Supplementary Materials for

Jumbo phages: A comparative genomic overview of core functions and adaptions for biological conflicts

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Abstract: Jumbo phages have attracted much attention by virtue of their extraordinary genome size and unusual aspects of biology. By performing a comparative genomics analysis of 224 jumbo phages, we suggest an objective inclusion criterion based on genome size distributions and present a synthetic overview of their manifold adaptations across major biological systems. By means of clustering and principle component analysis of the phyletic patterns of conserved genes, all known jumbo phages can be classified into 3 higher order groups, which include both myoviral and siphoviral morphologies indicating multiple independent origins from smaller predecessors. Our study uncovers several under-appreciated or unreported aspects of the DNA replication, recombination, transcription and virion maturation systems. Leveraging, sensitive sequence analysis methods we identify novel protein-modifying enzymes that might help hijack the host-machinery. Focusing on host-virus conflicts, we detect strategies used to counter different wings of the bacterial immune system, such as cyclic nucleotide- and NAD^+-dependent effector-activation, and prevention of superinfection during pseudolysogeny. We reconstruct the RNA-repair systems of jumbo phages that counter the consequences of RNA-targeting host effectors. These findings also suggest that several jumbo phage proteins provide a snapshot of the systems found in ancient replicons preceding the last universal ancestor of cellular life.

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Supplementary 2. Multiple sequence alignments of various protein domain families described in the text.

Supplementary 3. Counts of tRNA genes per genome in representative jumbo phages. The organism names, group type, and Genome assembly ids (GCA) are listed.

Supplementary 4. Relative gene positions of the 100 most frequent protein domains in a set of representative jumbo phage genomes.

Supplementary 5. Sequence clusters of all proteins of the 224 jumbo phages genomes. The clusters were obtained by combining BLASTCLUST (with the length and score thresholds as 0.3 each) followed by manual curation of the clusters. The architectures shown in column 3 were obtained using a combination of pfam profiles, custom local profiles and case-by-case sequence analysis. Clusters have unique cluster ids. Cluster ids containing “000000”are proteins that group in the un-clustered tail belonging to the architecture/family in column 3.

Phyletic patterns of Phage proteins

1.1 The phyletic patterns of 181 protein families in 224 phage genomes

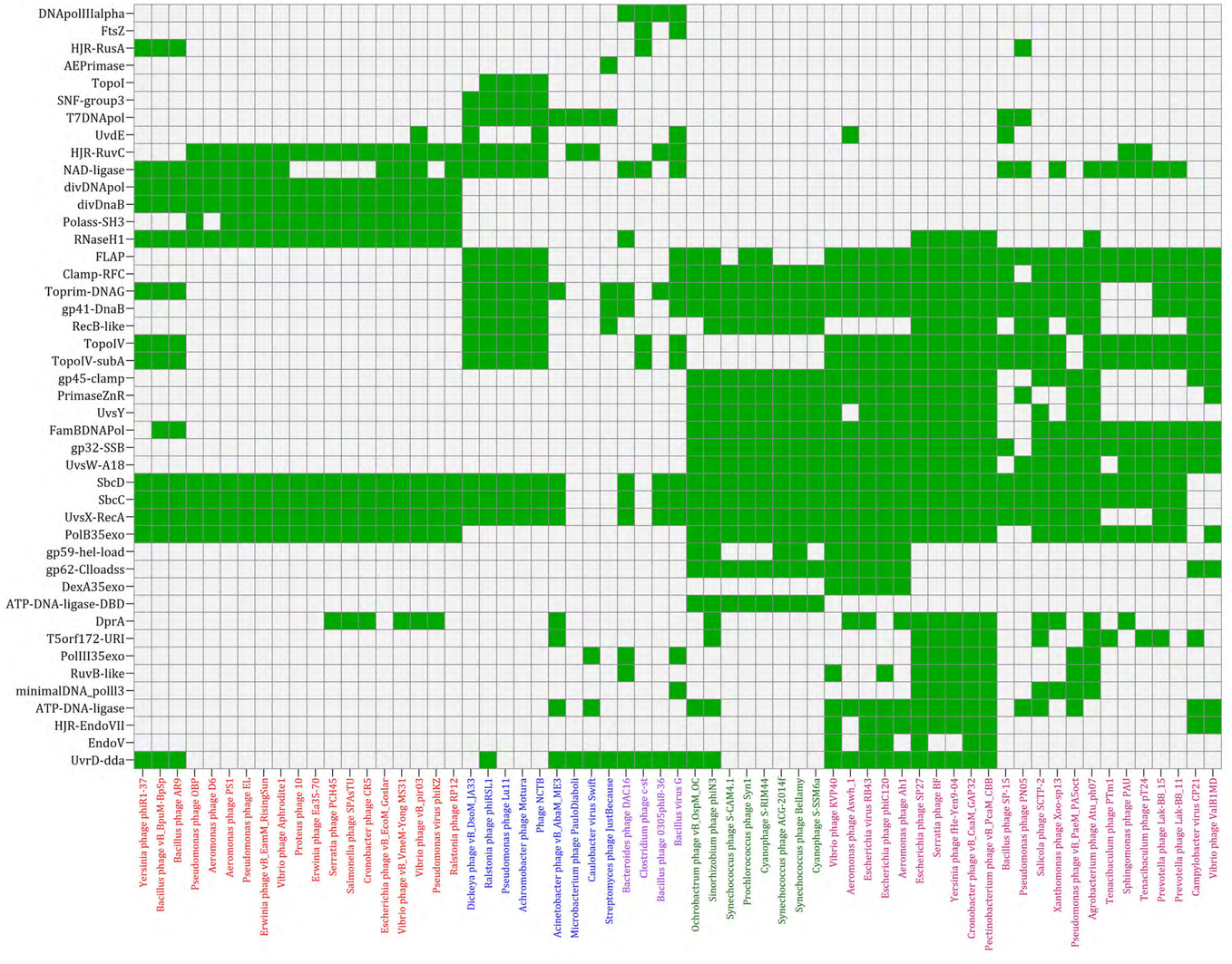


Phyletic patterns of Phage proteins

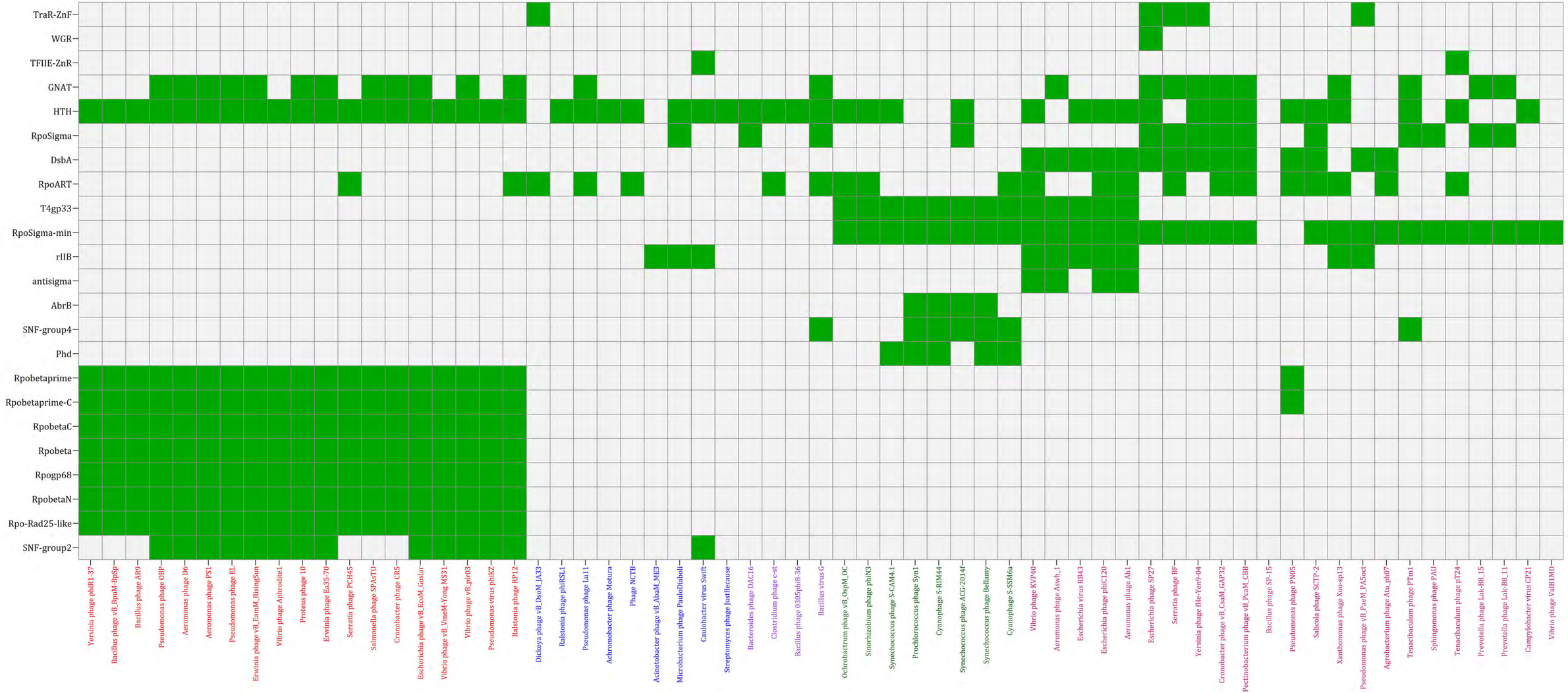
1.2 The phyletic patterns of 181 protein families in 154 phage genomes that show unique phyletic patterns



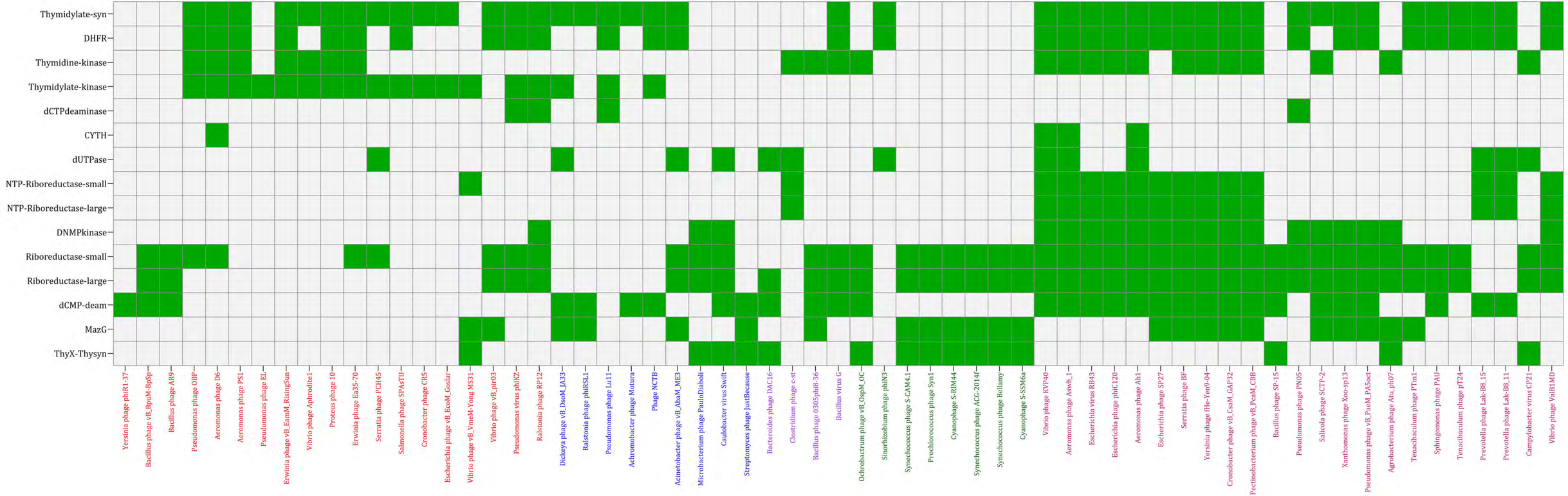
1.3 Phyletic patterns of Phage Replication proteins



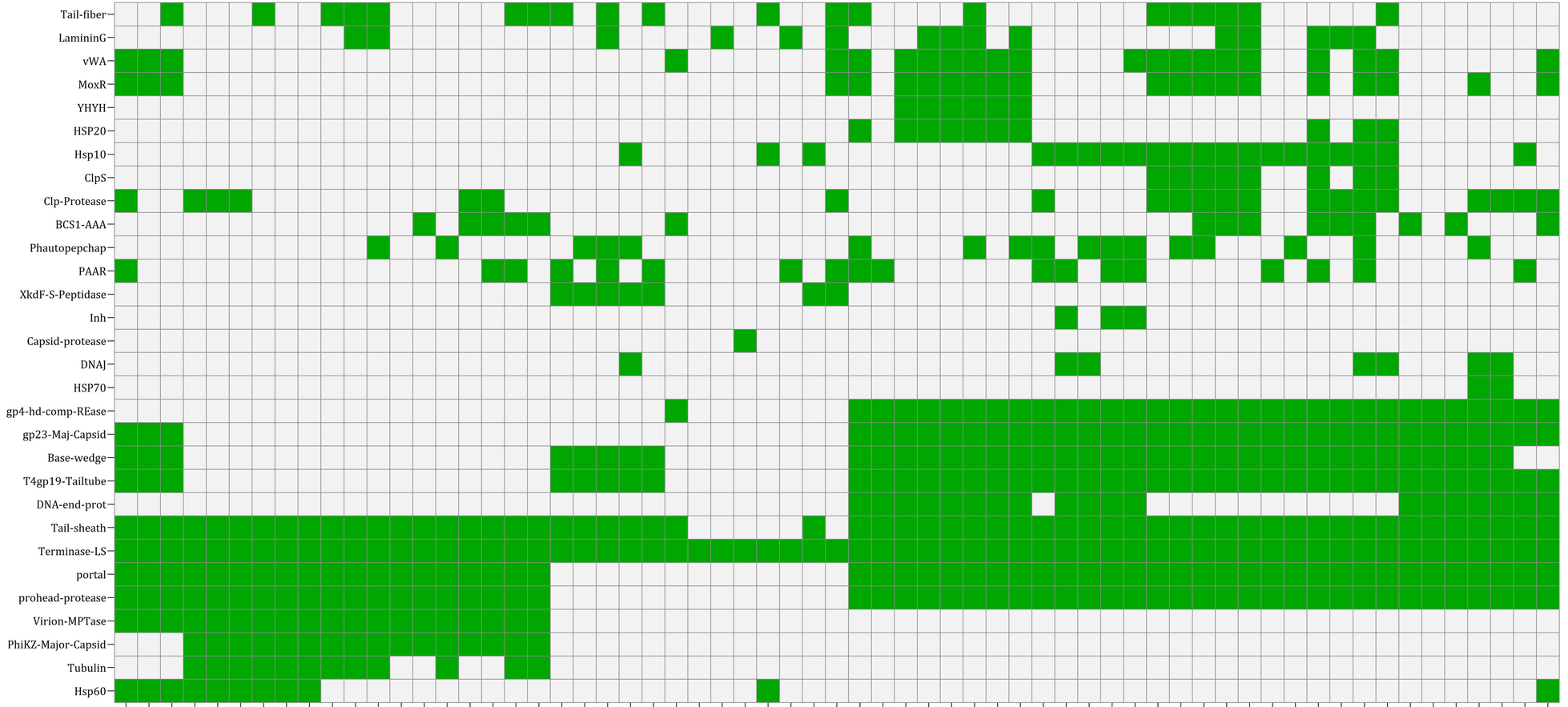
1.4 Phyletic patterns of Phage Transcription proteins



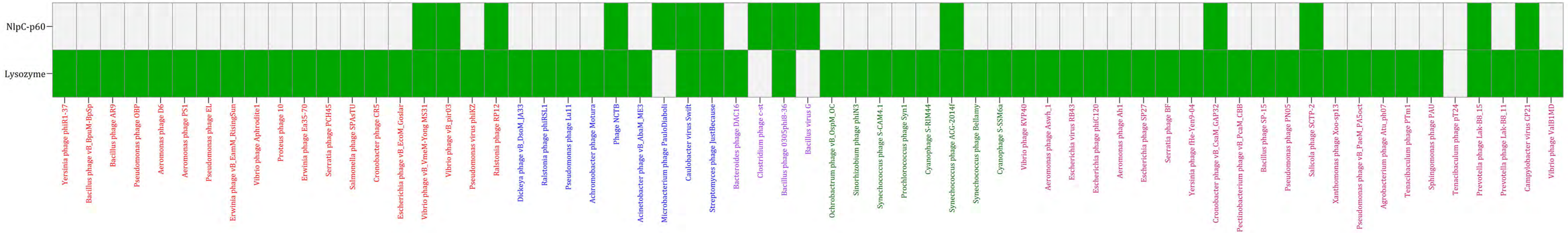
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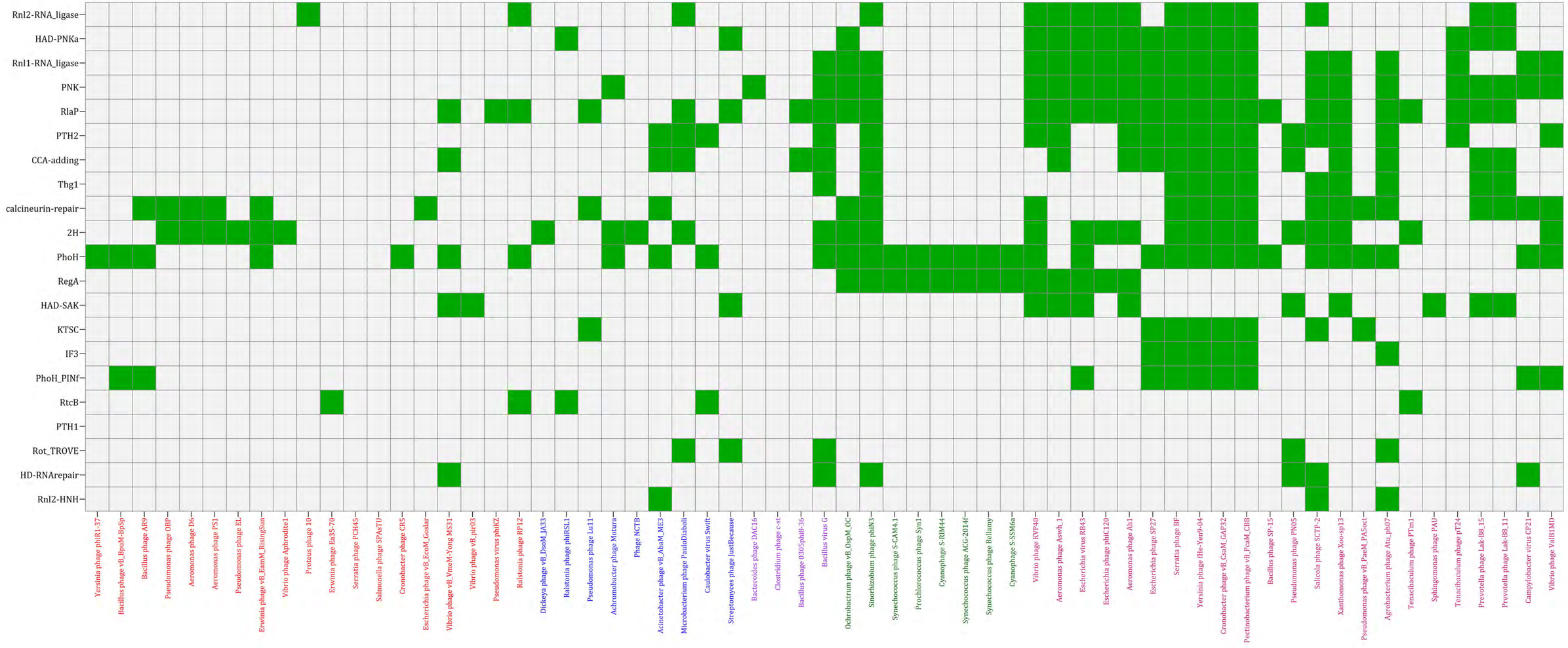
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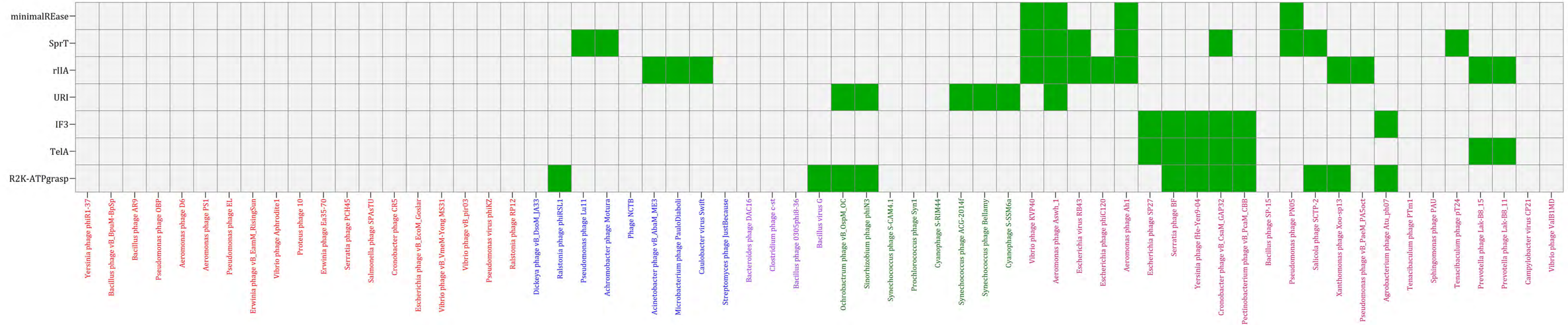
1.7 Phyletic patterns of Phage Cellwallpeptidase proteins



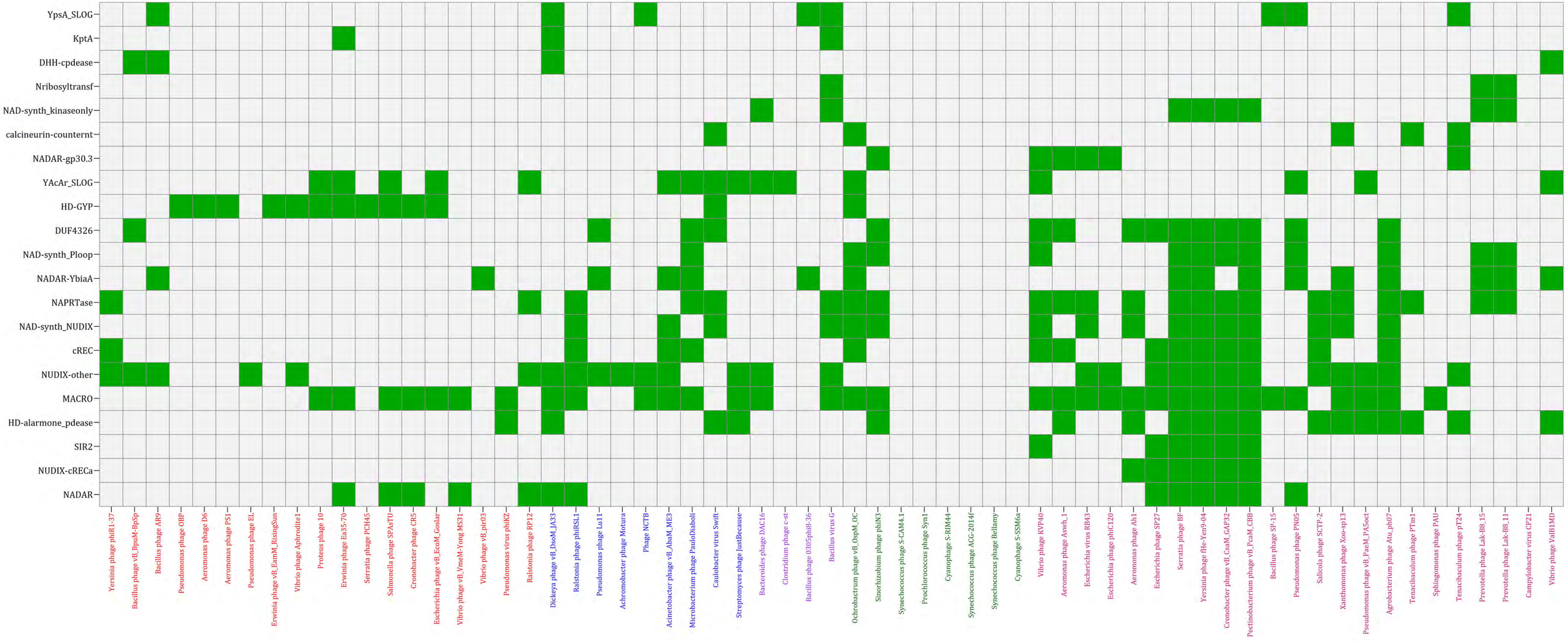
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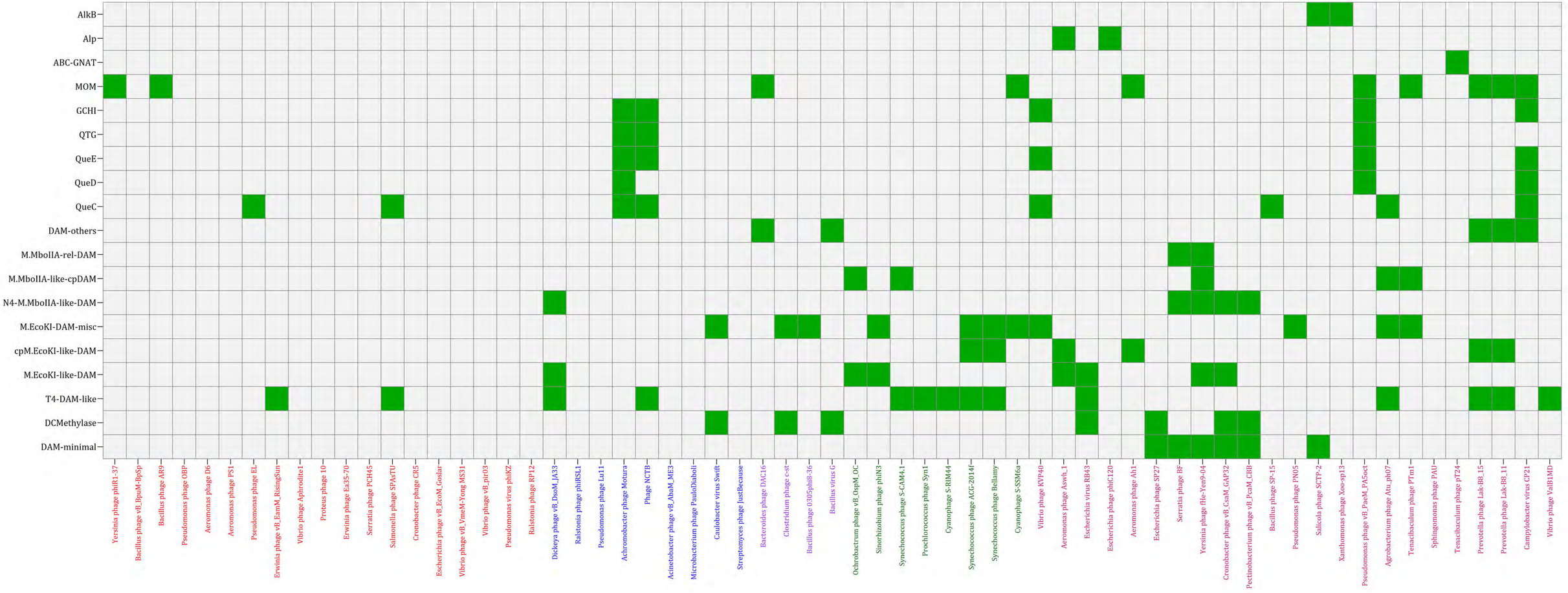
1.9 Phyletic patterns of Phage conflict proteins



1.10 Phyletic patterns of Phage counter-nt proteins



1.11 Phyletic patterns of Phage DNAmodification proteins

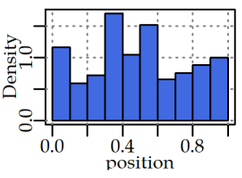
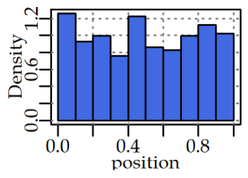
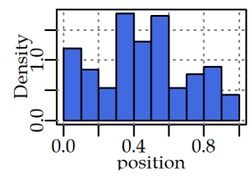
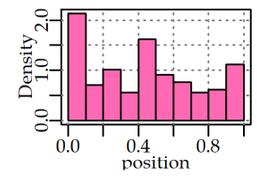
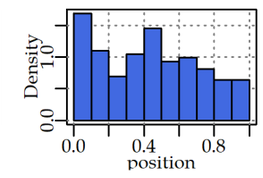
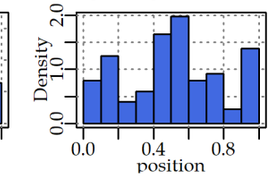
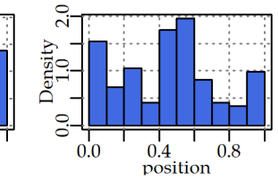
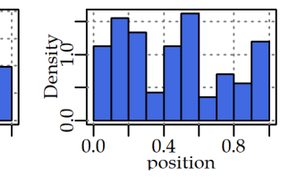
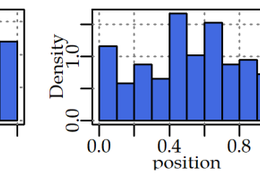
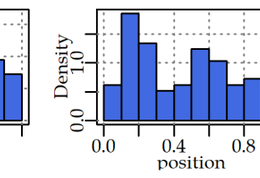
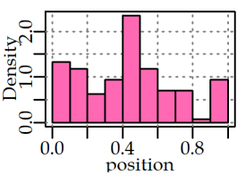
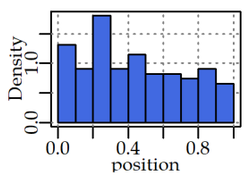
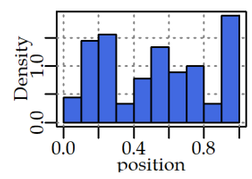
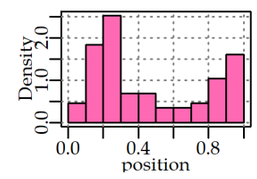
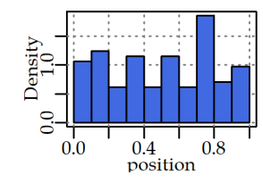
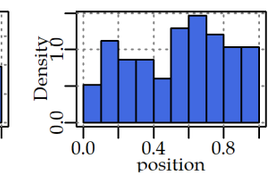
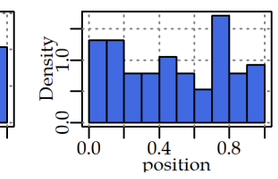
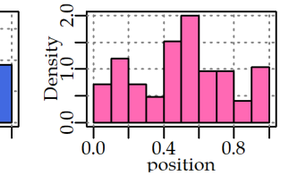
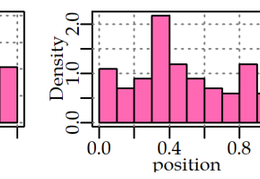
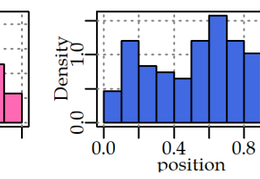
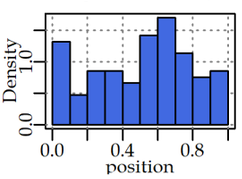
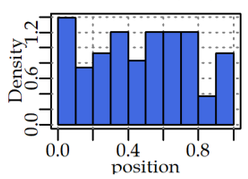
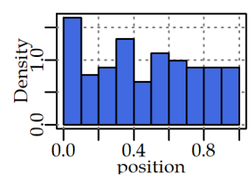
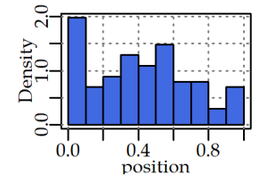
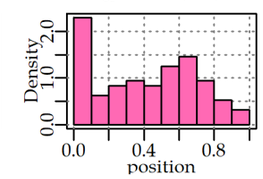
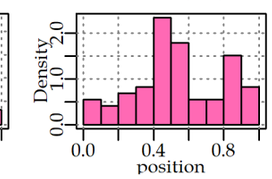
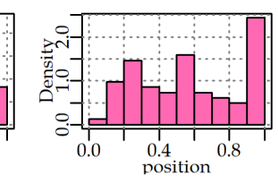
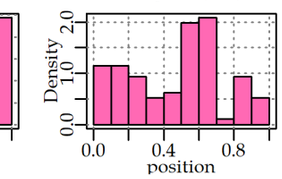
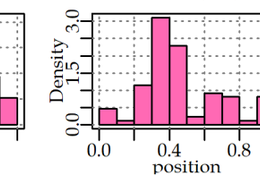
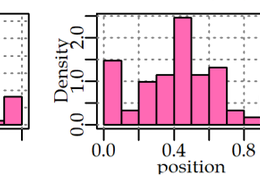
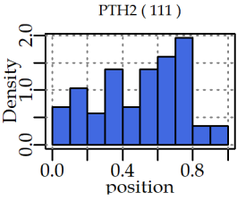
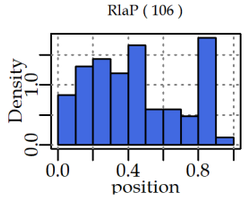
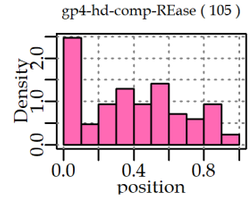
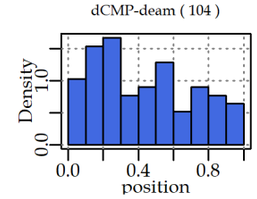
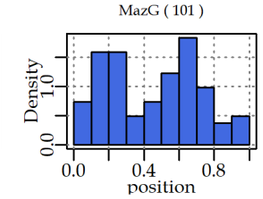
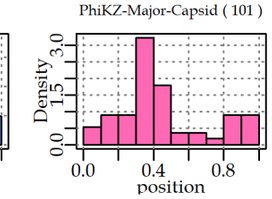
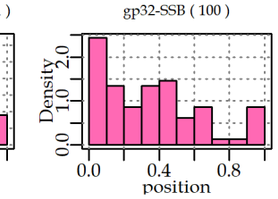
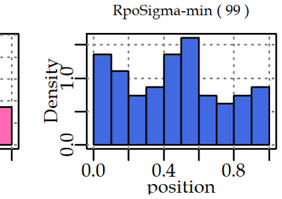
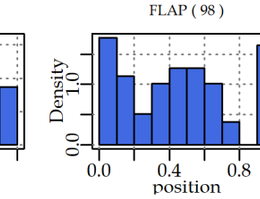
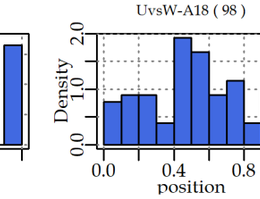


Supplementary 3: Counts of tRNA genes per genome in representative jumbo phages

virus name	group	GCA	tRNA.counts
Pseudomonas phage 201phi2-1	1.0	GCA_000875305.1	1
Erwinia phage Ea35-70	1.0	GCA_000914635.1	1
Bacillus virus PBS1	1.0	GCA_002601325.1	1
Ralstonia phage RP12	1.0	GCA_002617345.1	1
Ralstonia phage RP31	1.0	GCA_002617365.1	1
Erwinia phage vB_EamM_RAY	1.0	GCA_002624345.1	1
Erwinia phage vB_EamM_Simmy50	1.0	GCA_002624365.1	1
Erwinia phage vB_EamM_Bosolaphorus	1.0	GCA_002957735.1	1
Erwinia phage vB_EamM_Mortimer	1.0	GCA_002957765.1	1
Erwinia phage Rebecca	1.0	GCA_004521635.1	1
Edwardsiella virus pEt-SU	1.0	GCA_004800915.1	1
Salmonella phage vB_SalM_SA002	1.0	GCA_014131285.1	1
Escherichia phage vB_EcoM_EC001	1.0	GCA_014131305.1	1
Salmonella phage SPN3US	1.0	GCA_001042275.1	2
Aeromonas phage CF8	1.0	GCA_006384595.2	2
Serratia phage Moabite	1.0	GCA_006384735.1	2
Aeromonas phage PS1	1.0	GCA_007051165.2	2
Aeromonas phage PS2	1.0	GCA_009388305.2	2
Pseudomonas phage Phabio	1.0	GCA_002624965.1	3
Aeromonas phage D6	1.0	GCA_007051205.2	3
Klebsiella phage N1M2	1.0	GCA_010092605.1	3
Pseudomonas phage OBP	1.0	GCA_000896635.1	4
Pseudomonas phage Noxifer	1.0	GCA_002625005.1	4
Yersinia phage phiR1-37	1.0	GCA_000895615.1	5
Pseudomonas phage PhiPA3	1.0	GCA_001502095.1	5
Pseudomonas phage fnug	1.0	GCA_012837215.1	6
Pseudomonas virus phiKZ	1.0	GCA_000842965.1	7
Erwinia phage vB_EamM_Caitlin	1.0	GCA_001744955.1	7
Salmonella phage SPAsTU	1.0	GCA_003183805.1	7
Pseudomonas phage vB_PaeM_PS119XW	1.0	GCA_008375575.1	7
Erwinia phage vB_EamM_Kwan	1.0	GCA_001744315.1	8
Erwinia phage Wellington	1.0	GCA_003344985.1	8
Pseudomonas phage Psa21	1.0	GCA_004340405.1	8
Pseudomonas phage PA1C	1.0	GCA_004785505.1	8
Erwinia phage vB_EamM_Huxley	1.0	GCA_001745635.1	9
Erwinia phage Machina	1.0	GCA_002758035.1	9
Erwinia phage vB_EamM_Parshik	1.0	GCA_002758055.1	10
Erwinia phage vB_EamM_ChrisDB	1.0	GCA_001743655.1	11
Erwinia phage vB_EamM_Asesino	1.0	GCA_001744335.2	12
Erwinia phage vB_EamM_Stratton	1.0	GCA_002600675.1	12
Prochlorococcus phage P-SSM2	2.1	GCA_000859585.1	1
Cyanophage P-TIM40	2.1	GCA_001470935.1	1
Cyanophage S-RIM14	2.1	GCA_002599065.1	1
Cyanophage S-RIM14	2.1	GCA_002599125.1	1
Prochlorococcus phage P-SSM5	2.1	GCA_002991095.1	1
Cyanophage P-RSM6	2.1	GCA_000906155.1	3
Cyanophage S-SSM6b	2.1	GCA_002710425.1	3
Cyanophage S-RIM44	2.1	GCA_002599165.1	5
Cyanophage S-RIM44	2.1	GCA_002599205.1	5
Cyanophage S-RIM44	2.1	GCA_002599225.1	5
Cyanophage S-RIM44	2.1	GCA_002599265.1	5
Cyanophage S-SSM6a	2.1	GCA_002710385.1	5
Prochlorococcus phage Syn1	2.1	GCA_000892495.1	6
Sinorhizobium phage phiN3	2.1	GCA_001501175.1	6
Cyanophage S-RIM44	2.1	GCA_002599145.1	6
Cyanophage S-RIM44	2.1	GCA_002599185.1	6
Cyanophage S-RIM44	2.1	GCA_002599245.1	6
Cyanophage S-RIM44	2.1	GCA_002599285.1	6
Synechococcus phage S-CAM4	2.1	GCA_002922145.1	7
Synechococcus phage S-CAM4	2.1	GCA_002366065.1	8

virus name	group	GCA	tRNA.counts
Sinorhizobium phage phiM19	2.1	GCA_002605865.1	8
Sinorhizobium phage phiM7	2.1	GCA_002622405.1	8
Synechococcus phage S-CAM4	2.1	GCA_002922155.1	8
Sinorhizobium phage phiM12	2.1	GCA_001023565.1	10
Cyanophage S-RIM32	2.1	GCA_001754165.1	10
Synechococcus phage Bellamy	2.1	GCA_002627525.1	10
Synechococcus phage SynMITS9220M01	2.1	GCA_013187275.1	10
Synechococcus phage B23	2.1	GCA_009745195.1	19
Synechococcus phage B3	2.1	GCA_009745215.1	21
Ochrobactrum phage vB_OspM_OC	2.1	GCA_011067635.1	24
Pseudomonas phage PN05	2.2	GCA_009931935.1	1
Escherichia virus RB43	2.2	GCA_000863505.1	1
Citrobacter phage vB_CfrM_CfP1	2.2	GCA_001744555.1	1
Campylobacter virus CP21	2.2	GCA_000902535.1	2
Vibrio phage vB_VmeM-32	2.2	GCA_002608825.1	3
Tenacibaculum phage pT24	2.2	GCA_002611925.1	4
Escherichia phage SP27	2.2	GCA_008033345.1	6
Sphingomonas phage PAU	2.2	GCA_000902455.1	7
Klebsiella phage vB_KleM_RaK2	2.2	GCA_000903335.1	7
Escherichia phage 121Q	2.2	GCA_000926855.1	7
Escherichia phage vB_EcoM_G17	2.2	GCA_004521135.1	7
Escherichia phage vB_Eco_slurp01	2.2	GCA_900094095.1	7
Salmonella phage SE_PL	2.2	GCA_011067555.1	11
Salmonella phage Munch	2.2	GCA_004015485.1	12
Salmonella phage 7t3	2.2	GCA_006083215.1	12
Pseudomonas phage vB_PaeM_PA5oct	2.2	GCA_006516655.1	12
Aeromonas virus 65	2.2	GCA_000893255.1	16
Aeromonas phage 65.2	2.2	GCA_002618145.1	18
Aeromonas virus Aeh1	2.2	GCA_000843245.1	23
Aeromonas phage Ah1	2.2	GCA_002957415.1	23
Aeromonas phage PX29	2.2	GCA_000920195.1	25
Cronobacter phage S13	2.2	GCA_001503575.1	25
Cronobacter phage vB_CsaM_GAP32	2.2	GCA_000898015.1	26
Vibrio phage VH1_2019	2.2	GCA_009931825.1	27
Vibrio phage V09	2.2	GCA_012361135.1	27
Vibrio phage KVP40	2.2	GCA_000843785.1	29
Vibrio phage phi-ST2	2.2	GCA_002757135.1	29
Vibriophage phi-pp2	2.2	GCA_002630725.1	30
Vibrio phage phi-Grn1	2.2	GCA_002757115.1	30
Serratia phage BF	2.2	GCA_002619745.1	31
Yersinia phage fHe-Yen9-03	2.2	GCA_002990515.1	32
Vibrio phage V07	2.2	GCA_012361095.1	32
Yersinia phage fHe-Yen9-04	2.2	GCA_002990485.1	33
Xanthomonas phage XacN1	2.2	GCA_003173815.1	56
Ralstonia phage phiRSL1	3.1	GCA_000879455.1	2
Achromobacter phage Motura	3.1	GCA_006964305.1	2
Pseudomonas phage PaBG	3.1	GCA_000912555.1	5
Streptomyces phage Kela	3.1	GCA_012934305.1	11
Streptomyces phage Satis	3.1	GCA_003366315.1	12
Streptomyces phage Kradal	3.1	GCA_004799925.1	12
Streptomyces phage JustBecause	3.1	GCA_003613775.1	14
Caulobacter virus Rogue	3.1	GCA_000900555.1	23
Caulobacter virus phiCbK	3.1	GCA_000900535.1	26
Caulobacter virus Karma	3.1	GCA_000901575.1	26
Caulobacter phage Ccr10	3.1	GCA_002619445.1	26
Caulobacter phage Ccr2	3.1	GCA_002619465.1	26
Caulobacter phage Ccr29	3.1	GCA_002619485.1	26
Caulobacter phage Ccr32	3.1	GCA_002619505.1	26
Caulobacter phage Ccr34	3.1	GCA_002619525.1	26
Caulobacter phage CcrBL10	3.1	GCA_003443255.1	26

virus name	group	GCA	tRNA.counts
Caulobacter virus Swift	3.1	GCA_000899655.1	27
Caulobacter virus Magneto	3.1	GCA_000903095.1	27
Caulobacter phage Ccr5	3.1	GCA_002619545.1	27
Caulobacter phage CcrColossus	3.1	GCA_000899635.1	28
Caulobacter phage CcrBL9	3.1	GCA_003443295.1	28
Caulobacter phage CcrSC	3.1	GCA_003443315.1	28
Caulobacter phage CcrPW	3.1	GCA_003443275.1	29
Microbacterium phage PauloDiaboli	3.1	GCA_011067425.1	44
Acinetobacter phage vB_AbaM_ME3	3.2	GCA_002609765.1	4
Bacteroides phage DAC16	3.2	GCA_013387695.1	4
Bacteroides phage DAC19	3.2	GCA_013387715.1	4
Bacteroides phage DAC20	3.2	GCA_013387725.1	4
Bacteroides phage DAC22	3.2	GCA_013387735.1	4
Bacteroides phage DAC23	3.2	GCA_013387745.1	4
Bacillus virus G	3.2	GCA_000917535.1	18
Aeromonas phage AP1	NA	GCA_014183365.1	22
Pectobacterium phage CBB	NA	GCA_002609265.1	33

Lysozyme (701)

HTH (567)

Tailtube (316)

Terminase-LS (286)

Tail-sheath (235)

prohead-protease (227)

SbcC (204)

SbcD (203)

UvsX-RecA (198)

Rpobetaprime (189)

portal (185)

PolB35exo (177)

Rpobeta (167)

Rpobetaprime-C (162)

Thymidylate-syn (161)

Riboreductase-small (157)

GNAT (152)

gp23-Maj-Capsid (151)

MACRO (147)

Riboreductase-large (145)

Toprim-DNAG (133)

FamBDNAPol (130)

DHFR (128)

Base-wedge (122)

gp41-DnaB (122)

RNaseH1 (122)

PhoH (117)

Clamp-RFC (115)

Tail-fiber (112)

HJR-RuvC (111)

PTH2 (111)

RlaP (106)

gp4-hd-comp-REase (105)

dCMP-deam (104)

MazG (101)

PhiKZ-Major-Capsid (101)

gp32-SSB (100)

RpoSigma-min (99)

FLAP (98)

UvsW-A18 (98)

NUDIX-other (97)

UvrD-dda (95)

Hsp10 (93)

LaminiG (93)

gp45-clamp (91)

TopoIV (91)

NAPRTase (90)

TopoIV-subA (89)

DprA (87)

PrimaseZnR (87)

UvsY (87)

YAcAr_SLOG (85)

RpoART (84)

Thymidylate-kinase (84)

divDnaB (83)

divDNApol (83)

HD-alarmone_pdease (83)

Rpo-Rad25-like (82)

RpobetaC (82)

NAD-ligase (81)

ATP-DNA-ligase (79)

RpobetaN (79)

Rpogp68 (79)

Virion-MPTase (79)

Thymidine-kinase (77)

PNK (76)

2H (75)

DNMPkinase (75)

PAAR (75)

RecB-like (75)

DUF4326 (74)

Polass-SH3 (74)

CCA-adding (73)

dUTPase (71)

DNA-end-prot (70)

gp62-Clloadss (70)

NADAR (70)

RnlI1-RNA_ligase (70)

ThyX-Thysyn (70)

HD-GYP (69)

SNF-group2 (69)

RegA (68)

T4gp33 (67)

Clp-Protease (66)

NAD-synth_NUDIX (66)

BCS1-AAA (65)

Phautopepchap (63)

T4-DAM-like (63)

Rnl2-RNA_ligase (62)

HAD-PNKa (61)

NlpC-p60 (61)

vWA (61)

calcineurin-repair (60)

MoxR (57)

cREC (56)

NTP-Riboreductase-large (56)

rIIB (56)

HAD-SAK (55)

rIIA (54)

DsbA (53)

Supplementary 5: Sequence clusters of proteins

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG65775.1	000001	HAD	147	phiOC_p110	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AYD81402.1	000001	HAD	156	SEA_JUSTBECAUSE_247	Streptomyces phage JustBecause	GCA_003613775.1
QJD53806.1	000001	HAD	160	SEA_KELA_246	Streptomyces phage Kela	GCA_012934305.1
QBZ72131.1	000001	HAD	169	SEA_KRADAL_245	Streptomyces phage Kradal	GCA_004799925.1
AXH66393.1	000001	HAD	167	SEA_SATIS_244	Streptomyces phage Satis	GCA_003366315.1
APU01773.1	000002	PNK+HAD	303	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29068.1	000002	PNK+HAD	305	AP1_0361	Aeromonas phage AP1	GCA_014183365.1
ATI17525.1	000002	PNK+HAD	305	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00471.1	000002	PNK+HAD	304	HWB28_gp081	Aeromonas phage AS-zj	GCA_002627665.1
AUE22805.1	000002	PNK+HAD	305	Ah1_00287	Aeromonas phage Ah1	GCA_002957415.1
QAX98520.1	000002	PNK+HAD	305	ASfcp2_184	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97967.1	000002	PNK+HAD	304	ASswx1_325	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01174.1	000002	PNK+HAD	303	ASwh1_108	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39507.1	000002	PNK+HAD	305	CC2_208	Aeromonas phage CC2	GCA_000903495.1
ADQ52983.1	000002	PNK+HAD	305	PX29p264	Aeromonas phage PX29	GCA_000920195.1
ADM79907.1	000002	PNK+HAD	305	phiAS5_ORF0064	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53416.1	000002	PNK+HAD	303	65p409	Aeromonas virus 65	GCA_000893255.1
AAQ17932.1	000002	PNK+HAD	305	pseT	Aeromonas virus Aeh1	GCA_000843245.1
AXQ69208.1	000002	PNK+HAD	351	CcrBL9_gp184c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69761.1	000002	PNK+HAD	351	CcrSC_gp179c	Caulobacter phage CcrSC	GCA_003443315.1
ANS05978.1	000002	PNK+HAD	295	ABCD_0070	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64831.1	000002	PNK+HAD	293	S13_032	Cronobacter phage S13	GCA_001503575.1
AFC21532.1	000002	PNK+HAD	307	GAP32_084	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97084.1	000002	PNK+HAD	295	E_075	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14333.1	000002	PNK+HAD	310	PBI_121Q_443	Escherichia phage 121Q	GCA_000926855.1
QAY00609.1	000002	PNK+HAD	310	Ecwhy1_333	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34805.1	000002	PNK+HAD	310	ACQ29_gp125	Escherichia phage PBECO4	GCA_001041035.1
BBM62005.1	000002	PNK+HAD	310	EO157G_4160	Escherichia phage SP27	GCA_008033345.1
AXC36917.1	000002	PNK+HAD	310	-	Escherichia phage UB	GCA_003341455.1
ARM70776.1	000002	PNK+HAD	299	phiC120_c70	Escherichia phage phiC120	GCA_002621185.1
QBO61971.1	000002	PNK+HAD	310	G17_00482	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13996.1	000002	PNK+HAD	310	vBEcoMphAPEC6_gp372c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80320.1	000002	PNK+HAD	310	PSLUR01_00343	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78593.1	000002	PNK+HAD	295	RB43ORF071w	Escherichia virus RB43	GCA_000863505.1
AFA44743.1	000002	PNK+HAD	314	RaK2_00470	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78831.1	000002	PNK+HAD	293	-	Myoviridae sp.	GCA_012593985.1
AMM43652.1	000002	PNK+HAD	310	CBB_87	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18787.1	000002	PNK+HAD	309	7t3_0266	Salmonella phage 7t3	GCA_006083215.1
AZU98052.1	000002	PNK+HAD	309	CPT_Munch_108	Salmonella phage Munch	GCA_004015485.1
QIG62929.1	000002	PNK+HAD	309	SEPL_316	Salmonella phage SE_PL	GCA_011067555.1
AQW88601.1	000002	PNK+HAD	308	BF_0076	Serratia phage BF	GCA_002619745.1
BAV39374.1	000002	PNK+HAD	345	BPT24_255	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64161.1	000002	PNK+HAD	305	KVP40.0090	Vibrio phage KVP40	GCA_000843785.1
QIW90485.1	000002	PNK+HAD	305	GCAPEGMB_00138	Vibrio phage V07	GCA_012361095.1
QIW90944.1	000002	PNK+HAD	305	COHAPHLL_00081	Vibrio phage V09	GCA_012361135.1
QHJ74273.1	000002	PNK+HAD	305	VH12019_00354	Vibrio phage VH1_2019	GCA_009931825.1
AGB07098.1	000002	PNK+HAD	305	CF80_gp311	Vibrio phage VH7D	GCA_000914495.1
QBX05998.1	000002	PNK+HAD	305	ValB1HC_044	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61011.1	000002	PNK+HAD	305	AVU32_gp170	Vibrio phage ValKK3	GCA_001501635.1
AGN30140.1	000002	PNK+HAD	301	VPFG_00138	Vibrio phage nt-1	GCA_000910195.2
ALP47022.1	000002	PNK+HAD	305	phiGrn1_0205	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47402.1	000002	PNK+HAD	305	phiST2_0338	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54622.1	000002	PNK+HAD	305	vBValMR10Z_81	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07225.1	000002	PNK+HAD	315	VmeM32_00239	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37321.1	000002	PNK+HAD	385	pp2_088	Vibriophage phi-pp2	GCA_002630725.1
SOK58878.1	000002	PNK+HAD	308	g070	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58341.1	000002	PNK+HAD	308	g064	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000758	000002	PNK+HAD	314	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000510	000002	PNK+HAD	314	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AND75332.1	000003	NT5C-HAD	236	ME3_171	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75434.1	000003	NT5C-HAD	191	ME3_273	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01456.1	000003	NT5C-HAD	160	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29098.1	000003	NT5C-HAD	160	AP1_0391	Aeromonas phage AP1	GCA_014183365.1
ATI17441.1	000003	NT5C-HAD	160	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00154.1	000003	NT5C-HAD	160	HWB28_gp398	Aeromonas phage AS-zj	GCA_002627665.1
QAX97881.1	000003	NT5C-HAD	160	ASswx1_238	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01268.1	000003	NT5C-HAD	160	ASwh1_205	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39415.1	000003	NT5C-HAD	160	CC2_296	Aeromonas phage CC2	GCA_000903495.1
ADQ53076.1	000003	NT5C-HAD	81	65p066	Aeromonas virus 65	GCA_000893255.1
ADQ53077.1	000003	NT5C-HAD	58	65p067	Aeromonas virus 65	GCA_000893255.1
ASV44737.1	000003	NT5C-HAD	154	FDI40_gp301	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARB13745.1	000003	NT5C-HAD	212	Ccr10_gp215c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14090.1	000003	NT5C-HAD	212	Ccr2_gp214c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14779.1	000003	NT5C-HAD	212	Ccr29_gp223	Caulobacter phage Ccr29	GCA_002619485.1
ARB15123.1	000003	NT5C-HAD	212	Ccr32_gp205	Caulobacter phage Ccr32	GCA_002619505.1
ARB15457.1	000003	NT5C-HAD	212	Ccr34_gp215	Caulobacter phage Ccr34	GCA_002619525.1
ARB14432.1	000003	NT5C-HAD	212	Ccr5_gp212c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68411.1	000003	NT5C-HAD	231	CcrBL10_gp207c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69313.1	000003	NT5C-HAD	303	CcrBL9_gp289	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88146.1	000003	NT5C-HAD	244	CcrColossus_gp276	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68822.1	000003	NT5C-HAD	244	CcrPW_gp283	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69873.1	000003	NT5C-HAD	304	CcrSC_gp291	Caulobacter phage CcrSC	GCA_003443315.1
AFU87739.1	000003	NT5C-HAD	212	CcrKarma_gp222	Caulobacter virus Karma	GCA_000901575.1
AFU87387.1	000003	NT5C-HAD	212	CcrMagneto_gp217	Caulobacter virus Magneto	GCA_000903095.1
AFU86698.1	000003	NT5C-HAD	211	CcrRogue_gp216	Caulobacter virus Rogue	GCA_000900555.1
AFU88535.1	000003	NT5C-HAD	212	CcrSwift_gp217	Caulobacter virus Swift	GCA_000899655.1
AFU87042.1	000003	NT5C-HAD	212	CbK_gp210	Caulobacter virus phiCbK	GCA_000900535.1
ANS06047.1	000003	NT5C-HAD	154	ABCD_0227	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFO71436.1	000003	NT5C-HAD	182	CR5_216	Cronobacter phage CR5	GCA_000910235.1
AIA64859.1	000003	NT5C-HAD	158	S13_060	Cronobacter phage S13	GCA_001503575.1
AON97244.1	000003	NT5C-HAD	155	E_236	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AMR59900.1	000003	NT5C-HAD	197	SEGD1_253	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07649.1	000003	NT5C-HAD	185	DERBICUS_223	Erwinia phage Derbicus	GCA_004521655.1
ANZ49899.1	000003	NT5C-HAD	185	MACHINA_261	Erwinia phage Machina	GCA_002758035.1
AXF51400.1	000003	NT5C-HAD	183	WELLINGTON_274	Erwinia phage Wellington	GCA_003344985.1
AFQ96713.1	000003	NT5C-HAD	182	G173_gp168	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48283.1	000003	NT5C-HAD	182	ASESINO_270	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48555.1	000003	NT5C-HAD	183	CAITLIN_260	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48833.1	000003	NT5C-HAD	183	CHRISDB_271	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49073.1	000003	NT5C-HAD	182	EARLPHILLIPIV_224	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49342.1	000003	NT5C-HAD	185	HUXLEY_260	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49626.1	000003	NT5C-HAD	183	KWAN_274	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50170.1	000003	NT5C-HAD	185	PARSHIK_261	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50420.1	000003	NT5C-HAD	182	PHOBOS_230	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50695.1	000003	NT5C-HAD	182	STRATTON_270	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86089.1	000003	NT5C-HAD	182	ACEC001_2460	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AAX78762.1	000003	NT5C-HAD	153	RB43ORF240c	Escherichia virus RB43	GCA_000863505.1
AXH72491.1	000003	NT5C-HAD	159	-	Myoviridae sp.	GCA_003657725.1
QHJ79079.1	000003	NT5C-HAD	153	-	Myoviridae sp.	GCA_012593985.1
QNI20932.1	000003	NT5C-HAD	197	-	Salmonella phage JN03	GCA_014319805.1
AWN09105.1	000003	NT5C-HAD	182	MLDJOKPK_00192	Salmonella phage SPAsTU	GCA_003183805.1
AEP84081.1	000003	NT5C-HAD	182	SPN3US_0248	Salmonella phage SPN3US	GCA_001042275.1
AGR47829.1	000003	NT5C-HAD	167	SmphiM12_197	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13039.1	000003	NT5C-HAD	167	PHIM19_134	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12680.1	000003	NT5C-HAD	167	PHIM7_134	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13412.1	000003	NT5C-HAD	167	PHIN3_149	Sinorhizobium phage phiN3	GCA_001501175.1
AQT28114.1	000003	NT5C-HAD	175	pVa21_173	Vibrio phage pVa-21	GCA_002619305.1
ALY07019.1	000003	NT5C-HAD	147	VmeM32_00025	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21140.1	000003	NT5C-HAD	261	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65320.1	000003	NT5C-HAD	167	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96357.1	000003	NT5C-HAD	169	Xoosp13_170	Xanthomonas phage Xoo-sp13	GCA_013364725.1
APU01445.1	000004	HAD	204	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28930.1	000004	HAD	308	AP1_0223	Aeromonas phage AP1	GCA_014183365.1
ATI17454.1	000004	HAD	200	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00142.1	000004	HAD	200	HWB28_gp008	Aeromonas phage AS-zj	GCA_002627665.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22791.1	000004	HAD	219	Ah1_00273	Aeromonas phage Ah1	GCA_002957415.1
QAX98505.1	000004	HAD	221	ASfcp2_169	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97894.1	000004	HAD	200	ASswx1_251	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39531.1	000004	HAD	200	CC2_282	Aeromonas phage CC2	GCA_000903495.1
ADQ52968.1	000004	HAD	236	PX29p249	Aeromonas phage PX29	GCA_000920195.1
ADM79893.1	000004	HAD	221	phiAS5_ORF0050	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53065.1	000004	HAD	204	65p055	Aeromonas virus 65	GCA_000893255.1
AAQ17916.1	000004	HAD	234	30.2	Aeromonas virus Aeh1	GCA_000843245.1
ASV44740.1	000004	HAD	206	FDI40_gp310	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANS06007.1	000004	HAD	205	ABCD_0094	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64843.1	000004	HAD	277	S13_044	Cronobacter phage S13	GCA_001503575.1
AFC21778.1	000004	HAD	206	GAP32_328	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97106.1	000004	HAD	205	E_098	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT13958.1	000004	HAD	208	PBI_121Q_61	Escherichia phage 121Q	GCA_000926855.1
QAY00379.1	000004	HAD	208	Ecwhy1_98	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35124.1	000004	HAD	208	ACQ29_gp444	Escherichia phage PBECO4	GCA_001041035.1
BBM61650.1	000004	HAD	208	EO157G_0610	Escherichia phage SP27	GCA_008033345.1
AXC36698.1	000004	HAD	208	-	Escherichia phage UB	GCA_003341455.1
ARM70760.1	000004	HAD	274	phiC120_c54	Escherichia phage phiC120	GCA_002621185.1
QBO61735.1	000004	HAD	208	G17_00246	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13780.1	000004	HAD	208	vBEcoMphAPEC6_gp151c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80552.1	000004	HAD	208	PSLUR01_00575	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78616.1	000004	HAD	209	RB43ORF094w	Escherichia virus RB43	GCA_000863505.1
AFA44440.1	000004	HAD	207	RaK2_00167	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72561.1	000004	HAD	193	-	Myoviridae sp.	GCA_003657725.1
QHJ78819.1	000004	HAD	208	-	Myoviridae sp.	GCA_012593985.1
AMM43896.1	000004	HAD	206	CBB_333	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76174.1	000004	HAD	198	EST35_0293	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44141.1	000004	HAD	197	PBI_SCTP2_126	Salicola phage SCTP-2	GCA_002625545.1
QCW19055.1	000004	HAD	206	7t3_0535	Salmonella phage 7t3	GCA_006083215.1
AZU98302.1	000004	HAD	206	CPT_Munch_358	Salmonella phage Munch	GCA_004015485.1
QIG62682.1	000004	HAD	206	SEPL_069	Salmonella phage SE_PL	GCA_011067555.1
AQW88856.1	000004	HAD	207	BF_0331	Serratia phage BF	GCA_002619745.1
AGR47896.1	000004	HAD	194	SmphiM12_264	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13096.1	000004	HAD	194	PHIM19_191	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12736.1	000004	HAD	194	PHIM7_191	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13466.1	000004	HAD	194	PHIN3_203	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64126.1	000004	HAD	198	KVP40.0055	Vibrio phage KVP40	GCA_000843785.1
AAQ64331.1	000004	HAD	190	KVP40.0262	Vibrio phage KVP40	GCA_000843785.1
QIW90448.1	000004	HAD	198	GCAPEGMB_00101	Vibrio phage V07	GCA_012361095.1
QIW90646.1	000004	HAD	190	GCAPEGMB_00299	Vibrio phage V07	GCA_012361095.1
QIW90981.1	000004	HAD	198	COHAPHLL_00118	Vibrio phage V09	GCA_012361135.1
QIW91153.1	000004	HAD	190	COHAPHLL_00317	Vibrio phage V09	GCA_012361135.1
QHJ74441.1	000004	HAD	190	VH12019_00114	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74237.1	000004	HAD	198	VH12019_00318	Vibrio phage VH1_2019	GCA_009931825.1
AGB07062.1	000004	HAD	197	CF80_gp275	Vibrio phage VH7D	GCA_000914495.1
QBX06034.1	000004	HAD	197	ValB1HC_080	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04476.1	000004	HAD	186	ValB1MD_088	Vibrio phage ValB1MD	GCA_004138815.1
AJT61048.1	000004	HAD	197	AVU32_gp207	Vibrio phage ValKK3	GCA_001501635.1
AGN30104.1	000004	HAD	198	VPFG_00102	Vibrio phage nt-1	GCA_000910195.2
ALP47071.1	000004	HAD	197	phiGrn1_0169	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47450.1	000004	HAD	197	phiST2_0300	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54659.1	000004	HAD	197	vBValMR10Z_118	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37286.1	000004	HAD	198	pp2_052	Vibriophage phi-pp2	GCA_002630725.1
AFN37490.1	000004	HAD	190	pp2_257	Vibriophage phi-pp2	GCA_002630725.1
SOK59140.1	000004	HAD	208	g332	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58606.1	000004	HAD	208	g329	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDJ97362.1	000005	HAD+GNAT	381	D6_0203	Aeromonas phage D6	GCA_007051205.2
QDH47067.1	000005	HAD+GNAT	381	LAh10_118	Aeromonas phage LAh10	GCA_006863975.1
QDB70361.1	000006	HAD	213	CF8_0193	Aeromonas phage CF8	GCA_006384595.2
QDJ96706.1	000006	HAD	216	PS1_0195	Aeromonas phage PS1	GCA_007051165.2
QFR59339.1	000006	HAD	216	PS2_0197	Aeromonas phage PS2	GCA_009388305.2
AXG67251.1	000006	HAD	195	AD1_207	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79998.1	000006	HAD	191	JA11_193	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66596.1	000006	HAD	191	JA13_193	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66921.1	000006	HAD	191	JA29_195	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67567.1	000006	HAD	191	JA33_193	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBZ70744.1	000006	HAD	208	pETSU_163	Edwardsiella virus pEt-SU	GCA_004800915.1
AGX01800.1	000006	HAD	216	CF95_gp078	Erwinia phage PhiEaH1	GCA_000914555.1
AWY08481.1	000006	HAD	195	Alexandra_217	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ASU03808.1	000006	HAD	225	JOAD_107	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03563.1	000006	HAD	225	RISINGSUN_107	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ARW58851.1	000006	HAD	195	Y3_211	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28682.1	000006	HAD	192	YOLOSWAG_204	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QGH72051.1	000006	HAD	215	N1M2_188	Klebsiella phage N1M2	GCA_010092605.1
QGZ14458.1	000006	HAD	214	HWC77_gp095	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24030.1	000006	HAD	207	-	Proteus phage 10	GCA_014071245.1
AEV89676.1	000006	HAD	229	OBP_239	Pseudomonas phage OBP	GCA_000896635.1
QKE54349.1	000006	HAD	216	ACSA002_0350	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65599.1	000006	HAD	205	2050HW_00264	Serratia phage 2050HW	GCA_002628125.1
QDB71363.1	000006	HAD	205	CPT_Moabite_333	Serratia phage Moabite	GCA_006384735.1
QAU04276.1	000006	HAD	214	HWC03_gp121	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23301.1	000006	HAD	211	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81024.1	000006	HAD	211	Aphrodite1_0044	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47427.1	000006	HAD	211	HWC35_gp033	Vibrio phage USC-1	GCA_006864065.1
BAW98248.1	000006	HAD	212	FDH33_gp039	Vibrio phage pTD1	GCA_002618825.1
AIR93532.1	000007	HAD	112	AVU42_gp195	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76248.1	000007	HAD	102	PBI_BELLAMY_212	Synechococcus phage Bellamy	GCA_002627525.1
ARM70867.1	000007	HAD	128	phiC120_c162	Escherichia phage phiC120	GCA_002621185.1
AGH07746.1	000007	HAD	111	CYVG_00303	Cyanophage S-SSM6a	GCA_002710385.1
AXQ70508.1	000007	HAD	115	HOU04_gp109	Synechococcus phage S-T4	GCA_003443335.1
AAX44688.1	000007	HAD	114	PSSM2_311	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12288.1	000007	HAD	114	PRTG_00135	Prochlorococcus phage P-SSM5	GCA_002991095.1
QJT70212.1	000008	HAD+CTP_transf_like	250	SynMITS9220M01_206	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QIG63501.1	000009	CTP_transf_like	147	DAC19_10	Bacteroides phage DAC19	GCA_013387715.1
QIG63763.1	000009	CTP_transf_like	147	DAC20_10	Bacteroides phage DAC20	GCA_013387725.1
QIG64024.1	000009	CTP_transf_like	147	DAC22_10	Bacteroides phage DAC22	GCA_013387735.1
AGH07742.1	000009	CTP_transf_like	133	CYVG_00299	Cyanophage S-SSM6a	GCA_002710385.1
AAX44686.1	000009	CTP_transf_like	138	PSSM2_309	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12290.1	000009	CTP_transf_like	138	PRTG_00137	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93530.1	000009	CTP_transf_like	135	AVU42_gp193	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22980.1	000009	CTP_transf_like	108	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50516.1	000009	CTP_transf_like	164	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70512.1	000009	CTP_transf_like	136	HOU04_gp113	Synechococcus phage S-T4	GCA_003443335.1
QAU04462.1	000009	CTP_transf_like	154	ValB1MD_055	Vibrio phage ValB1MD	GCA_004138815.1
AFC21821.1	000010	SIG+NT5C	195	GAP32_370	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG57924.1	000010	SIG+NT5C	211	SEA_PAULODIABOLI_239	Microbacterium phage PauloDiaboli	GCA_011067425.1
AMM43943.1	000010	SIG+NT5C	195	CBB_380	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88902.1	000010	SIG+NT5C	193	BF_0377	Serratia phage BF	GCA_002619745.1
AAQ64142.1	000010	SIG+NT5C	170	KVP40.0071	Vibrio phage KVP40	GCA_000843785.1
QIW90465.1	000010	SIG+NT5C	170	GCAPEGMB_00118	Vibrio phage V07	GCA_012361095.1
QIW90964.1	000010	SIG+NT5C	170	COHAPHLL_00101	Vibrio phage V09	GCA_012361135.1
QHJ74254.1	000010	SIG+NT5C	170	VH12019_00335	Vibrio phage VH1_2019	GCA_009931825.1
AGB07078.1	000010	SIG+NT5C	166	CF80_gp291	Vibrio phage VH7D	GCA_000914495.1
QBX06017.1	000010	SIG+NT5C	166	ValB1HC_063	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61031.1	000010	SIG+NT5C	170	AVU32_gp190	Vibrio phage ValKK3	GCA_001501635.1
AGN30120.2	000010	SIG+NT5C	166	VPFG_00118	Vibrio phage nt-1	GCA_000910195.2
ALP47104.1	000010	SIG+NT5C	166	phiGrn1_0186	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47487.1	000010	SIG+NT5C	166	phiST2_0317	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54642.1	000010	SIG+NT5C	169	vBValMR10Z_101	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37302.1	000010	SIG+NT5C	161	pp2_069	Vibriophage phi-pp2	GCA_002630725.1
SOK59192.1	000010	SIG+NT5C	193	g384	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58656.1	000010	SIG+NT5C	193	g379	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BAS04952.2	000011	HAD	153	AVU11_gp160	Ralstonia phage RSF1	GCA_001500875.1
BAQ02677.2	000011	HAD	153	-	Ralstonia phage RSL2	GCA_001503055.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFF28093.1	000011	HAD	146	PAU_95	Sphingomonas phage PAU	GCA_000902455.1
prevph1000000340	000011	HAD	166	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000269	000011	HAD	166	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QAX96804.1	000012	HAD	193	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97123.1	000012	HAD	193	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96169.1	000012	HAD	193	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96487.1	000012	HAD	193	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX06632.1	000013	HAD	121	BcepSaruman_219	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74601.1	000013	HAD	121	BcepSauron_221	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41705.1	000013	HAD	114	RSL1_ORF257	Ralstonia phage phiRSL1	GCA_000879455.1
BAS04906.1	000014	HAD	484	AVU11_gp114	Ralstonia phage RSF1	GCA_001500875.1
BAQ02633.1	000014	HAD	487	AVU38_gp105	Ralstonia phage RSL2	GCA_001503055.1
prevph1000000262	000015	SIG+Nuc-Kinase	346	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000209	000015	SIG+Nuc-Kinase	346	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBA65341.1	000016	HAD	193	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96378.1	000016	HAD	208	Xoosp13_192	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AMM44933.1	000000	HAD	183	SP15_135	Bacillus phage SP-15	GCA_001754685.1
BAE47799.1	000000	NT5C	222	CST101	Clostridium phage c-st	GCA_000865225.1
ASV44111.1	000000	HAD	190	PBI_SCTP2_96	Salicola phage SCTP-2	GCA_002625545.1
QDH83552.1	000000	HAD	181	H1O15_gp236	Achromobacter phage Motura	GCA_006964305.1
SBV38545.1	000000	HAD	221	BN7874_298	Phage NCTB	GCA_900092385.1
BAG41677.1	000000	HAD-PNK	176	RSL1_ORF228	Ralstonia phage phiRSL1	GCA_000879455.1
AXH70998.1	000000	HAD-PNK	147	-	Vibrio phage BONAISHI	GCA_003441475.1
QHJ85941.1	000000	HAD-SAK	192	KKIINIFJ_00029	Pseudomonas phage PN05	GCA_009931935.1
AQT28136.1	000000	HAD-SAK	198	pVa21_195	Vibrio phage pVa-21	GCA_002619305.1
AUE22616.1	000017	HAD-SAK	96	Ah1_00075	Aeromonas phage Ah1	GCA_002957415.1
ADQ52801.1	000017	HAD-SAK	162	PX29p082	Aeromonas phage PX29	GCA_000920195.1
ADM80057.1	000017	HAD-SAK	161	phiAS5_ORF0214	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17744.1	000017	HAD-SAK	163	Aeh1ORF083c	Aeromonas virus Aeh1	GCA_000843245.1
AFU88182.1	000017	HAD-SAK	70	CcrColossus_gp312	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88183.1	000017	HAD-SAK	64	CcrColossus_gp313	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68859.1	000017	HAD-SAK	167	CcrPW_gp320	Caulobacter phage CcrPW	GCA_003443275.1
ANS06020.1	000017	HAD-SAK	187	ABCD_0224	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64872.1	000017	HAD-SAK	173	S13_073	Cronobacter phage S13	GCA_001503575.1
AON97241.1	000017	HAD-SAK	190	E_233	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78758.1	000017	HAD-SAK	157	RB43ORF236w	Escherichia virus RB43	GCA_000863505.1
QHJ79067.1	000017	HAD-SAK	111	-	Myoviridae sp.	GCA_012593985.1
AGS81975.1	000017	HAD-SAK	156	PaBG_00090	Pseudomonas phage PaBG	GCA_000912555.1
AFF28274.1	000017	HAD-SAK	175	PAU_276	Sphingomonas phage PAU	GCA_000902455.1
AAQ64230.1	000017	HAD-SAK	180	KVP40.0161	Vibrio phage KVP40	GCA_000843785.1
QIW90544.1	000017	HAD-SAK	172	GCAPEGMB_00197	Vibrio phage V07	GCA_012361095.1
QIW90878.1	000017	HAD-SAK	172	COHAPHLL_00015	Vibrio phage V09	GCA_012361135.1
QHJ74342.1	000017	HAD-SAK	172	VH12019_00015	Vibrio phage VH1_2019	GCA_009931825.1
AGB06835.1	000017	HAD-SAK	179	CF80_gp048	Vibrio phage VH7D	GCA_000914495.1
QBX06311.1	000017	HAD-SAK	171	ValB1HC_358	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60942.1	000017	HAD-SAK	171	AVU32_gp101	Vibrio phage ValKK3	GCA_001501635.1
AGN30208.1	000017	HAD-SAK	172	VPFG_00208	Vibrio phage nt-1	GCA_000910195.2
ALP47198.1	000017	HAD-SAK	101	phiGrn1_0272	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47588.1	000017	HAD-SAK	101	phiST2_0031	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54554.1	000017	HAD-SAK	171	vBValMR10Z_13	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07029.1	000017	HAD-SAK	158	VmeM32_00038	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96918.1	000017	HAD-SAK	243	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97223.1	000017	HAD-SAK	243	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96282.1	000017	HAD-SAK	243	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96600.1	000017	HAD-SAK	243	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21197.1	000017	HAD-SAK	262	-	Vibrio phage vB_pir03	GCA_014319855.1
AFN37389.1	000017	HAD-SAK	172	pp2_156	Vibriophage phi-pp2	GCA_002630725.1
BBA65436.1	000017	HAD-SAK	179	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96453.1	000017	HAD-SAK	179	Xoosp13_267	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000272	000017	HAD-SAK	186	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000217	000017	HAD-SAK	186	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01715.1	000018	HAD-SAK	169	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28751.1	000018	HAD-SAK	157	AP1_0033	Aeromonas phage AP1	GCA_014183365.1
ATI17581.1	000018	HAD-SAK	157	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00416.1	000018	HAD-SAK	157	HWB28_gp136	Aeromonas phage AS-zj	GCA_002627665.1
AUE22842.1	000018	HAD-SAK	167	Ah1_00324	Aeromonas phage Ah1	GCA_002957415.1
QAX98020.1	000018	HAD-SAK	157	ASswx1_380	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01121.1	000018	HAD-SAK	158	ASwh1_54	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39360.1	000018	HAD-SAK	157	CC2_152	Aeromonas phage CC2	GCA_000903495.1
ADQ53019.1	000018	HAD-SAK	167	PX29p300	Aeromonas phage PX29	GCA_000920195.1
ADM79943.1	000018	HAD-SAK	165	phiAS5_ORF0100	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53355.1	000018	HAD-SAK	158	65p347	Aeromonas virus 65	GCA_000893255.1
AAQ17972.1	000018	HAD-SAK	167	Aeh1ORF303c	Aeromonas virus Aeh1	GCA_000843245.1
AYD81240.1	000019	HAD-SAK	188	SEA_JUSTBECAUSE_71	Streptomyces phage JustBecause	GCA_003613775.1
QJD53643.1	000019	HAD-SAK	188	SEA_KELA_72	Streptomyces phage Kela	GCA_012934305.1
QBZ71974.1	000019	HAD-SAK	180	SEA_KRADAL_76	Streptomyces phage Kradal	GCA_004799925.1
AXH66237.1	000019	HAD-SAK	180	SEA_SATIS_76	Streptomyces phage Satis	GCA_003366315.1
AUE22617.1	000000	HAD-SAK	38	Ah1_00076	Aeromonas phage Ah1	GCA_002957415.1
CCH63532.1	000020	HD+PNK	340	CP21_070	Campylobacter virus CP21	GCA_000902535.1
AXH72845.1	000021	PNK	169	-	Myoviridae sp.	GCA_003657725.1
QIG65772.1	000021	PNK	176	phiOC_p107	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR48115.2	000021	PNK	110	SmphiM12_483	Sinorhizobium phage phiM12	GCA_001023565.1
AGR48117.2	000021	PNK	84	SmphiM12_485	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13658.1	000021	PNK	196	PHIN3_395	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54745.1	000021	PNK	150	b23_0130	Synechococcus phage B23	GCA_009745195.1
QGT54375.1	000021	PNK	150	b3_0131	Synechococcus phage B3	GCA_009745215.1
BBA65347.1	000021	PNK	164	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96381.1	000021	PNK	163	Xoosp13_195	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QIG63346.1	000022	PNK	160	DAC16_113	Bacteroides phage DAC16	GCA_013387695.1
QIG63612.1	000022	PNK	160	DAC19_121	Bacteroides phage DAC19	GCA_013387715.1
QIG63873.1	000022	PNK	160	DAC20_120	Bacteroides phage DAC20	GCA_013387725.1
QIG64136.1	000022	PNK	160	DAC22_122	Bacteroides phage DAC22	GCA_013387735.1
QIG64393.1	000022	PNK	160	DAC23_115	Bacteroides phage DAC23	GCA_013387745.1
QAU04501.1	000000	PNK	137	ValB1MD_148	Vibrio phage ValB1MD	GCA_004138815.1
ASV44095.1	000000	HD+PNK	374	PBI_SCTP2_80	Salicola phage SCTP-2	GCA_002625545.1
AEO93501.1	000000	PNK	286	G_242	Bacillus virus G	GCA_000917535.1
AEO93523.1	000000	PNK+HD	425	G_264	Bacillus virus G	GCA_000917535.1
QDH83522.1	000000	PNK	170	H1O15_gp284	Achromobacter phage Motura	GCA_006964305.1
AGR47987.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	411	SmphiM12_355	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13174.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	411	PHIM19_269	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12814.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	411	PHIM7_269	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13537.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	411	PHIN3_274	Sinorhizobium phage phiN3	GCA_001501175.1
QAU04503.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	448	ValB1MD_153	Vibrio phage ValB1MD	GCA_004138815.1
QAX96904.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	426	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97209.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	426	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96268.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	426	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96586.1	000023	PolyA_pol+PolyA_pol_RNAbd+HD	426	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AND75364.1	000024	PolyA_pol+PolyA_pol_RNAbd	220	ME3_203	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01757.1	000024	PolyA_pol+PolyA_pol_RNAbd	355	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29077.1	000024	PolyA_pol+PolyA_pol_RNAbd	330	AP1_0370	Aeromonas phage AP1	GCA_014183365.1
ATI17539.1	000024	PolyA_pol+PolyA_pol_RNAbd	330	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00458.1	000024	PolyA_pol+PolyA_pol_RNAbd	330	HWB28_gp094	Aeromonas phage AS-zj	GCA_002627665.1
AUE22829.1	000024	PolyA_pol+PolyA_pol_RNAbd	337	Ah1_00311	Aeromonas phage Ah1	GCA_002957415.1
QAX98543.1	000024	PolyA_pol+PolyA_pol_RNAbd	347	ASfcp2_208	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97980.1	000024	PolyA_pol+PolyA_pol_RNAbd	330	ASswx1_339	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01160.1	000024	PolyA_pol+PolyA_pol_RNAbd	353	ASwh1_94	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39504.1	000024	PolyA_pol+PolyA_pol_RNAbd	330	CC2_195	Aeromonas phage CC2	GCA_000903495.1
ADQ53007.1	000024	PolyA_pol+PolyA_pol_RNAbd	347	PX29p288	Aeromonas phage PX29	GCA_000920195.1
ADM79931.1	000024	PolyA_pol+PolyA_pol_RNAbd	351	phiAS5_ORF0088	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53399.1	000024	PolyA_pol+PolyA_pol_RNAbd	348	65p392	Aeromonas virus 65	GCA_000893255.1
AAQ17958.1	000024	PolyA_pol+PolyA_pol_RNAbd	347	Aeh1ORF289c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94830.1	000024	PolyA_pol+PolyA_pol_RNAbd	421	FDI40_gp018	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93780.1	000024	PolyA_pol+PolyA_pol_RNAbd	418	G_522	Bacillus virus G	GCA_000917535.1
AXQ69331.1	000024	PolyA_pol+PolyA_pol_RNAbd	394	CcrBL9_gp307	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88159.1	000024	PolyA_pol+PolyA_pol_RNAbd	384	CcrColossus_gp289	Caulobacter phage CcrColossus	GCA_000899635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ68835.1	000024	PolyA_pol+PolyA_pol_RNAbd	384	CcrPW_gp296	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69891.1	000024	PolyA_pol+PolyA_pol_RNAbd	394	CcrSC_gp309	Caulobacter phage CcrSC	GCA_003443315.1
AIA65003.1	000024	PolyA_pol+PolyA_pol_RNAbd	346	S13_206	Cronobacter phage S13	GCA_001503575.1
AFC21636.1	000024	PolyA_pol+PolyA_pol_RNAbd	371	GAP32_186	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14429.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	PBI_121Q_539	Escherichia phage 121Q	GCA_000926855.1
QAY00519.1	000024	PolyA_pol+PolyA_pol_RNAbd	371	Ecwhy1_240	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34713.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	ACQ29_gp033	Escherichia phage PBECO4	GCA_001041035.1
BBM62101.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	EO157G_5120	Escherichia phage SP27	GCA_008033345.1
AXC36832.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	-	Escherichia phage UB	GCA_003341455.1
QBO61872.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	G17_00383	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13912.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	vBEcoMphAPEC6_gp287c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80415.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	PSLUR01_00438	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44304.1	000024	PolyA_pol+PolyA_pol_RNAbd	368	RaK2_00031	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57956.1	000024	PolyA_pol+PolyA_pol_RNAbd	246	SEA_PAULODIABOLI_272	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72847.1	000024	PolyA_pol+PolyA_pol_RNAbd	526	-	Myoviridae sp.	GCA_003657725.1
QHJ78928.1	000024	PolyA_pol+PolyA_pol_RNAbd	382	-	Myoviridae sp.	GCA_012593985.1
AMM43757.1	000024	PolyA_pol+PolyA_pol_RNAbd	371	CBB_192	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18907.1	000024	PolyA_pol+PolyA_pol_RNAbd	374	7t3_0386	Salmonella phage 7t3	GCA_006083215.1
AZU98164.1	000024	PolyA_pol+PolyA_pol_RNAbd	374	CPT_Munch_220	Salmonella phage Munch	GCA_004015485.1
QIG62820.1	000024	PolyA_pol+PolyA_pol_RNAbd	374	SEPL_207	Salmonella phage SE_PL	GCA_011067555.1
AQW88713.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	BF_0188	Serratia phage BF	GCA_002619745.1
QGT54824.1	000024	PolyA_pol+PolyA_pol_RNAbd	243	b23_0209	Synechococcus phage B23	GCA_009745195.1
QGT54454.1	000024	PolyA_pol+PolyA_pol_RNAbd	243	b3_0211	Synechococcus phage B3	GCA_009745215.1
QIW90378.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	GCAPEGMB_00031	Vibrio phage V07	GCA_012361095.1
QIW91051.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	COHAPHLL_00188	Vibrio phage V09	GCA_012361135.1
QHJ74547.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	VH12019_00247	Vibrio phage VH1_2019	GCA_009931825.1
QBX06109.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	ValB1HC_155	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61121.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	AVU32_gp280	Vibrio phage ValKK3	GCA_001501635.1
AIE13788.1	000024	PolyA_pol+PolyA_pol_RNAbd	160	VPFG_p13	Vibrio phage nt-1	GCA_000910195.2
AIE13787.1	000024	PolyA_pol+PolyA_pol_RNAbd	197	VPFG_00029	Vibrio phage nt-1	GCA_000910195.2
ALP47001.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	phiGrn1_0099	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47382.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	phiST2_0230	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54734.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	vBValMR10Z_194	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07167.1	000024	PolyA_pol+PolyA_pol_RNAbd	332	VmeM32_00181	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37596.1	000024	PolyA_pol+PolyA_pol_RNAbd	365	pp2_364	Vibriophage phi-pp2	GCA_002630725.1
BBA65594.1	000024	PolyA_pol+PolyA_pol_RNAbd	352	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96573.1	000024	PolyA_pol+PolyA_pol_RNAbd	347	Xoosp13_387	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58995.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	g187	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58460.1	000024	PolyA_pol+PolyA_pol_RNAbd	370	g183	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000486	000024	PolyA_pol+PolyA_pol_RNAbd	424	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000367	000024	PolyA_pol+PolyA_pol_RNAbd	424	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83802.1	000025	PolyA_pol+PolyA_pol_RNAbd	550	0305phi8-36p102	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83661.1	000025	PolyA_pol+PolyA_pol_RNAbd	550	0305phi8-36p102R	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93458.1	000000	PolyA_pol	297	G_199	Bacillus virus G	GCA_000917535.1
QHJ86051.1	000000	PolyA_pol	208	KKIINIFJ_00139	Pseudomonas phage PN05	GCA_009931935.1
QIW90858.1	000000	PolyA_pol	50	GCAPEGMB_00543	Vibrio phage V07	GCA_012361095.1
APU01754.1	000026	HD	168	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29059.1	000026	HD	168	AP1_0352	Aeromonas phage AP1	GCA_014183665.1
ATI17542.1	000026	HD	168	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00455.1	000026	HD	168	HWB28_gp097	Aeromonas phage AS-zj	GCA_002627665.1
AUE22647.1	000026	HD	63	Ah1_00106	Aeromonas phage Ah1	GCA_002957415.1
AUE22648.1	000026	HD	70	Ah1_00107	Aeromonas phage Ah1	GCA_002957415.1
QAX98374.1	000026	HD	150	ASfcp2_28	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97983.1	000026	HD	168	ASswx1_342	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01157.1	000026	HD	168	ASwh1_91	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39488.1	000026	HD	168	CC2_193	Aeromonas phage CC2	GCA_000903495.1
ADQ52827.1	000026	HD	150	PX29p108	Aeromonas phage PX29	GCA_000920195.1
ADM80084.1	000026	HD	148	phiAS5_ORF0241	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53396.1	000026	HD	168	65p389	Aeromonas virus 65	GCA_000893255.1
AAQ17771.1	000026	HD	150	Aeh1ORF110c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95240.1	000026	HD	151	FDI40_gp481	Agrobacterium phage Atu_ph07	GCA_002628245.1
QBX06849.1	000026	HD	178	BcepSaruman_436	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74818.1	000026	HD	186	BcepSauron_438	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13695.1	000026	HD	203	Ccr10_gp165c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14040.1	000026	HD	203	Ccr2_gp164c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14727.1	000026	HD	203	Ccr29_gp171	Caulobacter phage Ccr29	GCA_002619485.1
ARB15082.1	000026	HD	203	Ccr32_gp164	Caulobacter phage Ccr32	GCA_002619505.1
ARB15416.1	000026	HD	203	Ccr34_gp174	Caulobacter phage Ccr34	GCA_002619525.1
ARB14383.1	000026	HD	203	Ccr5_gp163c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68365.1	000026	HD	204	CcrBL10_gp161c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69317.1	000026	HD	266	CcrBL9_gp293	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88082.1	000026	HD	307	CcrColossus_gp212	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68758.1	000026	HD	307	CcrPW_gp219c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69877.1	000026	HD	266	CcrSC_gp295	Caulobacter phage CcrSC	GCA_003443315.1
AFU87688.1	000026	HD	203	CcrKarma_gp171	Caulobacter virus Karma	GCA_000901575.1
AFU87337.1	000026	HD	203	CcrMagneto_gp167	Caulobacter virus Magneto	GCA_000903095.1
AFU86648.1	000026	HD	202	CcrRogue_gp166	Caulobacter virus Rogue	GCA_000900555.1
AFU88484.1	000026	HD	203	CcrSwift_gp166	Caulobacter virus Swift	GCA_000899655.1
AFU87001.1	000026	HD	203	CbK_gp169	Caulobacter virus phiCbK	GCA_000900535.1
AFC21522.1	000026	HD	214	GAP32_074	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXG67108.1	000026	HD	224	AD1_064	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79865.1	000026	HD	194	JA11_060	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66464.1	000026	HD	194	JA13_061	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66788.1	000026	HD	194	JA29_062	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67434.1	000026	HD	194	JA33_060	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08344.1	000026	HD	225	Alexandra_64	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58706.1	000026	HD	226	Y3_066	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AFA44730.1	000026	HD	205	RaK2_00457	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72877.1	000026	HD	201	-	Myoviridae sp.	GCA_003657725.1
AMM43642.1	000026	HD	233	CBB_77	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ABY63150.1	000026	HD	213	201phi2-1p325	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45056.1	000026	HD	218	KTN4_298	Pseudomonas phage KTN4	GCA_002607225.1
QBX32455.1	000026	HD	201	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03724.1	000026	HD	210	301	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02674.1	000026	HD	191	PSA21_147	Pseudomonas phage Psa21	GCA_004340405.1
ATN94659.1	000026	HD	218	SL2_082	Pseudomonas phage SL2	GCA_002956015.1
QJB22931.1	000026	HD	218	fnug_288	Pseudomonas phage fnug	GCA_012837215.1
QEM42027.1	000026	HD	201	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83147.1	000026	HD	218	PHIKZ246	Pseudomonas virus phiKZ	GCA_000842965.1
ASV44502.1	000026	HD	155	PBI_SCTP2_487	Salicola phage SCTP-2	GCA_002625545.1
QCW18773.1	000026	HD	203	7t3_0252	Salmonella phage 7t3	GCA_006083215.1
AZU98039.1	000026	HD	203	CPT_Munch_095	Salmonella phage Munch	GCA_004015485.1
QIG62941.1	000026	HD	203	SEPL_328	Salmonella phage SE_PL	GCA_011067555.1
ATA65552.1	000026	HD	228	2050HW_00217	Serratia phage 2050HW	GCA_002628125.1
AQW88592.1	000026	HD	232	BF_0067	Serratia phage BF	GCA_002619745.1
QDB71317.1	000026	HD	228	CPT_Moabite_287	Serratia phage Moabite	GCA_006384735.1
AGR48128.1	000026	HD	157	SmphiM12_496	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13665.1	000026	HD	157	PHIN3_402	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81290.1	000026	HD	180	SEA_JUSTBECAUSE_121	Streptomyces phage JustBecause	GCA_003613775.1
QJD53693.1	000026	HD	180	SEA_KELA_122	Streptomyces phage Kela	GCA_012934305.1
QBZ72021.1	000026	HD	173	SEA_KRADAL_123	Streptomyces phage Kradal	GCA_004799925.1
AXH66284.1	000026	HD	173	SEA_SATIS_123	Streptomyces phage Satis	GCA_003366315.1
QAU04460.1	000026	HD	175	ValB1MD_052	Vibrio phage ValB1MD	GCA_004138815.1
AQT28003.1	000026	HD	273	pVa21_061	Vibrio phage pVa-21	GCA_002619305.1
BBA65684.1	000026	HD	212	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65225.1	000026	HD	212	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96256.1	000026	HD	213	Xoosp13_69	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58868.1	000026	HD	234	g060	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58331.1	000026	HD	234	g054	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95268.1	000027	HD	159	FDI40_gp509	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72427.1	000027	HD	168	-	Myoviridae sp.	GCA_003657725.1
QCG76290.1	000027	HD	172	EST35_0422	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBI90576.1	000027	HD	325	HYO65_gp184	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90884.1	000027	HD	325	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBA65570.1	000027	HD	191	-	Xanthomonas phage XacN1	GCA_003173815.1

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QDJ96557.1	000027	HD	182	Xoosp13_371	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90623.1	000028	HD	173	HYO65_gp231	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90929.1	000028	HD	196	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39325.1	000028	HD	185	BPT24_201	Tenacibaculum phage pT24	GCA_002611925.1
AUE22587.1	000029	HJR-EndoVII	161	Ah1_00046	Aeromonas phage Ah1	GCA_002957415.1
QAX98624.1	000029	HJR-EndoVII	161	ASfcp2_291	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52764.1	000029	HJR-EndoVII	161	PX29p045	Aeromonas phage PX29	GCA_000920195.1
ADM80019.1	000029	HJR-EndoVII	161	phiAS5_ORF0176	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17709.1	000029	HJR-EndoVII	161	49	Aeromonas virus Aeh1	GCA_000843245.1
CCH63622.1	000029	HJR-EndoVII	79	CP21_160	Campylobacter virus CP21	GCA_000902535.1
ANS06043.1	000029	HJR-EndoVII	160	ABCD_0244	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65030.1	000029	HJR-EndoVII	159	S13_233	Cronobacter phage S13	GCA_001503575.1
AFC21691.1	000029	HJR-EndoVII	164	GAP32_241	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14484.1	000029	HJR-EndoVII	163	PBI_121Q_594	Escherichia phage 121Q	GCA_000926855.1
QAY00465.1	000029	HJR-EndoVII	163	Ecwhy1_185	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35207.1	000029	HJR-EndoVII	163	ACQ29_gp527	Escherichia phage PBECO4	GCA_001041035.1
BBM62156.1	000029	HJR-EndoVII	163	EO157G_5670	Escherichia phage SP27	GCA_008033345.1
AXC36779.1	000029	HJR-EndoVII	163	-	Escherichia phage UB	GCA_003341455.1
ARM70901.1	000029	HJR-EndoVII	157	phiC120_c196	Escherichia phage phiC120	GCA_002621185.1
QBO61819.1	000029	HJR-EndoVII	163	G17_00330	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13863.1	000029	HJR-EndoVII	163	vBEcoMphAPEC6_gp234	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80468.1	000029	HJR-EndoVII	163	PSLUR01_00491	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78781.1	000029	HJR-EndoVII	160	RB43ORF259w	Escherichia virus RB43	GCA_000863505.1
AFA44359.1	000029	HJR-EndoVII	164	RaK2_00086	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78902.1	000029	HJR-EndoVII	158	-	Myoviridae sp.	GCA_012593985.1
AMM43813.1	000029	HJR-EndoVII	158	CBB_248	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18964.1	000029	HJR-EndoVII	164	7t3_0443	Salmonella phage 7t3	GCA_006083215.1
AZU98217.1	000029	HJR-EndoVII	163	CPT_Munch_273	Salmonella phage Munch	GCA_004015485.1
QIG62767.1	000029	HJR-EndoVII	164	SEPL_154	Salmonella phage SE_PL	GCA_011067555.1
AQW88771.1	000029	HJR-EndoVII	160	BF_0246	Serratia phage BF	GCA_002619745.1
AAQ64202.1	000029	HJR-EndoVII	151	KVP40.0131	Vibrio phage KVP40	GCA_000843785.1
QIW90517.1	000029	HJR-EndoVII	169	GCAPEGMB_00170	Vibrio phage V07	GCA_012361095.1
QIW90905.1	000029	HJR-EndoVII	169	COHAPHLL_00042	Vibrio phage V09	GCA_012361135.1
QHJ74313.1	000029	HJR-EndoVII	169	VH12019_00394	Vibrio phage VH1_2019	GCA_009931825.1
QBX05958.1	000029	HJR-EndoVII	168	ValB1HC_004	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04571.1	000029	HJR-EndoVII	179	ValB1MD_293	Vibrio phage ValB1MD	GCA_004138815.1
AJT60970.1	000029	HJR-EndoVII	168	AVU32_gp129	Vibrio phage ValKK3	GCA_001501635.1
AGN30181.2	000029	HJR-EndoVII	168	VPFG_00179	Vibrio phage nt-1	GCA_000910195.2
ALP47218.1	000029	HJR-EndoVII	95	phiGrn1_0243	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47524.1	000029	HJR-EndoVII	142	phiST2_0381	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54583.1	000029	HJR-EndoVII	168	vBValMR10Z_42	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37362.1	000029	HJR-EndoVII	169	pp2_129	Vibriophage phi-pp2	GCA_002630725.1
SOK59052.1	000029	HJR-EndoVII	164	g244c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58517.1	000029	HJR-EndoVII	164	g240c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AQW88528.1	000030	HJR-EndoVII	138	BF_0003	Serratia phage BF	GCA_002619745.1
QCW23048.1	000030	HJR-EndoVII	147	-	Synechococcus phage S-B05	GCA_006083695.1
QGT54969.1	000031	HJR-EndoVII	111	b23_0363	Synechococcus phage B23	GCA_009745195.1
QGT54604.1	000031	HJR-EndoVII	111	b3_0369	Synechococcus phage B3	GCA_009745215.1
AFN37594.1	000032	HTH	280	pp2_362	Vibriophage phi-pp2	GCA_002630725.1
AIE13786.1	000032	HTH	279	VPFG_00027	Vibrio phage nt-1	GCA_000910195.2
QHJ74545.1	000032	HTH	280	VH12019_00245	Vibrio phage VH1_2019	GCA_009931825.1
QIW91053.1	000032	HTH	280	COHAPHLL_00190	Vibrio phage V09	GCA_012361135.1
QIW90376.1	000032	HTH	280	GCAPEGMB_00029	Vibrio phage V07	GCA_012361095.1
AAQ64431.1	000032	HTH	280	KVP40.0362	Vibrio phage KVP40	GCA_000843785.1
QMV29101.1	000033	PolB35exo-fragments	327	AP1_0394	Aeromonas phage AP1	GCA_014183365.1
BBI90939.1	000033	PolB35exo-fragments	137	-	Tenacibaculum phage PTm5	GCA_009730715.1
ALY07088.1	000033	PolB35exo-fragments	199	VmeM32_00099	Vibrio phage vB_VmeM-32	GCA_002608825.1
QDB70259.1	000034	PolB35exo	572	CF8_0091	Aeromonas phage CF8	GCA_006384595.2
QDJ97237.1	000034	PolB35exo	580	D6_0077	Aeromonas phage D6	GCA_007051205.2
QDH47034.1	000034	PolB35exo	580	LAh10_9	Aeromonas phage LAh10	GCA_006863975.1
QDJ96850.1	000034	PolB35exo	576	PS1_0091	Aeromonas phage PS1	GCA_007051165.2
QFR59482.1	000034	PolB35exo	576	PS2_0091	Aeromonas phage PS2	GCA_009388305.2
ALN97886.1	000034	PolB35exo	318	Bp8pS_207	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AFO71265.1	000034	PolB35exo	549	CR5_045	Cronobacter phage CR5	GCA_000910235.1
QBZ70620.1	000034	PolB35exo	581	pETSU_039	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59695.1	000034	PolB35exo	594	SEGD1_046	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07472.1	000034	PolB35exo	600	DERBICUS_46	Erwinia phage Derbicus	GCA_004521655.1
AHI60435.1	000034	PolB35exo	573	Ea357_281	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49698.1	000034	PolB35exo	592	MACHINA_60	Erwinia phage Machina	GCA_002758035.1
AGX01958.1	000034	PolB35exo	585	CF95_gp236	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07392.1	000034	PolB35exo	573	REBECCA_287	Erwinia phage Rebecca	GCA_004521635.1
AXF51187.1	000034	PolB35exo	590	WELLINGTON_57	Erwinia phage Wellington	GCA_003344985.1
AFQ96772.1	000034	PolB35exo	596	G173_gp227	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48074.1	000034	PolB35exo	596	ASESINO_61	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86074.1	000034	PolB35exo	573	BOSOLAPHORUS_288	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48349.1	000034	PolB35exo	592	CAITLIN_54	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48622.1	000034	PolB35exo	592	CHRISDB_60	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52390.1	000034	PolB35exo	573	DM_291	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86394.1	000034	PolB35exo	573	DESERTFOX_287	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48896.1	000034	PolB35exo	600	EARLPHILLIPIV_46	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49143.1	000034	PolB35exo	592	HUXLEY_61	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03859.1	000034	PolB35exo	583	JOAD_56	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49409.1	000034	PolB35exo	590	KWAN_57	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86715.1	000034	PolB35exo	573	MADMEL_288	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87040.1	000034	PolB35exo	573	MORTIMER_292	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49971.1	000034	PolB35exo	592	PARSHIK_62	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50237.1	000034	PolB35exo	595	PHOBOS_47	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52065.1	000034	PolB35exo	573	RAY_285	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03614.1	000034	PolB35exo	583	RISINGSUN_56	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51748.1	000034	PolB35exo	573	SIMMY50_290	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65100.1	000034	PolB35exo	573	SPECIALG_289	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50484.1	000034	PolB35exo	596	STRATTON_59	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85885.1	000034	PolB35exo	594	ACEC001_0470	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63861.1	000034	PolB35exo	499	Goslar_00068	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71936.1	000034	PolB35exo	579	N1M2_73	Klebsiella phage N1M2	GCA_010092605.1
QGZ14397.1	000034	PolB35exo	585	HWC77_gp034	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24188.1	000034	PolB35exo	578	-	Proteus phage 10	GCA_014071245.1
ABY62974.1	000034	PolB35exo	709	201phi2-1p144	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27145.1	000034	PolB35exo	601	PPEV_gp051	Pseudomonas phage EL	GCA_000866825.1
ANM44866.1	000034	PolB35exo	638	KTN4_108	Pseudomonas phage KTN4	GCA_002607225.1
ARV77505.1	000034	PolB35exo	638	NOXIFER_83	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89536.1	000034	PolB35exo	582	OBP_099	Pseudomonas phage OBP	GCA_000896635.1
QBX32238.1	000034	PolB35exo	647	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76759.1	000034	PolB35exo	678	PHABIO_128	Pseudomonas phage Phabio	GCA_002624965.1
AEH03509.1	000034	PolB35exo	608	085	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02620.1	000034	PolB35exo	651	PSA21_92	Pseudomonas phage Psa21	GCA_004340405.1
ATN94847.1	000034	PolB35exo	638	SL2_270	Pseudomonas phage SL2	GCA_002956015.1
QJB22744.1	000034	PolB35exo	638	fnug_101	Pseudomonas phage fnug	GCA_012837215.1
QEM41817.1	000034	PolB35exo	647	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82983.1	000034	PolB35exo	638	PHIKZ082	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19225.1	000034	PolB35exo	627	FDH28_gp170	Ralstonia phage RP12	GCA_002617345.1
BAW19511.1	000034	PolB35exo	627	-	Ralstonia phage RP31	GCA_002617365.1
BAS04981.2	000034	PolB35exo	678	AVU11_gp189	Ralstonia phage RSF1	GCA_001500875.1
BAQ02707.2	000034	PolB35exo	697	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20760.1	000034	PolB35exo	594	-	Salmonella phage JN03	GCA_014319805.1
AWN09053.1	000034	PolB35exo	594	MLDJOKPK_00122	Salmonella phage SPAsTU	GCA_003183805.1
AEP83877.1	000034	PolB35exo	594	SPN3US_0044	Salmonella phage SPN3US	GCA_001042275.1
QKE54612.1	000034	PolB35exo	576	ACSA002_2950	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65344.1	000034	PolB35exo	581	2050HW_00009	Serratia phage 2050HW	GCA_002628125.1
QDB71132.1	000034	PolB35exo	581	CPT_Moabite_102	Serratia phage Moabite	GCA_006384735.1
QFP93062.1	000034	PolB35exo	601	-	Serratia phage PCH45	GCA_009187865.1
AFF28103.1	000034	PolB35exo	487	PAU_105	Sphingomonas phage PAU	GCA_000902455.1
QAU04339.1	000034	PolB35exo	585	HWC03_gp184	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23237.1	000034	PolB35exo	588	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80935.1	000034	PolB35exo	588	Aphrodite1_0108	Vibrio phage Aphrodite1	GCA_002958015.1

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AXH70837.1	000034	PolB35exo	576	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47491.1	000034	PolB35exo	554	HWC35_gp097	Vibrio phage USC-1	GCA_006864065.1
BAW98311.1	000034	PolB35exo	550	FDH33_gp102	Vibrio phage pTD1	GCA_002618825.1
AQT28172.1	000034	PolB35exo	586	pVa21_231	Vibrio phage pVa-21	GCA_002619305.1
ALY07089.1	000034	PolB35exo	194	VmeM32_00100	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96656.1	000034	PolB35exo	574	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96974.1	000034	PolB35exo	574	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96020.1	000034	PolB35exo	574	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96338.1	000034	PolB35exo	574	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21085.1	000034	PolB35exo	575	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26194.1	000034	PolB35exo	576	g170	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000806	000034	PolB35exo	174	-	Prevotella_phage_Lak-B8	GCA_004379655.1
APU01413.1	000035	PolB35exo+FamBDNAPol	507	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28805.1	000035	PolB35exo+FamBDNAPol	506	AP1_0098	Aeromonas phage AP1	GCA_014183365.1
ATI17484.1	000035	PolB35exo+FamBDNAPol	506	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00513.1	000035	PolB35exo+FamBDNAPol	506	HWB28_gp039	Aeromonas phage AS-zj	GCA_002627665.1
AUE22561.1	000035	PolB35exo+FamBDNAPol	919	Ah1_00020	Aeromonas phage Ah1	GCA_002957415.1
QAX98598.1	000035	PolB35exo+FamBDNAPol	920	ASfcp2_265	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97924.1	000035	PolB35exo+FamBDNAPol	506	ASswx1_281	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01225.1	000035	PolB35exo+FamBDNAPol	505	ASwh1_160	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39514.1	000035	PolB35exo+FamBDNAPol	506	CC2_250	Aeromonas phage CC2	GCA_000903495.1
ADQ52734.1	000035	PolB35exo+FamBDNAPol	920	PX29p015	Aeromonas phage PX29	GCA_000920195.1
ADM79987.1	000035	PolB35exo+FamBDNAPol	919	phiAS5_ORF0144	Aeromonas phage phiAS5	GCA_000887715.1
AAR90916.1	000035	PolB35exo+FamBDNAPol	507	65p022	Aeromonas virus 65	GCA_000893255.1
AAQ17672.1	000035	PolB35exo+FamBDNAPol	919	43	Aeromonas virus Aeh1	GCA_000843245.1
ASV44732.1	000035	PolB35exo+FamBDNAPol	565	FDI40_gp277	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01216.1	000035	PolB35exo+FamBDNAPol	554	AR9_g132	Bacillus phage AR9	GCA_001743835.1
AST99841.1	000035	PolB35exo+FamBDNAPol	554	PBI_PBS1_19	Bacillus virus PBS1	GCA_002601325.1
ANS05923.1	000035	PolB35exo+FamBDNAPol	901	ABCD_0038	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65047.1	000035	PolB35exo+FamBDNAPol	885	S13_250	Cronobacter phage S13	GCA_001503575.1
AFC21707.1	000035	PolB35exo+FamBDNAPol	1010	GAP32_257	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97048.1	000035	PolB35exo+FamBDNAPol	901	E_039	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56853.1	000035	PolB35exo+FamBDNAPol	828	CPXG_00050	Cyanophage P-RSM6	GCA_000906155.1
AJK27640.1	000035	PolB35exo+FamBDNAPol	839	PTIM40_175	Cyanophage P-TIM40	GCA_001470935.1
AOO14358.1	000035	PolB35exo+FamBDNAPol	833	Sn110110_164	Cyanophage S-RIM14	GCA_002599065.1
AOO15007.1	000035	PolB35exo+FamBDNAPol	833	W1230910_161	Cyanophage S-RIM14	GCA_002599125.1
AMO43170.1	000035	PolB35exo+FamBDNAPol	829	R1080702_161	Cyanophage S-RIM32	GCA_001754165.1
AMO43396.1	000035	PolB35exo+FamBDNAPol	829	W270710_152	Cyanophage S-RIM44	GCA_002599145.1
AOO11640.1	000035	PolB35exo+FamBDNAPol	829	ES420910_159	Cyanophage S-RIM44	GCA_002599165.1
AOO11868.1	000035	PolB35exo+FamBDNAPol	829	Np050604_152	Cyanophage S-RIM44	GCA_002599185.1
AOO12106.1	000035	PolB35exo+FamBDNAPol	829	Np200711_160	Cyanophage S-RIM44	GCA_002599205.1
AOO12341.1	000035	PolB35exo+FamBDNAPol	829	Np420711_159	Cyanophage S-RIM44	GCA_002599225.1
AOO12569.1	000035	PolB35exo+FamBDNAPol	829	Sn080709_152	Cyanophage S-RIM44	GCA_002599245.1
AOO12806.1	000035	PolB35exo+FamBDNAPol	829	Sn130910_159	Cyanophage S-RIM44	GCA_002599265.1
AOO13035.1	000035	PolB35exo+FamBDNAPol	829	W2100709_153	Cyanophage S-RIM44	GCA_002599285.1
AGH07497.1	000035	PolB35exo+FamBDNAPol	834	CYVG_00053	Cyanophage S-SSM6a	GCA_002710385.1
AGG54450.1	000035	PolB35exo+FamBDNAPol	825	CYWG_00166	Cyanophage S-SSM6b	GCA_002710425.1
AIT14500.1	000035	PolB35exo+FamBDNAPol	1001	PBI_121Q_610	Escherichia phage 121Q	GCA_000926855.1
QAY00449.1	000035	PolB35exo+FamBDNAPol	1001	Ecwhy1_169	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35192.1	000035	PolB35exo+FamBDNAPol	1001	ACQ29_gp512	Escherichia phage PBECO4	GCA_001041035.1
BBM62172.1	000035	PolB35exo+FamBDNAPol	1001	EO157G_5830	Escherichia phage SP27	GCA_008033345.1
AXC36763.1	000035	PolB35exo+FamBDNAPol	1001	-	Escherichia phage UB	GCA_003341455.1
ARM70871.1	000035	PolB35exo+FamBDNAPol	903	phiC120_c166	Escherichia phage phiC120	GCA_002621185.1
QBO61803.1	000035	PolB35exo+FamBDNAPol	1001	G17_00314	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13847.1	000035	PolB35exo+FamBDNAPol	1001	vBEcoMphAPEC6_gp218c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80484.1	000035	PolB35exo+FamBDNAPol	1001	PSLUR01_00507	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78560.1	000035	PolB35exo+FamBDNAPol	901	RB43ORF038c	Escherichia virus RB43	GCA_000863505.1
AFA44373.1	000035	PolB35exo+FamBDNAPol	1000	RaK2_00100	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72916.1	000035	PolB35exo+FamBDNAPol	990	-	Myoviridae sp.	GCA_003657725.1
QHJ78885.1	000035	PolB35exo+FamBDNAPol	889	-	Myoviridae sp.	GCA_012593985.1
QIG65670.1	000035	PolB35exo+FamBDNAPol	841	phiOC_p004	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43827.1	000035	PolB35exo+FamBDNAPol	1010	CBB_263	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26288.1	000035	PolB35exo+FamBDNAPol	828	CPMG_00188	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44560.1	000035	PolB35exo+FamBDNAPol	831	PSSM2_182	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12412.1	000035	PolB35exo+FamBDNAPol	831	PRTG_00260	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93483.1	000035	PolB35exo+FamBDNAPol	831	AVU42_gp147	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99255.1	000035	PolB35exo+FamBDNAPol	829	Syn1_154	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76192.1	000035	PolB35exo+FamBDNAPol	803	EST35_0311	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44194.1	000035	PolB35exo+FamBDNAPol	1089	PBI_SCTP2_179	Salicola phage SCTP-2	GCA_002625545.1
QCW18986.1	000035	PolB35exo+FamBDNAPol	1006	7t3_0465	Salmonella phage 7t3	GCA_006083215.1
AZU98234.1	000035	PolB35exo+FamBDNAPol	1006	CPT_Munch_290	Salmonella phage Munch	GCA_004015485.1
QIG62750.1	000035	PolB35exo+FamBDNAPol	1006	SEPL_137	Salmonella phage SE_PL	GCA_011067555.1
AQW88786.1	000035	PolB35exo+FamBDNAPol	1010	BF_0261	Serratia phage BF	GCA_002619745.1
AGR47663.1	000035	PolB35exo+FamBDNAPol	845	SmphiM12_031	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12929.1	000035	PolB35exo+FamBDNAPol	845	PHIM19_22	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12569.1	000035	PolB35exo+FamBDNAPol	845	PHIM7_21	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13301.1	000035	PolB35exo+FamBDNAPol	845	PHIN3_36	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30647.1	000035	PolB35exo+FamBDNAPol	491	Syn7803US37_170	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54915.1	000035	PolB35exo+FamBDNAPol	830	b23_0302	Synechococcus phage B23	GCA_009745195.1
QGT54550.1	000035	PolB35exo+FamBDNAPol	830	b3_0309	Synechococcus phage B3	GCA_009745215.1
ASR76205.1	000035	PolB35exo+FamBDNAPol	831	PBI_BELLAMY_161	Synechococcus phage Bellamy	GCA_002627525.1
QDH50571.1	000035	PolB35exo+FamBDNAPol	760	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59621.1	000035	PolB35exo+FamBDNAPol	830	S330809_160	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59383.1	000035	PolB35exo+FamBDNAPol	830	C440309_160	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59859.1	000035	PolB35exo+FamBDNAPol	830	N231010_160	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70545.1	000035	PolB35exo+FamBDNAPol	806	HOU04_gp146	Synechococcus phage S-T4	GCA_003443335.1
QJT70157.1	000035	PolB35exo+FamBDNAPol	823	SynMITS9220M01_144	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90628.1	000035	PolB35exo+FamBDNAPol	497	HYO65_gp236	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90934.1	000035	PolB35exo+FamBDNAPol	497	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39291.1	000035	PolB35exo+FamBDNAPol	517	BPT24_165	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64153.1	000035	PolB35exo+FamBDNAPol	850	KVP40.0082	Vibrio phage KVP40	GCA_000843785.1
QIW90477.1	000035	PolB35exo+FamBDNAPol	850	GCAPEGMB_00130	Vibrio phage V07	GCA_012361095.1
QIW90952.1	000035	PolB35exo+FamBDNAPol	850	COHAPHLL_00089	Vibrio phage V09	GCA_012361135.1
QHJ74265.1	000035	PolB35exo+FamBDNAPol	850	VH12019_00346	Vibrio phage VH1_2019	GCA_009931825.1
AGB07090.1	000035	PolB35exo+FamBDNAPol	850	CF80_gp303	Vibrio phage VH7D	GCA_000914495.1
QBX06005.1	000035	PolB35exo+FamBDNAPol	850	ValB1HC_051	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04482.1	000035	PolB35exo+FamBDNAPol	538	ValB1MD_101	Vibrio phage ValB1MD	GCA_004138815.1
AJT61019.1	000035	PolB35exo+FamBDNAPol	850	AVU32_gp178	Vibrio phage ValKK3	GCA_001501635.1
AGN30132.1	000035	PolB35exo+FamBDNAPol	850	VPFG_00130	Vibrio phage nt-1	GCA_000910195.2
ALP46962.1	000035	PolB35exo+FamBDNAPol	850	phiGrn1_0197	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47342.1	000035	PolB35exo+FamBDNAPol	850	phiST2_0330	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54629.1	000035	PolB35exo+FamBDNAPol	850	vBValMR10Z_88	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37314.1	000035	PolB35exo+FamBDNAPol	850	pp2_081	Vibriophage phi-pp2	GCA_002630725.1
BBA65491.1	000035	PolB35exo+FamBDNAPol	882	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96499.1	000035	PolB35exo+FamBDNAPol	882	Xoosp13_313	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59067.1	000035	PolB35exo+FamBDNAPol	1008	g259	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58533.1	000035	PolB35exo+FamBDNAPol	1008	g256	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prev15ph1000000552	000035	PolB35exo+FamBDNAPol	517	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01412.1	000036	FamBDNAPol	390	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28804.1	000036	FamBDNAPol	405	AP1_0097	Aeromonas phage AP1	GCA_014183365.1
ATI17485.1	000036	FamBDNAPol	391	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00512.1	000036	FamBDNAPol	391	HWB28_gp040	Aeromonas phage AS-zj	GCA_002627665.1
QAX97925.1	000036	FamBDNAPol	391	ASswx1_282	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01223.1	000036	FamBDNAPol	390	ASwh1_158	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39513.1	000036	FamBDNAPol	391	CC2_249	Aeromonas phage CC2	GCA_000903495.1
AAR90917.1	000036	FamBDNAPol	390	65p021	Aeromonas virus 65	GCA_000893255.1
AUZ95050.1	000036	FamBDNAPol	417	FDI40_gp276	Agrobacterium phage Atu_ph07	GCA_002628245.1
ALN97885.1	000036	FamBDNAPol	258	Bp8pS_206	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
CCH63705.1	000036	FamBDNAPol	119	CP21_245	Campylobacter virus CP21	GCA_000902535.1
CCH63706.1	000036	FamBDNAPol	53	CP21_246	Campylobacter virus CP21	GCA_000902535.1
CCH63707.1	000036	FamBDNAPol	167	CP21_247	Campylobacter virus CP21	GCA_000902535.1
CCH63711.1	000036	FamBDNAPol	271	CP21_251	Campylobacter virus CP21	GCA_000902535.1
QCG76194.1	000036	FamBDNAPol	379	EST35_0313	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AFF28108.1	000036	FamBDNAPol	404	PAU_110	Sphingomonas phage PAU	GCA_000902455.1
AIX30650.1	000036	FamBDNAPol	389	Syn7803US37_173	Synechococcus phage ACG-2014f	GCA_002594065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW22927.1	000036	FamBDNAPol	626	-	Synechococcus phage S-B05	GCA_006083695.1
BBI90633.1	000036	FamBDNAPol	326	HYO65_gp241	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90940.1	000036	FamBDNAPol	147	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39294.1	000036	FamBDNAPol	470	BPT24_168	Tenacibaculum phage pT24	GCA_002611925.1
QAU04484.1	000036	FamBDNAPol	338	ValB1MD_105	Vibrio phage ValB1MD	GCA_004138815.1
ALY07083.1	000036	FamBDNAPol	201	VmeM32_00094	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07084.1	000036	FamBDNAPol	291	VmeM32_00095	Vibrio phage vB_VmeM-32	GCA_002608825.1
prevph1000000805	000036	FamBDNAPol	309	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000821	000036	FamBDNAPol	325	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000564	000036	FamBDNAPol	325	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBI90631.1	000037	FamBDNAPol+Intein	263	HYO65_gp239	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90937.1	000037	FamBDNAPol+Intein	254	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000824	000037	FamBDNAPol+Intein	271	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000568	000037	FamBDNAPol+Intein	271	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
CCH63709.1	000037	FamBDNAPol+Intein	119	CP21_249	Campylobacter virus CP21	GCA_000902535.1
CCH63710.1	000000	FamBDNAPol	121	CP21_250	Campylobacter virus CP21	GCA_000902535.1
ALY07086.1	000000	FamBDNAPol	107	VmeM32_00097	Vibrio phage vB_VmeM-32	GCA_002608825.1
QMV29172.1	000000	PolB35exo	149	AP1_0475	Aeromonas phage AP1	GCA_014183365.1
prev15ph1000000173	000000	LuxR-HTH+HNH	316	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
SOK58727.1	000038	HTH+HNH	165	g450	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18546.1	000038	HTH+HNH	220	7t3_016	Salmonella phage 7t3	GCA_006083215.1
QIG63136.1	000038	HTH+HNH	220	SEPL_523	Salmonella phage SE_PL	GCA_011067555.1
AGR47851.1	000039	HNH+HTH	145	SmphiM12_219	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12697.1	000039	HNH+HTH	145	PHIM7_151	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13056.1	000039	HNH+HTH	145	PHIM19_151	Sinorhizobium phage phiM19	GCA_002605865.1
SOK59271.1	000039	HNH+HTH	223	g463	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QDH50468.1	000040	HNH	102	-	Synechococcus phage S-B43	GCA_006869725.1
SOK59264.1	000040	HNH	140	g456	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58648.1	000040	HNH	242	g371	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21976.1	000040	HNH	259	GAP32_516	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
prevph1000000213	000040	HNH	96	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000167	000040	HNH	96	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44527.1	000040	HNH	91	PSSM2_149	Prochlorococcus phage P-SSM2	GCA_000859585.1
prev15ph1000000127	000040	HNH	219	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AOO12102.1	000040	HNH	51	Np200711_156	Cyanophage S-RIM44	GCA_002599205.1
AXC36569.1	000040	HNH	64	-	Escherichia phage UB	GCA_003341455.1
QGT54529.1	000041	HTH+HTH+REase+MOM	493	b3_0288	Synechococcus phage B3	GCA_009745215.1
QGT54894.1	000041	HTH+HTH+REase+MOM	493	b23_0281	Synechococcus phage B23	GCA_009745195.1
QCG76092.1	000041	HTH+HTH+REase+MOM	611	EST35_0211	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QIG64257.1	000042	HTH+REase+MOM	506	DAC22_247	Bacteroides phage DAC22	GCA_013387735.1
QIG63993.1	000042	HTH+REase+MOM	506	DAC20_244	Bacteroides phage DAC20	GCA_013387725.1
QIG63732.1	000042	HTH+REase+MOM	506	DAC19_245	Bacteroides phage DAC19	GCA_013387715.1
QIG64201.1	000042	HTH+REase+MOM	509	DAC22_190	Bacteroides phage DAC22	GCA_013387735.1
QIG63435.1	000042	HTH+REase+MOM	573	DAC16_206	Bacteroides phage DAC16	GCA_013387695.1
QIG63937.1	000042	HTH+REase+MOM	509	DAC20_187	Bacteroides phage DAC20	GCA_013387725.1
QIG63676.1	000042	HTH+REase+MOM	509	DAC19_188	Bacteroides phage DAC19	GCA_013387715.1
QIG64457.1	000042	HTH+REase+MOM	509	DAC23_182	Bacteroides phage DAC23	GCA_013387745.1
QIG63412.1	000042	HTH+REase+MOM	509	DAC16_182	Bacteroides phage DAC16	GCA_013387695.1
QIG64230.1	000042	HTH+REase+MOM	577	DAC22_220	Bacteroides phage DAC22	GCA_013387735.1
QIG63966.1	000042	HTH+REase+MOM	516	DAC20_217	Bacteroides phage DAC20	GCA_013387725.1
QIG63705.1	000042	HTH+REase+MOM	516	DAC19_218	Bacteroides phage DAC19	GCA_013387715.1
QIG63442.1	000042	HTH+REase+MOM	516	DAC16_213	Bacteroides phage DAC16	GCA_013387695.1
QIG64486.1	000042	HTH+REase+MOM	516	DAC23_212	Bacteroides phage DAC23	GCA_013387745.1
QIG64513.1	000042	HTH+REase+MOM	512	DAC23_239	Bacteroides phage DAC23	GCA_013387745.1
QIG63469.1	000042	HTH+REase+MOM	512	DAC16_240	Bacteroides phage DAC16	GCA_013387695.1
QCG76193.1	000042	HTH+REase+MOM	560	EST35_0312	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBI90695.1	000042	HTH+REase+MOM	465	HYO65_gp303	Tenacibaculum phage PTm1	GCA_009730695.1
CCE26253.1	000042	HTH+REase+MOM	469	g230	Yersinia phage phiR1-37	GCA_000895615.1
AUE22848.1	000042	HTH+REase+MOM	547	Ah1_00330	Aeromonas phage Ah1	GCA_002957415.1
AST99855.1	000042	HTH+REase+MOM	494	PBI_PBS1_33	Bacillus virus PBS1	GCA_002601325.1
CCE26175.1	000042	HTH+REase+MOM	585	g151	Yersinia phage phiR1-37	GCA_000895615.1
BBI91001.1	000042	HTH+REase+MOM	543	-	Tenacibaculum phage PTm5	GCA_009730715.1
AMS01230.1	000042	HTH+REase+MOM	494	AR9_g146	Bacillus phage AR9	GCA_001743835.1
AMS01272.1	000042	HTH+REase+MOM	582	AR9_g188	Bacillus phage AR9	GCA_001743835.1
AST99899.1	000042	HTH+REase+MOM	584	PBI_PBS1_77	Bacillus virus PBS1	GCA_002601325.1
CCH63533.1	000043	REase+MOM	399	CP21_071	Campylobacter virus CP21	GCA_000902535.1
AFA44431.1	000043	REase+MOM	569	RaK2_00158	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
CCE26195.1	000043	REase+MOM	561	g171	Yersinia phage phiR1-37	GCA_000895615.1
AXH72809.1	000043	REase+MOM	545	-	Myoviridae sp.	GCA_003657725.1
QCG76037.1	000043	REase+MOM	525	EST35_0155	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76220.1	000043	REase+MOM	498	EST35_0339	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AFA44407.1	000043	REase+MOM	577	RaK2_00134	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44312.1	000043	REase+MOM	667	RaK2_00039	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMS01349.1	000043	REase+MOM	565	AR9_g265	Bacillus phage AR9	GCA_001743835.1
AST99977.1	000043	REase+MOM	565	PBI_PBS1_156	Bacillus virus PBS1	GCA_002601325.1
QCG76077.1	000043	REase+MOM	538	EST35_0196	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
prevph1000000072	000043	REase+MOM	552	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000073	000043	REase+MOM	566	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000057	000043	REase+MOM	552	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000058	000043	REase+MOM	566	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000150	000044	HTH+REase	606	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000826	000044	HTH+REase	197	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000113	000044	HTH+REase	606	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000569	000044	HTH+REase	553	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QAX97689.1	000045	HTH+REase	432	ASswx1_43	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39413.1	000045	HTH+REase	307	CC2_293	Aeromonas phage CC2	GCA_000903495.1
AFN39330.1	000045	HTH+REase	362	CC2_068	Aeromonas phage CC2	GCA_000903495.1
APU01695.1	000045	HTH+REase	439	-	Aeromonas phage 65.2	GCA_002618145.1
QAX97931.1	000045	HTH+REase	316	ASswx1_288	Aeromonas phage Asswx_1	GCA_004146865.1
ATI17246.1	000045	HTH+REase	520	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00341.1	000045	HTH+REase	576	HWB28_gp211	Aeromonas phage AS-zj	GCA_002627665.1
QIG62757.1	000045	HTH+REase	373	SEPL_144	Salmonella phage SE_PL	GCA_011067555.1
AFC21749.1	000045	HTH+REase	245	GAP32_299	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44368.1	000045	HTH+REase	408	RaK2_00095	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18979.1	000045	HTH+REase	363	7t3_0458	Salmonella phage 7t3	GCA_006083215.1
ADQ53334.1	000046	HTH+REase	323	65p326	Aeromonas virus 65	GCA_000893255.1
AND75469.1	000046	HTH+REase	243	ME3_308	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
CCE26203.1	000046	HTH+REase	310	g179	Yersinia phage phiR1-37	GCA_000895615.1
AZU98218.1	000046	HTH+REase	318	CPT_Munch_274	Salmonella phage Munch	GCA_004015485.1
QNI20980.1	000046	HTH+REase	362	-	Vibrio phage vB_pir03	GCA_014319855.1
AST99856.1	000046	HTH+REase	302	PBI_PBS1_34	Bacillus virus PBS1	GCA_002601325.1
AMS01231.1	000046	HTH+REase	302	AR9_g147	Bacillus phage AR9	GCA_001743835.1
ASU00093.1	000046	HTH+REase	343	PBI_PBS1_271	Bacillus virus PBS1	GCA_002601325.1
ALN97828.1	000046	HTH+REase	305	Bp8pS_149	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
CCE26336.1	000046	HTH+REase	248	g313	Yersinia phage phiR1-37	GCA_000895615.1
QAX96128.1	000046	HTH+REase	234	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
SOK58400.1	000046	HTH+REase	310	g123	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASU00092.1	000046	HTH+REase	320	PBI_PBS1_270	Bacillus virus PBS1	GCA_002601325.1
AFC21724.1	000046	HTH+REase	302	GAP32_274	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QAX97082.1	000046	HTH+REase	362	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
AMS01163.1	000046	HTH+REase	274	AR9_g079	Bacillus phage AR9	GCA_001743835.1
AIT14474.1	000046	HTH+REase	254	PBI_121Q_584	Escherichia phage 121Q	GCA_000926855.1
QAX96763.1	000046	HTH+REase	362	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96446.1	000046	HTH+REase	362	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
CCE26359.1	000046	HTH+REase	282	g336	Yersinia phage phiR1-37	GCA_000895615.1
prev15ph1000000340	000046	HTH+REase	291	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000440	000046	HTH+REase	375	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXC36565.1	000047	ASwh1_70	487	-	Escherichia phage UB	GCA_003341455.1
AIT14111.1	000047	ASwh1_70	487	PBI_121Q_221	Escherichia phage 121Q	GCA_000926855.1
AND75163.1	000047	ASwh1_70	217	ME3_2	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AGC34986.1	000047	ASwh1_70	379	ACQ29_gp306	Escherichia phage PBECO4	GCA_001041035.1
QAY01136.1	000048	ASwh1_70+REase	320	ASwh1_70	Aeromonas phage Aswh_1	GCA_004146945.1
ASU00506.1	000048	ASwh1_70+REase	313	HWB28_gp046	Aeromonas phage AS-zj	GCA_002627665.1
ATI17491.1	000048	ASwh1_70+REase	313	-	Aeromonas phage AS-szw	GCA_002743635.1
ADQ52976.1	000048	ASwh1_70+REase	329	PX29p257	Aeromonas phage PX29	GCA_000920195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATI17394.1	000048	ASwh1_70+REase	278	-	Aeromonas phage AS-szw	GCA_002743635.1
BBM62166.1	000048	ASwh1_70+REase	365	EO157G_5770	Escherichia phage SP27	GCA_008033345.1
AFA44761.1	000048	ASwh1_70+REase	274	RaK2_00488	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44547.1	000048	ASwh1_70+REase	398	RaK2_00274	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
SCA80478.1	000048	ASwh1_70+REase	307	PSLUR01_00501	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QAX96381.1	000048	ASwh1_70+REase	373	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBO61809.1	000048	ASwh1_70+REase	307	G17_00320	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QAX96063.1	000048	ASwh1_70+REase	373	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAY00811.1	000048	ASwh1_70+REase	447	Ecwhy1_538	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00455.1	000048	ASwh1_70+REase	305	Ecwhy1_175	Escherichia phage Ecwhy_1	GCA_004146585.1
QAX97017.1	000048	ASwh1_70+REase	373	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
AON97220.1	000048	ASwh1_70+REase	241	E_212	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
QAX96699.1	000048	ASwh1_70+REase	373	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QDF13853.1	000048	ASwh1_70+REase	365	vBEcoMphAPEC6_gp224c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80104.1	000048	ASwh1_70+REase	628	PSLUR01_00127	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44388.1	000048	ASwh1_70+REase	382	RaK2_00115	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AZU98228.1	000048	ASwh1_70+REase	304	CPT_Munch_284	Salmonella phage Munch	GCA_004015485.1
QDF13650.1	000048	ASwh1_70+REase	628	vBEcoMphAPEC6_gp019c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AXC36769.1	000048	ASwh1_70+REase	365	-	Escherichia phage UB	GCA_003341455.1
AIT14494.1	000048	ASwh1_70+REase	365	PBI_121Q_604	Escherichia phage 121Q	GCA_000926855.1
QMV29092.1	000049	REase	178	AP1_0385	Aeromonas phage AP1	GCA_014183365.1
AGS82065.1	000050	REase	274	PaBG_00189	Pseudomonas phage PaBG	GCA_000912555.1
AGS82050.1	000050	REase	167	PaBG_00174	Pseudomonas phage PaBG	GCA_000912555.1
QAU04553.1	000050	REase	298	ValB1MD_269	Vibrio phage ValB1MD	GCA_004138815.1
AMS01317.1	000050	REase	238	AR9_g233	Bacillus phage AR9	GCA_001743835.1
ALN97867.1	000050	REase	314	Bp8pS_188	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97967.1	000050	REase	238	Bp8pS_288	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AFA44772.1	000050	REase	341	RaK2_00499	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AST99946.1	000050	REase	238	PBI_PBS1_124	Bacillus virus PBS1	GCA_002601325.1
QBO61588.1	000050	REase	372	G17_00092	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QIG63480.1	000050	REase	400	DAC16_251	Bacteroides phage DAC16	GCA_013387695.1
BAE47738.1	000050	REase	107	CST040	Clostridium phage c-st	GCA_000865225.1
SOK58935.1	000050	REase	154	g127	Yersinia phage fHe-Yen9-03	GCA_002990515.1
CCE26260.1	000050	REase	236	g237	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000825	000050	REase	356	-	Prevotella_phage_Lak-B8	GCA_004379655.1
CCE26093.1	000051	AP2	217	g069	Yersinia phage phiR1-37	GCA_000895615.1
AMM43910.1	000051	AP2	210	CBB_347	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QAX96574.1	000051	AP2	253	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63384.1	000051	AP2	252	DAC16_153	Bacteroides phage DAC16	GCA_013387695.1
QAX96349.1	000051	AP2	308	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ALY07069.1	000051	AP2	169	VmeM32_00078	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96256.1	000051	AP2	253	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96031.1	000051	AP2	308	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX97197.1	000051	AP2	253	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96985.1	000051	AP2	308	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96892.1	000051	AP2	253	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96667.1	000051	AP2	308	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
AFC21632.1	000051	AP2	81	GAP32_182	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AOO14993.1	000051	AP2	196	W1230910_147	Cyanophage S-RIM14	GCA_002599125.1
AFC21805.1	000051	AP2	208	GAP32_355	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AOO14344.1	000051	AP2	196	Sn110110_150	Cyanophage S-RIM14	GCA_002599065.1
QIG62825.1	000051	AP2	205	SEPL_212	Salmonella phage SE_PL	GCA_011067555.1
AMM43747.1	000051	AP2	202	CBB_182	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43628.1	000051	AP2	202	CBB_63	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ALP47448.1	000051	AP2	200	phiST2_0022	Vibrio phage phi-ST2	GCA_002757135.1
BBI90487.1	000051	AP2	118	HYO65_gp095	Tenacibaculum phage PTm1	GCA_009730695.1
ALY07101.1	000051	AP2	201	VmeM32_00114	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07127.1	000051	AP2	200	VmeM32_00140	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07205.1	000051	AP2	202	VmeM32_00219	Vibrio phage vB_VmeM-32	GCA_002608825.1
QCW18902.1	000051	AP2	205	7t3_0381	Salmonella phage 7t3	GCA_006083215.1
AZU98159.1	000051	AP2	205	CPT_Munch_215	Salmonella phage Munch	GCA_004015485.1
BBI90795.1	000051	AP2	118	-	Tenacibaculum phage PTm5	GCA_009730715.1
ALY07028.1	000051	AP2	169	VmeM32_00034	Vibrio phage vB_VmeM-32	GCA_002608825.1
SOK59036.1	000052	REase+HTH	384	g228	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58501.1	000052	REase+HTH	384	g224	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ATI17363.1	000053	MOM	219	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00231.1	000053	MOM	219	HWB28_gp321	Aeromonas phage AS-zj	GCA_002627665.1
QAX98625.1	000053	MOM	294	ASfcp2_292	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52765.1	000053	MOM	294	PX29p046	Aeromonas phage PX29	GCA_000920195.1
AGH07589.1	000053	MOM	207	CYVG_00145	Cyanophage S-SSM6a	GCA_002710385.1
AFA44422.1	000053	MOM	194	RaK2_00149	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
SOK58442.1	000054	REase	345	g165	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58976.1	000054	REase	345	g168	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AMM44079.1	000054	REase	324	CBB_516	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AXC36582.1	000054	REase	257	-	Escherichia phage UB	GCA_003341455.1
AFC21953.1	000054	REase	324	GAP32_494	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QNI21110.1	000054	REase	153	-	Vibrio phage vB_pir03	GCA_014319855.1
ADQ53333.1	000055	Cluster3573_1clades	73	65p325	Aeromonas virus 65	GCA_000893255.1
BBI90630.1	000055	Cluster3573_1clades	351	HYO65_gp238	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90936.1	000055	Cluster3573_1clades	351	-	Tenacibaculum phage PTm5	GCA_009730715.1
AFC21631.1	000055	Cluster3573_1clades	123	GAP32_181	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
prevph1000000017	000055	Cluster3573_1clades	204	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000313	000055	Cluster3573_1clades	89	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000409	000055	Cluster3573_1clades	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000620	000055	Cluster3573_1clades	284	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000015	000055	Cluster3573_1clades	391	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000243	000055	Cluster3573_1clades	370	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000324	000055	Cluster3573_1clades	379	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000439	000055	Cluster3573_1clades	337	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000565	000055	Cluster3573_1clades	130	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000570	000055	Cluster3573_1clades	407	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFA44358.1	000056	REase	343	RaK2_00085	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFC21703.1	000057	T5orf172	103	GAP32_253	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14496.1	000057	T5orf172	102	PBI_121Q_606	Escherichia phage 121Q	GCA_000926855.1
QAY00453.1	000057	T5orf172	102	Ecwhy1_173	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35196.1	000057	T5orf172	107	ACQ29_gp516	Escherichia phage PBECO4	GCA_001041035.1
BBM62168.1	000057	T5orf172	102	EO157G_5790	Escherichia phage SP27	GCA_008033345.1
AXC36767.1	000057	T5orf172	102	-	Escherichia phage UB	GCA_003341455.1
QBO61807.1	000057	T5orf172	102	G17_00318	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13851.1	000057	T5orf172	102	vBEcoMphAPEC6_gp222c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80480.1	000057	T5orf172	102	PSLUR01_00503	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43823.1	000057	T5orf172	103	CBB_259	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18982.1	000057	T5orf172	102	7t3_0461	Salmonella phage 7t3	GCA_006083215.1
AZU98230.1	000057	T5orf172	102	CPT_Munch_286	Salmonella phage Munch	GCA_004015485.1
QIG62754.1	000057	T5orf172	102	SEPL_141	Salmonella phage SE_PL	GCA_011067555.1
AQW88782.1	000057	T5orf172	103	BF_0257	Serratia phage BF	GCA_002619745.1
SOK59063.1	000057	T5orf172	103	g255	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58529.1	000057	T5orf172	103	g252	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95154.1	000058	T5orf172	94	FDI40_gp395	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGR47804.2	000058	T5orf172	96	SmphiM12_172	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13020.1	000058	T5orf172	96	PHIM19_114	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12660.1	000058	T5orf172	96	PHIM7_113	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13392.1	000058	T5orf172	96	PHIN3_127	Sinorhizobium phage phiN3	GCA_001501175.1
BBI90597.1	000059	T5orf172	106	HYO65_gp205	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90904.1	000059	T5orf172	106	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25563.1	000059	T5orf172	107	BPT24_258	Tenacibaculum phage pT24	GCA_002611925.1
prev15ph1000000516	000059	T5orf172	114	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
CCH63588.1	000000	SIG+T5orf172	421	CP21_126	Campylobacter virus CP21	GCA_000902535.1
AOO14982.1	000000	SIG+T5orf172	128	W1230910_136	Cyanophage S-RIM14	GCA_002599125.1
QAX98432.1	000000	T5orf172	195	ASfcp2_88	Aeromonas phage AsFcp_2	GCA_004146885.1
AND75366.1	000000	T5orf172	108	ME3_205	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ASV44151.1	000000	SIG+T5orf172	95	PBI_SCTP2_136	Salicola phage SCTP-2	GCA_002625545.1
AYD81344.1	000060	T5orf172	100	SEA_JUSTBECAUSE_179	Streptomyces phage JustBecause	GCA_003613775.1
QJD53747.1	000060	T5orf172	100	SEA_KELA_177	Streptomyces phage Kela	GCA_012934305.1
QBZ72073.1	000060	T5orf172	104	SEA_KRADAL_177	Streptomyces phage Kradal	GCA_004799925.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH66336.1	000060	T5orf172	227	SEA_SATIS_177	Streptomyces phage Satis	GCA_003366315.1
QBX06539.1	000061	GIY-YIG+T5orf172	301	BcepSaruman_126	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74505.1	000061	GIY-YIG+T5orf172	301	BcepSauron_125	Burkholderia phage BcepSauron	GCA_005394215.1
AFC21701.1	000000	T5orf172	77	GAP32_251	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXF51255.1	000062	HNH	156	WELLINGTON_125	Erwinia phage Wellington	GCA_003344985.1
ANH52334.1	000062	HNH	270	DM_234	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANZ49606.1	000062	HNH	217	KWAN_254	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86660.1	000062	HNH	270	MADMEL_232	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
BAW18975.1	000062	HNH	133	FDH28_gp001	Ralstonia phage RP12	GCA_002617345.1
ATA65426.1	000062	HNH	198	2050HW_00091	Serratia phage 2050HW	GCA_002628125.1
QDB71202.1	000062	HNH	198	CPT_Moabite_172	Serratia phage Moabite	GCA_006384735.1
QFP93153.1	000062	HNH	210	-	Serratia phage PCH45	GCA_009187865.1
QFP93154.1	000062	HNH	213	-	Serratia phage PCH45	GCA_009187865.1
BAW19356.1	000062	HNH	263	-	Ralstonia phage RP31	GCA_002617365.1
BAW19071.1	000062	HNH	263	FDH28_gp097	Ralstonia phage RP12	GCA_002617345.1
AFN39352.1	000063	HNH+AP2	210	CC2_121	Aeromonas phage CC2	GCA_000903495.1
AMS01274.1	000063	HNH+AP2	225	AR9_g190	Bacillus phage AR9	GCA_001743835.1
AST99901.1	000063	HNH+AP2	225	PBI_PBS1_79	Bacillus virus PBS1	GCA_002601325.1
AON97080.1	000063	HNH+AP2	178	E_071	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARB13697.1	000063	HNH+AP2	167	Ccr10_gp167c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14042.1	000063	HNH+AP2	167	Ccr2_gp166c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14729.1	000063	HNH+AP2	167	Ccr29_gp173	Caulobacter phage Ccr29	GCA_002619485.1
ARB15084.1	000063	HNH+AP2	167	Ccr32_gp166	Caulobacter phage Ccr32	GCA_002619505.1
ARB15418.1	000063	HNH+AP2	167	Ccr34_gp176	Caulobacter phage Ccr34	GCA_002619525.1
ARB14385.1	000063	HNH+AP2	167	Ccr5_gp165c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68367.1	000063	HNH+AP2	166	CcrBL10_gp163c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87690.1	000063	HNH+AP2	167	CcrKarma_gp173	Caulobacter virus Karma	GCA_000901575.1
AFU87339.1	000063	HNH+AP2	167	CcrMagneto_gp169	Caulobacter virus Magneto	GCA_000903095.1
AFU86650.1	000063	HNH+AP2	166	CcrRogue_gp168	Caulobacter virus Rogue	GCA_000900555.1
AFU88486.1	000063	HNH+AP2	167	CcrSwift_gp168	Caulobacter virus Swift	GCA_000899655.1
AFU87003.1	000063	HNH+AP2	167	CbK_gp171	Caulobacter virus phiCbK	GCA_000900535.1
AFC21950.1	000063	HNH+AP2	169	GAP32_491	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97075.1	000063	HNH+AP2	162	E_066	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97077.1	000063	HNH+AP2	179	E_068	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97136.1	000063	HNH+AP2	178	E_128	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78549.1	000063	HNH+AP2	165	RB43ORF027c	Escherichia virus RB43	GCA_000863505.1
AAX78615.1	000063	HNH+AP2	170	RB43ORF093w	Escherichia virus RB43	GCA_000863505.1
AAX78782.1	000063	HNH+AP2	168	RB43ORF260w	Escherichia virus RB43	GCA_000863505.1
QIG65803.1	000063	HNH+AP2	186	phiOC_p138	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65918.1	000063	HNH+AP2	177	phiOC_p269	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ABY62868.1	000063	HNH+AP2	273	201phi2-1p035	Pseudomonas phage 201phi2-1	GCA_000875305.1
BAG41778.1	000063	HNH+AP2	180	RSL1_ORF332	Ralstonia phage phiRSL1	GCA_000879455.1
AGR47930.1	000063	HNH+AP2	185	SmphiM12_298	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13130.1	000063	HNH+AP2	185	PHIM19_225	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12769.1	000063	HNH+AP2	185	PHIM7_224	Sinorhizobium phage phiM7	GCA_002622405.1
QCW23013.1	000063	HNH+AP2	160	-	Synechococcus phage S-B05	GCA_006083695.1
AXH70992.1	000000	AP2	182	-	Vibrio phage BONAISHI	GCA_003441475.1
AGS82192.1	000000	AP2	183	PaBG_00321	Pseudomonas phage PaBG	GCA_000912555.1
ATA65665.1	000064	HINT	299	2050HW_00330	Serratia phage 2050HW	GCA_002628125.1
QBX32389.1	000064	HINT	347	-	Pseudomonas phage PA1C	GCA_004785505.1
BAW98221.1	000065	D6	694	FDH33_gp012	Vibrio phage pTD1	GCA_002618825.1
QDB70380.1	000065	D6	1064	CF8_0211	Aeromonas phage CF8	GCA_006384595.2
QFR59355.1	000065	D6	708	PS2_0213	Aeromonas phage PS2	GCA_009388305.2
QBZ70764.1	000065	D6	670	pETSU_183	Edwardsiella virus pEt-SU	GCA_004800915.1
QBJ02797.1	000065	D6	716	PSA21_271	Pseudomonas phage Psa21	GCA_004340405.1
QBO63953.1	000065	D6	693	Goslar_00160	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QHB49872.1	000065	D6	663	PS1_0211	Aeromonas phage PS1	GCA_007051165.2
ARV76927.1	000065	D6	707	PHABIO_296	Pseudomonas phage Phabio	GCA_002624965.1
ANM45002.1	000065	D6	703	KTN4_244	Pseudomonas phage KTN4	GCA_002607225.1
ANH52234.1	000065	D6	707	DM_136	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86560.1	000065	D6	707	MADMEL_132	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
BAW19429.1	000065	D6	751	-	Ralstonia phage RP31	GCA_002617365.1
QDH47027.1	000065	D6	708	LAh10_134	Aeromonas phage LAh10	GCA_006863975.1
QCW23112.1	000065	D6	693	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUG85919.1	000065	D6	707	BOSOLAPHORUS_132	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86884.1	000065	D6	707	MORTIMER_135	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
QBP07239.1	000065	D6	707	REBECCA_132	Erwinia phage Rebecca	GCA_004521635.1
ARV77396.1	000065	D6	732	NOXIFER_231	Pseudomonas phage Noxifer	GCA_002625005.1
AHI60281.1	000065	D6	707	Ea357_130	Erwinia phage Ea35-70	GCA_000914635.1
QAX96561.1	000065	D6	738	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANH51912.1	000065	D6	707	RAY_131	Erwinia phage vB_EamM_RAY	GCA_002624345.1
QDB71116.1	000065	D6	641	CPT_Moabite_086	Serratia phage Moabite	GCA_006384735.1
QAX96243.1	000065	D6	738	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QDH47404.1	000065	D6	690	HWC35_gp010	Vibrio phage USC-1	GCA_006864065.1
ANH51596.1	000065	D6	707	SIMMY50_134	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
QNI21145.1	000065	D6	656	-	Vibrio phage vB_pir03	GCA_014319855.1
AUR80929.1	000065	D6	693	Aphrodite1_0019	Vibrio phage Aphrodite1	GCA_002958015.1
QDJ97379.1	000065	D6	708	D6_0220	Aeromonas phage D6	GCA_007051205.2
QGH72071.1	000065	D6	699	N1M2_208	Klebsiella phage N1M2	GCA_010092605.1
QKE54434.1	000065	D6	710	ACSA002_1200	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ANJ64943.1	000065	D6	707	SPECIALG_133	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QAX97184.1	000065	D6	738	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
AUG86238.1	000065	D6	707	DESERTFOX_131	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
BAW19143.1	000065	D6	751	FDH28_gp252	Ralstonia phage RP12	GCA_002617345.1
ABY63126.1	000065	D6	710	201phi2-1p300	Pseudomonas phage 201phi2-1	GCA_000875305.1
QAX96879.1	000065	D6	738	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
ASU03459.1	000065	D6	682	RISINGSUN_211	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65689.1	000065	D6	592	2050HW_00354	Serratia phage 2050HW	GCA_002628125.1
AAL83104.1	000065	D6	703	PHIKZ203	Pseudomonas virus phiKZ	GCA_000842965.1
AEV89700.1	000065	D6	706	OBP_263	Pseudomonas phage OBP	GCA_000896635.1
QJB22880.1	000065	D6	695	fnug_237	Pseudomonas phage fnug	GCA_012837215.1
QBX32388.1	000065	D6	723	-	Pseudomonas phage PA1C	GCA_004785505.1
QMP24061.1	000065	D6	703	-	Proteus phage 10	GCA_014071245.1
AXH70908.1	000065	D6	699	-	Vibrio phage BONAISHI	GCA_003441475.1
ASU03702.1	000065	D6	682	JOAD_213	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49690.1	000066	Rpo-Rad25-Helicase	568	MACHINA_52	Erwinia phage Machina	GCA_002758035.1
AFO71257.1	000066	Rpo-Rad25-Helicase	566	CR5_037	Cronobacter phage CR5	GCA_000910235.1
AUG86038.1	000066	Rpo-Rad25-Helicase	515	BOSOLAPHORUS_252	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AST99866.1	000066	Rpo-Rad25-Helicase	477	PBI_PBS1_44	Bacillus virus PBS1	GCA_002601325.1
ARV76745.1	000066	Rpo-Rad25-Helicase	510	PHABIO_114	Pseudomonas phage Phabio	GCA_002624965.1
AMS01240.1	000066	Rpo-Rad25-Helicase	477	AR9_g156	Bacillus phage AR9	GCA_001743835.1
AXH70826.1	000066	Rpo-Rad25-Helicase	513	-	Vibrio phage BONAISHI	GCA_003441475.1
BAW19241.1	000066	Rpo-Rad25-Helicase	494	FDH28_gp154	Ralstonia phage RP12	GCA_002617345.1
ANZ50228.1	000066	Rpo-Rad25-Helicase	565	PHOBOS_38	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANJ65065.1	000066	Rpo-Rad25-Helicase	515	SPECIALG_254	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ49963.1	000066	Rpo-Rad25-Helicase	568	PARSHIK_54	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AWN09059.1	000066	Rpo-Rad25-Helicase	568	MLDJOKPK_00129	Salmonella phage SPAsTU	GCA_003183805.1
ANH52355.1	000066	Rpo-Rad25-Helicase	515	DM_256	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86358.1	000066	Rpo-Rad25-Helicase	515	DESERTFOX_251	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AGX01728.1	000066	Rpo-Rad25-Helicase	506	CF95_gp006	Erwinia phage PhiEaH1	GCA_000914555.1
ALN97900.1	000066	Rpo-Rad25-Helicase	476	Bp8pS_221	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QEM41801.1	000066	Rpo-Rad25-Helicase	360	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ASU03625.1	000066	Rpo-Rad25-Helicase	510	RISINGSUN_45	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03870.1	000066	Rpo-Rad25-Helicase	510	JOAD_45	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49135.1	000066	Rpo-Rad25-Helicase	568	HUXLEY_53	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
AEP83869.1	000066	Rpo-Rad25-Helicase	568	SPN3US_0036	Salmonella phage SPN3US	GCA_001042275.1
QAU04351.1	000066	Rpo-Rad25-Helicase	510	HWC03_gp196	Vibrio phage 2 TSL-2019	GCA_006964105.1
AHI60400.1	000066	Rpo-Rad25-Helicase	515	Ea357_247	Erwinia phage Ea35-70	GCA_000914635.1
ANZ48888.1	000066	Rpo-Rad25-Helicase	566	EARLPHILLIPIV_38	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANH52030.1	000066	Rpo-Rad25-Helicase	515	RAY_250	Erwinia phage vB_EamM_RAY	GCA_002624345.1
AUG87004.1	000066	Rpo-Rad25-Helicase	515	MORTIMER_256	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
BAQ02734.2	000066	Rpo-Rad25-Helicase	522	-	Ralstonia phage RSL2	GCA_001503055.1
QBJ02606.1	000066	Rpo-Rad25-Helicase	508	PSA21_77	Pseudomonas phage Psa21	GCA_004340405.1
ANH51713.1	000066	Rpo-Rad25-Helicase	515	SIMMY50_255	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
QDB71088.1	000066	Rpo-Rad25-Helicase	505	CPT_Moabite_056	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48614.1	000066	Rpo-Rad25-Helicase	566	CHRISDB_52	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
BAS05004.2	000066	Rpo-Rad25-Helicase	529	AVU11_gp212	Ralstonia phage RSF1	GCA_001500875.1
ANZ48341.1	000066	Rpo-Rad25-Helicase	566	CAITLIN_46	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ATA65666.1	000066	Rpo-Rad25-Helicase	552	2050HW_00331	Serratia phage 2050HW	GCA_002628125.1
AEH03492.1	000066	Rpo-Rad25-Helicase	510	068	Pseudomonas phage PhiPA3	GCA_001502095.1
QBO63957.1	000066	Rpo-Rad25-Helicase	524	Goslar_00164	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QKE54576.1	000066	Rpo-Rad25-Helicase	699	ACSA002_2600	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ANZ50476.1	000066	Rpo-Rad25-Helicase	568	STRATTON_51	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AUG86680.1	000066	Rpo-Rad25-Helicase	515	MADMEL_253	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
ABY62963.1	000066	Rpo-Rad25-Helicase	487	201phi2-1p131	Pseudomonas phage 201phi2-1	GCA_000875305.1
AQT28163.1	000066	Rpo-Rad25-Helicase	457	pVa21_222	Vibrio phage pVa-21	GCA_002619305.1
BAW98322.1	000066	Rpo-Rad25-Helicase	510	FDH33_gp113	Vibrio phage pTD1	GCA_002618825.1
ANZ48066.1	000066	Rpo-Rad25-Helicase	568	ASESINO_53	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AFQ96764.1	000066	Rpo-Rad25-Helicase	568	G173_gp219	Erwinia phage phiEaH2	GCA_000902915.1
QCW23225.1	000066	Rpo-Rad25-Helicase	510	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AXF51179.1	000066	Rpo-Rad25-Helicase	565	WELLINGTON_48	Erwinia phage Wellington	GCA_003344985.1
QAX96668.1	000066	Rpo-Rad25-Helicase	506	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96350.1	000066	Rpo-Rad25-Helicase	506	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96032.1	000066	Rpo-Rad25-Helicase	506	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QFP93072.1	000066	Rpo-Rad25-Helicase	508	-	Serratia phage PCH45	GCA_009187865.1
QDH47503.1	000066	Rpo-Rad25-Helicase	510	HWC35_gp109	Vibrio phage USC-1	GCA_006864065.1
QGZ14385.1	000066	Rpo-Rad25-Helicase	510	HWC77_gp022	Photobacterium phage PDCC-1	GCA_009800445.1
AEV89521.1	000066	Rpo-Rad25-Helicase	514	OBP_084	Pseudomonas phage OBP	GCA_000896635.1
AUR80951.1	000066	Rpo-Rad25-Helicase	472	Aphrodite1_0120	Vibrio phage Aphrodite1	GCA_002958015.1
QBP07464.1	000066	Rpo-Rad25-Helicase	570	DERBICUS_38	Erwinia phage Derbicus	GCA_004521655.1
QAX96986.1	000066	Rpo-Rad25-Helicase	506	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
ARV77238.1	000066	Rpo-Rad25-Helicase	514	NOXIFER_67	Pseudomonas phage Noxifer	GCA_002625005.1
AMR59688.1	000066	Rpo-Rad25-Helicase	568	SEGD1_039	Enterobacteria phage SEGD1	GCA_002601865.1
BAW19527.1	000066	Rpo-Rad25-Helicase	517	-	Ralstonia phage RP31	GCA_002617365.1
QJB22733.1	000066	Rpo-Rad25-Helicase	512	fnug_90	Pseudomonas phage fnug	GCA_012837215.1
ATN94857.1	000066	Rpo-Rad25-Helicase	512	SL2_280	Pseudomonas phage SL2	GCA_002956015.1
AAL82976.1	000066	Rpo-Rad25-Helicase	537	PHIKZ075	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44856.1	000066	Rpo-Rad25-Helicase	512	KTN4_098	Pseudomonas phage KTN4	GCA_002607225.1
QDB70485.1	000066	Rpo-Rad25-Helicase	510	CF8_0074	Aeromonas phage CF8	GCA_006384595.2
QBZ70604.1	000066	Rpo-Rad25-Helicase	514	pETSU_023	Edwardsiella virus pEt-SU	GCA_004800915.1
QDH47043.1	000066	Rpo-Rad25-Helicase	519	LAh10_227	Aeromonas phage LAh10	GCA_006863975.1
CAG27134.1	000066	Rpo-Rad25-Helicase	760	PPEV_gp040	Pseudomonas phage EL	GCA_000866825.1
QBX32223.1	000066	Rpo-Rad25-Helicase	353	-	Pseudomonas phage PA1C	GCA_004785505.1
QGH71920.1	000066	Rpo-Rad25-Helicase	514	N1M2_57	Klebsiella phage N1M2	GCA_010092605.1
CCE26145.1	000066	Rpo-Rad25-Helicase	511	g121	Yersinia phage phiR1-37	GCA_000895615.1
QNI21072.1	000066	Rpo-Rad25-Helicase	462	-	Vibrio phage vB_pir03	GCA_014319855.1
QBX32222.1	000067	Rpo-Rad25-Helicase	163	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41800.1	000067	Rpo-Rad25-Helicase	145	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QKE54575.1	000000	Rpo-Rad25-Helicase	151	ACSA002_2590	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFR59462.1	000068	HINT+Rpo-Rad25-Helicase	713	PS2_0071	Aeromonas phage PS2	GCA_009388305.2
QNI20752.1	000068	HINT+Rpo-Rad25-Helicase	914	-	Salmonella phage JN03	GCA_014319805.1
QDJ96832.1	000068	HINT+Rpo-Rad25-Helicase	713	PS1_0073	Aeromonas phage PS1	GCA_007051165.2
QBP07356.1	000068	HINT+Rpo-Rad25-Helicase	860	REBECCA_251	Erwinia phage Rebecca	GCA_004521635.1
ANZ49400.1	000068	HINT+Rpo-Rad25-Helicase	907	KWAN_48	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QMP24167.1	000068	HINT+Rpo-Rad25-Helicase	861	-	Proteus phage 10	GCA_014071245.1
QKN85877.1	000068	HINT+Rpo-Rad25-Helicase	914	ACEC001_0390	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QDJ97225.1	000068	HINT+Rpo-Rad25-Helicase	861	D6_0065	Aeromonas phage D6	GCA_007051205.2
QEM41960.1	000069	HINT+D6	1049	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGZ14483.1	000069	HINT+D6	921	HWC77_gp120	Photobacterium phage PDCC-1	GCA_009800445.1
AEH03656.1	000069	HINT+D6	1056	233	Pseudomonas phage PhiPA3	GCA_001502095.1
CAG27260.1	000069	HINT+D6	940	PPEV_gp166	Pseudomonas phage EL	GCA_000866825.1
ATN94712.1	000069	HINT+D6	969	SL2_135	Pseudomonas phage SL2	GCA_002956015.1
QAU04251.1	000069	HINT+D6	921	HWC03_gp096	Vibrio phage 2 TSL-2019	GCA_006964105.1
AUR80915.1	000070	HINT+Terminase+coiled-coil	1071	Aphrodite1_0165	Vibrio phage Aphrodite1	GCA_002958015.1
CAG27133.1	000070	HINT+Terminase+coiled-coil	1036	PPEV_gp039	Pseudomonas phage EL	GCA_000866825.1
QDJ96766.1	000070	HINT+Terminase+coiled-coil	1122	PS1_0008	Aeromonas phage PS1	GCA_007051165.2
QFR59399.1	000070	HINT+Terminase+coiled-coil	1122	PS2_0008	Aeromonas phage PS2	GCA_009388305.2
QDH47014.1	000070	HINT+Terminase+coiled-coil	1113	LAh10_175	Aeromonas phage LAh10	GCA_006863975.1
QDH47552.1	000070	HINT+Terminase+coiled-coil	1071	HWC35_gp158	Vibrio phage USC-1	GCA_006864065.1
QGZ14552.1	000070	HINT+Terminase+coiled-coil	1070	HWC77_gp189	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04182.1	000070	HINT+Terminase+coiled-coil	1070	HWC03_gp027	Vibrio phage 2 TSL-2019	GCA_006964105.1
QGH72111.1	000070	HINT+Terminase+coiled-coil	1136	N1M2_248	Klebsiella phage N1M2	GCA_010092605.1
QCW23177.1	000070	HINT+Terminase+coiled-coil	1071	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
ASU03673.1	000070	HINT+Terminase+coiled-coil	1099	JOAD_242	Erwinia phage vB_EamM_Joad	GCA_002629065.1
QDB70421.1	000070	HINT+Terminase+coiled-coil	1128	CF8_0008	Aeromonas phage CF8	GCA_006384595.2
QDJ97427.1	000070	HINT+Terminase+coiled-coil	1113	D6_0001	Aeromonas phage D6	GCA_007051205.2
ASU03430.1	000070	HINT+Terminase+coiled-coil	1099	RISINGSUN_240	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27105.1	000070	HINT+Terminase+coiled-coil	1088	PPEV_gp011	Pseudomonas phage EL	GCA_000866825.1
QGT54881.1	000071	HINT+Terminase	880	b23_0267	Synechococcus phage B23	GCA_009745195.1
QGT54516.1	000071	HINT+Terminase	880	b3_0274	Synechococcus phage B3	GCA_009745215.1
AFA44384.1	000071	HINT+Terminase	889	RaK2_00111	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QAU04493.1	000072	REase+HINT+Terminase-LS	761	ValB1MD_136	Vibrio phage ValB1MD	GCA_004138815.1
BAW19286.1	000073	Terminase-LS	737	-	Ralstonia phage RP31	GCA_002617365.1
BAW18998.1	000073	Terminase-LS	737	FDH28_gp024	Ralstonia phage RP12	GCA_002617345.1
ANZ50429.1	000073	Terminase-LS	701	PHOBOS_239	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QMV29110.1	000073	Terminase-LS	106	AP1_0407	Aeromonas phage AP1	GCA_014183365.1
QNI21149.1	000073	Terminase-LS	321	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB71033.1	000073	Terminase-LS	704	CPT_Moabite_001	Serratia phage Moabite	GCA_006384735.1
ANZ49082.1	000073	Terminase-LS	701	EARLPHILLIPIV_233	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
QAY00437.1	000073	Terminase-LS	114	Ecwhy1_157	Escherichia phage Ecwhy_1	GCA_004146585.1
QBP07658.1	000073	Terminase-LS	701	DERBICUS_232	Erwinia phage Derbicus	GCA_004521655.1
QAX96919.1	000073	Terminase-LS	328	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
AFO71444.1	000073	Terminase-LS	701	CR5_224	Cronobacter phage CR5	GCA_000910235.1
ATA65607.1	000073	Terminase-LS	704	2050HW_00272	Serratia phage 2050HW	GCA_002628125.1
BAW98365.1	000073	Terminase-LS	777	FDH33_gp156	Vibrio phage pTD1	GCA_002618825.1
QAX97224.1	000073	Terminase-LS	328	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QBO64005.1	000073	Terminase-LS	743	Goslar_00213	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QAX96283.1	000073	Terminase-LS	328	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
AST99829.1	000073	Terminase-LS	201	PBI_PBS1_7	Bacillus virus PBS1	GCA_002601325.1
QAX96601.1	000073	Terminase-LS	328	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANZ48843.1	000073	Terminase-LS	703	CHRISDB_281	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48565.1	000073	Terminase-LS	703	CAITLIN_270	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
CCE26167.1	000073	Terminase-LS	210	g143	Yersinia phage phiR1-37	GCA_000895615.1
ARV76634.1	000073	Terminase-LS	738	PHABIO_3	Pseudomonas phage Phabio	GCA_002624965.1
ABY62839.1	000073	Terminase-LS	730	201phi2-1p005	Pseudomonas phage 201phi2-1	GCA_000875305.1
BAS04818.1	000073	Terminase-LS	726	AVU11_gp026	Ralstonia phage RSF1	GCA_001500875.1
ARV77174.1	000073	Terminase-LS	726	NOXIFER_3	Pseudomonas phage Noxifer	GCA_002625005.1
QBZ70813.1	000073	Terminase-LS	776	pETSU_232	Edwardsiella virus pEt-SU	GCA_004800915.1
QBP07292.1	000073	Terminase-LS	747	REBECCA_185	Erwinia phage Rebecca	GCA_004521635.1
ASV44708.1	000073	Terminase-LS	123	FDI40_gp110	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72830.1	000073	Terminase-LS	365	-	Myoviridae sp.	GCA_003657725.1
ASV44282.1	000073	Terminase-LS	297	PBI_SCTP2_267	Salicola phage SCTP-2	GCA_002625545.1
ADQ52931.1	000073	Terminase-LS	599	PX29p212	Aeromonas phage PX29	GCA_000920195.1
BAQ02551.1	000073	Terminase-LS	726	AVU38_gp023	Ralstonia phage RSL2	GCA_001503055.1
AAL82926.1	000073	Terminase-LS	717	PHIKZ025	Pseudomonas virus phiKZ	GCA_000842965.1
ANH51964.1	000073	Terminase-LS	731	RAY_183	Erwinia phage vB_EamM_RAY	GCA_002624345.1
AUG86937.1	000073	Terminase-LS	731	MORTIMER_188	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86613.1	000073	Terminase-LS	731	MADMEL_185	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
ANZ49636.1	000073	Terminase-LS	702	KWAN_284	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANH51648.1	000073	Terminase-LS	731	SIMMY50_186	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
AUG86291.1	000073	Terminase-LS	731	DESERTFOX_184	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANH52287.1	000073	Terminase-LS	731	DM_189	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ALY07096.1	000073	Terminase-LS	225	VmeM32_00107	Vibrio phage vB_VmeM-32	GCA_002608825.1
AUG85972.1	000073	Terminase-LS	731	BOSOLAPHORUS_185	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AXF51411.1	000073	Terminase-LS	702	WELLINGTON_285	Erwinia phage Wellington	GCA_003344985.1
AGX01793.1	000073	Terminase-LS	705	CF95_gp071	Erwinia phage PhiEaH1	GCA_000914555.1
QAX96736.1	000073	Terminase-LS	716	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
AQT28126.1	000073	Terminase-LS	706	pVa21_185	Vibrio phage pVa-21	GCA_002619305.1
AHI60333.1	000073	Terminase-LS	731	Ea357_181	Erwinia phage Ea35-70	GCA_000914635.1
QFP93056.1	000073	Terminase-LS	702	-	Serratia phage PCH45	GCA_009187865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX97055.1	000073	Terminase-LS	716	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96101.1	000073	Terminase-LS	716	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QKE54493.1	000073	Terminase-LS	726	ACSA002_1790	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QAX96419.1	000073	Terminase-LS	716	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21002.1	000073	Terminase-LS	729	-	Vibrio phage vB_pir03	GCA_014319855.1
CCH63587.1	000073	Terminase-LS	403	CP21_125	Campylobacter virus CP21	GCA_000902535.1
QMP24115.1	000073	Terminase-LS	733	-	Proteus phage 10	GCA_014071245.1
QEM41734.1	000073	Terminase-LS	728	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ALN97877.1	000073	Terminase-LS	658	Bp8pS_198	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ANJ64995.1	000073	Terminase-LS	731	SPECIALG_185	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANM44793.1	000073	Terminase-LS	717	KTN4_035	Pseudomonas phage KTN4	GCA_002607225.1
AEV89443.1	000073	Terminase-LS	780	OBP_006	Pseudomonas phage OBP	GCA_000896635.1
QDJ96428.1	000073	Terminase-LS	231	Xoosp13_242	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXH70782.1	000073	Terminase-LS	718	-	Vibrio phage BONAISHI	GCA_003441475.1
QBX32153.1	000073	Terminase-LS	729	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03433.1	000073	Terminase-LS	733	007	Pseudomonas phage PhiPA3	GCA_001502095.1
ASV44549.1	000073	Terminase-LS	130	PBI_SCTP2_534	Salicola phage SCTP-2	GCA_002625545.1
QBJ02537.1	000073	Terminase-LS	718	PSA21_7	Pseudomonas phage Psa21	GCA_004340405.1
ATN94918.1	000073	Terminase-LS	717	SL2_341	Pseudomonas phage SL2	GCA_002956015.1
QJB22672.1	000073	Terminase-LS	720	fnug_29	Pseudomonas phage fnug	GCA_012837215.1
AMR59913.1	000073	Terminase-LS	703	SEGD1_266	Enterobacteria phage SEGD1	GCA_002601865.1
QNI20943.1	000073	Terminase-LS	703	-	Salmonella phage JN03	GCA_014319805.1
AEP84093.1	000073	Terminase-LS	703	SPN3US_0260	Salmonella phage SPN3US	GCA_001042275.1
QKN86101.1	000073	Terminase-LS	703	ACEC001_2580	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AST99831.1	000073	Terminase-LS	404	PBI_PBS1_9	Bacillus virus PBS1	GCA_002601325.1
CCE26169.1	000073	Terminase-LS	469	g145	Yersinia phage phiR1-37	GCA_000895615.1
AMS01205.1	000073	Terminase-LS	653	AR9_g121	Bacillus phage AR9	GCA_001743835.1
ANZ48294.1	000073	Terminase-LS	702	ASESINO_281	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AFQ96723.1	000073	Terminase-LS	702	G173_gp178	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50181.1	000073	Terminase-LS	703	PARSHIK_272	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50705.1	000073	Terminase-LS	702	STRATTON_280	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ49353.1	000073	Terminase-LS	703	HUXLEY_271	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
AWN09093.1	000073	Terminase-LS	703	MLDJOKPK_00180	Salmonella phage SPAsTU	GCA_003183805.1
ANZ49910.1	000073	Terminase-LS	703	MACHINA_272	Erwinia phage Machina	GCA_002758035.1
AXH72905.1	000073	Terminase-LS	268	-	Myoviridae sp.	GCA_003657725.1
prev15ph1000000325	000073	Terminase-LS	721	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAV39261.1	000073	Terminase-LS	622	BPT24_136	Tenacibaculum phage pT24	GCA_002611925.1
ASV44707.1	000073	Terminase-LS	602	FDI40_gp109	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIW90369.1	000073	Terminase-LS	600	GCAPEGMB_00022	Vibrio phage V07	GCA_012361095.1
AGN30028.1	000073	Terminase-LS	600	VPFG_00020	Vibrio phage nt-1	GCA_000910195.2
AJT61130.1	000073	Terminase-LS	600	AVU32_gp289	Vibrio phage ValKK3	GCA_001501635.1
ALP46971.1	000073	Terminase-LS	600	phiGrn1_0089	Vibrio phage phi-Grn1	GCA_002757115.1
QIW91060.1	000073	Terminase-LS	600	COHAPHLL_00197	Vibrio phage V09	GCA_012361135.1
QHJ74538.1	000073	Terminase-LS	600	VH12019_00238	Vibrio phage VH1_2019	GCA_009931825.1
QNJ54743.1	000073	Terminase-LS	600	vBValMR10Z_203	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37587.1	000073	Terminase-LS	600	pp2_355	Vibriophage phi-pp2	GCA_002630725.1
QBX06118.1	000073	Terminase-LS	600	ValB1HC_164	Vibrio phage ValB1 HC	GCA_004771355.1
BBA65403.1	000073	Terminase-LS	548	-	Xanthomonas phage XacN1	GCA_003173815.1
ALP47351.1	000073	Terminase-LS	600	phiST2_0221	Vibrio phage phi-ST2	GCA_002757135.1
AAQ64424.1	000073	Terminase-LS	600	KVP40.0355	Vibrio phage KVP40	GCA_000843785.1
AFC21719.1	000073	Terminase-LS	549	GAP32_269	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AGR47745.1	000073	Terminase-LS	196	SmphiM12_113	Sinorhizobium phage phiM12	GCA_001023565.1
AEO93272.1	000073	Terminase-LS	560	G_1	Bacillus virus G	GCA_000917535.1
AKF12990.1	000073	Terminase-LS	196	PHIM19_83	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12630.1	000073	Terminase-LS	196	PHIM7_82	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13361.1	000073	Terminase-LS	194	PHIN3_97	Sinorhizobium phage phiN3	GCA_001501175.1
BBI90714.1	000073	Terminase-LS	614	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90405.1	000073	Terminase-LS	614	HYO65_gp013	Tenacibaculum phage PTm1	GCA_009730695.1
AFF28085.1	000073	Terminase-LS	734	PAU_87	Sphingomonas phage PAU	GCA_000902455.1
AXH72829.1	000073	Terminase-LS	313	-	Myoviridae sp.	GCA_003657725.1
ADQ52930.1	000073	Terminase-LS	406	PX29p211	Aeromonas phage PX29	GCA_000920195.1
AIT13901.1	000073	Terminase-LS	545	PBI_121Q_4	Escherichia phage 121Q	GCA_000926855.1
QAU04494.1	000073	Terminase-LS	386	ValB1MD_137	Vibrio phage ValB1MD	GCA_004138815.1
SOK59080.1	000073	Terminase-LS	546	g272	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58545.1	000073	Terminase-LS	546	g268	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QAX98470.1	000073	Terminase-LS	409	ASfcp2_130	Aeromonas phage AsFcp_2	GCA_004146885.1
AQW88798.1	000073	Terminase-LS	548	BF_0273	Serratia phage BF	GCA_002619745.1
SCA80496.1	000073	Terminase-LS	545	PSLUR01_00519	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDF13835.1	000073	Terminase-LS	545	vBEcoMphAPEC6_gp206c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QBO61791.1	000073	Terminase-LS	545	G17_00302	Escherichia phage vB_EcoM_G17	GCA_004521135.1
BBM61593.1	000073	Terminase-LS	545	EO157G_0040	Escherichia phage SP27	GCA_008033345.1
QAY00436.1	000073	Terminase-LS	445	Ecwhy1_156	Escherichia phage Ecwhy_1	GCA_004146585.1
AXC36752.1	000073	Terminase-LS	545	-	Escherichia phage UB	GCA_003341455.1
AMM43839.1	000073	Terminase-LS	549	CBB_275	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGC35180.1	000073	Terminase-LS	545	ACQ29_gp500	Escherichia phage PBECO4	GCA_001041035.1
ARM70726.1	000073	Terminase-LS	611	phiC120_c19	Escherichia phage phiC120	GCA_002621185.1
AAX78741.1	000073	Terminase-LS	609	RB43ORF219w	Escherichia virus RB43	GCA_000863505.1
APU01476.1	000073	Terminase-LS	642	-	Aeromonas phage 65.2	GCA_002618145.1
QHJ79052.1	000073	Terminase-LS	618	-	Myoviridae sp.	GCA_012593985.1
AGB06996.1	000073	Terminase-LS	576	CF80_gp209	Vibrio phage VH7D	GCA_000914495.1
QIG65739.1	000073	Terminase-LS	520	phiOC_p074	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26110.1	000073	Terminase-LS	560	CPMG_00009	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44506.1	000073	Terminase-LS	547	PSSM2_128	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12460.1	000073	Terminase-LS	547	PRTG_00313	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93438.1	000073	Terminase-LS	547	AVU42_gp098	Prochlorococcus phage P-TIM68	GCA_001503075.1
ALY06997.1	000073	Terminase-LS	704	VmeM32_00001	Vibrio phage vB_VmeM-32	GCA_002608825.1
ADO99217.1	000073	Terminase-LS	550	Syn1_116	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76085.1	000073	Terminase-LS	531	EST35_0204	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QMV28790.1	000073	Terminase-LS	509	AP1_0083	Aeromonas phage AP1	GCA_014183365.1
QCW18997.1	000073	Terminase-LS	543	7t3_0477	Salmonella phage 7t3	GCA_006083215.1
AZU98245.1	000073	Terminase-LS	543	CPT_Munch_301	Salmonella phage Munch	GCA_004015485.1
QIG62739.1	000073	Terminase-LS	543	SEPL_126	Salmonella phage SE_PL	GCA_011067555.1
AGG54497.1	000073	Terminase-LS	549	CYWG_00213	Cyanophage S-SSM6b	GCA_002710425.1
AGH07453.1	000073	Terminase-LS	552	CYVG_00009	Cyanophage S-SSM6a	GCA_002710385.1
AOO12998.1	000073	Terminase-LS	550	W2100709_116	Cyanophage S-RIM44	GCA_002599285.1
AOO12769.1	000073	Terminase-LS	550	Sn130910_122	Cyanophage S-RIM44	GCA_002599265.1
AOO12532.1	000073	Terminase-LS	550	Sn080709_115	Cyanophage S-RIM44	GCA_002599245.1
AOO12304.1	000073	Terminase-LS	550	Np420711_122	Cyanophage S-RIM44	GCA_002599225.1
AOO12068.1	000073	Terminase-LS	550	Np200711_122	Cyanophage S-RIM44	GCA_002599205.1
AOO11831.1	000073	Terminase-LS	550	Np050604_115	Cyanophage S-RIM44	GCA_002599185.1
AOO11603.1	000073	Terminase-LS	550	ES420910_122	Cyanophage S-RIM44	GCA_002599165.1
AMO43359.1	000073	Terminase-LS	550	W270710_115	Cyanophage S-RIM44	GCA_002599145.1
AMO43134.1	000073	Terminase-LS	549	R1080702_125	Cyanophage S-RIM32	GCA_001754165.1
AOO14955.1	000073	Terminase-LS	550	W1230910_109	Cyanophage S-RIM14	GCA_002599125.1
AOO14306.1	000073	Terminase-LS	550	Sn110110_112	Cyanophage S-RIM14	GCA_002599065.1
AJK27551.1	000073	Terminase-LS	549	PTIM40_124	Cyanophage P-TIM40	GCA_001470935.1
AGH56907.1	000073	Terminase-LS	557	CPXG_00104	Cyanophage P-RSM6	GCA_000906155.1
AON97223.1	000073	Terminase-LS	609	E_215	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGR47742.2	000073	Terminase-LS	543	SmphiM12_110	Sinorhizobium phage phiM12	GCA_001023565.1
AIA64887.1	000073	Terminase-LS	618	S13_088	Cronobacter phage S13	GCA_001503575.1
ANS05936.1	000073	Terminase-LS	609	ABCD_0208	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ATI17421.1	000073	Terminase-LS	639	-	Aeromonas phage AS-szw	GCA_002743635.1
AKF12989.1	000073	Terminase-LS	543	PHIM19_82	Sinorhizobium phage phiM19	GCA_002605865.1
AAQ17878.1	000073	Terminase-LS	633	17	Aeromonas virus Aeh1	GCA_000843245.1
ADQ53099.1	000073	Terminase-LS	642	65p089	Aeromonas virus 65	GCA_000893255.1
ADM79854.1	000073	Terminase-LS	633	phiAS5_ORF0011	Aeromonas phage phiAS5	GCA_000887715.1
AKF12629.1	000073	Terminase-LS	543	PHIM7_81	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13360.1	000073	Terminase-LS	543	PHIN3_96	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30609.1	000073	Terminase-LS	548	Syn7803US37_132	Synechococcus phage ACG-2014f	GCA_002594065.1
QDJ96427.1	000073	Terminase-LS	550	Xoosp13_241	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QJT70111.1	000073	Terminase-LS	549	SynMITS9220M01_098	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASR76169.1	000073	Terminase-LS	548	PBI_BELLAMY_124	Synechococcus phage Bellamy	GCA_002627525.1
QCW22879.1	000073	Terminase-LS	555	-	Synechococcus phage S-B05	GCA_006083695.1
AFN39543.1	000073	Terminase-LS	639	CC2_316	Aeromonas phage CC2	GCA_000903495.1
AXQ70583.1	000073	Terminase-LS	549	HOU04_gp184	Synechococcus phage S-T4	GCA_003443335.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY01289.1	000073	Terminase-LS	642	ASwh1_226	Aeromonas phage Aswh_1	GCA_004146945.1
QAX97861.1	000073	Terminase-LS	639	ASswx1_218	Aeromonas phage Asswx_1	GCA_004146865.1
QDH50478.1	000073	Terminase-LS	555	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59584.1	000073	Terminase-LS	550	S330809_123	Synechococcus phage S-CAM4	GCA_002366065.1
AUE22753.1	000073	Terminase-LS	633	Ah1_00235	Aeromonas phage Ah1	GCA_002957415.1
AOV59822.1	000073	Terminase-LS	550	N231010_123	Synechococcus phage S-CAM4	GCA_002922155.1
ASU00175.1	000073	Terminase-LS	639	HWB28_gp377	Aeromonas phage AS-zj	GCA_002627665.1
AOV59346.1	000073	Terminase-LS	550	C440309_123	Synechococcus phage S-CAM4	GCA_002922145.1
ASV44239.1	000073	Terminase-LS	694	PBI_SCTP2_224	Salicola phage SCTP-2	GCA_002625545.1
CCH63589.1	000073	Terminase-LS	261	CP21_127	Campylobacter virus CP21	GCA_000902535.1
ARB13854.1	000074	HINT+Terminase-LS	910	Ccr10_gp324	Caulobacter phage Ccr10	GCA_002619445.1
ARB14199.1	000074	HINT+Terminase-LS	910	Ccr2_gp323	Caulobacter phage Ccr2	GCA_002619465.1
ARB14893.1	000074	HINT+Terminase-LS	910	Ccr29_gp337	Caulobacter phage Ccr29	GCA_002619485.1
ARB15231.1	000074	HINT+Terminase-LS	910	Ccr32_gp313	Caulobacter phage Ccr32	GCA_002619505.1
ARB15565.1	000074	HINT+Terminase-LS	910	Ccr34_gp323	Caulobacter phage Ccr34	GCA_002619525.1
ARB14539.1	000074	HINT+Terminase-LS	910	Ccr5_gp319	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68523.1	000074	HINT+Terminase-LS	910	CcrBL10_gp319	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69541.1	000074	HINT+Terminase-LS	938	CcrBL9_gp517	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88318.1	000074	HINT+Terminase-LS	906	CcrColossus_gp448	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68989.1	000074	HINT+Terminase-LS	906	CcrPW_gp450	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70083.1	000074	HINT+Terminase-LS	938	CcrSC_gp501	Caulobacter phage CcrSC	GCA_003443315.1
AFU87850.1	000074	HINT+Terminase-LS	910	CcrKarma_gp333	Caulobacter virus Karma	GCA_000901575.1
AFU87498.1	000074	HINT+Terminase-LS	910	CcrMagneto_gp328	Caulobacter virus Magneto	GCA_000903095.1
AFU86813.1	000074	HINT+Terminase-LS	910	CcrRogue_gp331	Caulobacter virus Rogue	GCA_000900555.1
AFU88643.1	000074	HINT+Terminase-LS	910	CcrSwift_gp325	Caulobacter virus Swift	GCA_000899655.1
AFU87150.1	000074	HINT+Terminase-LS	910	CbK_gp318	Caulobacter virus phiCbK	GCA_000900535.1
ARB13528.1	000075	Terminase-LS	253	Ccr10_gp001	Caulobacter phage Ccr10	GCA_002619445.1
ARB13875.1	000075	Terminase-LS	230	Ccr2_gp001	Caulobacter phage Ccr2	GCA_002619465.1
ARB14920.1	000075	Terminase-LS	230	Ccr32_gp001	Caulobacter phage Ccr32	GCA_002619505.1
ARB15251.1	000075	Terminase-LS	230	Ccr34_gp001	Caulobacter phage Ccr34	GCA_002619525.1
ARB14219.1	000075	Terminase-LS	253	Ccr5_gp001	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68205.1	000075	Terminase-LS	194	CcrBL10_gp001	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69025.1	000075	Terminase-LS	123	CcrBL9_gp001	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69583.1	000075	Terminase-LS	229	CcrSC_gp001	Caulobacter phage CcrSC	GCA_003443315.1
QIG63461.1	000076	Terminase	555	DAC16_232	Bacteroides phage DAC16	GCA_013387695.1
QIG63724.1	000076	Terminase	555	DAC19_237	Bacteroides phage DAC19	GCA_013387715.1
QIG63985.1	000076	Terminase	555	DAC20_236	Bacteroides phage DAC20	GCA_013387725.1
QIG64249.1	000076	Terminase	555	DAC22_239	Bacteroides phage DAC22	GCA_013387735.1
QIG64505.1	000076	Terminase	555	DAC23_231	Bacteroides phage DAC23	GCA_013387745.1
QIG57807.1	000000	Terminase-LS	749	SEA_PAULODIABOLI_72	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIW90821.1	000000	Terminase-LS	476	GCAPEGMB_00506	Vibrio phage V07	GCA_012361095.1
ALY07097.1	000000	Terminase-LS	156	VmeM32_00108	Vibrio phage vB_VmeM-32	GCA_002608825.1
AND75174.1	000077	Terminase	760	ME3_13	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83675.1	000077	Terminase	635	0306phi8-36p117	Bacillus phage 0305phi8-36	GCA_000871045.1
QMV29102.1	000078	Terminase	244	AP1_0395	Aeromonas phage AP1	GCA_014183365.1
QIW90742.1	000078	Terminase	522	GCAPEGMB_00423	Vibrio phage V07	GCA_012361095.1
AUZ95386.1	000000	Terminase	244	FDI40_gp627	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARM70939.1	000000	Terminase	167	phiC120_c234	Escherichia phage phiC120	GCA_002621185.1
QHJ78949.1	000000	Terminase	166	-	Myoviridae sp.	GCA_012593985.1
prevph1000000411	000000	Terminase	95	-	Prevotella_phage_Lak-B8	GCA_004379655.1
BAE47866.1	000000	SIG+Terminase	580	CST168	Clostridium phage c-st	GCA_000865225.1
QDH83448.1	000079	Terminase	688	H1O15_gp040	Achromobacter phage Motura	GCA_006964305.1
QBX06657.1	000079	Terminase	752	BcepSaruman_244	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74625.1	000079	Terminase	734	BcepSauron_245	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67048.1	000079	Terminase	942	AD1_004	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79808.1	000079	Terminase	937	JA11_003	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66406.1	000079	Terminase	937	JA13_003	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66729.1	000079	Terminase	937	JA29_003	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67377.1	000079	Terminase	937	JA33_003	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08286.1	000079	Terminase	942	Alexandra_4	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58644.1	000079	Terminase	943	Y3_004	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28491.1	000079	Terminase	937	YOLOSWAG_4	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38263.1	000079	Terminase	678	BN7874_094	Phage NCTB	GCA_900092385.1
AFH14719.1	000079	Terminase	976	Lu11_0182	Pseudomonas phage Lu11	GCA_000897175.1
AGS81993.1	000079	Terminase	720	PaBG_00108	Pseudomonas phage PaBG	GCA_000912555.1
BAG41665.1	000079	Terminase	730	RSL1_ORF216	Ralstonia phage phiRSL1	GCA_000879455.1
AIT13900.1	000080	Terminase	227	PBI_121Q_3	Escherichia phage 121Q	GCA_000926855.1
QAY00438.1	000080	Terminase	228	Ecwhy1_158	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35181.1	000080	Terminase	227	ACQ29_gp501	Escherichia phage PBECO4	GCA_001041035.1
BBM61592.1	000080	Terminase	227	EO157G_0030	Escherichia phage SP27	GCA_008033345.1
AXC36753.1	000080	Terminase	227	-	Escherichia phage UB	GCA_003341455.1
QBO61792.1	000080	Terminase	227	G17_00303	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13836.1	000080	Terminase	227	vBEcoMphAPEC6_gp207c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80495.1	000080	Terminase	227	PSLUR01_00518	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44383.1	000080	Terminase	226	RaK2_00110	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFC21718.1	000081	Terminase	235	GAP32_268	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43838.1	000081	Terminase	235	CBB_274	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88797.1	000081	Terminase	236	BF_0272	Serratia phage BF	GCA_002619745.1
SOK59079.1	000081	Terminase	185	g271	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58544.1	000081	Terminase	185	g267	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD81189.1	000082	HINT+Terminase	789	SEA_JUSTBECAUSE_20	Streptomyces phage JustBecause	GCA_003613775.1
QJD53591.1	000082	HINT+Terminase	789	SEA_KELA_20	Streptomyces phage Kela	GCA_012934305.1
QBZ71922.1	000082	HINT+Terminase	788	SEA_KRADAL_23	Streptomyces phage Kradal	GCA_004799925.1
AXH66184.1	000082	HINT+Terminase	788	SEA_SATIS_23	Streptomyces phage Satis	GCA_003366315.1
AXF51285.1	000083	Terminase_6	391	WELLINGTON_156	Erwinia phage Wellington	GCA_003344985.1
ANZ49509.1	000083	Terminase_6	419	KWAN_157	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QIG57813.1	000084	Terminase-fragments	210	SEA_PAULODIABOLI_79	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57812.1	000084	Terminase-fragments	207	SEA_PAULODIABOLI_78	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57814.1	000084	Terminase-fragments	225	SEA_PAULODIABOLI_80	Microbacterium phage PauloDiaboli	GCA_011067425.1
ARB13853.1	000085	Terminase-SS	277	Ccr10_gp323	Caulobacter phage Ccr10	GCA_002619445.1
ARB14198.1	000085	Terminase-SS	277	Ccr2_gp322	Caulobacter phage Ccr2	GCA_002619465.1
ARB14892.1	000085	Terminase-SS	291	Ccr29_gp336	Caulobacter phage Ccr29	GCA_002619485.1
ARB15230.1	000085	Terminase-SS	291	Ccr32_gp312	Caulobacter phage Ccr32	GCA_002619505.1
ARB15564.1	000085	Terminase-SS	291	Ccr34_gp322	Caulobacter phage Ccr34	GCA_002619525.1
ARB14538.1	000085	Terminase-SS	277	Ccr5_gp318	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68522.1	000085	Terminase-SS	268	CcrBL10_gp318	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69537.1	000085	Terminase-SS	240	CcrBL9_gp513	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88317.1	000085	Terminase-SS	226	CcrColossus_gp447	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68988.1	000085	Terminase-SS	207	CcrPW_gp449	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70080.1	000085	Terminase-SS	240	CcrSC_gp498	Caulobacter phage CcrSC	GCA_003443315.1
AFU87849.1	000085	Terminase-SS	291	CcrKarma_gp332	Caulobacter virus Karma	GCA_000901575.1
AFU87497.1	000085	Terminase-SS	291	CcrMagneto_gp327	Caulobacter virus Magneto	GCA_000903095.1
AFU86812.1	000085	Terminase-SS	268	CcrRogue_gp330	Caulobacter virus Rogue	GCA_000900555.1
AFU88642.1	000085	Terminase-SS	291	CcrSwift_gp324	Caulobacter virus Swift	GCA_000899655.1
AFU87149.1	000085	Terminase-SS	291	CbK_gp317	Caulobacter virus phiCbK	GCA_000900535.1
QIW90738.1	000000	Terminase-SS	178	GCAPEGMB_00419	Vibrio phage V07	GCA_012361095.1
QIW90817.1	000000	Terminase-SS	138	GCAPEGMB_00502	Vibrio phage V07	GCA_012361095.1
APU01478.1	000086	Terminase-SS-DNA_Packaging	168	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17419.1	000086	Terminase-SS-DNA_Packaging	170	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00177.1	000086	Terminase-SS-DNA_Packaging	170	HWB28_gp375	Aeromonas phage AS-zj	GCA_002627665.1
AUE22752.1	000086	Terminase-SS-DNA_Packaging	172	Ah1_00234	Aeromonas phage Ah1	GCA_002957415.1
QAX98469.1	000086	Terminase-SS-DNA_Packaging	172	ASfcp2_129	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97859.1	000086	Terminase-SS-DNA_Packaging	170	ASswx1_216	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01291.1	000086	Terminase-SS-DNA_Packaging	168	ASwh1_228	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39544.1	000086	Terminase-SS-DNA_Packaging	170	CC2_318	Aeromonas phage CC2	GCA_000903495.1
ADQ52929.1	000086	Terminase-SS-DNA_Packaging	172	PX29p210	Aeromonas phage PX29	GCA_000920195.1
ADM79853.1	000086	Terminase-SS-DNA_Packaging	173	phiAS5_ORF0010	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53101.1	000086	Terminase-SS-DNA_Packaging	168	65p091	Aeromonas virus 65	GCA_000893255.1
AAQ17877.1	000086	Terminase-SS-DNA_Packaging	172	16	Aeromonas virus Aeh1	GCA_000843245.1
ANS06026.1	000086	Terminase-SS-DNA_Packaging	179	ABCD_0207	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64888.1	000086	Terminase-SS-DNA_Packaging	165	S13_089	Cronobacter phage S13	GCA_001503575.1
AON97222.1	000086	Terminase-SS-DNA_Packaging	180	E_214	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56919.1	000086	Terminase-SS-DNA_Packaging	135	CPXG_00116	Cyanophage P-RSM6	GCA_000906155.1
AJK27538.1	000086	Terminase-SS-DNA_Packaging	148	PTIM40_111	Cyanophage P-TIM40	GCA_001470935.1
AOO14297.1	000086	Terminase-SS-DNA_Packaging	134	Sn110110_103	Cyanophage S-RIM14	GCA_002599065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO14946.1	000086	Terminase-SS-DNA_Packaging	134	W1230910_100	Cyanophage S-RIM14	GCA_002599125.1
AMO43127.1	000086	Terminase-SS-DNA_Packaging	139	R1080702_118	Cyanophage S-RIM32	GCA_001754165.1
AMO43352.1	000086	Terminase-SS-DNA_Packaging	141	W270710_108	Cyanophage S-RIM44	GCA_002599145.1
AOO11596.1	000086	Terminase-SS-DNA_Packaging	141	ES420910_115	Cyanophage S-RIM44	GCA_002599165.1
AOO11824.1	000086	Terminase-SS-DNA_Packaging	141	Np050604_108	Cyanophage S-RIM44	GCA_002599185.1
AOO12061.1	000086	Terminase-SS-DNA_Packaging	141	Np200711_115	Cyanophage S-RIM44	GCA_002599205.1
AOO12297.1	000086	Terminase-SS-DNA_Packaging	141	Np420711_115	Cyanophage S-RIM44	GCA_002599225.1
AOO12525.1	000086	Terminase-SS-DNA_Packaging	141	Sn080709_108	Cyanophage S-RIM44	GCA_002599245.1
AOO12762.1	000086	Terminase-SS-DNA_Packaging	141	Sn130910_115	Cyanophage S-RIM44	GCA_002599265.1
AOO12991.1	000086	Terminase-SS-DNA_Packaging	141	W2100709_109	Cyanophage S-RIM44	GCA_002599285.1
AGH07451.1	000086	Terminase-SS-DNA_Packaging	145	CYVG_00007	Cyanophage S-SSM6a	GCA_002710385.1
AGG54287.1	000086	Terminase-SS-DNA_Packaging	145	CYWG_00003	Cyanophage S-SSM6b	GCA_002710425.1
ARM70725.1	000086	Terminase-SS-DNA_Packaging	164	phiC120_c18	Escherichia phage phiC120	GCA_002621185.1
AAX78740.1	000086	Terminase-SS-DNA_Packaging	178	RB43ORF218w	Escherichia virus RB43	GCA_000863505.1
QHJ79051.1	000086	Terminase-SS-DNA_Packaging	163	-	Myoviridae sp.	GCA_012593985.1
QIG65703.1	000086	Terminase-SS-DNA_Packaging	167	phiOC_p037	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26115.1	000086	Terminase-SS-DNA_Packaging	139	CPMG_00014	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44502.1	000086	Terminase-SS-DNA_Packaging	143	PSSM2_124	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12464.1	000086	Terminase-SS-DNA_Packaging	143	PRTG_00317	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93435.1	000086	Terminase-SS-DNA_Packaging	137	AVU42_gp095	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99210.1	000086	Terminase-SS-DNA_Packaging	141	Syn1_109	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47748.1	000086	Terminase-SS-DNA_Packaging	141	SmphiM12_116	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12991.1	000086	Terminase-SS-DNA_Packaging	141	PHIM19_84	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12631.1	000086	Terminase-SS-DNA_Packaging	141	PHIM7_83	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13362.1	000086	Terminase-SS-DNA_Packaging	141	PHIN3_98	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30604.1	000086	Terminase-SS-DNA_Packaging	141	Syn7803US37_127	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54879.1	000086	Terminase-SS-DNA_Packaging	150	b23_0265	Synechococcus phage B23	GCA_009745195.1
QGT54514.1	000086	Terminase-SS-DNA_Packaging	150	b3_0272	Synechococcus phage B3	GCA_009745215.1
ASR76165.1	000086	Terminase-SS-DNA_Packaging	135	PBI_BELLAMY_120	Synechococcus phage Bellamy	GCA_002627525.1
QCW22870.1	000086	Terminase-SS-DNA_Packaging	142	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50488.1	000086	Terminase-SS-DNA_Packaging	142	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59572.1	000086	Terminase-SS-DNA_Packaging	130	S330809_111	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59334.1	000086	Terminase-SS-DNA_Packaging	137	C440309_111	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59810.1	000086	Terminase-SS-DNA_Packaging	137	N231010_111	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70587.1	000086	Terminase-SS-DNA_Packaging	137	HOU04_gp188	Synechococcus phage S-T4	GCA_003443335.1
QJT70105.1	000086	Terminase-SS-DNA_Packaging	145	SynMITS9220M01_092	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64423.1	000086	Terminase-SS-DNA_Packaging	177	KVP40.0354	Vibrio phage KVP40	GCA_000843785.1
QIW90368.1	000086	Terminase-SS-DNA_Packaging	182	GCAPEGMB_00021	Vibrio phage V07	GCA_012361095.1
QIW91061.1	000086	Terminase-SS-DNA_Packaging	182	COHAPHLL_00198	Vibrio phage V09	GCA_012361135.1
QHJ74537.1	000086	Terminase-SS-DNA_Packaging	219	VH12019_00237	Vibrio phage VH1_2019	GCA_009931825.1
AGB06995.1	000086	Terminase-SS-DNA_Packaging	182	CF80_gp208	Vibrio phage VH7D	GCA_000914495.1
QBX06119.1	000086	Terminase-SS-DNA_Packaging	182	ValB1HC_165	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61131.1	000086	Terminase-SS-DNA_Packaging	182	AVU32_gp290	Vibrio phage ValKK3	GCA_001501635.1
AGN30027.2	000086	Terminase-SS-DNA_Packaging	181	VPFG_00019	Vibrio phage nt-1	GCA_000910195.2
ALP47086.1	000086	Terminase-SS-DNA_Packaging	182	phiGrn1_0088	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47467.1	000086	Terminase-SS-DNA_Packaging	182	phiST2_0220	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54744.1	000086	Terminase-SS-DNA_Packaging	182	vBValMR10Z_204	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07098.1	000086	Terminase-SS-DNA_Packaging	169	VmeM32_00109	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37586.1	000086	Terminase-SS-DNA_Packaging	182	pp2_354	Vibriophage phi-pp2	GCA_002630725.1
QMV29112.1	000000	Terminase-SS-DNA_Packaging	42	AP1_0409	Aeromonas phage AP1	GCA_014183365.1
APU01463.1	000087	Inh	267	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29103.1	000087	Inh	93	AP1_0396	Aeromonas phage AP1	GCA_014183365.1
QMV29139.1	000087	Inh	144	AP1_0436	Aeromonas phage AP1	GCA_014183365.1
ATI17434.1	000087	Inh	265	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00161.1	000087	Inh	265	HWB28_gp391	Aeromonas phage AS-zj	GCA_002627665.1
AUE22770.1	000087	Inh	232	Ah1_00252	Aeromonas phage Ah1	GCA_002957415.1
QAX98486.1	000087	Inh	233	ASfcp2_148	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97874.1	000087	Inh	265	ASswx1_231	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01275.1	000087	Inh	257	ASwh1_212	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39419.1	000087	Inh	290	CC2_303	Aeromonas phage CC2	GCA_000903495.1
ADQ52948.1	000087	Inh	233	PX29p229	Aeromonas phage PX29	GCA_000920195.1
ADM79872.1	000087	Inh	234	phiAS5_ORF0029	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53085.1	000087	Inh	267	65p075	Aeromonas virus 65	GCA_000893255.1
AAQ17894.1	000087	Inh	232	inh	Aeromonas virus Aeh1	GCA_000843245.1
ANS06001.1	000087	Inh	217	ABCD_0222	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64867.1	000087	Inh	214	S13_068	Cronobacter phage S13	GCA_001503575.1
AON97239.1	000087	Inh	219	E_231	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70741.1	000087	Inh	222	phiC120_c34	Escherichia phage phiC120	GCA_002621185.1
AAX78756.1	000087	Inh	306	RB43ORF234w	Escherichia virus RB43	GCA_000863505.1
QHJ79073.1	000087	Inh	211	-	Myoviridae sp.	GCA_012593985.1
AUE22769.1	000088	Inh	155	Ah1_00251	Aeromonas phage Ah1	GCA_002957415.1
QAX98485.1	000088	Inh	157	ASfcp2_147	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52947.1	000088	Inh	157	PX29p228	Aeromonas phage PX29	GCA_000920195.1
ADM79871.1	000088	Inh	187	phiAS5_ORF0028	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17893.1	000088	Inh	163	Aeh1ORF232c	Aeromonas virus Aeh1	GCA_000843245.1
ALY07008.1	000000	Inh	192	VmeM32_00014	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07007.1	000000	Inh	191	VmeM32_00013	Vibrio phage vB_VmeM-32	GCA_002608825.1
APU01730.1	000089	DUF5598+NAPRTase	509	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28739.1	000089	DUF5598+NAPRTase	508	AP1_0021	Aeromonas phage AP1	GCA_014183365.1
ATI17567.1	000089	DUF5598+NAPRTase	508	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00429.1	000089	DUF5598+NAPRTase	508	HWB28_gp123	Aeromonas phage AS-zj	GCA_002627665.1
AUE22655.1	000089	DUF5598+NAPRTase	481	Ah1_00114	Aeromonas phage Ah1	GCA_002957415.1
QAX98382.1	000089	DUF5598+NAPRTase	481	ASfcp2_36	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98007.1	000089	DUF5598+NAPRTase	508	ASswx1_367	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01135.1	000089	DUF5598+NAPRTase	511	ASwh1_69	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39500.1	000089	DUF5598+NAPRTase	503	CC2_165	Aeromonas phage CC2	GCA_000903495.1
ADQ52835.1	000089	DUF5598+NAPRTase	481	PX29p116	Aeromonas phage PX29	GCA_000920195.1
ADM80094.1	000089	DUF5598+NAPRTase	480	phiAS5_ORF0251	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53371.1	000089	DUF5598+NAPRTase	463	65p363	Aeromonas virus 65	GCA_000893255.1
AAQ17781.1	000089	DUF5598+NAPRTase	481	Aeh1ORF119c	Aeromonas virus Aeh1	GCA_000843245.1
QBX06526.1	000089	DUF5598+NAPRTase	488	BcepSaruman_113	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74492.1	000089	DUF5598+NAPRTase	488	BcepSauron_112	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13688.1	000089	DUF5598+NAPRTase	476	Ccr10_gp158c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14033.1	000089	DUF5598+NAPRTase	476	Ccr2_gp157c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14720.1	000089	DUF5598+NAPRTase	476	Ccr29_gp164	Caulobacter phage Ccr29	GCA_002619485.1
ARB15075.1	000089	DUF5598+NAPRTase	476	Ccr32_gp157	Caulobacter phage Ccr32	GCA_002619505.1
ARB15409.1	000089	DUF5598+NAPRTase	476	Ccr34_gp167	Caulobacter phage Ccr34	GCA_002619525.1
ARB14376.1	000089	DUF5598+NAPRTase	476	Ccr5_gp156c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68358.1	000089	DUF5598+NAPRTase	476	CcrBL10_gp154c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69258.1	000089	DUF5598+NAPRTase	472	CcrBL9_gp234c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88073.1	000089	DUF5598+NAPRTase	474	CcrColossus_gp203	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68750.1	000089	DUF5598+NAPRTase	474	CcrPW_gp211c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69814.1	000089	DUF5598+NAPRTase	280	CcrSC_gp232c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69815.1	000089	DUF5598+NAPRTase	191	CcrSC_gp233c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87681.1	000089	DUF5598+NAPRTase	476	CcrKarma_gp164	Caulobacter virus Karma	GCA_000901575.1
AFU87330.1	000089	DUF5598+NAPRTase	476	CcrMagneto_gp160	Caulobacter virus Magneto	GCA_000903095.1
AFU86641.1	000089	DUF5598+NAPRTase	485	CcrRogue_gp159	Caulobacter virus Rogue	GCA_000900555.1
AFU88477.1	000089	DUF5598+NAPRTase	476	CcrSwift_gp159	Caulobacter virus Swift	GCA_000899655.1
AFU86994.1	000089	DUF5598+NAPRTase	476	CbK_gp162	Caulobacter virus phiCbK	GCA_000900535.1
ANS05948.1	000089	DUF5598+NAPRTase	477	ABCD_0240	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65016.1	000089	DUF5598+NAPRTase	477	S13_219	Cronobacter phage S13	GCA_001503575.1
AFC21562.1	000089	DUF5598+NAPRTase	495	GAP32_114	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97258.1	000089	DUF5598+NAPRTase	317	E_250	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97259.1	000089	DUF5598+NAPRTase	161	E_251	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78777.1	000089	DUF5598+NAPRTase	476	RB43ORF255w	Escherichia virus RB43	GCA_000863505.1
AFA44773.1	000089	DUF5598+NAPRTase	490	RaK2_00500	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57938.1	000089	DUF5598+NAPRTase	523	SEA_PAULODIABOLI_253	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72853.1	000089	DUF5598+NAPRTase	473	-	Myoviridae sp.	GCA_003657725.1
QHJ78916.1	000089	DUF5598+NAPRTase	473	-	Myoviridae sp.	GCA_012593985.1
QIG65793.1	000089	DUF5598+NAPRTase	474	phiOC_p128	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43680.1	000089	DUF5598+NAPRTase	495	CBB_115	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QBX32439.1	000089	DUF5598+NAPRTase	588	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76978.1	000089	DUF5598+NAPRTase	576	PHABIO_347	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02830.1	000089	DUF5598+NAPRTase	609	PSA21_304	Pseudomonas phage Psa21	GCA_004340405.1
QEM42010.1	000089	DUF5598+NAPRTase	588	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAW19185.1	000089	DUF5598+NAPRTase	588	FDH28_gp210	Ralstonia phage RP12	GCA_002617345.1
BAW19471.1	000089	DUF5598+NAPRTase	588	-	Ralstonia phage RP31	GCA_002617365.1
BAG41550.1	000089	DUF5598+NAPRTase	472	pncB	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44119.1	000089	DUF5598+NAPRTase	456	PBI_SCTP2_104	Salicola phage SCTP-2	GCA_002625545.1
QCW18816.1	000089	DUF5598+NAPRTase	492	7t3_0295	Salmonella phage 7t3	GCA_006083215.1
AZU98080.1	000089	DUF5598+NAPRTase	492	CPT_Munch_136	Salmonella phage Munch	GCA_004015485.1
QIG62902.1	000089	DUF5598+NAPRTase	492	SEPL_289	Salmonella phage SE_PL	GCA_011067555.1
AQW88633.1	000089	DUF5598+NAPRTase	492	BF_0108	Serratia phage BF	GCA_002619745.1
AGR47913.1	000089	DUF5598+NAPRTase	302	SmphiM12_281	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13116.1	000089	DUF5598+NAPRTase	302	PHIM19_211	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12756.1	000089	DUF5598+NAPRTase	476	PHIM7_211	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13486.1	000089	DUF5598+NAPRTase	476	PHIN3_223	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54677.1	000089	DUF5598+NAPRTase	462	b23_0049	Synechococcus phage B23	GCA_009745195.1
QGT54307.1	000089	DUF5598+NAPRTase	462	b3_0049	Synechococcus phage B3	GCA_009745215.1
BBI90522.1	000089	DUF5598+NAPRTase	505	HYO65_gp130	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90830.1	000089	DUF5598+NAPRTase	505	-	Tenacibaculum phage PTm5	GCA_009730715.1
AXH70918.1	000089	DUF5598+NAPRTase	499	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64333.1	000089	DUF5598+NAPRTase	497	KVP40.0264	Vibrio phage KVP40	GCA_000843785.1
QIW90648.1	000089	DUF5598+NAPRTase	497	GCAPEGMB_00301	Vibrio phage V07	GCA_012361095.1
QIW91151.1	000089	DUF5598+NAPRTase	497	COHAPHLL_00315	Vibrio phage V09	GCA_012361135.1
QHJ74443.1	000089	DUF5598+NAPRTase	497	VH12019_00116	Vibrio phage VH1_2019	GCA_009931825.1
AGB06941.1	000089	DUF5598+NAPRTase	497	CF80_gp154	Vibrio phage VH7D	GCA_000914495.1
QBX06205.1	000089	DUF5598+NAPRTase	497	ValB1HC_252	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61222.1	000089	DUF5598+NAPRTase	497	AVU32_gp381	Vibrio phage ValKK3	GCA_001501635.1
AGN30309.1	000089	DUF5598+NAPRTase	497	VPFG_00310	Vibrio phage nt-1	GCA_000910195.2
ALP46980.1	000089	DUF5598+NAPRTase	497	phiGrn1_0377	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47363.1	000089	DUF5598+NAPRTase	497	phiST2_0132	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54830.1	000089	DUF5598+NAPRTase	497	vBValMR10Z_290	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07192.1	000089	DUF5598+NAPRTase	497	VmeM32_00206	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37493.1	000089	DUF5598+NAPRTase	497	pp2_260	Vibriophage phi-pp2	GCA_002630725.1
BBA65354.1	000089	DUF5598+NAPRTase	470	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96386.1	000089	DUF5598+NAPRTase	473	Xoosp13_200	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58910.1	000089	DUF5598+NAPRTase	492	g102	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58375.1	000089	DUF5598+NAPRTase	492	g098	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26094.1	000089	DUF5598+NAPRTase	584	g070	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000264	000089	DUF5598+NAPRTase	527	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000211	000089	DUF5598+NAPRTase	527	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAQ64328.1	000090	NAPRTase	297	KVP40.0259	Vibrio phage KVP40	GCA_000843785.1
QIW90643.1	000090	NAPRTase	297	GCAPEGMB_00296	Vibrio phage V07	GCA_012361095.1
QIW91156.1	000090	NAPRTase	297	COHAPHLL_00320	Vibrio phage V09	GCA_012361135.1
QHJ74438.1	000090	NAPRTase	297	VH12019_00111	Vibrio phage VH1_2019	GCA_009931825.1
AFN37487.1	000090	NAPRTase	210	pp2_254	Vibriophage phi-pp2	GCA_002630725.1
AEO93536.1	000000	NAPRTase_N+NAPRTase+NAPRTase_C	487	G_277	Bacillus virus G	GCA_000917535.1
AUZ95024.1	000000	NAPRTase_N+NAPRTase	432	FDI40_gp242	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUE22872.1	000091	NUDIX-cRECa	185	Ah1_00354	Aeromonas phage Ah1	GCA_002957415.1
QAX98582.1	000091	NUDIX-cRECa	186	ASfcp2_248	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53047.1	000091	NUDIX-cRECa	186	PX29p330	Aeromonas phage PX29	GCA_000920195.1
ADM79970.1	000091	NUDIX-cRECa	188	phiAS5_ORF0127	Aeromonas phage phiAS5	GCA_000887715.1
AAQ18001.1	000091	NUDIX-cRECa	183	nudE	Aeromonas virus Aeh1	GCA_000843245.1
AIT14367.1	000091	NUDIX-cRECa	183	PBI_121Q_477	Escherichia phage 121Q	GCA_000926855.1
QAY00581.1	000091	NUDIX-cRECa	183	Ecwhy1_302	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34774.1	000091	NUDIX-cRECa	183	ACQ29_gp094	Escherichia phage PBECO4	GCA_001041035.1
BBM62038.1	000091	NUDIX-cRECa	183	EO157G_4490	Escherichia phage SP27	GCA_008033345.1
AXC36889.1	000091	NUDIX-cRECa	183	-	Escherichia phage UB	GCA_003341455.1
QBO61937.1	000091	NUDIX-cRECa	183	G17_00448	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13967.1	000091	NUDIX-cRECa	183	vBEcoMphAPEC6_gp343c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80354.1	000091	NUDIX-cRECa	183	PSLUR01_00377	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44776.1	000091	NUDIX-cRECa	184	RaK2_00503	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18824.1	000091	NUDIX-cRECa	187	7t3_0303	Salmonella phage 7t3	GCA_006083215.1
AZU98088.1	000091	NUDIX-cRECa	187	CPT_Munch_144	Salmonella phage Munch	GCA_004015485.1
QIG62894.1	000091	NUDIX-cRECa	187	SEPL_281	Salmonella phage SE_PL	GCA_011067555.1
AFC21569.1	000092	NUDIX+cREC	301	GAP32_120	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43686.1	000092	NUDIX+cREC	299	CBB_121	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88638.1	000092	NUDIX+cREC	302	BF_0113	Serratia phage BF	GCA_002619745.1
SOK58918.1	000092	NUDIX+cREC	302	g110	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58383.1	000092	NUDIX+cREC	302	g106	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AND75441.1	000093	cREC	123	ME3_280	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01752.1	000093	cREC	111	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29057.1	000093	cREC	146	AP1_0350	Aeromonas phage AP1	GCA_014183665.1
ATI17544.1	000093	cREC	146	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00453.1	000093	cREC	146	HWB28_gp099	Aeromonas phage AS-zj	GCA_002627665.1
QAX97985.1	000093	cREC	146	ASswx1_344	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01155.1	000093	cREC	147	ASwh1_89	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39373.1	000093	cREC	146	CC2_191	Aeromonas phage CC2	GCA_000903495.1
ADQ53394.1	000093	cREC	144	65p387	Aeromonas virus 65	GCA_000893255.1
AUZ95316.1	000093	cREC	101	FDI40_gp557	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIT14368.1	000093	cREC	102	PBI_121Q_478	Escherichia phage 121Q	GCA_000926855.1
QAY00580.1	000093	cREC	106	Ecwhy1_301	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34773.1	000093	cREC	106	ACQ29_gp093	Escherichia phage PBECO4	GCA_001041035.1
BBM62039.1	000093	cREC	106	EO157G_4500	Escherichia phage SP27	GCA_008033345.1
AXC36888.1	000093	cREC	106	-	Escherichia phage UB	GCA_003341455.1
QBO61936.1	000093	cREC	106	G17_00447	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13966.1	000093	cREC	106	vBEcoMphAPEC6_gp342c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80355.1	000093	cREC	106	PSLUR01_00378	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44777.1	000093	cREC	111	RaK2_00504	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG65774.1	000093	cREC	114	phiOC_p109	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BAG41489.1	000093	cREC	116	RSL1_ORF044	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44422.1	000093	cREC	136	PBI_SCTP2_407	Salicola phage SCTP-2	GCA_002625545.1
QCW18825.1	000093	cREC	109	7t3_0304	Salmonella phage 7t3	GCA_006083215.1
AZU98089.1	000093	cREC	109	CPT_Munch_145	Salmonella phage Munch	GCA_004015485.1
QIG62893.1	000093	cREC	109	SEPL_280	Salmonella phage SE_PL	GCA_011067555.1
AFC21873.1	000094	cREC	121	GAP32_420	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21874.1	000094	cREC	118	GAP32_421	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44001.1	000094	cREC	121	CBB_438	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44002.1	000094	cREC	118	CBB_439	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44248.1	000094	cREC	123	PBI_SCTP2_233	Salicola phage SCTP-2	GCA_002625545.1
AQW88960.1	000094	cREC	121	BF_0435	Serratia phage BF	GCA_002619745.1
AQW88961.1	000094	cREC	118	BF_0436	Serratia phage BF	GCA_002619745.1
SOK59246.1	000094	cREC	120	g438	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59247.1	000094	cREC	119	g439	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58711.1	000094	cREC	120	g434	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58712.1	000094	cREC	119	g435	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26242.1	000094	cREC	119	g219	Yersinia phage phiR1-37	GCA_000895615.1
AAQ64374.1	000095	cREC	118	KVP40.0304	Vibrio phage KVP40	GCA_000843785.1
QIW90690.1	000095	cREC	118	GCAPEGMB_00343	Vibrio phage V07	GCA_012361095.1
QIW91108.1	000095	cREC	118	COHAPHLL_00272	Vibrio phage V09	GCA_012361135.1
QHJ74486.1	000095	cREC	119	VH12019_00159	Vibrio phage VH1_2019	GCA_009931825.1
QBX06164.1	000095	cREC	115	ValB1HC_211	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61181.1	000095	cREC	115	AVU32_gp340	Vibrio phage ValKK3	GCA_001501635.1
AGN30352.1	000095	cREC	119	VPFG_00355	Vibrio phage nt-1	GCA_000910195.2
ALP47173.1	000095	cREC	115	phiGrn1_0041	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47556.1	000095	cREC	116	phiST2_0173	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54790.1	000095	cREC	115	vBValMR10Z_250	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37536.1	000095	cREC	119	pp2_303	Vibriophage phi-pp2	GCA_002630725.1
BBA65627.1	000096	cREC	97	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65168.1	000096	cREC	97	-	Xanthomonas phage XacN1	GCA_003173815.1
QIG57979.1	000000	cREC	114	SEA_PAULODIABOLI_295	Microbacterium phage PauloDiaboli	GCA_011067425.1
AFC21559.1	000097	NLPC+IG+IG	303	GAP32_111	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ARB13621.1	000098	Phage-tail-tape+TM+TM+NLPC	1961	Ccr10_gp092	Caulobacter phage Ccr10	GCA_002619445.1
ARB13966.1	000098	Phage-tail-tape+TM+TM+NLPC	1961	Ccr2_gp091	Caulobacter phage Ccr2	GCA_002619465.1
ARB14655.1	000098	Phage-tail-tape+TM+TM+NLPC	1961	Ccr29_gp099	Caulobacter phage Ccr29	GCA_002619485.1
ARB15010.1	000098	Phage-tail-tape+TM+TM+NLPC	1964	Ccr32_gp092	Caulobacter phage Ccr32	GCA_002619505.1
ARB15341.1	000098	Phage-tail-tape+TM+TM+NLPC	1964	Ccr34_gp099	Caulobacter phage Ccr34	GCA_002619525.1
ARB14310.1	000098	Phage-tail-tape+TM+TM+NLPC	1961	Ccr5_gp092	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68293.1	000098	Phage-tail-tape+TM+TM+NLPC	2165	CcrBL10_gp089	Caulobacter phage CcrBL10	GCA_003443255.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU87613.1	000098	Phage-tail-tape+TM+TM+NLPC	1957	CcrKarma_gp096	Caulobacter virus Karma	GCA_000901575.1
AFU87262.1	000098	Phage-tail-tape+TM+TM+NLPC	1957	CcrMagneto_gp092	Caulobacter virus Magneto	GCA_000903095.1
AFU86576.1	000098	Phage-tail-tape+TM+TM+NLPC	2164	CcrRogue_gp094	Caulobacter virus Rogue	GCA_000900555.1
AFU88409.1	000098	Phage-tail-tape+TM+TM+NLPC	1960	CcrSwift_gp091	Caulobacter virus Swift	GCA_000899655.1
AFU86927.1	000098	Phage-tail-tape+TM+TM+NLPC	1964	CbK_gp095	Caulobacter virus phiCbK	GCA_000900535.1
AXQ69743.1	000099	Phage-tail-tape+TM+TM	2073	CcrSC_gp161	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69190.1	000099	Phage-tail-tape+TM+TM	2080	CcrBL9_gp166	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87988.1	000100	Phage-tail-tape+Lysozyme	2155	CcrColossus_gp118	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68664.1	000100	Phage-tail-tape+Lysozyme	2158	CcrPW_gp125	Caulobacter phage CcrPW	GCA_003443275.1
AIX30688.1	000101	NLPC+Phage_lysozyme	405	Syn7803US37_211	Synechococcus phage ACG-2014f	GCA_002594065.1
AND75169.1	000102	Phage_lysozyme	152	ME3_8	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ASV44718.1	000102	Phage_lysozyme	149	FDI40_gp141	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARB13630.1	000102	Phage_lysozyme	213	Ccr10_gp101	Caulobacter phage Ccr10	GCA_002619445.1
ARB13975.1	000102	Phage_lysozyme	213	Ccr2_gp100	Caulobacter phage Ccr2	GCA_002619465.1
ARB14664.1	000102	Phage_lysozyme	213	Ccr29_gp108	Caulobacter phage Ccr29	GCA_002619485.1
ARB15019.1	000102	Phage_lysozyme	213	Ccr32_gp101	Caulobacter phage Ccr32	GCA_002619505.1
ARB15351.1	000102	Phage_lysozyme	213	Ccr34_gp109	Caulobacter phage Ccr34	GCA_002619525.1
ARB14319.1	000102	Phage_lysozyme	213	Ccr5_gp101	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68300.1	000102	Phage_lysozyme	212	CcrBL10_gp096	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69204.1	000102	Phage_lysozyme	211	CcrBL9_gp180	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88004.1	000102	Phage_lysozyme	203	CcrColossus_gp134	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68680.1	000102	Phage_lysozyme	203	CcrPW_gp141	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69757.1	000102	Phage_lysozyme	211	CcrSC_gp175	Caulobacter phage CcrSC	GCA_003443315.1
AFU87622.1	000102	Phage_lysozyme	213	CcrKarma_gp105	Caulobacter virus Karma	GCA_000901575.1
AFU87271.1	000102	Phage_lysozyme	213	CcrMagneto_gp101	Caulobacter virus Magneto	GCA_000903095.1
AFU86583.1	000102	Phage_lysozyme	212	CcrRogue_gp101	Caulobacter virus Rogue	GCA_000900555.1
AFU88418.1	000102	Phage_lysozyme	213	CcrSwift_gp100	Caulobacter virus Swift	GCA_000899655.1
AFU86936.1	000102	Phage_lysozyme	213	CbK_gp104	Caulobacter virus phiCbK	GCA_000900535.1
AXH72913.1	000102	Phage_lysozyme	161	-	Myoviridae sp.	GCA_003657725.1
QCG76054.1	000102	Phage_lysozyme	171	EST35_0173	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ARB13624.1	000103	NLPC	141	Ccr10_gp095	Caulobacter phage Ccr10	GCA_002619445.1
ARB13969.1	000103	NLPC	141	Ccr2_gp094	Caulobacter phage Ccr2	GCA_002619465.1
ARB14658.1	000103	NLPC	141	Ccr29_gp102	Caulobacter phage Ccr29	GCA_002619485.1
ARB15013.1	000103	NLPC	141	Ccr32_gp095	Caulobacter phage Ccr32	GCA_002619505.1
ARB15344.1	000103	NLPC	141	Ccr34_gp102	Caulobacter phage Ccr34	GCA_002619525.1
ARB14313.1	000103	NLPC	141	Ccr5_gp095	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68296.1	000103	NLPC	141	CcrBL10_gp092	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69193.1	000103	NLPC	140	CcrBL9_gp169	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87991.1	000103	NLPC	140	CcrColossus_gp121	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68667.1	000103	NLPC	140	CcrPW_gp128	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69746.1	000103	NLPC	140	CcrSC_gp164	Caulobacter phage CcrSC	GCA_003443315.1
AFU87616.1	000103	NLPC	141	CcrKarma_gp099	Caulobacter virus Karma	GCA_000901575.1
AFU87265.1	000103	NLPC	141	CcrMagneto_gp095	Caulobacter virus Magneto	GCA_000903095.1
AFU86579.1	000103	NLPC	141	CcrRogue_gp097	Caulobacter virus Rogue	GCA_000900555.1
AFU88412.1	000103	NLPC	141	CcrSwift_gp094	Caulobacter virus Swift	GCA_000899655.1
AFU86930.1	000103	NLPC	141	CbK_gp098	Caulobacter virus phiCbK	GCA_000900535.1
AYD81280.1	000104	SIG+NLPC	155	SEA_JUSTBECAUSE_111	Streptomyces phage JustBecause	GCA_003613775.1
AYD81262.1	000104	SIG+NLPC	197	SEA_JUSTBECAUSE_93	Streptomyces phage JustBecause	GCA_003613775.1
QJD53683.1	000104	SIG+NLPC	160	SEA_KELA_112	Streptomyces phage Kela	GCA_012934305.1
QJD53665.1	000104	SIG+NLPC	197	SEA_KELA_94	Streptomyces phage Kela	GCA_012934305.1
QBZ72010.1	000104	SIG+NLPC	155	SEA_KRADAL_112	Streptomyces phage Kradal	GCA_004799925.1
QBZ71994.1	000104	SIG+NLPC	197	SEA_KRADAL_96	Streptomyces phage Kradal	GCA_004799925.1
AXH66273.1	000104	SIG+NLPC	155	SEA_SATIS_112	Streptomyces phage Satis	GCA_003366315.1
AXH66257.1	000104	SIG+NLPC	197	SEA_SATIS_96	Streptomyces phage Satis	GCA_003366315.1
AXH71035.1	000105	NLPC	154	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96800.1	000105	NLPC	148	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97119.1	000105	NLPC	148	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96165.1	000105	NLPC	148	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96483.1	000105	NLPC	148	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21278.1	000105	NLPC	143	-	Vibrio phage vB_pir03	GCA_014319855.1
prevph1000000200	000106	NLPC	201	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000161	000106	NLPC	299	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXQ69168.1	000107	NLPC	99	CcrBL9_gp144	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87955.1	000107	NLPC	96	CcrColossus_gp085	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68630.1	000107	NLPC	84	CcrPW_gp091c	Caulobacter phage CcrPW	GCA_003443275.1
QIG58043.1	000108	NLPC	250	SEA_PAULODIABOLI_359	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57742.1	000108	NLPC	250	SEA_PAULODIABOLI_4	Microbacterium phage PauloDiaboli	GCA_011067425.1
AGH56939.1	000109	NLPC	165	CPXG_00136	Cyanophage P-RSM6	GCA_000906155.1
AJK27517.1	000109	NLPC	159	PTIM40_90	Cyanophage P-TIM40	GCA_001470935.1
BAW19150.1	000110	NLPC	147	FDH28_gp245	Ralstonia phage RP12	GCA_002617345.1
BAW19436.1	000110	NLPC	147	-	Ralstonia phage RP31	GCA_002617365.1
AEO93471.1	000000	NLPC	157	G_212	Bacillus virus G	GCA_000917535.1
CCH63576.1	000000	NLPC	397	CP21_114	Campylobacter virus CP21	GCA_000902535.1
AGX01781.1	000000	NLPC	118	CF95_gp059	Erwinia phage PhiEaH1	GCA_000914555.1
SBV38413.1	000000	NLPC	133	BN7874_228	Phage NCTB	GCA_900092385.1
ASV44206.1	000000	NLPC	116	PBI_SCTP2_191	Salicola phage SCTP-2	GCA_002625545.1
QIW90760.1	000000	NLPC	151	GCAPEGMB_00441	Vibrio phage V07	GCA_012361095.1
ABS83705.1	000000	Lysozyme+NLPC	1903	0305phi8-36p147	Bacillus phage 0305phi8-36	GCA_000871045.1
BAE47829.1	000000	NLPC+Phage-tail-tape	558	CST131	Clostridium phage c-st	GCA_000865225.1
ARB15588.1	000000	SIG+NLPC	232	Ccr34_gp082	Caulobacter phage Ccr34	GCA_002619525.1
AEO93593.1	000000	Nuc_deoxyri_tr2+NUDIX	396	G_334	Bacillus virus G	GCA_000917535.1
AXQ69280.1	000111	Nuc_deoxyri_tr2	164	CcrBL9_gp256c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88058.1	000111	Nuc_deoxyri_tr2	159	CcrColossus_gp188	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ69837.1	000111	Nuc_deoxyri_tr2	164	CcrSC_gp255c	Caulobacter phage CcrSC	GCA_003443315.1
AXH72855.1	000111	Nuc_deoxyri_tr2	264	-	Myoviridae sp.	GCA_003657725.1
QBJ02940.1	000111	Nuc_deoxyri_tr2	138	PSA21_422	Pseudomonas phage Psa21	GCA_004340405.1
prevph1000000155	000111	Nuc_deoxyri_tr2	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000116	000111	Nuc_deoxyri_tr2	297	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000154	000000	SIG+Nuc_deoxyri_tr2	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
ATI17391.1	000112	PAAR+TM+TM+DUF4786	619	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97833.1	000112	PAAR+TM+TM+DUF4786	619	ASswx1_189	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39482.1	000112	PAAR+TM+TM+DUF4786	619	CC2_346	Aeromonas phage CC2	GCA_000903495.1
APU01506.1	000113	TM+TM+DUF4786	602	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29054.1	000113	TM+TM+DUF4786	494	AP1_0347	Aeromonas phage AP1	GCA_014183665.1
AUE22720.1	000113	TM+TM+DUF4786	617	Ah1_00202	Aeromonas phage Ah1	GCA_002957415.1
QAX98444.1	000113	TM+TM+DUF4786	618	ASfcp2_101	Aeromonas phage AsFcp_2	GCA_004146885.1
QAY01319.1	000113	TM+TM+DUF4786	630	ASwh1_257	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ52900.1	000113	TM+TM+DUF4786	618	PX29p181	Aeromonas phage PX29	GCA_000920195.1
ADM80167.1	000113	TM+TM+DUF4786	623	phiAS5_ORF0324	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53128.1	000113	TM+TM+DUF4786	602	65p120	Aeromonas virus 65	GCA_000893255.1
AAQ17853.1	000113	TM+TM+DUF4786	615	Aeh1ORF187c	Aeromonas virus Aeh1	GCA_000843245.1
ABY63076.1	000114	PAAR	88	201phi2-1p248	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77336.1	000114	PAAR	88	NOXIFER_167	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32346.1	000114	PAAR	88	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76867.1	000114	PAAR	86	PHABIO_236	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02748.1	000114	PAAR	87	PSA21_222	Pseudomonas phage Psa21	GCA_004340405.1
QEM41920.1	000114	PAAR	88	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANM44959.1	000114	PAAR	88	KTN4_201	Pseudomonas phage KTN4	GCA_002607225.1
AEH03611.1	000114	PAAR	88	188	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94755.1	000114	PAAR	88	SL2_178	Pseudomonas phage SL2	GCA_002956015.1
QJB22837.1	000114	PAAR	88	fnug_194	Pseudomonas phage fnug	GCA_012837215.1
AGC26338.1	000114	PAAR	88	PHIKZ163.1	Pseudomonas virus phiKZ	GCA_000842965.1
APU01493.1	000115	PAAR	98	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28802.1	000115	PAAR	98	AP1_0095	Aeromonas phage AP1	GCA_014183365.1
ATI17404.1	000115	PAAR	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00191.1	000115	PAAR	98	HWB28_gp361	Aeromonas phage AS-zj	GCA_002627665.1
AUE22732.1	000115	PAAR	97	Ah1_00214	Aeromonas phage Ah1	GCA_002957415.1
QAX98453.1	000115	PAAR	97	ASfcp2_111	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97844.1	000115	PAAR	98	ASswx1_201	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01308.1	000115	PAAR	98	ASwh1_245	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39480.1	000115	PAAR	98	CC2_334	Aeromonas phage CC2	GCA_000903495.1
ADQ52911.1	000115	PAAR	97	PX29p192	Aeromonas phage PX29	GCA_000920195.1
ADM80178.1	000115	PAAR	97	phiAS5_ORF0335	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53114.1	000115	PAAR	98	65p106	Aeromonas virus 65	GCA_000893255.1
AAQ17863.1	000115	PAAR	97	5.4	Aeromonas virus Aeh1	GCA_000843245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEO93380.1	000115	PAAR	95	G_118	Bacillus virus G	GCA_000917535.1
CCH63500.1	000115	PAAR	97	CP21_038	Campylobacter virus CP21	GCA_000902535.1
AXG67158.1	000115	PAAR	96	AD1_114	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79907.1	000115	PAAR	96	JA11_102	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66506.1	000115	PAAR	96	JA13_103	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66831.1	000115	PAAR	96	JA29_105	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67476.1	000115	PAAR	96	JA33_102	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08391.1	000115	PAAR	96	Alexandra_119	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58755.1	000115	PAAR	96	Y3_115	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28589.1	000115	PAAR	96	YOLOSWAG_107	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ARM70979.1	000115	PAAR	97	phiC120_c274	Escherichia phage phiC120	GCA_002621185.1
ARM70713.1	000115	PAAR	97	phiC120_c6	Escherichia phage phiC120	GCA_002621185.1
AXH72837.1	000115	PAAR	95	-	Myoviridae sp.	GCA_003657725.1
SBV38310.1	000115	PAAR	95	BN7874_141	Phage NCTB	GCA_900092385.1
AGH26140.1	000115	PAAR	112	CPMG_00039	Prochlorococcus phage MED4-213	GCA_000904535.1
AFH14761.1	000115	PAAR	97	Lu11_0224	Pseudomonas phage Lu11	GCA_000897175.1
AGS82112.1	000115	PAAR	109	PaBG_00238	Pseudomonas phage PaBG	GCA_000912555.1
ASV44143.1	000115	PAAR	99	PBI_SCTP2_128	Salicola phage SCTP-2	GCA_002625545.1
AKF13100.1	000115	PAAR	107	PHIM19_195	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12740.1	000115	PAAR	107	PHIM7_195	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13470.1	000115	PAAR	107	PHIN3_207	Sinorhizobium phage phiN3	GCA_001501175.1
AXH70746.1	000115	PAAR	98	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64406.1	000115	PAAR	98	KVP40.0337	Vibrio phage KVP40	GCA_000843785.1
QIW90351.1	000115	PAAR	98	GCAPEGMB_00004	Vibrio phage V07	GCA_012361095.1
QIW91078.1	000115	PAAR	98	COHAPHLL_00215	Vibrio phage V09	GCA_012361135.1
QHJ74519.1	000115	PAAR	98	VH12019_00219	Vibrio phage VH1_2019	GCA_009931825.1
AGB06980.1	000115	PAAR	98	CF80_gp193	Vibrio phage VH7D	GCA_000914495.1
QBX06136.1	000115	PAAR	98	ValB1HC_182	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61148.1	000115	PAAR	98	AVU32_gp307	Vibrio phage ValKK3	GCA_001501635.1
AGN30010.1	000115	PAAR	98	VPFG_00002	Vibrio phage nt-1	GCA_000910195.2
ALP47208.1	000115	PAAR	98	phiGrn1_0071	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47599.1	000115	PAAR	98	phiST2_0203	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54761.1	000115	PAAR	98	vBValMR10Z_221	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07245.1	000115	PAAR	95	VmeM32_00259	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI20955.1	000115	PAAR	99	-	Vibrio phage vB_pir03	GCA_014319855.1
AFN37569.1	000115	PAAR	98	pp2_337	Vibriophage phi-pp2	GCA_002630725.1
CCE26166.1	000115	PAAR	95	g142	Yersinia phage phiR1-37	GCA_000895615.1
QCG76126.1	000116	PAAR+Peptidase-M15	340	EST35_0245	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
SBV38281.1	000117	Peptidase-M15	193	BN7874_112	Phage NCTB	GCA_900092385.1
AGS82072.1	000117	Peptidase-M15	146	PaBG_00196	Pseudomonas phage PaBG	GCA_000912555.1
ASV44181.1	000117	Peptidase-M15	192	PBI_SCTP2_166	Salicola phage SCTP-2	GCA_002625545.1
CCE26108.1	000117	Peptidase-M15	119	g084	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000142	000117	Peptidase-M15	64	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000109	000117	Peptidase-M15	152	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGH56935.1	000118	PAAR	137	CPXG_00132	Cyanophage P-RSM6	GCA_000906155.1
AJK27521.1	000118	PAAR	176	PTIM40_94	Cyanophage P-TIM40	GCA_001470935.1
AOO14280.1	000118	PAAR	173	Sn110110_086	Cyanophage S-RIM14	GCA_002599065.1
AOO14929.1	000118	PAAR	173	W1230910_083	Cyanophage S-RIM14	GCA_002599125.1
AGG54303.1	000118	PAAR	164	CYWG_00019	Cyanophage S-SSM6b	GCA_002710425.1
AMO43104.1	000119	PAAR	112	R1080702_095	Cyanophage S-RIM32	GCA_001754165.1
AOO11565.1	000119	PAAR	111	ES420910_084	Cyanophage S-RIM44	GCA_002599165.1
AOO12030.1	000119	PAAR	111	Np200711_084	Cyanophage S-RIM44	GCA_002599205.1
AOO12266.1	000119	PAAR	111	Np420711_084	Cyanophage S-RIM44	GCA_002599225.1
AOO12731.1	000119	PAAR	111	Sn130910_084	Cyanophage S-RIM44	GCA_002599265.1
BAE47818.1	000000	PAAR	120	CST120	Clostridium phage c-st	GCA_000865225.1
AMM44851.1	000000	PAAR+PAAR	234	SP15_052	Bacillus phage SP-15	GCA_001754685.1
QDH50596.1	000000	PAAR	129	-	Synechococcus phage S-B43	GCA_006869725.1
AFC21849.1	000120	Cluster6251_1clades	77	GAP32_397	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21852.1	000120	Cluster6251_1clades	103	GAP32_399	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43969.1	000120	Cluster6251_1clades	77	CBB_406	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43971.1	000120	Cluster6251_1clades	107	CBB_408	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88931.1	000120	Cluster6251_1clades	70	BF_0406	Serratia phage BF	GCA_002619745.1
SOK59220.1	000120	Cluster6251_1clades	97	g412	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58686.1	000120	Cluster6251_1clades	97	g409	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMS01159.1	000121	PIN+PhoH	442	AR9_g075	Bacillus phage AR9	GCA_001743835.1
ALN97825.1	000121	PIN+PhoH	468	Bp8pS_146	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00088.1	000121	PIN+PhoH	442	PBI_PBS1_266	Bacillus virus PBS1	GCA_002601325.1
CCH63524.1	000121	PIN+PhoH	414	CP21_062	Campylobacter virus CP21	GCA_000902535.1
ANS05951.1	000121	PIN+PhoH	447	ABCD_0151	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFC21571.1	000121	PIN+PhoH	480	GAP32_122	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97163.1	000121	PIN+PhoH	447	E_155	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14370.1	000121	PIN+PhoH	479	PBI_121Q_480	Escherichia phage 121Q	GCA_000926855.1
QAY00578.1	000121	PIN+PhoH	479	Ecwhy1_299	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34771.1	000121	PIN+PhoH	479	ACQ29_gp091	Escherichia phage PBECO4	GCA_001041035.1
BBM62041.1	000121	PIN+PhoH	479	EO157G_4520	Escherichia phage SP27	GCA_008033345.1
AXC36886.1	000121	PIN+PhoH	479	-	Escherichia phage UB	GCA_003341455.1
QBO61934.1	000121	PIN+PhoH	479	G17_00445	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13965.1	000121	PIN+PhoH	479	vBEcoMphAPEC6_gp341c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80357.1	000121	PIN+PhoH	479	PSLUR01_00380	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78679.1	000121	PIN+PhoH	449	RB43ORF157c	Escherichia virus RB43	GCA_000863505.1
AFA44779.1	000121	PIN+PhoH	479	RaK2_00506	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43688.1	000121	PIN+PhoH	479	CBB_123	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18827.1	000121	PIN+PhoH	485	7t3_0306	Salmonella phage 7t3	GCA_006083215.1
AZU98091.1	000121	PIN+PhoH	485	CPT_Munch_147	Salmonella phage Munch	GCA_004015485.1
QIG62891.1	000121	PIN+PhoH	485	SEPL_278	Salmonella phage SE_PL	GCA_011067555.1
AQW88640.1	000121	PIN+PhoH	484	BF_0115	Serratia phage BF	GCA_002619745.1
QAU04516.1	000121	PIN+PhoH	463	ValB1MD_184	Vibrio phage ValB1MD	GCA_004138815.1
SOK58920.1	000121	PIN+PhoH	484	g112	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58385.1	000121	PIN+PhoH	484	g108	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDH83409.1	000122	PhoH	267	H1O15_gp072	Achromobacter phage Motura	GCA_006964305.1
AND75302.1	000122	PhoH	255	ME3_141	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ95075.1	000122	PhoH	254	FDI40_gp309	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMM45096.1	000122	PhoH	293	SP15_288	Bacillus phage SP-15	GCA_001754685.1
AEO93422.1	000122	PhoH	212	G_162	Bacillus virus G	GCA_000917535.1
ARB13613.1	000122	PhoH	288	Ccr10_gp084	Caulobacter phage Ccr10	GCA_002619445.1
ARB13958.1	000122	PhoH	288	Ccr2_gp083	Caulobacter phage Ccr2	GCA_002619465.1
ARB14648.1	000122	PhoH	288	Ccr29_gp091	Caulobacter phage Ccr29	GCA_002619485.1
ARB15003.1	000122	PhoH	288	Ccr32_gp084	Caulobacter phage Ccr32	GCA_002619505.1
ARB15334.1	000122	PhoH	288	Ccr34_gp091	Caulobacter phage Ccr34	GCA_002619525.1
ARB14302.1	000122	PhoH	288	Ccr5_gp084	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68284.1	000122	PhoH	288	CcrBL10_gp080	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69182.1	000122	PhoH	292	CcrBL9_gp158	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87979.1	000122	PhoH	274	CcrColossus_gp109	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68656.1	000122	PhoH	274	CcrPW_gp117	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69735.1	000122	PhoH	292	CcrSC_gp153	Caulobacter phage CcrSC	GCA_003443315.1
AFU87604.1	000122	PhoH	288	CcrKarma_gp087	Caulobacter virus Karma	GCA_000901575.1
AFU87253.1	000122	PhoH	288	CcrMagneto_gp083	Caulobacter virus Magneto	GCA_000903095.1
AFU86568.1	000122	PhoH	288	CcrRogue_gp086	Caulobacter virus Rogue	GCA_000900555.1
AFU88400.1	000122	PhoH	288	CcrSwift_gp082	Caulobacter virus Swift	GCA_000899655.1
AFU86918.1	000122	PhoH	288	CbK_gp086	Caulobacter virus phiCbK	GCA_000900535.1
AFO71309.1	000122	PhoH	250	CR5_089	Cronobacter phage CR5	GCA_000910235.1
AGH57021.1	000122	PhoH	251	CPXG_00218	Cyanophage P-RSM6	GCA_000906155.1
AJK27647.1	000122	PhoH	246	PTIM40_237	Cyanophage P-TIM40	GCA_001470935.1
AOO14412.1	000122	PhoH	255	Sn110110_219	Cyanophage S-RIM14	GCA_002599065.1
AOO15061.1	000122	PhoH	255	W1230910_216	Cyanophage S-RIM14	GCA_002599125.1
AMO43242.1	000122	PhoH	251	R1080702_237	Cyanophage S-RIM32	GCA_001754165.1
AMO43473.1	000122	PhoH	251	W270710_234	Cyanophage S-RIM44	GCA_002599145.1
AOO11715.1	000122	PhoH	251	ES420910_238	Cyanophage S-RIM44	GCA_002599165.1
AOO11945.1	000122	PhoH	251	Np050604_234	Cyanophage S-RIM44	GCA_002599185.1
AOO12181.1	000122	PhoH	251	Np200711_239	Cyanophage S-RIM44	GCA_002599205.1
AOO12416.1	000122	PhoH	251	Np420711_238	Cyanophage S-RIM44	GCA_002599225.1
AOO12646.1	000122	PhoH	251	Sn080709_234	Cyanophage S-RIM44	GCA_002599245.1
AOO12881.1	000122	PhoH	251	Sn130910_238	Cyanophage S-RIM44	GCA_002599265.1
AOO13112.1	000122	PhoH	251	W2100709_235	Cyanophage S-RIM44	GCA_002599285.1
AGH07625.1	000122	PhoH	253	CYVG_00182	Cyanophage S-SSM6a	GCA_002710385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGG54374.1	000122	PhoH	253	CYWG_00090	Cyanophage S-SSM6b	GCA_002710425.1
QBP07518.1	000122	PhoH	254	DERBICUS_92	Erwinia phage Derbicus	GCA_004521655.1
AGX01829.1	000122	PhoH	261	phoH	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ48941.1	000122	PhoH	251	EARLPHILLIPIV_92	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ASU03775.1	000122	PhoH	254	JOAD_140	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ50282.1	000122	PhoH	251	PHOBOS_92	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ASU03531.1	000122	PhoH	254	RISINGSUN_139	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXH72815.1	000122	PhoH	230	-	Myoviridae sp.	GCA_003657725.1
QIG65753.1	000122	PhoH	261	phiOC_p088	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26216.1	000122	PhoH	248	CPMG_00115	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44704.1	000122	PhoH	250	PSSM2_326	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12271.1	000122	PhoH	250	PRTG_00118	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93579.1	000122	PhoH	256	AVU42_gp244	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99334.1	000122	PhoH	251	Syn1_238	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76175.1	000122	PhoH	257	EST35_0294	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAW19031.1	000122	PhoH	257	FDH28_gp057	Ralstonia phage RP12	GCA_002617345.1
BAW19316.1	000122	PhoH	257	-	Ralstonia phage RP31	GCA_002617365.1
ASV44090.1	000122	PhoH	535	PBI_SCTP2_75	Salicola phage SCTP-2	GCA_002625545.1
ATA65539.1	000122	PhoH	258	2050HW_00204	Serratia phage 2050HW	GCA_002628125.1
QDB71304.1	000122	PhoH	258	CPT_Moabite_274	Serratia phage Moabite	GCA_006384735.1
AGR47898.1	000122	PhoH	85	SmphiM12_266	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13098.1	000122	PhoH	236	PHIM19_193	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12738.1	000122	PhoH	236	PHIM7_193	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13468.1	000122	PhoH	236	PHIN3_205	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30765.1	000122	PhoH	255	Syn7803US37_288	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54989.1	000122	PhoH	253	b23_0383	Synechococcus phage B23	GCA_009745195.1
QGT54624.1	000122	PhoH	253	b3_0389	Synechococcus phage B3	GCA_009745215.1
ASR76314.1	000122	PhoH	236	PBI_BELLAMY_278	Synechococcus phage Bellamy	GCA_002627525.1
QCW23063.1	000122	PhoH	254	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59696.1	000122	PhoH	251	S330809_235	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59458.1	000122	PhoH	251	C440309_235	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59933.1	000122	PhoH	250	N231010_234	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70453.1	000122	PhoH	252	HOU04_gp054	Synechococcus phage S-T4	GCA_003443335.1
QJT70259.1	000122	PhoH	250	SynMITS9220M01_253	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXH71002.1	000122	PhoH	331	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64362.1	000122	PhoH	235	KVP40.0292	Vibrio phage KVP40	GCA_000843785.1
QIW90676.1	000122	PhoH	235	GCAPEGMB_00329	Vibrio phage V07	GCA_012361095.1
QIW91122.1	000122	PhoH	235	COHAPHLL_00286	Vibrio phage V09	GCA_012361135.1
QHJ74471.1	000122	PhoH	235	VH12019_00144	Vibrio phage VH1_2019	GCA_009931825.1
AGB06965.1	000122	PhoH	234	CF80_gp178	Vibrio phage VH7D	GCA_000914495.1
QBX06180.1	000122	PhoH	234	ValB1HC_227	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61197.1	000122	PhoH	234	AVU32_gp356	Vibrio phage ValKK3	GCA_001501635.1
AGN30338.1	000122	PhoH	235	VPFG_00341	Vibrio phage nt-1	GCA_000910195.2
ALP47051.1	000122	PhoH	234	phiGrn1_0025	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47429.1	000122	PhoH	234	phiST2_0156	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54805.1	000122	PhoH	234	vBValMR10Z_265	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07074.1	000122	PhoH	275	VmeM32_00083	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96926.1	000122	PhoH	313	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97231.1	000122	PhoH	313	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96290.1	000122	PhoH	313	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96608.1	000122	PhoH	313	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFN37523.1	000122	PhoH	235	pp2_290	Vibriophage phi-pp2	GCA_002630725.1
BBA65336.1	000122	PhoH	259	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96373.1	000122	PhoH	267	Xoosp13_187	Xanthomonas phage Xoo-sp13	GCA_013364725.1
CCE26073.1	000122	PhoH	261	g049	Yersinia phage phiR1-37	GCA_000895615.1
CCH63519.1	000000	PhoH	71	CP21_057	Campylobacter virus CP21	GCA_000902535.1
QCG76197.1	000000	QTG	540	EST35_0316	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QIW90770.1	000000	QTG	316	GCAPEGMB_00451	Vibrio phage V07	GCA_012361095.1
QDH83434.1	000000	SIG+QTG	473	H1O15_gp026	Achromobacter phage Motura	GCA_006964305.1
SBV38183.1	000000	SIG+QTG	531	BN7874_014	Phage NCTB	GCA_900092385.1
AUZ94971.1	000000	DAM-div	325	FDI40_gp189	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21602.1	000123	N4-M.MboIIA-like-DAM	286	GAP32_152	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AGH56874.1	000123	N4-M.MboIIA-like-DAM	301	CPXG_00071	Cyanophage P-RSM6	GCA_000906155.1
AJK27489.1	000123	N4-M.MboIIA-like-DAM	280	PTIM40_60	Cyanophage P-TIM40	GCA_001470935.1
AJK27501.1	000123	N4-M.MboIIA-like-DAM	303	PTIM40_74	Cyanophage P-TIM40	GCA_001470935.1
AMO43224.1	000123	N4-M.MboIIA-like-DAM	251	R1080702_219	Cyanophage S-RIM32	GCA_001754165.1
AGG54440.1	000123	N4-M.MboIIA-like-DAM	316	CYWG_00156	Cyanophage S-SSM6b	GCA_002710425.1
AYD80040.1	000123	N4-M.MboIIA-like-DAM	407	JA11_235	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66639.1	000123	N4-M.MboIIA-like-DAM	407	JA13_236	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66963.1	000123	N4-M.MboIIA-like-DAM	407	JA29_237	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67610.1	000123	N4-M.MboIIA-like-DAM	407	JA33_236	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMM43722.1	000123	N4-M.MboIIA-like-DAM	286	CBB_157	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26175.1	000123	N4-M.MboIIA-like-DAM	335	CPMG_00074	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44419.1	000123	N4-M.MboIIA-like-DAM	322	PSSM2_041	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12232.1	000123	N4-M.MboIIA-like-DAM	327	PRTG_00074	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93494.1	000123	N4-M.MboIIA-like-DAM	258	AVU42_gp157	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93419.1	000123	N4-M.MboIIA-like-DAM	304	AVU42_gp049	Prochlorococcus phage P-TIM68	GCA_001503075.1
AQW88676.1	000123	N4-M.MboIIA-like-DAM	286	BF_0151	Serratia phage BF	GCA_002619745.1
SOK58958.1	000123	N4-M.MboIIA-like-DAM	286	g150	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58424.1	000123	N4-M.MboIIA-like-DAM	286	g147	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95158.1	000124	M.MboIIA-like-cpDAM+HTH	252	FDI40_gp399	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95002.1	000124	M.MboIIA-like-cpDAM+HTH	260	FDI40_gp220	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95017.1	000124	M.MboIIA-like-cpDAM+HTH	269	FDI40_gp235	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72825.1	000124	M.MboIIA-like-cpDAM+HTH	246	-	Myoviridae sp.	GCA_003657725.1
QIG65878.1	000124	M.MboIIA-like-cpDAM+HTH	230	phiOC_p213	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AAX44446.1	000124	M.MboIIA-like-cpDAM+HTH	306	PSSM2_068	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12206.1	000124	M.MboIIA-like-cpDAM+HTH	306	PRTG_00048	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59510.1	000124	M.MboIIA-like-cpDAM+HTH	165	S330809_049	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59272.1	000124	M.MboIIA-like-cpDAM+HTH	165	C440309_049	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59748.1	000124	M.MboIIA-like-cpDAM+HTH	165	N231010_049	Synechococcus phage S-CAM4	GCA_002922155.1
BBI90618.1	000124	M.MboIIA-like-cpDAM+HTH	260	HYO65_gp226	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90924.1	000124	M.MboIIA-like-cpDAM+HTH	260	-	Tenacibaculum phage PTm5	GCA_009730715.1
ALY07242.1	000124	M.MboIIA-like-cpDAM+HTH	243	VmeM32_00256	Vibrio phage vB_VmeM-32	GCA_002608825.1
SOK58518.1	000124	M.MboIIA-like-cpDAM+HTH	268	g241	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD80038.1	000125	M.EcoKI-like-DAM+inactive-DAM	389	JA11_233	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66637.1	000125	M.EcoKI-like-DAM+inactive-DAM	389	JA13_234	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66961.1	000125	M.EcoKI-like-DAM+inactive-DAM	389	JA29_235	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67608.1	000125	M.EcoKI-like-DAM+inactive-DAM	389	JA33_234	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
APU01582.1	000126	M.EcoKI-like-DAM	237	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28967.1	000126	M.EcoKI-like-DAM	238	AP1_0260	Aeromonas phage AP1	GCA_014183365.1
ATI17327.1	000126	M.EcoKI-like-DAM	238	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00267.1	000126	M.EcoKI-like-DAM	238	HWB28_gp285	Aeromonas phage AS-zj	GCA_002627665.1
QAX97770.1	000126	M.EcoKI-like-DAM	238	ASswx1_125	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01384.1	000126	M.EcoKI-like-DAM	238	ASwh1_324	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39571.1	000126	M.EcoKI-like-DAM	238	CC2_412	Aeromonas phage CC2	GCA_000903495.1
ADQ53205.1	000126	M.EcoKI-like-DAM	237	65p197	Aeromonas virus 65	GCA_000893255.1
ANS05992.1	000126	M.EcoKI-like-DAM	244	ABCD_0030	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFC21590.1	000126	M.EcoKI-like-DAM	247	GAP32_140	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97040.1	000126	M.EcoKI-like-DAM	243	E_031	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78552.1	000126	M.EcoKI-like-DAM	244	RB43ORF030c	Escherichia virus RB43	GCA_000863505.1
QHJ78960.1	000126	M.EcoKI-like-DAM	238	-	Myoviridae sp.	GCA_012593985.1
QIG66035.1	000126	M.EcoKI-like-DAM	257	phiOC_p393	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47996.1	000126	M.EcoKI-like-DAM	254	SmphiM12_364	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13183.1	000126	M.EcoKI-like-DAM	254	PHIM19_278	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12822.1	000126	M.EcoKI-like-DAM	254	PHIM7_277	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13545.1	000126	M.EcoKI-like-DAM	254	PHIN3_282	Sinorhizobium phage phiN3	GCA_001501175.1
SOK58945.1	000126	M.EcoKI-like-DAM	247	g137	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58411.1	000126	M.EcoKI-like-DAM	247	g134	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXH72592.1	000127	M.MboIIA-rel-DAM	172	-	Myoviridae sp.	GCA_003657725.1
AQW88654.1	000127	M.MboIIA-rel-DAM	176	BF_0129	Serratia phage BF	GCA_002619745.1
SOK58934.1	000127	M.MboIIA-rel-DAM	176	g126	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58399.1	000127	M.MboIIA-rel-DAM	176	g122	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS05983.1	000128	T4-DAM-like	283	ABCD_0242	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65007.1	000128	T4-DAM-like	258	S13_210	Cronobacter phage S13	GCA_001503575.1
AON97261.1	000128	T4-DAM-like	283	E_253	Cronobacter phage vB_CsaM_leE	GCA_002611805.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH56870.1	000128	T4-DAM-like	285	CPXG_00067	Cyanophage P-RSM6	GCA_000906155.1
AJK27585.1	000128	T4-DAM-like	283	PTIM40_158	Cyanophage P-TIM40	GCA_001470935.1
AOO14345.1	000128	T4-DAM-like	301	Sn110110_151	Cyanophage S-RIM14	GCA_002599065.1
AOO14994.1	000128	T4-DAM-like	301	W1230910_148	Cyanophage S-RIM14	GCA_002599125.1
AMO43163.1	000128	T4-DAM-like	246	R1080702_154	Cyanophage S-RIM32	GCA_001754165.1
AMO43387.1	000128	T4-DAM-like	282	W270710_143	Cyanophage S-RIM44	GCA_002599145.1
AOO11632.1	000128	T4-DAM-like	280	ES420910_151	Cyanophage S-RIM44	GCA_002599165.1
AOO11859.1	000128	T4-DAM-like	282	Np050604_143	Cyanophage S-RIM44	GCA_002599185.1
AOO12097.1	000128	T4-DAM-like	280	Np200711_151	Cyanophage S-RIM44	GCA_002599205.1
AOO12333.1	000128	T4-DAM-like	280	Np420711_151	Cyanophage S-RIM44	GCA_002599225.1
AOO12560.1	000128	T4-DAM-like	282	Sn080709_143	Cyanophage S-RIM44	GCA_002599245.1
AOO12798.1	000128	T4-DAM-like	280	Sn130910_151	Cyanophage S-RIM44	GCA_002599265.1
AOO13026.1	000128	T4-DAM-like	282	W2100709_144	Cyanophage S-RIM44	GCA_002599285.1
AGG54464.1	000128	T4-DAM-like	275	CYWG_00180	Cyanophage S-SSM6b	GCA_002710425.1
AXG67071.1	000128	T4-DAM-like	280	AD1_027	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79821.1	000128	T4-DAM-like	280	JA11_016	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66420.1	000128	T4-DAM-like	280	JA13_017	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66742.1	000128	T4-DAM-like	280	JA29_016	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67390.1	000128	T4-DAM-like	280	JA33_016	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMR59756.1	000128	T4-DAM-like	264	SEGD1_109	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49755.1	000128	T4-DAM-like	273	MACHINA_117	Erwinia phage Machina	GCA_002758035.1
AXF51263.1	000128	T4-DAM-like	273	WELLINGTON_133	Erwinia phage Wellington	GCA_003344985.1
AFQ96573.1	000128	T4-DAM-like	272	G173_gp028	Erwinia phage phiEaH2	GCA_000902915.1
AWY08307.1	000128	T4-DAM-like	280	Alexandra_27	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48134.1	000128	T4-DAM-like	243	ASESINO_121	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48411.1	000128	T4-DAM-like	274	CAITLIN_116	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48683.1	000128	T4-DAM-like	274	CHRISDB_121	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49199.1	000128	T4-DAM-like	273	HUXLEY_117	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03750.1	000128	T4-DAM-like	264	JOAD_165	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49484.1	000128	T4-DAM-like	273	KWAN_132	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50027.1	000128	T4-DAM-like	273	PARSHIK_118	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ASU03506.1	000128	T4-DAM-like	264	RISINGSUN_164	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANZ50548.1	000128	T4-DAM-like	272	STRATTON_123	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARW58669.1	000128	T4-DAM-like	280	Y3_029	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28801.1	000128	T4-DAM-like	279	YOLOSWAG_25	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QKN85946.1	000128	T4-DAM-like	272	ACEC001_1080	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AAX78779.1	000128	T4-DAM-like	283	RB43ORF257w	Escherichia virus RB43	GCA_000863505.1
QHJ78924.1	000128	T4-DAM-like	258	-	Myoviridae sp.	GCA_012593985.1
SBV38331.1	000128	T4-DAM-like	279	BN7874_162	Phage NCTB	GCA_900092385.1
AGH26298.1	000128	T4-DAM-like	279	CPMG_00198	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44543.1	000128	T4-DAM-like	264	PSSM2_165	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12428.1	000128	T4-DAM-like	264	PRTG_00278	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93477.1	000128	T4-DAM-like	274	AVU42_gp140	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99245.1	000128	T4-DAM-like	282	Syn1_144	Prochlorococcus phage Syn1	GCA_000892495.1
QNI20814.1	000128	T4-DAM-like	264	-	Salmonella phage JN03	GCA_014319805.1
AWN09003.2	000128	T4-DAM-like	272	MLDJOKPK_00052	Salmonella phage SPAsTU	GCA_003183805.1
AEP83938.1	000128	T4-DAM-like	264	SPN3US_0105	Salmonella phage SPN3US	GCA_001042275.1
AIX30665.1	000128	T4-DAM-like	299	Syn7803US37_188	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76200.1	000128	T4-DAM-like	284	PBI_BELLAMY_155	Synechococcus phage Bellamy	GCA_002627525.1
AOV59612.1	000128	T4-DAM-like	269	S330809_151	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59374.1	000128	T4-DAM-like	269	C440309_151	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59850.1	000128	T4-DAM-like	269	N231010_151	Synechococcus phage S-CAM4	GCA_002922155.1
QAU04531.1	000128	T4-DAM-like	268	ValB1MD_234	Vibrio phage ValB1MD	GCA_004138815.1
AQT28069.1	000128	T4-DAM-like	276	pVa21_128	Vibrio phage pVa-21	GCA_002619305.1
prevph1000000481	000128	T4-DAM-like	300	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000363	000128	T4-DAM-like	300	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QAX98355.1	000128	T4-DAM-like	289	ASfcp2_9	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52811.1	000128	T4-DAM-like	96	PX29p092	Aeromonas phage PX29	GCA_000920195.1
AIX30669.1	000128	T4-DAM-like	293	Syn7803US37_192	Synechococcus phage ACG-2014f	GCA_002594065.1
AUZ94846.1	000128	T4-DAM-like	234	FDI40_gp034	Agrobacterium phage Atu_ph07	GCA_002628245.1
APU01675.1	000129	cpM.EcoKI-like-DAM	386	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29014.1	000129	cpM.EcoKI-like-DAM	384	AP1_0307	Aeromonas phage AP1	GCA_014183365.1
ATI17620.1	000129	cpM.EcoKI-like-DAM	384	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00376.1	000129	cpM.EcoKI-like-DAM	349	HWB28_gp176	Aeromonas phage AS-zj	GCA_002627665.1
AUE22618.1	000129	cpM.EcoKI-like-DAM	415	Ah1_00077	Aeromonas phage Ah1	GCA_002957415.1
AUE22644.1	000129	cpM.EcoKI-like-DAM	166	Ah1_00103	Aeromonas phage Ah1	GCA_002957415.1
AUE22645.1	000129	cpM.EcoKI-like-DAM	545	Ah1_00104	Aeromonas phage Ah1	GCA_002957415.1
QAX97654.1	000129	cpM.EcoKI-like-DAM	384	ASswx1_8	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01088.1	000129	cpM.EcoKI-like-DAM	382	ASwh1_20	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39345.1	000129	cpM.EcoKI-like-DAM	383	CC2_106	Aeromonas phage CC2	GCA_000903495.1
ADQ52802.1	000129	cpM.EcoKI-like-DAM	415	PX29p083	Aeromonas phage PX29	GCA_000920195.1
ADM80058.1	000129	cpM.EcoKI-like-DAM	417	phiAS5_ORF0215	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53309.1	000129	cpM.EcoKI-like-DAM	386	p65301	Aeromonas virus 65	GCA_000893255.1
AAQ17745.1	000129	cpM.EcoKI-like-DAM	415	Aeh1ORF084c	Aeromonas virus Aeh1	GCA_000843245.1
AXH72787.1	000129	cpM.EcoKI-like-DAM	189	-	Myoviridae sp.	GCA_003657725.1
AAX44415.1	000129	cpM.EcoKI-like-DAM	132	PSSM2_037	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12236.1	000129	cpM.EcoKI-like-DAM	132	PRTG_00078	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIX30528.1	000129	cpM.EcoKI-like-DAM	134	Syn7803US37_51	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76133.1	000129	cpM.EcoKI-like-DAM	134	PBI_BELLAMY_88	Synechococcus phage Bellamy	GCA_002627525.1
ALP47484.1	000129	cpM.EcoKI-like-DAM	167	phiST2_0372	Vibrio phage phi-ST2	GCA_002757135.1
prev15ph1000000049	000129	cpM.EcoKI-like-DAM	146	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000063	000129	cpM.EcoKI-like-DAM	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000065	000129	cpM.EcoKI-like-DAM	449	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000051	000129	cpM.EcoKI-like-DAM	449	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000064	000129	cpM.EcoKI-like-DAM	168	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000050	000129	cpM.EcoKI-like-DAM	159	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFC21516.1	000130	DAM-minimal	180	GAP32_068	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14307.1	000130	DAM-minimal	173	PBI_121Q_417	Escherichia phage 121Q	GCA_000926855.1
QAY00631.1	000130	DAM-minimal	174	Ecwhy1_356	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34828.1	000130	DAM-minimal	173	ACQ29_gp148	Escherichia phage PBECO4	GCA_001041035.1
BBM61981.1	000130	DAM-minimal	173	EO157G_3920	Escherichia phage SP27	GCA_008033345.1
AXC36936.1	000130	DAM-minimal	173	-	Escherichia phage UB	GCA_003341455.1
QBO61997.1	000130	DAM-minimal	173	G17_00508	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14018.1	000130	DAM-minimal	173	vBEcoMphAPEC6_gp394c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80294.1	000130	DAM-minimal	173	PSLUR01_00317	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44720.1	000130	DAM-minimal	172	RaK2_00447	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43637.1	000130	DAM-minimal	180	CBB_72	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44390.1	000130	DAM-minimal	119	PBI_SCTP2_375	Salicola phage SCTP-2	GCA_002625545.1
QCW18768.1	000130	DAM-minimal	176	7t3_0247	Salmonella phage 7t3	GCA_006083215.1
AZU98034.1	000130	DAM-minimal	176	CPT_Munch_090	Salmonella phage Munch	GCA_004015485.1
QIG62946.1	000130	DAM-minimal	176	SEPL_333	Salmonella phage SE_PL	GCA_011067555.1
AQW88588.1	000130	DAM-minimal	179	BF_0063	Serratia phage BF	GCA_002619745.1
SOK58864.1	000130	DAM-minimal	179	g056	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58327.1	000130	DAM-minimal	179	g050	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13654.1	000131	DAM	215	Ccr10_gp125c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13999.1	000131	DAM	215	Ccr2_gp124c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14687.1	000131	DAM	215	Ccr29_gp131	Caulobacter phage Ccr29	GCA_002619485.1
ARB15041.1	000131	DAM	215	Ccr32_gp123	Caulobacter phage Ccr32	GCA_002619505.1
ARB15374.1	000131	DAM	215	Ccr34_gp132	Caulobacter phage Ccr34	GCA_002619525.1
ARB14342.1	000131	DAM	215	Ccr5_gp124c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68322.1	000131	DAM	204	CcrBL10_gp118c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69209.1	000131	DAM	213	CcrBL9_gp185	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88032.1	000131	DAM	267	CcrColossus_gp162	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68709.1	000131	DAM	267	CcrPW_gp170c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69763.1	000131	DAM	201	CcrSC_gp181	Caulobacter phage CcrSC	GCA_003443315.1
AFU87646.1	000131	DAM	204	CcrKarma_gp129	Caulobacter virus Karma	GCA_000901575.1
AFU87295.1	000131	DAM	215	CcrMagneto_gp125	Caulobacter virus Magneto	GCA_000903095.1
AFU86606.1	000131	DAM	204	CcrRogue_gp124	Caulobacter virus Rogue	GCA_000900555.1
AFU88442.1	000131	DAM	204	CcrSwift_gp124	Caulobacter virus Swift	GCA_000899655.1
AFU86959.1	000131	DAM	204	CbK_gp127	Caulobacter virus phiCbK	GCA_000900535.1
AXH72805.1	000131	DAM	190	-	Myoviridae sp.	GCA_003657725.1
AKF13105.1	000131	DAM	191	PHIM19_200	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12745.1	000131	DAM	191	PHIM7_200	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13475.1	000131	DAM	191	PHIN3_212	Sinorhizobium phage phiN3	GCA_001501175.1
AUZ95259.1	000132	DAM	301	FDI40_gp500	Agrobacterium phage Atu_ph07	GCA_002628245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69244.1	000132	DAM	230	CcrBL9_gp220	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87970.1	000132	DAM	211	CcrColossus_gp100	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68644.1	000132	DAM	231	CcrPW_gp105c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68647.1	000132	DAM	211	CcrPW_gp108	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69799.1	000132	DAM	142	CcrSC_gp217	Caulobacter phage CcrSC	GCA_003443315.1
QIG66036.1	000132	DAM	219	phiOC_p394	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47641.2	000132	DAM	211	SmphiM12_009	Sinorhizobium phage phiM12	GCA_001023565.1
AGR48098.1	000132	DAM	314	SmphiM12_466	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12908.1	000132	DAM	309	PHIM19_1	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12549.1	000132	DAM	344	PHIM7_1	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13631.1	000132	DAM	314	PHIN3_368	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13276.1	000132	DAM	211	PHIN3_9	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64207.1	000133	DAM	192	KVP40.0137	Vibrio phage KVP40	GCA_000843785.1
QIW90522.1	000133	DAM	192	GCAPEGMB_00175	Vibrio phage V07	GCA_012361095.1
QIW90900.1	000133	DAM	192	COHAPHLL_00037	Vibrio phage V09	GCA_012361135.1
QHJ74318.1	000133	DAM	192	VH12019_00399	Vibrio phage VH1_2019	GCA_009931825.1
AGB06812.1	000133	DAM	192	CF80_gp025	Vibrio phage VH7D	GCA_000914495.1
QBX06335.1	000133	DAM	192	ValB1HC_382	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60965.1	000133	DAM	192	AVU32_gp124	Vibrio phage ValKK3	GCA_001501635.1
AGN30186.1	000133	DAM	190	VPFG_00186	Vibrio phage nt-1	GCA_000910195.2
ALP47076.1	000133	DAM	192	phiGrn1_0248	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47456.1	000133	DAM	192	phiST2_0003	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54578.1	000133	DAM	192	vBValMR10Z_37	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37368.1	000133	DAM	192	pp2_135	Vibriophage phi-pp2	GCA_002630725.1
AYD81182.1	000134	DAM	186	SEA_JUSTBECAUSE_13	Streptomyces phage JustBecause	GCA_003613775.1
QJD53584.1	000134	DAM	212	SEA_KELA_13	Streptomyces phage Kela	GCA_012934305.1
QBZ71914.1	000134	DAM	186	SEA_KRADAL_15	Streptomyces phage Kradal	GCA_004799925.1
AXH66176.1	000134	DAM	186	SEA_SATIS_15	Streptomyces phage Satis	GCA_003366315.1
AIX30530.1	000135	DAM	393	Syn7803US37_53	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76131.1	000135	DAM	417	PBI_BELLAMY_86	Synechococcus phage Bellamy	GCA_002627525.1
BBI90669.1	000136	DAM	344	HYO65_gp277	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90974.1	000136	DAM	344	-	Tenacibaculum phage PTm5	GCA_009730715.1
AFU88228.1	000137	DAM	181	CcrColossus_gp358	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68905.1	000137	DAM	181	CcrPW_gp366	Caulobacter phage CcrPW	GCA_003443275.1
BBI90483.1	000138	DAM	163	HYO65_gp091	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90791.1	000138	DAM	163	-	Tenacibaculum phage PTm5	GCA_009730715.1
ABS83768.1	000000	DAM	220	0305phi8-36p210	Bacillus phage 0305phi8-36	GCA_000871045.1
BAE47709.1	000000	DAM	560	CST011	Clostridium phage c-st	GCA_000865225.1
ALY07195.1	000000	DAM	325	VmeM32_00209	Vibrio phage vB_VmeM-32	GCA_002608825.1
QIG63347.1	000139	DAM	387	DAC16_114	Bacteroides phage DAC16	GCA_013387695.1
QIG63613.1	000139	DAM	387	DAC19_122	Bacteroides phage DAC19	GCA_013387715.1
QIG63874.1	000139	DAM	387	DAC20_121	Bacteroides phage DAC20	GCA_013387725.1
QIG64137.1	000139	DAM	387	DAC22_123	Bacteroides phage DAC22	GCA_013387735.1
QIG64394.1	000139	DAM	387	DAC23_116	Bacteroides phage DAC23	GCA_013387745.1
CCH63598.1	000000	DAM	354	CP21_136	Campylobacter virus CP21	GCA_000902535.1
CCH63599.1	000000	DAM	148	CP21_137	Campylobacter virus CP21	GCA_000902535.1
AEO93553.1	000000	DAM	362	G_294	Bacillus virus G	GCA_000917535.1
CCH63513.1	000000	DAMT1	188	CP21_051	Campylobacter virus CP21	GCA_000902535.1
AGH07745.1	000140	MK-like Methylase	234	CYVG_00302	Cyanophage S-SSM6a	GCA_002710385.1
AAX44565.1	000140	MK-like Methylase	214	PSSM2_187	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12408.1	000140	MK-like Methylase	214	PRTG_00255	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGH07447.1	000141	2OGFeDO	232	CYVG_00003	Cyanophage S-SSM6a	GCA_002710385.1
AGH07735.1	000141	2OGFeDO	219	CYVG_00292	Cyanophage S-SSM6a	GCA_002710385.1
AGH07736.1	000142	Glycosyltransferase	397	CYVG_00293	Cyanophage S-SSM6a	GCA_002710385.1
AAX44684.1	000142	Glycosyltransferase	370	PSSM2_307	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12292.1	000142	Glycosyltransferase	370	PRTG_00139	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGH07737.1	000143	Carbamoyltransferase	600	CYVG_00294	Cyanophage S-SSM6a	GCA_002710385.1
AGH07595.1	000143	Carbamoyltransferase	511	CYVG_00151	Cyanophage S-SSM6a	GCA_002710385.1
AGG54489.1	000143	Carbamoyltransferase	513	CYWG_00205	Cyanophage S-SSM6b	GCA_002710425.1
AAX44685.1	000143	Carbamoyltransferase	600	PSSM2_308	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44555.1	000143	Carbamoyltransferase	571	PSSM2_177	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12291.1	000143	Carbamoyltransferase	600	PRTG_00138	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGH07466.1	000143	Carbamoyltransferase	524	CYVG_00022	Cyanophage S-SSM6a	GCA_002710385.1
AGH56867.1	000143	Carbamoyltransferase	484	CPXG_00064	Cyanophage P-RSM6	GCA_000906155.1
BBA65481.1	000143	Carbamoyltransferase	765	-	Xanthomonas phage XacN1	GCA_003173815.1
AXQ70462.1	000143	Carbamoyltransferase	501	HOU04_gp063	Synechococcus phage S-T4	GCA_003443335.1
QDJ96489.1	000143	Carbamoyltransferase	765	Xoosp13_303	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AOO12178.1	000143	Carbamoyltransferase	181	Np200711_236	Cyanophage S-RIM44	GCA_002599205.1
AOO11712.1	000143	Carbamoyltransferase	181	ES420910_235	Cyanophage S-RIM44	GCA_002599165.1
AOO12413.1	000143	Carbamoyltransferase	181	Np420711_235	Cyanophage S-RIM44	GCA_002599225.1
AOO12878.1	000143	Carbamoyltransferase	181	Sn130910_235	Cyanophage S-RIM44	GCA_002599265.1
QJT70214.1	000144	Glycosyltransferase+Carbamoyltransferase	839	SynMITS9220M01_208	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASR76259.1	000144	Glycosyltransferase+Carbamoyltransferase	524	PBI_BELLAMY_223	Synechococcus phage Bellamy	GCA_002627525.1
AOO11713.1	000145	Carbam_trans_N	337	ES420910_236	Cyanophage S-RIM44	GCA_002599165.1
AOO12879.1	000145	Carbam_trans_N	337	Sn130910_236	Cyanophage S-RIM44	GCA_002599265.1
AOO12414.1	000145	Carbam_trans_N	337	Np420711_236	Cyanophage S-RIM44	GCA_002599225.1
AOO12179.1	000145	Carbam_trans_N	337	Np200711_237	Cyanophage S-RIM44	GCA_002599205.1
AGH07739.1	000145	Carbam_trans_N	369	CYVG_00296	Cyanophage S-SSM6a	GCA_002710385.1
QGT54599.1	000146	Glycosyltransferase	316	b3_0364	Synechococcus phage B3	GCA_009745215.1
QGT54964.1	000146	Glycosyltransferase	316	b23_0358	Synechococcus phage B23	GCA_009745195.1
ASR76258.1	000146	Glycosyltransferase	317	PBI_BELLAMY_222	Synechococcus phage Bellamy	GCA_002627525.1
QJT70209.1	000146	Glycosyltransferase	312	SynMITS9220M01_203	Synechococcus phage SynMITS9220M01	GCA_013187275.1
CCH63630.1	000147	Trp_halogenase	399	CP21_168	Campylobacter virus CP21	GCA_000902535.1
AGH56986.1	000147	Trp_halogenase	526	CPXG_00183	Cyanophage P-RSM6	GCA_000906155.1
AGH56987.1	000147	Trp_halogenase	528	CPXG_00184	Cyanophage P-RSM6	GCA_000906155.1
AJK27650.1	000147	Trp_halogenase	379	PTIM40_228	Cyanophage P-TIM40	GCA_001470935.1
AJK27473.1	000147	Trp_halogenase	489	PTIM40_46	Cyanophage P-TIM40	GCA_001470935.1
AJK27474.1	000147	Trp_halogenase	545	PTIM40_47	Cyanophage P-TIM40	GCA_001470935.1
AOO14219.1	000147	Trp_halogenase	359	Sn110110_025	Cyanophage S-RIM14	GCA_002599065.1
AOO14871.1	000147	Trp_halogenase	359	W1230910_025	Cyanophage S-RIM14	GCA_002599125.1
AMO43443.1	000147	Trp_halogenase	478	W270710_203	Cyanophage S-RIM44	GCA_002599145.1
AOO11582.1	000147	Trp_halogenase	499	ES420910_101	Cyanophage S-RIM44	GCA_002599165.1
AOO11583.1	000147	Trp_halogenase	540	ES420910_102	Cyanophage S-RIM44	GCA_002599165.1
AOO11686.1	000147	Trp_halogenase	478	ES420910_208	Cyanophage S-RIM44	GCA_002599165.1
AOO11915.1	000147	Trp_halogenase	478	Np050604_203	Cyanophage S-RIM44	GCA_002599185.1
AOO12047.1	000147	Trp_halogenase	499	Np200711_101	Cyanophage S-RIM44	GCA_002599205.1
AOO12048.1	000147	Trp_halogenase	540	Np200711_102	Cyanophage S-RIM44	GCA_002599205.1
AOO12152.1	000147	Trp_halogenase	478	Np200711_209	Cyanophage S-RIM44	GCA_002599205.1
AOO12283.1	000147	Trp_halogenase	499	Np420711_101	Cyanophage S-RIM44	GCA_002599225.1
AOO12284.1	000147	Trp_halogenase	540	Np420711_102	Cyanophage S-RIM44	GCA_002599225.1
AOO12387.1	000147	Trp_halogenase	478	Np420711_208	Cyanophage S-RIM44	GCA_002599225.1
AOO12616.1	000147	Trp_halogenase	478	Sn080709_203	Cyanophage S-RIM44	GCA_002599245.1
AOO12748.1	000147	Trp_halogenase	499	Sn130910_101	Cyanophage S-RIM44	GCA_002599265.1
AOO12749.1	000147	Trp_halogenase	540	Sn130910_102	Cyanophage S-RIM44	GCA_002599265.1
AOO12852.1	000147	Trp_halogenase	478	Sn130910_208	Cyanophage S-RIM44	GCA_002599265.1
AOO13082.1	000147	Trp_halogenase	478	W2100709_204	Cyanophage S-RIM44	GCA_002599285.1
AGH07521.1	000147	Trp_halogenase	367	CYVG_00077	Cyanophage S-SSM6a	GCA_002710385.1
AGH07741.1	000147	Trp_halogenase	495	CYVG_00298	Cyanophage S-SSM6a	GCA_002710385.1
AAX44594.1	000147	Trp_halogenase	485	PSSM2_217	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12377.1	000147	Trp_halogenase	409	PRTG_00224	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99302.1	000147	Trp_halogenase	478	Syn1_205	Prochlorococcus phage Syn1	GCA_000892495.1
AGH07743.1	000148	PfkB	279	CYVG_00300	Cyanophage S-SSM6a	GCA_002710385.1
AAX44687.1	000148	PfkB	252	PSSM2_310	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12289.1	000148	PfkB	256	PRTG_00136	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93528.1	000148	PfkB	247	AVU42_gp191	Prochlorococcus phage P-TIM68	GCA_001503075.1
AXQ70511.1	000148	PfkB	220	HOU04_gp112	Synechococcus phage S-T4	GCA_003443335.1
AGH07747.1	000149	DSBH	133	CYVG_00304	Cyanophage S-SSM6a	GCA_002710385.1
AAX44689.1	000149	DSBH	118	PSSM2_312	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12287.1	000149	DSBH	125	PRTG_00134	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93531.1	000149	DSBH	143	AVU42_gp194	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76252.1	000149	DSBH	116	PBI_BELLAMY_216	Synechococcus phage Bellamy	GCA_002627525.1
AXQ70507.1	000149	DSBH	61	HOU04_gp108	Synechococcus phage S-T4	GCA_003443335.1
QJT70203.1	000149	DSBH	116	SynMITS9220M01_197	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXQ69461.1	000150	NAD_synthase	254	CcrBL9_gp437	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88243.1	000150	NAD_synthase	255	CcrColossus_gp373	Caulobacter phage CcrColossus	GCA_000899635.1

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AXQ68918.1	000150	NAD_synthase	255	CcrPW_gp379c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70010.1	000150	NAD_synthase	254	CcrSC_gp428	Caulobacter phage CcrSC	GCA_003443315.1
BBA65504.1	000150	NAD_synthase	246	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96509.1	000150	NAD_synthase	237	Xoosp13_323	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AND75459.1	000151	NAD_synthase	256	ME3_298	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ94924.1	000151	NAD_synthase	556	FDI40_gp135	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93542.1	000151	NAD_synthase	275	G_283	Bacillus virus G	GCA_000917535.1
AGH07570.1	000151	NAD_synthase	253	CYVG_00126	Cyanophage S-SSM6a	GCA_002710385.1
AIR93516.1	000151	NAD_synthase	246	AVU42_gp179	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76261.1	000151	NAD_synthase	246	PBI_BELLAMY_225	Synechococcus phage Bellamy	GCA_002627525.1
AMR59769.1	000152	QueC	297	SEGD1_122	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49772.1	000152	QueC	354	MACHINA_134	Erwinia phage Machina	GCA_002758035.1
AXF51275.1	000152	QueC	328	WELLINGTON_146	Erwinia phage Wellington	GCA_003344985.1
AFQ96587.1	000152	QueC	353	G173_gp042	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48148.1	000152	QueC	371	ASESINO_135	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48426.1	000152	QueC	344	CAITLIN_131	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48699.1	000152	QueC	352	CHRISDB_137	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49216.1	000152	QueC	354	HUXLEY_134	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49498.1	000152	QueC	328	KWAN_146	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50044.1	000152	QueC	354	PARSHIK_135	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50564.1	000152	QueC	370	STRATTON_139	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85959.1	000152	QueC	335	ACEC001_1210	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20823.1	000152	QueC	335	-	Salmonella phage JN03	GCA_014319805.1
AXF51066.1	000152	QueC	335	MLDJOKPK_00036	Salmonella phage SPAsTU	GCA_003183805.1
AEP83952.1	000152	QueC	335	SPN3US_0119	Salmonella phage SPN3US	GCA_001042275.1
QKE54344.1	000152	QueC	307	ACSA002_0300	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QDH83432.1	000153	QueC	200	H1O15_gp024	Achromobacter phage Motura	GCA_006964305.1
CCH63714.1	000153	QueC	219	CP21_254	Campylobacter virus CP21	GCA_000902535.1
AAQ64195.1	000153	QueC	238	KVP40.0124	Vibrio phage KVP40	GCA_000843785.1
QIW90511.1	000153	QueC	238	GCAPEGMB_00164	Vibrio phage V07	GCA_012361095.1
QIW90776.1	000153	QueC	462	GCAPEGMB_00457	Vibrio phage V07	GCA_012361095.1
QIW90911.1	000153	QueC	238	COHAPHLL_00048	Vibrio phage V09	GCA_012361135.1
QHJ74307.1	000153	QueC	238	VH12019_00388	Vibrio phage VH1_2019	GCA_009931825.1
AGB06801.1	000153	QueC	238	CF80_gp014	Vibrio phage VH7D	GCA_000914495.1
QBX05965.1	000153	QueC	238	ValB1HC_011	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60977.1	000153	QueC	238	AVU32_gp136	Vibrio phage ValKK3	GCA_001501635.1
AGN30174.1	000153	QueC	238	VPFG_00172	Vibrio phage nt-1	GCA_000910195.2
ALP47049.1	000153	QueC	238	phiGrn1_0236	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47426.1	000153	QueC	238	phiST2_0374	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54590.1	000153	QueC	238	vBValMR10Z_49	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37355.1	000153	QueC	238	pp2_122	Vibriophage phi-pp2	GCA_002630725.1
AXH72806.1	000154	QueC	204	-	Myoviridae sp.	GCA_003657725.1
ARV77198.1	000154	QueC	326	NOXIFER_27	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32403.1	000154	QueC	245	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41973.1	000154	QueC	245	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAS04945.1	000154	QueC	280	AVU11_gp153	Ralstonia phage RSF1	GCA_001500875.1
BAQ02669.1	000154	QueC	283	AVU38_gp141	Ralstonia phage RSL2	GCA_001503055.1
AAQ64327.1	000155	QueC	228	KVP40.0258	Vibrio phage KVP40	GCA_000843785.1
QIW90642.1	000155	QueC	227	GCAPEGMB_00295	Vibrio phage V07	GCA_012361095.1
QIW91157.1	000155	QueC	227	COHAPHLL_00321	Vibrio phage V09	GCA_012361135.1
QHJ74437.1	000155	QueC	227	VH12019_00110	Vibrio phage VH1_2019	GCA_009931825.1
AFN37486.1	000155	QueC	227	pp2_253	Vibriophage phi-pp2	GCA_002630725.1
SBV38455.1	000000	QueC	263	BN7874_252	Phage NCTB	GCA_900092385.1
AMM44912.1	000000	QueC	245	SP15_114	Bacillus phage SP-15	GCA_001754685.1
CAG27294.1	000000	QueC	305	PPEV_gp200	Pseudomonas phage EL	GCA_000866825.1
AQT27978.1	000000	QueC	354	pVa21_036	Vibrio phage pVa-21	GCA_002619305.1
QDH83436.1	000156	QueE	282	H1O15_gp028	Achromobacter phage Motura	GCA_006964305.1
CCH63607.1	000156	QueE	264	CP21_145	Campylobacter virus CP21	GCA_000902535.1
SBV38478.1	000156	QueE	291	BN7874_269	Phage NCTB	GCA_900092385.1
QCG76203.1	000156	QueE	290	EST35_0322	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAQ64354.1	000156	QueE	293	KVP40.0284	Vibrio phage KVP40	GCA_000843785.1
QIW90668.1	000156	QueE	293	GCAPEGMB_00321	Vibrio phage V07	GCA_012361095.1
QIW91130.1	000156	QueE	293	COHAPHLL_00294	Vibrio phage V09	GCA_012361135.1
QHJ74463.1	000156	QueE	293	VH12019_00136	Vibrio phage VH1_2019	GCA_009931825.1
AGB06957.1	000156	QueE	294	CF80_gp170	Vibrio phage VH7D	GCA_000914495.1
QBX06188.1	000156	QueE	294	ValB1HC_235	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61205.1	000156	QueE	294	AVU32_gp364	Vibrio phage ValKK3	GCA_001501635.1
AGN30330.1	000156	QueE	291	VPFG_00333	Vibrio phage nt-1	GCA_000910195.2
ALP47028.1	000156	QueE	294	phiGrn1_0017	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47407.1	000156	QueE	294	phiST2_0148	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54813.1	000156	QueE	294	vBValMR10Z_273	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37515.1	000156	QueE	293	pp2_282	Vibriophage phi-pp2	GCA_002630725.1
QIW90777.1	000000	QueE	234	GCAPEGMB_00458	Vibrio phage V07	GCA_012361095.1
AIA64870.1	000157	RnaseH	160	S13_071	Cronobacter phage S13	GCA_001503575.1
QHJ79069.1	000157	RnaseH	152	-	Myoviridae sp.	GCA_012593985.1
QFR59290.1	000000	RnaseH	42	PS2_0149	Aeromonas phage PS2	GCA_009388305.2
AUZ95397.1	000000	RnaseH	122	FDI40_gp638	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93431.1	000000	RnaseH	149	G_171	Bacillus virus G	GCA_000917535.1
BBA65342.1	000000	RnaseH	87	-	Xanthomonas phage XacN1	GCA_003173815.1
QDB70312.1	000158	RnaseH	181	CF8_0144	Aeromonas phage CF8	GCA_006384595.2
QDB70378.1	000158	RnaseH	473	CF8_0209	Aeromonas phage CF8	GCA_006384595.2
QDJ97296.1	000158	RnaseH	181	D6_0136	Aeromonas phage D6	GCA_007051205.2
QDJ97377.1	000158	RnaseH	474	D6_0218	Aeromonas phage D6	GCA_007051205.2
QDH47054.1	000158	RnaseH	474	LAh10_132	Aeromonas phage LAh10	GCA_006863975.1
QDH47183.1	000158	RnaseH	150	LAh10_61	Aeromonas phage LAh10	GCA_006863975.1
QDJ96659.1	000158	RnaseH	180	PS1_0148	Aeromonas phage PS1	GCA_007051165.2
QDJ96720.1	000158	RnaseH	474	PS1_0209	Aeromonas phage PS1	GCA_007051165.2
QFR59292.1	000158	RnaseH	180	PS2_0151	Aeromonas phage PS2	GCA_009388305.2
QFR59353.1	000158	RnaseH	474	PS2_0211	Aeromonas phage PS2	GCA_009388305.2
AMS01325.1	000158	RnaseH	177	AR9_g241	Bacillus phage AR9	GCA_001743835.1
ALN97976.1	000158	RnaseH	174	Bp8pS_297	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99954.1	000158	RnaseH	177	PBI_PBS1_132	Bacillus virus PBS1	GCA_002601325.1
AFO71406.1	000158	RnaseH	513	CR5_186	Cronobacter phage CR5	GCA_000910235.1
AFC21759.1	000158	RnaseH	144	GAP32_309	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QBZ70676.1	000158	RnaseH	161	pETSU_095	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70762.1	000158	RnaseH	473	pETSU_181	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59858.1	000158	RnaseH	504	SEGD1_211	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07618.1	000158	RnaseH	513	DERBICUS_192	Erwinia phage Derbicus	GCA_004521655.1
AHI60297.1	000158	RnaseH	506	Ea357_146	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49856.1	000158	RnaseH	506	MACHINA_218	Erwinia phage Machina	GCA_002758035.1
AGX01899.1	000158	RnaseH	526	rnhA	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07255.1	000158	RnaseH	506	REBECCA_148	Erwinia phage Rebecca	GCA_004521635.1
AXF51358.1	000158	RnaseH	506	WELLINGTON_232	Erwinia phage Wellington	GCA_003344985.1
AFQ96673.1	000158	RnaseH	503	G173_gp128	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48239.1	000158	RnaseH	503	ASESINO_226	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85935.1	000158	RnaseH	506	BOSOLAPHORUS_148	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48513.1	000158	RnaseH	508	CAITLIN_218	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48790.1	000158	RnaseH	508	CHRISDB_228	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52250.1	000158	RnaseH	506	DM_152	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86254.1	000158	RnaseH	506	DESERTFOX_147	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49042.1	000158	RnaseH	513	EARLPHILLIPIV_193	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49300.1	000158	RnaseH	506	HUXLEY_218	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03803.1	000158	RnaseH	182	JOAD_112	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03697.1	000158	RnaseH	502	JOAD_218	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49584.1	000158	RnaseH	506	KWAN_232	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86576.1	000158	RnaseH	506	MADMEL_148	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86900.1	000158	RnaseH	506	MORTIMER_151	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50128.1	000158	RnaseH	506	PARSHIK_219	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50390.1	000158	RnaseH	511	PHOBOS_200	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51928.1	000158	RnaseH	506	RAY_147	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03558.1	000158	RnaseH	182	RISINGSUN_112	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03454.1	000158	RnaseH	502	RISINGSUN_216	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51612.1	000158	RnaseH	506	SIMMY50_150	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64959.1	000158	RnaseH	506	SPECIALG_149	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50653.1	000158	RnaseH	503	STRATTON_228	Erwinia phage vB_EamM_Stratton	GCA_002600675.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIT13940.1	000158	RnaseH	142	PBI_121Q_43	Escherichia phage 121Q	GCA_000926855.1
QAY00397.1	000158	RnaseH	144	Ecwhy1_116	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35142.1	000158	RnaseH	142	ACQ29_gp462	Escherichia phage PBECO4	GCA_001041035.1
BBM61632.1	000158	RnaseH	142	EO157G_0430	Escherichia phage SP27	GCA_008033345.1
AXC36716.1	000158	RnaseH	142	-	Escherichia phage UB	GCA_003341455.1
QKN86047.1	000158	RnaseH	504	ACEC001_2040	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61753.1	000158	RnaseH	142	G17_00264	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO64037.1	000158	RnaseH	508	Goslar_00246	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13798.1	000158	RnaseH	142	vBEcoMphAPEC6_gp169c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80534.1	000158	RnaseH	142	PSLUR01_00557	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QGH71991.1	000158	RnaseH	123	N1M2_128	Klebsiella phage N1M2	GCA_010092605.1
QGH72069.1	000158	RnaseH	473	N1M2_206	Klebsiella phage N1M2	GCA_010092605.1
AMM43877.1	000158	RnaseH	144	CBB_314	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QGZ14464.1	000158	RnaseH	174	HWC77_gp101	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14498.1	000158	RnaseH	510	HWC77_gp135	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24078.1	000158	RnaseH	516	-	Proteus phage 10	GCA_014071245.1
ABY63069.1	000158	RnaseH	486	201phi2-1p240	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27218.1	000158	RnaseH	163	PPEV_gp124	Pseudomonas phage EL	GCA_000866825.1
CAG27265.1	000158	RnaseH	503	PPEV_gp171	Pseudomonas phage EL	GCA_000866825.1
ANM44949.1	000158	RnaseH	482	KTN4_191	Pseudomonas phage KTN4	GCA_002607225.1
ARV77338.1	000158	RnaseH	492	NOXIFER_169	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89595.1	000158	RnaseH	180	OBP_158	Pseudomonas phage OBP	GCA_000896635.1
AEV89698.1	000158	RnaseH	457	OBP_261	Pseudomonas phage OBP	GCA_000896635.1
QBX32336.1	000158	RnaseH	481	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76859.1	000158	RnaseH	481	PHABIO_228	Pseudomonas phage Phabio	GCA_002624965.1
AEH03601.1	000158	RnaseH	482	178	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02738.1	000158	RnaseH	482	PSA21_212	Pseudomonas phage Psa21	GCA_004340405.1
ATN94765.1	000158	RnaseH	482	SL2_188	Pseudomonas phage SL2	GCA_002956015.1
QJB22827.1	000158	RnaseH	482	fnug_184	Pseudomonas phage fnug	GCA_012837215.1
QEM41910.1	000158	RnaseH	481	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83056.1	000158	RnaseH	482	PHIKZ155	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19036.1	000158	RnaseH	533	FDH28_gp062	Ralstonia phage RP12	GCA_002617345.1
BAW19321.1	000158	RnaseH	533	-	Ralstonia phage RP31	GCA_002617365.1
BAS04849.2	000158	RnaseH	506	AVU11_gp057	Ralstonia phage RSF1	GCA_001500875.1
BAQ02582.1	000158	RnaseH	529	AVU38_gp054	Ralstonia phage RSL2	GCA_001503055.1
QCW19036.1	000158	RnaseH	144	7t3_0516	Salmonella phage 7t3	GCA_006083215.1
QNI20895.1	000158	RnaseH	504	-	Salmonella phage JN03	GCA_014319805.1
AZU98283.1	000158	RnaseH	144	CPT_Munch_339	Salmonella phage Munch	GCA_004015485.1
QIG62701.1	000158	RnaseH	144	SEPL_088	Salmonella phage SE_PL	GCA_011067555.1
AWN09140.1	000158	RnaseH	503	MLDJOKPK_00233	Salmonella phage SPAsTU	GCA_003183805.1
AEP84040.1	000158	RnaseH	504	SPN3US_0207	Salmonella phage SPN3US	GCA_001042275.1
QKE54451.1	000158	RnaseH	504	ACSA002_1370	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65409.1	000158	RnaseH	526	2050HW_00074	Serratia phage 2050HW	GCA_002628125.1
AQW88836.1	000158	RnaseH	145	BF_0311	Serratia phage BF	GCA_002619745.1
QDB71188.1	000158	RnaseH	526	CPT_Moabite_158	Serratia phage Moabite	GCA_006384735.1
QFP93068.1	000158	RnaseH	522	-	Serratia phage PCH45	GCA_009187865.1
QAU04270.1	000158	RnaseH	174	HWC03_gp115	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04236.1	000158	RnaseH	510	HWC03_gp081	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23095.1	000158	RnaseH	174	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23127.1	000158	RnaseH	510	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80943.1	000158	RnaseH	510	Aphrodite1_0004	Vibrio phage Aphrodite1	GCA_002958015.1
AUR81037.1	000158	RnaseH	174	Aphrodite1_0038	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70751.1	000158	RnaseH	460	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47421.1	000158	RnaseH	174	HWC35_gp027	Vibrio phage USC-1	GCA_006864065.1
QDH47600.1	000158	RnaseH	510	HWC35_gp206	Vibrio phage USC-1	GCA_006864065.1
BAW98241.1	000158	RnaseH	174	FDH33_gp032	Vibrio phage pTD1	GCA_002618825.1
BAW98415.1	000158	RnaseH	496	FDH33_gp206	Vibrio phage pTD1	GCA_002618825.1
AQT28081.1	000158	RnaseH	474	pVa21_140	Vibrio phage pVa-21	GCA_002619305.1
QAX96787.1	000158	RnaseH	484	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97106.1	000158	RnaseH	484	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96152.1	000158	RnaseH	484	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96470.1	000158	RnaseH	484	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20961.1	000158	RnaseH	453	-	Vibrio phage vB_pir03	GCA_014319855.1
SOK59120.1	000158	RnaseH	145	g312	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58586.1	000158	RnaseH	145	g309	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26236.1	000158	RnaseH	229	g213	Yersinia phage phiR1-37	GCA_000895615.1
QIG63358.1	000159	RnaseH	196	DAC16_125	Bacteroides phage DAC16	GCA_013387695.1
QIG63623.1	000159	RnaseH	196	DAC19_132	Bacteroides phage DAC19	GCA_013387715.1
QIG63884.1	000159	RnaseH	196	DAC20_131	Bacteroides phage DAC20	GCA_013387725.1
QIG64147.1	000159	RnaseH	196	DAC22_133	Bacteroides phage DAC22	GCA_013387735.1
QIG64404.1	000159	RnaseH	196	DAC23_126	Bacteroides phage DAC23	GCA_013387745.1
AUZ94847.1	000160	RecB_like_REase	226	FDI40_gp035	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21745.1	000160	RecB_like_REase	233	GAP32_295	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AGH57020.1	000160	RecB_like_REase	232	CPXG_00217	Cyanophage P-RSM6	GCA_000906155.1
AJK27664.1	000160	RecB_like_REase	224	PTIM40_1	Cyanophage P-TIM40	GCA_001470935.1
AOO14413.1	000160	RecB_like_REase	223	Sn110110_220	Cyanophage S-RIM14	GCA_002599065.1
AOO15062.1	000160	RecB_like_REase	223	W1230910_217	Cyanophage S-RIM14	GCA_002599125.1
AMO43243.1	000160	RecB_like_REase	216	R1080702_238	Cyanophage S-RIM32	GCA_001754165.1
AMO43474.1	000160	RecB_like_REase	225	W270710_235	Cyanophage S-RIM44	GCA_002599145.1
AOO11716.1	000160	RecB_like_REase	225	ES420910_239	Cyanophage S-RIM44	GCA_002599165.1
AOO11946.1	000160	RecB_like_REase	225	Np050604_235	Cyanophage S-RIM44	GCA_002599185.1
AOO12182.1	000160	RecB_like_REase	225	Np200711_240	Cyanophage S-RIM44	GCA_002599205.1
AOO12417.1	000160	RecB_like_REase	225	Np420711_239	Cyanophage S-RIM44	GCA_002599225.1
AOO12647.1	000160	RecB_like_REase	225	Sn080709_235	Cyanophage S-RIM44	GCA_002599245.1
AOO12882.1	000160	RecB_like_REase	225	Sn130910_239	Cyanophage S-RIM44	GCA_002599265.1
AOO13113.1	000160	RecB_like_REase	225	W2100709_236	Cyanophage S-RIM44	GCA_002599285.1
AGH07626.1	000160	RecB_like_REase	228	CYVG_00183	Cyanophage S-SSM6a	GCA_002710385.1
AGG54372.1	000160	RecB_like_REase	226	CYWG_00088	Cyanophage S-SSM6b	GCA_002710425.1
AIT13926.1	000160	RecB_like_REase	239	PBI_121Q_29	Escherichia phage 121Q	GCA_000926855.1
QAY00412.1	000160	RecB_like_REase	239	Ecwhy1_131	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35155.1	000160	RecB_like_REase	239	ACQ29_gp475	Escherichia phage PBECO4	GCA_001041035.1
BBM61618.1	000160	RecB_like_REase	239	EO157G_0290	Escherichia phage SP27	GCA_008033345.1
AXC36728.1	000160	RecB_like_REase	239	-	Escherichia phage UB	GCA_003341455.1
QBO61766.1	000160	RecB_like_REase	239	G17_00277	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13810.1	000160	RecB_like_REase	239	vBEcoMphAPEC6_gp181c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80521.1	000160	RecB_like_REase	239	PSLUR01_00544	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44410.1	000160	RecB_like_REase	235	RaK2_00137	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72836.1	000160	RecB_like_REase	231	-	Myoviridae sp.	GCA_003657725.1
AMM43864.1	000160	RecB_like_REase	233	CBB_300	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26215.1	000160	RecB_like_REase	222	CPMG_00114	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44707.1	000160	RecB_like_REase	229	PSSM2_329	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12269.1	000160	RecB_like_REase	229	PRTG_00115	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93581.1	000160	RecB_like_REase	223	AVU42_gp245	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99335.1	000160	RecB_like_REase	225	Syn1_239	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76121.1	000160	RecB_like_REase	221	EST35_0240	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44021.1	000160	RecB_like_REase	233	PBI_SCTP2_6	Salicola phage SCTP-2	GCA_002625545.1
QCW19023.1	000160	RecB_like_REase	235	7t3_0503	Salmonella phage 7t3	GCA_006083215.1
AZU98270.1	000160	RecB_like_REase	235	CPT_Munch_326	Salmonella phage Munch	GCA_004015485.1
QIG62714.1	000160	RecB_like_REase	235	SEPL_101	Salmonella phage SE_PL	GCA_011067555.1
AQW88823.1	000160	RecB_like_REase	233	BF_0298	Serratia phage BF	GCA_002619745.1
AKF13103.1	000160	RecB_like_REase	235	PHIM19_198	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12743.1	000160	RecB_like_REase	235	PHIM7_198	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13473.1	000160	RecB_like_REase	235	PHIN3_210	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30766.1	000160	RecB_like_REase	226	Syn7803US37_289	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54991.1	000160	RecB_like_REase	223	b23_0385	Synechococcus phage B23	GCA_009745195.1
QGT54626.1	000160	RecB_like_REase	223	b3_0391	Synechococcus phage B3	GCA_009745215.1
ASR76315.1	000160	RecB_like_REase	227	PBI_BELLAMY_279	Synechococcus phage Bellamy	GCA_002627525.1
QCW23064.1	000160	RecB_like_REase	221	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50688.1	000160	RecB_like_REase	221	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59697.1	000160	RecB_like_REase	225	S330809_236	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59459.1	000160	RecB_like_REase	225	C440309_236	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59934.1	000160	RecB_like_REase	225	N231010_235	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70452.1	000160	RecB_like_REase	221	HOU04_gp053	Synechococcus phage S-T4	GCA_003443335.1
QJT70260.1	000160	RecB_like_REase	227	SynMITS9220M01_254	Synechococcus phage SynMITS9220M01	GCA_013187275.1
SOK59106.1	000160	RecB_like_REase	233	g298	Yersinia phage fHe-Yen9-03	GCA_002990515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58570.1	000160	RecB_like_REase	233	g293	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDH83392.1	000161	RecB_like_REase	302	H1O15_gp070	Achromobacter phage Motura	GCA_006964305.1
QBX06701.1	000161	RecB_like_REase	272	BcepSaruman_288	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74669.1	000161	RecB_like_REase	309	BcepSauron_289	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67269.1	000161	RecB_like_REase	361	AD1_225	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80015.1	000161	RecB_like_REase	338	JA11_210	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66613.1	000161	RecB_like_REase	338	JA13_210	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66938.1	000161	RecB_like_REase	338	JA29_212	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67585.1	000161	RecB_like_REase	338	JA33_211	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08497.1	000161	RecB_like_REase	361	Alexandra_234	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58869.1	000161	RecB_like_REase	361	Y3_229	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28701.1	000161	RecB_like_REase	358	YOLOSWAG_223	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38180.1	000161	RecB_like_REase	379	BN7874_011	Phage NCTB	GCA_900092385.1
AFH14672.1	000161	RecB_like_REase	370	Lu11_0139	Pseudomonas phage Lu11	GCA_000897175.1
AGS82034.1	000161	RecB_like_REase	349	PaBG_00152	Pseudomonas phage PaBG	GCA_000912555.1
BAG41617.1	000161	RecB_like_REase	309	RSL1_ORF170	Ralstonia phage phiRSL1	GCA_000879455.1
AYD81236.1	000162	RecB_like_REase	280	SEA_JUSTBECAUSE_67	Streptomyces phage JustBecause	GCA_003613775.1
QJD53639.1	000162	RecB_like_REase	264	SEA_KELA_68	Streptomyces phage Kela	GCA_012934305.1
QBZ71970.1	000162	RecB_like_REase	280	SEA_KRADAL_72	Streptomyces phage Kradal	GCA_004799925.1
AXH66233.1	000162	RecB_like_REase	280	SEA_SATIS_72	Streptomyces phage Satis	GCA_003366315.1
CCH63664.1	000163	RecB_like_REase	230	CP21_202	Campylobacter virus CP21	GCA_000902535.1
QAU04524.1	000163	RecB_like_REase	227	ValB1MD_206	Vibrio phage ValB1MD	GCA_004138815.1
APU01414.1	000164	RegA	123	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28806.1	000164	RegA	129	AP1_0099	Aeromonas phage AP1	GCA_014183365.1
ATI17483.1	000164	RegA	129	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00514.1	000164	RegA	129	HWB28_gp038	Aeromonas phage AS-zj	GCA_002627665.1
AUE22562.1	000164	RegA	120	Ah1_00021	Aeromonas phage Ah1	GCA_002957415.1
QAX98600.1	000164	RegA	120	ASfcp2_267	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97923.1	000164	RegA	129	ASswx1_280	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01226.1	000164	RegA	121	ASwh1_161	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39515.1	000164	RegA	128	CC2_251	Aeromonas phage CC2	GCA_000903495.1
ADQ52735.1	000164	RegA	122	PX29p016	Aeromonas phage PX29	GCA_000920195.1
ADM79988.1	000164	RegA	120	phiAS5_ORF0145	Aeromonas phage phiAS5	GCA_000887715.1
AAR90915.1	000164	RegA	123	65p023	Aeromonas virus 65	GCA_000893255.1
AAQ17673.1	000164	RegA	122	regA	Aeromonas virus Aeh1	GCA_000843245.1
ANS06072.1	000164	RegA	120	ABCD_0040	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65046.1	000164	RegA	121	S13_249	Cronobacter phage S13	GCA_001503575.1
AON97050.1	000164	RegA	122	E_041	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56868.1	000164	RegA	137	CPXG_00065	Cyanophage P-RSM6	GCA_000906155.1
AJK27588.1	000164	RegA	143	PTIM40_161	Cyanophage P-TIM40	GCA_001470935.1
AOO14347.1	000164	RegA	148	Sn110110_153	Cyanophage S-RIM14	GCA_002599065.1
AOO14996.1	000164	RegA	148	W1230910_150	Cyanophage S-RIM14	GCA_002599125.1
AMO43166.1	000164	RegA	142	R1080702_157	Cyanophage S-RIM32	GCA_001754165.1
AMO43391.1	000164	RegA	141	W270710_147	Cyanophage S-RIM44	GCA_002599145.1
AOO11636.1	000164	RegA	141	ES420910_155	Cyanophage S-RIM44	GCA_002599165.1
AOO11863.1	000164	RegA	141	Np050604_147	Cyanophage S-RIM44	GCA_002599185.1
AOO12101.1	000164	RegA	141	Np200711_155	Cyanophage S-RIM44	GCA_002599205.1
AOO12337.1	000164	RegA	141	Np420711_155	Cyanophage S-RIM44	GCA_002599225.1
AOO12564.1	000164	RegA	141	Sn080709_147	Cyanophage S-RIM44	GCA_002599245.1
AOO12802.1	000164	RegA	141	Sn130910_155	Cyanophage S-RIM44	GCA_002599265.1
AOO13030.1	000164	RegA	141	W2100709_148	Cyanophage S-RIM44	GCA_002599285.1
AGH07490.1	000164	RegA	153	CYVG_00046	Cyanophage S-SSM6a	GCA_002710385.1
AGG54462.1	000164	RegA	139	CYWG_00178	Cyanophage S-SSM6b	GCA_002710425.1
ARM70872.1	000164	RegA	125	phiC120_c167	Escherichia phage phiC120	GCA_002621185.1
AAX78562.1	000164	RegA	122	RB43ORF040c	Escherichia virus RB43	GCA_000863505.1
QHJ78886.1	000164	RegA	121	-	Myoviridae sp.	GCA_012593985.1
QIG65673.1	000164	RegA	136	phiOC_p007	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26295.1	000164	RegA	140	CPMG_00195	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44550.1	000164	RegA	147	PSSM2_172	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12421.1	000164	RegA	139	PRTG_00270	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93479.1	000164	RegA	146	AVU42_gp142	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99249.1	000164	RegA	141	Syn1_148	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47667.1	000164	RegA	136	SmphiM12_035	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12931.1	000164	RegA	136	PHIM19_24	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12571.1	000164	RegA	136	PHIM7_23	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13303.1	000164	RegA	136	PHIN3_38	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30643.1	000164	RegA	142	Syn7803US37_166	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54913.1	000164	RegA	149	b23_0300	Synechococcus phage B23	GCA_009745195.1
QGT54548.1	000164	RegA	149	b3_0307	Synechococcus phage B3	GCA_009745215.1
ASR76202.1	000164	RegA	145	PBI_BELLAMY_157	Synechococcus phage Bellamy	GCA_002627525.1
QCW23083.1	000164	RegA	145	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50574.1	000164	RegA	145	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59616.1	000164	RegA	141	S330809_155	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59378.1	000164	RegA	141	C440309_155	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59854.1	000164	RegA	141	N231010_155	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70549.1	000164	RegA	145	HOU04_gp150	Synechococcus phage S-T4	GCA_003443335.1
QJT70151.1	000164	RegA	143	SynMITS9220M01_138	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64151.1	000164	RegA	126	KVP40.0080	Vibrio phage KVP40	GCA_000843785.1
QIW90475.1	000164	RegA	126	GCAPEGMB_00128	Vibrio phage V07	GCA_012361095.1
QIW90954.1	000164	RegA	126	COHAPHLL_00091	Vibrio phage V09	GCA_012361135.1
QHJ74263.1	000164	RegA	126	VH12019_00344	Vibrio phage VH1_2019	GCA_009931825.1
AGB07087.1	000164	RegA	127	CF80_gp300	Vibrio phage VH7D	GCA_000914495.1
QBX06008.1	000164	RegA	126	ValB1HC_054	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61021.1	000164	RegA	126	AVU32_gp180	Vibrio phage ValKK3	GCA_001501635.1
AGN30129.1	000164	RegA	126	VPFG_00127	Vibrio phage nt-1	GCA_000910195.2
ALP47156.1	000164	RegA	126	phiGrn1_0195	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47542.1	000164	RegA	127	phiST2_0327	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54632.1	000164	RegA	127	vBValMR10Z_91	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07132.1	000164	RegA	133	VmeM32_00145	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37311.1	000164	RegA	126	pp2_078	Vibriophage phi-pp2	GCA_002630725.1
AND75228.1	000165	ATPcone+Ribonuc_red_lg	687	ME3_67	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01436.1	000165	ATPcone+Ribonuc_red_lg	750	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28926.1	000165	ATPcone+Ribonuc_red_lg	749	AP1_0219	Aeromonas phage AP1	GCA_014183365.1
ATI17463.1	000165	ATPcone+Ribonuc_red_lg	749	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00534.1	000165	ATPcone+Ribonuc_red_lg	749	HWB28_gp018	Aeromonas phage AS-zj	GCA_002627665.1
AUE22584.1	000165	ATPcone+Ribonuc_red_lg	744	Ah1_00043	Aeromonas phage Ah1	GCA_002957415.1
QAX98619.1	000165	ATPcone+Ribonuc_red_lg	744	ASfcp2_286	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97903.1	000165	ATPcone+Ribonuc_red_lg	749	ASswx1_260	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01249.1	000165	ATPcone+Ribonuc_red_lg	752	ASwh1_184	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39526.1	000165	ATPcone+Ribonuc_red_lg	749	CC2_272	Aeromonas phage CC2	GCA_000903495.1
ADQ52759.1	000165	ATPcone+Ribonuc_red_lg	744	PX29p040	Aeromonas phage PX29	GCA_000920195.1
ADM80015.1	000165	ATPcone+Ribonuc_red_lg	744	phiAS5_ORF0172	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53055.1	000165	ATPcone+Ribonuc_red_lg	751	65p045	Aeromonas virus 65	GCA_000893255.1
AAQ17704.1	000165	ATPcone+Ribonuc_red_lg	473	nrdA-A	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17702.1	000165	ATPcone+Ribonuc_red_lg	323	nrdA-B	Aeromonas virus Aeh1	GCA_000843245.1
ASV44709.1	000165	ATPcone+Ribonuc_red_lg	546	FDI40_gp122	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83783.1	000165	ATPcone+Ribonuc_red_lg	767	0305phi8-36p225	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01307.1	000165	ATPcone+Ribonuc_red_lg	698	AR9_g223	Bacillus phage AR9	GCA_001743835.1
AMM44828.1	000165	ATPcone+Ribonuc_red_lg	780	SP15_029	Bacillus phage SP-15	GCA_001754685.1
ALN97957.1	000165	ATPcone+Ribonuc_red_lg	694	Bp8pS_278	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93353.1	000165	ATPcone+Ribonuc_red_lg	695	G_82	Bacillus virus G	GCA_000917535.1
AST99936.1	000165	ATPcone+Ribonuc_red_lg	698	PBI_PBS1_114	Bacillus virus PBS1	GCA_002601325.1
QIG63407.1	000165	ATPcone+Ribonuc_red_lg	1172	DAC16_177	Bacteroides phage DAC16	GCA_013387695.1
QIG63671.1	000165	ATPcone+Ribonuc_red_lg	851	DAC19_183	Bacteroides phage DAC19	GCA_013387715.1
QIG63932.1	000165	ATPcone+Ribonuc_red_lg	851	DAC20_182	Bacteroides phage DAC20	GCA_013387725.1
QIG64196.1	000165	ATPcone+Ribonuc_red_lg	851	DAC22_185	Bacteroides phage DAC22	GCA_013387735.1
QIG64452.1	000165	ATPcone+Ribonuc_red_lg	1172	DAC23_177	Bacteroides phage DAC23	GCA_013387745.1
CCH63683.1	000165	ATPcone+Ribonuc_red_lg	580	CP21_221	Campylobacter virus CP21	GCA_000902535.1
ARB13638.1	000165	ATPcone+Ribonuc_red_lg	935	Ccr10_gp109c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13983.1	000165	ATPcone+Ribonuc_red_lg	935	Ccr2_gp108c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14671.1	000165	ATPcone+Ribonuc_red_lg	935	Ccr29_gp115	Caulobacter phage Ccr29	GCA_002619485.1
ARB15026.1	000165	ATPcone+Ribonuc_red_lg	935	Ccr32_gp108	Caulobacter phage Ccr32	GCA_002619505.1
ARB15358.1	000165	ATPcone+Ribonuc_red_lg	935	Ccr34_gp116	Caulobacter phage Ccr34	GCA_002619525.1
ARB14327.1	000165	ATPcone+Ribonuc_red_lg	935	Ccr5_gp109c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68307.1	000165	ATPcone+Ribonuc_red_lg	936	CcrBL10_gp103c	Caulobacter phage CcrBL10	GCA_003443255.1

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AXQ69231.1	000165	ATPcone+Ribonuc_red_lg	906	CcrBL9_gp207	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88013.1	000165	ATPcone+Ribonuc_red_lg	936	CcrColossus_gp143	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68690.1	000165	ATPcone+Ribonuc_red_lg	937	CcrPW_gp151c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69785.1	000165	ATPcone+Ribonuc_red_lg	923	CcrSC_gp203	Caulobacter phage CcrSC	GCA_003443315.1
AFU87630.1	000165	ATPcone+Ribonuc_red_lg	935	CcrKarma_gp113	Caulobacter virus Karma	GCA_000901575.1
AFU87279.1	000165	ATPcone+Ribonuc_red_lg	935	CcrMagneto_gp109	Caulobacter virus Magneto	GCA_000903095.1
AFU86591.1	000165	ATPcone+Ribonuc_red_lg	937	CcrRogue_gp109	Caulobacter virus Rogue	GCA_000900555.1
AFU88426.1	000165	ATPcone+Ribonuc_red_lg	935	CcrSwift_gp108	Caulobacter virus Swift	GCA_000899655.1
AFU86944.1	000165	ATPcone+Ribonuc_red_lg	935	CbK_gp112	Caulobacter virus phiCbK	GCA_000900535.1
ANS05927.1	000165	ATPcone+Ribonuc_red_lg	751	ABCD_0063	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64817.1	000165	ATPcone+Ribonuc_red_lg	747	S13_018	Cronobacter phage S13	GCA_001503575.1
AFC21748.1	000165	ATPcone+Ribonuc_red_lg	777	GAP32_298	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97074.1	000165	ATPcone+Ribonuc_red_lg	748	E_065	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56833.1	000165	ATPcone+Ribonuc_red_lg	778	CPXG_00030	Cyanophage P-RSM6	GCA_000906155.1
AJK27653.1	000165	ATPcone+Ribonuc_red_lg	762	PTIM40_194	Cyanophage P-TIM40	GCA_001470935.1
AOO14379.1	000165	ATPcone+Ribonuc_red_lg	761	Sn110110_185	Cyanophage S-RIM14	GCA_002599065.1
AOO15027.1	000165	ATPcone+Ribonuc_red_lg	761	W1230910_181	Cyanophage S-RIM14	GCA_002599125.1
AMO43187.1	000165	ATPcone+Ribonuc_red_lg	771	R1080702_178	Cyanophage S-RIM32	GCA_001754165.1
AMO43413.1	000165	ATPcone+Ribonuc_red_lg	770	W270710_169	Cyanophage S-RIM44	GCA_002599145.1
AOO11657.1	000165	ATPcone+Ribonuc_red_lg	770	ES420910_176	Cyanophage S-RIM44	GCA_002599165.1
AOO11885.1	000165	ATPcone+Ribonuc_red_lg	770	Np050604_169	Cyanophage S-RIM44	GCA_002599185.1
AOO12123.1	000165	ATPcone+Ribonuc_red_lg	770	Np200711_177	Cyanophage S-RIM44	GCA_002599205.1
AOO12358.1	000165	ATPcone+Ribonuc_red_lg	770	Np420711_176	Cyanophage S-RIM44	GCA_002599225.1
AOO12586.1	000165	ATPcone+Ribonuc_red_lg	770	Sn080709_169	Cyanophage S-RIM44	GCA_002599245.1
AOO12823.1	000165	ATPcone+Ribonuc_red_lg	770	Sn130910_176	Cyanophage S-RIM44	GCA_002599265.1
AOO13052.1	000165	ATPcone+Ribonuc_red_lg	770	W2100709_170	Cyanophage S-RIM44	GCA_002599285.1
AGH07528.1	000165	ATPcone+Ribonuc_red_lg	766	CYVG_00084	Cyanophage S-SSM6a	GCA_002710385.1
AGG54423.1	000165	ATPcone+Ribonuc_red_lg	764	CYWG_00139	Cyanophage S-SSM6b	GCA_002710425.1
AIT13929.1	000165	ATPcone+Ribonuc_red_lg	772	PBI_121Q_32	Escherichia phage 121Q	GCA_000926855.1
QAY00409.1	000165	ATPcone+Ribonuc_red_lg	772	Ecwhy1_128	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35152.1	000165	ATPcone+Ribonuc_red_lg	772	ACQ29_gp472	Escherichia phage PBECO4	GCA_001041035.1
BBM61621.1	000165	ATPcone+Ribonuc_red_lg	772	EO157G_0320	Escherichia phage SP27	GCA_008033345.1
AXC36725.1	000165	ATPcone+Ribonuc_red_lg	772	-	Escherichia phage UB	GCA_003341455.1
ARM70786.1	000165	ATPcone+Ribonuc_red_lg	751	phiC120_c80	Escherichia phage phiC120	GCA_002621185.1
QBO61763.1	000165	ATPcone+Ribonuc_red_lg	772	G17_00274	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13807.1	000165	ATPcone+Ribonuc_red_lg	772	vBEcoMphAPEC6_gp178c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80524.1	000165	ATPcone+Ribonuc_red_lg	772	PSLUR01_00547	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78586.1	000165	ATPcone+Ribonuc_red_lg	751	RB43ORF064w	Escherichia virus RB43	GCA_000863505.1
AFA44413.1	000165	ATPcone+Ribonuc_red_lg	771	RaK2_00140	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57902.1	000165	ATPcone+Ribonuc_red_lg	717	SEA_PAULODIABOLI_216	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72883.1	000165	ATPcone+Ribonuc_red_lg	401	-	Myoviridae sp.	GCA_003657725.1
QHJ78847.1	000165	ATPcone+Ribonuc_red_lg	748	-	Myoviridae sp.	GCA_012593985.1
QIG66022.1	000165	ATPcone+Ribonuc_red_lg	705	phiOC_p380	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43866.1	000165	ATPcone+Ribonuc_red_lg	776	CBB_303	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26268.1	000165	ATPcone+Ribonuc_red_lg	769	CPMG_00168	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44585.1	000165	ATPcone+Ribonuc_red_lg	775	PSSM2_208	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12386.1	000165	ATPcone+Ribonuc_red_lg	775	PRTG_00233	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93504.1	000165	ATPcone+Ribonuc_red_lg	767	AVU42_gp167	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99272.1	000165	ATPcone+Ribonuc_red_lg	774	Syn1_171	Prochlorococcus phage Syn1	GCA_000892495.1
ABY63290.1	000165	ATPcone+Ribonuc_red_lg	764	201phi2-1p467	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45126.1	000165	ATPcone+Ribonuc_red_lg	762	KTN4_368	Pseudomonas phage KTN4	GCA_002607225.1
ARV77503.1	000165	ATPcone+Ribonuc_red_lg	826	NOXIFER_338	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32547.1	000165	ATPcone+Ribonuc_red_lg	522	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ86138.1	000165	ATPcone+Ribonuc_red_lg	318	KKIINIFJ_00227	Pseudomonas phage PN05	GCA_009931935.1
QHJ86158.1	000165	ATPcone+Ribonuc_red_lg	479	KKIINIFJ_00248	Pseudomonas phage PN05	GCA_009931935.1
ARV77098.1	000165	ATPcone+Ribonuc_red_lg	830	PHABIO_470	Pseudomonas phage Phabio	GCA_002624965.1
AEH03801.1	000165	ATPcone+Ribonuc_red_lg	762	378	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02946.1	000165	ATPcone+Ribonuc_red_lg	761	PSA21_428	Pseudomonas phage Psa21	GCA_004340405.1
ATN94585.1	000165	ATPcone+Ribonuc_red_lg	762	SL2_008	Pseudomonas phage SL2	GCA_002956015.1
QJB23003.1	000165	ATPcone+Ribonuc_red_lg	762	fnug_360	Pseudomonas phage fnug	GCA_012837215.1
QCG76124.1	000165	ATPcone+Ribonuc_red_lg	761	EST35_0243	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM42118.1	000165	ATPcone+Ribonuc_red_lg	761	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83207.2	000165	ATPcone+Ribonuc_red_lg	762	PHIKZ306	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19130.1	000165	ATPcone+Ribonuc_red_lg	886	FDH28_gp265	Ralstonia phage RP12	GCA_002617345.1
BAW19416.1	000165	ATPcone+Ribonuc_red_lg	886	-	Ralstonia phage RP31	GCA_002617365.1
BAS04910.1	000165	ATPcone+Ribonuc_red_lg	1005	AVU11_gp118	Ralstonia phage RSF1	GCA_001500875.1
BAQ02639.1	000165	ATPcone+Ribonuc_red_lg	1011	AVU38_gp111	Ralstonia phage RSL2	GCA_001503055.1
ASV44443.1	000165	ATPcone+Ribonuc_red_lg	889	PBI_SCTP2_428	Salicola phage SCTP-2	GCA_002625545.1
QCW19026.1	000165	ATPcone+Ribonuc_red_lg	781	7t3_0506	Salmonella phage 7t3	GCA_006083215.1
AZU98273.1	000165	ATPcone+Ribonuc_red_lg	781	CPT_Munch_329	Salmonella phage Munch	GCA_004015485.1
QIG62711.1	000165	ATPcone+Ribonuc_red_lg	781	SEPL_098	Salmonella phage SE_PL	GCA_011067555.1
AQW88826.1	000165	ATPcone+Ribonuc_red_lg	775	BF_0301	Serratia phage BF	GCA_002619745.1
AFF28244.1	000165	ATPcone+Ribonuc_red_lg	860	PAU_246	Sphingomonas phage PAU	GCA_000902455.1
AIX30680.1	000165	ATPcone+Ribonuc_red_lg	770	Syn7803US37_203	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54928.1	000165	ATPcone+Ribonuc_red_lg	756	b23_0315	Synechococcus phage B23	GCA_009745195.1
QGT54563.1	000165	ATPcone+Ribonuc_red_lg	756	b3_0322	Synechococcus phage B3	GCA_009745215.1
ASR76222.1	000165	ATPcone+Ribonuc_red_lg	765	PBI_BELLAMY_179	Synechococcus phage Bellamy	GCA_002627525.1
QCW22952.1	000165	ATPcone+Ribonuc_red_lg	766	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50529.1	000165	ATPcone+Ribonuc_red_lg	766	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59638.1	000165	ATPcone+Ribonuc_red_lg	773	S330809_177	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59400.1	000165	ATPcone+Ribonuc_red_lg	773	C440309_177	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59876.1	000165	ATPcone+Ribonuc_red_lg	773	N231010_177	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70530.1	000165	ATPcone+Ribonuc_red_lg	763	HOU04_gp131	Synechococcus phage S-T4	GCA_003443335.1
QJT70176.1	000165	ATPcone+Ribonuc_red_lg	769	SynMITS9220M01_164	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90441.1	000165	ATPcone+Ribonuc_red_lg	404	HYO65_gp049	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90748.1	000165	ATPcone+Ribonuc_red_lg	368	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39318.1	000165	ATPcone+Ribonuc_red_lg	809	BPT24_194	Tenacibaculum phage pT24	GCA_002611925.1
AXH70973.1	000165	ATPcone+Ribonuc_red_lg	303	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70974.1	000165	ATPcone+Ribonuc_red_lg	477	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64346.1	000165	ATPcone+Ribonuc_red_lg	741	KVP40.0277	Vibrio phage KVP40	GCA_000843785.1
QIW90851.1	000165	ATPcone+Ribonuc_red_lg	698	GCAPEGMB_00536	Vibrio phage V07	GCA_012361095.1
QIW90660.1	000165	ATPcone+Ribonuc_red_lg	741	GCAPEGMB_00313	Vibrio phage V07	GCA_012361095.1
QIW91138.1	000165	ATPcone+Ribonuc_red_lg	741	COHAPHLL_00302	Vibrio phage V09	GCA_012361135.1
QHJ74455.1	000165	ATPcone+Ribonuc_red_lg	741	VH12019_00128	Vibrio phage VH1_2019	GCA_009931825.1
AGB06949.1	000165	ATPcone+Ribonuc_red_lg	741	CF80_gp162	Vibrio phage VH7D	GCA_000914495.1
QBX06196.1	000165	ATPcone+Ribonuc_red_lg	741	ValB1HC_243	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04533.1	000165	ATPcone+Ribonuc_red_lg	781	ValB1MD_236	Vibrio phage ValB1MD	GCA_004138815.1
AJT61213.1	000165	ATPcone+Ribonuc_red_lg	741	AVU32_gp372	Vibrio phage ValKK3	GCA_001501635.1
AGN30323.2	000165	ATPcone+Ribonuc_red_lg	741	VPFG_00325	Vibrio phage nt-1	GCA_000910195.2
ALP46965.1	000165	ATPcone+Ribonuc_red_lg	741	phiGrn1_0009	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47345.1	000165	ATPcone+Ribonuc_red_lg	741	phiST2_0141	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54821.1	000165	ATPcone+Ribonuc_red_lg	741	vBValMR10Z_281	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07112.1	000165	ATPcone+Ribonuc_red_lg	792	VmeM32_00125	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21230.1	000165	ATPcone+Ribonuc_red_lg	762	-	Vibrio phage vB_pir03	GCA_014319855.1
AFN37506.1	000165	ATPcone+Ribonuc_red_lg	741	pp2_273	Vibriophage phi-pp2	GCA_002630725.1
BBA65525.1	000165	ATPcone+Ribonuc_red_lg	814	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96523.1	000165	ATPcone+Ribonuc_red_lg	810	Xoosp13_337	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59109.1	000165	ATPcone+Ribonuc_red_lg	774	g301	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58573.1	000165	ATPcone+Ribonuc_red_lg	774	g296	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBX32548.1	000165	ATPcone+Ribonuc_red_lg	239	-	Pseudomonas phage PA1C	GCA_004785505.1
BBI90440.1	000165	ATPcone+Ribonuc_red_lg	549	HYO65_gp048	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90747.1	000165	ATPcone+Ribonuc_red_lg	549	-	Tenacibaculum phage PTm5	GCA_009730715.1
CCH63681.1	000000	Intein_splicing	70	CP21_219	Campylobacter virus CP21	GCA_000902535.1
AXH72884.1	000000	Ribonuc_red_lgC	410	-	Myoviridae sp.	GCA_003657725.1
AND75227.1	000166	Ribonuc_red_sm	368	ME3_66	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01435.1	000166	Ribonuc_red_sm	376	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29122.1	000166	Ribonuc_red_sm	184	AP1_0419	Aeromonas phage AP1	GCA_014183365.1
QMV29129.1	000166	Ribonuc_red_sm	175	AP1_0426	Aeromonas phage AP1	GCA_014183365.1
QMV28767.1	000166	Ribonuc_red_sm	375	AP1_0049	Aeromonas phage AP1	GCA_014183365.1
ATI17464.1	000166	Ribonuc_red_sm	375	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00533.1	000166	Ribonuc_red_sm	375	HWB28_gp019	Aeromonas phage AS-zj	GCA_002627665.1
AUE22583.1	000166	Ribonuc_red_sm	376	Ah1_00042	Aeromonas phage Ah1	GCA_002957415.1
QAX98618.1	000166	Ribonuc_red_sm	376	ASfcp2_285	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97904.1	000166	Ribonuc_red_sm	375	ASswx1_261	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01248.1	000166	Ribonuc_red_sm	376	ASwh1_183	Aeromonas phage Aswh_1	GCA_004146945.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN39525.1	000166	Ribonuc_red_sm	375	CC2_271	Aeromonas phage CC2	GCA_000903495.1
QNH80849.1	000166	Ribonuc_red_sm	377	D6_0170	Aeromonas phage D6	GCA_007051205.2
QDH47068.1	000166	Ribonuc_red_sm	377	LAh10_90	Aeromonas phage LAh10	GCA_006863975.1
ADQ52758.1	000166	Ribonuc_red_sm	376	PX29p039	Aeromonas phage PX29	GCA_000920195.1
ADM80014.1	000166	Ribonuc_red_sm	376	phiAS5_ORF0171	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53054.1	000166	Ribonuc_red_sm	376	65p044	Aeromonas virus 65	GCA_000893255.1
AAQ17701.1	000166	Ribonuc_red_sm	376	nrdB	Aeromonas virus Aeh1	GCA_000843245.1
ASV44710.1	000166	Ribonuc_red_sm	332	FDI40_gp123	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83782.1	000166	Ribonuc_red_sm	352	0305phi8-36p224	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01306.1	000166	Ribonuc_red_sm	349	AR9_g222	Bacillus phage AR9	GCA_001743835.1
AMM44829.1	000166	Ribonuc_red_sm	348	SP15_030	Bacillus phage SP-15	GCA_001754685.1
ALN97956.1	000166	Ribonuc_red_sm	335	Bp8pS_277	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93354.1	000166	Ribonuc_red_sm	323	G_83	Bacillus virus G	GCA_000917535.1
AST99935.1	000166	Ribonuc_red_sm	349	PBI_PBS1_113	Bacillus virus PBS1	GCA_002601325.1
CCH63552.1	000166	Ribonuc_red_sm	369	CP21_090	Campylobacter virus CP21	GCA_000902535.1
ARB13637.1	000166	Ribonuc_red_sm	477	Ccr10_gp108c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13982.1	000166	Ribonuc_red_sm	477	Ccr2_gp107c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14670.1	000166	Ribonuc_red_sm	477	Ccr29_gp114	Caulobacter phage Ccr29	GCA_002619485.1
ARB15025.1	000166	Ribonuc_red_sm	477	Ccr32_gp107	Caulobacter phage Ccr32	GCA_002619505.1
ARB15357.1	000166	Ribonuc_red_sm	477	Ccr34_gp115	Caulobacter phage Ccr34	GCA_002619525.1
ARB14326.1	000166	Ribonuc_red_sm	477	Ccr5_gp108c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68306.1	000166	Ribonuc_red_sm	454	CcrBL10_gp102c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69232.1	000166	Ribonuc_red_sm	427	CcrBL9_gp208	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88012.1	000166	Ribonuc_red_sm	467	CcrColossus_gp142	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68689.1	000166	Ribonuc_red_sm	468	CcrPW_gp150c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69786.1	000166	Ribonuc_red_sm	426	CcrSC_gp204	Caulobacter phage CcrSC	GCA_003443315.1
AFU87629.1	000166	Ribonuc_red_sm	477	CcrKarma_gp112	Caulobacter virus Karma	GCA_000901575.1
AFU87278.1	000166	Ribonuc_red_sm	477	CcrMagneto_gp108	Caulobacter virus Magneto	GCA_000903095.1
AFU86590.1	000166	Ribonuc_red_sm	454	CcrRogue_gp108	Caulobacter virus Rogue	GCA_000900555.1
AFU88425.1	000166	Ribonuc_red_sm	477	CcrSwift_gp107	Caulobacter virus Swift	GCA_000899655.1
AFU86943.1	000166	Ribonuc_red_sm	477	CbK_gp111	Caulobacter virus phiCbK	GCA_000900535.1
ANS05955.1	000166	Ribonuc_red_sm	391	ABCD_0064	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64818.1	000166	Ribonuc_red_sm	383	S13_019	Cronobacter phage S13	GCA_001503575.1
AFC21750.1	000166	Ribonuc_red_sm	374	GAP32_300	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97076.1	000166	Ribonuc_red_sm	391	E_067	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56831.1	000166	Ribonuc_red_sm	378	CPXG_00028	Cyanophage P-RSM6	GCA_000906155.1
AJK27654.1	000166	Ribonuc_red_sm	388	PTIM40_195	Cyanophage P-TIM40	GCA_001470935.1
AOO14380.1	000166	Ribonuc_red_sm	386	Sn110110_186	Cyanophage S-RIM14	GCA_002599065.1
AOO15028.1	000166	Ribonuc_red_sm	386	W1230910_182	Cyanophage S-RIM14	GCA_002599125.1
AMO43188.1	000166	Ribonuc_red_sm	394	R1080702_179	Cyanophage S-RIM32	GCA_001754165.1
AMO43414.1	000166	Ribonuc_red_sm	395	W270710_170	Cyanophage S-RIM44	GCA_002599145.1
AOO11658.1	000166	Ribonuc_red_sm	395	ES420910_177	Cyanophage S-RIM44	GCA_002599165.1
AOO11886.1	000166	Ribonuc_red_sm	395	Np050604_170	Cyanophage S-RIM44	GCA_002599185.1
AOO12124.1	000166	Ribonuc_red_sm	395	Np200711_178	Cyanophage S-RIM44	GCA_002599205.1
AOO12359.1	000166	Ribonuc_red_sm	395	Np420711_177	Cyanophage S-RIM44	GCA_002599225.1
AOO12587.1	000166	Ribonuc_red_sm	395	Sn080709_170	Cyanophage S-RIM44	GCA_002599245.1
AOO12824.1	000166	Ribonuc_red_sm	395	Sn130910_177	Cyanophage S-RIM44	GCA_002599265.1
AOO13053.1	000166	Ribonuc_red_sm	395	W2100709_171	Cyanophage S-RIM44	GCA_002599285.1
AGH07529.1	000166	Ribonuc_red_sm	388	CYVG_00085	Cyanophage S-SSM6a	GCA_002710385.1
AGG54422.1	000166	Ribonuc_red_sm	386	CYWG_00138	Cyanophage S-SSM6b	GCA_002710425.1
QBZ70716.1	000166	Ribonuc_red_sm	376	pETSU_135	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60240.1	000166	Ribonuc_red_sm	377	Ea357_089	Erwinia phage Ea35-70	GCA_000914635.1
QBP07198.1	000166	Ribonuc_red_sm	378	REBECCA_91	Erwinia phage Rebecca	GCA_004521635.1
AUG85876.1	000166	Ribonuc_red_sm	377	BOSOLAPHORUS_89	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52192.1	000166	Ribonuc_red_sm	378	DM_94	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86196.1	000166	Ribonuc_red_sm	378	DESERTFOX_89	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86519.1	000166	Ribonuc_red_sm	378	MADMEL_91	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86841.1	000166	Ribonuc_red_sm	377	MORTIMER_92	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51869.1	000166	Ribonuc_red_sm	377	RAY_88	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51553.1	000166	Ribonuc_red_sm	377	SIMMY50_91	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64901.1	000166	Ribonuc_red_sm	377	SPECIALG_91	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT13930.1	000166	Ribonuc_red_sm	374	PBI_121Q_33	Escherichia phage 121Q	GCA_000926855.1
QAY00407.1	000166	Ribonuc_red_sm	374	Ecwhy1_126	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35151.1	000166	Ribonuc_red_sm	374	ACQ29_gp471	Escherichia phage PBECO4	GCA_001041035.1
BBM61622.1	000166	Ribonuc_red_sm	374	EO157G_0330	Escherichia phage SP27	GCA_008033345.1
AXC36724.1	000166	Ribonuc_red_sm	374	-	Escherichia phage UB	GCA_003341455.1
ARM70785.1	000166	Ribonuc_red_sm	391	phiC120_c79	Escherichia phage phiC120	GCA_002621185.1
QBO61762.1	000166	Ribonuc_red_sm	374	G17_00273	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13806.1	000166	Ribonuc_red_sm	374	vBEcoMphAPEC6_gp177c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80525.1	000166	Ribonuc_red_sm	374	PSLUR01_00548	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78587.1	000166	Ribonuc_red_sm	391	RB43ORF065w	Escherichia virus RB43	GCA_000863505.1
QGH72029.1	000166	Ribonuc_red_sm	377	N1M2_166	Klebsiella phage N1M2	GCA_010092605.1
AFA44414.1	000166	Ribonuc_red_sm	374	RaK2_00141	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57898.1	000166	Ribonuc_red_sm	320	SEA_PAULODIABOLI_212	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72885.1	000166	Ribonuc_red_sm	424	-	Myoviridae sp.	GCA_003657725.1
QHJ78845.1	000166	Ribonuc_red_sm	382	-	Myoviridae sp.	GCA_012593985.1
QIG66021.1	000166	Ribonuc_red_sm	316	phiOC_p379	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43868.1	000166	Ribonuc_red_sm	373	CBB_305	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26267.1	000166	Ribonuc_red_sm	388	CPMG_00167	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44586.1	000166	Ribonuc_red_sm	384	PSSM2_209	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12385.1	000166	Ribonuc_red_sm	384	PRTG_00232	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93505.1	000166	Ribonuc_red_sm	382	AVU42_gp168	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99273.1	000166	Ribonuc_red_sm	395	Syn1_172	Prochlorococcus phage Syn1	GCA_000892495.1
ABY63280.1	000166	Ribonuc_red_sm	386	201phi2-1p457	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45125.1	000166	Ribonuc_red_sm	387	KTN4_367	Pseudomonas phage KTN4	GCA_002607225.1
ARV77502.1	000166	Ribonuc_red_sm	390	NOXIFER_337	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89648.1	000166	Ribonuc_red_sm	377	OBP_211	Pseudomonas phage OBP	GCA_000896635.1
QBX32546.1	000166	Ribonuc_red_sm	385	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ86139.1	000166	Ribonuc_red_sm	502	KKIINIFJ_00228	Pseudomonas phage PN05	GCA_009931935.1
ARV77097.1	000166	Ribonuc_red_sm	375	PHABIO_469	Pseudomonas phage Phabio	GCA_002624965.1
AEH03800.1	000166	Ribonuc_red_sm	381	377	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02945.1	000166	Ribonuc_red_sm	405	PSA21_427	Pseudomonas phage Psa21	GCA_004340405.1
ATN94586.1	000166	Ribonuc_red_sm	387	SL2_009	Pseudomonas phage SL2	GCA_002956015.1
QJB23002.1	000166	Ribonuc_red_sm	387	fnug_359	Pseudomonas phage fnug	GCA_012837215.1
QCG76125.1	000166	Ribonuc_red_sm	379	EST35_0244	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM42117.1	000166	Ribonuc_red_sm	385	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83206.1	000166	Ribonuc_red_sm	387	PHIKZ305	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19129.1	000166	Ribonuc_red_sm	400	FDH28_gp266	Ralstonia phage RP12	GCA_002617345.1
BAW19415.1	000166	Ribonuc_red_sm	400	-	Ralstonia phage RP31	GCA_002617365.1
BAS04909.1	000166	Ribonuc_red_sm	377	AVU11_gp117	Ralstonia phage RSF1	GCA_001500875.1
BAQ02638.1	000166	Ribonuc_red_sm	379	AVU38_gp110	Ralstonia phage RSL2	GCA_001503055.1
ASV44442.1	000166	Ribonuc_red_sm	427	PBI_SCTP2_427	Salicola phage SCTP-2	GCA_002625545.1
QCW19027.1	000166	Ribonuc_red_sm	374	7t3_0507	Salmonella phage 7t3	GCA_006083215.1
AZU98274.1	000166	Ribonuc_red_sm	374	CPT_Munch_330	Salmonella phage Munch	GCA_004015485.1
QIG62710.1	000166	Ribonuc_red_sm	374	SEPL_097	Salmonella phage SE_PL	GCA_011067555.1
AQW88827.1	000166	Ribonuc_red_sm	374	BF_0302	Serratia phage BF	GCA_002619745.1
QFP93096.1	000166	Ribonuc_red_sm	368	-	Serratia phage PCH45	GCA_009187865.1
AFF28252.1	000166	Ribonuc_red_sm	331	PAU_254	Sphingomonas phage PAU	GCA_000902455.1
AIX30681.1	000166	Ribonuc_red_sm	388	Syn7803US37_204	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54929.1	000166	Ribonuc_red_sm	379	b23_0316	Synechococcus phage B23	GCA_009745195.1
QGT54564.1	000166	Ribonuc_red_sm	379	b3_0323	Synechococcus phage B3	GCA_009745215.1
ASR76223.1	000166	Ribonuc_red_sm	396	PBI_BELLAMY_180	Synechococcus phage Bellamy	GCA_002627525.1
QCW23015.1	000166	Ribonuc_red_sm	117	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22953.1	000166	Ribonuc_red_sm	306	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50528.1	000166	Ribonuc_red_sm	361	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59639.1	000166	Ribonuc_red_sm	394	S330809_178	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59401.1	000166	Ribonuc_red_sm	394	C440309_178	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59877.1	000166	Ribonuc_red_sm	394	N231010_178	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70529.1	000166	Ribonuc_red_sm	396	HOU04_gp130	Synechococcus phage S-T4	GCA_003443335.1
QJT70177.1	000166	Ribonuc_red_sm	376	SynMITS9220M01_165	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90448.1	000166	Ribonuc_red_sm	684	HYO65_gp056	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90756.1	000166	Ribonuc_red_sm	684	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV31392.1	000166	Ribonuc_red_sm	330	BPT24_193	Tenacibaculum phage pT24	GCA_002611925.1
AXH70977.1	000166	Ribonuc_red_sm	128	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70975.1	000166	Ribonuc_red_sm	235	-	Vibrio phage BONAISHI	GCA_003441475.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAQ64347.1	000166	Ribonuc_red_sm	374	KVP40.0278	Vibrio phage KVP40	GCA_000843785.1
QIW90661.1	000166	Ribonuc_red_sm	374	GCAPEGMB_00314	Vibrio phage V07	GCA_012361095.1
QIW91137.1	000166	Ribonuc_red_sm	374	COHAPHLL_00301	Vibrio phage V09	GCA_012361135.1
QHJ74456.1	000166	Ribonuc_red_sm	374	VH12019_00129	Vibrio phage VH1_2019	GCA_009931825.1
AGB06950.1	000166	Ribonuc_red_sm	374	CF80_gp163	Vibrio phage VH7D	GCA_000914495.1
QBX06195.1	000166	Ribonuc_red_sm	374	ValB1HC_242	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04532.1	000166	Ribonuc_red_sm	380	ValB1MD_235	Vibrio phage ValB1MD	GCA_004138815.1
AJT61212.1	000166	Ribonuc_red_sm	374	AVU32_gp371	Vibrio phage ValKK3	GCA_001501635.1
AGN30324.1	000166	Ribonuc_red_sm	374	VPFG_00326	Vibrio phage nt-1	GCA_000910195.2
ALP46998.1	000166	Ribonuc_red_sm	374	phiGrn1_0010	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47379.1	000166	Ribonuc_red_sm	374	phiST2_0142	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54820.1	000166	Ribonuc_red_sm	374	vBValMR10Z_280	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07113.1	000166	Ribonuc_red_sm	367	VmeM32_00126	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21233.1	000166	Ribonuc_red_sm	372	-	Vibrio phage vB_pir03	GCA_014319855.1
AFN37508.1	000166	Ribonuc_red_sm	374	pp2_275	Vibriophage phi-pp2	GCA_002630725.1
BBA65526.1	000166	Ribonuc_red_sm	350	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96524.1	000166	Ribonuc_red_sm	363	Xoosp13_338	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59111.1	000166	Ribonuc_red_sm	374	g303	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58575.1	000166	Ribonuc_red_sm	236	g298	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58577.1	000166	Ribonuc_red_sm	142	g300	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIW90850.1	000166	Ribonuc_red_sm	339	GCAPEGMB_00535	Vibrio phage V07	GCA_012361095.1
APU01747.1	000167	RlaP	321	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28918.1	000167	RlaP	322	AP1_0211	Aeromonas phage AP1	GCA_014183365.1
ATI17551.1	000167	RlaP	322	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00446.1	000167	RlaP	322	HWB28_gp106	Aeromonas phage AS-zj	GCA_002627665.1
AUE22659.1	000167	RlaP	317	Ah1_00118	Aeromonas phage Ah1	GCA_002957415.1
QAX98385.1	000167	RlaP	324	ASfcp2_40	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97992.1	000167	RlaP	322	ASswx1_351	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01148.1	000167	RlaP	323	ASwh1_82	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39503.1	000167	RlaP	322	CC2_184	Aeromonas phage CC2	GCA_000903495.1
ADQ52839.1	000167	RlaP	324	PX29p120	Aeromonas phage PX29	GCA_000920195.1
ADM80099.1	000167	RlaP	317	phiAS5_ORF0256	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17786.1	000167	RlaP	317	nrdC.11	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94977.1	000167	RlaP	330	FDI40_gp195	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93477.1	000167	RlaP	519	G_218	Bacillus virus G	GCA_000917535.1
AXQ69141.1	000167	RlaP	295	CcrBL9_gp117	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69695.1	000167	RlaP	295	CcrSC_gp113	Caulobacter phage CcrSC	GCA_003443315.1
ANS05966.1	000167	RlaP	332	ABCD_0131	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65012.1	000167	RlaP	329	S13_215	Cronobacter phage S13	GCA_001503575.1
AFC21604.1	000167	RlaP	413	GAP32_154	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97140.1	000167	RlaP	333	E_132	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14396.1	000167	RlaP	410	PBL_121Q_506	Escherichia phage 121Q	GCA_000926855.1
QAY00552.1	000167	RlaP	412	Ecwhy1_273	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34746.1	000167	RlaP	410	ACQ29_gp066	Escherichia phage PBECO4	GCA_001041035.1
BBM62067.1	000167	RlaP	410	EO157G_4780	Escherichia phage SP27	GCA_008033345.1
AXC36861.1	000167	RlaP	410	-	Escherichia phage UB	GCA_003341455.1
ARM70917.1	000167	RlaP	328	phiC120_c212	Escherichia phage phiC120	GCA_002621185.1
QBO61906.1	000167	RlaP	410	G17_00417	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13941.1	000167	RlaP	410	vBEcoMphAPEC6_gp316c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80385.1	000167	RlaP	410	PSLUR01_00408	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78653.1	000167	RlaP	328	RB43ORF131c	Escherichia virus RB43	GCA_000863505.1
AFA44278.1	000167	RlaP	414	RaK2_00005	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57911.1	000167	RlaP	244	SEA_PAULODIABOLI_226	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72866.1	000167	RlaP	301	-	Myoviridae sp.	GCA_003657725.1
QHJ78921.1	000167	RlaP	326	-	Myoviridae sp.	GCA_012593985.1
QIG65805.1	000167	RlaP	300	phiOC_p140	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43724.1	000167	RlaP	416	CBB_159	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18860.1	000167	RlaP	413	7t3_0339	Salmonella phage 7t3	GCA_006083215.1
AZU98121.1	000167	RlaP	413	CPT_Munch_177	Salmonella phage Munch	GCA_004015485.1
QIG62861.1	000167	RlaP	413	SEPL_248	Salmonella phage SE_PL	GCA_011067555.1
AQW88678.1	000167	RlaP	414	BF_0153	Serratia phage BF	GCA_002619745.1
AGR47950.1	000167	RlaP	341	SmphiM12_318	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13144.1	000167	RlaP	341	PHIM19_239	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12783.1	000167	RlaP	341	PHIM7_238	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13512.1	000167	RlaP	324	PHIN3_249	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81202.1	000167	RlaP	230	SEA_JUSTBECAUSE_33	Streptomyces phage JustBecause	GCA_003613775.1
QJD53604.1	000167	RlaP	230	SEA_KELA_33	Streptomyces phage Kela	GCA_012934305.1
QBZ71941.1	000167	RlaP	230	SEA_KRADAL_42	Streptomyces phage Kradal	GCA_004799925.1
AXH66203.1	000167	RlaP	230	SEA_SATIS_42	Streptomyces phage Satis	GCA_003366315.1
BBI90542.1	000167	RlaP	372	HYO65_gp150	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90850.1	000167	RlaP	372	-	Tenacibaculum phage PTm5	GCA_009730715.1
AAQ64222.1	000167	RlaP	346	KVP40.0153	Vibrio phage KVP40	GCA_000843785.1
QIW90536.1	000167	RlaP	346	GCAPEGMB_00189	Vibrio phage V07	GCA_012361095.1
QIW90886.1	000167	RlaP	346	COHAPHLL_00023	Vibrio phage V09	GCA_012361135.1
QHJ74334.1	000167	RlaP	346	VH12019_00007	Vibrio phage VH1_2019	GCA_009931825.1
AGB06826.1	000167	RlaP	337	CF80_gp039	Vibrio phage VH7D	GCA_000914495.1
QBX06320.1	000167	RlaP	337	ValB1HC_367	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60951.1	000167	RlaP	337	AVU32_gp110	Vibrio phage ValKK3	GCA_001501635.1
AGN30198.1	000167	RlaP	337	VPFG_00198	Vibrio phage nt-1	GCA_000910195.2
ALP47009.1	000167	RlaP	337	phiGrn1_0263	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47389.1	000167	RlaP	337	phiST2_0021	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54563.1	000167	RlaP	337	vBValMR10Z_22	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07212.1	000167	RlaP	318	VmeM32_00226	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96903.1	000167	RlaP	344	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97208.1	000167	RlaP	344	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96267.1	000167	RlaP	344	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96585.1	000167	RlaP	344	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFN37381.1	000167	RlaP	346	pp2_148	Vibriophage phi-pp2	GCA_002630725.1
BBA65547.1	000167	RlaP	287	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96543.1	000167	RlaP	286	Xoosp13_357	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58960.1	000167	RlaP	413	g152	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58426.1	000167	RlaP	413	g149	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AEO93371.1	000168	RlaP	202	G_109	Bacillus virus G	GCA_000917535.1
AFC21573.1	000168	RlaP	232	GAP32_124	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43690.1	000168	RlaP	230	CBB_125	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44420.1	000168	RlaP	212	PBL_SCTP2_405	Salicola phage SCTP-2	GCA_002625545.1
QCW18830.1	000168	RlaP	237	7t3_0309	Salmonella phage 7t3	GCA_006083215.1
AZU98094.1	000168	RlaP	237	CPT_Munch_150	Salmonella phage Munch	GCA_004015485.1
QIG62888.1	000168	RlaP	237	SEPL_275	Salmonella phage SE_PL	GCA_011067555.1
AQW88643.1	000168	RlaP	241	BF_0118	Serratia phage BF	GCA_002619745.1
BBA65356.1	000168	RlaP	203	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96387.1	000168	RlaP	211	Xoosp13_201	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58923.1	000168	RlaP	239	g115	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58388.1	000168	RlaP	239	g111	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000304	000168	RlaP	223	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000236	000168	RlaP	223	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBX06787.1	000169	RlaP	278	BcepSaruman_374	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74757.1	000169	RlaP	281	BcepSauron_377	Burkholderia phage BcepSauron	GCA_005394215.1
AFU88042.1	000169	RlaP	285	CcrColossus_gp172	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68719.1	000169	RlaP	285	CcrPW_gp180c	Caulobacter phage CcrPW	GCA_003443275.1
QBX32435.1	000169	RlaP	275	-	Pseudomonas phage PA1C	GCA_004785505.1
QKE11199.1	000169	RlaP	290	PaBG_00003	Pseudomonas phage PaBG	GCA_000912555.1
QBJ02579.1	000169	RlaP	266	PSA21_49	Pseudomonas phage Psa21	GCA_004340405.1
ATN94669.1	000169	RlaP	277	SL2_092	Pseudomonas phage SL2	GCA_002956015.1
QEM42005.1	000169	RlaP	274	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83138.1	000169	RlaP	277	PHIKZ237	Pseudomonas virus phiKZ	GCA_000842965.1
prevph1000000853	000170	RlaP	766	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000591	000170	RlaP	766	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19091.1	000171	RlaP	332	FDH28_gp117	Ralstonia phage RP12	GCA_002617345.1
BAW19377.1	000171	RlaP	332	-	Ralstonia phage RP31	GCA_002617365.1
BAW19092.1	000172	RlaP	301	FDH28_gp118	Ralstonia phage RP12	GCA_002617345.1
BAW19378.1	000172	RlaP	301	-	Ralstonia phage RP31	GCA_002617365.1
AMM45106.1	000000	RlaP	252	SP15_298	Bacillus phage SP-15	GCA_001754685.1
AFH14868.1	000000	RlaP	297	Lu11_0330	Pseudomonas phage Lu11	GCA_000897175.1
ASV44469.1	000000	RlaP	265	PBL_SCTP2_454	Salicola phage SCTP-2	GCA_002625545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAV39380.1	000000	RlaP	243	BPT24_262	Tenacibaculum phage pT24	GCA_002611925.1
ABS83642.1	000000	RlaP	260	0305phi8-36p082	Bacillus phage 0305phi8-36	GCA_000871045.1
APU01702.1	000173	Rnl1-RNA_ligase	346	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28899.1	000173	Rnl1-RNA_ligase	392	AP1_0192	Aeromonas phage AP1	GCA_014183365.1
ATI17596.1	000173	Rnl1-RNA_ligase	392	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00401.1	000173	Rnl1-RNA_ligase	392	HWB28_gp151	Aeromonas phage AS-zj	GCA_002627665.1
AUE22839.1	000173	Rnl1-RNA_ligase	389	Ah1_00321	Aeromonas phage Ah1	GCA_002957415.1
QAX98552.1	000173	Rnl1-RNA_ligase	389	ASfcp2_217	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98035.1	000173	Rnl1-RNA_ligase	392	ASswx1_395	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01110.1	000173	Rnl1-RNA_ligase	395	ASwh1_42	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39495.1	000173	Rnl1-RNA_ligase	392	CC2_136	Aeromonas phage CC2	GCA_000903495.1
ADQ53016.1	000173	Rnl1-RNA_ligase	389	PX29p297	Aeromonas phage PX29	GCA_000920195.1
ADM79940.1	000173	Rnl1-RNA_ligase	385	phiAS5_ORF0097	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53341.1	000173	Rnl1-RNA_ligase	391	65p333	Aeromonas virus 65	GCA_000893255.1
AAQ17969.1	000173	Rnl1-RNA_ligase	389	rnlA	Aeromonas virus Aeh1	GCA_000843245.1
ASV44727.1	000173	Rnl1-RNA_ligase	397	FDI40_gp261	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93524.1	000173	Rnl1-RNA_ligase	457	G_265	Bacillus virus G	GCA_000917535.1
QBX06783.1	000173	Rnl1-RNA_ligase	383	BcepSaruman_370	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74753.1	000173	Rnl1-RNA_ligase	383	BcepSauron_373	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63568.1	000173	Rnl1-RNA_ligase	240	CP21_106	Campylobacter virus CP21	GCA_000902535.1
AXQ69246.1	000173	Rnl1-RNA_ligase	363	CcrBL9_gp222	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69801.1	000173	Rnl1-RNA_ligase	384	CcrSC_gp219	Caulobacter phage CcrSC	GCA_003443315.1
ANS05958.1	000173	Rnl1-RNA_ligase	370	ABCD_0067	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64821.1	000173	Rnl1-RNA_ligase	374	S13_022	Cronobacter phage S13	GCA_001503575.1
AFC21528.1	000173	Rnl1-RNA_ligase	383	GAP32_080	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97079.1	000173	Rnl1-RNA_ligase	370	E_070	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14328.1	000173	Rnl1-RNA_ligase	380	PBI_121Q_438	Escherichia phage 121Q	GCA_000926855.1
QAY00613.1	000173	Rnl1-RNA_ligase	380	Ecwhy1_337	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34809.1	000173	Rnl1-RNA_ligase	377	ACQ29_gp129	Escherichia phage PBECO4	GCA_001041035.1
BBM62001.1	000173	Rnl1-RNA_ligase	380	EO157G_4120	Escherichia phage SP27	GCA_008033345.1
AXC36920.1	000173	Rnl1-RNA_ligase	380	-	Escherichia phage UB	GCA_003341455.1
ARM70783.1	000173	Rnl1-RNA_ligase	374	phiC120_c77	Escherichia phage phiC120	GCA_002621185.1
QBO61976.1	000173	Rnl1-RNA_ligase	380	G17_00487	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14000.1	000173	Rnl1-RNA_ligase	380	vBEcoMphAPEC6_gp376c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80315.1	000173	Rnl1-RNA_ligase	380	PSLUR01_00338	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78590.1	000173	Rnl1-RNA_ligase	370	RB43ORF068w	Escherichia virus RB43	GCA_000863505.1
AFA44737.1	000173	Rnl1-RNA_ligase	381	RaK2_00464	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72893.1	000173	Rnl1-RNA_ligase	396	-	Myoviridae sp.	GCA_003657725.1
QHJ78842.1	000173	Rnl1-RNA_ligase	386	-	Myoviridae sp.	GCA_012593985.1
QIG65773.1	000173	Rnl1-RNA_ligase	386	phiOC_p108	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43648.1	000173	Rnl1-RNA_ligase	382	CBB_83	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44065.1	000173	Rnl1-RNA_ligase	403	PBI_SCTP2_50	Salicola phage SCTP-2	GCA_002625545.1
QCW18783.1	000173	Rnl1-RNA_ligase	383	7t3_0262	Salmonella phage 7t3	GCA_006083215.1
AZU98048.1	000173	Rnl1-RNA_ligase	383	CPT_Munch_104	Salmonella phage Munch	GCA_004015485.1
QIG62932.1	000173	Rnl1-RNA_ligase	383	SEPL_319	Salmonella phage SE_PL	GCA_011067555.1
AQW88597.1	000173	Rnl1-RNA_ligase	386	BF_0072	Serratia phage BF	GCA_002619745.1
AGR47967.1	000173	Rnl1-RNA_ligase	412	SmphiM12_335	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13158.1	000173	Rnl1-RNA_ligase	412	PHIM19_253	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12797.1	000173	Rnl1-RNA_ligase	412	PHIM7_252	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13520.1	000173	Rnl1-RNA_ligase	410	PHIN3_257	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54743.1	000173	Rnl1-RNA_ligase	397	b23_0128	Synechococcus phage B23	GCA_009745195.1
QGT54373.1	000173	Rnl1-RNA_ligase	397	b3_0129	Synechococcus phage B3	GCA_009745215.1
BAX25564.1	000173	Rnl1-RNA_ligase	352	BPT24_259	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64155.1	000173	Rnl1-RNA_ligase	381	KVP40.0084	Vibrio phage KVP40	GCA_000843785.1
QIW90479.1	000173	Rnl1-RNA_ligase	381	GCAPEGMB_00132	Vibrio phage V07	GCA_012361095.1
QIW90950.1	000173	Rnl1-RNA_ligase	381	COHAPHLL_00087	Vibrio phage V09	GCA_012361135.1
QHJ74267.1	000173	Rnl1-RNA_ligase	381	VH12019_00348	Vibrio phage VH1_2019	GCA_009931825.1
AGB07092.1	000173	Rnl1-RNA_ligase	381	CF80_gp305	Vibrio phage VH7D	GCA_000914495.1
QBX06003.1	000173	Rnl1-RNA_ligase	381	ValB1HC_049	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61017.1	000173	Rnl1-RNA_ligase	381	AVU32_gp176	Vibrio phage ValKK3	GCA_001501635.1
AGN30134.1	000173	Rnl1-RNA_ligase	379	VPFG_00132	Vibrio phage nt-1	GCA_000910195.2
ALP46996.1	000173	Rnl1-RNA_ligase	381	phiGrn1_0199	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47377.1	000173	Rnl1-RNA_ligase	381	phiST2_0332	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54627.1	000173	Rnl1-RNA_ligase	381	vBValMR10Z_86	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07152.1	000173	Rnl1-RNA_ligase	375	VmeM32_00166	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37316.1	000173	Rnl1-RNA_ligase	381	pp2_083	Vibriophage phi-pp2	GCA_002630725.1
QDJ96308.1	000173	Rnl1-RNA_ligase	389	Xoosp13_121	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58874.1	000173	Rnl1-RNA_ligase	386	g066	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58337.1	000173	Rnl1-RNA_ligase	386	g060	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXQ69217.1	000174	Rnl1-RNA_ligase	194	CcrBL9_gp193	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69771.1	000174	Rnl1-RNA_ligase	194	CcrSC_gp189	Caulobacter phage CcrSC	GCA_003443315.1
QAU04498.1	000000	Rnl1-RNA_ligase	296	ValB1MD_145	Vibrio phage ValB1MD	GCA_004138815.1
APU01459.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29005.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	333	AP1_0298	Aeromonas phage AP1	GCA_014183365.1
ATI17438.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	333	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00157.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	333	HWB28_gp395	Aeromonas phage AS-zj	GCA_002627665.1
AUE22774.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	341	Ah1_00256	Aeromonas phage Ah1	GCA_002957415.1
QAX98490.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	341	ASfcp2_152	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97878.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	333	ASswx1_235	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01272.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	333	ASwh1_209	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39535.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	333	CC2_299	Aeromonas phage CC2	GCA_000903495.1
ADQ52952.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	341	PX29p233	Aeromonas phage PX29	GCA_000920195.1
ADM79877.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	341	phiAS5_ORF0034	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53080.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	65p070	Aeromonas virus 65	GCA_000893255.1
AAQ17898.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	269	rnlB-B	Aeromonas virus Aeh1	GCA_000843245.1
ANS05962.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	347	ABCD_0235	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64863.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	334	S13_064	Cronobacter phage S13	GCA_001503575.1
AON97253.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	347	E_245	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70737.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	phiC120_c30	Escherichia phage phiC120	GCA_002621185.1
AAX78771.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	347	RB43ORF249w	Escherichia virus RB43	GCA_000863505.1
QHJ79075.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	331	-	Myoviridae sp.	GCA_012593985.1
AAQ64204.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	KVP40.0133	Vibrio phage KVP40	GCA_000843785.1
QIW90519.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	GCAPEGMB_00172	Vibrio phage V07	GCA_012361095.1
QIW90903.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	COHAPHLL_00040	Vibrio phage V09	GCA_012361135.1
QHJ74315.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	VH12019_00396	Vibrio phage VH1_2019	GCA_009931825.1
AGB06809.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	CF80_gp022	Vibrio phage VH7D	GCA_000914495.1
QBX05956.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	ValB1HC_002	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60968.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	AVU32_gp127	Vibrio phage ValKK3	GCA_001501635.1
AIE13795.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	327	VPFG_00181	Vibrio phage nt-1	GCA_000910195.2
ALP47010.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	phiGrn1_0245	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47390.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	phiST2_0383	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54581.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	vBValMR10Z_40	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37364.1	000175	Rnl2-RNA_ligase+T4_Rnl2_C	335	pp2_131	Vibriophage phi-pp2	GCA_002630725.1
QBX06573.1	000176	Rnl2-RNA_ligase	372	BcepSaruman_160	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74540.1	000176	Rnl2-RNA_ligase	372	BcepSauron_160	Burkholderia phage BcepSauron	GCA_005394215.1
AFC21625.1	000176	Rnl2-RNA_ligase	421	GAP32_175	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG57864.1	000176	Rnl2-RNA_ligase	360	SEA_PAULODIABOLI_169	Microbacterium phage PauloDiaboli	GCA_011067425.1
AMM43746.1	000176	Rnl2-RNA_ligase	418	CBB_181	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QMP24171.1	000176	Rnl2-RNA_ligase	443	-	Proteus phage 10	GCA_014071245.1
ABY63181.1	000176	Rnl2-RNA_ligase	468	201phi2-1p355	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32442.1	000176	Rnl2-RNA_ligase	451	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76938.1	000176	Rnl2-RNA_ligase	475	PHABIO_307	Pseudomonas phage Phabio	GCA_002624965.1
AEH03712.1	000176	Rnl2-RNA_ligase	463	289	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02838.1	000176	Rnl2-RNA_ligase	446	PSA21_312	Pseudomonas phage Psa21	GCA_004340405.1
QEM42013.1	000176	Rnl2-RNA_ligase	451	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAW19183.1	000176	Rnl2-RNA_ligase	430	FDH28_gp212	Ralstonia phage RP12	GCA_002617345.1
BAW19469.1	000176	Rnl2-RNA_ligase	430	-	Ralstonia phage RP31	GCA_002617365.1
ASV44479.1	000176	Rnl2-RNA_ligase	369	PBI_SCTP2_464	Salicola phage SCTP-2	GCA_002625545.1
QCW18894.1	000176	Rnl2-RNA_ligase	402	7t3_0373	Salmonella phage 7t3	GCA_006083215.1
AZU98152.1	000176	Rnl2-RNA_ligase	402	CPT_Munch_208	Salmonella phage Munch	GCA_004015485.1
QIG62831.1	000176	Rnl2-RNA_ligase	402	SEPL_218	Salmonella phage SE_PL	GCA_011067555.1
AQW88703.1	000176	Rnl2-RNA_ligase	419	BF_0178	Serratia phage BF	GCA_002619745.1
AGR47935.1	000176	Rnl2-RNA_ligase	354	SmphiM12_303	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13133.1	000176	Rnl2-RNA_ligase	354	PHIM19_228	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12772.1	000176	Rnl2-RNA_ligase	354	PHIM7_227	Sinorhizobium phage phiM7	GCA_002622405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF13501.1	000176	RnlI2-RNA_ligase	354	PHIN3_238	Sinorhizobium phage phiN3	GCA_001501175.1
SOK58985.1	000176	RnlI2-RNA_ligase	417	g177	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58451.1	000176	RnlI2-RNA_ligase	417	g174	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGT54652.1	000177	RnlI2-RNA_ligase	441	b23_0024	Synechococcus phage B23	GCA_009745195.1
QGT54282.1	000177	RnlI2-RNA_ligase	441	b3_0024	Synechococcus phage B3	GCA_009745215.1
BBA65728.1	000177	RnlI2-RNA_ligase	435	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65269.1	000177	RnlI2-RNA_ligase	435	-	Xanthomonas phage XacN1	GCA_003173815.1
prevph1000000242	000177	RnlI2-RNA_ligase	504	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000192	000177	RnlI2-RNA_ligase	514	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AND75422.1	000178	RnlI2-HNH	359	ME3_261	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ94893.1	000178	RnlI2-HNH	214	FDI40_gp086	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69499.1	000178	RnlI2-HNH	359	CcrBL9_gp475	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70049.1	000178	RnlI2-HNH	359	CcrSC_gp467	Caulobacter phage CcrSC	GCA_003443315.1
AXH72860.1	000178	RnlI2-HNH	339	-	Myoviridae sp.	GCA_003657725.1
ASV44116.1	000178	RnlI2-HNH	340	PBI_SCTP2_101	Salicola phage SCTP-2	GCA_002625545.1
BBA65408.1	000178	RnlI2-HNH	216	-	Xanthomonas phage XacN1	GCA_003173815.1
QDB70286.1	000179	RpobetaN	565	CF8_0118	Aeromonas phage CF8	GCA_006384595.2
QDJ97263.1	000179	RpobetaN	575	D6_0103	Aeromonas phage D6	GCA_007051205.2
QDH47036.1	000179	RpobetaN	575	LAh10_35	Aeromonas phage LAh10	GCA_006863975.1
QDJ96877.1	000179	RpobetaN	566	PS1_0118	Aeromonas phage PS1	GCA_007051165.2
QFR59509.1	000179	RpobetaN	566	PS2_0118	Aeromonas phage PS2	GCA_009388305.2
AFO71293.1	000179	RpobetaN	524	CR5_073	Cronobacter phage CR5	GCA_000910235.1
QBZ70645.1	000179	RpobetaN	576	pETSU_064	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59727.1	000179	RpobetaN	592	SEGD1_078	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07501.1	000179	RpobetaN	591	DERBICUS_75	Erwinia phage Derbicus	GCA_004521655.1
AHI60152.1	000179	RpobetaN	562	Ea357_002	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49727.1	000179	RpobetaN	589	MACHINA_89	Erwinia phage Machina	GCA_002758035.1
AGX01935.1	000179	RpobetaN	554	CF95_gp213	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07110.1	000179	RpobetaN	562	REBECCA_2	Erwinia phage Rebecca	GCA_004521635.1
AXF51224.1	000179	RpobetaN	589	WELLINGTON_94	Erwinia phage Wellington	GCA_003344985.1
AFQ96547.1	000179	RpobetaN	591	G173_gp002	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48107.1	000179	RpobetaN	591	ASESINO_94	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85790.1	000179	RpobetaN	562	BOSOLAPHORUS_2	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48380.1	000179	RpobetaN	589	CAITLIN_85	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48653.1	000179	RpobetaN	589	CHRISDB_91	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52100.1	000179	RpobetaN	562	DM_2	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86110.1	000179	RpobetaN	562	DESERTFOX_2	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48925.1	000179	RpobetaN	591	EARLPHILLIPIV_75	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49172.1	000179	RpobetaN	589	HUXLEY_90	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03830.1	000179	RpobetaN	551	JOAD_85	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49445.1	000179	RpobetaN	589	KWAN_93	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86430.1	000179	RpobetaN	562	MADMEL_2	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86751.1	000179	RpobetaN	562	MORTIMER_2	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50000.1	000179	RpobetaN	589	PARSHIK_91	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50266.1	000179	RpobetaN	591	PHOBOS_76	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51783.1	000179	RpobetaN	562	RAY_2	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03585.1	000179	RpobetaN	551	RISINGSUN_85	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51464.1	000179	RpobetaN	562	SIMMY50_2	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64812.1	000179	RpobetaN	562	SPECIALG_2	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50521.1	000179	RpobetaN	591	STRATTON_96	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85917.1	000179	RpobetaN	592	ACEC001_0790	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63832.1	000179	RpobetaN	598	Goslar_00039	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71962.1	000179	RpobetaN	564	N1M2_99	Klebsiella phage N1M2	GCA_010092605.1
QGZ14436.1	000179	RpobetaN	557	HWC77_gp073	Photobacterium phage PDCC-1	GCA_009800445.1
QMP23996.1	000179	RpobetaN	563	-	Proteus phage 10	GCA_014071245.1
ABY63032.1	000179	RpobetaN	544	201phi2-1p203	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27174.1	000179	RpobetaN	570	PPEV_gp080	Pseudomonas phage EL	GCA_000866825.1
ANM44916.1	000179	RpobetaN	543	KTN4_158	Pseudomonas phage KTN4	GCA_002607225.1
ARV77294.1	000179	RpobetaN	549	NOXIFER_125	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89563.1	000179	RpobetaN	563	OBP_126	Pseudomonas phage OBP	GCA_000896635.1
QBX32300.1	000179	RpobetaN	541	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76821.1	000179	RpobetaN	541	PHABIO_190	Pseudomonas phage Phabio	GCA_002624965.1
AEH03562.1	000179	RpobetaN	540	139	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02700.1	000179	RpobetaN	543	PSA21_173	Pseudomonas phage Psa21	GCA_004340405.1
ATN94798.1	000179	RpobetaN	543	SL2_221	Pseudomonas phage SL2	GCA_002956015.1
QJB22794.1	000179	RpobetaN	543	fnug_151	Pseudomonas phage fnug	GCA_012837215.1
QEM41873.1	000179	RpobetaN	541	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83024.1	000179	RpobetaN	543	PHIKZ123	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19066.1	000179	RpobetaN	558	FDH28_gp092	Ralstonia phage RP12	GCA_002617345.1
BAW19351.1	000179	RpobetaN	558	-	Ralstonia phage RP31	GCA_002617365.1
BAS04914.2	000179	RpobetaN	527	AVU11_gp122	Ralstonia phage RSF1	GCA_001500875.1
BAQ02643.1	000179	RpobetaN	559	AVU38_gp115	Ralstonia phage RSL2	GCA_001503055.1
QNI20788.1	000179	RpobetaN	596	-	Salmonella phage JN03	GCA_014319805.1
AWN09023.2	000179	RpobetaN	592	MLDJOKPK_00082	Salmonella phage SPAsTU	GCA_003183805.1
AEP83910.1	000179	RpobetaN	592	SPN3US_0077	Salmonella phage SPN3US	GCA_001042275.1
QKE54316.1	000179	RpobetaN	561	ACSA002_0020	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65376.1	000179	RpobetaN	537	2050HW_00041	Serratia phage 2050HW	GCA_002628125.1
QDB71160.1	000179	RpobetaN	537	CPT_Moabite_130	Serratia phage Moabite	GCA_006384735.1
QFP93067.1	000179	RpobetaN	535	-	Serratia phage PCH45	GCA_009187865.1
QAU04300.1	000179	RpobetaN	557	HWC03_gp145	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23278.1	000179	RpobetaN	557	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80936.1	000179	RpobetaN	557	Aphrodite1_0067	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70856.1	000179	RpobetaN	523	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47450.1	000179	RpobetaN	557	HWC35_gp056	Vibrio phage USC-1	GCA_006864065.1
BAW98272.1	000179	RpobetaN	559	FDH33_gp063	Vibrio phage pTD1	GCA_002618825.1
AQT27955.1	000179	RpobetaN	559	pVa21_013	Vibrio phage pVa-21	GCA_002619305.1
QAX96633.1	000179	RpobetaN	534	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96951.1	000179	RpobetaN	534	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95997.1	000179	RpobetaN	534	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96315.1	000179	RpobetaN	534	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21106.1	000179	RpobetaN	523	-	Vibrio phage vB_pir03	GCA_014319855.1
AMS01189.1	000180	RpobetaN	496	AR9_g105	Bacillus phage AR9	GCA_001743835.1
ALN97864.1	000180	RpobetaN	505	Bp8pS_185	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00123.1	000180	RpobetaN	496	PBI_PBS1_301	Bacillus virus PBS1	GCA_002601325.1
CCE26218.1	000180	RpobetaN	516	g194	Yersinia phage phiR1-37	GCA_000895615.1
ANZ50227.1	000181	beta-prime-C	703	PHOBOS_37	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ABY62962.1	000181	beta-prime-C	659	201phi2-1p130	Pseudomonas phage 201phi2-1	GCA_000875305.1
QFR59459.1	000181	beta-prime-C	674	PS2_0068	Aeromonas phage PS2	GCA_009388305.2
QHJ86093.1	000181	beta-prime-C	515	KKIINIFJ_00181	Pseudomonas phage PN05	GCA_009931935.1
BAS05006.2	000181	beta-prime-C	643	AVU11_gp214	Ralstonia phage RSF1	GCA_001500875.1
BAQ02736.2	000181	beta-prime-C	658	-	Ralstonia phage RSL2	GCA_001503055.1
ANZ49962.1	000181	beta-prime-C	699	PARSHIK_53	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANH52029.1	000181	beta-prime-C	655	RAY_249	Erwinia phage vB_EamM_RAY	GCA_002624345.1
QEM41799.1	000181	beta-prime-C	657	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AUG87003.1	000181	beta-prime-C	655	MORTIMER_255	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ASU03626.1	000181	beta-prime-C	661	RISINGSUN_44	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AUG86679.1	000181	beta-prime-C	655	MADMEL_252	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
CCE26126.1	000181	beta-prime-C	603	g102	Yersinia phage phiR1-37	GCA_000895615.1
ANZ49399.1	000181	beta-prime-C	699	KWAN_47	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03871.1	000181	beta-prime-C	661	JOAD_44	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49134.1	000181	beta-prime-C	699	HUXLEY_52	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
AXH70825.1	000181	beta-prime-C	657	-	Vibrio phage BONAISHI	GCA_003441475.1
ANH51712.1	000181	beta-prime-C	655	SIMMY50_254	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANZ48887.1	000181	beta-prime-C	703	EARLPHILLIPIV_37	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANJ65064.1	000181	beta-prime-C	655	SPECIALG_253	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AUG86357.1	000181	beta-prime-C	655	DESERTFOX_250	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
QDB71087.1	000181	beta-prime-C	663	CPT_Moabite_055	Serratia phage Moabite	GCA_006384735.1
ANZ50475.1	000181	beta-prime-C	701	STRATTON_50	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QBJ02605.1	000181	beta-prime-C	657	PSA21_76	Pseudomonas phage Psa21	GCA_004340405.1
ANH52354.1	000181	beta-prime-C	655	DM_255	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANZ48613.1	000181	beta-prime-C	699	CHRISDB_51	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48340.1	000181	beta-prime-C	712	CAITLIN_45	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
AUG86037.1	000181	beta-prime-C	655	BOSOLAPHORUS_251	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
QDJ97221.1	000181	beta-prime-C	670	D6_0061	Aeromonas phage D6	GCA_007051205.2
AUR80932.1	000181	beta-prime-C	661	Aphrodite1_0121	Vibrio phage Aphrodite1	GCA_002958015.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48065.1	000181	beta-prime-C	701	ASESINO_52	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
QDH47504.1	000181	beta-prime-C	661	HWC35_gp110	Vibrio phage USC-1	GCA_006864065.1
QDH47030.1	000181	beta-prime-C	670	LAh10_226	Aeromonas phage LAh10	GCA_006863975.1
AFQ96763.1	000181	beta-prime-C	630	G173_gp218	Erwinia phage phiEaH2	GCA_000902915.1
AXF51178.1	000181	beta-prime-C	699	WELLINGTON_47	Erwinia phage Wellington	GCA_003344985.1
AFO71256.1	000181	beta-prime-C	703	CR5_036	Cronobacter phage CR5	GCA_000910235.1
QBP07355.1	000181	beta-prime-C	655	REBECCA_250	Erwinia phage Rebecca	GCA_004521635.1
QFP93057.1	000181	beta-prime-C	667	-	Serratia phage PCH45	GCA_009187865.1
AGX01729.1	000181	beta-prime-C	662	CF95_gp007	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ49689.1	000181	beta-prime-C	699	MACHINA_51	Erwinia phage Machina	GCA_002758035.1
AEV89511.1	000181	beta-prime-C	674	OBP_074	Pseudomonas phage OBP	GCA_000896635.1
AHI60399.1	000181	beta-prime-C	655	Ea357_246	Erwinia phage Ea35-70	GCA_000914635.1
QBP07463.1	000181	beta-prime-C	703	DERBICUS_37	Erwinia phage Derbicus	GCA_004521655.1
AMR59687.1	000181	beta-prime-C	701	SEGD1_038	Enterobacteria phage SEGD1	GCA_002601865.1
ARV77237.1	000181	beta-prime-C	658	NOXIFER_66	Pseudomonas phage Noxifer	GCA_002625005.1
QCW23224.1	000181	beta-prime-C	661	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QNI20751.1	000181	beta-prime-C	701	-	Salmonella phage JN03	GCA_014319805.1
ATA65663.1	000181	beta-prime-C	479	2050HW_00328	Serratia phage 2050HW	GCA_002628125.1
QAX96672.1	000181	beta-prime-C	649	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
BAW98323.1	000181	beta-prime-C	661	FDH33_gp114	Vibrio phage pTD1	GCA_002618825.1
QKN85876.1	000181	beta-prime-C	701	ACEC001_0380	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QAU04352.1	000181	beta-prime-C	661	HWC03_gp197	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAX96990.1	000181	beta-prime-C	649	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QKE54574.1	000181	beta-prime-C	655	ACSA002_2580	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AMS01238.1	000181	beta-prime-C	631	AR9_g154	Bacillus phage AR9	GCA_001743835.1
QGZ14384.1	000181	beta-prime-C	661	HWC77_gp021	Photobacterium phage PDCC-1	GCA_009800445.1
QDJ96829.1	000181	beta-prime-C	674	PS1_0070	Aeromonas phage PS1	GCA_007051165.2
ALN97898.1	000181	beta-prime-C	632	Bp8pS_219	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QNI21070.1	000181	beta-prime-C	654	-	Vibrio phage vB_pir03	GCA_014319855.1
AST99864.1	000181	beta-prime-C	631	PBI_PBS1_42	Bacillus virus PBS1	GCA_002601325.1
QMP24166.1	000181	beta-prime-C	675	-	Proteus phage 10	GCA_014071245.1
QGH71915.1	000181	beta-prime-C	673	N1M2_52	Klebsiella phage N1M2	GCA_010092605.1
QAX96036.1	000181	beta-prime-C	649	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
AEP83868.1	000181	beta-prime-C	701	SPN3US_0035	Salmonella phage SPN3US	GCA_001042275.1
AWN09060.1	000181	beta-prime-C	701	MLDJOKPK_00130	Salmonella phage SPAsTU	GCA_003183805.1
QAX96354.1	000181	beta-prime-C	649	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AQT28162.1	000181	beta-prime-C	668	pVa21_221	Vibrio phage pVa-21	GCA_002619305.1
BAW19248.1	000181	beta-prime-C	680	FDH28_gp147	Ralstonia phage RP12	GCA_002617345.1
AAL82975.1	000181	beta-prime-C	677	PHIKZ074	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19534.1	000181	beta-prime-C	680	-	Ralstonia phage RP31	GCA_002617365.1
QBZ70599.1	000181	beta-prime-C	672	pETSU_018	Edwardsiella virus pEt-SU	GCA_004800915.1
ANM44855.1	000181	beta-prime-C	677	KTN4_097	Pseudomonas phage KTN4	GCA_002607225.1
QBX32221.1	000181	beta-prime-C	657	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76744.1	000181	beta-prime-C	661	PHABIO_113	Pseudomonas phage Phabio	GCA_002624965.1
QJB22732.1	000181	beta-prime-C	677	fnug_89	Pseudomonas phage fnug	GCA_012837215.1
QBO63958.1	000181	beta-prime-C	668	Goslar_00165	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDB70481.1	000181	beta-prime-C	672	CF8_0070	Aeromonas phage CF8	GCA_006384595.2
ATN94858.1	000181	beta-prime-C	677	SL2_281	Pseudomonas phage SL2	GCA_002956015.1
QMV29132.1	000182	beta-prime-C	136	AP1_0429	Aeromonas phage AP1	GCA_014183365.1
QDB70249.1	000182	beta-prime-C	431	CF8_0081	Aeromonas phage CF8	GCA_006384595.2
QNH80841.1	000182	beta-prime-C	435	D6_0068	Aeromonas phage D6	GCA_007051205.2
QDH47059.1	000182	beta-prime-C	437	LAh10_1	Aeromonas phage LAh10	GCA_006863975.1
QDJ96838.1	000182	beta-prime-C	434	PS1_0079	Aeromonas phage PS1	GCA_007051165.2
QFR59468.1	000182	beta-prime-C	434	PS2_0077	Aeromonas phage PS2	GCA_009388305.2
AMS01348.1	000182	beta-prime-C	401	AR9_g264	Bacillus phage AR9	GCA_001743835.1
ALN97982.1	000182	beta-prime-C	402	Bp8pS_303	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99976.1	000182	beta-prime-C	401	PBI_PBS1_155	Bacillus virus PBS1	GCA_002601325.1
AFO71263.1	000182	beta-prime-C	431	CR5_043	Cronobacter phage CR5	GCA_000910235.1
QBZ70611.1	000182	beta-prime-C	435	pETSU_030	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59693.1	000182	beta-prime-C	431	SEGD1_044	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07470.1	000182	beta-prime-C	431	DERBICUS_44	Erwinia phage Derbicus	GCA_004521655.1
AHI60420.1	000182	beta-prime-C	436	Ea357_266	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49696.1	000182	beta-prime-C	432	MACHINA_58	Erwinia phage Machina	GCA_002758035.1
AGX01961.1	000182	beta-prime-C	466	CF95_gp239	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07377.1	000182	beta-prime-C	436	REBECCA_272	Erwinia phage Rebecca	GCA_004521635.1
AXF51185.1	000182	beta-prime-C	434	WELLINGTON_54	Erwinia phage Wellington	GCA_003344985.1
AFQ96770.1	000182	beta-prime-C	435	G173_gp225	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48072.1	000182	beta-prime-C	435	ASESINO_59	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86059.1	000182	beta-prime-C	436	BOSOLAPHORUS_273	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48347.1	000182	beta-prime-C	434	CAITLIN_52	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48620.1	000182	beta-prime-C	434	CHRISDB_58	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52375.1	000182	beta-prime-C	436	DM_276	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86379.1	000182	beta-prime-C	436	DESERTFOX_272	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48894.1	000182	beta-prime-C	431	EARLPHILLIPIV_44	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49141.1	000182	beta-prime-C	432	HUXLEY_59	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03865.1	000182	beta-prime-C	434	JOAD_50	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49406.1	000182	beta-prime-C	434	KWAN_54	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86700.1	000182	beta-prime-C	436	MADMEL_273	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87025.1	000182	beta-prime-C	436	MORTIMER_277	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49969.1	000182	beta-prime-C	432	PARSHIK_60	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50234.1	000182	beta-prime-C	431	PHOBOS_44	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52050.1	000182	beta-prime-C	436	RAY_270	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03620.1	000182	beta-prime-C	434	RISINGSUN_50	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51733.1	000182	beta-prime-C	436	SIMMY50_275	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65085.1	000182	beta-prime-C	436	SPECIALG_274	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50482.1	000182	beta-prime-C	435	STRATTON_57	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85883.1	000182	beta-prime-C	431	ACEC001_0450	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63871.1	000182	beta-prime-C	433	Goslar_00078	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71927.1	000182	beta-prime-C	435	N1M2_64	Klebsiella phage N1M2	GCA_010092605.1
QGZ14390.1	000182	beta-prime-C	433	HWC77_gp027	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24180.1	000182	beta-prime-C	433	-	Proteus phage 10	GCA_014071245.1
ABY62970.1	000182	beta-prime-C	447	201phi2-1p139	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27138.1	000182	beta-prime-C	433	PPEV_gp044	Pseudomonas phage EL	GCA_000866825.1
ANM44864.1	000182	beta-prime-C	449	KTN4_106	Pseudomonas phage KTN4	GCA_002607225.1
ARV77247.1	000182	beta-prime-C	463	NOXIFER_76	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89527.1	000182	beta-prime-C	436	OBP_090	Pseudomonas phage OBP	GCA_000896635.1
QBX32234.1	000182	beta-prime-C	447	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76755.1	000182	beta-prime-C	450	PHABIO_124	Pseudomonas phage Phabio	GCA_002624965.1
AEH03501.1	000182	beta-prime-C	446	077	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02615.1	000182	beta-prime-C	448	PSA21_87	Pseudomonas phage Psa21	GCA_004340405.1
ATN94849.1	000182	beta-prime-C	449	SL2_272	Pseudomonas phage SL2	GCA_002956015.1
QJB22742.1	000182	beta-prime-C	449	fnug_99	Pseudomonas phage fnug	GCA_012837215.1
QEM41813.1	000182	beta-prime-C	447	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82981.1	000182	beta-prime-C	449	PHIKZ080	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19232.1	000182	beta-prime-C	442	FDH28_gp163	Ralstonia phage RP12	GCA_002617345.1
BAW19518.1	000182	beta-prime-C	442	-	Ralstonia phage RP31	GCA_002617365.1
BAS04991.1	000182	beta-prime-C	443	AVU11_gp199	Ralstonia phage RSF1	GCA_001500875.1
BAQ02720.1	000182	beta-prime-C	432	AVU38_gp192	Ralstonia phage RSL2	GCA_001503055.1
QNI20758.1	000182	beta-prime-C	432	-	Salmonella phage JN03	GCA_014319805.1
AWN09055.1	000182	beta-prime-C	433	MLDJOKPK_00124	Salmonella phage SPAsTU	GCA_003183805.1
AEP83875.1	000182	beta-prime-C	431	SPN3US_0042	Salmonella phage SPN3US	GCA_001042275.1
QKE54600.1	000182	beta-prime-C	436	ACSA002_2830	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65698.1	000182	beta-prime-C	261	2050HW_00363	Serratia phage 2050HW	GCA_002628125.1
QDB71125.1	000182	beta-prime-C	462	CPT_Moabite_095	Serratia phage Moabite	GCA_006384735.1
QFP93082.1	000182	beta-prime-C	455	-	Serratia phage PCH45	GCA_009187865.1
QAU04346.1	000182	beta-prime-C	433	HWC03_gp191	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23230.1	000182	beta-prime-C	432	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80959.1	000182	beta-prime-C	432	Aphrodite1_0115	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70833.1	000182	beta-prime-C	419	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47498.1	000182	beta-prime-C	432	HWC35_gp104	Vibrio phage USC-1	GCA_006864065.1
BAW98318.1	000182	beta-prime-C	432	FDH33_gp109	Vibrio phage pTD1	GCA_002618825.1
AQT28169.1	000182	beta-prime-C	435	pVa21_228	Vibrio phage pVa-21	GCA_002619305.1
QAX96660.1	000182	beta-prime-C	417	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96978.1	000182	beta-prime-C	417	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96024.1	000182	beta-prime-C	417	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96342.1	000182	beta-prime-C	417	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21080.1	000182	beta-prime-C	409	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26254.1	000182	beta-prime-C	424	g231	Yersinia phage phiR1-37	GCA_000895615.1
ATA65336.1	000182	beta-prime-C	138	2050HW_00001	Serratia phage 2050HW	GCA_002628125.1
QMV29140.1	000183	beta-prime-C	246	AP1_0437	Aeromonas phage AP1	GCA_014183365.1
APU01660.1	000184	beta-prime-C	127	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17226.1	000184	beta-prime-C	126	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00361.1	000184	beta-prime-C	126	HWB28_gp191	Aeromonas phage AS-zj	GCA_002627665.1
QAX97669.1	000184	beta-prime-C	126	ASswx1_23	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01470.1	000184	beta-prime-C	126	ASwh1_411	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39340.1	000184	beta-prime-C	130	CC2_092	Aeromonas phage CC2	GCA_000903495.1
ADQ53291.1	000184	beta-prime-C	127	65p283	Aeromonas virus 65	GCA_000893255.1
QMV29152.1	000000	beta-prime-C	232	AP1_0451	Aeromonas phage AP1	GCA_014183365.1
ATA65664.1	000000	beta-prime-C	186	2050HW_00329	Serratia phage 2050HW	GCA_002628125.1
QMV29113.1	000185	DDRP-betaprime	211	AP1_0410	Aeromonas phage AP1	GCA_014183365.1
QDB70466.1	000185	DDRP-betaprime	469	CF8_0053	Aeromonas phage CF8	GCA_006384595.2
QDB70394.1	000185	DDRP-betaprime	493	CF8_0225	Aeromonas phage CF8	GCA_006384595.2
QDJ97206.1	000185	DDRP-betaprime	533	D6_0046	Aeromonas phage D6	GCA_007051205.2
QDJ97393.1	000185	DDRP-betaprime	539	D6_0234	Aeromonas phage D6	GCA_007051205.2
QDH47038.1	000185	DDRP-betaprime	539	LAh10_148	Aeromonas phage LAh10	GCA_006863975.1
QDH47039.1	000185	DDRP-betaprime	533	LAh10_213	Aeromonas phage LAh10	GCA_006863975.1
QDJ96808.1	000185	DDRP-betaprime	475	PS1_0049	Aeromonas phage PS1	GCA_007051165.2
QDJ96738.1	000185	DDRP-betaprime	490	PS1_0227	Aeromonas phage PS1	GCA_007051165.2
QFR59439.1	000185	DDRP-betaprime	475	PS2_0048	Aeromonas phage PS2	GCA_009388305.2
QFR59371.1	000185	DDRP-betaprime	490	PS2_0229	Aeromonas phage PS2	GCA_009388305.2
AMS01229.1	000185	DDRP-betaprime	503	AR9_g145	Bacillus phage AR9	GCA_001743835.1
AMS01354.1	000185	DDRP-betaprime	426	AR9_g270	Bacillus phage AR9	GCA_001743835.1
ALN97697.1	000185	DDRP-betaprime	428	Bp8pS_018	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97891.1	000185	DDRP-betaprime	504	Bp8pS_212	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99985.1	000185	DDRP-betaprime	382	PBI_PBS1_164	Bacillus virus PBS1	GCA_002601325.1
AST99857.1	000185	DDRP-betaprime	390	PBI_PBS1_35	Bacillus virus PBS1	GCA_002601325.1
AFO71244.1	000185	DDRP-betaprime	540	CR5_024	Cronobacter phage CR5	GCA_000910235.1
AFO71428.1	000185	DDRP-betaprime	543	CR5_208	Cronobacter phage CR5	GCA_000910235.1
QBZ70584.1	000185	DDRP-betaprime	529	pETSU_003	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70779.1	000185	DDRP-betaprime	521	pETSU_198	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59892.1	000185	DDRP-betaprime	537	SEGD1_245	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07641.1	000185	DDRP-betaprime	543	DERBICUS_215	Erwinia phage Derbicus	GCA_004521655.1
QBP07451.1	000185	DDRP-betaprime	540	DERBICUS_25	Erwinia phage Derbicus	GCA_004521655.1
AHI60313.1	000185	DDRP-betaprime	538	Ea357_162	Erwinia phage Ea35-70	GCA_000914635.1
AHI60373.1	000185	DDRP-betaprime	495	Ea357_220	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49891.1	000185	DDRP-betaprime	537	MACHINA_253	Erwinia phage Machina	GCA_002758035.1
ANZ49677.1	000185	DDRP-betaprime	530	MACHINA_39	Erwinia phage Machina	GCA_002758035.1
AGX01868.1	000185	DDRP-betaprime	542	CF95_gp146	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01743.1	000185	DDRP-betaprime	469	rpoBC	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07272.1	000185	DDRP-betaprime	538	REBECCA_165	Erwinia phage Rebecca	GCA_004521635.1
QBP07330.1	000185	DDRP-betaprime	495	REBECCA_225	Erwinia phage Rebecca	GCA_004521635.1
AXF51392.1	000185	DDRP-betaprime	537	WELLINGTON_266	Erwinia phage Wellington	GCA_003344985.1
AXF51166.1	000185	DDRP-betaprime	529	WELLINGTON_35	Erwinia phage Wellington	GCA_003344985.1
AFQ96750.1	000185	DDRP-betaprime	533	G173_gp205	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96705.1	000185	DDRP-betaprime	537	G173_gp160	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48275.1	000185	DDRP-betaprime	537	ASESINO_262	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48053.1	000185	DDRP-betaprime	533	ASESINO_40	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85952.1	000185	DDRP-betaprime	538	BOSOLAPHORUS_165	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86011.1	000185	DDRP-betaprime	495	BOSOLAPHORUS_225	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48547.1	000185	DDRP-betaprime	537	CAITLIN_252	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48328.1	000185	DDRP-betaprime	530	CAITLIN_33	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48825.1	000185	DDRP-betaprime	537	CHRISDB_263	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48601.1	000185	DDRP-betaprime	530	CHRISDB_39	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52267.2	000185	DDRP-betaprime	538	DM_169	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52328.1	000185	DDRP-betaprime	495	DM_228	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86271.1	000185	DDRP-betaprime	538	DESERTFOX_164	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86330.1	000185	DDRP-betaprime	495	DESERTFOX_223	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49065.1	000185	DDRP-betaprime	543	EARLPHILLIPIV_216	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48875.1	000185	DDRP-betaprime	540	EARLPHILLIPIV_25	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49334.1	000185	DDRP-betaprime	537	HUXLEY_252	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49122.1	000185	DDRP-betaprime	530	HUXLEY_40	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03684.1	000185	DDRP-betaprime	539	JOAD_231	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03886.1	000185	DDRP-betaprime	543	JOAD_29	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49618.1	000185	DDRP-betaprime	537	KWAN_266	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49387.1	000185	DDRP-betaprime	529	KWAN_35	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86593.1	000185	DDRP-betaprime	538	MADMEL_165	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86653.1	000185	DDRP-betaprime	495	MADMEL_225	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86917.1	000185	DDRP-betaprime	538	MORTIMER_168	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86976.1	000185	DDRP-betaprime	495	MORTIMER_228	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50162.1	000185	DDRP-betaprime	537	PARSHIK_253	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ49950.1	000185	DDRP-betaprime	530	PARSHIK_41	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50412.1	000185	DDRP-betaprime	543	PHOBOS_222	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50215.1	000185	DDRP-betaprime	539	PHOBOS_25	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51944.1	000185	DDRP-betaprime	538	RAY_163	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52003.1	000185	DDRP-betaprime	495	RAY_223	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03441.1	000185	DDRP-betaprime	538	RISINGSUN_229	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03641.1	000185	DDRP-betaprime	543	RISINGSUN_29	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51628.1	000185	DDRP-betaprime	538	SIMMY50_166	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51687.1	000185	DDRP-betaprime	495	SIMMY50_228	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64975.1	000185	DDRP-betaprime	538	SPECIALG_165	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65037.1	000185	DDRP-betaprime	495	SPECIALG_226	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50687.1	000185	DDRP-betaprime	537	STRATTON_262	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50463.1	000185	DDRP-betaprime	533	STRATTON_38	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85863.1	000185	DDRP-betaprime	502	ACEC001_0250	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86081.1	000185	DDRP-betaprime	537	ACEC001_2380	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63980.1	000185	DDRP-betaprime	423	Goslar_00188	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64022.1	000185	DDRP-betaprime	502	Goslar_00231	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72085.1	000185	DDRP-betaprime	538	N1M2_222	Klebsiella phage N1M2	GCA_010092605.1
QGH71900.1	000185	DDRP-betaprime	529	N1M2_37	Klebsiella phage N1M2	GCA_010092605.1
QGZ14512.1	000185	DDRP-betaprime	477	HWC77_gp149	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14368.1	000185	DDRP-betaprime	488	HWC77_gp005	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24146.1	000185	DDRP-betaprime	483	-	Proteus phage 10	GCA_014071245.1
QMP24094.1	000185	DDRP-betaprime	543	-	Proteus phage 10	GCA_014071245.1
ABY62939.1	000185	DDRP-betaprime	487	201phi2-1p107	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63102.1	000185	DDRP-betaprime	550	201phi2-1p275	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27118.1	000185	DDRP-betaprime	480	PPEV_gp024	Pseudomonas phage EL	GCA_000866825.1
CAG27278.1	000185	DDRP-betaprime	481	PPEV_gp184	Pseudomonas phage EL	GCA_000866825.1
ANM44832.1	000185	DDRP-betaprime	379	KTN4_074	Pseudomonas phage KTN4	GCA_002607225.1
ANM44978.1	000185	DDRP-betaprime	550	KTN4_220	Pseudomonas phage KTN4	GCA_002607225.1
ARV77365.1	000185	DDRP-betaprime	556	NOXIFER_196	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77222.1	000185	DDRP-betaprime	490	NOXIFER_51	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89495.1	000185	DDRP-betaprime	530	OBP_058	Pseudomonas phage OBP	GCA_000896635.1
AEV89714.1	000185	DDRP-betaprime	518	OBP_277	Pseudomonas phage OBP	GCA_000896635.1
QBX32207.1	000185	DDRP-betaprime	476	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32368.1	000185	DDRP-betaprime	550	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76895.1	000185	DDRP-betaprime	550	PHABIO_264	Pseudomonas phage Phabio	GCA_002624965.1
ARV76715.1	000185	DDRP-betaprime	487	PHABIO_84	Pseudomonas phage Phabio	GCA_002624965.1
AEH03481.1	000185	DDRP-betaprime	488	054	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03635.1	000185	DDRP-betaprime	550	212	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02771.1	000185	DDRP-betaprime	550	PSA21_245	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02587.1	000185	DDRP-betaprime	489	PSA21_58	Pseudomonas phage Psa21	GCA_004340405.1
ATN94736.1	000185	DDRP-betaprime	550	SL2_159	Pseudomonas phage SL2	GCA_002956015.1
ATN94880.1	000185	DDRP-betaprime	379	SL2_303	Pseudomonas phage SL2	GCA_002956015.1
QJB22856.1	000185	DDRP-betaprime	550	fnug_213	Pseudomonas phage fnug	GCA_012837215.1
QJB22710.1	000185	DDRP-betaprime	379	fnug_67	Pseudomonas phage fnug	GCA_012837215.1
QEM41784.1	000185	DDRP-betaprime	436	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41942.1	000185	DDRP-betaprime	550	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82956.1	000185	DDRP-betaprime	420	PHIKZ055	Pseudomonas virus phiKZ	GCA_000842965.1
AAL83081.1	000185	DDRP-betaprime	490	PHIKZ180	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19261.1	000185	DDRP-betaprime	505	FDH28_gp134	Ralstonia phage RP12	GCA_002617345.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAW19016.1	000185	DDRP-betaprime	664	FDH28_gp042	Ralstonia phage RP12	GCA_002617345.1
BAW19548.1	000185	DDRP-betaprime	505	-	Ralstonia phage RP31	GCA_002617365.1
BAW19302.1	000185	DDRP-betaprime	664	-	Ralstonia phage RP31	GCA_002617365.1
BAS04833.2	000185	DDRP-betaprime	538	AVU11_agp10	Ralstonia phage RSF1	GCA_001500875.1
BAS05019.2	000185	DDRP-betaprime	539	AVU11_gp227	Ralstonia phage RSF1	GCA_001500875.1
BAQ02749.2	000185	DDRP-betaprime	537	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02566.2	000185	DDRP-betaprime	538	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20925.1	000185	DDRP-betaprime	401	-	Salmonella phage JN03	GCA_014319805.1
QNI20739.1	000185	DDRP-betaprime	445	-	Salmonella phage JN03	GCA_014319805.1
AXF51098.1	000185	DDRP-betaprime	539	MLDJOKPK_00143	Salmonella phage SPAsTU	GCA_003183805.1
AWN09112.2	000185	DDRP-betaprime	537	MLDJOKPK_00200	Salmonella phage SPAsTU	GCA_003183805.1
AEP83856.1	000185	DDRP-betaprime	531	SPN3US_0023	Salmonella phage SPN3US	GCA_001042275.1
AEP84073.1	000185	DDRP-betaprime	537	SPN3US_0240	Salmonella phage SPN3US	GCA_001042275.1
QKE54470.1	000185	DDRP-betaprime	538	ACSA002_1560	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54547.1	000185	DDRP-betaprime	490	ACSA002_2310	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65432.1	000185	DDRP-betaprime	192	2050HW_00097	Serratia phage 2050HW	GCA_002628125.1
ATA65648.1	000185	DDRP-betaprime	435	2050HW_00313	Serratia phage 2050HW	GCA_002628125.1
QDB71073.1	000185	DDRP-betaprime	483	CPT_Moabite_041	Serratia phage Moabite	GCA_006384735.1
QDB71207.1	000185	DDRP-betaprime	545	CPT_Moabite_177	Serratia phage Moabite	GCA_006384735.1
QFP93077.1	000185	DDRP-betaprime	474	-	Serratia phage PCH45	GCA_009187865.1
QFP93065.1	000185	DDRP-betaprime	545	-	Serratia phage PCH45	GCA_009187865.1
QAU04222.1	000185	DDRP-betaprime	477	HWC03_gp067	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04368.1	000185	DDRP-betaprime	488	HWC03_gp213	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23207.1	000185	DDRP-betaprime	495	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23140.1	000185	DDRP-betaprime	535	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80946.1	000185	DDRP-betaprime	495	Aphrodite1_0137	Vibrio phage Aphrodite1	GCA_002958015.1
AUR80938.1	000185	DDRP-betaprime	535	Aphrodite1_0200	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70813.1	000185	DDRP-betaprime	497	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70765.1	000185	DDRP-betaprime	555	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47521.1	000185	DDRP-betaprime	495	HWC35_gp127	Vibrio phage USC-1	GCA_006864065.1
QDH47587.1	000185	DDRP-betaprime	535	HWC35_gp193	Vibrio phage USC-1	GCA_006864065.1
BAW98338.1	000185	DDRP-betaprime	533	FDH33_gp129	Vibrio phage pTD1	GCA_002618825.1
BAW98402.1	000185	DDRP-betaprime	536	FDH33_gp193	Vibrio phage pTD1	GCA_002618825.1
AQT28107.1	000185	DDRP-betaprime	530	pVa21_166	Vibrio phage pVa-21	GCA_002619305.1
AQT28150.1	000185	DDRP-betaprime	510	pVa21_209	Vibrio phage pVa-21	GCA_002619305.1
QAX96695.1	000185	DDRP-betaprime	446	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96767.1	000185	DDRP-betaprime	484	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97013.1	000185	DDRP-betaprime	446	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX97086.1	000185	DDRP-betaprime	484	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96059.1	000185	DDRP-betaprime	446	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96132.1	000185	DDRP-betaprime	484	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96377.1	000185	DDRP-betaprime	446	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96450.1	000185	DDRP-betaprime	484	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21051.1	000185	DDRP-betaprime	451	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20974.1	000185	DDRP-betaprime	500	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26202.1	000185	DDRP-betaprime	472	g178	Yersinia phage phiR1-37	GCA_000895615.1
CCE26297.1	000185	DDRP-betaprime	452	g274	Yersinia phage phiR1-37	GCA_000895615.1
ATA65434.1	000185	DDRP-betaprime	290	2050HW_00099	Serratia phage 2050HW	GCA_002628125.1
AHI60221.1	000186	DDRP-betaprime	233	Ea357_070	Erwinia phage Ea35-70	GCA_000914635.1
QBP07180.1	000186	DDRP-betaprime	233	REBECCA_72	Erwinia phage Rebecca	GCA_004521635.1
AUG85859.1	000186	DDRP-betaprime	233	BOSOLAPHORUS_71	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52171.1	000186	DDRP-betaprime	233	DM_73	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86178.1	000186	DDRP-betaprime	233	DESERTFOX_70	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86500.1	000186	DDRP-betaprime	233	MADMEL_72	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86821.1	000186	DDRP-betaprime	233	MORTIMER_72	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51851.1	000186	DDRP-betaprime	233	RAY_70	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51535.1	000186	DDRP-betaprime	233	SIMMY50_73	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64883.1	000186	DDRP-betaprime	233	SPECIALG_73	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGY75118.1	000187	DDRP-betaprime	59	CF8_0054	Aeromonas phage CF8	GCA_006384595.2
QDJ96811.1	000187	DDRP-betaprime	59	PS1_0052	Aeromonas phage PS1	GCA_007051165.2
QFR59442.1	000187	DDRP-betaprime	59	PS2_0051	Aeromonas phage PS2	GCA_009388305.2
QGZ14369.1	000187	DDRP-betaprime	63	HWC77_gp006	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27120.1	000187	DDRP-betaprime	93	PPEV_gp026	Pseudomonas phage EL	GCA_000866825.1
QAU04367.1	000187	DDRP-betaprime	63	HWC03_gp212	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23209.1	000187	DDRP-betaprime	62	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81098.1	000187	DDRP-betaprime	62	Aphrodite1_0136	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47519.1	000187	DDRP-betaprime	62	HWC35_gp125	Vibrio phage USC-1	GCA_006864065.1
ANM44835.1	000188	DDRP-betaprime	61	KTN4_077	Pseudomonas phage KTN4	GCA_002607225.1
ATN94878.1	000188	DDRP-betaprime	61	SL2_301	Pseudomonas phage SL2	GCA_002956015.1
QJB22713.1	000188	DDRP-betaprime	71	fnug_70	Pseudomonas phage fnug	GCA_012837215.1
QEM41785.1	000188	DDRP-betaprime	62	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26315.1	000188	DDRP-betaprime	61	PHIKZ056.1	Pseudomonas virus phiKZ	GCA_000842965.1
QHJ86094.1	000000	SIG+DDRP-ZNR+DDRP-betaprime	491	KKIINIFJ_00182	Pseudomonas phage PN05	GCA_009931935.1
QMV29155.1	000000	DDRP-betaprime	193	AP1_0454	Aeromonas phage AP1	GCA_014183365.1
QKN85864.1	000000	DDRP-betaprime	79	ACEC001_0260	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63978.1	000000	DDRP-betaprime	79	Goslar_00185	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ATA65433.1	000000	DDRP-betaprime	73	2050HW_00098	Serratia phage 2050HW	GCA_002628125.1
ATA65649.1	000000	DDRP-betaprime	56	2050HW_00314	Serratia phage 2050HW	GCA_002628125.1
QNI21056.1	000000	DDRP-betaprime	125	-	Vibrio phage vB_pir03	GCA_014319855.1
AGN30336.1	000189	Rpo-ART	368	VPFG_00339	Vibrio phage nt-1	GCA_000910195.2
ASV44416.1	000189	Rpo-ART	372	PBI_SCTP2_401	Salicola phage SCTP-2	GCA_002625545.1
AAQ64360.1	000189	Rpo-ART	372	KVP40.0290	Vibrio phage KVP40	GCA_000843785.1
QIW90674.1	000189	Rpo-ART	372	GCAPEGMB_00327	Vibrio phage V07	GCA_012361095.1
QIW91124.1	000189	Rpo-ART	372	COHAPHLL_00288	Vibrio phage V09	GCA_012361135.1
QHJ74469.1	000189	Rpo-ART	372	VH12019_00142	Vibrio phage VH1_2019	GCA_009931825.1
AGB06963.1	000189	Rpo-ART	362	CF80_gp176	Vibrio phage VH7D	GCA_000914495.1
QBX06182.1	000189	Rpo-ART	362	ValB1HC_229	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61199.1	000189	Rpo-ART	369	AVU32_gp358	Vibrio phage ValKK3	GCA_001501635.1
ALP46999.1	000189	Rpo-ART	369	phiGrn1_0023	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47380.1	000189	Rpo-ART	369	phiST2_0154	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54807.1	000189	Rpo-ART	362	vBValMR10Z_267	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37521.1	000189	Rpo-ART	372	pp2_288	Vibriophage phi-pp2	GCA_002630725.1
AFC21890.1	000190	Rpo-ART	199	GAP32_436	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AYD79995.1	000190	Rpo-ART	225	JA11_190	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66593.1	000190	Rpo-ART	225	JA13_190	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66918.1	000190	Rpo-ART	225	JA29_192	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67564.1	000190	Rpo-ART	225	JA33_190	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMM44018.1	000190	Rpo-ART	199	CBB_455	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18557.1	000190	Rpo-ART	230	7t3_034	Salmonella phage 7t3	GCA_006083215.1
AZU98386.1	000190	Rpo-ART	229	CPT_Munch_453	Salmonella phage Munch	GCA_004015485.1
QIG63126.1	000190	Rpo-ART	230	SEPL_513	Salmonella phage SE_PL	GCA_011067555.1
AQW88978.1	000190	Rpo-ART	199	BF_0453	Serratia phage BF	GCA_002619745.1
BAV39282.1	000190	Rpo-ART	205	BPT24_156	Tenacibaculum phage pT24	GCA_002611925.1
BAV39283.1	000190	Rpo-ART	176	BPT24_157	Tenacibaculum phage pT24	GCA_002611925.1
SOK59262.1	000190	Rpo-ART	199	g454	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AAQ64130.1	000191	Rpo-ART	554	KVP40.0059	Vibrio phage KVP40	GCA_000843785.1
QIW90453.1	000191	Rpo-ART	554	GCAPEGMB_00106	Vibrio phage V07	GCA_012361095.1
QIW90976.1	000191	Rpo-ART	554	COHAPHLL_00113	Vibrio phage V09	GCA_012361135.1
QHJ74242.1	000191	Rpo-ART	554	VH12019_00323	Vibrio phage VH1_2019	GCA_009931825.1
QBX06029.1	000191	Rpo-ART	542	ValB1HC_075	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61043.1	000191	Rpo-ART	542	AVU32_gp202	Vibrio phage ValKK3	GCA_001501635.1
AGN30108.2	000191	Rpo-ART	547	VPFG_00106	Vibrio phage nt-1	GCA_000910195.2
ALP46977.1	000191	Rpo-ART	513	phiGrn1_0174	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47357.1	000191	Rpo-ART	532	phiST2_0305	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54654.1	000191	Rpo-ART	542	vBValMR10Z_113	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37290.1	000191	Rpo-ART	554	pp2_057	Vibriophage phi-pp2	GCA_002630725.1
AUE22785.1	000192	Rpo-ART	581	Ah1_00267	Aeromonas phage Ah1	GCA_002957415.1
QAX98499.1	000192	Rpo-ART	653	ASfcp2_163	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52962.1	000192	Rpo-ART	653	PX29p243	Aeromonas phage PX29	GCA_000920195.1
ADM79888.1	000192	Rpo-ART	647	phiAS5_ORF0045	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17910.1	000192	Rpo-ART	646	alt	Aeromonas virus Aeh1	GCA_000843245.1
AIA64847.1	000192	Rpo-ART	693	S13_048	Cronobacter phage S13	GCA_001503575.1
ARM70756.1	000192	Rpo-ART	695	phiC120_c50	Escherichia phage phiC120	GCA_002621185.1
QHJ78816.1	000192	Rpo-ART	672	-	Myoviridae sp.	GCA_012593985.1
ALY07011.1	000192	Rpo-ART	629	VmeM32_00017	Vibrio phage vB_VmeM-32	GCA_002608825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22667.1	000193	Rpo-ART	1212	Ah1_00126	Aeromonas phage Ah1	GCA_002957415.1
QAX98394.1	000193	Rpo-ART	1186	ASfcp2_49	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52849.1	000193	Rpo-ART	1186	PX29p130	Aeromonas phage PX29	GCA_000920195.1
ADM80108.1	000193	Rpo-ART	1183	phiAS5_ORF0265	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17796.1	000193	Rpo-ART	1211	Aeh1ORF131c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47801.1	000194	Rpo-ART	167	SmphiM12_169	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13017.1	000194	Rpo-ART	167	PHIM19_111	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12657.1	000194	Rpo-ART	167	PHIM7_110	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13389.1	000194	Rpo-ART	167	PHIN3_124	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67233.1	000195	Rpo-ART	169	AD1_189	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08464.1	000195	Rpo-ART	169	Alexandra_199	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58833.1	000195	Rpo-ART	170	Y3_193	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BBA65562.1	000196	WGR+Rpo-ART	423	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96554.1	000196	WGR+Rpo-ART	420	Xoosp13_368	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AEO93510.1	000197	Rpo-ART	177	G_251	Bacillus virus G	GCA_000917535.1
AEO93324.1	000197	Rpo-ART	377	G_53	Bacillus virus G	GCA_000917535.1
BAW19101.1	000198	Rpo-ART	211	FDH28_gp127	Ralstonia phage RP12	GCA_002617345.1
BAW19387.1	000198	Rpo-ART	211	-	Ralstonia phage RP31	GCA_002617365.1
AUZ95140.1	000000	Rpo-ART	170	FDI40_gp381	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFH14742.1	000000	Rpo-ART	150	Lu11_0205	Pseudomonas phage Lu11	GCA_000897175.1
AQT28037.1	000000	Rpo-ART	739	pVa21_096	Vibrio phage pVa-21	GCA_002619305.1
BAE47846.1	000000	SIG+Rpo-ART	251	CST148	Clostridium phage c-st	GCA_000865225.1
ALY07179.1	000000	Rpo-ART	254	VmeM32_00193	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX97715.1	000000	Rpo-ART	224	ASswx1_69	Aeromonas phage Asswx_1	GCA_004146865.1
ARM70838.1	000000	Rpo-ART	202	phiC120_c132	Escherichia phage phiC120	GCA_002621185.1
QIG66047.1	000000	Rpo-ART	1502	phiOC_p405	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QBX06544.1	000199	RtcB	408	BcepSaruman_131	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74510.1	000199	RtcB	408	BcepSauron_130	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13704.1	000199	RtcB	410	Ccr10_gp174c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14049.1	000199	RtcB	410	Ccr2_gp173c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14736.1	000199	RtcB	410	Ccr29_gp180	Caulobacter phage Ccr29	GCA_002619485.1
ARB15091.1	000199	RtcB	410	Ccr32_gp173	Caulobacter phage Ccr32	GCA_002619505.1
ARB15425.1	000199	RtcB	410	Ccr34_gp183	Caulobacter phage Ccr34	GCA_002619525.1
ARB14392.1	000199	RtcB	410	Ccr5_gp172c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68374.1	000199	RtcB	410	CcrBL10_gp170c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88086.1	000199	RtcB	409	CcrColossus_gp216	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68762.1	000199	RtcB	409	CcrPW_gp223c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87697.1	000199	RtcB	410	CcrKarma_gp180	Caulobacter virus Karma	GCA_000901575.1
AFU87346.1	000199	RtcB	410	CcrMagneto_gp176	Caulobacter virus Magneto	GCA_000903095.1
AFU86657.1	000199	RtcB	410	CcrRogue_gp175	Caulobacter virus Rogue	GCA_000900555.1
AFU88493.1	000199	RtcB	410	CcrSwift_gp175	Caulobacter virus Swift	GCA_000899655.1
AFU87010.1	000199	RtcB	410	CbK_gp178	Caulobacter virus phiCbK	GCA_000900535.1
AHI60198.1	000199	RtcB	412	Ea357_048	Erwinia phage Ea35-70	GCA_000914635.1
QBP07157.1	000199	RtcB	412	REBECCA_49	Erwinia phage Rebecca	GCA_004521635.1
AUG85837.1	000199	RtcB	412	BOSOLAPHORUS_49	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52149.1	000199	RtcB	412	DM_51	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86156.1	000199	RtcB	412	DESERTFOX_48	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86477.1	000199	RtcB	412	MADMEL_49	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86798.1	000199	RtcB	412	MORTIMER_49	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51829.1	000199	RtcB	412	RAY_48	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANJ64860.1	000199	RtcB	412	SPECIALG_50	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBX32437.1	000199	RtcB	417	-	Pseudomonas phage PA1C	GCA_004785505.1
QBJ02922.1	000199	RtcB	420	PSA21_396	Pseudomonas phage Psa21	GCA_004340405.1
QEM42008.1	000199	RtcB	734	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAW19187.1	000199	RtcB	422	FDH28_gp208	Ralstonia phage RP12	GCA_002617345.1
BAW19473.1	000199	RtcB	422	-	Ralstonia phage RP31	GCA_002617365.1
BAG41528.1	000199	RtcB	417	RSL1_ORF082	Ralstonia phage phiRSL1	GCA_000879455.1
BBI90595.1	000199	RtcB	375	HYO65_gp203	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90902.1	000199	RtcB	553	-	Tenacibaculum phage PTm5	GCA_009730715.1
APU01528.1	000200	ZetaToxin	282	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28768.1	000200	ZetaToxin	283	AP1_0050	Aeromonas phage AP1	GCA_014183365.1
ATI17372.1	000200	ZetaToxin	283	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00222.1	000200	ZetaToxin	283	HWB28_gp330	Aeromonas phage AS-zj	GCA_002627665.1
QAX97813.1	000200	ZetaToxin	283	ASswx1_169	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01338.1	000200	ZetaToxin	283	ASwh1_277	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39434.1	000200	ZetaToxin	283	CC2_367	Aeromonas phage CC2	GCA_000903495.1
ADQ53150.1	000200	ZetaToxin	282	65p142	Aeromonas virus 65	GCA_000893255.1
ANS05984.1	000200	ZetaToxin	277	ABCD_0228	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64990.1	000200	ZetaToxin	289	S13_193	Cronobacter phage S13	GCA_001503575.1
AON97245.1	000200	ZetaToxin	277	E_237	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78763.1	000200	ZetaToxin	277	RB43ORF241c	Escherichia virus RB43	GCA_000863505.1
QHJ78942.1	000200	ZetaToxin	289	-	Myoviridae sp.	GCA_012593985.1
ASV44275.1	000200	ZetaToxin	276	PBI_SCTP2_260	Salicola phage SCTP-2	GCA_002625545.1
BBI90579.1	000200	ZetaToxin	613	HYO65_gp187	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90887.1	000200	ZetaToxin	613	-	Tenacibaculum phage PTm5	GCA_009730715.1
AAQ64136.1	000200	ZetaToxin	481	KVP40.0065	Vibrio phage KVP40	GCA_000843785.1
QIW90459.1	000200	ZetaToxin	481	GCAPEGMB_00112	Vibrio phage V07	GCA_012361095.1
QIW90970.1	000200	ZetaToxin	481	COHAPHLL_00107	Vibrio phage V09	GCA_012361135.1
QHJ74248.1	000200	ZetaToxin	481	VH12019_00329	Vibrio phage VH1_2019	GCA_009931825.1
AGB07072.1	000200	ZetaToxin	481	CF80_gp285	Vibrio phage VH7D	GCA_000914495.1
QBX06023.1	000200	ZetaToxin	481	ValB1HC_069	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61037.1	000200	ZetaToxin	481	AVU32_gp196	Vibrio phage ValKK3	GCA_001501635.1
AGN30114.1	000200	ZetaToxin	481	VPFG_00112	Vibrio phage nt-1	GCA_000910195.2
ALP46982.1	000200	ZetaToxin	481	phiGrn1_0180	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47365.1	000200	ZetaToxin	481	phiST2_0311	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54648.1	000200	ZetaToxin	481	vBValMR10Z_107	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07021.1	000200	ZetaToxin	287	VmeM32_00027	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37296.1	000200	ZetaToxin	481	pp2_063	Vibriophage phi-pp2	GCA_002630725.1
AUZ95003.1	000201	RuvB-like-ATPase	348	FDI40_gp221	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG63312.1	000201	RuvB-like-ATPase	354	DAC16_79	Bacteroides phage DAC16	GCA_013387695.1
QIG63573.1	000201	RuvB-like-ATPase	354	DAC19_82	Bacteroides phage DAC19	GCA_013387715.1
QIG63834.1	000201	RuvB-like-ATPase	354	DAC20_81	Bacteroides phage DAC20	GCA_013387725.1
QIG64096.1	000201	RuvB-like-ATPase	354	DAC22_82	Bacteroides phage DAC22	GCA_013387735.1
QIG64356.1	000201	RuvB-like-ATPase	354	DAC23_78	Bacteroides phage DAC23	GCA_013387745.1
AIA64800.1	000201	RuvB-like-ATPase	328	S13_001	Cronobacter phage S13	GCA_001503575.1
AFC21981.1	000201	RuvB-like-ATPase	260	GAP32_521	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14113.1	000201	RuvB-like-ATPase	256	PBI_121Q_223	Escherichia phage 121Q	GCA_000926855.1
QAY00810.1	000201	RuvB-like-ATPase	256	Ecwhy1_537	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34984.1	000201	RuvB-like-ATPase	256	ACQ29_gp304	Escherichia phage PBECO4	GCA_001041035.1
BBM61792.1	000201	RuvB-like-ATPase	256	EO157G_2030	Escherichia phage SP27	GCA_008033345.1
AXC36563.1	000201	RuvB-like-ATPase	256	-	Escherichia phage UB	GCA_003341455.1
ARM70915.1	000201	RuvB-like-ATPase	326	phiC120_c210	Escherichia phage phiC120	GCA_002621185.1
QBO61587.1	000201	RuvB-like-ATPase	256	G17_00091	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13649.1	000201	RuvB-like-ATPase	256	vBEcoMphAPEC6_gp018c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80105.1	000201	RuvB-like-ATPase	256	PSLUR01_00128	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44580.1	000201	RuvB-like-ATPase	256	RaK2_00307	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78863.1	000201	RuvB-like-ATPase	330	-	Myoviridae sp.	GCA_012593985.1
AMM44101.1	000201	RuvB-like-ATPase	260	CBB_538	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76239.1	000201	RuvB-like-ATPase	384	EST35_0359	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18635.1	000201	RuvB-like-ATPase	255	7t3_0114	Salmonella phage 7t3	GCA_006083215.1
AZU98460.1	000201	RuvB-like-ATPase	255	CPT_Munch_528	Salmonella phage Munch	GCA_004015485.1
QIG63054.1	000201	RuvB-like-ATPase	255	SEPL_441	Salmonella phage SE_PL	GCA_011067555.1
AQW89055.1	000201	RuvB-like-ATPase	260	BF_0530	Serratia phage BF	GCA_002619745.1
AAQ64351.1	000201	RuvB-like-ATPase	334	KVP40.0281	Vibrio phage KVP40	GCA_000843785.1
QIW90665.1	000201	RuvB-like-ATPase	334	GCAPEGMB_00318	Vibrio phage V07	GCA_012361095.1
QIW91133.1	000201	RuvB-like-ATPase	334	COHAPHLL_00297	Vibrio phage V09	GCA_012361135.1
QHJ74460.1	000201	RuvB-like-ATPase	334	VH12019_00133	Vibrio phage VH1_2019	GCA_009931825.1
AGB06954.1	000201	RuvB-like-ATPase	334	CF80_gp167	Vibrio phage VH7D	GCA_000914495.1
QBX06191.1	000201	RuvB-like-ATPase	334	ValB1HC_238	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61208.1	000201	RuvB-like-ATPase	334	AVU32_gp367	Vibrio phage ValKK3	GCA_001501635.1
AGN30328.1	000201	RuvB-like-ATPase	343	VPFG_00330	Vibrio phage nt-1	GCA_000910195.2
ALP47011.1	000201	RuvB-like-ATPase	334	phiGrn1_0014	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47391.1	000201	RuvB-like-ATPase	334	phiST2_0145	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54816.1	000201	RuvB-like-ATPase	334	vBValMR10Z_276	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37512.1	000201	RuvB-like-ATPase	334	pp2_279	Vibriophage phi-pp2	GCA_002630725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK59333.1	000201	RuvB-like-ATPase	260	g525	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58795.1	000201	RuvB-like-ATPase	260	g518	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21568.1	000202	SIR2	265	GAP32_119	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14366.1	000202	SIR2	250	PBI_121Q_476	Escherichia phage 121Q	GCA_000926855.1
QAY00582.1	000202	SIR2	249	Ecwhy1_303	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34775.1	000202	SIR2	250	ACQ29_gp095	Escherichia phage PBECO4	GCA_001041035.1
BBM62037.1	000202	SIR2	250	EO157G_4480	Escherichia phage SP27	GCA_008033345.1
AXC36890.1	000202	SIR2	250	-	Escherichia phage UB	GCA_003414555.1
QBO61938.1	000202	SIR2	250	G17_00449	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13968.1	000202	SIR2	250	vBEcoMphAPEC6_gp344c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80353.1	000202	SIR2	250	PSLUR01_00376	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44775.1	000202	SIR2	245	RaK2_00502	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72864.1	000202	SIR2	270	-	Myoviridae sp.	GCA_003657725.1
AMM43685.1	000202	SIR2	263	CBB_120	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18822.1	000202	SIR2	253	7t3_0301	Salmonella phage 7t3	GCA_006083215.1
AZU98086.1	000202	SIR2	253	CPT_Munch_142	Salmonella phage Munch	GCA_004015485.1
QIG62896.1	000202	SIR2	253	SEPL_283	Salmonella phage SE_PL	GCA_011067555.1
AQW88637.1	000202	SIR2	263	BF_0112	Serratia phage BF	GCA_002619745.1
AAQ64114.1	000202	SIR2	246	KVP40.0043	Vibrio phage KVP40	GCA_000843785.1
QIW90437.1	000202	SIR2	214	GCAPEGMB_00090	Vibrio phage V07	GCA_012361095.1
QIW90992.1	000202	SIR2	214	COHAPHLL_00129	Vibrio phage V09	GCA_012361135.1
QHJ74226.1	000202	SIR2	246	VH12019_00307	Vibrio phage VH1_2019	GCA_009931825.1
AGB07050.1	000202	SIR2	253	CF80_gp263	Vibrio phage VH7D	GCA_000914495.1
QBX06046.1	000202	SIR2	253	ValB1HC_092	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61060.1	000202	SIR2	253	AVU32_gp219	Vibrio phage ValKK3	GCA_001501635.1
AGN30093.1	000202	SIR2	253	VPFG_00091	Vibrio phage nt-1	GCA_000910195.2
ALP47040.1	000202	SIR2	253	phiGrn1_0157	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47418.1	000202	SIR2	253	phiST2_0288	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54672.1	000202	SIR2	253	vBValMR10Z_131	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37276.1	000202	SIR2	221	pp2_042	Vibriophage phi-pp2	GCA_002630725.1
SOK58917.1	000202	SIR2	263	g109	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58382.1	000202	SIR2	263	g105	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01425.1	000203	RpoSigma-min	178	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28758.1	000203	RpoSigma-min	183	AP1_0040	Aeromonas phage AP1	GCA_014183665.1
ATI17473.1	000203	RpoSigma-min	183	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00524.1	000203	RpoSigma-min	183	HWB28_gp028	Aeromonas phage AS-zj	GCA_002627665.1
AUE22573.1	000203	RpoSigma-min	173	Ah1_00032	Aeromonas phage Ah1	GCA_002957415.1
QAX98609.1	000203	RpoSigma-min	174	ASfcp2_276	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97913.1	000203	RpoSigma-min	183	ASswx1_270	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01237.1	000203	RpoSigma-min	184	ASwh1_172	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39522.1	000203	RpoSigma-min	183	CC2_262	Aeromonas phage CC2	GCA_000903495.1
ADQ52746.1	000203	RpoSigma-min	174	PX29p027	Aeromonas phage PX29	GCA_000920195.1
ADM80002.1	000203	RpoSigma-min	174	phiAS5_ORF0159	Aeromonas phage phiAS5	GCA_000887715.1
AAR90904.1	000203	RpoSigma-min	178	65p034	Aeromonas virus 65	GCA_000893255.1
AAQ17688.1	000203	RpoSigma-min	173	55	Aeromonas virus Aeh1	GCA_000843245.1
ASV44763.1	000203	RpoSigma-min	277	FDI40_gp694	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63544.1	000203	RpoSigma-min	255	CP21_082	Campylobacter virus CP21	GCA_000902535.1
ANS06033.1	000203	RpoSigma-min	171	ABCD_0050	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65037.1	000203	RpoSigma-min	175	S13_240	Cronobacter phage S13	GCA_001503575.1
AFC21688.1	000203	RpoSigma-min	286	GAP32_238	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97061.1	000203	RpoSigma-min	171	E_052	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56885.1	000203	RpoSigma-min	159	CPXG_00082	Cyanophage P-RSM6	GCA_000906155.1
AJK27572.1	000203	RpoSigma-min	156	PTIM40_145	Cyanophage P-TIM40	GCA_001470935.1
AOO14320.1	000203	RpoSigma-min	157	Sn110110_126	Cyanophage S-RIM14	GCA_002599065.1
AOO14969.1	000203	RpoSigma-min	157	W1230910_123	Cyanophage S-RIM14	GCA_002599125.1
AMO43150.1	000203	RpoSigma-min	164	R1080702_141	Cyanophage S-RIM32	GCA_001754165.1
AMO43374.1	000203	RpoSigma-min	164	W270710_130	Cyanophage S-RIM44	GCA_002599145.1
AOO11618.1	000203	RpoSigma-min	164	ES420910_137	Cyanophage S-RIM44	GCA_002599165.1
AOO11846.1	000203	RpoSigma-min	164	Np050604_130	Cyanophage S-RIM44	GCA_002599185.1
AOO12083.1	000203	RpoSigma-min	164	Np200711_137	Cyanophage S-RIM44	GCA_002599205.1
AOO12319.1	000203	RpoSigma-min	164	Np420711_137	Cyanophage S-RIM44	GCA_002599225.1
AOO12547.1	000203	RpoSigma-min	164	Sn080709_130	Cyanophage S-RIM44	GCA_002599245.1
AOO12784.1	000203	RpoSigma-min	164	Sn130910_137	Cyanophage S-RIM44	GCA_002599265.1
AOO13013.1	000203	RpoSigma-min	164	W2100709_131	Cyanophage S-RIM44	GCA_002599285.1
AGH07468.1	000203	RpoSigma-min	160	CYVG_00024	Cyanophage S-SSM6a	GCA_002710385.1
AGG54483.1	000203	RpoSigma-min	163	CYWG_00199	Cyanophage S-SSM6b	GCA_002710425.1
AIT14481.1	000203	RpoSigma-min	279	PBI_121Q_591	Escherichia phage 121Q	GCA_000926855.1
QAY00467.1	000203	RpoSigma-min	312	Ecwhy1_188	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35210.1	000203	RpoSigma-min	279	ACQ29_gp530	Escherichia phage PBECO4	GCA_001041035.1
BBM62153.1	000203	RpoSigma-min	279	EO157G_5640	Escherichia phage SP27	GCA_008033345.1
AXC36782.1	000203	RpoSigma-min	279	-	Escherichia phage UB	GCA_003414555.1
ARM70886.1	000203	RpoSigma-min	185	phiC120_c181	Escherichia phage phiC120	GCA_002621185.1
QBO61822.1	000203	RpoSigma-min	279	G17_00333	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13866.1	000203	RpoSigma-min	279	vBEcoMphAPEC6_gp237c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80465.1	000203	RpoSigma-min	279	PSLUR01_00488	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78572.1	000203	RpoSigma-min	171	RB43ORF050w	Escherichia virus RB43	GCA_000863505.1
AFA44355.1	000203	RpoSigma-min	292	RaK2_00082	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72818.1	000203	RpoSigma-min	312	-	Myoviridae sp.	GCA_003657725.1
QHJ78895.1	000203	RpoSigma-min	175	-	Myoviridae sp.	GCA_012593985.1
QIG65686.1	000203	RpoSigma-min	178	phiOC_p020	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43809.1	000203	RpoSigma-min	286	CBB_244	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26311.1	000203	RpoSigma-min	156	CPMG_00212	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44522.1	000203	RpoSigma-min	159	PSSM2_144	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12445.1	000203	RpoSigma-min	159	PRTG_00297	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93454.1	000203	RpoSigma-min	159	AVU42_gp116	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99232.1	000203	RpoSigma-min	164	Syn1_131	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76019.1	000203	RpoSigma-min	280	EST35_0137	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44200.1	000203	RpoSigma-min	342	PBI_SCTP2_185	Salicola phage SCTP-2	GCA_002625545.1
QCW18961.1	000203	RpoSigma-min	281	7t3_0440	Salmonella phage 7t3	GCA_006083215.1
AZU98214.1	000203	RpoSigma-min	281	CPT_Munch_270	Salmonella phage Munch	GCA_004015485.1
QIG62770.1	000203	RpoSigma-min	281	SEPL_157	Salmonella phage SE_PL	GCA_011067555.1
AQW88768.1	000203	RpoSigma-min	286	BF_0243	Serratia phage BF	GCA_002619745.1
AGR47681.1	000203	RpoSigma-min	193	SmphiM12_049	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12943.1	000203	RpoSigma-min	193	PHIM19_36	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12583.1	000203	RpoSigma-min	193	PHIM7_35	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13317.1	000203	RpoSigma-min	193	PHIN3_52	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28110.1	000203	RpoSigma-min	155	PAU_112	Sphingomonas phage PAU	GCA_000902455.1
AIX30627.1	000203	RpoSigma-min	158	Syn7803US37_150	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76186.1	000203	RpoSigma-min	164	PBI_BELLAMY_141	Synechococcus phage Bellamy	GCA_002627525.1
QCW22896.1	000203	RpoSigma-min	181	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50662.1	000203	RpoSigma-min	159	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59599.1	000203	RpoSigma-min	164	S330809_138	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59361.1	000203	RpoSigma-min	164	C440309_138	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59837.1	000203	RpoSigma-min	169	N231010_138	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70569.1	000203	RpoSigma-min	168	HOU04_gp170	Synechococcus phage S-T4	GCA_003443335.1
QJT70127.1	000203	RpoSigma-min	164	SynMITS9220M01_114	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BAV39297.1	000203	RpoSigma-min	119	BPT24_171	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64135.1	000203	RpoSigma-min	170	KVP40.0064	Vibrio phage KVP40	GCA_000843785.1
QIW90458.1	000203	RpoSigma-min	170	GCAPEGMB_00111	Vibrio phage V07	GCA_012361095.1
QIW90971.1	000203	RpoSigma-min	170	COHAPHLL_00108	Vibrio phage V09	GCA_012361135.1
QHJ74247.1	000203	RpoSigma-min	170	VH12019_00328	Vibrio phage VH1_2019	GCA_009931825.1
AGB07071.1	000203	RpoSigma-min	170	CF80_gp284	Vibrio phage VH7D	GCA_000914495.1
QBX06024.1	000203	RpoSigma-min	170	ValB1HC_070	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04570.1	000203	RpoSigma-min	286	ValB1MD_290	Vibrio phage ValB1MD	GCA_004138815.1
AJT61038.1	000203	RpoSigma-min	170	AVU32_gp197	Vibrio phage ValKK3	GCA_001501635.1
AGN30113.1	000203	RpoSigma-min	171	VPFG_00111	Vibrio phage nt-1	GCA_000910195.2
ALP47096.1	000203	RpoSigma-min	170	phiGrn1_0179	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47478.1	000203	RpoSigma-min	170	phiST2_0310	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54649.1	000203	RpoSigma-min	170	vBValMR10Z_108	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07123.1	000203	RpoSigma-min	194	VmeM32_00136	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37295.1	000203	RpoSigma-min	170	pp2_062	Vibriophage phi-pp2	GCA_002630725.1
BBA65451.1	000203	RpoSigma-min	197	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96466.1	000203	RpoSigma-min	195	Xoosp13_280	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59049.1	000203	RpoSigma-min	287	g241	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58514.1	000203	RpoSigma-min	287	g237	Yersinia phage fHe-Yen9-04	GCA_002990485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000626	000203	RpoSigma-min	58	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000445	000203	RpoSigma-min	129	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QGT54902.1	000204	RpoSigma-min+HINT	504	b23_0289	Synechococcus phage B23	GCA_009745195.1
QGT54537.1	000204	RpoSigma-min+HINT	504	b3_0296	Synechococcus phage B3	GCA_009745215.1
BBI90635.1	000205	RpoSigma-min	120	HYO65_gp243	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90942.1	000205	RpoSigma-min	85	-	Tenacibaculum phage PTm5	GCA_009730715.1
AFC21949.1	000206	SIGMA-HTH	331	GAP32_490	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14057.1	000206	SIGMA-HTH	321	PBI_121Q_167	Escherichia phage 121Q	GCA_000926855.1
AGC35036.1	000206	SIGMA-HTH	321	ACQ29_gp356	Escherichia phage PBECO4	GCA_001041035.1
BBM61740.1	000206	SIGMA-HTH	321	EO157G_1510	Escherichia phage SP27	GCA_008033345.1
AXC36614.1	000206	SIGMA-HTH	321	-	Escherichia phage UB	GCA_003341455.1
QBO61642.1	000206	SIGMA-HTH	321	G17_00146	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13696.1	000206	SIGMA-HTH	321	vBEcoMphAPEC6_gp066c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80052.1	000206	SIGMA-HTH	321	PSLUR01_00075	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44517.1	000206	SIGMA-HTH	298	RaK2_00244	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44076.1	000206	SIGMA-HTH	330	CBB_513	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18591.1	000206	SIGMA-HTH	322	7t3_070	Salmonella phage 7t3	GCA_006083215.1
AZU98419.1	000206	SIGMA-HTH	322	CPT_Munch_487	Salmonella phage Munch	GCA_004015485.1
QIG63094.1	000206	SIGMA-HTH	322	SEPL_481	Salmonella phage SE_PL	GCA_011067555.1
AQW89032.1	000206	SIGMA-HTH	330	BF_0507	Serratia phage BF	GCA_002619745.1
SOK59311.1	000206	SIGMA-HTH	330	g503	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58775.1	000206	SIGMA-HTH	330	g498	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFF28006.1	000207	SIGMA-HTH	362	PAU_1	Sphingomonas phage PAU	GCA_000902455.1
BBI90560.1	000207	SIGMA-HTH	280	HYO65_gp168	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90868.1	000207	SIGMA-HTH	280	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIX30670.1	000208	SIGMA-HTH	230	Syn7803US37_193	Synechococcus phage ACG-2014f	GCA_002594065.1
prevph1000000271	000208	SIGMA-HTH	330	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000216	000208	SIGMA-HTH	338	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASV44054.1	000000	SIGMA-HTH	282	PBI_SCTP2_39	Salicola phage SCTP-2	GCA_002625545.1
AEO93340.1	000000	SIGMA-HTH+SIGMA-HTH	206	G_69	Bacillus virus G	GCA_000917535.1
QIG63376.1	000209	SIGMA-HTH	176	DAC16_143	Bacteroides phage DAC16	GCA_013387695.1
QIG63641.1	000209	SIGMA-HTH	176	DAC19_150	Bacteroides phage DAC19	GCA_013387715.1
QIG63902.1	000209	SIGMA-HTH	176	DAC20_149	Bacteroides phage DAC20	GCA_013387725.1
QIG64165.1	000209	SIGMA-HTH	176	DAC22_151	Bacteroides phage DAC22	GCA_013387735.1
QIG64422.1	000209	SIGMA-HTH	176	DAC23_144	Bacteroides phage DAC23	GCA_013387745.1
prevph1000000516	000210	SIGMA-HTH	312	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000390	000210	SIGMA-HTH	312	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG58077.1	000211	SIGMA-HTH	201	SEA_PAULODIABOLI_396	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57776.1	000211	SIGMA-HTH	201	SEA_PAULODIABOLI_41	Microbacterium phage PauloDiaboli	GCA_011067425.1
QDB70476.1	000212	Rpogp68	532	CF8_0065	Aeromonas phage CF8	GCA_006384595.2
QDJ97216.1	000212	Rpogp68	533	D6_0056	Aeromonas phage D6	GCA_007051205.2
QDH47040.1	000212	Rpogp68	533	LAh10_222	Aeromonas phage LAh10	GCA_006863975.1
QDJ96824.1	000212	Rpogp68	533	PS1_0065	Aeromonas phage PS1	GCA_007051165.2
QFR59454.1	000212	Rpogp68	533	PS2_0063	Aeromonas phage PS2	GCA_009388305.2
AFO71251.1	000212	Rpogp68	546	CR5_031	Cronobacter phage CR5	GCA_000910235.1
QBZ70594.1	000212	Rpogp68	541	pETSU_013	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59681.1	000212	Rpogp68	544	SEGD1_032	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07458.1	000212	Rpogp68	546	DERBICUS_32	Erwinia phage Derbicus	GCA_004521655.1
AHI60394.1	000212	Rpogp68	514	Ea357_241	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49684.1	000212	Rpogp68	541	MACHINA_46	Erwinia phage Machina	GCA_002758035.1
AGX01736.1	000212	Rpogp68	517	CF95_gp014	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07350.1	000212	Rpogp68	514	REBECCA_245	Erwinia phage Rebecca	GCA_004521635.1
AXF51173.1	000212	Rpogp68	537	WELLINGTON_42	Erwinia phage Wellington	GCA_003344985.1
AFQ96757.1	000212	Rpogp68	548	G173_gp212	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48060.1	000212	Rpogp68	548	ASESINO_47	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86032.1	000212	Rpogp68	514	BOSOLAPHORUS_246	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48335.1	000212	Rpogp68	541	CAITLIN_40	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48608.1	000212	Rpogp68	541	CHRISDB_46	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52349.1	000212	Rpogp68	514	DM_249	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86351.1	000212	Rpogp68	514	DESERTFOX_244	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48882.1	000212	Rpogp68	546	EARLPHILLIPIV_32	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49129.1	000212	Rpogp68	541	HUXLEY_47	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03876.1	000212	Rpogp68	520	JOAD_39	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49394.1	000212	Rpogp68	537	KWAN_42	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86674.1	000212	Rpogp68	514	MADMEL_247	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86997.1	000212	Rpogp68	514	MORTIMER_249	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49957.1	000212	Rpogp68	541	PARSHIK_48	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50222.1	000212	Rpogp68	546	PHOBOS_32	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52023.1	000212	Rpogp68	514	RAY_243	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03631.1	000212	Rpogp68	520	RISINGSUN_39	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51707.1	000212	Rpogp68	514	SIMMY50_248	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65058.1	000212	Rpogp68	514	SPECIALG_247	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50470.1	000212	Rpogp68	548	STRATTON_45	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85871.1	000212	Rpogp68	544	ACEC001_0330	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63968.1	000212	Rpogp68	528	Goslar_00175	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71910.1	000212	Rpogp68	546	N1M2_47	Klebsiella phage N1M2	GCA_010092605.1
QGZ14378.1	000212	Rpogp68	524	HWC77_gp015	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24161.1	000212	Rpogp68	510	-	Proteus phage 10	GCA_014071245.1
ABY62956.1	000212	Rpogp68	527	201phi2-1p124	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27127.1	000212	Rpogp68	517	PPEV_gp033	Pseudomonas phage EL	GCA_000866825.1
ANM44848.1	000212	Rpogp68	521	KTN4_090	Pseudomonas phage KTN4	GCA_002607225.1
ARV77232.1	000212	Rpogp68	519	NOXIFER_61	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89506.1	000212	Rpogp68	543	OBP_069	Pseudomonas phage OBP	GCA_000896635.1
QBX32216.1	000212	Rpogp68	525	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76735.1	000212	Rpogp68	525	PHABIO_104	Pseudomonas phage Phabio	GCA_002624965.1
AEH03489.1	000212	Rpogp68	525	062	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02600.1	000212	Rpogp68	524	PSA21_71	Pseudomonas phage Psa21	GCA_004340405.1
ATN94865.1	000212	Rpogp68	521	SL2_288	Pseudomonas phage SL2	GCA_002956015.1
QJB22726.1	000212	Rpogp68	521	fnug_83	Pseudomonas phage fnug	GCA_012837215.1
QEM41794.1	000212	Rpogp68	525	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82969.1	000212	Rpogp68	521	PHIKZ068	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19253.1	000212	Rpogp68	573	FDH28_gp142	Ralstonia phage RP12	GCA_002617345.1
BAW19539.1	000212	Rpogp68	573	-	Ralstonia phage RP31	GCA_002617365.1
BAS05011.2	000212	Rpogp68	523	AVU11_gp219	Ralstonia phage RSF1	GCA_001500875.1
BAQ02741.2	000212	Rpogp68	523	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20746.1	000212	Rpogp68	544	-	Salmonella phage JN03	GCA_014319805.1
AWN09065.1	000212	Rpogp68	544	MLDJOKPK_00135	Salmonella phage SPAsTU	GCA_003183805.1
AEP83863.1	000212	Rpogp68	535	SPN3US_0030	Salmonella phage SPN3US	GCA_001042275.1
QKE54569.1	000212	Rpogp68	512	ACSA002_2530	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65657.1	000212	Rpogp68	505	2050HW_00322	Serratia phage 2050HW	GCA_002628125.1
QDB71081.1	000212	Rpogp68	505	CPT_Moabite_049	Serratia phage Moabite	GCA_006384735.1
QFP93069.1	000212	Rpogp68	517	-	Serratia phage PCH45	GCA_009187865.1
QAU04358.1	000212	Rpogp68	524	HWC03_gp203	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23218.1	000212	Rpogp68	524	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80940.1	000212	Rpogp68	524	Aphrodite1_0127	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47510.1	000212	Rpogp68	524	HWC35_gp116	Vibrio phage USC-1	GCA_006864065.1
BAW98329.1	000212	Rpogp68	524	FDH33_gp120	Vibrio phage pTD1	GCA_002618825.1
AXH70820.1	000213	Rpogp68	516	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96677.1	000213	Rpogp68	488	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96995.1	000213	Rpogp68	488	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96041.1	000213	Rpogp68	488	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96359.1	000213	Rpogp68	488	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21065.1	000213	Rpogp68	487	-	Vibrio phage vB_pir03	GCA_014319855.1
AQT28157.1	000000	Rpogp68	516	pVa21_216	Vibrio phage pVa-21	GCA_002619305.1
CCE26268.1	000214	Rpogp68	500	g245	Yersinia phage phiR1-37	GCA_000895615.1
AMS01310.1	000214	Rpogp68	464	AR9_g226	Bacillus phage AR9	GCA_001743835.1
ALN97960.1	000214	Rpogp68	464	Bp8pS_281	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99939.1	000214	Rpogp68	464	PBI_PBS1_117	Bacillus virus PBS1	GCA_002601325.1
APU01454.1	000215	UvsW-A18	501	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29070.1	000215	UvsW-A18	501	AP1_0363	Aeromonas phage AP1	GCA_014183365.1
ATI17443.1	000215	UvsW-A18	501	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00152.1	000215	UvsW-A18	501	HWB28_gp400	Aeromonas phage AS-zj	GCA_002627665.1
AUE22777.1	000215	UvsW-A18	503	Ah1_00259	Aeromonas phage Ah1	GCA_002957415.1
QAX98492.1	000215	UvsW-A18	501	ASfcp2_155	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97883.1	000215	UvsW-A18	501	ASswx1_240	Aeromonas phage Asswx_1	GCA_004146865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY01265.1	000215	UvsW-A18	501	ASwh1_202	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39534.1	000215	UvsW-A18	501	CC2_294	Aeromonas phage CC2	GCA_000903495.1
ADQ52955.1	000215	UvsW-A18	503	PX29p236	Aeromonas phage PX29	GCA_000920195.1
ADM79880.1	000215	UvsW-A18	503	phiAS5_ORF0037	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53074.1	000215	UvsW-A18	501	65p064	Aeromonas virus 65	GCA_000893255.1
AAQ17902.1	000215	UvsW-A18	503	uvsW	Aeromonas virus Aeh1	GCA_000843245.1
ASV44698.2	000215	UvsW-A18	460	FDI40_gp080	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93480.1	000215	UvsW-A18	323	G_221	Bacillus virus G	GCA_000917535.1
AEO93482.1	000215	UvsW-A18	422	G_223	Bacillus virus G	GCA_000917535.1
AEO93659.1	000215	UvsW-A18	456	G_400	Bacillus virus G	GCA_000917535.1
CCH63663.1	000215	UvsW-A18	472	CP21_201	Campylobacter virus CP21	GCA_000902535.1
ANS05946.1	000215	UvsW-A18	499	ABCD_0221	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64858.1	000215	UvsW-A18	500	S13_059	Cronobacter phage S13	GCA_001503575.1
AFC21726.1	000215	UvsW-A18	494	GAP32_276	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97238.1	000215	UvsW-A18	499	E_230	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56887.1	000215	UvsW-A18	486	CPXG_00084	Cyanophage P-RSM6	GCA_000906155.1
AJK27570.1	000215	UvsW-A18	494	PTIM40_143	Cyanophage P-TIM40	GCA_001470935.1
AOO14318.1	000215	UvsW-A18	487	Sn110110_124	Cyanophage S-RIM14	GCA_002599065.1
AOO14967.1	000215	UvsW-A18	487	W1230910_121	Cyanophage S-RIM14	GCA_002599125.1
AMO43148.1	000215	UvsW-A18	490	R1080702_139	Cyanophage S-RIM32	GCA_001754165.1
AMO43372.1	000215	UvsW-A18	490	W270710_128	Cyanophage S-RIM44	GCA_002599145.1
AOO11616.1	000215	UvsW-A18	490	ES420910_135	Cyanophage S-RIM44	GCA_002599165.1
AOO11844.1	000215	UvsW-A18	490	Np050604_128	Cyanophage S-RIM44	GCA_002599185.1
AOO12081.1	000215	UvsW-A18	490	Np200711_135	Cyanophage S-RIM44	GCA_002599205.1
AOO12317.1	000215	UvsW-A18	490	Np420711_135	Cyanophage S-RIM44	GCA_002599225.1
AOO12545.1	000215	UvsW-A18	490	Sn080709_128	Cyanophage S-RIM44	GCA_002599245.1
AOO12782.1	000215	UvsW-A18	490	Sn130910_135	Cyanophage S-RIM44	GCA_002599265.1
AOO13011.1	000215	UvsW-A18	490	W2100709_129	Cyanophage S-RIM44	GCA_002599285.1
AGH07465.1	000215	UvsW-A18	484	CYVG_00021	Cyanophage S-SSM6a	GCA_002710385.1
AGG54485.1	000215	UvsW-A18	486	CYWG_00201	Cyanophage S-SSM6b	GCA_002710425.1
AIT13907.1	000215	UvsW-A18	494	PBI_121Q_10	Escherichia phage 121Q	GCA_000926855.1
QAY00430.1	000215	UvsW-A18	494	Ecwhy1_150	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35174.1	000215	UvsW-A18	468	ACQ29_gp494	Escherichia phage PBECO4	GCA_001041035.1
BBM61599.1	000215	UvsW-A18	494	EO157G_0100	Escherichia phage SP27	GCA_008033345.1
AXC36746.1	000215	UvsW-A18	468	-	Escherichia phage UB	GCA_003341455.1
ARM70742.1	000215	UvsW-A18	504	phiC120_c35	Escherichia phage phiC120	GCA_002621185.1
QBO61785.1	000215	UvsW-A18	494	G17_00296	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13829.1	000215	UvsW-A18	494	vBEcoMphAPEC6_gp200c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80502.1	000215	UvsW-A18	494	PSLUR01_00525	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78755.1	000215	UvsW-A18	499	RB43ORF233c	Escherichia virus RB43	GCA_000863505.1
AFA44391.1	000215	UvsW-A18	511	RaK2_00118	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72832.1	000215	UvsW-A18	540	-	Myoviridae sp.	GCA_003657725.1
QHJ79080.1	000215	UvsW-A18	498	-	Myoviridae sp.	GCA_012593985.1
QIG65687.1	000215	UvsW-A18	503	phiOC_p021	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43845.1	000215	UvsW-A18	494	CBB_281	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26313.1	000215	UvsW-A18	492	CPMG_00214	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44520.1	000215	UvsW-A18	487	PSSM2_142	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12447.1	000215	UvsW-A18	487	PRTG_00299	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93452.1	000215	UvsW-A18	490	AVU42_gp114	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99230.1	000215	UvsW-A18	483	Syn1_129	Prochlorococcus phage Syn1	GCA_000892495.1
QHJ86005.1	000215	UvsW-A18	491	KKIINIFJ_00093	Pseudomonas phage PN05	GCA_009931935.1
QCG76096.1	000215	UvsW-A18	483	EST35_0215	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44158.1	000215	UvsW-A18	494	PBI_SCTP2_143	Salicola phage SCTP-2	GCA_002625545.1
QCW19004.1	000215	UvsW-A18	494	7t3_0484	Salmonella phage 7t3	GCA_006083215.1
AZU98251.1	000215	UvsW-A18	494	CPT_Munch_307	Salmonella phage Munch	GCA_004015485.1
QIG62733.1	000215	UvsW-A18	494	SEPL_120	Salmonella phage SE_PL	GCA_011067555.1
AQW88804.1	000215	UvsW-A18	494	BF_0279	Serratia phage BF	GCA_002619745.1
AGR47684.1	000215	UvsW-A18	489	SmphiM12_052	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12946.1	000215	UvsW-A18	489	PHIM19_39	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12586.1	000215	UvsW-A18	489	PHIM7_38	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13319.1	000215	UvsW-A18	489	PHIN3_54	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28172.1	000215	UvsW-A18	499	PAU_174	Sphingomonas phage PAU	GCA_000902455.1
AIX30625.1	000215	UvsW-A18	487	Syn7803US37_148	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54897.1	000215	UvsW-A18	488	b23_0284	Synechococcus phage B23	GCA_009745195.1
QGT54532.1	000215	UvsW-A18	488	b3_0291	Synechococcus phage B3	GCA_009745215.1
ASR76184.1	000215	UvsW-A18	491	PBI_BELLAMY_139	Synechococcus phage Bellamy	GCA_002627525.1
QCW22894.1	000215	UvsW-A18	488	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50660.1	000215	UvsW-A18	488	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59597.1	000215	UvsW-A18	489	S330809_136	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59359.1	000215	UvsW-A18	489	C440309_136	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59835.1	000215	UvsW-A18	490	N231010_136	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70571.1	000215	UvsW-A18	487	HOU04_gp172	Synechococcus phage S-T4	GCA_003443335.1
QJT70125.1	000215	UvsW-A18	494	SynMITS9220M01_112	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90432.1	000215	UvsW-A18	498	HYO65_gp040	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90739.1	000215	UvsW-A18	498	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39234.1	000215	UvsW-A18	531	BPT24_109	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64446.1	000215	UvsW-A18	507	KVP40.0378	Vibrio phage KVP40	GCA_000843785.1
QIW90782.1	000215	UvsW-A18	570	GCAPEGMB_00464	Vibrio phage V07	GCA_012361095.1
QIW90391.1	000215	UvsW-A18	507	GCAPEGMB_00044	Vibrio phage V07	GCA_012361095.1
QIW91038.1	000215	UvsW-A18	507	COHAPHLL_00175	Vibrio phage V09	GCA_012361135.1
QHJ74558.1	000215	UvsW-A18	507	VH12019_00258	Vibrio phage VH1_2019	GCA_009931825.1
AGB07007.1	000215	UvsW-A18	510	CF80_gp220	Vibrio phage VH7D	GCA_000914495.1
QBX06096.1	000215	UvsW-A18	510	ValB1HC_142	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04530.1	000215	UvsW-A18	512	ValB1MD_226	Vibrio phage ValB1MD	GCA_004138815.1
AJT61110.1	000215	UvsW-A18	510	AVU32_gp269	Vibrio phage ValKK3	GCA_001501635.1
AGN30046.1	000215	UvsW-A18	507	VPFG_00041	Vibrio phage nt-1	GCA_000910195.2
ALP46979.1	000215	UvsW-A18	510	phiGrn1_0110	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47362.1	000215	UvsW-A18	509	phiST2_0241	Vibrio phage phi-ST2	GCA_002757135.1
ALY07010.1	000215	UvsW-A18	503	VmeM32_00016	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37609.1	000215	UvsW-A18	507	pp2_377	Vibriophage phi-pp2	GCA_002630725.1
BBA65396.1	000215	UvsW-A18	513	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96422.1	000215	UvsW-A18	513	Xoosp13_236	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59087.1	000215	UvsW-A18	494	g279	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58551.1	000215	UvsW-A18	494	g274	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000594	000215	UvsW-A18	191	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000596	000215	UvsW-A18	253	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000419	000215	UvsW-A18	342	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000421	000215	UvsW-A18	326	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QHJ86110.1	000216	UvsW-A18	707	KKIINIFJ_00199	Pseudomonas phage PN05	GCA_009931935.1
AEO93344.1	000217	SFII-RAD3	542	G_73	Bacillus virus G	GCA_000917535.1
QHJ86046.1	000217	SFII-RAD3	556	KKIINIFJ_00134	Pseudomonas phage PN05	GCA_009931935.1
AFF28237.1	000217	SFII-RAD3	642	PAU_239	Sphingomonas phage PAU	GCA_000902455.1
BBI90513.1	000217	SFII-RAD3	667	HYO65_gp121	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90821.1	000217	SFII-RAD3	667	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39279.1	000217	SFII-RAD3	736	BPT24_153	Tenacibaculum phage pT24	GCA_002611925.1
BBA65460.1	000217	SFII-RAD3	559	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96470.1	000217	SFII-RAD3	557	Xoosp13_284	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000349	000217	SFII-RAD3	610	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000275	000217	SFII-RAD3	640	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGH56973.1	000218	UvsW-A18	427	CPXG_00170	Cyanophage P-RSM6	GCA_000906155.1
AJK27484.1	000218	UvsW-A18	430	PTIM40_57	Cyanophage P-TIM40	GCA_001470935.1
AOO14249.1	000218	UvsW-A18	413	Sn110110_055	Cyanophage S-RIM14	GCA_002599065.1
AOO14901.1	000218	UvsW-A18	413	W1230910_055	Cyanophage S-RIM14	GCA_002599125.1
AMO43053.1	000218	UvsW-A18	402	R1080702_044	Cyanophage S-RIM32	GCA_001754165.1
AMO43292.1	000218	UvsW-A18	413	W270710_048	Cyanophage S-RIM44	GCA_002599145.1
AOO11526.1	000218	UvsW-A18	413	ES420910_045	Cyanophage S-RIM44	GCA_002599165.1
AOO11764.1	000218	UvsW-A18	413	Np050604_048	Cyanophage S-RIM44	GCA_002599185.1
AOO11991.1	000218	UvsW-A18	413	Np200711_045	Cyanophage S-RIM44	GCA_002599205.1
AOO12227.1	000218	UvsW-A18	413	Np420711_045	Cyanophage S-RIM44	GCA_002599225.1
AOO12465.1	000218	UvsW-A18	413	Sn080709_048	Cyanophage S-RIM44	GCA_002599245.1
AOO12692.1	000218	UvsW-A18	413	Sn130910_045	Cyanophage S-RIM44	GCA_002599265.1
AOO12930.1	000218	UvsW-A18	413	W2100709_048	Cyanophage S-RIM44	GCA_002599285.1
AGH07669.1	000218	UvsW-A18	405	CYVG_00226	Cyanophage S-SSM6a	GCA_002710385.1
AGG54336.1	000218	UvsW-A18	416	CYWG_00052	Cyanophage S-SSM6b	GCA_002710425.1
AAX44417.1	000218	UvsW-A18	396	PSSM2_039	Prochlorococcus phage P-SSM2	GCA_000859585.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN12234.1	000218	UvsW-A18	396	PRTG_00076	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93423.1	000218	UvsW-A18	390	AVU42_gp053	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99146.1	000218	UvsW-A18	413	Syn1_045	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30578.1	000218	UvsW-A18	417	Syn7803US37_101	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30531.1	000218	UvsW-A18	483	Syn7803US37_54	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54651.1	000218	UvsW-A18	410	b23_0023	Synechococcus phage B23	GCA_009745195.1
QGT54281.1	000218	UvsW-A18	410	b3_0023	Synechococcus phage B3	GCA_009745215.1
ASR76128.1	000218	UvsW-A18	407	PBI_BELLAMY_83	Synechococcus phage Bellamy	GCA_002627525.1
ASR76130.1	000218	UvsW-A18	465	PBI_BELLAMY_85	Synechococcus phage Bellamy	GCA_002627525.1
QCW23012.1	000218	UvsW-A18	392	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50721.1	000218	UvsW-A18	392	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70427.1	000218	UvsW-A18	391	HOU04_gp028	Synechococcus phage S-T4	GCA_003443335.1
QJT70068.1	000218	UvsW-A18	383	SynMITS9220M01_055	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXH72839.1	000000	REase+UvsW-A18	762	-	Myoviridae sp.	GCA_003657725.1
QDH83416.1	000219	A18	524	H1O15_gp007	Achromobacter phage Motura	GCA_006964305.1
QBX06721.1	000219	A18	490	BcepSaruman_308	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74689.1	000219	A18	513	BcepSauron_309	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67211.1	000219	A18	533	AD1_167	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79960.1	000219	A18	297	JA11_155	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79961.1	000219	A18	378	JA11_156	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66559.1	000219	A18	536	JA13_156	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66884.1	000219	A18	536	JA29_158	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67529.1	000219	A18	297	JA33_155	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67530.1	000219	A18	378	JA33_156	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08442.1	000219	A18	533	Alexandra_172	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58808.1	000219	A18	532	Y3_168	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28643.1	000219	A18	534	YOLOSWAG_163	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38467.1	000219	A18	555	BN7874_262	Phage NCTB	GCA_900092385.1
AFH14620.1	000219	A18	558	Lu11_0088	Pseudomonas phage Lu11	GCA_000897175.1
AGS82085.1	000219	A18	531	PaBG_00210	Pseudomonas phage PaBG	GCA_000912555.1
BAG41599.1	000219	A18	509	RSL1_ORF153	Ralstonia phage phiRSL1	GCA_000879455.1
ARB13658.1	000220	SNF	648	Ccr10_gp129c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14003.1	000220	SNF	648	Ccr2_gp128c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14691.1	000220	SNF	648	Ccr29_gp135	Caulobacter phage Ccr29	GCA_002619485.1
ARB15045.1	000220	SNF	648	Ccr32_gp127	Caulobacter phage Ccr32	GCA_002619505.1
ARB15378.1	000220	SNF	648	Ccr34_gp136	Caulobacter phage Ccr34	GCA_002619525.1
ARB14346.1	000220	SNF	648	Ccr5_gp127c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68326.1	000220	SNF	648	CcrBL10_gp122c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69239.1	000220	SNF	626	CcrBL9_gp215c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88035.1	000220	SNF	645	CcrColossus_gp165	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68712.1	000220	SNF	645	CcrPW_gp173c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69793.1	000220	SNF	626	CcrSC_gp211c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87650.1	000220	SNF	648	CcrKarma_gp133	Caulobacter virus Karma	GCA_000901575.1
AFU87299.1	000220	SNF	648	CcrMagneto_gp129	Caulobacter virus Magneto	GCA_000903095.1
AFU86611.1	000220	SNF	648	CcrRogue_gp129	Caulobacter virus Rogue	GCA_000900555.1
AFU88446.1	000220	SNF	648	CcrSwift_gp128	Caulobacter virus Swift	GCA_000899655.1
AFU86963.1	000220	SNF	648	CbK_gp131	Caulobacter virus phiCbK	GCA_000900535.1
QMV29148.1	000000	SNF	101	AP1_0447	Aeromonas phage AP1	GCA_014183365.1
QIG57848.1	000000	SNF	616	SEA_PAULODIABOLI_114	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXG67219.1	000221	SNF+MIP-T3	1948	AD1_175	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79969.1	000221	SNF+MIP-T3	1944	JA11_164	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66567.1	000221	SNF+MIP-T3	1944	JA13_164	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66892.1	000221	SNF+MIP-T3	1944	JA29_166	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67538.1	000221	SNF+MIP-T3	1944	JA33_164	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08449.1	000221	SNF+MIP-T3	1948	Alexandra_180	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58816.1	000221	SNF+MIP-T3	1951	Y3_176	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28650.1	000221	SNF+MIP-T3	1951	YOLOSWAG_171	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38484.1	000221	SNF+MIP-T3	1942	BN7874_272	Phage NCTB	GCA_900092385.1
AFH14631.1	000221	SNF+MIP-T3	2020	Lu11_0099	Pseudomonas phage Lu11	GCA_000897175.1
AGS82077.1	000221	SNF+MIP-T3	1969	PaBG_00202	Pseudomonas phage PaBG	GCA_000912555.1
ABS83630.1	000222	SNF	624	0305phi8-36p070	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93839.1	000222	SNF	498	G_594	Bacillus virus G	GCA_000917535.1
AYD81291.1	000222	SNF	548	SEA_JUSTBECAUSE_122	Streptomyces phage JustBecause	GCA_003613775.1
QJD53694.1	000222	SNF	548	SEA_KELA_123	Streptomyces phage Kela	GCA_012934305.1
QBZ72022.1	000222	SNF	547	SEA_KRADAL_124	Streptomyces phage Kradal	GCA_004799925.1
AXH66285.1	000222	SNF	547	SEA_SATIS_124	Streptomyces phage Satis	GCA_003366315.1
QDH83606.1	000223	SNF	1528	H1O15_gp182	Achromobacter phage Motura	GCA_006964305.1
QBX06501.1	000223	SNF	1534	BcepSaruman_088	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74468.1	000223	SNF	1534	BcepSauron_088	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41574.1	000223	SNF	1555	RSL1_ORF129	Ralstonia phage phiRSL1	GCA_000879455.1
AFF28066.1	000224	A18	1304	PAU_68	Sphingomonas phage PAU	GCA_000902455.1
BBI90509.1	000224	A18	1336	HYO65_gp117	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90817.1	000224	A18	1336	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39135.1	000224	A18	1479	BPT24_013	Tenacibaculum phage pT24	GCA_002611925.1
AXH72820.1	000225	SbcC	589	-	Myoviridae sp.	GCA_003657725.1
QMV28811.1	000225	SbcC	265	AP1_0104	Aeromonas phage AP1	GCA_014183365.1
QMV28753.1	000225	SbcC	277	AP1_0035	Aeromonas phage AP1	GCA_014183365.1
ARM70878.1	000225	SbcC	562	phiC120_c173	Escherichia phage phiC120	GCA_002621185.1
AZU98216.1	000225	SbcC	718	CPT_Munch_272	Salmonella phage Munch	GCA_004015485.1
AUE22567.1	000225	SbcC	772	Ah1_00026	Aeromonas phage Ah1	GCA_002957415.1
AKF12938.1	000225	SbcC	570	PHIM19_31	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13311.1	000225	SbcC	570	PHIN3_46	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54541.1	000225	SbcC	571	b3_0300	Synechococcus phage B3	GCA_009745215.1
QGT54906.1	000225	SbcC	571	b23_0293	Synechococcus phage B23	GCA_009745195.1
AKF12578.1	000225	SbcC	570	PHIM7_30	Sinorhizobium phage phiM7	GCA_002622405.1
ASV44554.1	000225	SbcC	921	PBI_SCTP2_539	Salicola phage SCTP-2	GCA_002625545.1
AGR47675.1	000225	SbcC	570	SmphiM12_043	Sinorhizobium phage phiM12	GCA_001023565.1
SOK58516.1	000225	SbcC	713	g239	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK59051.1	000225	SbcC	713	g243	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AQW88770.1	000225	SbcC	713	BF_0245	Serratia phage BF	GCA_002619745.1
prev15ph1000000095	000225	SbcC	559	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AOO14323.1	000225	SbcC	573	Sn110110_129	Cyanophage S-RIM14	GCA_002599065.1
AOO14972.1	000225	SbcC	573	W1230910_126	Cyanophage S-RIM14	GCA_002599125.1
AGH56881.1	000225	SbcC	572	CPXG_00078	Cyanophage P-RSM6	GCA_000906155.1
QHJ78891.1	000225	SbcC	566	-	Myoviridae sp.	GCA_012593985.1
AGH26307.1	000225	SbcC	573	CPMG_00208	Prochlorococcus phage MED4-213	GCA_000904535.1
AGB07081.1	000225	SbcC	745	CF80_gp294	Vibrio phage VH7D	GCA_000914495.1
QBX06014.1	000225	SbcC	745	ValB1HC_060	Vibrio phage ValB1 HC	GCA_004771355.1
AOO11850.1	000225	SbcC	576	Np050604_134	Cyanophage S-RIM44	GCA_002599185.1
AOO11622.1	000225	SbcC	576	ES420910_141	Cyanophage S-RIM44	GCA_002599165.1
QDF13864.1	000225	SbcC	715	vBEcoMphAPEC6_gp235c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ADQ52742.1	000225	SbcC	772	PX29p023	Aeromonas phage PX29	GCA_000920195.1
AMO43154.1	000225	SbcC	564	R1080702_145	Cyanophage S-RIM32	GCA_001754165.1
SCA80467.1	000225	SbcC	715	PSLUR01_00490	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44357.1	000225	SbcC	714	RaK2_00084	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AGC35208.1	000225	SbcC	715	ACQ29_gp528	Escherichia phage PBECO4	GCA_001041035.1
AMM43811.1	000225	SbcC	713	CBB_246	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AOO13017.1	000225	SbcC	576	W2100709_135	Cyanophage S-RIM44	GCA_002599285.1
ALP47344.1	000225	SbcC	745	phiST2_0320	Vibrio phage phi-ST2	GCA_002757135.1
AOO12323.1	000225	SbcC	576	Np420711_141	Cyanophage S-RIM44	GCA_002599225.1
AIR93457.1	000225	SbcC	575	AVU42_gp119	Prochlorococcus phage P-TIM68	GCA_001503075.1
AOO12551.1	000225	SbcC	576	Sn080709_134	Cyanophage S-RIM44	GCA_002599245.1
AOO12788.1	000225	SbcC	576	Sn130910_141	Cyanophage S-RIM44	GCA_002599265.1
ASR76189.1	000225	SbcC	570	PBI_BELLAMY_144	Synechococcus phage Bellamy	GCA_002627525.1
BBM62155.1	000225	SbcC	715	EO157G_5660	Escherichia phage SP27	GCA_008033345.1
ADO99236.1	000225	SbcC	576	Syn1_135	Prochlorococcus phage Syn1	GCA_000892495.1
ALP46964.1	000225	SbcC	745	phiGrn1_0189	Vibrio phage phi-Grn1	GCA_002757115.1
AOV59364.1	000225	SbcC	576	C440309_141	Synechococcus phage S-CAM4	GCA_002922145.1
AJT61027.1	000225	SbcC	745	AVU32_gp186	Vibrio phage ValKK3	GCA_001501635.1
AGG54480.1	000225	SbcC	572	CYWG_00196	Cyanophage S-SSM6b	GCA_002710425.1
QCG76021.1	000225	SbcC	584	EST35_0139	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QIW90468.1	000225	SbcC	745	GCAPEGMB_00121	Vibrio phage V07	GCA_012361095.1
AOO12087.1	000225	SbcC	576	Np200711_141	Cyanophage S-RIM44	GCA_002599205.1
ANS05940.1	000225	SbcC	567	ABCD_0055	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97066.1	000225	SbcC	563	E_057	Cronobacter phage vB_CsaM_leE	GCA_002611805.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59602.1	000225	SbcC	576	S330809_141	Synechococcus phage S-CAM4	GCA_002366065.1
AAX44525.1	000225	SbcC	570	PSSM2_147	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAQ17679.1	000225	SbcC	772	46	Aeromonas virus Aeh1	GCA_000843245.1
QIG65682.1	000225	SbcC	573	phiOC_p016	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QAX98605.1	000225	SbcC	772	ASfcp2_272	Aeromonas phage AsFcp_2	GCA_004146885.1
AXQ70565.1	000225	SbcC	569	HOU04_gp166	Synechococcus phage S-T4	GCA_003443335.1
AXC36780.1	000225	SbcC	715	-	Escherichia phage UB	GCA_003341455.1
AOV59840.1	000225	SbcC	576	N231010_141	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70132.1	000225	SbcC	569	SynMITS9220M01_119	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH07473.1	000225	SbcC	574	CYVG_00029	Cyanophage S-SSM6a	GCA_002710385.1
QIW90961.1	000225	SbcC	745	COHAPHLL_00098	Vibrio phage V09	GCA_012361135.1
AAQ64145.1	000225	SbcC	745	KVP40.0074	Vibrio phage KVP40	GCA_000843785.1
AAX78577.1	000225	SbcC	567	RB43ORF055w	Escherichia virus RB43	GCA_000863505.1
ASV44761.1	000225	SbcC	591	FDI40_gp691	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFN37305.1	000225	SbcC	745	pp2_072	Vibriophage phi-pp2	GCA_002630725.1
AGN30123.1	000225	SbcC	745	VPFG_00121	Vibrio phage nt-1	GCA_000910195.2
QHJ74257.1	000225	SbcC	745	VH12019_00338	Vibrio phage VH1_2019	GCA_009931825.1
QBO61820.1	000225	SbcC	715	G17_00331	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AIT14483.1	000225	SbcC	715	PBI_121Q_593	Escherichia phage 121Q	GCA_000926855.1
QNJ54639.1	000225	SbcC	745	vBValMR10Z_98	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AJK27575.1	000225	SbcC	572	PTIM40_148	Cyanophage P-TIM40	GCA_001470935.1
AFC21690.1	000225	SbcC	713	GAP32_240	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QCW18963.1	000225	SbcC	718	7t3_0442	Salmonella phage 7t3	GCA_006083215.1
QIG62768.1	000225	SbcC	718	SEPL_155	Salmonella phage SE_PL	GCA_011067555.1
AAR90909.1	000225	SbcC	775	65p029	Aeromonas virus 65	GCA_000893255.1
APU01420.1	000225	SbcC	776	-	Aeromonas phage 65.2	GCA_002618145.1
QAX97918.1	000225	SbcC	776	ASswx1_275	Aeromonas phage Asswx_1	GCA_004146865.1
ATI17478.1	000225	SbcC	776	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00519.1	000225	SbcC	776	HWB28_gp033	Aeromonas phage AS-zj	GCA_002627665.1
AMO43378.1	000225	SbcC	576	W270710_134	Cyanophage S-RIM44	GCA_002599145.1
AIX30631.1	000225	SbcC	575	Syn7803US37_154	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW22900.1	000225	SbcC	569	-	Synechococcus phage S-B05	GCA_006083695.1
AFN39519.1	000225	SbcC	776	CC2_257	Aeromonas phage CC2	GCA_000903495.1
ALY07126.1	000225	SbcC	794	VmeM32_00139	Vibrio phage vB_VmeM-32	GCA_002608825.1
AIA65041.1	000225	SbcC	567	S13_244	Cronobacter phage S13	GCA_001503575.1
QAY01232.1	000225	SbcC	780	ASwh1_167	Aeromonas phage Aswh_1	GCA_004146945.1
ADM79994.1	000225	SbcC	769	phiAS5_ORF0151	Aeromonas phage phiAS5	GCA_000887715.1
QDB70304.1	000226	SbcC	826	CF8_0136	Aeromonas phage CF8	GCA_006384595.2
QDJ97281.1	000226	SbcC	826	D6_0121	Aeromonas phage D6	GCA_007051205.2
QDH47021.1	000226	SbcC	826	LAh10_53	Aeromonas phage LAh10	GCA_006863975.1
QDJ96898.1	000226	SbcC	827	PS1_0139	Aeromonas phage PS1	GCA_007051165.2
QFR59528.1	000226	SbcC	827	PS2_0137	Aeromonas phage PS2	GCA_009388305.2
AFO71390.1	000226	SbcC	836	CR5_170	Cronobacter phage CR5	GCA_000910235.1
QBZ70667.1	000226	SbcC	825	pETSU_086	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59837.1	000226	SbcC	822	SEGD1_190	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07601.1	000226	SbcC	836	DERBICUS_175	Erwinia phage Derbicus	GCA_004521655.1
AHI60173.1	000226	SbcC	830	Ea357_023	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49835.1	000226	SbcC	837	MACHINA_197	Erwinia phage Machina	GCA_002758035.1
AGX01909.1	000226	SbcC	825	sbcC	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07131.1	000226	SbcC	830	REBECCA_23	Erwinia phage Rebecca	GCA_004521635.1
AXF51334.1	000226	SbcC	837	WELLINGTON_206	Erwinia phage Wellington	GCA_003344985.1
AFQ96655.1	000226	SbcC	822	G173_gp110	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48220.1	000226	SbcC	836	ASESINO_207	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85811.1	000226	SbcC	830	BOSOLAPHORUS_23	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48491.1	000226	SbcC	836	CAITLIN_196	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48770.1	000226	SbcC	836	CHRISDB_208	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52121.1	000226	SbcC	830	DM_23	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86131.1	000226	SbcC	830	DESERTFOX_23	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49024.1	000226	SbcC	836	EARLPHILLIPIV_175	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49279.1	000226	SbcC	837	HUXLEY_197	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03812.1	000226	SbcC	819	JOAD_103	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49559.1	000226	SbcC	837	KWAN_207	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86451.1	000226	SbcC	830	MADMEL_23	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86772.1	000226	SbcC	830	MORTIMER_23	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50107.1	000226	SbcC	837	PARSHIK_198	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50371.1	000226	SbcC	837	PHOBOS_181	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51804.1	000226	SbcC	830	RAY_23	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03567.1	000226	SbcC	819	RISINGSUN_103	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51486.1	000226	SbcC	830	SIMMY50_24	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64833.1	000226	SbcC	830	SPECIALG_23	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50632.1	000226	SbcC	836	STRATTON_207	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86027.1	000226	SbcC	836	ACEC001_1860	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63805.1	000226	SbcC	818	Goslar_00012	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71983.1	000226	SbcC	826	N1M2_120	Klebsiella phage N1M2	GCA_010092605.1
QGZ14455.1	000226	SbcC	825	HWC77_gp092	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24015.1	000226	SbcC	830	-	Proteus phage 10	GCA_014071245.1
ABY63078.1	000226	SbcC	829	201phi2-1p250	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27212.1	000226	SbcC	822	PPEV_gp118	Pseudomonas phage EL	GCA_000866825.1
ANM44961.1	000226	SbcC	830	KTN4_203	Pseudomonas phage KTN4	GCA_002607225.1
ARV77334.1	000226	SbcC	834	NOXIFER_165	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89584.1	000226	SbcC	825	OBP_147	Pseudomonas phage OBP	GCA_000896635.1
QBX32348.1	000226	SbcC	830	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76869.1	000226	SbcC	831	PHABIO_238	Pseudomonas phage Phabio	GCA_002624965.1
AEH03613.1	000226	SbcC	798	190	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02750.1	000226	SbcC	832	PSA21_224	Pseudomonas phage Psa21	GCA_004340405.1
ATN94753.1	000226	SbcC	830	SL2_176	Pseudomonas phage SL2	GCA_002956015.1
QJB22839.1	000226	SbcC	830	fnug_196	Pseudomonas phage fnug	GCA_012837215.1
QEM41922.1	000226	SbcC	830	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83066.1	000226	SbcC	830	PHIKZ165	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19043.1	000226	SbcC	830	FDH28_gp069	Ralstonia phage RP12	GCA_002617345.1
BAW19328.1	000226	SbcC	830	-	Ralstonia phage RP31	GCA_002617365.1
BAS04855.1	000226	SbcC	836	AVU11_gp063	Ralstonia phage RSF1	GCA_001500875.1
BAQ02589.2	000226	SbcC	812	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20882.1	000226	SbcC	836	-	Salmonella phage JN03	GCA_014319805.1
AWN09152.2	000226	SbcC	839	MLDJOKPK_00254	Salmonella phage SPAsTU	GCA_003183805.1
AEP84019.1	000226	SbcC	836	SPN3US_0186	Salmonella phage SPN3US	GCA_001042275.1
QKE54337.1	000226	SbcC	829	ACSA002_0230	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65399.1	000226	SbcC	737	2050HW_00064	Serratia phage 2050HW	GCA_002628125.1
QDB71179.1	000226	SbcC	826	CPT_Moabite_149	Serratia phage Moabite	GCA_006384735.1
QFP93050.1	000226	SbcC	820	-	Serratia phage PCH45	GCA_009187865.1
QAU04279.1	000226	SbcC	825	HWC03_gp124	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23298.1	000226	SbcC	825	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80921.1	000226	SbcC	825	Aphrodite1_0047	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70742.1	000226	SbcC	366	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47430.1	000226	SbcC	825	HWC35_gp036	Vibrio phage USC-1	GCA_006864065.1
BAW98251.1	000226	SbcC	825	FDH33_gp042	Vibrio phage pTD1	GCA_002618825.1
AQT28072.1	000226	SbcC	828	pVa21_131	Vibrio phage pVa-21	GCA_002619305.1
QAX96785.1	000226	SbcC	827	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97104.1	000226	SbcC	827	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96150.1	000226	SbcC	827	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96468.1	000226	SbcC	827	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20953.1	000226	SbcC	902	-	Vibrio phage vB_pir03	GCA_014319855.1
AXG67243.1	000227	SbcC	776	AD1_199	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79991.1	000227	SbcC	766	JA11_186	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66589.1	000227	SbcC	766	JA13_186	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66914.1	000227	SbcC	766	JA29_188	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67560.1	000227	SbcC	766	JA33_186	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08473.1	000227	SbcC	775	Alexandra_209	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58842.1	000227	SbcC	777	Y3_202	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28673.1	000227	SbcC	769	YOLOSWAG_194	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38521.1	000227	SbcC	819	BN7874_288	Phage NCTB	GCA_900092385.1
AFH14650.1	000227	SbcC	770	Lu11_0118	Pseudomonas phage Lu11	GCA_000897175.1
AGS82062.1	000227	SbcC	814	PaBG_00186	Pseudomonas phage PaBG	GCA_000912555.1
QIG63485.1	000228	SbcC+SbcC	696	DAC16_256	Bacteroides phage DAC16	GCA_013387695.1
QIG63747.1	000228	SbcC+SbcC	696	DAC19_260	Bacteroides phage DAC19	GCA_013387715.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG64008.1	000228	SbcC+SbcC	696	DAC20_259	Bacteroides phage DAC20	GCA_013387725.1
QIG64272.1	000228	SbcC+SbcC	696	DAC22_262	Bacteroides phage DAC22	GCA_013387735.1
QIG64529.1	000228	SbcC+SbcC	696	DAC23_255	Bacteroides phage DAC23	GCA_013387745.1
AMS01223.1	000229	SbcC+SbcC	911	AR9_g139	Bacillus phage AR9	GCA_001743835.1
ALN97887.1	000229	SbcC+SbcC	902	Bp8pS_208	Bacillus phage vB_BpuM-Bp8p	GCA_002607645.1
AST99848.1	000229	SbcC+SbcC	911	PBI_PBS1_26	Bacillus virus PBS1	GCA_002601325.1
CCE26085.1	000229	SbcC+SbcC	929	g061	Yersinia phage phiR1-37	GCA_000895615.1
QDH83405.1	000230	SbcC+SbcC	731	H1O15_gp057	Achromobacter phage Motura	GCA_006964305.1
QBX06709.1	000230	SbcC+SbcC	750	BcepSaruman_296	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74677.1	000230	SbcC+SbcC	750	BcepSauron_297	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41608.1	000230	SbcC+SbcC	754	RSL1_ORF161	Ralstonia phage phiRSL1	GCA_000879455.1
ABS83570.1	000000	SbcC	236	0305phi8-36p005	Bacillus phage 0305phi8-36	GCA_000871045.1
ATA65400.1	000000	SbcC	101	2050HW_00065	Serratia phage 2050HW	GCA_002628125.1
AXH70743.1	000000	SbcC	144	-	Vibrio phage BONAISHI	GCA_003441475.1
prevph1000000126	000000	SbcC	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000127	000000	SbcC	164	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AEO93574.1	000000	AAA_17	331	G_315	Bacillus virus G	GCA_000917535.1
AND75218.1	000000	SbcC+SbcC	625	ME3_57	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AEO93634.1	000000	SbcC+SbcC	694	G_375	Bacillus virus G	GCA_000917535.1
QHJ86024.1	000000	SbcC+SbcC	646	KKIINIFJ_00112	Pseudomonas phage PN05	GCA_009931935.1
ABS83573.1	000000	Calcineurin-SbcD+SbcC	769	0305phi8-36p008	Bacillus phage 0305phi8-36	GCA_000871045.1
QHJ86056.1	000000	Calcineurin-SbcD+SbcC+SbcC	926	KKIINIFJ_00144	Pseudomonas phage PN05	GCA_009931935.1
AMM44935.1	000000	SbcC+PspA+SbcC	622	SP15_137	Bacillus phage SP-15	GCA_001754685.1
QMV29157.1	000000	SbcC	186	AP1_0456	Aeromonas phage AP1	GCA_014183365.1
QDJ96467.1	000231	Calcineurin-SbcD+SbcC	1110	Xoosp13_281	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65453.1	000231	Calcineurin-SbcD+SbcC	1099	-	Xanthomonas phage XacN1	GCA_003173815.1
prevph1000000123	000232	Calcineurin-SbcD	257	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AXH72819.1	000232	Calcineurin-SbcD	344	-	Myoviridae sp.	GCA_003657725.1
QIG63481.1	000232	Calcineurin-SbcD	346	DAC16_252	Bacteroides phage DAC16	GCA_013387695.1
QIG63743.1	000232	Calcineurin-SbcD	335	DAC19_256	Bacteroides phage DAC19	GCA_013387715.1
QIG64004.1	000232	Calcineurin-SbcD	335	DAC20_255	Bacteroides phage DAC20	GCA_013387725.1
QIG64268.1	000232	Calcineurin-SbcD	335	DAC22_258	Bacteroides phage DAC22	GCA_013387735.1
QIG64525.1	000232	Calcineurin-SbcD	335	DAC23_251	Bacteroides phage DAC23	GCA_013387745.1
QGT54539.1	000232	Calcineurin-SbcD	343	b3_0298	Synechococcus phage B3	GCA_009745215.1
ASR76187.1	000232	Calcineurin-SbcD	348	PBI_BELLAMY_142	Synechococcus phage Bellamy	GCA_002627525.1
AGG54482.1	000232	Calcineurin-SbcD	343	CYWG_00198	Cyanophage S-SSM6b	GCA_002710425.1
AXC36781.1	000232	Calcineurin-SbcD	343	-	Escherichia phage UB	GCA_003341455.1
QGT54904.1	000232	Calcineurin-SbcD	343	b23_0291	Synechococcus phage B23	GCA_009745195.1
AFN39520.1	000232	Calcineurin-SbcD	361	CC2_259	Aeromonas phage CC2	GCA_000903495.1
AZU98215.1	000232	Calcineurin-SbcD	343	CPT_Munch_271	Salmonella phage Munch	GCA_004015485.1
ALY07125.1	000232	Calcineurin-SbcD	341	VmeM32_00138	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAY01234.1	000232	Calcineurin-SbcD	341	ASwh1_169	Aeromonas phage Aswh_1	GCA_004146945.1
AGH07471.1	000232	Calcineurin-SbcD	347	CYVG_00027	Cyanophage S-SSM6a	GCA_002710385.1
AAX44523.1	000232	Calcineurin-SbcD	346	PSSM2_145	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGC35209.1	000232	Calcineurin-SbcD	343	ACQ29_gp529	Escherichia phage PBECO4	GCA_001041035.1
ARM70881.1	000232	Calcineurin-SbcD	339	phiC120_c176	Escherichia phage phiC120	GCA_002621185.1
ALP47005.1	000232	Calcineurin-SbcD	347	phiGrn1_0187	Vibrio phage phi-Grn1	GCA_002757115.1
QCW22898.1	000232	Calcineurin-SbcD	300	-	Synechococcus phage S-B05	GCA_006083695.1
AOO13015.1	000232	Calcineurin-SbcD	347	W2100709_133	Cyanophage S-RIM44	GCA_002599285.1
AAQ17680.1	000232	Calcineurin-SbcD	342	47	Aeromonas virus Aeh1	GCA_000843245.1
AXQ70567.1	000232	Calcineurin-SbcD	349	HOU04_gp168	Synechococcus phage S-T4	GCA_003443335.1
QAX97916.1	000232	Calcineurin-SbcD	343	ASswx1_273	Aeromonas phage Asswx_1	GCA_004146865.1
AOO12786.1	000232	Calcineurin-SbcD	347	Sn130910_139	Cyanophage S-RIM44	GCA_002599265.1
AKF12580.1	000232	Calcineurin-SbcD	354	PHIM7_32	Sinorhizobium phage phiM7	GCA_002622405.1
AOO12549.1	000232	Calcineurin-SbcD	347	Sn080709_132	Cyanophage S-RIM44	GCA_002599245.1
QCW18962.1	000232	Calcineurin-SbcD	343	7t3_0441	Salmonella phage 7t3	GCA_006083215.1
QAY00466.1	000232	Calcineurin-SbcD	343	Ecwhy1_187	Escherichia phage Ecwhy_1	GCA_004146585.1
ASV44555.1	000232	Calcineurin-SbcD	344	PBI_SCTP2_540	Salicola phage SCTP-2	GCA_002625545.1
SOK59050.1	000232	Calcineurin-SbcD	344	g242	Yersinia phage fHe-Yen9-03	GCA_002990515.1
ASV44762.1	000232	Calcineurin-SbcD	340	FDI40_gp693	Agrobacterium phage Atu_ph07	GCA_002628245.1
AOO12321.1	000232	Calcineurin-SbcD	347	Np420711_139	Cyanophage S-RIM44	GCA_002599225.1
AIX30629.1	000232	Calcineurin-SbcD	349	Syn7803US37_152	Synechococcus phage ACG-2014f	GCA_002594065.1
QBO61821.1	000232	Calcineurin-SbcD	343	G17_00332	Escherichia phage vB_EcoM_G17	GCA_004521135.1
ADQ52743.1	000232	Calcineurin-SbcD	353	PX29p024	Aeromonas phage PX29	GCA_000920195.1
AOO12085.1	000232	Calcineurin-SbcD	347	Np200711_139	Cyanophage S-RIM44	GCA_002599205.1
AOO11848.1	000232	Calcineurin-SbcD	347	Np050604_132	Cyanophage S-RIM44	GCA_002599185.1
AMM44934.1	000232	Calcineurin-SbcD	344	SP15_136	Bacillus phage SP-15	GCA_001754685.1
ALP47386.1	000232	Calcineurin-SbcD	347	phiST2_0318	Vibrio phage phi-ST2	GCA_002757135.1
AOO11620.1	000232	Calcineurin-SbcD	347	ES420910_139	Cyanophage S-RIM44	GCA_002599165.1
AOV59600.1	000232	Calcineurin-SbcD	346	S330809_139	Synechococcus phage S-CAM4	GCA_002366065.1
QDF13865.1	000232	Calcineurin-SbcD	343	vBEcoMphAPEC6_gp236c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QIG65683.1	000232	Calcineurin-SbcD	349	phiOC_p017	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QDH50664.1	000232	Calcineurin-SbcD	199	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70130.1	000232	Calcineurin-SbcD	346	SynMITS9220M01_117	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBM62154.1	000232	Calcineurin-SbcD	343	EO157G_5650	Escherichia phage SP27	GCA_008033345.1
QNJ54641.1	000232	Calcineurin-SbcD	347	vBValMR10Z_100	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
SCA80466.1	000232	Calcineurin-SbcD	343	PSLUR01_00489	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SOK58515.1	000232	Calcineurin-SbcD	344	g238	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMO43152.1	000232	Calcineurin-SbcD	347	R1080702_143	Cyanophage S-RIM32	GCA_001754165.1
AAR90907.1	000232	Calcineurin-SbcD	341	65p031	Aeromonas virus 65	GCA_000893255.1
AJT61030.1	000232	Calcineurin-SbcD	347	AVU32_gp189	Vibrio phage ValKK3	GCA_001501635.1
AOO14970.1	000232	Calcineurin-SbcD	347	W1230910_124	Cyanophage S-RIM14	GCA_002599125.1
ADM79995.1	000232	Calcineurin-SbcD	342	phiAS5_ORF0152	Aeromonas phage phiAS5	GCA_000887715.1
AOO14321.1	000232	Calcineurin-SbcD	347	Sn110110_127	Cyanophage S-RIM14	GCA_002599065.1
ASU00521.1	000232	Calcineurin-SbcD	343	HWB28_gp031	Aeromonas phage AS-zj	GCA_002627665.1
QIW90963.1	000232	Calcineurin-SbcD	346	COHAPHLL_00100	Vibrio phage V09	GCA_012361135.1
QAX98606.1	000232	Calcineurin-SbcD	342	ASfcp2_273	Aeromonas phage AsFcp_2	GCA_004146885.1
AFA44356.1	000232	Calcineurin-SbcD	346	RaK2_00083	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ATI17476.1	000232	Calcineurin-SbcD	343	-	Aeromonas phage AS-szw	GCA_002743635.1
QCG76020.1	000232	Calcineurin-SbcD	337	EST35_0138	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AFN37303.1	000232	Calcineurin-SbcD	346	pp2_070	Vibriophage phi-pp2	GCA_002630725.1
AJK27573.1	000232	Calcineurin-SbcD	341	PTIM40_146	Cyanophage P-TIM40	GCA_001470935.1
AAQ64143.1	000232	Calcineurin-SbcD	346	KVP40.0072	Vibrio phage KVP40	GCA_000843785.1
AUE22568.1	000232	Calcineurin-SbcD	342	Ah1_00027	Aeromonas phage Ah1	GCA_002957415.1
ADO99234.1	000232	Calcineurin-SbcD	268	Syn1_133	Prochlorococcus phage Syn1	GCA_000892495.1
prev15ph1000000093	000232	Calcineurin-SbcD	373	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QMV28755.1	000232	Calcineurin-SbcD	343	AP1_0037	Aeromonas phage AP1	GCA_014183365.1
AGH56883.1	000232	Calcineurin-SbcD	344	CPXG_00080	Cyanophage P-RSM6	GCA_000906155.1
AIT14482.1	000232	Calcineurin-SbcD	343	PBI_121Q_592	Escherichia phage 121Q	GCA_000926855.1
AGR47678.1	000232	Calcineurin-SbcD	354	SmphiM12_046	Sinorhizobium phage phiM12	GCA_001023565.1
AIR93455.1	000232	Calcineurin-SbcD	348	AVU42_gp117	Prochlorococcus phage P-TIM68	GCA_001503075.1
QBX06016.1	000232	Calcineurin-SbcD	347	ValB1HC_062	Vibrio phage ValB1 HC	GCA_004771355.1
QIG62769.1	000232	Calcineurin-SbcD	343	SEPL_156	Salmonella phage SE_PL	GCA_011067555.1
QHJ74255.1	000232	Calcineurin-SbcD	346	VH12019_00336	Vibrio phage VH1_2019	GCA_009931825.1
AGN12444.1	000232	Calcineurin-SbcD	346	PRTG_00296	Prochlorococcus phage P-SSM5	GCA_002991095.1
AQW88769.1	000232	Calcineurin-SbcD	343	BF_0244	Serratia phage BF	GCA_002619745.1
AMM43810.1	000232	Calcineurin-SbcD	343	CBB_245	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AKF12940.1	000232	Calcineurin-SbcD	354	PHIM19_33	Sinorhizobium phage phiM19	GCA_002605865.1
AFC21689.1	000232	Calcineurin-SbcD	343	GAP32_239	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIW90466.1	000232	Calcineurin-SbcD	346	GCAPEGMB_00119	Vibrio phage V07	GCA_012361095.1
AAX78575.1	000232	Calcineurin-SbcD	339	RB43ORF053w	Escherichia virus RB43	GCA_000863505.1
AGH26309.1	000232	Calcineurin-SbcD	348	CPMG_00210	Prochlorococcus phage MED4-213	GCA_000904535.1
AOV59838.1	000232	Calcineurin-SbcD	346	N231010_139	Synechococcus phage S-CAM4	GCA_002922155.1
ANS05964.1	000232	Calcineurin-SbcD	339	ABCD_0053	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97064.1	000232	Calcineurin-SbcD	339	E_055	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AMO43376.1	000232	Calcineurin-SbcD	347	W270710_132	Cyanophage S-RIM44	GCA_002599145.1
QHJ78892.1	000232	Calcineurin-SbcD	343	-	Myoviridae sp.	GCA_012593985.1
AOV59362.1	000232	Calcineurin-SbcD	346	C440309_139	Synechococcus phage S-CAM4	GCA_002922145.1
AGB07079.1	000232	Calcineurin-SbcD	347	CF80_gp292	Vibrio phage VH7D	GCA_000914495.1
APU01422.1	000232	Calcineurin-SbcD	341	-	Aeromonas phage 65.2	GCA_002618145.1
AIA65040.1	000232	Calcineurin-SbcD	343	S13_243	Cronobacter phage S13	GCA_001503575.1
AKF13315.1	000232	Calcineurin-SbcD	354	PHIN3_50	Sinorhizobium phage phiN3	GCA_001501175.1
AGN30121.1	000232	Calcineurin-SbcD	346	VPFG_00119	Vibrio phage nt-1	GCA_000910195.2
AND75219.1	000232	Calcineurin-SbcD	369	ME3_58	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QHJ86023.1	000232	Calcineurin-SbcD	348	KKIINIFJ_00111	Pseudomonas phage PN05	GCA_009931935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDB70473.1	000233	Calcineurin-SbcD	376	CF8_0061	Aeromonas phage CF8	GCA_006384595.2
QDJ97213.1	000233	Calcineurin-SbcD	380	D6_0053	Aeromonas phage D6	GCA_007051205.2
QDH47066.1	000233	Calcineurin-SbcD	387	LAh10_219	Aeromonas phage LAh10	GCA_006863975.1
QDJ96820.1	000233	Calcineurin-SbcD	377	PS1_0061	Aeromonas phage PS1	GCA_007051165.2
QFR59449.1	000233	Calcineurin-SbcD	377	PS2_0058	Aeromonas phage PS2	GCA_009388305.2
AMS01087.1	000233	Calcineurin-SbcD	370	AR9_g002	Bacillus phage AR9	GCA_001743835.1
ALN97722.1	000233	Calcineurin-SbcD	368	Bp8pS_043	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00009.1	000233	Calcineurin-SbcD	370	PBI_PBS1_187	Bacillus virus PBS1	GCA_002601325.1
AFO71248.1	000233	Calcineurin-SbcD	379	CR5_028	Cronobacter phage CR5	GCA_000910235.1
QBZ70591.1	000233	Calcineurin-SbcD	378	pETSU_010	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59678.1	000233	Calcineurin-SbcD	382	SEGD1_029	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07455.1	000233	Calcineurin-SbcD	375	DERBICUS_29	Erwinia phage Derbicus	GCA_004521655.1
AHI60389.1	000233	Calcineurin-SbcD	368	Ea357_236	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49681.1	000233	Calcineurin-SbcD	388	MACHINA_43	Erwinia phage Machina	GCA_002758035.1
AGX01739.1	000233	Calcineurin-SbcD	381	CF95_gp017	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07345.1	000233	Calcineurin-SbcD	368	REBECCA_240	Erwinia phage Rebecca	GCA_004521635.1
AXF51170.1	000233	Calcineurin-SbcD	388	WELLINGTON_39	Erwinia phage Wellington	GCA_003344985.1
AFQ96754.1	000233	Calcineurin-SbcD	383	G173_gp209	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48057.1	000233	Calcineurin-SbcD	406	ASESINO_44	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86027.1	000233	Calcineurin-SbcD	378	BOSOLAPHORUS_241	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48332.1	000233	Calcineurin-SbcD	395	CAITLIN_37	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48605.1	000233	Calcineurin-SbcD	395	CHRISDB_43	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52344.2	000233	Calcineurin-SbcD	378	DM_244	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86346.1	000233	Calcineurin-SbcD	378	DESERTFOX_239	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48879.1	000233	Calcineurin-SbcD	375	EARLPHILLIPIV_29	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49126.1	000233	Calcineurin-SbcD	388	HUXLEY_44	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03879.1	000233	Calcineurin-SbcD	394	JOAD_36	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49391.1	000233	Calcineurin-SbcD	388	KWAN_39	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86669.1	000233	Calcineurin-SbcD	378	MADMEL_242	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86992.1	000233	Calcineurin-SbcD	378	MORTIMER_244	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49954.1	000233	Calcineurin-SbcD	388	PARSHIK_45	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50219.1	000233	Calcineurin-SbcD	375	PHOBOS_29	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52018.2	000233	Calcineurin-SbcD	378	RAY_238	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03634.1	000233	Calcineurin-SbcD	394	RISINGSUN_36	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51702.1	000233	Calcineurin-SbcD	368	SIMMY50_243	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65053.3	000233	Calcineurin-SbcD	378	SPECIALG_242	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50467.1	000233	Calcineurin-SbcD	383	STRATTON_42	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85868.1	000233	Calcineurin-SbcD	382	ACEC001_0300	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63971.1	000233	Calcineurin-SbcD	380	Goslar_00178	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71907.1	000233	Calcineurin-SbcD	378	N1M2_44	Klebsiella phage N1M2	GCA_010092605.1
QGZ14375.1	000233	Calcineurin-SbcD	374	HWC77_gp012	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24158.1	000233	Calcineurin-SbcD	375	-	Proteus phage 10	GCA_014071245.1
ABY62953.1	000233	Calcineurin-SbcD	381	201phi2-1p121	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27124.1	000233	Calcineurin-SbcD	371	PPEV_gp030	Pseudomonas phage EL	GCA_000866825.1
ANM44845.1	000233	Calcineurin-SbcD	379	KTN4_087	Pseudomonas phage KTN4	GCA_002607225.1
ARV77229.1	000233	Calcineurin-SbcD	385	NOXIFER_58	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89502.1	000233	Calcineurin-SbcD	377	OBP_065	Pseudomonas phage OBP	GCA_000896635.1
QBX32213.1	000233	Calcineurin-SbcD	397	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76732.1	000233	Calcineurin-SbcD	382	PHABIO_101	Pseudomonas phage Phabio	GCA_002624965.1
AEH03486.1	000233	Calcineurin-SbcD	381	059	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02596.1	000233	Calcineurin-SbcD	379	PSA21_67	Pseudomonas phage Psa21	GCA_004340405.1
ATN94868.1	000233	Calcineurin-SbcD	379	SL2_291	Pseudomonas phage SL2	GCA_002956015.1
QJB22723.1	000233	Calcineurin-SbcD	358	fnug_80	Pseudomonas phage fnug	GCA_012837215.1
QEM41791.1	000233	Calcineurin-SbcD	332	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82966.2	000233	Calcineurin-SbcD	387	PHIKZ065	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19256.1	000233	Calcineurin-SbcD	401	FDH28_gp139	Ralstonia phage RP12	GCA_002617345.1
BAW19542.1	000233	Calcineurin-SbcD	401	-	Ralstonia phage RP31	GCA_002617365.1
BAS05015.2	000233	Calcineurin-SbcD	359	AVU11_gp223	Ralstonia phage RSF1	GCA_001500875.1
BAQ02745.2	000233	Calcineurin-SbcD	359	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20743.1	000233	Calcineurin-SbcD	382	-	Salmonella phage JN03	GCA_014319805.1
AWN09068.1	000233	Calcineurin-SbcD	382	MLDJOKPK_00138	Salmonella phage SPAsTU	GCA_003183805.1
AEP83860.1	000233	Calcineurin-SbcD	382	SPN3US_0027	Salmonella phage SPN3US	GCA_001042275.1
QKE54565.1	000233	Calcineurin-SbcD	366	ACSA002_2490	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65653.1	000233	Calcineurin-SbcD	374	2050HW_00318	Serratia phage 2050HW	GCA_002628125.1
QDB71077.1	000233	Calcineurin-SbcD	374	CPT_Moabite_045	Serratia phage Moabite	GCA_006384735.1
QFP93089.1	000233	Calcineurin-SbcD	394	-	Serratia phage PCH45	GCA_009187865.1
QAU04361.1	000233	Calcineurin-SbcD	374	HWC03_gp206	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23215.1	000233	Calcineurin-SbcD	374	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80975.1	000233	Calcineurin-SbcD	374	Aphrodite1_0130	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70817.1	000233	Calcineurin-SbcD	390	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47513.1	000233	Calcineurin-SbcD	374	HWC35_gp119	Vibrio phage USC-1	GCA_006864065.1
BAW98332.1	000233	Calcineurin-SbcD	375	FDH33_gp123	Vibrio phage pTD1	GCA_002618825.1
AQT28154.1	000233	Calcineurin-SbcD	339	pVa21_213	Vibrio phage pVa-21	GCA_002619305.1
QAX96680.1	000233	Calcineurin-SbcD	378	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96998.1	000233	Calcineurin-SbcD	383	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96044.1	000233	Calcineurin-SbcD	383	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96362.1	000233	Calcineurin-SbcD	383	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21062.1	000233	Calcineurin-SbcD	400	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26357.1	000233	Calcineurin-SbcD	413	g334	Yersinia phage phiR1-37	GCA_000895615.1
QDH83449.1	000234	Calcineurin-SbcD	347	H1O15_gp041	Achromobacter phage Motura	GCA_006964305.1
QBX06605.1	000234	Calcineurin-SbcD	340	BcepSaruman_192	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74571.1	000234	Calcineurin-SbcD	340	BcepSauron_191	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67229.1	000234	Calcineurin-SbcD	357	AD1_185	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79979.1	000234	Calcineurin-SbcD	376	JA11_174	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66577.1	000234	Calcineurin-SbcD	376	JA13_174	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66902.1	000234	Calcineurin-SbcD	376	JA29_176	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67548.1	000234	Calcineurin-SbcD	376	JA33_174	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08458.1	000234	Calcineurin-SbcD	357	Alexandra_190	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58826.1	000234	Calcineurin-SbcD	358	Y3_186	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28660.1	000234	Calcineurin-SbcD	349	YOLOSWAG_181	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38505.1	000234	Calcineurin-SbcD	352	BN7874_283	Phage NCTB	GCA_900092385.1
AFH14643.1	000234	Calcineurin-SbcD	351	Lu11_0111	Pseudomonas phage Lu11	GCA_000897175.1
AGS82066.2	000234	Calcineurin-SbcD	355	PaBG_00190	Pseudomonas phage PaBG	GCA_000912555.1
BAG41742.1	000234	Calcineurin-SbcD	337	RSL1_ORF296	Ralstonia phage phiRSL1	GCA_000879455.1
AFF28286.1	000235	SbcC+SidE+SbcC	1301	PAU_288	Sphingomonas phage PAU	GCA_000902455.1
BBI90467.1	000235	SbcC+SidE+SbcC	1318	HYO65_gp075	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90774.1	000235	SbcC+SidE+SbcC	1318	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39141.1	000235	SbcC+SidE+SbcC	1310	BPT24_019	Tenacibaculum phage pT24	GCA_002611925.1
AEO93615.1	000000	Calcineurin-SbcD	379	G_356	Bacillus virus G	GCA_000917535.1
AMM43830.1	000236	Calcineurin	204	CBB_266	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18989.1	000236	Calcineurin	207	7t3_0468	Salmonella phage 7t3	GCA_006083215.1
AZU98237.1	000236	Calcineurin	207	CPT_Munch_293	Salmonella phage Munch	GCA_004015485.1
QIG62747.1	000236	Calcineurin	207	SEPL_134	Salmonella phage SE_PL	GCA_011067555.1
AND75391.1	000236	Calcineurin	159	ME3_230	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QDJ97347.1	000236	Calcineurin	202	D6_0188	Aeromonas phage D6	GCA_007051205.2
QDH47143.1	000236	Calcineurin	202	LAh10_106	Aeromonas phage LAh10	GCA_006863975.1
QDJ96700.1	000236	Calcineurin	167	PS1_0189	Aeromonas phage PS1	GCA_007051165.2
QFR59333.1	000236	Calcineurin	167	PS2_0191	Aeromonas phage PS2	GCA_009388305.2
AMS01102.1	000236	Calcineurin	244	AR9_g017	Bacillus phage AR9	GCA_001743835.1
ASU00024.1	000236	Calcineurin	244	PBI_PBS1_202	Bacillus virus PBS1	GCA_002601325.1
QBX06540.1	000236	Calcineurin	199	BcepSaruman_127	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74506.1	000236	Calcineurin	199	BcepSauron_126	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63653.1	000236	Calcineurin	181	CP21_191	Campylobacter virus CP21	GCA_000902535.1
AFU88083.1	000236	Calcineurin	183	CcrColossus_gp213	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68759.1	000236	Calcineurin	183	CcrPW_gp220c	Caulobacter phage CcrPW	GCA_003443275.1
AIA64998.1	000236	Calcineurin	184	S13_201	Cronobacter phage S13	GCA_001503575.1
AFC21710.1	000236	Calcineurin	201	GAP32_260	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QBZ70734.1	000236	Calcineurin	172	pETSU_153	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03767.1	000236	Calcineurin	170	JOAD_148	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03523.1	000236	Calcineurin	170	RISINGSUN_147	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AQT28708.1	000236	Calcineurin	177	YOLOSWAG_230	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QBO63950.1	000236	Calcineurin	185	Goslar_00157	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72045.1	000236	Calcineurin	175	N1M2_182	Klebsiella phage N1M2	GCA_010092605.1
AXH72888.1	000236	Calcineurin	174	-	Myoviridae sp.	GCA_003657725.1
QHJ78933.1	000236	Calcineurin	185	-	Myoviridae sp.	GCA_012593985.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG65770.1	000236	Calcineurin	169	phiOC_p105	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AFH14569.1	000236	Calcineurin	214	Lu11_0038	Pseudomonas phage Lu11	GCA_000897175.1
AEV89666.1	000236	Calcineurin	184	OBP_229	Pseudomonas phage OBP	GCA_000896635.1
AGS82186.1	000236	Calcineurin	201	PaBG_00315	Pseudomonas phage PaBG	GCA_000912555.1
ASV44532.1	000236	Calcineurin	179	PBI_SCTP2_517	Salicola phage SCTP-2	GCA_002625545.1
AQW88789.1	000236	Calcineurin	204	BF_0264	Serratia phage BF	GCA_002619745.1
AGR48111.1	000236	Calcineurin	200	SmphiM12_479	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13656.1	000236	Calcineurin	200	PHIN3_393	Sinorhizobium phage phiN3	GCA_001501175.1
AXH70941.1	000236	Calcineurin	210	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64087.1	000236	Calcineurin	174	KVP40.0016	Vibrio phage KVP40	GCA_000843785.1
QIW90410.1	000236	Calcineurin	174	GCAPEGMB_00063	Vibrio phage V07	GCA_012361095.1
QIW91019.1	000236	Calcineurin	174	COHAPHLL_00156	Vibrio phage V09	GCA_012361135.1
QHJ74199.1	000236	Calcineurin	174	VH12019_00280	Vibrio phage VH1_2019	GCA_009931825.1
AGB07023.1	000236	Calcineurin	174	CF80_gp236	Vibrio phage VH7D	GCA_000914495.1
QBX06073.1	000236	Calcineurin	174	ValB1HC_119	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04495.1	000236	Calcineurin	193	ValB1MD_142	Vibrio phage ValB1MD	GCA_004138815.1
AJT61087.1	000236	Calcineurin	174	AVU32_gp246	Vibrio phage ValKK3	GCA_001501635.1
AGN30068.1	000236	Calcineurin	174	VPFG_00065	Vibrio phage nt-1	GCA_000910195.2
ALP47093.1	000236	Calcineurin	174	phiGrn1_0131	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47473.1	000236	Calcineurin	174	phiST2_0261	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54699.1	000236	Calcineurin	174	vBValMR10Z_158	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07045.1	000236	Calcineurin	241	VmeM32_00054	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37250.1	000236	Calcineurin	174	pp2_016	Vibriophage phi-pp2	GCA_002630725.1
BBA65441.1	000236	Calcineurin	187	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96457.1	000236	Calcineurin	158	Xoosp13_271	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59070.1	000236	Calcineurin	216	g262	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58536.1	000236	Calcineurin	204	g259	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000225	000236	Calcineurin	240	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000175	000236	Calcineurin	240	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ95032.1	000237	PNK+Calcineurin	418	FDI40_gp253	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72921.1	000237	PNK+Calcineurin	428	-	Myoviridae sp.	GCA_003657725.1
QCG76129.1	000237	PNK+Calcineurin	253	EST35_0248	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44730.1	000000	Calcineurin	296	FDI40_gp267	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93600.1	000000	Calcineurin	347	G_341	Bacillus virus G	GCA_000917535.1
ARB13653.1	000238	Calcineurin	567	Ccr10_gp124c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13998.1	000238	Calcineurin	567	Ccr2_gp123c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14686.1	000238	Calcineurin	567	Ccr29_gp130	Caulobacter phage Ccr29	GCA_002619485.1
ARB15040.1	000238	Calcineurin	567	Ccr32_gp122	Caulobacter phage Ccr32	GCA_002619505.1
ARB15373.1	000238	Calcineurin	567	Ccr34_gp131	Caulobacter phage Ccr34	GCA_002619525.1
ARB14341.1	000238	Calcineurin	567	Ccr5_gp123c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68321.1	000238	Calcineurin	568	CcrBL10_gp117c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69210.1	000238	Calcineurin	595	CcrBL9_gp186	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88031.1	000238	Calcineurin	610	CcrColossus_gp161	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68708.1	000238	Calcineurin	595	CcrPW_gp169c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69764.1	000238	Calcineurin	630	CcrSC_gp182	Caulobacter phage CcrSC	GCA_003443315.1
AFU87645.1	000238	Calcineurin	567	CcrKarma_gp128	Caulobacter virus Karma	GCA_000901575.1
AFU87294.1	000238	Calcineurin	567	CcrMagneto_gp124	Caulobacter virus Magneto	GCA_000903095.1
AFU86605.1	000238	Calcineurin	566	CcrRogue_gp123	Caulobacter virus Rogue	GCA_000900555.1
AFU88441.1	000238	Calcineurin	567	CcrSwift_gp123	Caulobacter virus Swift	GCA_000899655.1
AFU86958.1	000238	Calcineurin	567	CbK_gp126	Caulobacter virus phiCbK	GCA_000900535.1
QIG66054.1	000238	Calcineurin	608	phiOC_p412	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BBI90680.1	000238	Calcineurin	470	HYO65_gp288	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90987.1	000238	Calcineurin	470	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39268.1	000238	Calcineurin	578	BPT24_142	Tenacibaculum phage pT24	GCA_002611925.1
AXH70997.1	000238	Calcineurin	623	-	Vibrio phage BONAISHI	GCA_003441475.1
BBA65411.1	000238	Calcineurin	564	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96434.1	000238	Calcineurin	566	Xoosp13_248	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54655.1	000239	PP2A	226	b23_0027	Synechococcus phage B23	GCA_009745195.1
QGT54285.1	000239	PP2A	226	b3_0027	Synechococcus phage B3	GCA_009745215.1
AND75288.1	000240	Calcineurin	248	ME3_127	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AEO93607.1	000240	Calcineurin	280	G_348	Bacillus virus G	GCA_000917535.1
AFU87972.1	000240	Calcineurin	253	CcrColossus_gp102	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68649.1	000240	Calcineurin	253	CcrPW_gp110	Caulobacter phage CcrPW	GCA_003443275.1
AFC21549.1	000240	Calcineurin	263	GAP32_101	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14351.1	000240	Calcineurin	263	PBI_121Q_461	Escherichia phage 121Q	GCA_000926855.1
QAY00593.1	000240	Calcineurin	263	Ecwhy1_316	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34788.1	000240	Calcineurin	263	ACQ29_gp108	Escherichia phage PBECO4	GCA_001041035.1
BBM62022.1	000240	Calcineurin	263	EO157G_4330	Escherichia phage SP27	GCA_008033345.1
AXC36904.1	000240	Calcineurin	263	-	Escherichia phage UB	GCA_003341455.1
QBO61953.1	000240	Calcineurin	263	G17_00464	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13980.1	000240	Calcineurin	263	vBEcoMphAPEC6_gp356c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80338.1	000240	Calcineurin	263	PSLUR01_00361	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43667.1	000240	Calcineurin	263	CBB_102	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44264.1	000240	Calcineurin	268	PBI_SCTP2_249	Salicola phage SCTP-2	GCA_002625545.1
QCW18803.1	000240	Calcineurin	263	7t3_0282	Salmonella phage 7t3	GCA_006083215.1
AZU98068.1	000240	Calcineurin	263	CPT_Munch_124	Salmonella phage Munch	GCA_004015485.1
QIG62914.1	000240	Calcineurin	263	SEPL_301	Salmonella phage SE_PL	GCA_011067555.1
AQW88620.1	000240	Calcineurin	267	BF_0095	Serratia phage BF	GCA_002619745.1
QGT54707.1	000240	Calcineurin	261	b23_0092	Synechococcus phage B23	GCA_009745195.1
QGT54337.1	000240	Calcineurin	261	b3_0093	Synechococcus phage B3	GCA_009745215.1
AAQ64122.1	000240	Calcineurin	242	KVP40.0051	Vibrio phage KVP40	GCA_000843785.1
QIW90444.1	000240	Calcineurin	242	GCAPEGMB_00097	Vibrio phage V07	GCA_012361095.1
QIW90985.1	000240	Calcineurin	242	COHAPHLL_00122	Vibrio phage V09	GCA_012361135.1
QHJ74233.1	000240	Calcineurin	242	VH12019_00314	Vibrio phage VH1_2019	GCA_009931825.1
AGB07057.1	000240	Calcineurin	242	CF80_gp270	Vibrio phage VH7D	GCA_000914495.1
QBX06039.1	000240	Calcineurin	242	ValB1HC_085	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61053.1	000240	Calcineurin	242	AVU32_gp212	Vibrio phage ValKK3	GCA_001501635.1
AGN30100.1	000240	Calcineurin	242	VPFG_00098	Vibrio phage nt-1	GCA_000910195.2
ALP47046.1	000240	Calcineurin	242	phiGrn1_0164	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47424.1	000240	Calcineurin	242	phiST2_0295	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54664.1	000240	Calcineurin	242	vBValMR10Z_123	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37283.1	000240	Calcineurin	242	pp2_049	Vibriophage phi-pp2	GCA_002630725.1
BBA65531.1	000240	Calcineurin	293	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96528.1	000240	Calcineurin	295	Xoosp13_342	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58896.1	000240	Calcineurin	267	g088	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58361.1	000240	Calcineurin	267	g084	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AEO93611.1	000241	LTD+Calcineurin	866	G_352	Bacillus virus G	GCA_000917535.1
QIG63318.1	000241	LTD+Calcineurin	1177	DAC16_85	Bacteroides phage DAC16	GCA_013387695.1
QIG63579.1	000241	LTD+Calcineurin	1177	DAC19_88	Bacteroides phage DAC19	GCA_013387715.1
QIG63840.1	000241	LTD+Calcineurin	1177	DAC20_87	Bacteroides phage DAC20	GCA_013387725.1
QIG64102.1	000241	LTD+Calcineurin	1177	DAC22_88	Bacteroides phage DAC22	GCA_013387735.1
QIG64362.1	000241	LTD+Calcineurin	1177	DAC23_84	Bacteroides phage DAC23	GCA_013387745.1
prev15ph1000000478	000241	LTD+Calcineurin	1571	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ95385.1	000242	Calcineurin	192	FDI40_gp626	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72579.1	000242	Calcineurin	190	-	Myoviridae sp.	GCA_003657725.1
QIG65988.1	000242	Calcineurin	204	phiOC_p346	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47928.1	000242	Calcineurin	201	SmphiM12_296	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13129.1	000242	Calcineurin	201	PHIM19_224	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12768.1	000242	Calcineurin	201	PHIM7_223	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13498.1	000242	Calcineurin	201	PHIN3_235	Sinorhizobium phage phiN3	GCA_001501175.1
prevph1000000510	000243	Calcineurin	297	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000385	000243	Calcineurin	297	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXQ69133.1	000244	Calcineurin	264	CcrBL9_gp109	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69687.1	000244	Calcineurin	265	CcrSC_gp105	Caulobacter phage CcrSC	GCA_003443315.1
QIG57916.1	000000	Calcineurin	285	SEA_PAULODIABOLI_231	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57914.1	000000	Calcineurin	226	SEA_PAULODIABOLI_229	Microbacterium phage PauloDiaboli	GCA_011067425.1
CCE26211.1	000000	Calcineurin	203	g187	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000237	000245	PP2A	260	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000187	000245	PP2A	260	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01791.1	000246	SprT-like	257	-	Aeromonas phage 65.2	GCA_002618145.1
APU01787.1	000246	SprT-like	131	-	Aeromonas phage 65.2	GCA_002618145.1
APU01690.1	000246	SprT-like	176	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28993.1	000246	SprT-like	258	AP1_0286	Aeromonas phage AP1	GCA_014183365.1
ATI17514.1	000246	SprT-like	258	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00482.1	000246	SprT-like	258	HWB28_gp070	Aeromonas phage AS-zj	GCA_002627665.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU00396.1	000246	SprT-like	177	HWB28_gp156	Aeromonas phage AS-zj	GCA_002627665.1
AUE22599.1	000246	SprT-like	293	Ah1_00058	Aeromonas phage Ah1	GCA_002957415.1
QAX98637.1	000246	SprT-like	305	ASfcp2_304	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97954.1	000246	SprT-like	258	ASswx1_312	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01190.1	000246	SprT-like	232	ASwh1_125	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39384.1	000246	SprT-like	258	CC2_220	Aeromonas phage CC2	GCA_000903495.1
ADQ52777.1	000246	SprT-like	305	PX29p058	Aeromonas phage PX29	GCA_000920195.1
ADM80033.1	000246	SprT-like	302	phiAS5_ORF0190	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53328.1	000246	SprT-like	176	65p320	Aeromonas virus 65	GCA_000893255.1
ADQ53430.1	000246	SprT-like	131	65p424	Aeromonas virus 65	GCA_000893255.1
ADQ53434.1	000246	SprT-like	257	65p428	Aeromonas virus 65	GCA_000893255.1
AAQ17722.1	000246	SprT-like	293	Aeh1ORF062c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06023.1	000246	SprT-like	180	ABCD_0005	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65029.1	000246	SprT-like	235	S13_232	Cronobacter phage S13	GCA_001503575.1
AFC21883.1	000246	SprT-like	191	GAP32_430	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97013.1	000246	SprT-like	179	E_004	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78525.1	000246	SprT-like	180	RB43ORF003c	Escherichia virus RB43	GCA_000863505.1
QHJ78905.1	000246	SprT-like	239	-	Myoviridae sp.	GCA_012593985.1
ASV44326.1	000246	SprT-like	218	PBI_SCTP2_311	Salicola phage SCTP-2	GCA_002625545.1
QAU04471.1	000246	SprT-like	168	ValB1MD_070	Vibrio phage ValB1MD	GCA_004138815.1
ALY07202.1	000246	SprT-like	181	VmeM32_00216	Vibrio phage vB_VmeM-32	GCA_002608825.1
BBA65652.1	000246	SprT-like	171	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65193.1	000246	SprT-like	171	-	Xanthomonas phage XacN1	GCA_003173815.1
AAQ64132.1	000247	SprT-like+S13_232	270	KVP40.0061	Vibrio phage KVP40	GCA_000843785.1
QIW90455.1	000247	SprT-like+S13_232	270	GCAPEGMB_00108	Vibrio phage V07	GCA_012361095.1
QIW90974.1	000247	SprT-like+S13_232	278	COHAPHLL_00111	Vibrio phage V09	GCA_012361135.1
QHJ74244.1	000247	SprT-like+S13_232	278	VH12019_00325	Vibrio phage VH1_2019	GCA_009931825.1
AGB07068.1	000247	SprT-like+S13_232	275	CF80_gp281	Vibrio phage VH7D	GCA_000914495.1
QBX06027.1	000247	SprT-like+S13_232	275	ValB1HC_073	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61041.1	000247	SprT-like+S13_232	275	AVU32_gp200	Vibrio phage ValKK3	GCA_001501635.1
AGN30110.1	000247	SprT-like+S13_232	271	VPFG_00108	Vibrio phage nt-1	GCA_000910195.2
ALP47038.1	000247	SprT-like+S13_232	271	phiGrn1_0176	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47414.1	000247	SprT-like+S13_232	275	phiST2_0307	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54652.1	000247	SprT-like+S13_232	275	vBValMR10Z_111	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37292.1	000247	SprT-like+S13_232	270	pp2_059	Vibriophage phi-pp2	GCA_002630725.1
AAQ64264.1	000248	S13_232	199	KVP40.0195	Vibrio phage KVP40	GCA_000843785.1
QIW90580.1	000248	S13_232	199	GCAPEGMB_00233	Vibrio phage V07	GCA_012361095.1
QIW91218.1	000248	S13_232	199	COHAPHLL_00382	Vibrio phage V09	GCA_012361135.1
QHJ74378.1	000248	S13_232	199	VH12019_00051	Vibrio phage VH1_2019	GCA_009931825.1
AGB06876.1	000248	S13_232	188	CF80_gp089	Vibrio phage VH7D	GCA_000914495.1
QBX06270.1	000248	S13_232	194	ValB1HC_317	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60896.1	000248	S13_232	194	AVU32_gp055	Vibrio phage ValKK3	GCA_001501635.1
AGN30252.1	000248	S13_232	185	VPFG_00253	Vibrio phage nt-1	GCA_000910195.2
ALP47074.1	000248	S13_232	194	phiGrn1_0315	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47454.1	000248	S13_232	194	phiST2_0071	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54897.1	000248	S13_232	194	vBValMR10Z_357	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37425.1	000248	S13_232	204	pp2_192	Vibriophage phi-pp2	GCA_002630725.1
QDH83610.1	000000	SIG+SprT-like	459	H1O15_gp178	Achromobacter phage Motura	GCA_006964305.1
ARB13649.1	000249	SIG+35exo+T7DNApol	748	Ccr10_gp120c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13994.1	000249	SIG+35exo+T7DNApol	748	Ccr2_gp119c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14682.1	000249	SIG+35exo+T7DNApol	748	Ccr29_gp126	Caulobacter phage Ccr29	GCA_002619485.1
ARB15037.1	000249	SIG+35exo+T7DNApol	748	Ccr32_gp119	Caulobacter phage Ccr32	GCA_002619505.1
ARB15369.1	000249	SIG+35exo+T7DNApol	748	Ccr34_gp127	Caulobacter phage Ccr34	GCA_002619525.1
ARB14338.1	000249	SIG+35exo+T7DNApol	748	Ccr5_gp120c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68318.1	000249	SIG+35exo+T7DNApol	748	CcrBL10_gp114c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69212.1	000249	SIG+35exo+T7DNApol	758	CcrBL9_gp188	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88028.1	000249	SIG+35exo+T7DNApol	788	CcrColossus_gp158	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68705.1	000249	SIG+35exo+T7DNApol	787	CcrPW_gp166c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69766.1	000249	SIG+35exo+T7DNApol	758	CcrSC_gp184	Caulobacter phage CcrSC	GCA_003443315.1
AFU87642.1	000249	SIG+35exo+T7DNApol	748	CcrKarma_gp125	Caulobacter virus Karma	GCA_000901575.1
AFU87291.1	000249	SIG+35exo+T7DNApol	748	CcrMagneto_gp121	Caulobacter virus Magneto	GCA_000903095.1
AFU86602.1	000249	SIG+35exo+T7DNApol	748	CcrRogue_gp120	Caulobacter virus Rogue	GCA_000900555.1
AFU88438.1	000249	SIG+35exo+T7DNApol	748	CcrSwift_gp120	Caulobacter virus Swift	GCA_000899655.1
AFU86955.1	000249	SIG+35exo+T7DNApol	748	CbK_gp123	Caulobacter virus phiCbK	GCA_000900535.1
QDH83419.1	000250	35exo+T7DNApol	1055	H1O15_gp010	Achromobacter phage Motura	GCA_006964305.1
QBX06635.1	000250	35exo+T7DNApol	1056	BcepSaruman_222	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74605.1	000250	35exo+T7DNApol	1056	BcepSauron_225	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67216.1	000250	35exo+T7DNApol	1053	AD1_172	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79966.1	000250	35exo+T7DNApol	1051	JA11_161	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66564.1	000250	35exo+T7DNApol	1051	JA13_161	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66889.1	000250	35exo+T7DNApol	1051	JA29_163	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67535.1	000250	35exo+T7DNApol	1051	JA33_161	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08446.1	000250	35exo+T7DNApol	1056	Alexandra_177	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58813.1	000250	35exo+T7DNApol	1054	Y3_173	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28647.1	000250	35exo+T7DNApol	1053	YOLOSWAG_168	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38480.1	000250	35exo+T7DNApol	1044	BN7874_270	Phage NCTB	GCA_900092385.1
AFH14628.1	000250	35exo+T7DNApol	983	Lu11_0096	Pseudomonas phage Lu11	GCA_000897175.1
AGS82080.1	000250	35exo+T7DNApol	1032	PaBG_00205	Pseudomonas phage PaBG	GCA_000912555.1
BAG41704.1	000250	35exo+T7DNApol	1050	RSL1_ORF256	Ralstonia phage phiRSL1	GCA_000879455.1
AYD81231.1	000251	35exo+T7DNApol	655	SEA_JUSTBECAUSE_62	Streptomyces phage JustBecause	GCA_003613775.1
QJD53634.1	000251	35exo+T7DNApol	655	SEA_KELA_63	Streptomyces phage Kela	GCA_012934305.1
QBZ71965.1	000251	35exo+T7DNApol	654	SEA_KRADAL_67	Streptomyces phage Kradal	GCA_004799925.1
AXH66228.1	000251	35exo+T7DNApol	654	SEA_SATIS_67	Streptomyces phage Satis	GCA_003366315.1
AMM44908.1	000000	35exo+T7DNApol	1177	SP15_109	Bacillus phage SP-15	GCA_001754685.1
QIG57851.1	000000	35exo+T7DNApol	622	SEA_PAULODIABOLI_117	Microbacterium phage PauloDiaboli	GCA_011067425.1
QHJ86116.1	000000	35exo+T7DNApol	899	KKIINIFJ_00205	Pseudomonas phage PN05	GCA_009931935.1
QIW90845.1	000000	35exo+T7DNApol	605	GCAPEGMB_00530	Vibrio phage V07	GCA_012361095.1
AND75221.1	000000	T7DNApol	87	ME3_60	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QHJ86038.1	000000	T7DNApol	1023	KKIINIFJ_00126	Pseudomonas phage PN05	GCA_009931935.1
QHJ86136.1	000000	T7DNApol	194	KKIINIFJ_00225	Pseudomonas phage PN05	GCA_009931935.1
AND75222.1	000000	T7DNApol+HINT+T7DNApol	931	ME3_61	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ARB13756.1	000252	DNA_pol_A-Fragments	81	Ccr10_gp226c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14101.1	000252	DNA_pol_A-Fragments	81	Ccr2_gp225c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14790.1	000252	DNA_pol_A-Fragments	81	Ccr29_gp234	Caulobacter phage Ccr29	GCA_002619485.1
ARB15134.1	000252	DNA_pol_A-Fragments	81	Ccr32_gp216	Caulobacter phage Ccr32	GCA_002619505.1
ARB15468.1	000252	DNA_pol_A-Fragments	81	Ccr34_gp226	Caulobacter phage Ccr34	GCA_002619525.1
ARB14443.1	000252	DNA_pol_A-Fragments	81	Ccr5_gp223c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68423.1	000252	DNA_pol_A-Fragments	83	CcrBL10_gp219c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87750.1	000252	DNA_pol_A-Fragments	81	CcrKarma_gp233	Caulobacter virus Karma	GCA_000901575.1
AFU87398.1	000252	DNA_pol_A-Fragments	81	CcrMagneto_gp228	Caulobacter virus Magneto	GCA_000903095.1
AFU86709.1	000252	DNA_pol_A-Fragments	83	CcrRogue_gp227	Caulobacter virus Rogue	GCA_000900555.1
AFU88546.1	000252	DNA_pol_A-Fragments	81	CcrSwift_gp228	Caulobacter virus Swift	GCA_000899655.1
AFU87053.1	000252	DNA_pol_A-Fragments	81	CbK_gp221	Caulobacter virus phiCbK	GCA_000900535.1
AYD79999.1	000253	DNA_pol_A-Fragments	110	JA11_194	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66597.1	000253	DNA_pol_A-Fragments	110	JA13_194	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66922.1	000253	DNA_pol_A-Fragments	110	JA29_196	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67568.1	000253	DNA_pol_A-Fragments	110	JA33_194	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
BAG41502.1	000000	SIG+DNA_pol_A-Fragments	188	RSL1_ORF056	Ralstonia phage phiRSL1	GCA_000879455.1
QHJ86191.1	000000	DNA_pol_A-Fragments	57	KKIINIFJ_00281	Pseudomonas phage PN05	GCA_009931935.1
ARB13787.1	000254	TFIIE-HTH	71	Ccr10_gp257	Caulobacter phage Ccr10	GCA_002619445.1
ARB14132.1	000254	TFIIE-HTH	71	Ccr2_gp256	Caulobacter phage Ccr2	GCA_002619465.1
ARB14826.1	000254	TFIIE-HTH	71	Ccr29_gp270	Caulobacter phage Ccr29	GCA_002619485.1
ARB15166.1	000254	TFIIE-HTH	71	Ccr32_gp248	Caulobacter phage Ccr32	GCA_002619505.1
ARB15500.1	000254	TFIIE-HTH	71	Ccr34_gp258	Caulobacter phage Ccr34	GCA_002619525.1
ARB14474.1	000254	TFIIE-HTH	69	Ccr5_gp254	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68452.1	000254	TFIIE-HTH	49	CcrBL10_gp248	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87783.1	000254	TFIIE-HTH	73	CcrKarma_gp266	Caulobacter virus Karma	GCA_000901575.1
AFU87430.1	000254	TFIIE-HTH	73	CcrMagneto_gp260	Caulobacter virus Magneto	GCA_000903095.1
AFU86739.1	000254	TFIIE-HTH	73	CcrRogue_gp257	Caulobacter virus Rogue	GCA_000900555.1
AFU88577.1	000254	TFIIE-HTH	71	CcrSwift_gp259	Caulobacter virus Swift	GCA_000899655.1
AFU87085.1	000254	TFIIE-HTH	71	CbK_gp253	Caulobacter virus phiCbK	GCA_000900535.1
BAV39190.1	000000	HTH	64	BPT24_067	Tenacibaculum phage pT24	GCA_002611925.1
AXQ69276.1	000255	TelA	334	CcrBL9_gp252c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88092.1	000255	TelA	362	CcrColossus_gp222	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68768.1	000255	TelA	362	CcrPW_gp229c	Caulobacter phage CcrPW	GCA_003443275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69833.1	000255	TelA	326	CcrSC_gp251c	Caulobacter phage CcrSC	GCA_003443315.1
AFC21785.1	000255	TelA	382	GAP32_335	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13963.1	000255	TelA	378	PBI_121Q_66	Escherichia phage 121Q	GCA_000926855.1
QAY00374.1	000255	TelA	380	Ecwhy1_93	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35119.1	000255	TelA	378	ACQ29_gp439	Escherichia phage PBECO4	GCA_001041035.1
BBM61655.1	000255	TelA	378	EO157G_0660	Escherichia phage SP27	GCA_008033345.1
AXC36693.1	000255	TelA	378	-	Escherichia phage UB	GCA_003341455.1
QBO61730.1	000255	TelA	378	G17_00241	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13775.1	000255	TelA	378	vBEcoMphAPEC6_gp146c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80557.1	000255	TelA	378	PSLUR01_00580	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44445.1	000255	TelA	375	RaK2_00172	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43903.1	000255	TelA	380	CBB_340	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19062.1	000255	TelA	380	7t3_0542	Salmonella phage 7t3	GCA_006083215.1
AZU98308.1	000255	TelA	380	CPT_Munch_364	Salmonella phage Munch	GCA_004015485.1
QIG62676.1	000255	TelA	380	SEPL_063	Salmonella phage SE_PL	GCA_011067555.1
AQW88863.1	000255	TelA	379	BF_0338	Serratia phage BF	GCA_002619745.1
SOK59147.1	000255	TelA	378	g339	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58613.1	000255	TelA	378	g336	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000235	000255	TelA	374	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000185	000255	TelA	374	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AYD81386.1	000256	TerD	227	SEA_JUSTBECAUSE_231	Streptomyces phage JustBecause	GCA_003613775.1
QJD53790.1	000256	TerD	227	SEA_KELA_230	Streptomyces phage Kela	GCA_012934305.1
QBZ72115.1	000256	TerD	245	SEA_KRADAL_229	Streptomyces phage Kradal	GCA_004799925.1
AXH66377.1	000256	TerD	245	SEA_SATIS_228	Streptomyces phage Satis	GCA_003366315.1
AND75451.1	000257	TerD	203	ME3_290	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXQ69273.1	000257	TerD	209	CcrBL9_gp249c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88089.1	000257	TerD	218	CcrColossus_gp219	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68765.1	000257	TerD	232	CcrPW_gp226c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69830.1	000257	TerD	209	CcrSC_gp248c	Caulobacter phage CcrSC	GCA_003443315.1
CCH63465.1	000000	ROT+TerD	459	CP21_003	Campylobacter virus CP21	GCA_000902535.1
AND75445.1	000258	div-TerD-PPC	671	ME3_284	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AMM44929.1	000258	div-TerD-PPC	691	SP15_131	Bacillus phage SP-15	GCA_001754685.1
ARB13807.1	000258	div-TerD-PPC	676	Ccr10_gp277	Caulobacter phage Ccr10	GCA_002619445.1
ARB14152.1	000258	div-TerD-PPC	676	Ccr2_gp276	Caulobacter phage Ccr2	GCA_002619465.1
ARB14846.1	000258	div-TerD-PPC	676	Ccr29_gp290	Caulobacter phage Ccr29	GCA_002619485.1
ARB15186.1	000258	div-TerD-PPC	676	Ccr32_gp268	Caulobacter phage Ccr32	GCA_002619505.1
ARB15520.1	000258	div-TerD-PPC	676	Ccr34_gp278	Caulobacter phage Ccr34	GCA_002619525.1
ARB14495.1	000258	div-TerD-PPC	676	Ccr5_gp275	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68472.1	000258	div-TerD-PPC	677	CcrBL10_gp268	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87805.1	000258	div-TerD-PPC	676	CcrKarma_gp288	Caulobacter virus Karma	GCA_000901575.1
AFU87452.1	000258	div-TerD-PPC	676	CcrMagneto_gp282	Caulobacter virus Magneto	GCA_000903095.1
AFU86757.1	000258	div-TerD-PPC	677	CcrRogue_gp275	Caulobacter virus Rogue	GCA_000900555.1
AFU88597.1	000258	div-TerD-PPC	676	CcrSwift_gp279	Caulobacter virus Swift	GCA_000899655.1
AFU87105.1	000258	div-TerD-PPC	676	CbK_gp273	Caulobacter virus phiCbK	GCA_000900535.1
AXH72496.1	000258	div-TerD-PPC	668	-	Myoviridae sp.	GCA_003657725.1
AFH14890.1	000258	div-TerD-PPC	703	Lu11_0352	Pseudomonas phage Lu11	GCA_000897175.1
AGS81897.1	000258	div-TerD-PPC	538	PaBG_00013	Pseudomonas phage PaBG	GCA_000912555.1
BAG41503.1	000258	div-TerD-PPC	683	RSL1_ORF057	Ralstonia phage phiRSL1	GCA_000879455.1
ATA65517.1	000258	div-TerD-PPC	552	2050HW_00182	Serratia phage 2050HW	GCA_002628125.1
QDB71284.1	000258	div-TerD-PPC	552	CPT_Moabite_254	Serratia phage Moabite	GCA_006384735.1
ALY07177.1	000258	div-TerD-PPC	572	VmeM32_00191	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07176.1	000258	div-TerD-PPC	96	VmeM32_00190	Vibrio phage vB_VmeM-32	GCA_002608825.1
AND75453.1	000259	SIG+TerC	370	ME3_292	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXQ69274.1	000259	SIG+TerC	343	CcrBL9_gp250c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88090.1	000259	SIG+TerC	343	CcrColossus_gp220	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68766.1	000259	SIG+TerC	343	CcrPW_gp227c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69831.1	000259	SIG+TerC	343	CcrSC_gp249c	Caulobacter phage CcrSC	GCA_003443315.1
AYD81385.1	000260	Lowcomp-Cluster4692_1clades	52	SEA_JUSTBECAUSE_230	Streptomyces phage JustBecause	GCA_003613775.1
QJD53789.1	000260	Lowcomp-Cluster4692_1clades	52	SEA_KELA_229	Streptomyces phage Kela	GCA_012934305.1
QBZ72114.1	000260	Lowcomp-Cluster4692_1clades	50	SEA_KRADAL_228	Streptomyces phage Kradal	GCA_004799925.1
AXH66376.1	000260	Lowcomp-Cluster4692_1clades	50	SEA_SATIS_227	Streptomyces phage Satis	GCA_003366315.1
AYD81387.1	000261	Lowcomp+Bact_X	281	SEA_JUSTBECAUSE_232	Streptomyces phage JustBecause	GCA_003613775.1
QJD53791.1	000261	Lowcomp+Bact_X	281	SEA_KELA_231	Streptomyces phage Kela	GCA_012934305.1
QBZ72116.1	000261	Lowcomp+Bact_X	260	SEA_KRADAL_230	Streptomyces phage Kradal	GCA_004799925.1
AXH66378.1	000261	Lowcomp+Bact_X	260	SEA_SATIS_229	Streptomyces phage Satis	GCA_003366315.1
AND75447.1	000000	PRTase+PELOTA	355	ME3_286	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75449.1	000000	PRTase	375	ME3_288	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
CCH63570.1	000000	PRTase	137	CP21_108	Campylobacter virus CP21	GCA_000902535.1
ARM70967.1	000000	PRTase	120	phiC120_c262	Escherichia phage phiC120	GCA_002621185.1
QCG76202.1	000000	PRTase	144	EST35_0321	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AFF28112.1	000000	PRTase	268	PAU_114	Sphingomonas phage PAU	GCA_000902455.1
AND75448.1	000262	HAD	239	ME3_287	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AAX44672.1	000263	Phagesheath	1170	PSSM2_295	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12305.1	000263	Phagesheath	1170	PRTG_00152	Prochlorococcus phage P-SSM5	GCA_002991095.1
QDH83596.1	000264	Phagesheath	652	H1O15_gp192	Achromobacter phage Motura	GCA_006964305.1
APU01475.1	000264	Phagesheath	678	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28789.1	000264	Phagesheath	678	AP1_0082	Aeromonas phage AP1	GCA_014183365.1
ATI17422.1	000264	Phagesheath	678	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00174.1	000264	Phagesheath	678	HWB28_gp378	Aeromonas phage AS-zj	GCA_002627665.1
AUE22754.1	000264	Phagesheath	679	Ah1_00236	Aeromonas phage Ah1	GCA_002957415.1
QAX98471.1	000264	Phagesheath	679	ASfcp2_132	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97862.1	000264	Phagesheath	678	ASswx1_219	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01288.1	000264	Phagesheath	678	ASwh1_225	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39542.1	000264	Phagesheath	678	CC2_315	Aeromonas phage CC2	GCA_000903495.1
ADQ52932.1	000264	Phagesheath	679	PX29p213	Aeromonas phage PX29	GCA_000920195.1
ADM79855.1	000264	Phagesheath	679	phiAS5_ORF0012	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53098.1	000264	Phagesheath	678	65p088	Aeromonas virus 65	GCA_000893255.1
AAQ17879.1	000264	Phagesheath	679	18	Aeromonas virus Aeh1	GCA_000843245.1
ASV44714.1	000264	Phagesheath	1086	FDI40_gp132	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01210.1	000264	Phagesheath	987	AR9_g126	Bacillus phage AR9	GCA_001743835.1
AMM44842.1	000264	Phagesheath	494	SP15_043	Bacillus phage SP-15	GCA_001754685.1
ALN97881.1	000264	Phagesheath	986	Bp8pS_202	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99835.1	000264	Phagesheath	987	PBI_PBS1_13	Bacillus virus PBS1	GCA_002601325.1
QBX06491.1	000264	Phagesheath	665	BcepSaruman_078	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74458.1	000264	Phagesheath	665	BcepSauron_078	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63536.1	000264	Phagesheath	145	CP21_074	Campylobacter virus CP21	GCA_000902535.1
CCH63538.1	000264	Phagesheath	311	CP21_076	Campylobacter virus CP21	GCA_000902535.1
ANS05933.1	000264	Phagesheath	663	ABCD_0209	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64886.1	000264	Phagesheath	669	S13_087	Cronobacter phage S13	GCA_001503575.1
AFC21648.1	000264	Phagesheath	883	GAP32_198	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97224.1	000264	Phagesheath	669	E_216	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56905.1	000264	Phagesheath	932	CPXG_00102	Cyanophage P-RSM6	GCA_000906155.1
AJK27557.1	000264	Phagesheath	923	PTIM40_130	Cyanophage P-TIM40	GCA_001470935.1
AOO14307.1	000264	Phagesheath	759	Sn110110_113	Cyanophage S-RIM14	GCA_002599065.1
AOO14956.1	000264	Phagesheath	759	W1230910_110	Cyanophage S-RIM14	GCA_002599125.1
AMO43135.1	000264	Phagesheath	643	R1080702_126	Cyanophage S-RIM32	GCA_001754165.1
AMO43361.1	000264	Phagesheath	635	W270710_117	Cyanophage S-RIM44	GCA_002599145.1
AOO11605.1	000264	Phagesheath	635	ES420910_124	Cyanophage S-RIM44	GCA_002599165.1
AOO11833.1	000264	Phagesheath	635	Np050604_117	Cyanophage S-RIM44	GCA_002599185.1
AOO12070.1	000264	Phagesheath	635	Np200711_124	Cyanophage S-RIM44	GCA_002599205.1
AOO12306.1	000264	Phagesheath	635	Np420711_124	Cyanophage S-RIM44	GCA_002599225.1
AOO12534.1	000264	Phagesheath	635	Sn080709_117	Cyanophage S-RIM44	GCA_002599245.1
AOO12771.1	000264	Phagesheath	635	Sn130910_124	Cyanophage S-RIM44	GCA_002599265.1
AOO13000.1	000264	Phagesheath	635	W2100709_118	Cyanophage S-RIM44	GCA_002599285.1
AGH07455.1	000264	Phagesheath	806	CYVG_00011	Cyanophage S-SSM6a	GCA_002710385.1
AGG54496.1	000264	Phagesheath	800	CYWG_00212	Cyanophage S-SSM6b	GCA_002710425.1
AXG67178.1	000264	Phagesheath	561	AD1_134	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67201.1	000264	Phagesheath	558	AD1_157	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79928.1	000264	Phagesheath	561	JA11_123	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79952.1	000264	Phagesheath	558	JA11_147	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66527.1	000264	Phagesheath	561	JA13_124	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66551.1	000264	Phagesheath	558	JA13_148	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66852.1	000264	Phagesheath	561	JA29_126	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66876.1	000264	Phagesheath	558	JA29_150	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67497.1	000264	Phagesheath	561	JA33_123	Dickeya phage vB_DsoM_JA33	GCA_003568495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG67521.1	000264	Phagesheath	558	JA33_147	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08411.1	000264	Phagesheath	561	Alexandra_139	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08434.1	000264	Phagesheath	558	Alexandra_162	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58775.1	000264	Phagesheath	561	Y3_135	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58798.1	000264	Phagesheath	559	Y3_158	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28804.1	000264	Phagesheath	563	YOLOSWAG_133	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28636.1	000264	Phagesheath	561	YOLOSWAG_156	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14441.1	000264	Phagesheath	887	PBI_121Q_551	Escherichia phage 121Q	GCA_000926855.1
QAY00508.1	000264	Phagesheath	887	Ecwhy1_229	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34702.1	000264	Phagesheath	887	ACQ29_gp022	Escherichia phage PBECO4	GCA_001041035.1
BBM62113.1	000264	Phagesheath	887	EO157G_5240	Escherichia phage SP27	GCA_008033345.1
AXC36822.1	000264	Phagesheath	887	-	Escherichia phage UB	GCA_003341455.1
ARM70727.1	000264	Phagesheath	660	phiC120_c20	Escherichia phage phiC120	GCA_002621185.1
QBO61861.1	000264	Phagesheath	887	G17_00372	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13902.1	000264	Phagesheath	887	vBEcoMphAPEC6_gp277c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80426.1	000264	Phagesheath	887	PSLUR01_00449	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78742.1	000264	Phagesheath	664	RB43ORF220w	Escherichia virus RB43	GCA_000863505.1
AFA44314.1	000264	Phagesheath	888	RaK2_00041	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72827.1	000264	Phagesheath	975	-	Myoviridae sp.	GCA_003657725.1
QHJ79053.1	000264	Phagesheath	670	-	Myoviridae sp.	GCA_012593985.1
QIG65702.1	000264	Phagesheath	638	phiOC_p036	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43769.1	000264	Phagesheath	884	CBB_204	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38397.1	000264	Phagesheath	536	BN7874_216	Phage NCTB	GCA_900092385.1
SBV38453.1	000264	Phagesheath	546	BN7874_251	Phage NCTB	GCA_900092385.1
AGH26109.1	000264	Phagesheath	669	CPMG_00008	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44507.1	000264	Phagesheath	729	PSSM2_129	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12459.1	000264	Phagesheath	729	PRTG_00312	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93441.1	000264	Phagesheath	740	AVU42_gp102	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99219.1	000264	Phagesheath	635	Syn1_118	Prochlorococcus phage Syn1	GCA_000892495.1
AFH14592.1	000264	Phagesheath	530	Lu11_0061	Pseudomonas phage Lu11	GCA_000897175.1
AFH14613.1	000264	Phagesheath	546	Lu11_0081	Pseudomonas phage Lu11	GCA_000897175.1
QHJ85973.1	000264	Phagesheath	512	KKIINIFJ_00061	Pseudomonas phage PN05	GCA_009931935.1
QHJ86168.1	000264	Phagesheath	334	KKIINIFJ_00258	Pseudomonas phage PN05	GCA_009931935.1
AGS81960.1	000264	Phagesheath	528	PaBG_00076	Pseudomonas phage PaBG	GCA_000912555.1
AGS82088.2	000264	Phagesheath	547	PaBG_00213	Pseudomonas phage PaBG	GCA_000912555.1
QCG76076.1	000264	Phagesheath	879	EST35_0195	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41585.1	000264	Phagesheath	648	18	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44492.1	000264	Phagesheath	955	PBI_SCTP2_477	Salicola phage SCTP-2	GCA_002625545.1
QCW18917.1	000264	Phagesheath	885	7t3_0396	Salmonella phage 7t3	GCA_006083215.1
AZU98174.1	000264	Phagesheath	885	CPT_Munch_230	Salmonella phage Munch	GCA_004015485.1
QIG62810.1	000264	Phagesheath	885	SEPL_197	Salmonella phage SE_PL	GCA_011067555.1
AQW88725.1	000264	Phagesheath	883	BF_0200	Serratia phage BF	GCA_002619745.1
AGR47739.1	000264	Phagesheath	605	SmphiM12_107	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12988.1	000264	Phagesheath	605	PHIM19_81	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12628.1	000264	Phagesheath	605	PHIM7_80	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13359.1	000264	Phagesheath	605	PHIN3_95	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30610.1	000264	Phagesheath	731	Syn7803US37_133	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54882.1	000264	Phagesheath	728	b23_0268	Synechococcus phage B23	GCA_009745195.1
QGT54517.1	000264	Phagesheath	728	b3_0275	Synechococcus phage B3	GCA_009745215.1
ASR76171.1	000264	Phagesheath	742	PBI_BELLAMY_126	Synechococcus phage Bellamy	GCA_002627525.1
QCW22881.1	000264	Phagesheath	809	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50476.1	000264	Phagesheath	809	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59585.1	000264	Phagesheath	634	S330809_124	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59347.1	000264	Phagesheath	634	C440309_124	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59823.1	000264	Phagesheath	634	N231010_124	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70581.1	000264	Phagesheath	726	HOU04_gp182	Synechococcus phage S-T4	GCA_003443335.1
QJT70113.1	000264	Phagesheath	742	SynMITS9220M01_100	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64425.1	000264	Phagesheath	671	KVP40.0356	Vibrio phage KVP40	GCA_000843785.1
QIW90370.1	000264	Phagesheath	671	GCAPEGMB_00023	Vibrio phage V07	GCA_012361095.1
QIW91059.1	000264	Phagesheath	671	COHAPHLL_00196	Vibrio phage V09	GCA_012361135.1
QHJ74539.1	000264	Phagesheath	671	VH12019_00239	Vibrio phage VH1_2019	GCA_009931825.1
AGB06997.1	000264	Phagesheath	671	CF80_gp210	Vibrio phage VH7D	GCA_000914495.1
QBX06117.1	000264	Phagesheath	671	ValB1HC_163	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04544.1	000264	Phagesheath	648	ValB1MD_258	Vibrio phage ValB1MD	GCA_004138815.1
AJT61129.1	000264	Phagesheath	671	AVU32_gp288	Vibrio phage ValKK3	GCA_001501635.1
AGN30029.1	000264	Phagesheath	671	VPFG_00021	Vibrio phage nt-1	GCA_000910195.2
ALP46967.1	000264	Phagesheath	671	phiGrn1_0090	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47347.1	000264	Phagesheath	671	phiST2_0222	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54742.1	000264	Phagesheath	671	vBValMR10Z_202	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY06998.1	000264	Phagesheath	675	VmeM32_00002	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37588.1	000264	Phagesheath	671	pp2_356	Vibriophage phi-pp2	GCA_002630725.1
BBA65515.1	000264	Phagesheath	714	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96515.1	000264	Phagesheath	714	Xoosp13_329	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59007.1	000264	Phagesheath	883	g199	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58472.1	000264	Phagesheath	883	g195	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26173.1	000264	Phagesheath	590	g149	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000149	000264	Phagesheath	224	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QDB70415.1	000265	Phagesheath	736	CF8_0002	Aeromonas phage CF8	GCA_006384595.2
QDJ97423.1	000265	Phagesheath	733	D6_0264	Aeromonas phage D6	GCA_007051205.2
QDH47023.1	000265	Phagesheath	733	LAh10_171	Aeromonas phage LAh10	GCA_006863975.1
QDJ96760.1	000265	Phagesheath	732	PS1_0002	Aeromonas phage PS1	GCA_007051165.2
QFR59393.1	000265	Phagesheath	732	PS2_0002	Aeromonas phage PS2	GCA_009388305.2
AFO71440.1	000265	Phagesheath	679	CR5_220	Cronobacter phage CR5	GCA_000910235.1
QBZ70809.1	000265	Phagesheath	732	pETSU_228	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59908.1	000265	Phagesheath	681	SEGD1_261	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07654.1	000265	Phagesheath	679	DERBICUS_228	Erwinia phage Derbicus	GCA_004521655.1
AHI60329.1	000265	Phagesheath	695	Ea357_177	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49906.1	000265	Phagesheath	680	MACHINA_268	Erwinia phage Machina	GCA_002758035.1
AGX01797.1	000265	Phagesheath	693	CF95_gp075	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07288.1	000265	Phagesheath	708	REBECCA_181	Erwinia phage Rebecca	GCA_004521635.1
AXF51407.1	000265	Phagesheath	681	WELLINGTON_281	Erwinia phage Wellington	GCA_003344985.1
AFQ96719.1	000265	Phagesheath	680	G173_gp174	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48290.1	000265	Phagesheath	680	ASESINO_277	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85968.1	000265	Phagesheath	695	BOSOLAPHORUS_181	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48561.1	000265	Phagesheath	685	CAITLIN_266	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48839.1	000265	Phagesheath	685	CHRISDB_277	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52283.1	000265	Phagesheath	695	DM_185	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86287.1	000265	Phagesheath	695	DESERTFOX_180	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49078.1	000265	Phagesheath	679	EARLPHILLIPIV_229	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49349.1	000265	Phagesheath	680	HUXLEY_267	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03914.1	000265	Phagesheath	713	JOAD_1	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49632.1	000265	Phagesheath	681	KWAN_280	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86609.1	000265	Phagesheath	695	MADMEL_181	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86933.1	000265	Phagesheath	695	MORTIMER_184	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50177.1	000265	Phagesheath	680	PARSHIK_268	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50425.1	000265	Phagesheath	679	PHOBOS_235	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51960.1	000265	Phagesheath	695	RAY_179	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03669.1	000265	Phagesheath	713	RISINGSUN_1	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51644.1	000265	Phagesheath	695	SIMMY50_182	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64991.1	000265	Phagesheath	695	SPECIALG_181	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50701.1	000265	Phagesheath	680	STRATTON_276	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86097.1	000265	Phagesheath	681	ACEC001_2540	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64009.1	000265	Phagesheath	690	Goslar_00217	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72107.1	000265	Phagesheath	731	N1M2_244	Klebsiella phage N1M2	GCA_010092605.1
QGZ14546.1	000265	Phagesheath	712	HWC77_gp183	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24111.1	000265	Phagesheath	684	-	Proteus phage 10	GCA_014071245.1
ABY62864.1	000265	Phagesheath	700	201phi2-1p030	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27100.1	000265	Phagesheath	722	PPEV_gp006	Pseudomonas phage EL	GCA_000866825.1
ANM44797.1	000265	Phagesheath	695	KTN4_039	Pseudomonas phage KTN4	GCA_002607225.1
ARV77192.1	000265	Phagesheath	690	NOXIFER_21	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89439.1	000265	Phagesheath	733	OBP_002	Pseudomonas phage OBP	GCA_000896635.1
QBX32158.1	000265	Phagesheath	697	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76650.1	000265	Phagesheath	695	PHABIO_19	Pseudomonas phage Phabio	GCA_002624965.1
AEH03437.1	000265	Phagesheath	698	011	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02541.1	000265	Phagesheath	695	PSA21_11	Pseudomonas phage Psa21	GCA_004340405.1

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ATN94914.1	000265	Phagesheath	695	SL2_337	Pseudomonas phage SL2	GCA_002956015.1
QJB22676.1	000265	Phagesheath	695	fnug_33	Pseudomonas phage fnug	GCA_012837215.1
QEM41739.1	000265	Phagesheath	697	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82930.1	000265	Phagesheath	695	PHIKZ029	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19003.1	000265	Phagesheath	696	FDH28_gp029	Ralstonia phage RP12	GCA_002617345.1
BAW19290.1	000265	Phagesheath	696	-	Ralstonia phage RP31	GCA_002617365.1
BAS04822.2	000265	Phagesheath	705	AVU11_gp030	Ralstonia phage RSF1	GCA_001500875.1
BAQ02555.2	000265	Phagesheath	705	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20939.1	000265	Phagesheath	681	-	Salmonella phage JN03	GCA_014319805.1
AWN09097.1	000265	Phagesheath	680	MLDJOKPK_00184	Salmonella phage SPAsTU	GCA_003183805.1
AEP84089.1	000265	Phagesheath	681	SPN3US_0256	Salmonella phage SPN3US	GCA_001042275.1
QKE54489.1	000265	Phagesheath	694	ACSA002_1750	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65603.1	000265	Phagesheath	692	2050HW_00268	Serratia phage 2050HW	GCA_002628125.1
QDB71367.1	000265	Phagesheath	692	CPT_Moabite_337	Serratia phage Moabite	GCA_006384735.1
QFP93059.1	000265	Phagesheath	692	-	Serratia phage PCH45	GCA_009187865.1
QAU04188.1	000265	Phagesheath	712	HWC03_gp033	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23171.1	000265	Phagesheath	711	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80926.1	000265	Phagesheath	711	Aphrodite1_0171	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70778.1	000265	Phagesheath	682	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47558.1	000265	Phagesheath	711	HWC35_gp164	Vibrio phage USC-1	GCA_006864065.1
BAW98373.1	000265	Phagesheath	712	FDH33_gp164	Vibrio phage pTD1	GCA_002618825.1
AQT28122.1	000265	Phagesheath	680	pVa21_181	Vibrio phage pVa-21	GCA_002619305.1
QAX96740.1	000265	Phagesheath	678	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97059.1	000265	Phagesheath	678	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96105.1	000265	Phagesheath	678	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96423.1	000265	Phagesheath	678	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20997.1	000265	Phagesheath	676	-	Vibrio phage vB_pir03	GCA_014319855.1
AFF28088.1	000266	Phagesheath	926	PAU_90	Sphingomonas phage PAU	GCA_000902455.1
BBI90408.1	000266	Phagesheath	1032	HYO65_gp016	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90717.1	000266	Phagesheath	1032	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39260.1	000266	Phagesheath	944	BPT24_135	Tenacibaculum phage pT24	GCA_002611925.1
AYD79820.1	000267	Phagesheath	59	JA11_015	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66419.1	000267	Phagesheath	59	JA13_016	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66741.1	000267	Phagesheath	85	JA29_015	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67389.1	000267	Phagesheath	59	JA33_015	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67097.1	000268	Phagesheath	117	AD1_053	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08332.1	000268	Phagesheath	133	Alexandra_52	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
CCH63540.1	000000	Phagesheath+Toast-rack	526	CP21_078	Campylobacter virus CP21	GCA_000902535.1
AFH14646.1	000000	HTH_37	166	Lu11_0114	Pseudomonas phage Lu11	GCA_000897175.1
QDH83656.1	000000	Phagesheath	111	H1O15_gp094	Achromobacter phage Motura	GCA_006964305.1
ARW58696.1	000000	Phagesheath	112	Y3_056	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QHJ86147.1	000000	Phagesheath	384	KKIINIFJ_00236	Pseudomonas phage PN05	GCA_009931935.1
AGS82136.2	000000	Phagesheath	990	PaBG_00262	Pseudomonas phage PaBG	GCA_000912555.1
AGS82164.1	000000	Phagesheath	224	PaBG_00291	Pseudomonas phage PaBG	GCA_000912555.1
BAG41689.1	000000	Phagesheath	243	RSL1_ORF240	Ralstonia phage phiRSL1	GCA_000879455.1
AND75190.1	000000	Phagesheath	665	ME3_29	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83695.1	000000	Phagesheath	530	0305phi8-36p137	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83697.1	000000	Phagesheath	717	0305phi8-36p139	Bacillus phage 0305phi8-36	GCA_000871045.1
CCH63633.1	000000	Phagesheath	517	CP21_171	Campylobacter virus CP21	GCA_000902535.1
prevph1000000145	000000	Phagesheath	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000112	000000	Phagesheath	1254	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG63440.1	000269	Phagesheath	525	DAC16_211	Bacteroides phage DAC16	GCA_013387695.1
QIG63703.1	000269	Phagesheath	525	DAC19_216	Bacteroides phage DAC19	GCA_013387715.1
QIG63964.1	000269	Phagesheath	525	DAC20_215	Bacteroides phage DAC20	GCA_013387725.1
QIG64228.1	000269	Phagesheath	525	DAC22_218	Bacteroides phage DAC22	GCA_013387735.1
QIG64484.1	000269	Phagesheath	525	DAC23_210	Bacteroides phage DAC23	GCA_013387745.1
AEO93438.1	000000	SIG+Phagesheath	579	G_178	Bacillus virus G	GCA_000917535.1
QDH83592.1	000270	Phage_T4_gp19	169	H1O15_gp196	Achromobacter phage Motura	GCA_006964305.1
QDH83644.1	000270	Phage_T4_gp19	365	H1O15_gp144	Achromobacter phage Motura	GCA_006964305.1
APU01474.1	000270	Phage_T4_gp19	162	-	Aeromonas phage 65.2	GCA_002618145.1
APU01504.1	000270	Phage_T4_gp19	315	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28788.1	000270	Phage_T4_gp19	162	AP1_0081	Aeromonas phage AP1	GCA_014183365.1
QMV28987.1	000270	Phage_T4_gp19	313	AP1_0280	Aeromonas phage AP1	GCA_014183365.1
ATI17423.1	000270	Phage_T4_gp19	162	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17393.1	000270	Phage_T4_gp19	313	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00172.1	000270	Phage_T4_gp19	162	HWB28_gp380	Aeromonas phage AS-zj	GCA_002627665.1
ASU00201.1	000270	Phage_T4_gp19	313	HWB28_gp351	Aeromonas phage AS-zj	GCA_002627665.1
AUE22723.1	000270	Phage_T4_gp19	239	Ah1_00205	Aeromonas phage Ah1	GCA_002957415.1
AUE22755.1	000270	Phage_T4_gp19	162	Ah1_00237	Aeromonas phage Ah1	GCA_002957415.1
QAX98446.1	000270	Phage_T4_gp19	329	ASfcp2_103	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98472.1	000270	Phage_T4_gp19	162	ASfcp2_133	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97835.1	000270	Phage_T4_gp19	313	ASswx1_191	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97863.1	000270	Phage_T4_gp19	162	ASswx1_220	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01287.1	000270	Phage_T4_gp19	162	ASwh1_224	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01317.1	000270	Phage_T4_gp19	312	ASwh1_255	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39541.1	000270	Phage_T4_gp19	162	CC2_314	Aeromonas phage CC2	GCA_000903495.1
AFN39562.1	000270	Phage_T4_gp19	318	CC2_344	Aeromonas phage CC2	GCA_000903495.1
ADQ52933.1	000270	Phage_T4_gp19	162	PX29p214	Aeromonas phage PX29	GCA_000920195.1
ADQ52903.1	000270	Phage_T4_gp19	329	PX29p184	Aeromonas phage PX29	GCA_000920195.1
ADM79856.1	000270	Phage_T4_gp19	162	phiAS5_ORF0013	Aeromonas phage phiAS5	GCA_000887715.1
ADM80170.1	000270	Phage_T4_gp19	323	phiAS5_ORF0327	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53097.1	000270	Phage_T4_gp19	162	65p087	Aeromonas virus 65	GCA_000893255.1
ADQ53125.1	000270	Phage_T4_gp19	315	65p117	Aeromonas virus 65	GCA_000893255.1
AAQ17880.1	000270	Phage_T4_gp19	162	19	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17855.1	000270	Phage_T4_gp19	331	54	Aeromonas virus Aeh1	GCA_000843245.1
ASV44712.1	000270	Phage_T4_gp19	193	FDI40_gp127	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMM44843.1	000270	Phage_T4_gp19	175	SP15_044	Bacillus phage SP-15	GCA_001754685.1
QBX06489.1	000270	Phage_T4_gp19	167	BcepSaruman_076	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06665.1	000270	Phage_T4_gp19	269	BcepSaruman_252	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74456.1	000270	Phage_T4_gp19	167	BcepSauron_076	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74635.1	000270	Phage_T4_gp19	382	BcepSauron_255	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63529.1	000270	Phage_T4_gp19	196	CP21_067	Campylobacter virus CP21	GCA_000902535.1
CCH63562.1	000270	Phage_T4_gp19	250	CP21_100	Campylobacter virus CP21	GCA_000902535.1
CCH63648.1	000270	Phage_T4_gp19	252	CP21_186	Campylobacter virus CP21	GCA_000902535.1
ANS05979.1	000270	Phage_T4_gp19	287	ABCD_0106	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS06042.1	000270	Phage_T4_gp19	161	ABCD_0210	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64885.1	000270	Phage_T4_gp19	162	S13_086	Cronobacter phage S13	GCA_001503575.1
AIA64962.1	000270	Phage_T4_gp19	323	S13_163	Cronobacter phage S13	GCA_001503575.1
AFC21649.1	000270	Phage_T4_gp19	229	GAP32_199	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21650.1	000270	Phage_T4_gp19	258	GAP32_200	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97116.1	000270	Phage_T4_gp19	287	E_108	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97225.1	000270	Phage_T4_gp19	161	E_217	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56904.1	000270	Phage_T4_gp19	222	CPXG_00101	Cyanophage P-RSM6	GCA_000906155.1
AGH57011.1	000270	Phage_T4_gp19	260	CPXG_00208	Cyanophage P-RSM6	GCA_000906155.1
AJK27558.1	000270	Phage_T4_gp19	214	PTIM40_131	Cyanophage P-TIM40	GCA_001470935.1
AJK27444.1	000270	Phage_T4_gp19	276	PTIM40_17	Cyanophage P-TIM40	GCA_001470935.1
AOO14202.1	000270	Phage_T4_gp19	285	Sn110110_008	Cyanophage S-RIM14	GCA_002599065.1
AOO14308.1	000270	Phage_T4_gp19	235	Sn110110_114	Cyanophage S-RIM14	GCA_002599065.1
AOO14854.1	000270	Phage_T4_gp19	285	W1230910_008	Cyanophage S-RIM14	GCA_002599125.1
AOO14957.1	000270	Phage_T4_gp19	235	W1230910_111	Cyanophage S-RIM14	GCA_002599125.1
AMO43022.1	000270	Phage_T4_gp19	266	R1080702_007	Cyanophage S-RIM32	GCA_001754165.1
AMO43136.1	000270	Phage_T4_gp19	204	R1080702_127	Cyanophage S-RIM32	GCA_001754165.1
AMO43253.1	000270	Phage_T4_gp19	263	W270710_008	Cyanophage S-RIM44	GCA_002599145.1
AMO43362.1	000270	Phage_T4_gp19	205	W270710_118	Cyanophage S-RIM44	GCA_002599145.1
AOO11490.1	000270	Phage_T4_gp19	263	ES420910_008	Cyanophage S-RIM44	GCA_002599165.1
AOO11606.1	000270	Phage_T4_gp19	205	ES420910_125	Cyanophage S-RIM44	GCA_002599165.1
AOO11725.1	000270	Phage_T4_gp19	263	Np050604_008	Cyanophage S-RIM44	GCA_002599185.1
AOO11834.1	000270	Phage_T4_gp19	205	Np050604_118	Cyanophage S-RIM44	GCA_002599185.1
AOO11955.1	000270	Phage_T4_gp19	263	Np200711_008	Cyanophage S-RIM44	GCA_002599205.1
AOO12071.1	000270	Phage_T4_gp19	205	Np200711_125	Cyanophage S-RIM44	GCA_002599205.1
AOO12191.1	000270	Phage_T4_gp19	263	Np420711_008	Cyanophage S-RIM44	GCA_002599225.1
AOO12307.1	000270	Phage_T4_gp19	205	Np420711_125	Cyanophage S-RIM44	GCA_002599225.1
AOO12426.1	000270	Phage_T4_gp19	263	Sn080709_008	Cyanophage S-RIM44	GCA_002599245.1
AOO12535.1	000270	Phage_T4_gp19	205	Sn080709_118	Cyanophage S-RIM44	GCA_002599245.1
AOO12656.1	000270	Phage_T4_gp19	263	Sn130910_008	Cyanophage S-RIM44	GCA_002599265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12772.1	000270	Phage_T4_gp19	205	Sn130910_125	Cyanophage S-RIM44	GCA_002599265.1
AOO12891.1	000270	Phage_T4_gp19	263	W2100709_008	Cyanophage S-RIM44	GCA_002599285.1
AOO13001.1	000270	Phage_T4_gp19	205	W2100709_119	Cyanophage S-RIM44	GCA_002599285.1
AGH07456.1	000270	Phage_T4_gp19	227	CYVG_00012	Cyanophage S-SSM6a	GCA_002710385.1
AGH07635.1	000270	Phage_T4_gp19	324	CYVG_00192	Cyanophage S-SSM6a	GCA_002710385.1
AGG54362.1	000270	Phage_T4_gp19	318	CYWG_00078	Cyanophage S-SSM6b	GCA_002710425.1
AGG54495.1	000270	Phage_T4_gp19	196	CYWG_00211	Cyanophage S-SSM6b	GCA_002710425.1
AXG67175.1	000270	Phage_T4_gp19	170	AD1_131	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67177.1	000270	Phage_T4_gp19	170	AD1_133	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79925.1	000270	Phage_T4_gp19	170	JA11_120	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79927.1	000270	Phage_T4_gp19	171	JA11_122	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66524.1	000270	Phage_T4_gp19	170	JA13_121	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66526.1	000270	Phage_T4_gp19	171	JA13_123	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66849.1	000270	Phage_T4_gp19	170	JA29_123	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66851.1	000270	Phage_T4_gp19	171	JA29_125	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67494.1	000270	Phage_T4_gp19	170	JA33_120	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67496.1	000270	Phage_T4_gp19	171	JA33_122	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08408.1	000270	Phage_T4_gp19	170	Alexandra_136	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08410.1	000270	Phage_T4_gp19	169	Alexandra_138	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58772.1	000270	Phage_T4_gp19	170	Y3_132	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58774.1	000270	Phage_T4_gp19	169	Y3_134	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28611.1	000270	Phage_T4_gp19	171	YOLOSWAG_130	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28613.1	000270	Phage_T4_gp19	172	YOLOSWAG_132	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14442.1	000270	Phage_T4_gp19	228	PBI_121Q_552	Escherichia phage 121Q	GCA_000926855.1
AIT14443.1	000270	Phage_T4_gp19	258	PBI_121Q_553	Escherichia phage 121Q	GCA_000926855.1
QAY00505.1	000270	Phage_T4_gp19	258	Ecwhy1_226	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00506.1	000270	Phage_T4_gp19	228	Ecwhy1_227	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34701.1	000270	Phage_T4_gp19	228	ACQ29_gp021	Escherichia phage PBECO4	GCA_001041035.1
AGC34700.1	000270	Phage_T4_gp19	258	ACQ29_gp020	Escherichia phage PBECO4	GCA_001041035.1
BBM62115.1	000270	Phage_T4_gp19	228	EO157G_5260	Escherichia phage SP27	GCA_008033345.1
BBM62116.1	000270	Phage_T4_gp19	258	EO157G_5270	Escherichia phage SP27	GCA_008033345.1
AXC36821.1	000270	Phage_T4_gp19	228	-	Escherichia phage UB	GCA_003341455.1
AXC36820.1	000270	Phage_T4_gp19	258	-	Escherichia phage UB	GCA_003341455.1
ARM70728.1	000270	Phage_T4_gp19	163	phiC120_c21	Escherichia phage phiC120	GCA_002621185.1
ARM70754.1	000270	Phage_T4_gp19	320	phiC120_c48	Escherichia phage phiC120	GCA_002621185.1
QBO61859.1	000270	Phage_T4_gp19	258	G17_00370	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61860.1	000270	Phage_T4_gp19	228	G17_00371	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13899.1	000270	Phage_T4_gp19	258	vBEcoMphAPEC6_gp274c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13900.1	000270	Phage_T4_gp19	228	vBEcoMphAPEC6_gp275c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80427.1	000270	Phage_T4_gp19	228	PSLUR01_00450	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80428.1	000270	Phage_T4_gp19	258	PSLUR01_00451	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78743.1	000270	Phage_T4_gp19	161	RB43ORF221w	Escherichia virus RB43	GCA_000863505.1
AAX78628.1	000270	Phage_T4_gp19	287	RB43ORF106w	Escherichia virus RB43	GCA_000863505.1
AFA44315.1	000270	Phage_T4_gp19	227	RaK2_00042	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44316.1	000270	Phage_T4_gp19	257	RaK2_00043	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72758.1	000270	Phage_T4_gp19	198	-	Myoviridae sp.	GCA_003657725.1
QHJ79054.1	000270	Phage_T4_gp19	162	-	Myoviridae sp.	GCA_012593985.1
QHJ78972.1	000270	Phage_T4_gp19	323	-	Myoviridae sp.	GCA_012593985.1
QIG65701.1	000270	Phage_T4_gp19	179	phiOC_p035	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65735.1	000270	Phage_T4_gp19	180	phiOC_p070	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43770.1	000270	Phage_T4_gp19	229	CBB_205	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43771.1	000270	Phage_T4_gp19	258	CBB_206	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38389.1	000270	Phage_T4_gp19	156	BN7874_212	Phage NCTB	GCA_900092385.1
SBV38395.1	000270	Phage_T4_gp19	171	BN7874_215	Phage NCTB	GCA_900092385.1
AGH26108.1	000270	Phage_T4_gp19	204	CPMG_00007	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26198.1	000270	Phage_T4_gp19	228	CPMG_00097	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44391.1	000270	Phage_T4_gp19	277	PSSM2_013	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44508.1	000270	Phage_T4_gp19	195	PSSM2_130	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12458.1	000270	Phage_T4_gp19	195	PRTG_00311	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93442.1	000270	Phage_T4_gp19	209	AVU42_gp103	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93395.1	000270	Phage_T4_gp19	244	AVU42_gp009	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99111.1	000270	Phage_T4_gp19	296	Syn1_009	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99220.1	000270	Phage_T4_gp19	205	Syn1_119	Prochlorococcus phage Syn1	GCA_000892495.1
AFH14590.1	000270	Phage_T4_gp19	167	Lu11_0059	Pseudomonas phage Lu11	GCA_000897175.1
AFH14591.1	000270	Phage_T4_gp19	170	Lu11_0060	Pseudomonas phage Lu11	GCA_000897175.1
QHJ85971.1	000270	Phage_T4_gp19	240	KKIINIFJ_00059	Pseudomonas phage PN05	GCA_009931935.1
QHJ85972.1	000270	Phage_T4_gp19	170	KKIINIFJ_00060	Pseudomonas phage PN05	GCA_009931935.1
QHJ86167.1	000270	Phage_T4_gp19	380	KKIINIFJ_00257	Pseudomonas phage PN05	GCA_009931935.1
AGS81958.1	000270	Phage_T4_gp19	167	PaBG_00074	Pseudomonas phage PaBG	GCA_000912555.1
AGS81959.2	000270	Phage_T4_gp19	168	PaBG_00075	Pseudomonas phage PaBG	GCA_000912555.1
QCG76078.1	000270	Phage_T4_gp19	206	EST35_0197	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41587.1	000270	Phage_T4_gp19	169	RSL1_ORF142	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41657.1	000270	Phage_T4_gp19	372	RSL1_ORF208	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44462.1	000270	Phage_T4_gp19	215	PBI_SCTP2_447	Salicola phage SCTP-2	GCA_002625545.1
ASV44463.1	000270	Phage_T4_gp19	260	PBI_SCTP2_448	Salicola phage SCTP-2	GCA_002625545.1
ASV44464.1	000270	Phage_T4_gp19	259	PBI_SCTP2_449	Salicola phage SCTP-2	GCA_002625545.1
QCW18918.1	000270	Phage_T4_gp19	228	7t3_0397	Salmonella phage 7t3	GCA_006083215.1
QCW18919.1	000270	Phage_T4_gp19	257	7t3_0398	Salmonella phage 7t3	GCA_006083215.1
AZU98175.1	000270	Phage_T4_gp19	228	CPT_Munch_231	Salmonella phage Munch	GCA_004015485.1
AZU98176.1	000270	Phage_T4_gp19	257	CPT_Munch_232	Salmonella phage Munch	GCA_004015485.1
QIG62808.1	000270	Phage_T4_gp19	257	SEPL_195	Salmonella phage SE_PL	GCA_011067555.1
QIG62809.1	000270	Phage_T4_gp19	228	SEPL_196	Salmonella phage SE_PL	GCA_011067555.1
AQW88726.1	000270	Phage_T4_gp19	156	BF_0201	Serratia phage BF	GCA_002619745.1
AQW88727.1	000270	Phage_T4_gp19	257	BF_0202	Serratia phage BF	GCA_002619745.1
AGR47706.1	000270	Phage_T4_gp19	171	SmphiM12_074	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47792.1	000270	Phage_T4_gp19	261	SmphiM12_160	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13011.1	000270	Phage_T4_gp19	261	PHIM19_105	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12962.1	000270	Phage_T4_gp19	171	PHIM19_55	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12651.1	000270	Phage_T4_gp19	261	PHIM7_104	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12602.1	000270	Phage_T4_gp19	171	PHIM7_54	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13383.1	000270	Phage_T4_gp19	261	PHIN3_118	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13335.1	000270	Phage_T4_gp19	171	PHIN3_70	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30611.1	000270	Phage_T4_gp19	198	Syn7803US37_134	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30482.1	000270	Phage_T4_gp19	248	Syn7803US37_5	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54634.1	000270	Phage_T4_gp19	233	b23_0006	Synechococcus phage B23	GCA_009745195.1
QGT54883.1	000270	Phage_T4_gp19	207	b23_0269	Synechococcus phage B23	GCA_009745195.1
QGT54264.1	000270	Phage_T4_gp19	233	b3_0006	Synechococcus phage B3	GCA_009745215.1
QGT54518.1	000270	Phage_T4_gp19	207	b3_0276	Synechococcus phage B3	GCA_009745215.1
ASR76172.1	000270	Phage_T4_gp19	209	PBI_BELLAMY_127	Synechococcus phage Bellamy	GCA_002627525.1
ASR76056.1	000270	Phage_T4_gp19	285	PBI_BELLAMY_9	Synechococcus phage Bellamy	GCA_002627525.1
QCW22882.1	000270	Phage_T4_gp19	210	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22923.1	000270	Phage_T4_gp19	229	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50475.1	000270	Phage_T4_gp19	210	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50638.1	000270	Phage_T4_gp19	229	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59468.1	000270	Phage_T4_gp19	216	S330809_007	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59586.1	000270	Phage_T4_gp19	195	S330809_125	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59230.1	000270	Phage_T4_gp19	216	C440309_007	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59348.1	000270	Phage_T4_gp19	195	C440309_125	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59706.1	000270	Phage_T4_gp19	216	N231010_007	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59824.1	000270	Phage_T4_gp19	195	N231010_125	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70580.1	000270	Phage_T4_gp19	198	HOU04_gp181	Synechococcus phage S-T4	GCA_003443335.1
AXQ70444.1	000270	Phage_T4_gp19	277	HOU04_gp045	Synechococcus phage S-T4	GCA_003443335.1
QJT70024.1	000270	Phage_T4_gp19	266	SynMITS9220M01_008	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70114.1	000270	Phage_T4_gp19	196	SynMITS9220M01_101	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64426.1	000270	Phage_T4_gp19	166	KVP40.0357	Vibrio phage KVP40	GCA_000843785.1
AAQ64399.1	000270	Phage_T4_gp19	248	KVP40.0329	Vibrio phage KVP40	GCA_000843785.1
QIW90371.1	000270	Phage_T4_gp19	166	GCAPEGMB_00024	Vibrio phage V07	GCA_012361095.1
QIW90711.1	000270	Phage_T4_gp19	248	GCAPEGMB_00392	Vibrio phage V07	GCA_012361095.1
QIW91058.1	000270	Phage_T4_gp19	166	COHAPHLL_00195	Vibrio phage V09	GCA_012361135.1
QIW91086.1	000270	Phage_T4_gp19	248	COHAPHLL_00223	Vibrio phage V09	GCA_012361135.1
QHJ74511.1	000270	Phage_T4_gp19	248	VH12019_00211	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74540.1	000270	Phage_T4_gp19	166	VH12019_00240	Vibrio phage VH1_2019	GCA_009931825.1
AGB06998.1	000270	Phage_T4_gp19	166	CF80_gp211	Vibrio phage VH7D	GCA_000914495.1
QBX06116.1	000270	Phage_T4_gp19	166	ValB1HC_162	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06144.1	000270	Phage_T4_gp19	248	ValB1HC_190	Vibrio phage ValB1 HC	GCA_004771355.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAU04546.1	000270	Phage_T4_gp19	258	ValB1MD_260	Vibrio phage ValB1MD	GCA_004138815.1
QAU04547.1	000270	Phage_T4_gp19	250	ValB1MD_261	Vibrio phage ValB1MD	GCA_004138815.1
QAU04548.1	000270	Phage_T4_gp19	193	ValB1MD_262	Vibrio phage ValB1MD	GCA_004138815.1
AJT61128.1	000270	Phage_T4_gp19	166	AVU32_gp287	Vibrio phage ValKK3	GCA_001501635.1
AJT61156.1	000270	Phage_T4_gp19	248	AVU32_gp315	Vibrio phage ValKK3	GCA_001501635.1
AGN30030.1	000270	Phage_T4_gp19	166	VPFG_00022	Vibrio phage nt-1	GCA_000910195.2
AGN30380.1	000270	Phage_T4_gp19	248	VPFG_00383	Vibrio phage nt-1	GCA_000910195.2
ALP47043.1	000270	Phage_T4_gp19	248	phiGrn1_0063	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47103.1	000270	Phage_T4_gp19	166	phiGrn1_0091	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47421.1	000270	Phage_T4_gp19	248	phiST2_0195	Vibrio phage phi-ST2	GCA_002757135.1
ALP47486.1	000270	Phage_T4_gp19	166	phiST2_0223	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54741.1	000270	Phage_T4_gp19	166	vBValMR10Z_201	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54769.1	000270	Phage_T4_gp19	248	vBValMR10Z_229	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07000.1	000270	Phage_T4_gp19	162	VmeM32_00004	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07100.1	000270	Phage_T4_gp19	302	VmeM32_00111	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37561.1	000270	Phage_T4_gp19	248	pp2_329	Vibriophage phi-pp2	GCA_002630725.1
AFN37589.1	000270	Phage_T4_gp19	166	pp2_357	Vibriophage phi-pp2	GCA_002630725.1
BBA65499.1	000270	Phage_T4_gp19	194	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96507.1	000270	Phage_T4_gp19	194	Xoosp13_321	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59009.1	000270	Phage_T4_gp19	229	g201	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59010.1	000270	Phage_T4_gp19	257	g202	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58474.1	000270	Phage_T4_gp19	229	g197	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58475.1	000270	Phage_T4_gp19	257	g198	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01507.1	000271	Phage_T4_gp19	189	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29055.1	000271	Phage_T4_gp19	185	AP1_0348	Aeromonas phage AP1	GCA_014183365.1
ATI17390.1	000271	Phage_T4_gp19	185	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00203.1	000271	Phage_T4_gp19	187	HWB28_gp349	Aeromonas phage AS-zj	GCA_002627665.1
AUE22719.1	000271	Phage_T4_gp19	189	Ah1_00201	Aeromonas phage Ah1	GCA_002957415.1
QAX98443.1	000271	Phage_T4_gp19	189	ASfcp2_100	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97832.1	000271	Phage_T4_gp19	185	ASswx1_188	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01320.1	000271	Phage_T4_gp19	192	ASwh1_258	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39564.1	000271	Phage_T4_gp19	185	CC2_347	Aeromonas phage CC2	GCA_000903495.1
ADQ52899.1	000271	Phage_T4_gp19	189	PX29p180	Aeromonas phage PX29	GCA_000920195.1
ADM80166.1	000271	Phage_T4_gp19	190	phiAS5_ORF0323	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53129.1	000271	Phage_T4_gp19	189	65p121	Aeromonas virus 65	GCA_000893255.1
AAQ17852.1	000271	Phage_T4_gp19	189	3	Aeromonas virus Aeh1	GCA_000843245.1
ANS06025.1	000271	Phage_T4_gp19	179	ABCD_0189	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64965.1	000271	Phage_T4_gp19	194	S13_166	Cronobacter phage S13	GCA_001503575.1
AON97203.1	000271	Phage_T4_gp19	179	E_195	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56889.1	000271	Phage_T4_gp19	200	CPXG_00086	Cyanophage P-RSM6	GCA_000906155.1
AJK27568.1	000271	Phage_T4_gp19	190	PTIM40_141	Cyanophage P-TIM40	GCA_001470935.1
AOO14314.1	000271	Phage_T4_gp19	188	Sn110110_120	Cyanophage S-RIM14	GCA_002599065.1
AOO14963.1	000271	Phage_T4_gp19	188	W1230910_117	Cyanophage S-RIM14	GCA_002599125.1
AMO43146.1	000271	Phage_T4_gp19	168	R1080702_137	Cyanophage S-RIM32	GCA_001754165.1
AMO43370.1	000271	Phage_T4_gp19	168	W270710_126	Cyanophage S-RIM44	GCA_002599145.1
AOO11614.1	000271	Phage_T4_gp19	168	ES420910_133	Cyanophage S-RIM44	GCA_002599165.1
AOO11842.1	000271	Phage_T4_gp19	168	Np050604_126	Cyanophage S-RIM44	GCA_002599185.1
AOO12079.1	000271	Phage_T4_gp19	168	Np200711_133	Cyanophage S-RIM44	GCA_002599205.1
AOO12315.1	000271	Phage_T4_gp19	168	Np420711_133	Cyanophage S-RIM44	GCA_002599225.1
AOO12543.1	000271	Phage_T4_gp19	168	Sn080709_126	Cyanophage S-RIM44	GCA_002599245.1
AOO12780.1	000271	Phage_T4_gp19	168	Sn130910_133	Cyanophage S-RIM44	GCA_002599265.1
AOO13009.1	000271	Phage_T4_gp19	168	W2100709_127	Cyanophage S-RIM44	GCA_002599285.1
AGH07463.1	000271	Phage_T4_gp19	186	CYVG_00019	Cyanophage S-SSM6a	GCA_002710385.1
AGG54488.1	000271	Phage_T4_gp19	190	CYWG_00204	Cyanophage S-SSM6b	GCA_002710425.1
ARM70973.1	000271	Phage_T4_gp19	194	phiC120_c268	Escherichia phage phiC120	GCA_002621185.1
AAX78721.1	000271	Phage_T4_gp19	177	RB43ORF199c	Escherichia virus RB43	GCA_000863505.1
QHJ78969.1	000271	Phage_T4_gp19	193	-	Myoviridae sp.	GCA_012593985.1
QIG65694.1	000271	Phage_T4_gp19	180	phiOC_p028	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26315.1	000271	Phage_T4_gp19	185	CPMG_00216	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44515.1	000271	Phage_T4_gp19	177	PSSM2_137	Prochlorococcus phage P-SSM2	GCA_000859585.1
AIR93450.1	000271	Phage_T4_gp19	183	AVU42_gp112	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99228.1	000271	Phage_T4_gp19	168	Syn1_127	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47686.1	000271	Phage_T4_gp19	165	SmphiM12_054	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12948.1	000271	Phage_T4_gp19	165	PHIM19_41	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12588.1	000271	Phage_T4_gp19	165	PHIM7_40	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13322.1	000271	Phage_T4_gp19	165	PHIN3_57	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30621.1	000271	Phage_T4_gp19	193	Syn7803US37_144	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54895.1	000271	Phage_T4_gp19	190	b23_0282	Synechococcus phage B23	GCA_009745195.1
QGT54530.1	000271	Phage_T4_gp19	190	b3_0289	Synechococcus phage B3	GCA_009745215.1
ASR76180.1	000271	Phage_T4_gp19	195	PBI_BELLAMY_135	Synechococcus phage Bellamy	GCA_002627525.1
QCW22891.1	000271	Phage_T4_gp19	182	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50657.1	000271	Phage_T4_gp19	182	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59595.1	000271	Phage_T4_gp19	173	S330809_134	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59357.1	000271	Phage_T4_gp19	173	C440309_134	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59833.1	000271	Phage_T4_gp19	173	N231010_134	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70573.1	000271	Phage_T4_gp19	183	HOU04_gp174	Synechococcus phage S-T4	GCA_003443335.1
QJT70122.1	000271	Phage_T4_gp19	182	SynMITS9220M01_109	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64395.1	000271	Phage_T4_gp19	177	KVP40.0325	Vibrio phage KVP40	GCA_000843785.1
QIW90707.1	000271	Phage_T4_gp19	177	GCAPEGMB_00388	Vibrio phage V07	GCA_012361095.1
QIW91090.1	000271	Phage_T4_gp19	177	COHAPHLL_00227	Vibrio phage V09	GCA_012361135.1
QHJ74507.1	000271	Phage_T4_gp19	177	VH12019_00207	Vibrio phage VH1_2019	GCA_009931825.1
QBX06148.1	000271	Phage_T4_gp19	178	ValB1HC_194	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61160.1	000271	Phage_T4_gp19	178	AVU32_gp319	Vibrio phage ValKK3	GCA_001501635.1
AGN30376.1	000271	Phage_T4_gp19	179	VPFG_00379	Vibrio phage nt-1	GCA_000910195.2
ALP47091.1	000271	Phage_T4_gp19	178	phiGrn1_0059	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47471.1	000271	Phage_T4_gp19	178	phiST2_0191	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54773.1	000271	Phage_T4_gp19	178	vBValMR10Z_233	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07107.1	000271	Phage_T4_gp19	151	VmeM32_00120	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37557.1	000271	Phage_T4_gp19	177	pp2_325	Vibriophage phi-pp2	GCA_002630725.1
AUZ94920.1	000272	Phage_T4_gp19	328	FDI40_gp126	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21651.1	000272	Phage_T4_gp19	364	GAP32_201	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14444.1	000272	Phage_T4_gp19	364	PBI_121Q_554	Escherichia phage 121Q	GCA_000926855.1
QAY00504.1	000272	Phage_T4_gp19	364	Ecwhy1_225	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34699.1	000272	Phage_T4_gp19	364	ACQ29_gp019	Escherichia phage PBECO4	GCA_001041035.1
BBM62117.1	000272	Phage_T4_gp19	364	EO157G_5280	Escherichia phage SP27	GCA_008033345.1
AXC36819.1	000272	Phage_T4_gp19	364	-	Escherichia phage UB	GCA_003341455.1
QBO61858.1	000272	Phage_T4_gp19	364	G17_00369	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13898.1	000272	Phage_T4_gp19	364	vBEcoMphAPEC6_gp273c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80429.1	000272	Phage_T4_gp19	364	PSLUR01_00452	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44317.1	000272	Phage_T4_gp19	364	RaK2_00044	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72759.1	000272	Phage_T4_gp19	414	-	Myoviridae sp.	GCA_003657725.1
AMM43772.1	000272	Phage_T4_gp19	364	CBB_207	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76079.1	000272	Phage_T4_gp19	492	EST35_0198	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18920.1	000272	Phage_T4_gp19	363	7t3_0399	Salmonella phage 7t3	GCA_006083215.1
AZU98177.1	000272	Phage_T4_gp19	363	CPT_Munch_233	Salmonella phage Munch	GCA_004015485.1
QIG62807.1	000272	Phage_T4_gp19	363	SEPL_194	Salmonella phage SE_PL	GCA_011067555.1
AQW88728.1	000272	Phage_T4_gp19	364	BF_0203	Serratia phage BF	GCA_002619745.1
SOK59011.1	000272	Phage_T4_gp19	364	g203	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58476.1	000272	Phage_T4_gp19	364	g199	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFF28090.1	000273	Phage_T4_gp19	184	PAU_92	Sphingomonas phage PAU	GCA_000902455.1
BBI90411.1	000273	Phage_T4_gp19	180	HYO65_gp019	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90719.1	000273	Phage_T4_gp19	180	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39258.1	000273	Phage_T4_gp19	180	BPT24_133	Tenacibaculum phage pT24	GCA_002611925.1
prevph1000000196	000273	Phage_T4_gp19	209	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000159	000273	Phage_T4_gp19	209	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBA65497.1	000274	Phage_T4_gp19	259	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96505.1	000274	Phage_T4_gp19	242	Xoosp13_319	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QAU04558.1	000275	Phage_T4_gp19	170	ValB1MD_275	Vibrio phage ValB1MD	GCA_004138815.1
CCH63685.1	000275	Phage_T4_gp19	229	CP21_223	Campylobacter virus CP21	GCA_000902535.1
CCH63579.1	000276	Phage_T4_gp19	167	CP21_117	Campylobacter virus CP21	GCA_000902535.1
QAU04569.1	000276	Phage_T4_gp19	154	ValB1MD_289	Vibrio phage ValB1MD	GCA_004138815.1
AMS01297.1	000277	Phage_T4_gp19	310	AR9_g213	Bacillus phage AR9	GCA_001743835.1
ALN97948.1	000277	Phage_T4_gp19	312	Bp8pS_269	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99926.1	000277	Phage_T4_gp19	310	PBI_PBS1_104	Bacillus virus PBS1	GCA_002601325.1
CCE26231.1	000277	Phage_T4_gp19	336	g208	Yersinia phage phiR1-37	GCA_000895615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFF28125.1	000278	Phage_T4_gp19	223	PAU_127	Sphingomonas phage PAU	GCA_000902455.1
BBI90636.1	000278	Phage_T4_gp19	196	HYO65_gp244	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90943.1	000278	Phage_T4_gp19	196	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39299.1	000278	Phage_T4_gp19	197	BPT24_173	Tenacibaculum phage pT24	GCA_002611925.1
AUE22722.1	000000	Phage_T4_gp19	80	Ah1_00204	Aeromonas phage Ah1	GCA_002957415.1
QHJ86161.1	000000	Phage_T4_gp19	167	KKIINIFJ_00251	Pseudomonas phage PN05	GCA_009931935.1
ASV44465.1	000000	Phage_T4_gp19	408	PBI_SCTP2_450	Salicola phage SCTP-2	GCA_002625545.1
prev15ph1000000424	000000	Phage_T4_gp19	252	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ95009.1	000279	THG1+THG1-C	262	FDI40_gp227	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93637.1	000279	THG1+THG1-C	246	G_378	Bacillus virus G	GCA_000917535.1
QBX06745.1	000279	THG1+THG1-C	283	BcepSaruman_332	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74714.1	000279	THG1+THG1-C	272	BcepSauron_334	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ69361.1	000279	THG1+THG1-C	282	CcrBL9_gp337	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88170.1	000279	THG1+THG1-C	279	CcrColossus_gp300	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68847.1	000279	THG1+THG1-C	279	CcrPW_gp308	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69921.1	000279	THG1+THG1-C	282	CcrSC_gp339	Caulobacter phage CcrSC	GCA_003443315.1
AFC21597.1	000279	THG1+THG1-C	259	GAP32_147	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXH72867.1	000279	THG1+THG1-C	290	-	Myoviridae sp.	GCA_003657725.1
AMM43717.1	000279	THG1+THG1-C	259	CBB_152	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ABY63144.1	000279	THG1+THG1-C	270	201phi2-1p319	Pseudomonas phage 201phi2-1	GCA_000875305.1
ASV44433.1	000279	THG1+THG1-C	246	PBI_SCTP2_418	Salicola phage SCTP-2	GCA_002625545.1
AQW88671.1	000279	THG1+THG1-C	256	BF_0146	Serratia phage BF	GCA_002619745.1
AGR47633.1	000279	THG1+THG1-C	260	SmphiM12_001	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13268.1	000279	THG1+THG1-C	260	PHIN3_1	Sinorhizobium phage phiN3	GCA_001501175.1
BBA65274.1	000279	THG1+THG1-C	249	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65733.1	000279	THG1+THG1-C	249	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96314.1	000279	THG1+THG1-C	247	Xoosp13_127	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58953.1	000279	THG1+THG1-C	251	g145	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58419.1	000279	THG1+THG1-C	251	g142	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000248	000279	THG1+THG1-C	271	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000196	000279	THG1+THG1-C	271	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASV44724.1	000280	Thy1	316	FDI40_gp246	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMM44808.1	000280	Thy1	278	SP15_009	Bacillus phage SP-15	GCA_001754685.1
AGH56804.1	000280	Thy1	91	CPXG_00001	Cyanophage P-RSM6	GCA_000906155.1
AGH57023.1	000280	Thy1	234	CPXG_00220	Cyanophage P-RSM6	GCA_000906155.1
AJK27648.1	000280	Thy1	229	PTIM40_235	Cyanophage P-TIM40	GCA_001470935.1
AOO14410.1	000280	Thy1	233	Sn110110_217	Cyanophage S-RIM14	GCA_002599065.1
AOO15059.1	000280	Thy1	233	W1230910_214	Cyanophage S-RIM14	GCA_002599125.1
AMO43240.1	000280	Thy1	211	R1080702_235	Cyanophage S-RIM32	GCA_001754165.1
AMO43471.1	000280	Thy1	215	W270710_232	Cyanophage S-RIM44	GCA_002599145.1
AOO11711.1	000280	Thy1	212	ES420910_234	Cyanophage S-RIM44	GCA_002599165.1
AOO11943.1	000280	Thy1	215	Np050604_232	Cyanophage S-RIM44	GCA_002599185.1
AOO12177.1	000280	Thy1	212	Np200711_235	Cyanophage S-RIM44	GCA_002599205.1
AOO12412.1	000280	Thy1	216	Np420711_234	Cyanophage S-RIM44	GCA_002599225.1
AOO12644.1	000280	Thy1	215	Sn080709_232	Cyanophage S-RIM44	GCA_002599245.1
AOO12877.1	000280	Thy1	212	Sn130910_234	Cyanophage S-RIM44	GCA_002599265.1
AOO13110.1	000280	Thy1	215	W2100709_233	Cyanophage S-RIM44	GCA_002599285.1
AGH07623.1	000280	Thy1	237	CYVG_00180	Cyanophage S-SSM6a	GCA_002710385.1
AGG54378.1	000280	Thy1	232	CYWG_00094	Cyanophage S-SSM6b	GCA_002710425.1
QIG57858.1	000280	Thy1	252	SEA_PAULODIABOLI_141	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG66025.1	000280	Thy1	285	phiOC_p383	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26218.1	000280	Thy1	212	CPMG_00117	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44700.1	000280	Thy1	211	PSSM2_322	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12275.1	000280	Thy1	211	PRTG_00122	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93578.1	000280	Thy1	213	AVU42_gp242	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99332.1	000280	Thy1	228	Syn1_236	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76312.1	000280	Thy1	214	PBI_BELLAMY_276	Synechococcus phage Bellamy	GCA_002627525.1
QCW23061.1	000280	Thy1	211	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59693.1	000280	Thy1	216	S330809_232	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59455.1	000280	Thy1	158	C440309_232	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59930.1	000280	Thy1	158	N231010_231	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70455.1	000280	Thy1	211	HOU04_gp056	Synechococcus phage S-T4	GCA_003443335.1
QJT70257.1	000280	Thy1	214	SynMITS9220M01_251	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QBX06650.1	000281	Thy1	311	BcepSaruman_237	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74618.1	000281	Thy1	306	BcepSauron_238	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13642.1	000281	Thy1	319	Ccr10_gp113c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13987.1	000281	Thy1	319	Ccr2_gp112c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14675.1	000281	Thy1	319	Ccr29_gp119	Caulobacter phage Ccr29	GCA_002619485.1
ARB15030.1	000281	Thy1	319	Ccr32_gp112	Caulobacter phage Ccr32	GCA_002619505.1
ARB15362.1	000281	Thy1	319	Ccr34_gp120	Caulobacter phage Ccr34	GCA_002619525.1
ARB14331.1	000281	Thy1	319	Ccr5_gp113c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68311.1	000281	Thy1	311	CcrBL10_gp107c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69221.1	000281	Thy1	309	CcrBL9_gp197	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88020.1	000281	Thy1	323	CcrColossus_gp150	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68697.1	000281	Thy1	323	CcrPW_gp158c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69775.1	000281	Thy1	309	CcrSC_gp193	Caulobacter phage CcrSC	GCA_003443315.1
AFU87634.1	000281	Thy1	319	CcrKarma_gp117	Caulobacter virus Karma	GCA_000901575.1
AFU87283.1	000281	Thy1	319	CcrMagneto_gp113	Caulobacter virus Magneto	GCA_000903095.1
AFU86595.1	000281	Thy1	311	CcrRogue_gp113	Caulobacter virus Rogue	GCA_000900555.1
AFU88430.1	000281	Thy1	319	CcrSwift_gp112	Caulobacter virus Swift	GCA_000899655.1
AFU86948.1	000281	Thy1	319	CbK_gp116	Caulobacter virus phiCbK	GCA_000900535.1
AXH71010.1	000282	Thy1	480	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96891.1	000282	Thy1	461	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97196.1	000282	Thy1	461	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96255.1	000282	Thy1	461	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96573.1	000282	Thy1	461	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63487.1	000283	Thy1	270	DAC16_258	Bacteroides phage DAC16	GCA_013387695.1
QIG63749.1	000283	Thy1	270	DAC19_262	Bacteroides phage DAC19	GCA_013387715.1
QIG64010.1	000283	Thy1	270	DAC20_261	Bacteroides phage DAC20	GCA_013387725.1
QIG64274.1	000283	Thy1	270	DAC22_264	Bacteroides phage DAC22	GCA_013387735.1
QIG64531.1	000283	Thy1	270	DAC23_257	Bacteroides phage DAC23	GCA_013387745.1
AYD81175.1	000284	Thy1	260	SEA_JUSTBECAUSE_6	Streptomyces phage JustBecause	GCA_003613775.1
QJD53577.1	000284	Thy1	260	SEA_KELA_6	Streptomyces phage Kela	GCA_012934305.1
QBZ71905.1	000284	Thy1	262	SEA_KRADAL_6	Streptomyces phage Kradal	GCA_004799925.1
AXH66167.1	000284	Thy1	262	SEA_SATIS_6	Streptomyces phage Satis	GCA_003366315.1
AIX30763.1	000285	Thy1	250	Syn7803US37_286	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54986.1	000285	Thy1	250	b23_0380	Synechococcus phage B23	GCA_009745195.1
QGT54621.1	000285	Thy1	250	b3_0386	Synechococcus phage B3	GCA_009745215.1
CCH63550.1	000000	SIG+Thy1	211	CP21_088	Campylobacter virus CP21	GCA_000902535.1
AMM44928.1	000000	SIG+Thy1	413	SP15_130	Bacillus phage SP-15	GCA_001754685.1
QIW90838.1	000000	Thy1	65	GCAPEGMB_00523	Vibrio phage V07	GCA_012361095.1
APU01720.1	000286	DHFR	174	-	Aeromonas phage 65.2	GCA_002618145.1
SOK59119.1	000286	DHFR	173	g311	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QDJ96372.1	000286	DHFR	176	Xoosp13_185	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QMV28746.1	000286	DHFR	177	AP1_0028	Aeromonas phage AP1	GCA_014183365.1
ATI17575.1	000286	DHFR	181	-	Aeromonas phage AS-szw	GCA_002743635.1
BBA65334.1	000286	DHFR	184	-	Xanthomonas phage XacN1	GCA_003173815.1
ASU00421.1	000286	DHFR	181	HWB28_gp131	Aeromonas phage AS-zj	GCA_002627665.1
AFN37240.1	000286	DHFR	181	pp2_006	Vibriophage phi-pp2	GCA_002630725.1
AUE22847.1	000286	DHFR	172	Ah1_00329	Aeromonas phage Ah1	GCA_002957415.1
QNI21156.1	000286	DHFR	243	-	Vibrio phage vB_pir03	GCA_014319855.1
ALY07133.1	000286	DHFR	191	VmeM32_00146	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX98559.1	000286	DHFR	173	ASfcp2_225	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98015.1	000286	DHFR	181	ASswx1_375	Aeromonas phage Asswx_1	GCA_004146865.1
QNJ54709.1	000286	DHFR	181	vBValMR10Z_168	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALP47469.1	000286	DHFR	181	phiST2_0252	Vibrio phage phi-ST2	GCA_002757135.1
QAY01128.1	000286	DHFR	173	ASwh1_61	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39498.1	000286	DHFR	178	CC2_157	Aeromonas phage CC2	GCA_000903495.1
ALP47088.1	000286	DHFR	181	phiGrn1_0121	Vibrio phage phi-Grn1	GCA_002757115.1
AQT28183.1	000286	DHFR	168	pVa21_066	Vibrio phage pVa-21	GCA_002619305.1
QDB70364.1	000286	DHFR	185	CF8_0196	Aeromonas phage CF8	GCA_006384595.2
BAW98387.1	000286	DHFR	167	FDH33_gp178	Vibrio phage pTD1	GCA_002618825.1
AND75401.1	000286	DHFR	179	ME3_240	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AJT61097.1	000286	DHFR	181	AVU32_gp256	Vibrio phage ValKK3	GCA_001501635.1
QDH47149.1	000286	DHFR	193	LAh10_119	Aeromonas phage LAh10	GCA_006863975.1

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QDJ96708.1	000286	DHFR	177	PS1_0197	Aeromonas phage PS1	GCA_007051165.2
QFR59341.1	000286	DHFR	177	PS2_0199	Aeromonas phage PS2	GCA_009388305.2
ADQ53024.1	000286	DHFR	173	PX29p305	Aeromonas phage PX29	GCA_000920195.1
QAU04555.1	000286	DHFR	173	ValB1MD_271	Vibrio phage ValB1MD	GCA_004138815.1
QBX06083.1	000286	DHFR	181	ValB1HC_129	Vibrio phage ValB1 HC	GCA_004771355.1
ADM79948.1	000286	DHFR	174	phiAS5_ORF0105	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53360.1	000286	DHFR	155	65p352	Aeromonas virus 65	GCA_000893255.1
AGB07013.1	000286	DHFR	181	CF80_gp226	Vibrio phage VH7D	GCA_000914495.1
AAQ17977.1	000286	DHFR	172	frd	Aeromonas virus Aeh1	GCA_000843245.1
QHJ74189.1	000286	DHFR	181	VH12019_00270	Vibrio phage VH1_2019	GCA_009931825.1
QIW91026.1	000286	DHFR	181	COHAPHLL_00163	Vibrio phage V09	GCA_012361135.1
AEO93387.1	000286	DHFR	159	G_125	Bacillus virus G	GCA_000917535.1
QIW90403.1	000286	DHFR	181	GCAPEGMB_00056	Vibrio phage V07	GCA_012361095.1
AAQ64077.1	000286	DHFR	181	KVP40.0006	Vibrio phage KVP40	GCA_000843785.1
BAV39334.1	000286	DHFR	176	BPT24_210	Tenacibaculum phage pT24	GCA_002611925.1
BBI90927.1	000286	DHFR	75	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIA64815.1	000286	DHFR	177	S13_016	Cronobacter phage S13	GCA_001503575.1
SOK58585.1	000286	DHFR	173	g308	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BBI90621.1	000286	DHFR	75	HYO65_gp229	Tenacibaculum phage PTm1	GCA_009730695.1
AFC21758.1	000286	DHFR	172	GAP32_308	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QDJ97363.1	000286	DHFR	193	D6_0204	Aeromonas phage D6	GCA_007051205.2
AFF28156.1	000286	DHFR	179	PAU_158	Sphingomonas phage PAU	GCA_000902455.1
AKF13617.1	000286	DHFR	163	PHIN3_354	Sinorhizobium phage phiN3	GCA_001501175.1
AKF12894.1	000286	DHFR	163	PHIM7_349	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13254.1	000286	DHFR	163	PHIM19_349	Sinorhizobium phage phiM19	GCA_002605865.1
AGR48082.1	000286	DHFR	163	SmphiM12_450	Sinorhizobium phage phiM12	GCA_001023565.1
QDB71279.1	000286	DHFR	174	CPT_Moabite_249	Serratia phage Moabite	GCA_006384735.1
AQW88835.1	000286	DHFR	174	BF_0310	Serratia phage BF	GCA_002619745.1
ATA65511.1	000286	DHFR	174	2050HW_00176	Serratia phage 2050HW	GCA_002628125.1
QBZ70745.1	000286	DHFR	227	pETSU_164	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59709.1	000286	DHFR	183	SEGD1_060	Enterobacteria phage SEGD1	GCA_002601865.1
QKE54430.1	000286	DHFR	564	ACSA002_1160	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AEP83891.1	000286	DHFR	175	SPN3US_0058	Salmonella phage SPN3US	GCA_001042275.1
AWN09040.1	000286	DHFR	201	MLDJOKPK_00107	Salmonella phage SPAsTU	GCA_003183805.1
AHI60272.1	000286	DHFR	546	Ea357_121	Erwinia phage Ea35-70	GCA_000914635.1
QIG62702.1	000286	DHFR	167	SEPL_089	Salmonella phage SE_PL	GCA_011067555.1
ANZ49711.1	000286	DHFR	180	MACHINA_73	Erwinia phage Machina	GCA_002758035.1
AZU98282.1	000286	DHFR	167	CPT_Munch_338	Salmonella phage Munch	GCA_004015485.1
QBP07230.1	000286	DHFR	537	REBECCA_123	Erwinia phage Rebecca	GCA_004521635.1
QNI20774.1	000286	DHFR	175	-	Salmonella phage JN03	GCA_014319805.1
QCW19035.1	000286	DHFR	167	7t3_0515	Salmonella phage 7t3	GCA_006083215.1
AXF51201.1	000286	DHFR	172	WELLINGTON_71	Erwinia phage Wellington	GCA_003344985.1
AFQ96787.1	000286	DHFR	200	G173_gp242	Erwinia phage phiEaH2	GCA_000902915.1
BAQ02602.1	000286	DHFR	203	AVU38_gp074	Ralstonia phage RSL2	GCA_001503055.1
BAQ02601.1	000286	DHFR	178	AVU38_gp073	Ralstonia phage RSL2	GCA_001503055.1
BAS04870.1	000286	DHFR	192	AVU11_gp078	Ralstonia phage RSF1	GCA_001500875.1
ANZ48088.1	000286	DHFR	200	ASESINO_75	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85910.1	000286	DHFR	537	BOSOLAPHORUS_123	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
BAS04869.1	000286	DHFR	178	AVU11_gp077	Ralstonia phage RSF1	GCA_001500875.1
BAW19445.1	000286	DHFR	174	-	Ralstonia phage RP31	GCA_002617365.1
ANZ48362.1	000286	DHFR	178	CAITLIN_67	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
BAW19159.1	000286	DHFR	174	FDH28_gp236	Ralstonia phage RP12	GCA_002617345.1
ANZ48635.1	000286	DHFR	175	CHRISDB_73	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52225.1	000286	DHFR	537	DM_127	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AAL82905.1	000286	DHFR	173	PHIKZ004	Pseudomonas virus phiKZ	GCA_000842965.1
AUG86229.1	000286	DHFR	537	DESERTFOX_122	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
QCG76057.1	000286	DHFR	156	EST35_0176	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QJB22647.1	000286	DHFR	173	fnug_4	Pseudomonas phage fnug	GCA_012837215.1
ATN94581.1	000286	DHFR	173	SL2_004	Pseudomonas phage SL2	GCA_002956015.1
ANZ49156.1	000286	DHFR	180	HUXLEY_74	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03796.1	000286	DHFR	192	JOAD_119	Erwinia phage vB_EamM_Joad	GCA_002629065.1
QBJ02534.1	000286	DHFR	159	PSA21_4	Pseudomonas phage Psa21	GCA_004340405.1
AEH03429.1	000286	DHFR	173	003	Pseudomonas phage PhiPA3	GCA_001502095.1
ARV76633.1	000286	DHFR	186	PHABIO_2	Pseudomonas phage Phabio	GCA_002624965.1
ANZ49423.1	000286	DHFR	172	KWAN_71	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86551.1	000286	DHFR	537	MADMEL_123	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AGS81924.2	000286	DHFR	182	PaBG_00040	Pseudomonas phage PaBG	GCA_000912555.1
AUG86875.1	000286	DHFR	546	MORTIMER_126	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ARM70789.1	000286	DHFR	195	phiC120_c83	Escherichia phage phiC120	GCA_002621185.1
QBX32151.1	000286	DHFR	174	-	Pseudomonas phage PA1C	GCA_004785505.1
ANZ49984.1	000286	DHFR	180	PARSHIK_75	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ARV77172.1	000286	DHFR	161	NOXIFER_1	Pseudomonas phage Noxifer	GCA_002625005.1
ANH51903.1	000286	DHFR	546	RAY_122	Erwinia phage vB_EamM_RAY	GCA_002624345.1
AFH14752.1	000286	DHFR	173	Lu11_0215	Pseudomonas phage Lu11	GCA_000897175.1
ASU03551.1	000286	DHFR	192	RISINGSUN_119	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANM44762.1	000286	DHFR	173	KTN4_004	Pseudomonas phage KTN4	GCA_002607225.1
ABY63292.1	000286	DHFR	183	201phi2-1p003	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANH51587.1	000286	DHFR	546	SIMMY50_125	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
SBV38338.1	000286	DHFR	203	BN7874_169	Phage NCTB	GCA_900092385.1
ANJ64934.1	000286	DHFR	546	SPECIALG_124	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMM43876.1	000286	DHFR	172	CBB_313	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QHJ78849.1	000286	DHFR	177	-	Myoviridae sp.	GCA_012593985.1
ANZ50499.1	000286	DHFR	200	STRATTON_74	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85899.1	000286	DHFR	183	ACEC001_0610	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXH72924.1	000286	DHFR	162	-	Myoviridae sp.	GCA_003657725.1
AIT13939.1	000286	DHFR	170	PBI_121Q_42	Escherichia phage 121Q	GCA_000926855.1
AFA44421.1	000286	DHFR	190	RaK2_00148	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QAY00398.1	000286	DHFR	173	Ecwhy1_117	Escherichia phage Ecwhy_1	GCA_004146585.1
QGH72052.1	000286	DHFR	207	N1M2_189	Klebsiella phage N1M2	GCA_010092605.1
AGC35143.1	000286	DHFR	173	ACQ29_gp463	Escherichia phage PBECO4	GCA_001041035.1
SCA80533.1	000286	DHFR	173	PSLUR01_00556	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
BBM61631.1	000286	DHFR	173	EO157G_0420	Escherichia phage SP27	GCA_008033345.1
QDF13799.1	000286	DHFR	173	vBEcoMphAPEC6_gp170c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AXC36717.1	000286	DHFR	173	-	Escherichia phage UB	GCA_003341455.1
QBO61754.1	000286	DHFR	173	G17_00265	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AON97072.1	000286	DHFR	193	E_063	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ANS06014.1	000286	DHFR	193	ABCD_0061	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
QEM41732.1	000286	DHFR	173	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AEV89678.1	000286	DHFR	236	OBP_241	Pseudomonas phage OBP	GCA_000896635.1
AAX78584.1	000286	DHFR	193	RB43ORF062w	Escherichia virus RB43	GCA_000863505.1
AGN30056.2	000286	DHFR	186	VPFG_00053	Vibrio phage nt-1	GCA_000910195.2
prev15ph1000000582	000287	DHFR+Thymidylate-synthase	517	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000840	000287	DHFR+Thymidylate-synthase	517	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QMP24058.1	000000	SIG+DHFR_1	579	-	Proteus phage 10	GCA_014071245.1
QHJ86039.1	000288	Thymidylate-synthase	229	KKIINIFJ_00127	Pseudomonas phage PN05	GCA_009931935.1
BBI90867.1	000288	Thymidylate-synthase	223	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90559.1	000288	Thymidylate-synthase	225	HYO65_gp167	Tenacibaculum phage PTm1	GCA_009730695.1
QFP93091.1	000288	Thymidylate-synthase	390	-	Serratia phage PCH45	GCA_009187865.1
QDB71264.1	000288	Thymidylate-synthase	284	CPT_Moabite_234	Serratia phage Moabite	GCA_006384735.1
ATA65497.1	000288	Thymidylate-synthase	284	2050HW_00162	Serratia phage 2050HW	GCA_002628125.1
SCA80443.1	000288	Thymidylate-synthase	309	PSLUR01_00466	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGC34685.1	000288	Thymidylate-synthase	309	ACQ29_gp005	Escherichia phage PBECO4	GCA_001041035.1
AAX78585.1	000288	Thymidylate-synthase	285	RB43ORF063w	Escherichia virus RB43	GCA_000863505.1
QGH72047.1	000288	Thymidylate-synthase	396	N1M2_184	Klebsiella phage N1M2	GCA_010092605.1
QAY00490.1	000288	Thymidylate-synthase	309	Ecwhy1_211	Escherichia phage Ecwhy_1	GCA_004146585.1
AIT14458.1	000288	Thymidylate-synthase	309	PBI_121Q_568	Escherichia phage 121Q	GCA_000926855.1
AFA44332.1	000288	Thymidylate-synthase	309	RaK2_00059	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AQT28523.1	000288	Thymidylate-synthase	366	YOLOSWAG_38	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ARW58685.1	000288	Thymidylate-synthase	366	Y3_045	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ANZ50677.1	000288	Thymidylate-synthase	305	STRATTON_252	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QHJ78848.1	000288	Thymidylate-synthase	284	-	Myoviridae sp.	GCA_012593985.1
AMM43788.1	000288	Thymidylate-synthase	309	CBB_223	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ANJ64880.1	000288	Thymidylate-synthase	383	SPECIALG_70	Erwinia phage vB_EamM_Special G	GCA_002624385.1
SBV38326.1	000288	Thymidylate-synthase	471	BN7874_157	Phage NCTB	GCA_900092385.1
ANH51532.1	000288	Thymidylate-synthase	383	SIMMY50_70	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGZ14531.1	000288	Thymidylate-synthase	302	HWC77_gp168	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24038.1	000288	Thymidylate-synthase	393	-	Proteus phage 10	GCA_014071245.1
ASU03482.1	000288	Thymidylate-synthase	99	RISINGSUN_188	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ABY63176.1	000288	Thymidylate-synthase	457	201phi2-1p350	Pseudomonas phage 201phi2-1	GCA_000875305.1
ASU03484.1	000288	Thymidylate-synthase	286	RISINGSUN_186	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANM45042.1	000288	Thymidylate-synthase	488	KTN4_284	Pseudomonas phage KTN4	GCA_002607225.1
ANH51848.1	000288	Thymidylate-synthase	383	RAY_67	Erwinia phage vB_EamM_RAY	GCA_002624345.1
AFH14760.1	000288	Thymidylate-synthase	426	Lu11_0223	Pseudomonas phage Lu11	GCA_000897175.1
ANZ50301.1	000288	Thymidylate-synthase	339	PHOBOS_111	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ARV77412.1	000288	Thymidylate-synthase	522	NOXIFER_247	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89671.1	000288	Thymidylate-synthase	392	OBP_234	Pseudomonas phage OBP	GCA_000896635.1
QDF13884.1	000288	Thymidylate-synthase	309	vBEcoMphAPEC6_gp259c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ANZ50151.1	000288	Thymidylate-synthase	353	PARSHIK_242	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QBX32432.1	000288	Thymidylate-synthase	476	-	Pseudomonas phage PA1C	GCA_004785505.1
AUG86818.1	000288	Thymidylate-synthase	383	MORTIMER_69	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
QHJ86156.1	000288	Thymidylate-synthase	353	KKIINIFJ_00246	Pseudomonas phage PN05	GCA_009931935.1
AUG86497.1	000288	Thymidylate-synthase	383	MADMEL_69	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AGS82110.1	000288	Thymidylate-synthase	375	PaBG_00236	Pseudomonas phage PaBG	GCA_000912555.1
ANZ49610.1	000288	Thymidylate-synthase	372	KWAN_258	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ARV76982.1	000288	Thymidylate-synthase	465	PHABIO_351	Pseudomonas phage Phabio	GCA_002624965.1
ASU03725.1	000288	Thymidylate-synthase	99	JOAD_190	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AEH03697.1	000288	Thymidylate-synthase	476	274	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02832.1	000288	Thymidylate-synthase	473	PSA21_306	Pseudomonas phage Psa21	GCA_004340405.1
ASU03727.1	000288	Thymidylate-synthase	292	JOAD_188	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49323.1	000288	Thymidylate-synthase	351	HUXLEY_241	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ATN94670.1	000288	Thymidylate-synthase	75	SL2_093	Pseudomonas phage SL2	GCA_002956015.1
ATN94672.1	000288	Thymidylate-synthase	359	SL2_095	Pseudomonas phage SL2	GCA_002956015.1
QJB22918.1	000288	Thymidylate-synthase	488	fnug_275	Pseudomonas phage fnug	GCA_012837215.1
ANZ48959.1	000288	Thymidylate-synthase	342	EARLPHILLIPIV_110	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
AUG86175.1	000288	Thymidylate-synthase	383	DESERTFOX_67	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
QCG76132.1	000288	Thymidylate-synthase	298	EST35_0251	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBM62131.1	000288	Thymidylate-synthase	309	EO157G_5420	Escherichia phage SP27	GCA_008033345.1
QEM42003.1	000288	Thymidylate-synthase	476	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBO63934.1	000288	Thymidylate-synthase	339	Goslar_00141	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
AAL83136.1	000288	Thymidylate-synthase	488	PHIKZ235	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ48813.1	000288	Thymidylate-synthase	372	CHRISDB_251	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
BAW19189.1	000288	Thymidylate-synthase	300	FDH28_gp206	Ralstonia phage RP12	GCA_002617345.1
ANZ48537.1	000288	Thymidylate-synthase	343	CAITLIN_242	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
BAW19475.1	000288	Thymidylate-synthase	300	-	Ralstonia phage RP31	GCA_002617365.1
AUG85856.1	000288	Thymidylate-synthase	383	BOSOLAPHORUS_68	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48264.1	000288	Thymidylate-synthase	339	ASESINO_251	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
BAS04956.1	000288	Thymidylate-synthase	420	AVU11_gp164	Ralstonia phage RSF1	GCA_001500875.1
AWY08321.1	000288	Thymidylate-synthase	365	Alexandra_41	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AFQ96695.1	000288	Thymidylate-synthase	342	G173_gp150	Erwinia phage phiEaH2	GCA_000902915.1
BAQ02681.1	000288	Thymidylate-synthase	420	AVU38_gp153	Ralstonia phage RSL2	GCA_001503055.1
BAG41679.1	000288	Thymidylate-synthase	414	RSL1_ORF230	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44093.1	000288	Thymidylate-synthase	293	PBI_SCTP2_78	Salicola phage SCTP-2	GCA_002625545.1
QCW18938.1	000288	Thymidylate-synthase	310	7t3_0417	Salmonella phage 7t3	GCA_006083215.1
AXF51383.1	000288	Thymidylate-synthase	340	WELLINGTON_257	Erwinia phage Wellington	GCA_003344985.1
QBP07176.1	000288	Thymidylate-synthase	383	REBECCA_68	Erwinia phage Rebecca	GCA_004521635.1
QNI20916.1	000288	Thymidylate-synthase	345	-	Salmonella phage JN03	GCA_014319805.1
AZU98193.1	000288	Thymidylate-synthase	310	CPT_Munch_249	Salmonella phage Munch	GCA_004015485.1
AGX01835.1	000288	Thymidylate-synthase	388	thyA	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ49880.1	000288	Thymidylate-synthase	353	MACHINA_242	Erwinia phage Machina	GCA_002758035.1
QIG62792.1	000288	Thymidylate-synthase	310	SEPL_179	Salmonella phage SE_PL	GCA_011067555.1
AHI60218.1	000288	Thymidylate-synthase	383	Ea357_067	Erwinia phage Ea35-70	GCA_000914635.1
AWN09123.1	000288	Thymidylate-synthase	344	MLDJOKPK_00211	Salmonella phage SPAsTU	GCA_003183805.1
QBP07536.1	000288	Thymidylate-synthase	342	DERBICUS_110	Erwinia phage Derbicus	GCA_004521655.1
AEP84062.1	000288	Thymidylate-synthase	338	SPN3US_0229	Salmonella phage SPN3US	GCA_001042275.1
QKE54371.1	000288	Thymidylate-synthase	383	ACSA002_0570	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AMR59880.1	000288	Thymidylate-synthase	345	SEGD1_233	Enterobacteria phage SEGD1	GCA_002601865.1
QBO61844.1	000288	Thymidylate-synthase	309	G17_00355	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBZ70737.1	000288	Thymidylate-synthase	394	pETSU_156	Edwardsiella virus pEt-SU	GCA_004800915.1
AQW88744.1	000288	Thymidylate-synthase	309	BF_0219	Serratia phage BF	GCA_002619745.1
AXG67399.1	000288	Thymidylate-synthase	367	JA33_025	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXC36805.1	000288	Thymidylate-synthase	309	-	Escherichia phage UB	GCA_003341455.1
AXG66753.1	000288	Thymidylate-synthase	117	JA29_027	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
QKN86070.1	000288	Thymidylate-synthase	343	ACEC001_2270	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXG66751.1	000288	Thymidylate-synthase	254	JA29_025	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AGR48078.1	000288	Thymidylate-synthase	306	SmphiM12_446	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13253.1	000288	Thymidylate-synthase	306	PHIM19_348	Sinorhizobium phage phiM19	GCA_002605865.1
AXG66429.1	000288	Thymidylate-synthase	367	JA13_026	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AKF12893.1	000288	Thymidylate-synthase	306	PHIM7_348	Sinorhizobium phage phiM7	GCA_002622405.1
AYD79830.1	000288	Thymidylate-synthase	367	JA11_025	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AKF13616.1	000288	Thymidylate-synthase	306	PHIN3_353	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67087.1	000288	Thymidylate-synthase	368	AD1_043	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AON97073.1	000288	Thymidylate-synthase	284	E_064	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AFF28180.1	000288	Thymidylate-synthase	235	PAU_182	Sphingomonas phage PAU	GCA_000902455.1
AFF28023.1	000288	Thymidylate-synthase	443	PAU_25	Sphingomonas phage PAU	GCA_000902455.1
ARM70864.1	000288	Thymidylate-synthase	238	phiC120_c158	Escherichia phage phiC120	GCA_002621185.1
AFC21667.1	000288	Thymidylate-synthase	309	GAP32_217	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
BBI90677.1	000288	Thymidylate-synthase	527	HYO65_gp285	Tenacibaculum phage PTm1	GCA_009730695.1
AIA64816.1	000288	Thymidylate-synthase	284	S13_017	Cronobacter phage S13	GCA_001503575.1
AFO71327.1	000288	Thymidylate-synthase	337	CR5_107	Cronobacter phage CR5	GCA_000910235.1
BBI90984.1	000288	Thymidylate-synthase	527	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39316.1	000288	Thymidylate-synthase	319	BPT24_191	Tenacibaculum phage pT24	GCA_002611925.1
ANS05981.1	000288	Thymidylate-synthase	285	ABCD_0062	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
QAU04203.1	000288	Thymidylate-synthase	302	HWC03_gp048	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23157.1	000288	Thymidylate-synthase	302	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80992.1	000288	Thymidylate-synthase	302	Aphrodite1_0183	Vibrio phage Aphrodite1	GCA_002958015.1
ANH52168.1	000288	Thymidylate-synthase	383	DM_70	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AAQ64102.1	000288	Thymidylate-synthase	300	KVP40.0031	Vibrio phage KVP40	GCA_000843785.1
QDH47571.1	000288	Thymidylate-synthase	302	HWC35_gp177	Vibrio phage USC-1	GCA_006864065.1
AEO93578.1	000288	Thymidylate-synthase	348	G_319	Bacillus virus G	GCA_000917535.1
QIW90425.1	000288	Thymidylate-synthase	299	GCAPEGMB_00078	Vibrio phage V07	GCA_012361095.1
AEO93386.1	000288	Thymidylate-synthase	278	G_124	Bacillus virus G	GCA_000917535.1
QIW91004.1	000288	Thymidylate-synthase	299	COHAPHLL_00141	Vibrio phage V09	GCA_012361135.1
AAQ17973.1	000288	Thymidylate-synthase	277	td	Aeromonas virus Aeh1	GCA_000843245.1
QHJ74214.1	000288	Thymidylate-synthase	299	VH12019_00295	Vibrio phage VH1_2019	GCA_009931825.1
ADQ53358.1	000288	Thymidylate-synthase	313	65p350	Aeromonas virus 65	GCA_000893255.1
AGB07038.1	000288	Thymidylate-synthase	299	CF80_gp251	Vibrio phage VH7D	GCA_000914495.1
QBX06058.1	000288	Thymidylate-synthase	299	ValB1HC_104	Vibrio phage ValB1 HC	GCA_004771355.1
ADM79944.1	000288	Thymidylate-synthase	277	phiAS5_ORF0101	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53020.1	000288	Thymidylate-synthase	277	PX29p301	Aeromonas phage PX29	GCA_000920195.1
QAU04556.1	000288	Thymidylate-synthase	287	ValB1MD_273	Vibrio phage ValB1MD	GCA_004138815.1
QDH47053.1	000288	Thymidylate-synthase	475	LAh10_114	Aeromonas phage LAh10	GCA_006863975.1
AJT61071.1	000288	Thymidylate-synthase	299	AVU32_gp230	Vibrio phage ValKK3	GCA_001501635.1
ARM70788.1	000288	Thymidylate-synthase	286	phiC120_c82	Escherichia phage phiC120	GCA_002621185.1
AGN30081.2	000288	Thymidylate-synthase	299	VPFG_00079	Vibrio phage nt-1	GCA_000910195.2
QDJ97355.1	000288	Thymidylate-synthase	460	D6_0196	Aeromonas phage D6	GCA_007051205.2
BAW98385.1	000288	Thymidylate-synthase	302	FDH33_gp176	Vibrio phage pTD1	GCA_002618825.1
AQT27999.1	000288	Thymidylate-synthase	451	pVa21_057	Vibrio phage pVa-21	GCA_002619305.1
QDB70355.1	000288	Thymidylate-synthase	338	CF8_0186	Aeromonas phage CF8	GCA_006384595.2
AFN39497.1	000288	Thymidylate-synthase	290	CC2_155	Aeromonas phage CC2	GCA_000903495.1
ALP47026.1	000288	Thymidylate-synthase	299	phiGrn1_0146	Vibrio phage phi-Grn1	GCA_002757115.1
QAY01126.1	000288	Thymidylate-synthase	284	ASwh1_59	Aeromonas phage Aswh_1	GCA_004146945.1
ALP47405.1	000288	Thymidylate-synthase	299	phiST2_0276	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54684.1	000288	Thymidylate-synthase	299	vBValMR10Z_143	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QAX98017.1	000288	Thymidylate-synthase	290	ASswx1_377	Aeromonas phage Asswx_1	GCA_004146865.1
QAX98555.1	000288	Thymidylate-synthase	277	ASfcp2_221	Aeromonas phage AsFcp_2	GCA_004146885.1
ALY07135.1	000288	Thymidylate-synthase	407	VmeM32_00148	Vibrio phage vB_VmeM-32	GCA_002608825.1
AUE22843.1	000288	Thymidylate-synthase	277	Ah1_00325	Aeromonas phage Ah1	GCA_002957415.1
QNI21270.1	000288	Thymidylate-synthase	308	-	Vibrio phage vB_pir03	GCA_014319855.1
ASU00419.1	000288	Thymidylate-synthase	284	HWB28_gp133	Aeromonas phage AS-zj	GCA_002627665.1
AFN37265.1	000288	Thymidylate-synthase	299	pp2_031	Vibriophage phi-pp2	GCA_002630725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATI17578.1	000288	Thymidylate-synthase	284	-	Aeromonas phage AS-szw	GCA_002743635.1
BBA65540.1	000288	Thymidylate-synthase	296	-	Xanthomonas phage XacN1	GCA_003173815.1
QMV28748.1	000288	Thymidylate-synthase	290	AP1_0030	Aeromonas phage AP1	GCA_014183365.1
QDJ96537.1	000288	Thymidylate-synthase	310	Xoosp13_351	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59027.1	000288	Thymidylate-synthase	312	g219	Yersinia phage fHe-Yen9-03	GCA_002990515.1
APU01718.1	000288	Thymidylate-synthase	313	-	Aeromonas phage 65.2	GCA_002618145.1
SOK58492.1	000288	Thymidylate-synthase	312	g215	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AND75269.1	000288	Thymidylate-synthase	241	ME3_108	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXH72923.1	000288	Thymidylate-synthase	274	-	Myoviridae sp.	GCA_003657725.1
QDH83428.1	000288	Thymidylate-synthase	326	H1O15_gp020	Achromobacter phage Motura	GCA_006964305.1
QDJ96702.1	000289	Thymidylate-synthase+HINT	752	PS1_0191	Aeromonas phage PS1	GCA_007051165.2
QFR59335.1	000289	Thymidylate-synthase+HINT	752	PS2_0193	Aeromonas phage PS2	GCA_009388305.2
AND75268.1	000000	Thymidylate-synthase	79	ME3_107	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QHJ86027.1	000000	Thymidylate-synthase	127	KKIINIFJ_00115	Pseudomonas phage PN05	GCA_009931935.1
QDH83578.1	000290	Topoisom_I	541	H1O15_gp210	Achromobacter phage Motura	GCA_006964305.1
SBV38411.1	000290	Topoisom_I	561	BN7874_227	Phage NCTB	GCA_900092385.1
AFH14734.1	000290	Topoisom_I	561	Lu11_0197	Pseudomonas phage Lu11	GCA_000897175.1
AGS81969.1	000290	Topoisom_I	562	PaBG_00084	Pseudomonas phage PaBG	GCA_000912555.1
BAG41552.1	000290	Topoisom_I	559	RSL1_ORF108	Ralstonia phage phiRSL1	GCA_000879455.1
APU01441.1	000291	Phage_DsbA	103	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28794.1	000291	Phage_DsbA	107	AP1_0087	Aeromonas phage AP1	GCA_014183365.1
ATI17458.1	000291	Phage_DsbA	107	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00138.1	000291	Phage_DsbA	107	HWB28_gp012	Aeromonas phage AS-zj	GCA_002627665.1
AUE22852.1	000291	Phage_DsbA	95	Ah1_00334	Aeromonas phage Ah1	GCA_002957415.1
QAX98563.1	000291	Phage_DsbA	95	ASfcp2_229	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97898.1	000291	Phage_DsbA	107	ASswx1_255	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01255.1	000291	Phage_DsbA	100	ASwh1_190	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39304.1	000291	Phage_DsbA	107	CC2_278	Aeromonas phage CC2	GCA_000903495.1
ADQ53028.1	000291	Phage_DsbA	95	PX29p309	Aeromonas phage PX29	GCA_000920195.1
ADM79952.1	000291	Phage_DsbA	95	phiAS5_ORF0109	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53061.1	000291	Phage_DsbA	103	65p051	Aeromonas virus 65	GCA_000893255.1
AAQ17981.1	000291	Phage_DsbA	95	dsbA	Aeromonas virus Aeh1	GCA_000843245.1
ANS06127.1	000291	Phage_DsbA	87	ABCD_0048	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64811.1	000291	Phage_DsbA	118	S13_012	Cronobacter phage S13	GCA_001503575.1
AON97058.1	000291	Phage_DsbA	87	E_049	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70796.1	000291	Phage_DsbA	89	phiC120_c90	Escherichia phage phiC120	GCA_002621185.1
AAX78570.1	000291	Phage_DsbA	87	RB43ORF048c	Escherichia virus RB43	GCA_000863505.1
QHJ78853.1	000291	Phage_DsbA	110	-	Myoviridae sp.	GCA_012593985.1
AAQ64073.1	000291	Phage_DsbA	90	KVP40.0002	Vibrio phage KVP40	GCA_000843785.1
QIW90399.1	000291	Phage_DsbA	90	GCAPEGMB_00052	Vibrio phage V07	GCA_012361095.1
QIW91030.1	000291	Phage_DsbA	90	COHAPHLL_00167	Vibrio phage V09	GCA_012361135.1
QHJ74185.1	000291	Phage_DsbA	90	VH12019_00266	Vibrio phage VH1_2019	GCA_009931825.1
AGB07009.1	000291	Phage_DsbA	93	CF80_gp222	Vibrio phage VH7D	GCA_000914495.1
QBX06087.1	000291	Phage_DsbA	93	ValB1HC_133	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61101.1	000291	Phage_DsbA	93	AVU32_gp260	Vibrio phage ValKK3	GCA_001501635.1
AGN30053.1	000291	Phage_DsbA	91	VPFG_00049	Vibrio phage nt-1	GCA_000910195.2
ALP47223.1	000291	Phage_DsbA	93	phiGrn1_0117	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47611.1	000291	Phage_DsbA	93	phiST2_0248	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54713.1	000291	Phage_DsbA	93	vBValMR10Z_172	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07093.1	000291	Phage_DsbA	97	VmeM32_00104	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37236.1	000291	Phage_DsbA	90	pp2_002	Vibriophage phi-pp2	GCA_002630725.1
AFC21706.1	000292	Phage_DsbA	100	GAP32_256	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14499.1	000292	Phage_DsbA	100	PBI_121Q_609	Escherichia phage 121Q	GCA_000926855.1
QAY00450.1	000292	Phage_DsbA	101	Ecwhy1_170	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35193.1	000292	Phage_DsbA	105	ACQ29_gp513	Escherichia phage PBECO4	GCA_001041035.1
BBM62171.1	000292	Phage_DsbA	100	EO157G_5820	Escherichia phage SP27	GCA_008033345.1
AXC36764.1	000292	Phage_DsbA	100	-	Escherichia phage UB	GCA_003341455.1
QBO61804.1	000292	Phage_DsbA	100	G17_00315	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13848.1	000292	Phage_DsbA	100	vBEcoMphAPEC6_gp219c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80483.1	000292	Phage_DsbA	100	PSLUR01_00506	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44372.1	000292	Phage_DsbA	97	RaK2_00099	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43826.1	000292	Phage_DsbA	100	CBB_262	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18985.1	000292	Phage_DsbA	98	7t3_0464	Salmonella phage 7t3	GCA_006083215.1
AZU98233.1	000292	Phage_DsbA	98	CPT_Munch_289	Salmonella phage Munch	GCA_004015485.1
QIG62751.1	000292	Phage_DsbA	98	SEPL_138	Salmonella phage SE_PL	GCA_011067555.1
AQW88785.1	000292	Phage_DsbA	100	BF_0260	Serratia phage BF	GCA_002619745.1
SOK59066.1	000292	Phage_DsbA	100	g258	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58532.1	000292	Phage_DsbA	100	g255	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95053.1	000293	Phage_DsbA	85	FDI40_gp281	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72731.1	000293	Phage_DsbA	99	-	Myoviridae sp.	GCA_003657725.1
QCG76191.1	000293	Phage_DsbA	91	EST35_0310	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44195.1	000293	Phage_DsbA	87	PBI_SCTP2_180	Salicola phage SCTP-2	GCA_002625545.1
APU01403.1	000294	PrimaseZnR+Toprim-DNAG	348	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28893.1	000294	PrimaseZnR+Toprim-DNAG	351	AP1_0186	Aeromonas phage AP1	GCA_014183365.1
ATI17493.1	000294	PrimaseZnR+Toprim-DNAG	351	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00504.1	000294	PrimaseZnR+Toprim-DNAG	351	HWB28_gp048	Aeromonas phage AS-zj	GCA_002627665.1
AUE22554.1	000294	PrimaseZnR+Toprim-DNAG	345	Ah1_00013	Aeromonas phage Ah1	GCA_002957415.1
QAX98593.1	000294	PrimaseZnR+Toprim-DNAG	344	ASfcp2_260	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97932.1	000294	PrimaseZnR+Toprim-DNAG	351	ASswx1_290	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01216.1	000294	PrimaseZnR+Toprim-DNAG	353	ASwh1_151	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39511.1	000294	PrimaseZnR+Toprim-DNAG	351	CC2_241	Aeromonas phage CC2	GCA_000903495.1
ADQ52729.1	000294	PrimaseZnR+Toprim-DNAG	337	PX29p010	Aeromonas phage PX29	GCA_000920195.1
ADM79982.1	000294	PrimaseZnR+Toprim-DNAG	343	phiAS5_ORF0139	Aeromonas phage phiAS5	GCA_000887715.1
AAR90927.1	000294	PrimaseZnR+Toprim-DNAG	348	65p011	Aeromonas virus 65	GCA_000893255.1
AAQ17666.1	000294	PrimaseZnR+Toprim-DNAG	344	58	Aeromonas virus Aeh1	GCA_000843245.1
ASV44693.1	000294	PrimaseZnR+Toprim-DNAG	340	FDI40_gp071	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANS05963.1	000294	PrimaseZnR+Toprim-DNAG	341	ABCD_0028	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65052.1	000294	PrimaseZnR+Toprim-DNAG	368	S13_255	Cronobacter phage S13	GCA_001503575.1
AFC21735.1	000294	PrimaseZnR+Toprim-DNAG	348	GAP32_285	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97037.1	000294	PrimaseZnR+Toprim-DNAG	341	E_028	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56834.1	000294	PrimaseZnR+Toprim-DNAG	328	CPXG_00031	Cyanophage P-RSM6	GCA_000906155.1
AJK27652.1	000294	PrimaseZnR+Toprim-DNAG	325	PTIM40_193	Cyanophage P-TIM40	GCA_001470935.1
AOO14378.1	000294	PrimaseZnR+Toprim-DNAG	331	Sn110110_184	Cyanophage S-RIM14	GCA_002599065.1
AOO15026.1	000294	PrimaseZnR+Toprim-DNAG	331	W1230910_180	Cyanophage S-RIM14	GCA_002599125.1
AMO43186.1	000294	PrimaseZnR+Toprim-DNAG	329	R1080702_177	Cyanophage S-RIM32	GCA_001754165.1
AMO43412.1	000294	PrimaseZnR+Toprim-DNAG	329	W270710_168	Cyanophage S-RIM44	GCA_002599145.1
AOO11656.1	000294	PrimaseZnR+Toprim-DNAG	329	ES420910_175	Cyanophage S-RIM44	GCA_002599165.1
AOO11884.1	000294	PrimaseZnR+Toprim-DNAG	329	Np050604_168	Cyanophage S-RIM44	GCA_002599185.1
AOO12122.1	000294	PrimaseZnR+Toprim-DNAG	329	Np200711_176	Cyanophage S-RIM44	GCA_002599205.1
AOO12357.1	000294	PrimaseZnR+Toprim-DNAG	329	Np420711_175	Cyanophage S-RIM44	GCA_002599225.1
AOO12585.1	000294	PrimaseZnR+Toprim-DNAG	329	Sn080709_168	Cyanophage S-RIM44	GCA_002599245.1
AOO12822.1	000294	PrimaseZnR+Toprim-DNAG	329	Sn130910_175	Cyanophage S-RIM44	GCA_002599265.1
AOO13051.1	000294	PrimaseZnR+Toprim-DNAG	329	W2100709_169	Cyanophage S-RIM44	GCA_002599285.1
AGH07527.1	000294	PrimaseZnR+Toprim-DNAG	333	CYVG_00083	Cyanophage S-SSM6a	GCA_002710385.1
AIT13916.1	000294	PrimaseZnR+Toprim-DNAG	351	PBI_121Q_19	Escherichia phage 121Q	GCA_000926855.1
QAY00422.1	000294	PrimaseZnR+Toprim-DNAG	351	Ecwhy1_141	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35165.1	000294	PrimaseZnR+Toprim-DNAG	351	ACQ29_gp485	Escherichia phage PBECO4	GCA_001041035.1
BBM61608.1	000294	PrimaseZnR+Toprim-DNAG	351	EO157G_0190	Escherichia phage SP27	GCA_008033345.1
AXC36738.1	000294	PrimaseZnR+Toprim-DNAG	351	-	Escherichia phage UB	GCA_003341455.1
ARM70849.1	000294	PrimaseZnR+Toprim-DNAG	340	phiC120_c143	Escherichia phage phiC120	GCA_002621185.1
QBO61776.1	000294	PrimaseZnR+Toprim-DNAG	351	G17_00287	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80511.1	000294	PrimaseZnR+Toprim-DNAG	351	PSLUR01_00534	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78550.1	000294	PrimaseZnR+Toprim-DNAG	342	RB43ORF028c	Escherichia virus RB43	GCA_000863505.1
AFA44400.1	000294	PrimaseZnR+Toprim-DNAG	352	RaK2_00127	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72834.1	000294	PrimaseZnR+Toprim-DNAG	354	-	Myoviridae sp.	GCA_003657725.1
QHJ78880.1	000294	PrimaseZnR+Toprim-DNAG	373	-	Myoviridae sp.	GCA_012593985.1
QIG66026.1	000294	PrimaseZnR+Toprim-DNAG	343	phiOC_p384	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43854.1	000294	PrimaseZnR+Toprim-DNAG	348	CBB_290	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26269.1	000294	PrimaseZnR+Toprim-DNAG	330	CPMG_00169	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44584.1	000294	PrimaseZnR+Toprim-DNAG	323	PSSM2_207	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12387.1	000294	PrimaseZnR+Toprim-DNAG	324	PRTG_00234	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93500.1	000294	PrimaseZnR+Toprim-DNAG	331	AVU42_gp166	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99271.1	000294	PrimaseZnR+Toprim-DNAG	329	Syn1_170	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76104.1	000294	PrimaseZnR+Toprim-DNAG	342	EST35_0223	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW19013.1	000294	PrimaseZnR+Toprim-DNAG	352	7t3_0493	Salmonella phage 7t3	GCA_006083215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AZU98260.1	000294	PrimaseZnR+Toprim-DNAG	352	CPT_Munch_316	Salmonella phage Munch	GCA_004015485.1
QIG62724.1	000294	PrimaseZnR+Toprim-DNAG	352	SEPL_111	Salmonella phage SE_PL	GCA_011067555.1
AQW88813.1	000294	PrimaseZnR+Toprim-DNAG	347	BF_0288	Serratia phage BF	GCA_002619745.1
AGR48085.1	000294	PrimaseZnR+Toprim-DNAG	351	SmphiM12_453	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13256.1	000294	PrimaseZnR+Toprim-DNAG	351	PHIM19_351	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12896.1	000294	PrimaseZnR+Toprim-DNAG	351	PHIM7_351	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13619.1	000294	PrimaseZnR+Toprim-DNAG	351	PHIN3_356	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30679.1	000294	PrimaseZnR+Toprim-DNAG	326	Syn7803US37_202	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54927.1	000294	PrimaseZnR+Toprim-DNAG	320	b23_0314	Synechococcus phage B23	GCA_009745195.1
QGT54562.1	000294	PrimaseZnR+Toprim-DNAG	320	b3_0321	Synechococcus phage B3	GCA_009745215.1
ASR76221.1	000294	PrimaseZnR+Toprim-DNAG	322	PBI_BELLAMY_178	Synechococcus phage Bellamy	GCA_002627525.1
QCW22951.1	000294	PrimaseZnR+Toprim-DNAG	330	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50530.1	000294	PrimaseZnR+Toprim-DNAG	321	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59637.1	000294	PrimaseZnR+Toprim-DNAG	329	S330809_176	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59399.1	000294	PrimaseZnR+Toprim-DNAG	329	C440309_176	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59875.1	000294	PrimaseZnR+Toprim-DNAG	329	N231010_176	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70531.1	000294	PrimaseZnR+Toprim-DNAG	322	HOU04_gp132	Synechococcus phage S-T4	GCA_003443335.1
QJT70175.1	000294	PrimaseZnR+Toprim-DNAG	323	SynMITS9220M01_163	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64091.1	000294	PrimaseZnR+Toprim-DNAG	352	KVP40.0020	Vibrio phage KVP40	GCA_000843785.1
QIW90414.1	000294	PrimaseZnR+Toprim-DNAG	352	GCAPEGMB_00067	Vibrio phage V07	GCA_012361095.1
QIW91015.1	000294	PrimaseZnR+Toprim-DNAG	352	COHAPHLL_00152	Vibrio phage V09	GCA_012361135.1
QHJ74203.1	000294	PrimaseZnR+Toprim-DNAG	352	VH12019_00284	Vibrio phage VH1_2019	GCA_009931825.1
AGB07027.1	000294	PrimaseZnR+Toprim-DNAG	331	CF80_gp240	Vibrio phage VH7D	GCA_000914495.1
QBX06069.1	000294	PrimaseZnR+Toprim-DNAG	352	ValB1HC_115	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04522.1	000294	PrimaseZnR+Toprim-DNAG	332	ValB1MD_202	Vibrio phage ValB1MD	GCA_004138815.1
AJT61083.1	000294	PrimaseZnR+Toprim-DNAG	352	AVU32_gp242	Vibrio phage ValKK3	GCA_001501635.1
AGN30071.2	000294	PrimaseZnR+Toprim-DNAG	352	VPFG_00069	Vibrio phage nt-1	GCA_000910195.2
ALP47003.1	000294	PrimaseZnR+Toprim-DNAG	352	phiGrn1_0135	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47384.1	000294	PrimaseZnR+Toprim-DNAG	352	phiST2_0265	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54695.1	000294	PrimaseZnR+Toprim-DNAG	352	vBValMR10Z_154	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07075.1	000294	PrimaseZnR+Toprim-DNAG	349	VmeM32_00084	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37254.1	000294	PrimaseZnR+Toprim-DNAG	352	pp2_020	Vibriophage phi-pp2	GCA_002630725.1
SOK59096.1	000294	PrimaseZnR+Toprim-DNAG	348	g288	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58560.1	000294	PrimaseZnR+Toprim-DNAG	348	g283	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCH63597.1	000295	Toprim-DNAG	291	CP21_135	Campylobacter virus CP21	GCA_000902535.1
AGG54424.1	000295	Toprim-DNAG	282	CYWG_00140	Cyanophage S-SSM6b	GCA_002710425.1
QDF13820.1	000295	Toprim-DNAG	279	vBEcoMphAPEC6_gp191c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ASV44169.1	000295	Toprim-DNAG	312	PBI_SCTP2_154	Salicola phage SCTP-2	GCA_002625545.1
BBA65324.1	000295	Toprim-DNAG	293	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96363.1	000295	Toprim-DNAG	344	Xoosp13_176	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000143	000295	Toprim-DNAG	377	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000110	000295	Toprim-DNAG	377	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDH83421.1	000296	CHC2+Toprim-DNAG	329	H1O15_gp012	Achromobacter phage Motura	GCA_006964305.1
QBX06638.1	000296	CHC2+Toprim-DNAG	355	BcepSaruman_225	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74608.1	000296	CHC2+Toprim-DNAG	355	BcepSauron_228	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67267.1	000296	CHC2+Toprim-DNAG	352	AD1_223	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80013.1	000296	CHC2+Toprim-DNAG	351	JA11_208	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66611.1	000296	CHC2+Toprim-DNAG	351	JA13_208	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66936.1	000296	CHC2+Toprim-DNAG	354	JA29_210	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67583.1	000296	CHC2+Toprim-DNAG	351	JA33_209	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08495.1	000296	CHC2+Toprim-DNAG	360	Alexandra_232	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58867.1	000296	CHC2+Toprim-DNAG	363	Y3_227	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28699.1	000296	CHC2+Toprim-DNAG	357	YOLO5WAG_221	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38177.1	000296	CHC2+Toprim-DNAG	348	BN7874_008	Phage NCTB	GCA_900092385.1
AFH14671.1	000296	CHC2+Toprim-DNAG	346	Lu11_0137	Pseudomonas phage Lu11	GCA_000897175.1
AGS82035.1	000296	CHC2+Toprim-DNAG	353	PaBG_00153	Pseudomonas phage PaBG	GCA_000912555.1
BAG41701.1	000296	CHC2+Toprim-DNAG	345	RSL1_ORF253	Ralstonia phage phiRSL1	GCA_000879455.1
QIG63466.1	000297	Toprim-DNAG	348	DAC16_237	Bacteroides phage DAC16	GCA_013387695.1
QIG63729.1	000297	Toprim-DNAG	348	DAC19_242	Bacteroides phage DAC19	GCA_013387715.1
QIG63990.1	000297	Toprim-DNAG	348	DAC20_241	Bacteroides phage DAC20	GCA_013387725.1
QIG64254.1	000297	Toprim-DNAG	348	DAC22_244	Bacteroides phage DAC22	GCA_013387735.1
QIG64510.1	000297	Toprim-DNAG	348	DAC23_236	Bacteroides phage DAC23	GCA_013387745.1
AYD81354.1	000298	CHC2+Toprim-DNAG	510	SEA_JUSTBECAUSE_189	Streptomyces phage JustBecause	GCA_003613775.1
QJD53757.1	000298	CHC2+Toprim-DNAG	510	SEA_KELA_187	Streptomyces phage Kela	GCA_012934305.1
QBZ72084.1	000298	CHC2+Toprim-DNAG	503	SEA_KRADAL_188	Streptomyces phage Kradal	GCA_004799925.1
AXH66346.1	000298	CHC2+Toprim-DNAG	503	SEA_SATIS_187	Streptomyces phage Satis	GCA_003366315.1
AMS01309.1	000299	Toprim-DNAG	345	AR9_g225	Bacillus phage AR9	GCA_001743835.1
ALN97959.1	000299	Toprim-DNAG	344	Bp8pS_280	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99938.1	000299	Toprim-DNAG	345	PBI_PBS1_116	Bacillus virus PBS1	GCA_002601325.1
CCE26270.1	000299	Toprim-DNAG	353	g247	Yersinia phage phiR1-37	GCA_000895615.1
ABS83794.1	000300	CHC2+Toprim-DNAG	424	0305phi8-36p236	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93677.1	000300	CHC2+Toprim-DNAG	235	G_419	Bacillus virus G	GCA_000917535.1
QGT54831.1	000301	Toprim-DNAG	176	b23_0216	Synechococcus phage B23	GCA_009745195.1
QGT54461.1	000301	Toprim-DNAG	176	b3_0218	Synechococcus phage B3	GCA_009745215.1
AMM45090.1	000000	Toprim-DNAG	367	SP15_282	Bacillus phage SP-15	GCA_001754685.1
QHJ86149.1	000000	Toprim-DNAG	338	KKIINIFJ_00238	Pseudomonas phage PN05	GCA_009931935.1
QHJ86007.1	000000	Toprim-DNAG	309	KKIINIFJ_00095	Pseudomonas phage PN05	GCA_009931935.1
AND75223.1	000000	Toprim-DNAG+DnaB	596	ME3_62	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QIW90843.1	000000	Toprim-DNAG+DnaB	566	GCAPEGMB_00528	Vibrio phage V07	GCA_012361095.1
AMM44890.1	000000	CHC2+Toprim-DNAG	319	SP15_091	Bacillus phage SP-15	GCA_001754685.1
QDH83475.1	000302	TopoIV-subB	672	H1O15_gp331	Achromobacter phage Motura	GCA_006964305.1
APU01396.1	000302	TopoIV-subB	667	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28873.1	000302	TopoIV-subB	667	AP1_0166	Aeromonas phage AP1	GCA_014183365.1
ATI17499.1	000302	TopoIV-subB	667	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00498.1	000302	TopoIV-subB	667	HWB28_gp054	Aeromonas phage AS-zj	GCA_002627665.1
AUE22546.1	000302	TopoIV-subB	210	Ah1_00005	Aeromonas phage Ah1	GCA_002957415.1
AUE22547.1	000302	TopoIV-subB	388	Ah1_00006	Aeromonas phage Ah1	GCA_002957415.1
QAX98587.1	000302	TopoIV-subB	614	ASfcp2_254	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97938.1	000302	TopoIV-subB	667	ASswx1_296	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01208.1	000302	TopoIV-subB	668	ASwh1_143	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39509.1	000302	TopoIV-subB	667	CC2_235	Aeromonas phage CC2	GCA_000903495.1
ADQ52723.1	000302	TopoIV-subB	614	PX29p004	Aeromonas phage PX29	GCA_000920195.1
ADM79975.1	000302	TopoIV-subB	614	phiAS5_ORF0132	Aeromonas phage phiAS5	GCA_000887715.1
AAR90934.2	000302	TopoIV-subB	667	65p005	Aeromonas virus 65	GCA_000893255.1
AAQ17660.1	000302	TopoIV-subB	613	60	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94816.1	000302	TopoIV-subB	604	FDI40_gp004	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01109.1	000302	TopoIV-subB	767	AR9_g024	Bacillus phage AR9	GCA_001743835.1
AMM44879.1	000302	TopoIV-subB	657	SP15_080	Bacillus phage SP-15	GCA_001754685.1
ALN97756.1	000302	TopoIV-subB	513	Bp8pS_077	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93511.1	000302	TopoIV-subB	656	G_252	Bacillus virus G	GCA_000917535.1
ASU00031.1	000302	TopoIV-subB	767	PBI_PBS1_209	Bacillus virus PBS1	GCA_002601325.1
QBX06583.1	000302	TopoIV-subB	859	BcepSaruman_170	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74549.1	000302	TopoIV-subB	863	BcepSauron_169	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63592.1	000302	TopoIV-subB	392	CP21_130	Campylobacter virus CP21	GCA_000902535.1
ANS05935.1	000302	TopoIV-subB	630	ABCD_0007	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47797.1	000302	TopoIV-subB	678	CST099	Clostridium phage c-st	GCA_000865225.1
AIA65059.1	000302	TopoIV-subB	624	S13_262	Cronobacter phage S13	GCA_001503575.1
AFC21769.1	000302	TopoIV-subB	655	GAP32_319	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97015.1	000302	TopoIV-subB	631	E_006	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXG67368.1	000302	TopoIV-subB	676	AD1_324	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80120.1	000302	TopoIV-subB	686	JA11_315	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66720.1	000302	TopoIV-subB	686	JA13_317	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67038.1	000302	TopoIV-subB	691	JA29_312	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67689.1	000302	TopoIV-subB	686	JA33_315	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08591.1	000302	TopoIV-subB	675	Alexandra_342	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58967.1	000302	TopoIV-subB	679	Y3_327	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28793.1	000302	TopoIV-subB	677	YOLO5WAG_325	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT13949.1	000302	TopoIV-subB	654	PBI_121Q_52	Escherichia phage 121Q	GCA_000926855.1
QAY00388.1	000302	TopoIV-subB	654	Ecwhy1_107	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35133.1	000302	TopoIV-subB	654	ACQ29_gp453	Escherichia phage PBECO4	GCA_001041035.1
BBM61641.1	000302	TopoIV-subB	654	EO157G_0520	Escherichia phage SP27	GCA_008033345.1
AXC36707.1	000302	TopoIV-subB	654	-	Escherichia phage UB	GCA_003341455.1
ARM70825.1	000302	TopoIV-subB	606	phiC120_c119	Escherichia phage phiC120	GCA_002621185.1
QBO61744.1	000302	TopoIV-subB	654	G17_00255	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13789.1	000302	TopoIV-subB	654	vBEcoMphAPEC6_gp160c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SCA80543.1	000302	TopoIV-subB	654	PSLUR01_00566	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78527.1	000302	TopoIV-subB	630	RB43ORF005c	Escherichia virus RB43	GCA_000863505.1
AFA44430.1	000302	TopoIV-subB	655	RaK2_00157	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72907.1	000302	TopoIV-subB	635	-	Myoviridae sp.	GCA_003657725.1
QHJ78871.1	000302	TopoIV-subB	615	-	Myoviridae sp.	GCA_012593985.1
AMM43887.1	000302	TopoIV-subB	657	CBB_324	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38251.1	000302	TopoIV-subB	673	BN7874_082	Phage NCTB	GCA_900092385.1
AFH14678.1	000302	TopoIV-subB	698	Lu11_0145	Pseudomonas phage Lu11	GCA_000897175.1
QHJ86002.1	000302	TopoIV-subB	602	KKIINIFJ_00090	Pseudomonas phage PN05	GCA_009931935.1
AGS82030.1	000302	TopoIV-subB	671	PaBG_00147	Pseudomonas phage PaBG	GCA_000912555.1
BAG41779.1	000302	TopoIV-subB	882	gyrB	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44212.1	000302	TopoIV-subB	615	PBI_SCTP2_197	Salicola phage SCTP-2	GCA_002625545.1
QCW19046.1	000302	TopoIV-subB	657	7t3_0526	Salmonella phage 7t3	GCA_006083215.1
AZU98293.1	000302	TopoIV-subB	657	CPT_Munch_349	Salmonella phage Munch	GCA_004015485.1
QIG62691.1	000302	TopoIV-subB	657	SEPL_078	Salmonella phage SE_PL	GCA_011067555.1
AQW88847.1	000302	TopoIV-subB	662	BF_0322	Serratia phage BF	GCA_002619745.1
AFF28039.1	000302	TopoIV-subB	640	PAU_41	Sphingomonas phage PAU	GCA_000902455.1
BBI90589.1	000302	TopoIV-subB	461	HYO65_gp197	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90896.1	000302	TopoIV-subB	461	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV31393.1	000302	TopoIV-subB	672	BPT24_252	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64116.1	000302	TopoIV-subB	597	KVP40.0045	Vibrio phage KVP40	GCA_000843785.1
QIW90438.1	000302	TopoIV-subB	597	GCAPEGMB_00091	Vibrio phage V07	GCA_012361095.1
QIW90991.1	000302	TopoIV-subB	597	COHAPHLL_00128	Vibrio phage V09	GCA_012361135.1
QHJ74227.1	000302	TopoIV-subB	597	VH12019_00308	Vibrio phage VH1_2019	GCA_009931825.1
AGB07051.1	000302	TopoIV-subB	598	CF80_gp264	Vibrio phage VH7D	GCA_000914495.1
QBX06045.1	000302	TopoIV-subB	597	ValB1HC_091	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04513.1	000302	TopoIV-subB	600	ValB1MD_175	Vibrio phage ValB1MD	GCA_004138815.1
AJT61059.1	000302	TopoIV-subB	598	AVU32_gp218	Vibrio phage ValKK3	GCA_001501635.1
AGN30094.2	000302	TopoIV-subB	597	VPFG_00092	Vibrio phage nt-1	GCA_000910195.2
ALP46972.1	000302	TopoIV-subB	597	phiGrn1_0158	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47352.1	000302	TopoIV-subB	597	phiST2_0289	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54670.1	000302	TopoIV-subB	597	vBValMR10Z_129	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07070.1	000302	TopoIV-subB	613	VmeM32_00079	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37277.1	000302	TopoIV-subB	597	pp2_043	Vibriophage phi-pp2	GCA_002630725.1
BBA65329.1	000302	TopoIV-subB	623	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96367.1	000302	TopoIV-subB	623	Xoosp13_180	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59131.1	000302	TopoIV-subB	662	g323	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58597.1	000302	TopoIV-subB	662	g320	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26334.1	000302	TopoIV-subB	441	g311	Yersinia phage phiR1-37	GCA_000895615.1
CCE26337.1	000302	TopoIV-subB	357	g314	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000005	000302	TopoIV-subB	635	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000006	000302	TopoIV-subB	635	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ALN97757.1	000302	TopoIV-subB	260	Bp8pS_078	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
BBI90588.1	000303	TopoIV-subB	64	HYO65_gp196	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90895.1	000303	TopoIV-subB	82	-	Tenacibaculum phage PTm5	GCA_009730715.1
QHJ86152.1	000000	TopoIV-subB	485	KKIINIFJ_00241	Pseudomonas phage PN05	GCA_009931935.1
CCH63563.1	000000	TopoIV-subB	168	CP21_101	Campylobacter virus CP21	GCA_000902535.1
QDH83476.1	000304	DNA_topoisoIV	538	H1O15_gp330	Achromobacter phage Motura	GCA_006964305.1
APU01552.1	000304	DNA_topoisoIV	450	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29007.1	000304	DNA_topoisoIV	448	AP1_0300	Aeromonas phage AP1	GCA_014183365.1
ATI17348.1	000304	DNA_topoisoIV	448	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00245.1	000304	DNA_topoisoIV	448	HWB28_gp307	Aeromonas phage AS-zj	GCA_002627665.1
AUE22869.1	000304	DNA_topoisoIV	438	Ah1_00351	Aeromonas phage Ah1	GCA_002957415.1
QAX98579.1	000304	DNA_topoisoIV	438	ASfcp2_245	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97793.1	000304	DNA_topoisoIV	448	ASswx1_148	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01361.1	000304	DNA_topoisoIV	450	ASwh1_301	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39570.1	000304	DNA_topoisoIV	447	CC2_389	Aeromonas phage CC2	GCA_000903495.1
ADQ53044.1	000304	DNA_topoisoIV	438	PX29p327	Aeromonas phage PX29	GCA_000920195.1
ADM79967.1	000304	DNA_topoisoIV	438	phiAS5_ORF0124	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53175.1	000304	DNA_topoisoIV	450	65p167	Aeromonas virus 65	GCA_000893255.1
AAQ17997.1	000304	DNA_topoisoIV	438	52	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94817.1	000304	DNA_topoisoIV	453	FDI40_gp005	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01129.1	000304	DNA_topoisoIV	809	AR9_g044	Bacillus phage AR9	GCA_001743835.1
AMM44881.1	000304	DNA_topoisoIV	608	SP15_082	Bacillus phage SP-15	GCA_001754685.1
ALN97785.1	000304	DNA_topoisoIV	722	Bp8pS_106	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93513.1	000304	DNA_topoisoIV	823	G_254	Bacillus virus G	GCA_000917535.1
ASU00057.1	000304	DNA_topoisoIV	700	PBI_PBS1_235	Bacillus virus PBS1	GCA_002601325.1
QBX06582.1	000304	DNA_topoisoIV	505	BcepSaruman_169	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74548.1	000304	DNA_topoisoIV	505	BcepSauron_168	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63660.1	000304	DNA_topoisoIV	257	CP21_198	Campylobacter virus CP21	GCA_000902535.1
ANS05954.1	000304	DNA_topoisoIV	428	ABCD_0006	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47798.1	000304	DNA_topoisoIV	752	CST100	Clostridium phage c-st	GCA_000865225.1
AIA65067.1	000304	DNA_topoisoIV	442	S13_270	Cronobacter phage S13	GCA_001503575.1
AFC21770.1	000304	DNA_topoisoIV	468	GAP32_320	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97014.1	000304	DNA_topoisoIV	428	E_005	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXG67369.1	000304	DNA_topoisoIV	548	AD1_325	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80121.1	000304	DNA_topoisoIV	560	JA11_316	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66721.1	000304	DNA_topoisoIV	560	JA13_318	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67039.1	000304	DNA_topoisoIV	560	JA29_313	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67690.1	000304	DNA_topoisoIV	560	JA33_316	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08592.1	000304	DNA_topoisoIV	552	Alexandra_344	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58969.1	000304	DNA_topoisoIV	550	Y3_329	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28796.1	000304	DNA_topoisoIV	541	YOLOSWAG_328	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT13950.1	000304	DNA_topoisoIV	470	PBI_121Q_53	Escherichia phage 121Q	GCA_000926855.1
QAY00387.1	000304	DNA_topoisoIV	470	Ecwhy1_106	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35132.1	000304	DNA_topoisoIV	470	ACQ29_gp452	Escherichia phage PBECO4	GCA_001041035.1
BBM61642.1	000304	DNA_topoisoIV	470	EO157G_0530	Escherichia phage SP27	GCA_008033345.1
AXC36706.1	000304	DNA_topoisoIV	470	-	Escherichia phage UB	GCA_003341455.1
ARM70812.1	000304	DNA_topoisoIV	441	phiC120_c106	Escherichia phage phiC120	GCA_002621185.1
QBO61743.1	000304	DNA_topoisoIV	470	G17_00254	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13788.1	000304	DNA_topoisoIV	470	vBEcoMphAPEC6_gp159c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80544.1	000304	DNA_topoisoIV	470	PSLUR01_00567	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78526.1	000304	DNA_topoisoIV	387	RB43ORF004c	Escherichia virus RB43	GCA_000863505.1
AFA44432.1	000304	DNA_topoisoIV	468	RaK2_00159	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72909.1	000304	DNA_topoisoIV	452	-	Myoviridae sp.	GCA_003657725.1
QHJ78864.1	000304	DNA_topoisoIV	441	-	Myoviridae sp.	GCA_012593985.1
AMM43888.1	000304	DNA_topoisoIV	468	CBB_325	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38255.1	000304	DNA_topoisoIV	526	BN7874_086	Phage NCTB	GCA_900092385.1
AFH14679.1	000304	DNA_topoisoIV	541	Lu11_0146	Pseudomonas phage Lu11	GCA_000897175.1
QHJ86004.1	000304	DNA_topoisoIV	433	KKIINIFJ_00092	Pseudomonas phage PN05	GCA_009931935.1
AGS82029.1	000304	DNA_topoisoIV	538	PaBG_00146	Pseudomonas phage PaBG	GCA_000912555.1
BAG41783.2	000304	DNA_topoisoIV	514	gyrA	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44211.1	000304	DNA_topoisoIV	453	PBI_SCTP2_196	Salicola phage SCTP-2	GCA_002625545.1
QCW19047.1	000304	DNA_topoisoIV	472	7t3_0527	Salmonella phage 7t3	GCA_006083215.1
AZU98294.1	000304	DNA_topoisoIV	472	CPT_Munch_350	Salmonella phage Munch	GCA_004015485.1
QIG62690.1	000304	DNA_topoisoIV	472	SEPL_077	Salmonella phage SE_PL	GCA_011067555.1
AQW88848.1	000304	DNA_topoisoIV	469	BF_0323	Serratia phage BF	GCA_002619745.1
AFF28043.1	000304	DNA_topoisoIV	496	PAU_45	Sphingomonas phage PAU	GCA_000902455.1
BBI90591.1	000304	DNA_topoisoIV	321	HYO65_gp199	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90899.1	000304	DNA_topoisoIV	321	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25565.1	000304	DNA_topoisoIV	450	BPT24_267	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64352.1	000304	DNA_topoisoIV	428	KVP40.0282	Vibrio phage KVP40	GCA_000843785.1
QIW90666.1	000304	DNA_topoisoIV	428	GCAPEGMB_00319	Vibrio phage V07	GCA_012361095.1
QIW91132.1	000304	DNA_topoisoIV	428	COHAPHLL_00296	Vibrio phage V09	GCA_012361135.1
QHJ74461.1	000304	DNA_topoisoIV	428	VH12019_00134	Vibrio phage VH1_2019	GCA_009931825.1
AGB06955.1	000304	DNA_topoisoIV	428	CF80_gp168	Vibrio phage VH7D	GCA_000914495.1
QBX06190.1	000304	DNA_topoisoIV	428	ValB1HC_237	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04514.1	000304	DNA_topoisoIV	446	ValB1MD_180	Vibrio phage ValB1MD	GCA_004138815.1
AJT61207.1	000304	DNA_topoisoIV	428	AVU32_gp366	Vibrio phage ValKK3	GCA_001501635.1
AIE13779.1	000304	DNA_topoisoIV	428	VPFG_00331	Vibrio phage nt-1	GCA_000910195.2
ALP46989.1	000304	DNA_topoisoIV	428	phiGrn1_0015	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47370.1	000304	DNA_topoisoIV	428	phiST2_0146	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54815.1	000304	DNA_topoisoIV	428	vBValMR10Z_275	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07206.1	000304	DNA_topoisoIV	436	VmeM32_00220	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37513.1	000304	DNA_topoisoIV	428	pp2_280	Vibriophage phi-pp2	GCA_002630725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65330.1	000304	DNA_topoisoIV	441	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96368.1	000304	DNA_topoisoIV	440	Xoosp13_181	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59132.1	000304	DNA_topoisoIV	469	g324	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58598.1	000304	DNA_topoisoIV	469	g321	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26352.1	000304	DNA_topoisoIV	749	g329	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000018	000304	DNA_topoisoIV	475	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000016	000304	DNA_topoisoIV	475	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ALN97784.1	000305	DNA_topoisoIV	71	Bp8pS_105	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00054.1	000305	DNA_topoisoIV	72	PBI_PBS1_232	Bacillus virus PBS1	GCA_002601325.1
QHJ86184.1	000000	DNA_topoisoIV	313	KKIINIFJ_00274	Pseudomonas phage PN05	GCA_009931935.1
CCE26350.1	000000	DNA_topoisoIV	70	g327	Yersinia phage phiR1-37	GCA_000895615.1
CCH63659.1	000000	DNA_topoisoIV	63	CP21_197	Campylobacter virus CP21	GCA_000902535.1
BAE47887.1	000000	FtsZ	358	CST189	Clostridium phage c-st	GCA_000865225.1
AEO93400.1	000000	FtsZ	376	G_138	Bacillus virus G	GCA_000917535.1
QDB70454.1	000306	Tubulin	317	CF8_0042	Aeromonas phage CF8	GCA_006384595.2
QDJ97195.1	000306	Tubulin	318	D6_0035	Aeromonas phage D6	GCA_007051205.2
QDH47086.1	000306	Tubulin	318	LAh10_202	Aeromonas phage LAh10	GCA_006863975.1
QDJ96797.1	000306	Tubulin	316	PS1_0038	Aeromonas phage PS1	GCA_007051165.2
QFR59428.1	000306	Tubulin	316	PS2_0037	Aeromonas phage PS2	GCA_009388305.2
QBZ70858.1	000306	Tubulin	315	pETSU_277	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60360.1	000306	Tubulin	324	Ea357_207	Erwinia phage Ea35-70	GCA_000914635.1
AGX01756.1	000306	Tubulin	322	CF95_gp034	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07317.1	000306	Tubulin	324	REBECCA_212	Erwinia phage Rebecca	GCA_004521635.1
AUG85998.1	000306	Tubulin	324	BOSOLAPHORUS_212	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52315.1	000306	Tubulin	324	DM_215	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86317.1	000306	Tubulin	324	DESERTFOX_210	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03898.1	000306	Tubulin	321	JOAD_17	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86640.1	000306	Tubulin	324	MADMEL_212	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86963.1	000306	Tubulin	324	MORTIMER_215	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51990.1	000306	Tubulin	324	RAY_210	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03653.1	000306	Tubulin	321	RISINGSUN_17	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51674.1	000306	Tubulin	324	SIMMY50_215	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65024.1	000306	Tubulin	324	SPECIALG_213	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBO63993.1	000306	Tubulin	326	Goslar_00201	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71890.1	000306	Tubulin	316	N1M2_27	Klebsiella phage N1M2	GCA_010092605.1
QGZ14571.1	000306	Tubulin	321	HWC77_gp208	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24134.1	000306	Tubulin	324	-	Proteus phage 10	GCA_014071245.1
ABY62892.1	000306	Tubulin	315	201phi2-1p059	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27110.1	000306	Tubulin	320	PPEV_gp016	Pseudomonas phage EL	GCA_000866825.1
ANM44810.1	000306	Tubulin	326	KTN4_052	Pseudomonas phage KTN4	GCA_002607225.1
ARV77202.1	000306	Tubulin	344	NOXIFER_31	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89484.1	000306	Tubulin	318	OBP_047	Pseudomonas phage OBP	GCA_000896635.1
QBX32179.1	000306	Tubulin	315	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76677.1	000306	Tubulin	314	PHABIO_46	Pseudomonas phage Phabio	GCA_002624965.1
AEH03455.1	000306	Tubulin	315	028	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02557.1	000306	Tubulin	314	PSA21_27	Pseudomonas phage Psa21	GCA_004340405.1
ATN94901.1	000306	Tubulin	326	SL2_324	Pseudomonas phage SL2	GCA_002956015.1
QJB22689.1	000306	Tubulin	326	fnug_46	Pseudomonas phage fnug	GCA_012837215.1
QEM41757.1	000306	Tubulin	315	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82940.1	000306	Tubulin	327	PHIKZ039	Pseudomonas virus phiKZ	GCA_000842965.1
BAW18988.1	000306	Tubulin	334	FDH28_gp014	Ralstonia phage RP12	GCA_002617345.1
BAW19276.1	000306	Tubulin	334	-	Ralstonia phage RP31	GCA_002617365.1
BAS04803.1	000306	Tubulin	332	AVU11_gp011	Ralstonia phage RSF1	GCA_001500875.1
BAQ02539.2	000306	Tubulin	332	-	Ralstonia phage RSL2	GCA_001503055.1
QKE54534.1	000306	Tubulin	326	ACSA002_2180	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65630.1	000306	Tubulin	320	2050HW_00295	Serratia phage 2050HW	GCA_002628125.1
QDB71058.1	000306	Tubulin	320	CPT_Moabite_026	Serratia phage Moabite	GCA_006384735.1
QFP93107.1	000306	Tubulin	324	-	Serratia phage PCH45	GCA_009187865.1
QAU04162.1	000306	Tubulin	321	HWC03_gp007	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23196.1	000306	Tubulin	321	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80988.1	000306	Tubulin	321	Aphrodite1_0147	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70800.1	000306	Tubulin	329	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47533.1	000306	Tubulin	321	HWC35_gp139	Vibrio phage USC-1	GCA_006864065.1
APU01727.1	000307	UvdE	326	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17569.1	000307	UvdE	326	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00427.1	000307	UvdE	326	HWB28_gp125	Aeromonas phage AS-zj	GCA_002627665.1
QAX98009.1	000307	UvdE	326	ASswx1_369	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01133.1	000307	UvdE	326	ASwh1_67	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39499.1	000307	UvdE	326	CC2_163	Aeromonas phage CC2	GCA_000903495.1
ADM80086.1	000307	UvdE	307	phiAS5_ORF0243	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53368.1	000307	UvdE	326	65p360	Aeromonas virus 65	GCA_000893255.1
AAQ17773.1	000307	UvdE	309	Aeh1ORF111c	Aeromonas virus Aeh1	GCA_000843245.1
AMM44906.1	000307	UvdE	324	SP15_107	Bacillus phage SP-15	GCA_001754685.1
AEO93769.1	000307	UvdE	295	G_511	Bacillus virus G	GCA_000917535.1
AXG67327.1	000307	UvdE	326	AD1_283	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80074.1	000307	UvdE	311	JA11_269	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66675.1	000307	UvdE	311	JA13_272	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66995.1	000307	UvdE	311	JA29_269	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67644.1	000307	UvdE	311	JA33_270	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08554.1	000307	UvdE	326	Alexandra_298	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58927.1	000307	UvdE	324	Y3_287	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28751.1	000307	UvdE	327	YOLOSWAG_279	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38239.1	000307	UvdE	338	BN7874_070	Phage NCTB	GCA_900092385.1
ALY07193.1	000307	UvdE	344	VmeM32_00207	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21154.1	000307	UvdE	323	-	Vibrio phage vB_pir03	GCA_014319855.1
APU01450.1	000308	UvrD-helicase	434	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28935.1	000308	UvrD-helicase	434	AP1_0228	Aeromonas phage AP1	GCA_014183365.1
ATI17449.1	000308	UvrD-helicase	434	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00147.1	000308	UvrD-helicase	434	HWB28_gp003	Aeromonas phage AS-zj	GCA_002627665.1
AUE22782.1	000308	UvrD-helicase	454	Ah1_00264	Aeromonas phage Ah1	GCA_002957415.1
QAX98497.1	000308	UvrD-helicase	453	ASfcp2_161	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97889.1	000308	UvrD-helicase	434	ASswx1_246	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01262.1	000308	UvrD-helicase	433	ASwh1_198	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39411.1	000308	UvrD-helicase	420	CC2_287	Aeromonas phage CC2	GCA_000903495.1
ADQ52960.1	000308	UvrD-helicase	453	PX29p241	Aeromonas phage PX29	GCA_000920195.1
ADM79886.1	000308	UvrD-helicase	454	phiAS5_ORF0043	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53070.1	000308	UvrD-helicase	434	65p060	Aeromonas virus 65	GCA_000893255.1
AAQ17908.1	000308	UvrD-helicase	454	dda	Aeromonas virus Aeh1	GCA_000843245.1
AMS01101.1	000308	UvrD-helicase	405	AR9_g016	Bacillus phage AR9	GCA_001743835.1
ALN97744.1	000308	UvrD-helicase	154	Bp8pS_065	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97745.1	000308	UvrD-helicase	251	Bp8pS_066	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00023.1	000308	UvrD-helicase	405	PBI_PBS1_201	Bacillus virus PBS1	GCA_002601325.1
QBX06629.1	000308	UvrD-helicase	537	BcepSaruman_216	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74598.1	000308	UvrD-helicase	537	BcepSauron_218	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13644.1	000308	UvrD-helicase	444	Ccr10_gp115c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13989.1	000308	UvrD-helicase	444	Ccr2_gp114c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14677.1	000308	UvrD-helicase	444	Ccr29_gp121	Caulobacter phage Ccr29	GCA_002619485.1
ARB15032.1	000308	UvrD-helicase	444	Ccr32_gp114	Caulobacter phage Ccr32	GCA_002619505.1
ARB15364.1	000308	UvrD-helicase	444	Ccr34_gp122	Caulobacter phage Ccr34	GCA_002619525.1
ARB14333.1	000308	UvrD-helicase	444	Ccr5_gp115c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68313.1	000308	UvrD-helicase	444	CcrBL10_gp109c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69219.1	000308	UvrD-helicase	440	CcrBL9_gp195	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88023.1	000308	UvrD-helicase	427	CcrColossus_gp153	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68700.1	000308	UvrD-helicase	441	CcrPW_gp161c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69773.1	000308	UvrD-helicase	440	CcrSC_gp191	Caulobacter phage CcrSC	GCA_003443315.1
AFU87636.1	000308	UvrD-helicase	420	CcrKarma_gp119	Caulobacter virus Karma	GCA_000901575.1
AFU87285.1	000308	UvrD-helicase	444	CcrMagneto_gp115	Caulobacter virus Magneto	GCA_000903095.1
AFU86597.1	000308	UvrD-helicase	420	CcrRogue_gp115	Caulobacter virus Rogue	GCA_000900555.1
AFU88432.1	000308	UvrD-helicase	420	CcrSwift_gp114	Caulobacter virus Swift	GCA_000899655.1
AFU86950.1	000308	UvrD-helicase	420	CbK_gp118	Caulobacter virus phiCbK	GCA_000900535.1
ANS05952.1	000308	UvrD-helicase	443	ABCD_0025	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64849.1	000308	UvrD-helicase	426	S13_050	Cronobacter phage S13	GCA_001503575.1
AFC21760.1	000308	UvrD-helicase	446	GAP32_310	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97033.1	000308	UvrD-helicase	443	E_024	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT13941.1	000308	UvrD-helicase	446	PBI_121Q_44	Escherichia phage 121Q	GCA_000926855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY00396.1	000308	UvrD-helicase	446	Ecwhy1_115	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35141.1	000308	UvrD-helicase	454	ACQ29_gp461	Escherichia phage PBECO4	GCA_001041035.1
BBM61633.1	000308	UvrD-helicase	454	EO157G_0440	Escherichia phage SP27	GCA_008033345.1
AXC36715.1	000308	UvrD-helicase	446	-	Escherichia phage UB	GCA_003341455.1
ARM70835.1	000308	UvrD-helicase	437	phiC120_c129	Escherichia phage phiC120	GCA_002621185.1
QBO61752.1	000308	UvrD-helicase	446	G17_00263	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13797.1	000308	UvrD-helicase	447	vBEcoMphAPEC6_gp168c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80535.1	000308	UvrD-helicase	446	PSLUR01_00558	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78546.1	000308	UvrD-helicase	443	RB43ORF024c	Escherichia virus RB43	GCA_000863505.1
AFA44423.1	000308	UvrD-helicase	452	RaK2_00150	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78815.1	000308	UvrD-helicase	425	-	Myoviridae sp.	GCA_012593985.1
AMM43878.1	000308	UvrD-helicase	446	CBB_315	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAG41737.1	000308	UvrD-helicase	417	RSL1_ORF291	Ralstonia phage phiRSL1	GCA_000879455.1
QCW19037.1	000308	UvrD-helicase	448	7t3_0517	Salmonella phage 7t3	GCA_006083215.1
AZU98284.1	000308	UvrD-helicase	448	CPT_Munch_340	Salmonella phage Munch	GCA_004015485.1
QIG62700.1	000308	UvrD-helicase	448	SEPL_087	Salmonella phage SE_PL	GCA_011067555.1
AQW88837.1	000308	UvrD-helicase	446	BF_0312	Serratia phage BF	GCA_002619745.1
AGR48005.1	000308	UvrD-helicase	414	SmphiM12_373	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13191.1	000308	UvrD-helicase	414	PHIM19_286	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12831.1	000308	UvrD-helicase	414	PHIM7_286	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13553.1	000308	UvrD-helicase	414	PHIN3_290	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64225.1	000308	UvrD-helicase	411	KVP40.0156	Vibrio phage KVP40	GCA_000843785.1
QIW90539.1	000308	UvrD-helicase	411	GCAPEGMB_00192	Vibrio phage V07	GCA_012361095.1
QIW90883.1	000308	UvrD-helicase	411	COHAPHLL_00020	Vibrio phage V09	GCA_012361135.1
QHJ74337.1	000308	UvrD-helicase	421	VH12019_00010	Vibrio phage VH1_2019	GCA_009931825.1
AGB06830.1	000308	UvrD-helicase	421	CF80_gp043	Vibrio phage VH7D	GCA_000914495.1
QBX06316.1	000308	UvrD-helicase	421	ValB1HC_363	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60947.1	000308	UvrD-helicase	421	AVU32_gp106	Vibrio phage ValKK3	GCA_001501635.1
AGN30203.1	000308	UvrD-helicase	421	VPFG_00203	Vibrio phage nt-1	GCA_000910195.2
ALP46992.1	000308	UvrD-helicase	421	phiGrn1_0267	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47373.1	000308	UvrD-helicase	421	phiST2_0026	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54559.1	000308	UvrD-helicase	421	vBValMR10Z_18	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07016.1	000308	UvrD-helicase	426	VmeM32_00022	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37384.1	000308	UvrD-helicase	421	pp2_151	Vibriophage phi-pp2	GCA_002630725.1
SOK59121.1	000308	UvrD-helicase	446	g313	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58587.1	000308	UvrD-helicase	446	g310	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26309.1	000308	UvrD-helicase	477	g286	Yersinia phage phiR1-37	GCA_000895615.1
QIG63252.1	000309	UvrD-helicase	498	DAC16_19	Bacteroides phage DAC16	GCA_013387695.1
QIG63514.1	000309	UvrD-helicase	498	DAC19_23	Bacteroides phage DAC19	GCA_013387715.1
QIG63776.1	000309	UvrD-helicase	498	DAC20_23	Bacteroides phage DAC20	GCA_013387725.1
QIG64037.1	000309	UvrD-helicase	498	DAC22_23	Bacteroides phage DAC22	GCA_013387735.1
QIG64298.1	000309	UvrD-helicase	498	DAC23_20	Bacteroides phage DAC23	GCA_013387745.1
QIG65868.1	000309	UvrD-helicase	543	phiOC_p203	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QGT54841.1	000309	UvrD-helicase	493	b23_0226	Synechococcus phage B23	GCA_009745195.1
QGT54475.1	000309	UvrD-helicase	493	b3_0232	Synechococcus phage B3	GCA_009745215.1
AYD81249.1	000310	UvrD-helicase	495	SEA_JUSTBECAUSE_80	Streptomyces phage JustBecause	GCA_003613775.1
QJD53652.1	000310	UvrD-helicase	495	SEA_KELA_81	Streptomyces phage Kela	GCA_012934305.1
QBZ71981.1	000310	UvrD-helicase	501	SEA_KRADAL_83	Streptomyces phage Kradal	GCA_004799925.1
AXH66244.1	000310	UvrD-helicase	501	SEA_SATIS_83	Streptomyces phage Satis	GCA_003366315.1
ABS83588.1	000311	UvrD-helicase	657	0305phi8-36p023	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93558.1	000311	UvrD-helicase	650	G_299	Bacillus virus G	GCA_000917535.1
BAE47881.1	000311	UvrD-helicase	592	CST183	Clostridium phage c-st	GCA_000865225.1
AND75280.1	000312	UvrD-helicase	415	ME3_119	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QIG57888.1	000312	UvrD-helicase	420	SEA_PAULODIABOLI_201	Microbacterium phage PauloDiaboli	GCA_011067425.1
BAE47760.1	000000	UvrD-helicase+DYN-MID-AAA	746	CST062	Clostridium phage c-st	GCA_000865225.1
AMM44888.1	000313	DnaB	443	SP15_089	Bacillus phage SP-15	GCA_001754685.1
QHJ86062.1	000313	DnaB	276	KKIINIFJ_00150	Pseudomonas phage PN05	GCA_009931935.1
QDH83418.1	000314	DnaB	449	H1O15_gp009	Achromobacter phage Motura	GCA_006964305.1
APU01405.1	000314	DnaB	520	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28895.1	000314	DnaB	520	AP1_0188	Aeromonas phage AP1	GCA_014183365.1
ATI17490.1	000314	DnaB	519	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00507.1	000314	DnaB	519	HWB28_gp045	Aeromonas phage AS-zj	GCA_002627665.1
AUE22556.1	000314	DnaB	486	Ah1_00015	Aeromonas phage Ah1	GCA_002957415.1
QAX98595.1	000314	DnaB	484	ASfcp2_262	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97930.1	000314	DnaB	519	ASswx1_287	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01218.1	000314	DnaB	522	ASwh1_153	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39512.1	000314	DnaB	520	CC2_243	Aeromonas phage CC2	GCA_000903495.1
ADQ52731.1	000314	DnaB	484	PX29p012	Aeromonas phage PX29	GCA_000920195.1
ADM79984.1	000314	DnaB	484	phiAS5_ORF0141	Aeromonas phage phiAS5	GCA_000887715.1
AAR90925.1	000314	DnaB	520	65p013	Aeromonas virus 65	GCA_000893255.1
AAQ17668.1	000314	DnaB	485	41	Aeromonas virus Aeh1	GCA_000843245.1
ASV44692.2	000314	DnaB	440	FDI40_gp070	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93485.1	000314	DnaB	470	G_226	Bacillus virus G	GCA_000917535.1
QBX06729.1	000314	DnaB	441	BcepSaruman_316	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74698.1	000314	DnaB	457	BcepSauron_318	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63692.1	000314	DnaB	345	CP21_232	Campylobacter virus CP21	GCA_000902535.1
ANS05947.1	000314	DnaB	478	ABCD_0035	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65050.1	000314	DnaB	475	S13_253	Cronobacter phage S13	GCA_001503575.1
AFC21736.1	000314	DnaB	500	GAP32_286	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97045.1	000314	DnaB	479	E_036	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56850.1	000314	DnaB	434	CPXG_00047	Cyanophage P-RSM6	GCA_000906155.1
AJK27643.1	000314	DnaB	455	PTIM40_178	Cyanophage P-TIM40	GCA_001470935.1
AOO14362.1	000314	DnaB	459	Sn110110_168	Cyanophage S-RIM14	GCA_002599065.1
AOO15011.1	000314	DnaB	459	W1230910_165	Cyanophage S-RIM14	GCA_002599125.1
AMO43172.1	000314	DnaB	453	R1080702_163	Cyanophage S-RIM32	GCA_001754165.1
AMO43398.1	000314	DnaB	463	W270710_154	Cyanophage S-RIM44	GCA_002599145.1
AOO11642.1	000314	DnaB	463	ES420910_161	Cyanophage S-RIM44	GCA_002599165.1
AOO11870.1	000314	DnaB	463	Np050604_154	Cyanophage S-RIM44	GCA_002599185.1
AOO12108.1	000314	DnaB	463	Np200711_162	Cyanophage S-RIM44	GCA_002599205.1
AOO12343.1	000314	DnaB	463	Np420711_161	Cyanophage S-RIM44	GCA_002599225.1
AOO12571.1	000314	DnaB	463	Sn080709_154	Cyanophage S-RIM44	GCA_002599245.1
AOO12808.1	000314	DnaB	463	Sn130910_161	Cyanophage S-RIM44	GCA_002599265.1
AOO13037.1	000314	DnaB	463	W2100709_155	Cyanophage S-RIM44	GCA_002599285.1
AGH07503.1	000314	DnaB	461	CYVG_00059	Cyanophage S-SSM6a	GCA_002710385.1
AGG54447.1	000314	DnaB	436	CYWG_00163	Cyanophage S-SSM6b	GCA_002710425.1
AXG67045.1	000314	DnaB	473	AD1_001	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79806.1	000314	DnaB	459	JA11_001	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66404.1	000314	DnaB	459	JA13_001	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66727.1	000314	DnaB	487	JA29_001	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67375.1	000314	DnaB	459	JA33_001	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08283.1	000314	DnaB	502	Alexandra_1	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58641.1	000314	DnaB	498	Y3_001	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28488.1	000314	DnaB	473	YOLOSWAG_1	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT13917.1	000314	DnaB	506	PBI_121Q_20	Escherichia phage 121Q	GCA_000926855.1
QAY00421.1	000314	DnaB	506	Ecwhy1_140	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35164.1	000314	DnaB	506	ACQ29_gp484	Escherichia phage PBECO4	GCA_001041035.1
BBM61609.1	000314	DnaB	506	EO157G_0200	Escherichia phage SP27	GCA_008033345.1
AXC36737.1	000314	DnaB	506	-	Escherichia phage UB	GCA_003341455.1
ARM70859.1	000314	DnaB	480	phiC120_c153	Escherichia phage phiC120	GCA_002621185.1
QBO61775.1	000314	DnaB	506	G17_00286	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13819.1	000314	DnaB	506	vBEcoMphAPEC6_gp190c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80512.1	000314	DnaB	506	PSLUR01_00535	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78557.1	000314	DnaB	478	RB43ORF035c	Escherichia virus RB43	GCA_000863505.1
AFA44401.1	000314	DnaB	522	RaK2_00128	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72835.1	000314	DnaB	463	-	Myoviridae sp.	GCA_003657725.1
QHJ78882.1	000314	DnaB	479	-	Myoviridae sp.	GCA_012593985.1
QIG65667.1	000314	DnaB	459	phiOC_p001	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43855.1	000314	DnaB	498	CBB_291	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38261.1	000314	DnaB	423	BN7874_092	Phage NCTB	GCA_900092385.1
AGH26285.1	000314	DnaB	457	CPMG_00185	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44564.1	000314	DnaB	460	PSSM2_186	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12409.1	000314	DnaB	467	PRTG_00256	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93489.1	000314	DnaB	459	AVU42_gp152	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99257.1	000314	DnaB	467	Syn1_156	Prochlorococcus phage Syn1	GCA_000892495.1
AFH14717.1	000314	DnaB	492	Lu11_0180	Pseudomonas phage Lu11	GCA_000897175.1

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QHJ86006.1	000314	DnaB	455	KKIINIFJ_00094	Pseudomonas phage PN05	GCA_009931935.1
AGS81995.1	000314	DnaB	488	PaBG_00110	Pseudomonas phage PaBG	GCA_000912555.1
QCG76105.1	000314	DnaB	479	EST35_0224	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41595.1	000314	DnaB	447	RSL1_ORF149	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44170.1	000314	DnaB	500	PBI_SCTP2_155	Salicola phage SCTP-2	GCA_002625545.1
QCW19014.1	000314	DnaB	514	7t3_0494	Salmonella phage 7t3	GCA_006083215.1
AZU98261.1	000314	DnaB	514	CPT_Munch_317	Salmonella phage Munch	GCA_004015485.1
QIG62723.1	000314	DnaB	514	SEPL_110	Salmonella phage SE_PL	GCA_011067555.1
AQW88814.1	000314	DnaB	493	BF_0289	Serratia phage BF	GCA_002619745.1
AGR47659.1	000314	DnaB	473	SmphiM12_027	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12925.1	000314	DnaB	473	PHIM19_18	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12565.1	000314	DnaB	473	PHIM7_17	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13297.1	000314	DnaB	473	PHIN3_32	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81350.1	000314	DnaB	458	SEA_JUSTBECAUSE_185	Streptomyces phage JustBecause	GCA_003613775.1
QJD53753.1	000314	DnaB	453	SEA_KELA_183	Streptomyces phage Kela	GCA_012934305.1
QBZ72079.1	000314	DnaB	459	SEA_KRADAL_183	Streptomyces phage Kradal	GCA_004799925.1
AXH66342.1	000314	DnaB	459	SEA_SATIS_183	Streptomyces phage Satis	GCA_003366315.1
AIX30655.1	000314	DnaB	456	Syn7803US37_178	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54918.1	000314	DnaB	455	b23_0305	Synechococcus phage B23	GCA_009745195.1
QGT54553.1	000314	DnaB	455	b3_0312	Synechococcus phage B3	GCA_009745215.1
ASR76209.1	000314	DnaB	458	PBI_BELLAMY_165	Synechococcus phage Bellamy	GCA_002627525.1
QCW22929.1	000314	DnaB	457	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50614.1	000314	DnaB	312	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59624.1	000314	DnaB	462	S330809_163	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59386.1	000314	DnaB	462	C440309_163	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59862.1	000314	DnaB	462	N231010_163	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70542.1	000314	DnaB	455	HOU04_gp143	Synechococcus phage S-T4	GCA_003443335.1
QJT70162.1	000314	DnaB	458	SynMITS9220M01_149	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64081.1	000314	DnaB	466	KVP40.0010	Vibrio phage KVP40	GCA_000843785.1
QIW90406.1	000314	DnaB	466	GCAPEGMB_00059	Vibrio phage V07	GCA_012361095.1
QIW91023.1	000314	DnaB	466	COHAPHLL_00160	Vibrio phage V09	GCA_012361135.1
QHJ74193.1	000314	DnaB	427	VH12019_00274	Vibrio phage VH1_2019	GCA_009931825.1
AGB07017.1	000314	DnaB	427	CF80_gp230	Vibrio phage VH7D	GCA_000914495.1
QBX06079.1	000314	DnaB	466	ValB1HC_125	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04491.1	000314	DnaB	516	ValB1MD_130	Vibrio phage ValB1MD	GCA_004138815.1
AJT61093.1	000314	DnaB	466	AVU32_gp252	Vibrio phage ValKK3	GCA_001501635.1
AGN30060.2	000314	DnaB	429	VPFG_00057	Vibrio phage nt-1	GCA_000910195.2
ALP46990.1	000314	DnaB	427	phiGrn1_0125	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47371.1	000314	DnaB	427	phiST2_0256	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54705.1	000314	DnaB	466	vBValMR10Z_164	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37244.1	000314	DnaB	427	pp2_010	Vibriophage phi-pp2	GCA_002630725.1
BBA65414.1	000314	DnaB	519	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96437.1	000314	DnaB	517	Xoosp13_251	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59097.1	000314	DnaB	493	g289	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58561.1	000314	DnaB	493	g284	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000246	000314	DnaB	397	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000195	000314	DnaB	503	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG63464.1	000315	DnaB	453	DAC16_235	Bacteroides phage DAC16	GCA_013387695.1
QIG63727.1	000315	DnaB	450	DAC19_240	Bacteroides phage DAC19	GCA_013387715.1
QIG63988.1	000315	DnaB	450	DAC20_239	Bacteroides phage DAC20	GCA_013387725.1
QIG64252.1	000315	DnaB	453	DAC22_242	Bacteroides phage DAC22	GCA_013387735.1
QIG64508.1	000315	DnaB	453	DAC23_234	Bacteroides phage DAC23	GCA_013387745.1
AND75248.1	000316	UvsX-RecA	263	ME3_87	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01410.1	000316	UvsX-RecA	368	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29093.1	000316	UvsX-RecA	378	AP1_0386	Aeromonas phage AP1	GCA_014183365.1
ATI17487.1	000316	UvsX-RecA	369	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00511.1	000316	UvsX-RecA	369	HWB28_gp041	Aeromonas phage AS-zj	GCA_002627665.1
AUE22560.1	000316	UvsX-RecA	408	Ah1_00019	Aeromonas phage Ah1	GCA_002957415.1
QAX98597.1	000316	UvsX-RecA	411	ASfcp2_264	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97927.1	000316	UvsX-RecA	369	ASswx1_284	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01222.1	000316	UvsX-RecA	369	ASwh1_157	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39398.1	000316	UvsX-RecA	369	CC2_247	Aeromonas phage CC2	GCA_000903495.1
ADQ52733.1	000316	UvsX-RecA	411	PX29p014	Aeromonas phage PX29	GCA_000920195.1
ADM79986.1	000316	UvsX-RecA	410	phiAS5_ORF0143	Aeromonas phage phiAS5	GCA_000887715.1
AAR90919.1	000316	UvsX-RecA	368	65p019	Aeromonas virus 65	GCA_000893255.1
AAQ17671.1	000316	UvsX-RecA	411	uvsX	Aeromonas virus Aeh1	GCA_000843245.1
ASV44705.1	000316	UvsX-RecA	368	FDI40_gp106	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83593.1	000316	UvsX-RecA	457	0305phi8-36p241	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44893.1	000316	UvsX-RecA	239	SP15_094	Bacillus phage SP-15	GCA_001754685.1
AEO93665.1	000316	UvsX-RecA	401	G_407	Bacillus virus G	GCA_000917535.1
QIG63484.1	000316	UvsX-RecA	469	DAC16_255	Bacteroides phage DAC16	GCA_013387695.1
QIG63746.1	000316	UvsX-RecA	469	DAC19_259	Bacteroides phage DAC19	GCA_013387715.1
QIG64007.1	000316	UvsX-RecA	469	DAC20_258	Bacteroides phage DAC20	GCA_013387725.1
QIG64271.1	000316	UvsX-RecA	469	DAC22_261	Bacteroides phage DAC22	GCA_013387735.1
QIG64528.1	000316	UvsX-RecA	469	DAC23_254	Bacteroides phage DAC23	GCA_013387745.1
ANS05957.1	000316	UvsX-RecA	380	ABCD_0037	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65048.1	000316	UvsX-RecA	356	S13_251	Cronobacter phage S13	GCA_001503575.1
AFC21722.1	000316	UvsX-RecA	376	GAP32_272	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97047.1	000316	UvsX-RecA	382	E_038	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56852.1	000316	UvsX-RecA	339	CPXG_00049	Cyanophage P-RSM6	GCA_000906155.1
AJK27641.1	000316	UvsX-RecA	339	PTIM40_176	Cyanophage P-TIM40	GCA_001470935.1
AOO14360.1	000316	UvsX-RecA	336	Sn110110_166	Cyanophage S-RIM14	GCA_002599065.1
AOO15009.1	000316	UvsX-RecA	336	W1230910_163	Cyanophage S-RIM14	GCA_002599125.1
AMO43171.1	000316	UvsX-RecA	355	R1080702_162	Cyanophage S-RIM32	GCA_001754165.1
AMO43397.1	000316	UvsX-RecA	344	W270710_153	Cyanophage S-RIM44	GCA_002599145.1
AOO11641.1	000316	UvsX-RecA	344	ES420910_160	Cyanophage S-RIM44	GCA_002599165.1
AOO11869.1	000316	UvsX-RecA	344	Np050604_153	Cyanophage S-RIM44	GCA_002599185.1
AOO12107.1	000316	UvsX-RecA	344	Np200711_161	Cyanophage S-RIM44	GCA_002599205.1
AOO12342.1	000316	UvsX-RecA	344	Np420711_160	Cyanophage S-RIM44	GCA_002599225.1
AOO12570.1	000316	UvsX-RecA	344	Sn080709_153	Cyanophage S-RIM44	GCA_002599245.1
AOO12807.1	000316	UvsX-RecA	344	Sn130910_160	Cyanophage S-RIM44	GCA_002599265.1
AOO13036.1	000316	UvsX-RecA	344	W2100709_154	Cyanophage S-RIM44	GCA_002599285.1
AGH07501.1	000316	UvsX-RecA	333	CYVG_00057	Cyanophage S-SSM6a	GCA_002710385.1
AGG54449.1	000316	UvsX-RecA	336	CYWG_00165	Cyanophage S-SSM6b	GCA_002710425.1
AIT13904.1	000316	UvsX-RecA	372	PBI_121Q_7	Escherichia phage 121Q	GCA_000926855.1
QAY00433.1	000316	UvsX-RecA	372	Ecwhy1_153	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35177.1	000316	UvsX-RecA	372	ACQ29_gp497	Escherichia phage PBECO4	GCA_001041035.1
BBM61596.1	000316	UvsX-RecA	372	EO157G_0070	Escherichia phage SP27	GCA_008033345.1
AXC36749.1	000316	UvsX-RecA	372	-	Escherichia phage UB	GCA_003341455.1
ARM70861.1	000316	UvsX-RecA	390	phiC120_c155	Escherichia phage phiC120	GCA_002621185.1
QBO61788.1	000316	UvsX-RecA	372	G17_00299	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13832.1	000316	UvsX-RecA	372	vBEcoMphAPEC6_gp203c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80499.1	000316	UvsX-RecA	372	PSLUR01_00522	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78559.1	000316	UvsX-RecA	386	RB43ORF037c	Escherichia virus RB43	GCA_000863505.1
AFA44387.1	000316	UvsX-RecA	370	RaK2_00114	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72831.1	000316	UvsX-RecA	378	-	Myoviridae sp.	GCA_003657725.1
QHJ78884.1	000316	UvsX-RecA	356	-	Myoviridae sp.	GCA_012593985.1
QIG65668.1	000316	UvsX-RecA	369	phiOC_p002	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43842.1	000316	UvsX-RecA	376	CBB_278	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26287.1	000316	UvsX-RecA	338	CPMG_00187	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44563.1	000316	UvsX-RecA	335	PSSM2_185	Prochlorococcus phage P-SSM2	GCA_000859585.1
AIR93487.1	000316	UvsX-RecA	333	AVU42_gp150	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99256.1	000316	UvsX-RecA	344	Syn1_155	Prochlorococcus phage Syn1	GCA_000892495.1
QHJ86017.1	000316	UvsX-RecA	433	KKIINIFJ_00105	Pseudomonas phage PN05	GCA_009931935.1
QCG76091.1	000316	UvsX-RecA	423	EST35_0210	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44219.1	000316	UvsX-RecA	656	PBI_SCTP2_204	Salicola phage SCTP-2	GCA_002625545.1
QCW19001.1	000316	UvsX-RecA	373	7t3_0481	Salmonella phage 7t3	GCA_006083215.1
AZU98248.1	000316	UvsX-RecA	373	CPT_Munch_304	Salmonella phage Munch	GCA_004015485.1
QIG62736.1	000316	UvsX-RecA	373	SEPL_123	Salmonella phage SE_PL	GCA_011067555.1
AQW88801.1	000316	UvsX-RecA	378	BF_0276	Serratia phage BF	GCA_002619745.1
AGR47660.1	000316	UvsX-RecA	355	SmphiM12_028	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12926.1	000316	UvsX-RecA	355	PHIM19_19	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12566.1	000316	UvsX-RecA	355	PHIM7_18	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13298.1	000316	UvsX-RecA	355	PHIN3_33	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30653.1	000316	UvsX-RecA	335	Syn7803US37_176	Synechococcus phage ACG-2014f	GCA_002594065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54916.1	000316	UvsX-RecA	351	b23_0303	Synechococcus phage B23	GCA_009745195.1
QGT54551.1	000316	UvsX-RecA	351	b3_0310	Synechococcus phage B3	GCA_009745215.1
ASR76207.1	000316	UvsX-RecA	334	PBI_BELLAMY_163	Synechococcus phage Bellamy	GCA_002627525.1
QCW22928.1	000316	UvsX-RecA	335	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59623.1	000316	UvsX-RecA	337	S330809_162	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59385.1	000316	UvsX-RecA	337	C440309_162	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59861.1	000316	UvsX-RecA	337	N231010_162	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70543.1	000316	UvsX-RecA	334	HOU04_gp144	Synechococcus phage S-T4	GCA_003443335.1
QJT70159.1	000316	UvsX-RecA	334	SynMITS9220M01_146	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64079.1	000316	UvsX-RecA	366	KVP40.0008	Vibrio phage KVP40	GCA_000843785.1
QIW90405.1	000316	UvsX-RecA	366	GCAPEGMB_00058	Vibrio phage V07	GCA_012361095.1
QIW91024.1	000316	UvsX-RecA	366	COHAPHLL_00161	Vibrio phage V09	GCA_012361135.1
QHJ74191.1	000316	UvsX-RecA	366	VH12019_00272	Vibrio phage VH1_2019	GCA_009931825.1
AGB07015.1	000316	UvsX-RecA	366	CF80_gp228	Vibrio phage VH7D	GCA_000914495.1
QBX06081.1	000316	UvsX-RecA	366	ValB1HC_127	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61095.1	000316	UvsX-RecA	366	AVU32_gp254	Vibrio phage ValKK3	GCA_001501635.1
AGN30058.1	000316	UvsX-RecA	366	VPFG_00055	Vibrio phage nt-1	GCA_000910195.2
ALP47000.1	000316	UvsX-RecA	366	phiGrn1_0123	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47381.1	000316	UvsX-RecA	366	phiST2_0254	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54707.1	000316	UvsX-RecA	366	vBValMR10Z_166	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07082.1	000316	UvsX-RecA	304	VmeM32_00093	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37242.1	000316	UvsX-RecA	366	pp2_008	Vibriophage phi-pp2	GCA_002630725.1
BBA65399.1	000316	UvsX-RecA	377	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96424.1	000316	UvsX-RecA	367	Xoosp13_238	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59084.1	000316	UvsX-RecA	378	g276	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58548.1	000316	UvsX-RecA	378	g271	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000830	000316	UvsX-RecA	305	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000573	000316	UvsX-RecA	325	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ALY07080.1	000316	UvsX-RecA	183	VmeM32_00091	Vibrio phage vB_VmeM-32	GCA_002608825.1
prevph1000000484	000317	HINT	158	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000365	000317	HINT	158	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70383.1	000318	UvsX-RecA	488	CF8_0214	Aeromonas phage CF8	GCA_006384595.2
QDJ97382.1	000318	UvsX-RecA	487	D6_0223	Aeromonas phage D6	GCA_007051205.2
QDH47052.1	000318	UvsX-RecA	487	LAh10_137	Aeromonas phage LAh10	GCA_006863975.1
QDJ96725.1	000318	UvsX-RecA	488	PS1_0214	Aeromonas phage PS1	GCA_007051165.2
QFR59358.1	000318	UvsX-RecA	488	PS2_0216	Aeromonas phage PS2	GCA_009388305.2
AFO71411.1	000318	UvsX-RecA	492	CR5_191	Cronobacter phage CR5	GCA_000910235.1
QBZ70768.1	000318	UvsX-RecA	491	pETSU_187	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59868.1	000318	UvsX-RecA	497	SEGD1_221	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07624.1	000318	UvsX-RecA	492	DERBICUS_198	Erwinia phage Derbicus	GCA_004521655.1
AHI60300.1	000318	UvsX-RecA	461	Ea357_149	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49867.1	000318	UvsX-RecA	499	MACHINA_229	Erwinia phage Machina	GCA_002758035.1
AGX01896.1	000318	UvsX-RecA	475	uvsX	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07258.1	000318	UvsX-RecA	461	REBECCA_151	Erwinia phage Rebecca	GCA_004521635.1
AXF51370.1	000318	UvsX-RecA	496	WELLINGTON_244	Erwinia phage Wellington	GCA_003344985.1
AFQ96684.1	000318	UvsX-RecA	494	G173_gp139	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48251.1	000318	UvsX-RecA	494	ASESINO_238	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85938.1	000318	UvsX-RecA	461	BOSOLAPHORUS_151	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48524.1	000318	UvsX-RecA	498	CAITLIN_229	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48801.1	000318	UvsX-RecA	498	CHRISDB_239	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52253.1	000318	UvsX-RecA	461	DM_155	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86257.1	000318	UvsX-RecA	461	DESERTFOX_150	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49048.1	000318	UvsX-RecA	492	EARLPHILLIPIV_199	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49311.1	000318	UvsX-RecA	499	HUXLEY_229	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03695.1	000318	UvsX-RecA	475	JOAD_220	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49596.1	000318	UvsX-RecA	496	KWAN_244	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86579.1	000318	UvsX-RecA	461	MADMEL_151	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86903.1	000318	UvsX-RecA	461	MORTIMER_154	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50139.1	000318	UvsX-RecA	499	PARSHIK_230	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50395.1	000318	UvsX-RecA	492	PHOBOS_205	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51931.1	000318	UvsX-RecA	461	RAY_150	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03452.1	000318	UvsX-RecA	475	RISINGSUN_218	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51615.1	000318	UvsX-RecA	461	SIMMY50_153	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64962.1	000318	UvsX-RecA	461	SPECIALG_152	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50664.1	000318	UvsX-RecA	494	STRATTON_239	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86057.1	000318	UvsX-RecA	497	ACEC001_2140	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64034.1	000318	UvsX-RecA	496	Goslar_00243	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72074.1	000318	UvsX-RecA	489	N1M2_211	Klebsiella phage N1M2	GCA_010092605.1
QGZ14500.1	000318	UvsX-RecA	477	HWC77_gp137	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24080.1	000318	UvsX-RecA	466	-	Proteus phage 10	GCA_014071245.1
ABY63066.1	000318	UvsX-RecA	487	201phi2-1p237	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27267.1	000318	UvsX-RecA	489	PPEV_gp173	Pseudomonas phage EL	GCA_000866825.1
ANM44946.1	000318	UvsX-RecA	479	KTN4_188	Pseudomonas phage KTN4	GCA_002607225.1
ARV77331.1	000318	UvsX-RecA	495	NOXIFER_162	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89703.1	000318	UvsX-RecA	491	OBP_266	Pseudomonas phage OBP	GCA_000896635.1
QBX32334.1	000318	UvsX-RecA	479	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76856.1	000318	UvsX-RecA	477	PHABIO_225	Pseudomonas phage Phabio	GCA_002624965.1
AEH03598.1	000318	UvsX-RecA	476	175	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02735.1	000318	UvsX-RecA	476	PSA21_209	Pseudomonas phage Psa21	GCA_004340405.1
ATN94768.1	000318	UvsX-RecA	479	SL2_191	Pseudomonas phage SL2	GCA_002956015.1
QJB22824.1	000318	UvsX-RecA	479	fnug_181	Pseudomonas phage fnug	GCA_012837215.1
QEM41907.1	000318	UvsX-RecA	479	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83053.1	000318	UvsX-RecA	479	PHIKZ152	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19033.1	000318	UvsX-RecA	468	FDH28_gp059	Ralstonia phage RP12	GCA_002617345.1
BAW19318.1	000318	UvsX-RecA	468	-	Ralstonia phage RP31	GCA_002617365.1
BAS04845.2	000318	UvsX-RecA	466	AVU11_gp053	Ralstonia phage RSF1	GCA_001500875.1
BAQ02578.2	000318	UvsX-RecA	483	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20904.1	000318	UvsX-RecA	497	-	Salmonella phage JN03	GCA_014319805.1
AWN09131.1	000318	UvsX-RecA	493	MLDJOKPK_00224	Salmonella phage SPAsTU	GCA_003183805.1
AEP84049.1	000318	UvsX-RecA	497	SPN3US_0216	Salmonella phage SPN3US	GCA_001042275.1
QKE54454.1	000318	UvsX-RecA	462	ACSA002_1400	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65412.1	000318	UvsX-RecA	474	2050HW_00077	Serratia phage 2050HW	GCA_002628125.1
QDB71191.1	000318	UvsX-RecA	474	CPT_Moabite_161	Serratia phage Moabite	GCA_006384735.1
QFP93076.1	000318	UvsX-RecA	478	-	Serratia phage PCH45	GCA_009187865.1
QAU04234.1	000318	UvsX-RecA	477	HWC03_gp079	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23129.1	000318	UvsX-RecA	478	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80950.1	000318	UvsX-RecA	478	Aphrodite1_0002	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70753.1	000318	UvsX-RecA	491	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47598.1	000318	UvsX-RecA	478	HWC35_gp204	Vibrio phage USC-1	GCA_006864065.1
BAW98413.1	000318	UvsX-RecA	478	FDH33_gp204	Vibrio phage pTD1	GCA_002618825.1
AQT28089.1	000318	UvsX-RecA	486	pVa21_148	Vibrio phage pVa-21	GCA_002619305.1
QAX96781.1	000318	UvsX-RecA	487	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97100.1	000318	UvsX-RecA	487	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96146.1	000318	UvsX-RecA	487	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96464.1	000318	UvsX-RecA	487	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20963.1	000318	UvsX-RecA	575	-	Vibrio phage vB_pir03	GCA_014319855.1
QDH83446.1	000319	SIG+UvsX-RecA	533	H1O15_gp038	Achromobacter phage Motura	GCA_006964305.1
QBX06655.1	000319	SIG+UvsX-RecA	498	BcepSaruman_242	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74623.1	000319	SIG+UvsX-RecA	498	BcepSauron_243	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67283.1	000319	SIG+UvsX-RecA	841	AD1_239	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80027.1	000319	SIG+UvsX-RecA	501	JA11_222	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66626.1	000319	SIG+UvsX-RecA	501	JA13_223	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66950.1	000319	SIG+UvsX-RecA	501	JA29_224	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67597.1	000319	SIG+UvsX-RecA	501	JA33_223	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08507.1	000319	SIG+UvsX-RecA	844	Alexandra_248	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58883.1	000319	SIG+UvsX-RecA	830	Y3_243	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28715.1	000319	SIG+UvsX-RecA	836	YOLOSWAG_238	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38190.1	000319	SIG+UvsX-RecA	503	BN7874_021	Phage NCTB	GCA_900092385.1
AFH14708.1	000319	SIG+UvsX-RecA	506	Lu11_0173	Pseudomonas phage Lu11	GCA_000897175.1
AGS82000.1	000319	SIG+UvsX-RecA	501	PaBG_00116	Pseudomonas phage PaBG	GCA_000912555.1
BAG41670.1	000319	SIG+UvsX-RecA	481	RSL1_ORF221	Ralstonia phage phiRSL1	GCA_000879455.1
AMS01170.1	000320	UvsX-RecA	421	AR9_g086	Bacillus phage AR9	GCA_001743835.1
ALN97833.1	000320	UvsX-RecA	426	Bp8pS_154	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00102.1	000320	UvsX-RecA	421	PBI_PBS1_280	Bacillus virus PBS1	GCA_002601325.1
CCE26273.1	000320	UvsX-RecA	407	g250	Yersinia phage phiR1-37	GCA_000895615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QMV29138.1	000000	UvsX-RecA	112	AP1_0435	Aeromonas phage AP1	GCA_014183365.1
QCG76089.1	000000	UvsX-RecA	81	EST35_0208	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ABY63291.1	000000	UvsX-RecA	166	201phi2-1p468	Pseudomonas phage 201phi2-1	GCA_000875305.1
APU01452.1	000321	UvsY	138	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29080.1	000321	UvsY	138	AP1_0373	Aeromonas phage AP1	GCA_014183365.1
ATI17447.1	000321	UvsY	138	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00149.1	000321	UvsY	138	HWB28_gp001	Aeromonas phage AS-zj	GCA_002627665.1
AUE22779.1	000321	UvsY	136	Ah1_00261	Aeromonas phage Ah1	GCA_002957415.1
QAX97887.1	000321	UvsY	138	ASswx1_244	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39533.1	000321	UvsY	138	CC2_289	Aeromonas phage CC2	GCA_000903495.1
ADQ52957.1	000321	UvsY	136	PX29p238	Aeromonas phage PX29	GCA_000920195.1
ADM79883.1	000321	UvsY	136	phiAS5_ORF0040	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53072.1	000321	UvsY	138	65p062	Aeromonas virus 65	GCA_000893255.1
AAQ17905.1	000321	UvsY	136	uvsY	Aeromonas virus Aeh1	GCA_000843245.1
ANS06054.1	000321	UvsY	140	ABCD_0218	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64854.1	000321	UvsY	136	S13_055	Cronobacter phage S13	GCA_001503575.1
AON97234.1	000321	UvsY	140	E_226	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56888.1	000321	UvsY	132	CPXG_00085	Cyanophage P-RSM6	GCA_000906155.1
AJK27569.1	000321	UvsY	142	PTIM40_142	Cyanophage P-TIM40	GCA_001470935.1
AOO14316.1	000321	UvsY	142	Sn110110_122	Cyanophage S-RIM14	GCA_002599065.1
AOO14965.1	000321	UvsY	142	W1230910_119	Cyanophage S-RIM14	GCA_002599125.1
AMO43147.1	000321	UvsY	157	R1080702_138	Cyanophage S-RIM32	GCA_001754165.1
AMO43371.1	000321	UvsY	157	W270710_127	Cyanophage S-RIM44	GCA_002599145.1
AOO11615.1	000321	UvsY	157	ES420910_134	Cyanophage S-RIM44	GCA_002599165.1
AOO11843.1	000321	UvsY	157	Np050604_127	Cyanophage S-RIM44	GCA_002599185.1
AOO12080.1	000321	UvsY	157	Np200711_134	Cyanophage S-RIM44	GCA_002599205.1
AOO12316.1	000321	UvsY	157	Np420711_134	Cyanophage S-RIM44	GCA_002599225.1
AOO12544.1	000321	UvsY	157	Sn080709_127	Cyanophage S-RIM44	GCA_002599245.1
AOO12781.1	000321	UvsY	157	Sn130910_134	Cyanophage S-RIM44	GCA_002599265.1
AOO13010.1	000321	UvsY	157	W2100709_128	Cyanophage S-RIM44	GCA_002599285.1
AGH07464.1	000321	UvsY	141	CYVG_00020	Cyanophage S-SSM6a	GCA_002710385.1
AGG54486.1	000321	UvsY	142	CYWG_00202	Cyanophage S-SSM6b	GCA_002710425.1
ARM70746.1	000321	UvsY	164	phiC120_c39	Escherichia phage phiC120	GCA_002621185.1
AAX78751.1	000321	UvsY	140	RB43ORF229w	Escherichia virus RB43	GCA_000863505.1
QHJ78811.1	000321	UvsY	136	-	Myoviridae sp.	GCA_012593985.1
QIG65688.1	000321	UvsY	143	phiOC_p022	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26314.1	000321	UvsY	137	CPMG_00215	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44516.1	000321	UvsY	142	PSSM2_138	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12451.1	000321	UvsY	142	PRTG_00303	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93451.1	000321	UvsY	144	AVU42_gp113	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99229.1	000321	UvsY	157	Syn1_128	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47685.1	000321	UvsY	145	SmphiM12_053	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12947.1	000321	UvsY	145	PHIM19_40	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12587.1	000321	UvsY	145	PHIM7_39	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13321.1	000321	UvsY	146	PHIN3_56	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30622.1	000321	UvsY	144	Syn7803US37_145	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54896.1	000321	UvsY	141	b23_0283	Synechococcus phage B23	GCA_009745195.1
QGT54531.1	000321	UvsY	141	b3_0290	Synechococcus phage B3	GCA_009745215.1
ASR76181.1	000321	UvsY	144	PBI_BELLAMY_136	Synechococcus phage Bellamy	GCA_002627525.1
QCW22892.1	000321	UvsY	144	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50658.1	000321	UvsY	144	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59596.1	000321	UvsY	157	S330809_135	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59358.1	000321	UvsY	157	C440309_135	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59834.1	000321	UvsY	157	N231010_135	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70572.1	000321	UvsY	142	HOU04_gp173	Synechococcus phage S-T4	GCA_003443335.1
QJT70123.1	000321	UvsY	145	SynMITS9220M01_110	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64450.1	000321	UvsY	137	KVP40.0382	Vibrio phage KVP40	GCA_000843785.1
QIW90395.1	000321	UvsY	137	GCAPEGMB_00048	Vibrio phage V07	GCA_012361095.1
QIW91034.1	000321	UvsY	137	COHAPHLL_00171	Vibrio phage V09	GCA_012361135.1
QHJ74562.1	000321	UvsY	137	VH12019_00262	Vibrio phage VH1_2019	GCA_009931825.1
QBX06091.1	000321	UvsY	137	ValB1HC_137	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61105.1	000321	UvsY	137	AVU32_gp264	Vibrio phage ValKK3	GCA_001501635.1
AGN30050.1	000321	UvsY	137	VPFG_00045	Vibrio phage nt-1	GCA_000910195.2
ALP47144.1	000321	UvsY	137	phiGrn1_0113	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47531.1	000321	UvsY	137	phiST2_0244	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54717.1	000321	UvsY	137	vBValMR10Z_176	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07012.1	000321	UvsY	135	VmeM32_00018	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37613.1	000321	UvsY	137	pp2_381	Vibriophage phi-pp2	GCA_002630725.1
ASV44701.1	000322	UvsY	155	FDI40_gp092	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21723.1	000322	UvsY	154	GAP32_273	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13905.1	000322	UvsY	153	PBI_121Q_8	Escherichia phage 121Q	GCA_000926855.1
QAY00432.1	000322	UvsY	153	Ecwhy1_152	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35176.1	000322	UvsY	153	ACQ29_gp496	Escherichia phage PBECO4	GCA_001041035.1
BBM61597.1	000322	UvsY	153	EO157G_0080	Escherichia phage SP27	GCA_008033345.1
AXC36748.1	000322	UvsY	153	-	Escherichia phage UB	GCA_003341455.1
QBO61787.1	000322	UvsY	153	G17_00298	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13831.1	000322	UvsY	153	vBEcoMphAPEC6_gp202c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80500.1	000322	UvsY	153	PSLUR01_00523	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44389.1	000322	UvsY	154	RaK2_00116	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72765.1	000322	UvsY	156	-	Myoviridae sp.	GCA_003657725.1
AMM43843.1	000322	UvsY	154	CBB_279	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76095.1	000322	UvsY	154	EST35_0214	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44214.1	000322	UvsY	156	PBI_SCTP2_199	Salicola phage SCTP-2	GCA_002625545.1
QCW19002.1	000322	UvsY	153	7t3_0482	Salmonella phage 7t3	GCA_006083215.1
AZU98249.1	000322	UvsY	153	CPT_Munch_305	Salmonella phage Munch	GCA_004015485.1
QIG62735.1	000322	UvsY	153	SEPL_122	Salmonella phage SE_PL	GCA_011067555.1
AQW88802.1	000322	UvsY	154	BF_0277	Serratia phage BF	GCA_002619745.1
SOK59085.1	000322	UvsY	154	g277	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58549.1	000322	UvsY	154	g272	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BBA65397.1	000000	UvsY	154	-	Xanthomonas phage XacN1	GCA_003173815.1
QDB70260.1	000323	Virion-MPTase+TM+TM	457	CF8_0092	Aeromonas phage CF8	GCA_006384595.2
QDJ97238.1	000323	Virion-MPTase+TM+TM	451	D6_0078	Aeromonas phage D6	GCA_007051205.2
QDH47055.1	000323	Virion-MPTase+TM+TM	451	LAh10_10	Aeromonas phage LAh10	GCA_006863975.1
QDJ96851.1	000323	Virion-MPTase+TM+TM	449	PS1_0092	Aeromonas phage PS1	GCA_007051165.2
QFR59483.1	000323	Virion-MPTase+TM+TM	449	PS2_0092	Aeromonas phage PS2	GCA_009388305.2
AFO71266.1	000323	Virion-MPTase+TM+TM	446	CR5_046	Cronobacter phage CR5	GCA_000910235.1
QBZ70621.1	000323	Virion-MPTase+TM+TM	441	pETSU_040	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59696.1	000323	Virion-MPTase+TM+TM	450	SEGD1_047	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07473.1	000323	Virion-MPTase+TM+TM	447	DERBICUS_47	Erwinia phage Derbicus	GCA_004521655.1
AHI60436.1	000323	Virion-MPTase+TM+TM	420	Ea357_282	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49699.1	000323	Virion-MPTase+TM+TM	452	MACHINA_61	Erwinia phage Machina	GCA_002758035.1
AGX01957.1	000323	Virion-MPTase+TM+TM	431	CF95_gp235	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07393.1	000323	Virion-MPTase+TM+TM	448	REBECCA_288	Erwinia phage Rebecca	GCA_004521635.1
AXF51188.1	000323	Virion-MPTase+TM+TM	451	WELLINGTON_58	Erwinia phage Wellington	GCA_003344985.1
AFQ96773.1	000323	Virion-MPTase+TM+TM	451	G173_gp228	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48075.1	000323	Virion-MPTase+TM+TM	449	ASESINO_62	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86075.1	000323	Virion-MPTase+TM+TM	420	BOSOLAPHORUS_289	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48350.1	000323	Virion-MPTase+TM+TM	450	CAITLIN_55	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48623.1	000323	Virion-MPTase+TM+TM	449	CHRISDB_61	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52391.2	000323	Virion-MPTase+TM+TM	420	DM_292	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86395.1	000323	Virion-MPTase+TM+TM	420	DESERTFOX_288	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48897.1	000323	Virion-MPTase+TM+TM	447	EARLPHILLIPIV_47	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49144.1	000323	Virion-MPTase+TM+TM	452	HUXLEY_62	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03858.1	000323	Virion-MPTase+TM+TM	481	JOAD_57	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49410.1	000323	Virion-MPTase+TM+TM	451	KWAN_58	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86716.1	000323	Virion-MPTase+TM+TM	420	MADMEL_289	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87041.1	000323	Virion-MPTase+TM+TM	420	MORTIMER_293	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49972.1	000323	Virion-MPTase+TM+TM	452	PARSHIK_63	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50238.1	000323	Virion-MPTase+TM+TM	447	PHOBOS_48	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52066.1	000323	Virion-MPTase+TM+TM	420	RAY_286	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03613.1	000323	Virion-MPTase+TM+TM	481	RISINGSUN_57	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51749.1	000323	Virion-MPTase+TM+TM	420	SIMMY50_291	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65101.2	000323	Virion-MPTase+TM+TM	420	SPECIALG_290	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50485.1	000323	Virion-MPTase+TM+TM	451	STRATTON_60	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85886.1	000323	Virion-MPTase+TM+TM	450	ACEC001_0480	Escherichia phage vB_EcoM_EC001	GCA_014131305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBO63860.1	000323	Virion-MPTase+TM+TM	436	Goslar_00067	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71937.1	000323	Virion-MPTase+TM+TM	447	N1M2_74	Klebsiella phage N1M2	GCA_010092605.1
QGZ14398.1	000323	Virion-MPTase+TM+TM	442	HWC77_gp035	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24189.1	000323	Virion-MPTase+TM+TM	420	-	Proteus phage 10	GCA_014071245.1
ABY62975.1	000323	Virion-MPTase+TM+TM	425	201phi2-1p145	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27146.1	000323	Virion-MPTase+TM+TM	453	PPEV_gp052	Pseudomonas phage EL	GCA_000866825.1
ANM44869.1	000323	Virion-MPTase+TM+TM	413	KTN4_111	Pseudomonas phage KTN4	GCA_002607225.1
ARV77254.1	000323	Virion-MPTase+TM+TM	448	NOXIFER_84	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89537.1	000323	Virion-MPTase+TM+TM	443	OBP_100	Pseudomonas phage OBP	GCA_000896635.1
QBX32240.1	000323	Virion-MPTase+TM+TM	337	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76760.1	000323	Virion-MPTase+TM+TM	416	PHABIO_129	Pseudomonas phage Phabio	GCA_002624965.1
AEH03510.1	000323	Virion-MPTase+TM+TM	414	086	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02621.1	000323	Virion-MPTase+TM+TM	412	PSA21_93	Pseudomonas phage Psa21	GCA_004340405.1
ATN94844.1	000323	Virion-MPTase+TM+TM	413	SL2_267	Pseudomonas phage SL2	GCA_002956015.1
QJB22746.1	000323	Virion-MPTase+TM+TM	413	fnug_103	Pseudomonas phage fnug	GCA_012837215.1
QEM41818.1	000323	Virion-MPTase+TM+TM	415	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82985.1	000323	Virion-MPTase+TM+TM	413	PHIKZ084	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19224.1	000323	Virion-MPTase+TM+TM	433	FDH28_gp171	Ralstonia phage RP12	GCA_002617345.1
BAW19510.1	000323	Virion-MPTase+TM+TM	433	-	Ralstonia phage RP31	GCA_002617365.1
BAS04980.2	000323	Virion-MPTase+TM+TM	443	AVU11_gp188	Ralstonia phage RSF1	GCA_001500875.1
BAQ02706.2	000323	Virion-MPTase+TM+TM	443	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20761.1	000323	Virion-MPTase+TM+TM	450	-	Salmonella phage JN03	GCA_014319805.1
AWN09052.1	000323	Virion-MPTase+TM+TM	448	MLDJOKPK_00121	Salmonella phage SPAsTU	GCA_003183805.1
AEP83878.1	000323	Virion-MPTase+TM+TM	450	SPN3US_0045	Salmonella phage SPN3US	GCA_001042275.1
QKE54613.1	000323	Virion-MPTase+TM+TM	418	ACSA002_2960	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65345.1	000323	Virion-MPTase+TM+TM	440	2050HW_00010	Serratia phage 2050HW	GCA_002628125.1
QDB71133.1	000323	Virion-MPTase+TM+TM	440	CPT_Moabite_103	Serratia phage Moabite	GCA_006384735.1
QFP93086.1	000323	Virion-MPTase+TM+TM	427	-	Serratia phage PCH45	GCA_009187865.1
QAU04338.1	000323	Virion-MPTase+TM+TM	442	HWC03_gp183	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23238.1	000323	Virion-MPTase+TM+TM	442	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80958.1	000323	Virion-MPTase+TM+TM	442	Aphrodite1_0107	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70838.1	000323	Virion-MPTase+TM+TM	431	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47490.1	000323	Virion-MPTase+TM+TM	442	HWC35_gp096	Vibrio phage USC-1	GCA_006864065.1
BAW98310.1	000323	Virion-MPTase+TM+TM	444	FDH33_gp101	Vibrio phage pTD1	GCA_002618825.1
AQT28174.1	000323	Virion-MPTase+TM+TM	425	pVa21_233	Vibrio phage pVa-21	GCA_002619305.1
QAX96655.1	000323	Virion-MPTase+TM+TM	449	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96973.1	000323	Virion-MPTase+TM+TM	449	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96019.1	000323	Virion-MPTase+TM+TM	449	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96337.1	000323	Virion-MPTase+TM+TM	449	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21086.1	000323	Virion-MPTase+TM+TM	420	-	Vibrio phage vB_pir03	GCA_014319855.1
AMS01136.1	000324	Virion-MPTase	425	AR9_g051	Bacillus phage AR9	GCA_001743835.1
ALN97801.1	000324	Virion-MPTase	413	Bp8pS_122	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00063.1	000324	Virion-MPTase	421	PBI_PBS1_241	Bacillus virus PBS1	GCA_002601325.1
CCE26227.1	000000	Virion-MPTase	505	g204	Yersinia phage phiR1-37	GCA_000895615.1
BBI90457.1	000325	SprT-like	186	HYO65_gp065	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90765.1	000325	SprT-like	186	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39281.1	000325	SprT-like	260	BPT24_155	Tenacibaculum phage pT24	GCA_002611925.1
AFH14730.1	000326	SprT-like	442	Lu11_0193	Pseudomonas phage Lu11	GCA_000897175.1
AGS81974.1	000326	SprT-like	448	PaBG_00089	Pseudomonas phage PaBG	GCA_000912555.1
QAY00573.1	000327	WGR	323	Ecwhy1_294	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34766.1	000327	WGR	323	ACQ29_gp086	Escherichia phage PBECO4	GCA_001041035.1
BBM62046.1	000327	WGR	323	EO157G_4570	Escherichia phage SP27	GCA_008033345.1
AXC36881.1	000327	WGR	323	-	Escherichia phage UB	GCA_003341455.1
QBO61928.1	000327	WGR	323	G17_00439	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13960.1	000327	WGR	323	vBEcoMphAPEC6_gp336c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80363.1	000327	WGR	323	PSLUR01_00386	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ABS83631.1	000000	WGR	310	0305phi8-36p071	Bacillus phage 0305phi8-36	GCA_000871045.1
BBA65562.1	000328	WGR+Rpo-ART	423	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96554.1	000328	WGR+Rpo-ART	420	Xoosp13_368	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDH83603.1	000329	XkdF-S-Peptidase	251	H1O15_gp185	Achromobacter phage Motura	GCA_006964305.1
AEO93290.1	000329	XkdF-S-Peptidase	300	G_19	Bacillus virus G	GCA_000917535.1
QBX06498.1	000329	XkdF-S-Peptidase	297	BcepSaruman_085	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74465.1	000329	XkdF-S-Peptidase	297	BcepSauron_085	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67186.1	000329	XkdF-S-Peptidase	259	AD1_142	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79936.1	000329	XkdF-S-Peptidase	273	JA11_131	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66535.1	000329	XkdF-S-Peptidase	272	JA13_132	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66860.1	000329	XkdF-S-Peptidase	272	JA29_134	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67505.1	000329	XkdF-S-Peptidase	273	JA33_131	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08419.1	000329	XkdF-S-Peptidase	259	Alexandra_147	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58783.1	000329	XkdF-S-Peptidase	259	Y3_143	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28621.1	000329	XkdF-S-Peptidase	257	YOLOSWAG_141	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38416.1	000329	XkdF-S-Peptidase	260	BN7874_230	Phage NCTB	GCA_900092385.1
AFH14603.1	000329	XkdF-S-Peptidase	269	Lu11_0071	Pseudomonas phage Lu11	GCA_000897175.1
AGS82101.2	000329	XkdF-S-Peptidase	254	PaBG_00226	Pseudomonas phage PaBG	GCA_000912555.1
BAG41577.1	000329	XkdF-S-Peptidase	266	RSL1_ORF132	Ralstonia phage phiRSL1	GCA_000879455.1
ABS83681.1	000330	XkdF-S-Peptidase	489	0306phi8-36p123	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83808.1	000331	CCDC158	257	0305phi8-36p123*	Bacillus phage 0305phi8-36	GCA_000871045.1
APU01547.1	000332	AsiA	97	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29012.1	000332	AsiA	90	AP1_0305	Aeromonas phage AP1	GCA_014183365.1
ATI17353.1	000332	AsiA	90	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00240.1	000332	AsiA	90	HWB28_gp312	Aeromonas phage AS-zj	GCA_002627665.1
AUE22863.1	000332	AsiA	97	Ah1_00345	Aeromonas phage Ah1	GCA_002957415.1
QAX98573.1	000332	AsiA	99	ASfcp2_239	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97798.1	000332	AsiA	90	ASswx1_153	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01357.1	000332	AsiA	90	ASwh1_297	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39569.1	000332	AsiA	90	CC2_384	Aeromonas phage CC2	GCA_000903495.1
ADQ53038.1	000332	AsiA	99	PX29p321	Aeromonas phage PX29	GCA_000920195.1
ADM79962.1	000332	AsiA	97	phiAS5_ORF0119	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53169.1	000332	AsiA	97	65p161	Aeromonas virus 65	GCA_000893255.1
AAQ17991.1	000332	AsiA	97	asiA	Aeromonas virus Aeh1	GCA_000843245.1
AIA64803.1	000332	AsiA	90	S13_004	Cronobacter phage S13	GCA_001503575.1
ARM70804.1	000332	AsiA	90	phiC120_c98	Escherichia phage phiC120	GCA_002621185.1
QHJ78860.1	000332	AsiA	89	-	Myoviridae sp.	GCA_012593985.1
AAQ64365.1	000332	AsiA	99	KVP40.0295	Vibrio phage KVP40	GCA_000843785.1
QIW90680.1	000332	AsiA	99	GCAPEGMB_00333	Vibrio phage V07	GCA_012361095.1
QIW91118.1	000332	AsiA	99	COHAPHLL_00282	Vibrio phage V09	GCA_012361135.1
QHJ74475.1	000332	AsiA	99	VH12019_00148	Vibrio phage VH1_2019	GCA_009931825.1
AGB06968.1	000332	AsiA	99	CF80_gp181	Vibrio phage VH7D	GCA_000914495.1
QBX06176.1	000332	AsiA	99	ValB1HC_223	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61193.1	000332	AsiA	99	AVU32_gp352	Vibrio phage ValKK3	GCA_001501635.1
AGN30341.1	000332	AsiA	99	VPFG_00344	Vibrio phage nt-1	GCA_000910195.2
ALP47202.1	000332	AsiA	99	phiGrn1_0028	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47593.1	000332	AsiA	99	phiST2_0161	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54802.1	000332	AsiA	99	vBValMR10Z_262	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07209.1	000332	AsiA	97	VmeM32_00223	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37526.1	000332	AsiA	99	pp2_293	Vibriophage phi-pp2	GCA_002630725.1
ABY63156.1	000333	dCTPdeaminase	195	201phi2-1p331	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45016.1	000333	dCTPdeaminase	189	KTN4_258	Pseudomonas phage KTN4	GCA_002607225.1
AFH14580.1	000333	dCTPdeaminase	247	Lu11_0049	Pseudomonas phage Lu11	GCA_000897175.1
ARV77403.1	000333	dCTPdeaminase	247	NOXIFER_238	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32408.1	000333	dCTPdeaminase	214	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ86111.1	000333	dCTPdeaminase	187	KKIINIFJ_00200	Pseudomonas phage PN05	GCA_009931935.1
AGS81949.1	000333	dCTPdeaminase	222	PaBG_00065	Pseudomonas phage PaBG	GCA_000912555.1
ARV76960.1	000333	dCTPdeaminase	208	PHABIO_329	Pseudomonas phage Phabio	GCA_002624965.1
AEH03678.1	000333	dCTPdeaminase	192	255	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02809.1	000333	dCTPdeaminase	208	PSA21_283	Pseudomonas phage Psa21	GCA_004340405.1
ATN94698.1	000333	dCTPdeaminase	189	SL2_121	Pseudomonas phage SL2	GCA_002956015.1
QJB22893.1	000333	dCTPdeaminase	189	fnug_250	Pseudomonas phage fnug	GCA_012837215.1
QEM41979.1	000333	dCTPdeaminase	214	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83115.1	000333	dCTPdeaminase	189	PHIKZ214	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19108.1	000333	dCTPdeaminase	200	FDH28_gp287	Ralstonia phage RP12	GCA_002617345.1
BAW19394.1	000333	dCTPdeaminase	200	-	Ralstonia phage RP31	GCA_002617365.1
APU01401.1	000334	dUTPase	163	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28869.1	000334	dUTPase	163	AP1_0162	Aeromonas phage AP1	GCA_014183365.1
ATI17495.1	000334	dUTPase	163	-	Aeromonas phage AS-szw	GCA_002743635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU00502.1	000334	dUTPase	163	HWB28_gp050	Aeromonas phage AS-zj	GCA_002627665.1
AUE22552.1	000334	dUTPase	161	Ah1_00011	Aeromonas phage Ah1	GCA_002957415.1
QAX98592.1	000334	dUTPase	161	ASfcp2_259	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97934.1	000334	dUTPase	163	ASswx1_292	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01213.1	000334	dUTPase	163	ASwh1_148	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39492.1	000334	dUTPase	163	CC2_239	Aeromonas phage CC2	GCA_000903495.1
ADQ52728.1	000334	dUTPase	166	PX29p009	Aeromonas phage PX29	GCA_000920195.1
ADM79981.1	000334	dUTPase	159	phiAS5_ORF0138	Aeromonas phage phiAS5	GCA_000887715.1
AAR90929.1	000334	dUTPase	163	65p009	Aeromonas virus 65	GCA_000893255.1
AAQ17665.1	000334	dUTPase	161	Aeh1ORF010c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63465.1	000334	dUTPase	172	DAC16_236	Bacteroides phage DAC16	GCA_013387695.1
QIG63728.1	000334	dUTPase	172	DAC19_241	Bacteroides phage DAC19	GCA_013387715.1
QIG63989.1	000334	dUTPase	172	DAC20_240	Bacteroides phage DAC20	GCA_013387725.1
QIG64253.1	000334	dUTPase	172	DAC22_243	Bacteroides phage DAC22	GCA_013387735.1
QIG64509.1	000334	dUTPase	172	DAC23_235	Bacteroides phage DAC23	GCA_013387745.1
CCH63595.1	000334	dUTPase	152	CP21_133	Campylobacter virus CP21	GCA_000902535.1
ARB13636.1	000334	dUTPase	227	Ccr10_gp107c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13981.1	000334	dUTPase	227	Ccr2_gp106c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14669.1	000334	dUTPase	227	Ccr29_gp113	Caulobacter phage Ccr29	GCA_002619485.1
ARB15024.1	000334	dUTPase	227	Ccr32_gp106	Caulobacter phage Ccr32	GCA_002619505.1
ARB15356.1	000334	dUTPase	227	Ccr34_gp114	Caulobacter phage Ccr34	GCA_002619525.1
ARB14325.1	000334	dUTPase	227	Ccr5_gp107c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68305.1	000334	dUTPase	244	CcrBL10_gp101c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69233.1	000334	dUTPase	146	CcrBL9_gp209	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88011.1	000334	dUTPase	215	CcrColossus_gp141	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68688.1	000334	dUTPase	215	CcrPW_gp149c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69787.1	000334	dUTPase	146	CcrSC_gp205	Caulobacter phage CcrSC	GCA_003443315.1
AFU87628.1	000334	dUTPase	227	CcrKarma_gp111	Caulobacter virus Karma	GCA_000901575.1
AFU87277.1	000334	dUTPase	227	CcrMagneto_gp107	Caulobacter virus Magneto	GCA_000903095.1
AFU86589.1	000334	dUTPase	227	CcrRogue_gp107	Caulobacter virus Rogue	GCA_000900555.1
AFU88424.1	000334	dUTPase	227	CcrSwift_gp106	Caulobacter virus Swift	GCA_000899655.1
AFU86942.1	000334	dUTPase	227	CbK_gp110	Caulobacter virus phiCbK	GCA_000900535.1
BAE47776.1	000334	dUTPase	155	CST078	Clostridium phage c-st	GCA_000865225.1
AIA65053.1	000334	dUTPase	153	S13_256	Cronobacter phage S13	GCA_001503575.1
AXG67337.1	000334	dUTPase	189	AD1_293	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80087.1	000334	dUTPase	188	JA11_282	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66688.1	000334	dUTPase	188	JA13_285	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67008.1	000334	dUTPase	188	JA29_282	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67657.1	000334	dUTPase	188	JA33_283	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGX01845.1	000334	dUTPase	549	dut	Erwinia phage PhiEaH1	GCA_000914555.1
AWY08565.1	000334	dUTPase	178	Alexandra_310	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58940.1	000334	dUTPase	178	Y3_300	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28764.1	000334	dUTPase	163	YOLOSWAG_294	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QHJ78879.1	000334	dUTPase	98	-	Myoviridae sp.	GCA_012593985.1
ATA65473.1	000334	dUTPase	380	2050HW_00138	Serratia phage 2050HW	GCA_002628125.1
QDB71242.1	000334	dUTPase	411	CPT_Moabite_212	Serratia phage Moabite	GCA_006384735.1
QFP93124.1	000334	dUTPase	264	-	Serratia phage PCH45	GCA_009187865.1
AGR47666.1	000334	dUTPase	180	SmphiM12_034	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12930.1	000334	dUTPase	180	PHIM19_23	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12570.1	000334	dUTPase	180	PHIM7_22	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13302.1	000334	dUTPase	180	PHIN3_37	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64092.1	000334	dUTPase	165	KVP40.0021	Vibrio phage KVP40	GCA_000843785.1
QIW90415.1	000334	dUTPase	192	GCAPEGMB_00068	Vibrio phage V07	GCA_012361095.1
QIW91014.1	000334	dUTPase	165	COHAPHLL_00151	Vibrio phage V09	GCA_012361135.1
QHJ74204.1	000334	dUTPase	165	VH12019_00285	Vibrio phage VH1_2019	GCA_009931825.1
AGB07028.1	000334	dUTPase	199	CF80_gp241	Vibrio phage VH7D	GCA_000914495.1
QBX06068.1	000334	dUTPase	165	ValB1HC_114	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61082.1	000334	dUTPase	194	AVU32_gp241	Vibrio phage ValKK3	GCA_001501635.1
AGN30072.1	000334	dUTPase	203	VPFG_00070	Vibrio phage nt-1	GCA_000910195.2
AQT28046.1	000334	dUTPase	352	pVa21_105	Vibrio phage pVa-21	GCA_002619305.1
ALP47106.1	000334	dUTPase	165	phiGrn1_0136	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47489.1	000334	dUTPase	165	phiST2_0266	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54694.1	000334	dUTPase	165	vBValMR10Z_153	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07073.1	000334	dUTPase	205	VmeM32_00082	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37255.1	000334	dUTPase	165	pp2_021	Vibriophage phi-pp2	GCA_002630725.1
prevph1000000308	000334	dUTPase	136	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000240	000334	dUTPase	178	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AND75272.1	000000	dUTPase	120	ME3_111	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ANS06027.1	000335	dUTPase	177	ABCD_0027	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97036.1	000335	dUTPase	177	E_027	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70847.1	000335	dUTPase	173	phiC120_c141	Escherichia phage phiC120	GCA_002621185.1
AAX78548.1	000335	dUTPase	177	RB43ORF026c	Escherichia virus RB43	GCA_000863505.1
AFF28104.1	000335	dUTPase	167	PAU_106	Sphingomonas phage PAU	GCA_000902455.1
QIG63470.1	000336	dUTPase	165	DAC16_241	Bacteroides phage DAC16	GCA_013387695.1
QIG63733.1	000336	dUTPase	165	DAC19_246	Bacteroides phage DAC19	GCA_013387715.1
QIG63994.1	000336	dUTPase	165	DAC20_245	Bacteroides phage DAC20	GCA_013387725.1
QIG64258.1	000336	dUTPase	165	DAC22_248	Bacteroides phage DAC22	GCA_013387735.1
QIG64514.1	000336	dUTPase	165	DAC23_240	Bacteroides phage DAC23	GCA_013387745.1
QDH83443.1	000337	dUTPase	242	H1O15_gp035	Achromobacter phage Motura	GCA_006964305.1
QHJ86103.1	000337	dUTPase	240	KKIINIFJ_00192	Pseudomonas phage PN05	GCA_009931935.1
QHJ86003.1	000337	dUTPase	310	KKIINIFJ_00091	Pseudomonas phage PN05	GCA_009931935.1
QMV29125.1	000338	divDnaB_helicase	358	AP1_0422	Aeromonas phage AP1	GCA_014183365.1
QMV29134.1	000338	divDnaB_helicase	141	AP1_0431	Aeromonas phage AP1	GCA_014183365.1
QDB70282.1	000338	divDnaB_helicase	511	CF8_0114	Aeromonas phage CF8	GCA_006384595.2
QDJ97259.1	000338	divDnaB_helicase	511	D6_0099	Aeromonas phage D6	GCA_007051205.2
QDH47046.1	000338	divDnaB_helicase	511	LAh10_31	Aeromonas phage LAh10	GCA_006863975.1
QDJ96873.1	000338	divDnaB_helicase	512	PS1_0114	Aeromonas phage PS1	GCA_007051165.2
QFR59505.1	000338	divDnaB_helicase	512	PS2_0114	Aeromonas phage PS2	GCA_009388305.2
AMS01092.1	000338	divDnaB_helicase	561	AR9_g007	Bacillus phage AR9	GCA_001743835.1
ALN97723.1	000338	divDnaB_helicase	578	Bp8pS_044	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00014.1	000338	divDnaB_helicase	561	PBI_PBS1_192	Bacillus virus PBS1	GCA_002601325.1
AFO71289.1	000338	divDnaB_helicase	513	CR5_069	Cronobacter phage CR5	GCA_000910235.1
QBZ70641.1	000338	divDnaB_helicase	514	pETSU_060	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59721.1	000338	divDnaB_helicase	520	SEGD1_072	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07497.1	000338	divDnaB_helicase	513	DERBICUS_71	Erwinia phage Derbicus	GCA_004521655.1
AHI60465.1	000338	divDnaB_helicase	510	Ea357_311	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49722.1	000338	divDnaB_helicase	521	MACHINA_84	Erwinia phage Machina	GCA_002758035.1
AGX01939.1	000338	divDnaB_helicase	522	CF95_gp217	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07422.1	000338	divDnaB_helicase	510	REBECCA_317	Erwinia phage Rebecca	GCA_004521635.1
AXF51217.1	000338	divDnaB_helicase	523	WELLINGTON_87	Erwinia phage Wellington	GCA_003344985.1
AFQ96803.1	000338	divDnaB_helicase	521	G173_gp258	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48102.1	000338	divDnaB_helicase	521	ASESINO_89	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86104.1	000338	divDnaB_helicase	510	BOSOLAPHORUS_318	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48375.1	000338	divDnaB_helicase	521	CAITLIN_80	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48648.1	000338	divDnaB_helicase	521	CHRISDB_86	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52420.1	000338	divDnaB_helicase	510	DM_321	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86424.1	000338	divDnaB_helicase	510	DESERTFOX_317	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48921.1	000338	divDnaB_helicase	513	EARLPHILLIPIV_71	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49167.1	000338	divDnaB_helicase	521	HUXLEY_85	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03834.1	000338	divDnaB_helicase	516	JOAD_81	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49438.1	000338	divDnaB_helicase	523	KWAN_86	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86745.1	000338	divDnaB_helicase	510	MADMEL_318	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87070.1	000338	divDnaB_helicase	510	MORTIMER_322	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49995.1	000338	divDnaB_helicase	521	PARSHIK_86	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50262.1	000338	divDnaB_helicase	513	PHOBOS_72	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52095.1	000338	divDnaB_helicase	510	RAY_315	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03589.1	000338	divDnaB_helicase	516	RISINGSUN_81	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51778.1	000338	divDnaB_helicase	510	SIMMY50_320	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65130.1	000338	divDnaB_helicase	510	SPECIALG_319	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50516.1	000338	divDnaB_helicase	521	STRATTON_91	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85913.1	000338	divDnaB_helicase	520	ACEC001_0750	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63836.1	000338	divDnaB_helicase	536	Goslar_00043	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71958.1	000338	divDnaB_helicase	512	N1M2_95	Klebsiella phage N1M2	GCA_010092605.1
QGZ14432.1	000338	divDnaB_helicase	512	HWC77_gp069	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24224.1	000338	divDnaB_helicase	510	-	Proteus phage 10	GCA_014071245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ABY63027.1	000338	divDnaB_helicase	510	201phi2-1p197	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27170.1	000338	divDnaB_helicase	510	PPEV_gp076	Pseudomonas phage EL	GCA_000866825.1
ANM44911.1	000338	divDnaB_helicase	515	KTN4_153	Pseudomonas phage KTN4	GCA_002607225.1
ARV77289.1	000338	divDnaB_helicase	512	NOXIFER_120	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89559.1	000338	divDnaB_helicase	514	OBP_122	Pseudomonas phage OBP	GCA_000896635.1
QBX32295.1	000338	divDnaB_helicase	512	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76816.1	000338	divDnaB_helicase	510	PHABIO_185	Pseudomonas phage Phabio	GCA_002624965.1
AEH03557.1	000338	divDnaB_helicase	389	134	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02695.1	000338	divDnaB_helicase	510	PSA21_168	Pseudomonas phage Psa21	GCA_004340405.1
ATN94803.1	000338	divDnaB_helicase	515	SL2_226	Pseudomonas phage SL2	GCA_002956015.1
QJB22789.1	000338	divDnaB_helicase	515	fnug_146	Pseudomonas phage fnug	GCA_012837215.1
QEM41869.1	000338	divDnaB_helicase	512	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83019.2	000338	divDnaB_helicase	491	PHIKZ118	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19070.1	000338	divDnaB_helicase	511	FDH28_gp096	Ralstonia phage RP12	GCA_002617345.1
BAW19355.1	000338	divDnaB_helicase	511	-	Ralstonia phage RP31	GCA_002617365.1
BAS04918.2	000338	divDnaB_helicase	474	AVU11_agp29	Ralstonia phage RSF1	GCA_001500875.1
BAQ02647.2	000338	divDnaB_helicase	495	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20784.1	000338	divDnaB_helicase	520	-	Salmonella phage JN03	GCA_014319805.1
AWN09029.1	000338	divDnaB_helicase	521	MLDJOKPK_00089	Salmonella phage SPAsTU	GCA_003183805.1
AEP83906.1	000338	divDnaB_helicase	520	SPN3US_0073	Salmonella phage SPN3US	GCA_001042275.1
QKE54646.1	000338	divDnaB_helicase	510	ACSA002_3290	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65372.1	000338	divDnaB_helicase	433	2050HW_00037	Serratia phage 2050HW	GCA_002628125.1
QDB71156.1	000338	divDnaB_helicase	519	CPT_Moabite_126	Serratia phage Moabite	GCA_006384735.1
QFP93071.1	000338	divDnaB_helicase	515	-	Serratia phage PCH45	GCA_009187865.1
QAU04304.1	000338	divDnaB_helicase	512	HWC03_gp149	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23274.1	000338	divDnaB_helicase	512	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80942.1	000338	divDnaB_helicase	512	Aphrodite1_0071	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70852.1	000338	divDnaB_helicase	536	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47454.1	000338	divDnaB_helicase	512	HWC35_gp060	Vibrio phage USC-1	GCA_006864065.1
BAW98276.1	000338	divDnaB_helicase	512	FDH33_gp067	Vibrio phage pTD1	GCA_002618825.1
AQT27951.1	000338	divDnaB_helicase	508	pVa21_009	Vibrio phage pVa-21	GCA_002619305.1
QAX96638.1	000338	divDnaB_helicase	525	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96956.1	000338	divDnaB_helicase	525	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96002.1	000338	divDnaB_helicase	525	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96320.1	000338	divDnaB_helicase	525	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21100.1	000338	divDnaB_helicase	515	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26360.1	000338	divDnaB_helicase	357	g337	Yersinia phage phiR1-37	GCA_000895615.1
ABY62886.1	000000	divDnaB	139	201phi2-1p053	Pseudomonas phage 201phi2-1	GCA_000875305.1
AGS82046.2	000000	divDnaB	157	PaBG_00165	Pseudomonas phage PaBG	GCA_000912555.1
AEH03555.1	000000	divDnaB	104	131	Pseudomonas phage PhiPA3	GCA_001502095.1
ATA65371.1	000000	divDnaB	87	2050HW_00036	Serratia phage 2050HW	GCA_002628125.1
AQT28018.1	000000	divDnaB	279	pVa21_077	Vibrio phage pVa-21	GCA_002619305.1
ARV76670.1	000000	SIG+divDnaB	171	PHABIO_39	Pseudomonas phage Phabio	GCA_002624965.1
QNI21183.1	000000	SIG+divDnaB	354	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26358.1	000000	SIG+divDnaB	251	g335	Yersinia phage phiR1-37	GCA_000895615.1
QGY75132.1	000339	LAh10_145	731	CF8_0223	Aeromonas phage CF8	GCA_006384595.2
QDJ97390.1	000339	LAh10_145	731	D6_0231	Aeromonas phage D6	GCA_007051205.2
QDH47024.1	000339	LAh10_145	731	LAh10_145	Aeromonas phage LAh10	GCA_006863975.1
QDJ96736.1	000339	LAh10_145	732	PS1_0225	Aeromonas phage PS1	GCA_007051165.2
QFR59369.1	000339	LAh10_145	732	PS2_0227	Aeromonas phage PS2	GCA_009388305.2
AMS01289.1	000339	LAh10_145	490	AR9_g205	Bacillus phage AR9	GCA_001743835.1
ALN97943.1	000339	LAh10_145	489	Bp8pS_264	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99918.1	000339	LAh10_145	342	PBI_PBS1_96	Bacillus virus PBS1	GCA_002601325.1
AFO71426.1	000339	LAh10_145	730	CR5_206	Cronobacter phage CR5	GCA_000910235.1
QBZ70777.1	000339	LAh10_145	734	pETSU_196	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59889.1	000339	LAh10_145	740	SEGD1_242	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07639.1	000339	LAh10_145	728	DERBICUS_213	Erwinia phage Derbicus	GCA_004521655.1
AHI60311.1	000339	LAh10_145	662	Ea357_160	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49889.1	000339	LAh10_145	729	MACHINA_251	Erwinia phage Machina	GCA_002758035.1
AGX01870.1	000339	LAh10_145	727	CF95_gp148	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07270.1	000339	LAh10_145	662	REBECCA_163	Erwinia phage Rebecca	GCA_004521635.1
AXF51390.1	000339	LAh10_145	732	WELLINGTON_264	Erwinia phage Wellington	GCA_003344985.1
AFQ96703.1	000339	LAh10_145	736	G173_gp158	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48273.1	000339	LAh10_145	736	ASESINO_260	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85950.1	000339	LAh10_145	662	BOSOLAPHORUS_163	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48545.1	000339	LAh10_145	726	CAITLIN_250	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48823.1	000339	LAh10_145	727	CHRISDB_261	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52265.1	000339	LAh10_145	662	DM_167	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86269.1	000339	LAh10_145	662	DESERTFOX_162	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49063.1	000339	LAh10_145	728	EARLPHILLIPIV_214	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49332.1	000339	LAh10_145	729	HUXLEY_250	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03686.1	000339	LAh10_145	714	JOAD_229	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49616.1	000339	LAh10_145	732	KWAN_264	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86591.1	000339	LAh10_145	662	MADMEL_163	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86915.1	000339	LAh10_145	662	MORTIMER_166	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50160.1	000339	LAh10_145	729	PARSHIK_251	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50410.1	000339	LAh10_145	730	PHOBOS_220	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51942.1	000339	LAh10_145	662	RAY_161	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03443.1	000339	LAh10_145	714	RISINGSUN_227	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51626.1	000339	LAh10_145	662	SIMMY50_164	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64973.1	000339	LAh10_145	662	SPECIALG_163	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50685.1	000339	LAh10_145	736	STRATTON_260	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86079.1	000339	LAh10_145	740	ACEC001_2360	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64024.1	000339	LAh10_145	713	Goslar_00233	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72083.1	000339	LAh10_145	734	N1M2_220	Klebsiella phage N1M2	GCA_010092605.1
QGZ14510.1	000339	LAh10_145	725	HWC77_gp147	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24092.1	000339	LAh10_145	662	-	Proteus phage 10	GCA_014071245.1
ABY63104.1	000339	LAh10_145	666	201phi2-1p277	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27276.1	000339	LAh10_145	730	PPEV_gp182	Pseudomonas phage EL	GCA_000866825.1
ANM44980.1	000339	LAh10_145	664	KTN4_222	Pseudomonas phage KTN4	GCA_002607225.1
ARV77367.1	000339	LAh10_145	657	NOXIFER_198	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89712.1	000339	LAh10_145	733	OBP_275	Pseudomonas phage OBP	GCA_000896635.1
QBX32371.1	000339	LAh10_145	658	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76897.1	000339	LAh10_145	659	PHABIO_266	Pseudomonas phage Phabio	GCA_002624965.1
AEH03637.1	000339	LAh10_145	658	214	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02773.1	000339	LAh10_145	659	PSA21_247	Pseudomonas phage Psa21	GCA_004340405.1
ATN94734.1	000339	LAh10_145	664	SL2_157	Pseudomonas phage SL2	GCA_002956015.1
QJB22858.1	000339	LAh10_145	664	fnug_215	Pseudomonas phage fnug	GCA_012837215.1
QEM41944.1	000339	LAh10_145	658	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83083.1	000339	LAh10_145	664	PHIKZ182	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19018.1	000339	LAh10_145	704	FDH28_gp044	Ralstonia phage RP12	GCA_002617345.1
BAW19304.1	000339	LAh10_145	704	-	Ralstonia phage RP31	GCA_002617365.1
BAS04835.1	000339	LAh10_145	631	AVU11_gp043	Ralstonia phage RSF1	GCA_001500875.1
BAQ02568.2	000339	LAh10_145	621	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20923.1	000339	LAh10_145	704	-	Salmonella phage JN03	GCA_014319805.1
AWN09114.2	000339	LAh10_145	736	MLDJOKPK_00202	Salmonella phage SPAsTU	GCA_003183805.1
AEP84071.1	000339	LAh10_145	740	SPN3US_0238	Salmonella phage SPN3US	GCA_001042275.1
QKE54468.1	000339	LAh10_145	666	ACSA002_1540	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65430.1	000339	LAh10_145	576	2050HW_00095	Serratia phage 2050HW	GCA_002628125.1
QDB71205.1	000339	LAh10_145	722	CPT_Moabite_175	Serratia phage Moabite	GCA_006384735.1
QFP93048.1	000339	LAh10_145	784	-	Serratia phage PCH45	GCA_009187865.1
QAU04224.1	000339	LAh10_145	725	HWC03_gp069	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23138.1	000339	LAh10_145	724	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80924.1	000339	LAh10_145	724	Aphrodite1_0202	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70763.1	000339	LAh10_145	704	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47589.1	000339	LAh10_145	724	HWC35_gp195	Vibrio phage USC-1	GCA_006864065.1
BAW98404.1	000339	LAh10_145	726	FDH33_gp195	Vibrio phage pTD1	GCA_002618825.1
AQT28105.1	000339	LAh10_145	697	pVa21_164	Vibrio phage pVa-21	GCA_002619305.1
QAX96769.1	000339	LAh10_145	664	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97088.1	000339	LAh10_145	664	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96134.1	000339	LAh10_145	664	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96452.1	000339	LAh10_145	664	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20972.1	000339	LAh10_145	674	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26109.1	000339	LAh10_145	457	g085	Yersinia phage phiR1-37	GCA_000895615.1
QDB70462.1	000340	FamB-divDNAPol	689	CF8_0049	Aeromonas phage CF8	GCA_006384595.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ97202.1	000340	FamB-divDNAPol	687	D6_0042	Aeromonas phage D6	GCA_007051205.2
QDH47029.1	000340	FamB-divDNAPol	687	LAh10_209	Aeromonas phage LAh10	GCA_006863975.1
QDJ96804.1	000340	FamB-divDNAPol	688	PS1_0045	Aeromonas phage PS1	GCA_007051165.2
QFR59435.1	000340	FamB-divDNAPol	688	PS2_0044	Aeromonas phage PS2	GCA_009388305.2
AMS01236.1	000340	FamB-divDNAPol	641	AR9_g152	Bacillus phage AR9	GCA_001743835.1
ALN97896.1	000340	FamB-divDNAPol	628	Bp8pS_217	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99862.1	000340	FamB-divDNAPol	641	PBI_PBS1_40	Bacillus virus PBS1	GCA_002601325.1
AFO71240.1	000340	FamB-divDNAPol	733	CR5_020	Cronobacter phage CR5	GCA_000910235.1
QBZ70865.1	000340	FamB-divDNAPol	692	pETSU_284	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59668.1	000340	FamB-divDNAPol	759	SEGD1_017	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07447.1	000340	FamB-divDNAPol	733	DERBICUS_21	Erwinia phage Derbicus	GCA_004521655.1
AHI60370.1	000340	FamB-divDNAPol	703	Ea357_217	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49671.1	000340	FamB-divDNAPol	770	MACHINA_33	Erwinia phage Machina	GCA_002758035.1
AGX01746.1	000340	FamB-divDNAPol	716	CF95_gp024	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07327.1	000340	FamB-divDNAPol	703	REBECCA_222	Erwinia phage Rebecca	GCA_004521635.1
AXF51159.1	000340	FamB-divDNAPol	762	WELLINGTON_28	Erwinia phage Wellington	GCA_003344985.1
AFQ96745.1	000340	FamB-divDNAPol	761	G173_gp200	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48048.1	000340	FamB-divDNAPol	761	ASESINO_35	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86008.1	000340	FamB-divDNAPol	703	BOSOLAPHORUS_222	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48322.1	000340	FamB-divDNAPol	769	CAITLIN_27	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48595.1	000340	FamB-divDNAPol	769	CHRISDB_33	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52325.1	000340	FamB-divDNAPol	703	DM_225	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86327.1	000340	FamB-divDNAPol	703	DESERTFOX_220	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48871.1	000340	FamB-divDNAPol	733	EARLPHILLIPIV_21	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49116.1	000340	FamB-divDNAPol	770	HUXLEY_34	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03890.1	000340	FamB-divDNAPol	690	JOAD_25	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49380.1	000340	FamB-divDNAPol	762	KWAN_28	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86650.1	000340	FamB-divDNAPol	703	MADMEL_222	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86973.1	000340	FamB-divDNAPol	703	MORTIMER_225	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49944.1	000340	FamB-divDNAPol	770	PARSHIK_35	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50211.1	000340	FamB-divDNAPol	731	PHOBOS_21	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52000.1	000340	FamB-divDNAPol	703	RAY_220	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03645.1	000340	FamB-divDNAPol	690	RISINGSUN_25	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51684.1	000340	FamB-divDNAPol	703	SIMMY50_225	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65034.1	000340	FamB-divDNAPol	703	SPECIALG_223	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50458.1	000340	FamB-divDNAPol	761	STRATTON_33	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85856.1	000340	FamB-divDNAPol	763	ACEC001_0190	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63983.1	000340	FamB-divDNAPol	717	Goslar_00191	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71897.1	000340	FamB-divDNAPol	692	N1M2_34	Klebsiella phage N1M2	GCA_010092605.1
QGZ14365.1	000340	FamB-divDNAPol	690	HWC77_gp002	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24143.1	000340	FamB-divDNAPol	715	-	Proteus phage 10	GCA_014071245.1
ABY62916.1	000340	FamB-divDNAPol	715	201phi2-1p083	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27115.1	000340	FamB-divDNAPol	700	PPEV_gp021	Pseudomonas phage EL	GCA_000866825.1
ANM44826.1	000340	FamB-divDNAPol	731	KTN4_068	Pseudomonas phage KTN4	GCA_002607225.1
ARV77215.1	000340	FamB-divDNAPol	723	NOXIFER_44	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89492.1	000340	FamB-divDNAPol	692	OBP_055	Pseudomonas phage OBP	GCA_000896635.1
QBX32200.1	000340	FamB-divDNAPol	716	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76698.1	000340	FamB-divDNAPol	716	PHABIO_67	Pseudomonas phage Phabio	GCA_002624965.1
AEH03474.1	000340	FamB-divDNAPol	716	047	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02578.1	000340	FamB-divDNAPol	715	PSA21_48	Pseudomonas phage Psa21	GCA_004340405.1
ATN94886.1	000340	FamB-divDNAPol	731	SL2_309	Pseudomonas phage SL2	GCA_002956015.1
QJB22704.1	000340	FamB-divDNAPol	731	fnug_61	Pseudomonas phage fnug	GCA_012837215.1
QEM41777.1	000340	FamB-divDNAPol	716	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82951.1	000340	FamB-divDNAPol	731	PHIKZ050	Pseudomonas virus phiKZ	GCA_000842965.1
BAW18977.1	000340	FamB-divDNAPol	728	FDH28_gp003	Ralstonia phage RP12	GCA_002617345.1
BAW19265.1	000340	FamB-divDNAPol	728	-	Ralstonia phage RP31	GCA_002617365.1
BAS04795.1	000340	FamB-divDNAPol	713	AVU11_gp003	Ralstonia phage RSF1	GCA_001500875.1
BAQ02531.1	000340	FamB-divDNAPol	716	AVU38_gp003	Ralstonia phage RSL2	GCA_001503055.1
QNI20736.1	000340	FamB-divDNAPol	708	-	Salmonella phage JN03	GCA_014319805.1
AWN09076.2	000340	FamB-divDNAPol	801	MLDJOKPK_00149	Salmonella phage SPAsTU	GCA_003183805.1
AEP83851.1	000340	FamB-divDNAPol	759	SPN3US_0018	Salmonella phage SPN3US	GCA_001042275.1
QKE54544.1	000340	FamB-divDNAPol	703	ACSA002_2280	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65642.1	000340	FamB-divDNAPol	742	2050HW_00307	Serratia phage 2050HW	GCA_002628125.1
QDB71070.1	000340	FamB-divDNAPol	742	CPT_Moabite_038	Serratia phage Moabite	GCA_006384735.1
QFP93052.1	000340	FamB-divDNAPol	733	-	Serratia phage PCH45	GCA_009187865.1
QAU04371.1	000340	FamB-divDNAPol	690	HWC03_gp216	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23204.1	000340	FamB-divDNAPol	690	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80930.1	000340	FamB-divDNAPol	690	Aphrodite1_0140	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70810.1	000340	FamB-divDNAPol	728	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47524.1	000340	FamB-divDNAPol	690	HWC35_gp130	Vibrio phage USC-1	GCA_006864065.1
BAW98341.1	000340	FamB-divDNAPol	690	FDH33_gp132	Vibrio phage pTD1	GCA_002618825.1
AQT28147.1	000340	FamB-divDNAPol	723	pVa21_206	Vibrio phage pVa-21	GCA_002619305.1
QAX96700.1	000340	FamB-divDNAPol	722	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97018.1	000340	FamB-divDNAPol	722	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96064.1	000340	FamB-divDNAPol	722	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96382.1	000340	FamB-divDNAPol	722	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21046.1	000340	FamB-divDNAPol	723	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26188.1	000340	FamB-divDNAPol	242	g164	Yersinia phage phiR1-37	GCA_000895615.1
CCE26191.1	000340	FamB-divDNAPol	420	g167	Yersinia phage phiR1-37	GCA_000895615.1
QMV29126.1	000000	FamB-divDNAPol	182	AP1_0423	Aeromonas phage AP1	GCA_014183365.1
QMV29159.1	000000	FamB-divDNAPol	85	AP1_0458	Aeromonas phage AP1	GCA_014183365.1
QMP24043.1	000000	FamB-divDNAPol	154	-	Proteus phage 10	GCA_014071245.1
QBZ70684.1	000000	FamB-divDNAPol	260	pETSU_103	Edwardsiella virus pEt-SU	GCA_004800915.1
BAE47759.1	000341	PHP+DNApolIIIalpha+HHH	1032	CST061	Clostridium phage c-st	GCA_000865225.1
AEO93598.1	000341	PHP+DNApolIIIalpha+HHH	606	G_339	Bacillus virus G	GCA_000917535.1
QIG63474.1	000341	PHP+DNApolIIIalpha+HHH	1277	DAC16_245	Bacteroides phage DAC16	GCA_013387695.1
QIG63737.1	000341	PHP+DNApolIIIalpha+HHH	1274	DAC19_250	Bacteroides phage DAC19	GCA_013387715.1
QIG63998.1	000341	PHP+DNApolIIIalpha+HHH	1274	DAC20_249	Bacteroides phage DAC20	GCA_013387725.1
QIG64262.1	000341	PHP+DNApolIIIalpha+HHH	1274	DAC22_252	Bacteroides phage DAC22	GCA_013387735.1
QIG64518.1	000341	PHP+DNApolIIIalpha+HHH	1277	DAC23_244	Bacteroides phage DAC23	GCA_013387745.1
AEO93588.1	000000	PHP+DNApolIIIalpha+HINT	765	G_329	Bacillus virus G	GCA_000917535.1
ABS83797.1	000000	PHP+DNApolIIIalpha+HHH	1348	0305phi8-36p240	Bacillus phage 0305phi8-36	GCA_000871045.1
AUZ94883.1	000342	DNApolIIIalpha-NTPBD	164	FDI40_gp074	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21732.1	000342	DNApolIIIalpha-NTPBD	216	GAP32_282	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13913.1	000342	DNApolIIIalpha-NTPBD	212	PBI_121Q_16	Escherichia phage 121Q	GCA_000926855.1
QAY00425.1	000342	DNApolIIIalpha-NTPBD	212	Ecwhy1_144	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35168.1	000342	DNApolIIIalpha-NTPBD	212	ACQ29_gp488	Escherichia phage PBECO4	GCA_001041035.1
BBM61605.1	000342	DNApolIIIalpha-NTPBD	212	EO157G_0160	Escherichia phage SP27	GCA_008033345.1
AXC36741.1	000342	DNApolIIIalpha-NTPBD	212	-	Escherichia phage UB	GCA_003341455.1
QBO61779.1	000342	DNApolIIIalpha-NTPBD	212	G17_00290	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13823.1	000342	DNApolIIIalpha-NTPBD	212	vBEcoMphAPEC6_gp194c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80508.1	000342	DNApolIIIalpha-NTPBD	212	PSLUR01_00531	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44397.1	000342	DNApolIIIalpha-NTPBD	213	RaK2_00124	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72833.1	000342	DNApolIIIalpha-NTPBD	192	-	Myoviridae sp.	GCA_003657725.1
AMM43851.1	000342	DNApolIIIalpha-NTPBD	216	CBB_287	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76101.1	000342	DNApolIIIalpha-NTPBD	200	EST35_0220	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44166.1	000342	DNApolIIIalpha-NTPBD	193	PBI_SCTP2_151	Salicola phage SCTP-2	GCA_002625545.1
QCW19010.1	000342	DNApolIIIalpha-NTPBD	210	7t3_0490	Salmonella phage 7t3	GCA_006083215.1
AZU98257.1	000342	DNApolIIIalpha-NTPBD	210	CPT_Munch_313	Salmonella phage Munch	GCA_004015485.1
QIG62727.1	000342	DNApolIIIalpha-NTPBD	210	SEPL_114	Salmonella phage SE_PL	GCA_011067555.1
AQW88810.1	000342	DNApolIIIalpha-NTPBD	216	BF_0285	Serratia phage BF	GCA_002619745.1
BBA65376.1	000342	DNApolIIIalpha-NTPBD	188	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96404.1	000342	DNApolIIIalpha-NTPBD	188	Xoosp13_218	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59093.1	000342	DNApolIIIalpha-NTPBD	216	g285	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58557.1	000342	DNApolIIIalpha-NTPBD	216	g280	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44743.1	000343	DNApolIIIalpha-NTPBD	177	FDI40_gp316	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21773.1	000343	DNApolIIIalpha-NTPBD	172	GAP32_323	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13953.1	000343	DNApolIIIalpha-NTPBD	172	PBI_121Q_56	Escherichia phage 121Q	GCA_000926855.1
QAY00384.1	000343	DNApolIIIalpha-NTPBD	172	Ecwhy1_103	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35129.1	000343	DNApolIIIalpha-NTPBD	172	ACQ29_gp449	Escherichia phage PBECO4	GCA_001041035.1
BBM61645.1	000343	DNApolIIIalpha-NTPBD	172	EO157G_0560	Escherichia phage SP27	GCA_008033345.1
AXC36703.1	000343	DNApolIIIalpha-NTPBD	172	-	Escherichia phage UB	GCA_003341455.1
QBO61740.1	000343	DNApolIIIalpha-NTPBD	172	G17_00251	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13785.1	000343	DNApolIIIalpha-NTPBD	158	vBEcoMphAPEC6_gp156c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80547.1	000343	DNApolIIIalpha-NTPBD	172	PSLUR01_00570	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFA44435.1	000343	DNApolIIIalpha-NTPBD	172	RaK2_00162	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72812.1	000343	DNApolIIIalpha-NTPBD	176	-	Myoviridae sp.	GCA_003657725.1
AMM43891.1	000343	DNApolIIIalpha-NTPBD	172	CBB_328	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76169.1	000343	DNApolIIIalpha-NTPBD	169	EST35_0288	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44306.1	000343	DNApolIIIalpha-NTPBD	181	PBI_SCTP2_291	Salicola phage SCTP-2	GCA_002625545.1
QCW19050.1	000343	DNApolIIIalpha-NTPBD	172	7t3_0530	Salmonella phage 7t3	GCA_006083215.1
AZU98297.1	000343	DNApolIIIalpha-NTPBD	172	CPT_Munch_353	Salmonella phage Munch	GCA_004015485.1
QIG62687.1	000343	DNApolIIIalpha-NTPBD	135	SEPL_074	Salmonella phage SE_PL	GCA_011067555.1
AQW88851.1	000343	DNApolIIIalpha-NTPBD	179	BF_0326	Serratia phage BF	GCA_002619745.1
BBA65393.1	000343	DNApolIIIalpha-NTPBD	182	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK59135.1	000343	DNApolIIIalpha-NTPBD	172	g327	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58601.1	000343	DNApolIIIalpha-NTPBD	172	g324	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AEO93590.1	000000	DNApolIIIalpha-NTPBD	158	G_331	Bacillus virus G	GCA_000917535.1
APU01444.1	000344	gp32-SSB	315	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28791.1	000344	gp32-SSB	323	AP1_0084	Aeromonas phage AP1	GCA_014183365.1
ATI17455.1	000344	gp32-SSB	323	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00141.1	000344	gp32-SSB	323	HWB28_gp009	Aeromonas phage AS-zj	GCA_002627665.1
AUE22849.1	000344	gp32-SSB	302	Ah1_00331	Aeromonas phage Ah1	GCA_002957415.1
QAX98560.1	000344	gp32-SSB	301	ASfcp2_226	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97895.1	000344	gp32-SSB	323	ASswx1_252	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01258.1	000344	gp32-SSB	317	ASwh1_193	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39530.1	000344	gp32-SSB	323	CC2_281	Aeromonas phage CC2	GCA_000903495.1
ADQ53025.1	000344	gp32-SSB	301	PX29p306	Aeromonas phage PX29	GCA_000920195.1
ADM79949.1	000344	gp32-SSB	301	phiAS5_ORF0106	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53064.1	000344	gp32-SSB	290	65p054	Aeromonas virus 65	GCA_000893255.1
AAQ17978.1	000344	gp32-SSB	302	32	Aeromonas virus Aeh1	GCA_000843245.1
ASV44706.1	000344	gp32-SSB	333	FDI40_gp107	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63564.1	000344	gp32-SSB	305	CP21_102	Campylobacter virus CP21	GCA_000902535.1
ANS05968.1	000344	gp32-SSB	326	ABCD_0045	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64814.1	000344	gp32-SSB	295	S13_015	Cronobacter phage S13	GCA_001503575.1
AFC21721.1	000344	gp32-SSB	347	GAP32_271	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97055.1	000344	gp32-SSB	326	E_046	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH57017.1	000344	gp32-SSB	301	CPXG_00214	Cyanophage P-RSM6	GCA_000906155.1
AJK27433.1	000344	gp32-SSB	311	PTIM40_6	Cyanophage P-TIM40	GCA_001470935.1
AOO14197.1	000344	gp32-SSB	320	Sn110110_003	Cyanophage S-RIM14	GCA_002599065.1
AOO14849.1	000344	gp32-SSB	320	W1230910_003	Cyanophage S-RIM14	GCA_002599125.1
AMO43016.1	000344	gp32-SSB	291	R1080702_001	Cyanophage S-RIM32	GCA_001754165.1
AMO43247.1	000344	gp32-SSB	290	W270710_002	Cyanophage S-RIM44	GCA_002599145.1
AOO11484.1	000344	gp32-SSB	290	ES420910_002	Cyanophage S-RIM44	GCA_002599165.1
AOO11719.1	000344	gp32-SSB	290	Np050604_002	Cyanophage S-RIM44	GCA_002599185.1
AOO11949.1	000344	gp32-SSB	290	Np200711_002	Cyanophage S-RIM44	GCA_002599205.1
AOO12185.1	000344	gp32-SSB	290	Np420711_002	Cyanophage S-RIM44	GCA_002599225.1
AOO12420.1	000344	gp32-SSB	290	Sn080709_002	Cyanophage S-RIM44	GCA_002599245.1
AOO12650.1	000344	gp32-SSB	290	Sn130910_002	Cyanophage S-RIM44	GCA_002599265.1
AOO12885.1	000344	gp32-SSB	290	W2100709_002	Cyanophage S-RIM44	GCA_002599285.1
AGH07630.1	000344	gp32-SSB	306	CYVG_00187	Cyanophage S-SSM6a	GCA_002710385.1
AGG54367.1	000344	gp32-SSB	306	CYWG_00083	Cyanophage S-SSM6b	GCA_002710425.1
AIT13903.1	000344	gp32-SSB	350	PBI_121Q_6	Escherichia phage 121Q	GCA_000926855.1
QAY00434.1	000344	gp32-SSB	349	Ecwhy1_154	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35178.1	000344	gp32-SSB	350	ACQ29_gp498	Escherichia phage PBECO4	GCA_001041035.1
BBM61595.1	000344	gp32-SSB	341	EO157G_0060	Escherichia phage SP27	GCA_008033345.1
AXC36750.1	000344	gp32-SSB	350	-	Escherichia phage UB	GCA_003341455.1
ARM70793.1	000344	gp32-SSB	300	phiC120_c87	Escherichia phage phiC120	GCA_002621185.1
QBO61789.1	000344	gp32-SSB	350	G17_00300	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13833.1	000344	gp32-SSB	350	vBEcoMphAPEC6_gp204c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80498.1	000344	gp32-SSB	350	PSLUR01_00521	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78567.1	000344	gp32-SSB	326	RB43ORF045c	Escherichia virus RB43	GCA_000863505.1
AFA44386.1	000344	gp32-SSB	361	RaK2_00113	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72764.1	000344	gp32-SSB	326	-	Myoviridae sp.	GCA_003657725.1
QHJ78850.1	000344	gp32-SSB	292	-	Myoviridae sp.	GCA_012593985.1
QIG65749.1	000344	gp32-SSB	323	phiOC_p084	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43841.1	000344	gp32-SSB	347	CBB_277	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26203.1	000344	gp32-SSB	290	CPMG_00102	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44386.1	000344	gp32-SSB	272	PSSM2_008	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12262.1	000344	gp32-SSB	297	PRTG_00107	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93390.1	000344	gp32-SSB	313	AVU42_gp004	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99105.1	000344	gp32-SSB	290	Syn1_003	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76088.1	000344	gp32-SSB	328	EST35_0207	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44218.1	000344	gp32-SSB	336	PBI_SCTP2_203	Salicola phage SCTP-2	GCA_002625545.1
QCW19000.1	000344	gp32-SSB	350	7t3_0480	Salmonella phage 7t3	GCA_006083215.1
AZU98247.1	000344	gp32-SSB	350	CPT_Munch_303	Salmonella phage Munch	GCA_004015485.1
QIG62737.1	000344	gp32-SSB	350	SEPL_124	Salmonella phage SE_PL	GCA_011067555.1
AQW88800.1	000344	gp32-SSB	351	BF_0275	Serratia phage BF	GCA_002619745.1
AGR47820.1	000344	gp32-SSB	312	SmphiM12_188	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13034.1	000344	gp32-SSB	312	PHIM19_129	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12674.1	000344	gp32-SSB	312	PHIM7_128	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13406.1	000344	gp32-SSB	312	PHIN3_143	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28171.1	000344	gp32-SSB	349	PAU_173	Sphingomonas phage PAU	GCA_000902455.1
AIX30478.1	000344	gp32-SSB	309	Syn7803US37_1	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54629.1	000344	gp32-SSB	316	b23_0001	Synechococcus phage B23	GCA_009745195.1
QGT54259.1	000344	gp32-SSB	316	b3_0001	Synechococcus phage B3	GCA_009745215.1
ASR76051.1	000344	gp32-SSB	308	PBI_BELLAMY_4	Synechococcus phage Bellamy	GCA_002627525.1
QCW23071.1	000344	gp32-SSB	320	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50681.1	000344	gp32-SSB	298	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59462.1	000344	gp32-SSB	313	S330809_001	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59224.1	000344	gp32-SSB	313	C440309_001	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59700.1	000344	gp32-SSB	313	N231010_001	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70449.1	000344	gp32-SSB	305	HOU04_gp050	Synechococcus phage S-T4	GCA_003443335.1
QJT70019.1	000344	gp32-SSB	302	SynMITS9220M01_003	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90431.1	000344	gp32-SSB	340	HYO65_gp039	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90738.1	000344	gp32-SSB	347	-	Tenacibaculum phage PTm5	GCA_009730715.1
AAQ64076.1	000344	gp32-SSB	302	KVP40.0005	Vibrio phage KVP40	GCA_000843785.1
QIW90402.1	000344	gp32-SSB	303	GCAPEGMB_00055	Vibrio phage V07	GCA_012361095.1
QIW91027.1	000344	gp32-SSB	304	COHAPHLL_00164	Vibrio phage V09	GCA_012361135.1
QHJ74188.1	000344	gp32-SSB	303	VH12019_00269	Vibrio phage VH1_2019	GCA_009931825.1
AGB07012.1	000344	gp32-SSB	306	CF80_gp225	Vibrio phage VH7D	GCA_000914495.1
QBX06084.1	000344	gp32-SSB	308	ValB1HC_130	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04520.1	000344	gp32-SSB	314	ValB1MD_199	Vibrio phage ValB1MD	GCA_004138815.1
AJT61098.1	000344	gp32-SSB	308	AVU32_gp257	Vibrio phage ValKK3	GCA_001501635.1
AGN30055.2	000344	gp32-SSB	306	VPFG_00052	Vibrio phage nt-1	GCA_000910195.2
ALP47019.1	000344	gp32-SSB	308	phiGrn1_0120	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47399.1	000344	gp32-SSB	308	phiST2_0251	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54710.1	000344	gp32-SSB	308	vBValMR10Z_169	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07090.1	000344	gp32-SSB	314	VmeM32_00101	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37239.1	000344	gp32-SSB	303	pp2_005	Vibriophage phi-pp2	GCA_002630725.1
BBA65400.1	000344	gp32-SSB	337	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96425.1	000344	gp32-SSB	329	Xoosp13_239	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59083.1	000344	gp32-SSB	350	g275	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58547.1	000344	gp32-SSB	350	g270	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000831	000344	gp32-SSB	303	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000574	000344	gp32-SSB	379	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44892.1	000345	gp32-SSB	477	SP15_093	Bacillus phage SP-15	GCA_001754685.1
BAV39235.1	000000	gp32-SSB	382	BPT24_110	Tenacibaculum phage pT24	GCA_002611925.1
AND75171.1	000346	gp4-TnsA-REase	150	ME3_10	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01501.1	000346	gp4-TnsA-REase	156	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28989.1	000346	gp4-TnsA-REase	156	AP1_0282	Aeromonas phage AP1	GCA_014183365.1
ATI17396.1	000346	gp4-TnsA-REase	156	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00199.1	000346	gp4-TnsA-REase	156	HWB28_gp353	Aeromonas phage AS-zj	GCA_002627665.1
AUE22725.1	000346	gp4-TnsA-REase	156	Ah1_00207	Aeromonas phage Ah1	GCA_002957415.1
QAX98448.1	000346	gp4-TnsA-REase	156	ASfcp2_105	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97837.1	000346	gp4-TnsA-REase	156	ASswx1_193	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01315.1	000346	gp4-TnsA-REase	156	ASwh1_253	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39560.1	000346	gp4-TnsA-REase	156	CC2_342	Aeromonas phage CC2	GCA_000903495.1
ADQ52905.1	000346	gp4-TnsA-REase	156	PX29p186	Aeromonas phage PX29	GCA_000920195.1
ADM80172.1	000346	gp4-TnsA-REase	154	phiAS5_ORF0329	Aeromonas phage phiAS5	GCA_000887715.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADQ53122.1	000346	gp4-TnsA-REase	156	65p114	Aeromonas virus 65	GCA_000893255.1
AAQ17857.1	000346	gp4-TnsA-REase	156	4	Aeromonas virus Aeh1	GCA_000843245.1
ASV44711.1	000346	gp4-TnsA-REase	160	FDI40_gp125	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63649.1	000346	gp4-TnsA-REase	141	CP21_187	Campylobacter virus CP21	GCA_000902535.1
ANS06051.1	000346	gp4-TnsA-REase	144	ABCD_0192	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64960.1	000346	gp4-TnsA-REase	154	S13_161	Cronobacter phage S13	GCA_001503575.1
AFC21652.1	000346	gp4-TnsA-REase	152	GAP32_202	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97206.1	000346	gp4-TnsA-REase	144	E_198	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH57013.1	000346	gp4-TnsA-REase	146	CPXG_00210	Cyanophage P-RSM6	GCA_000906155.1
AJK27442.1	000346	gp4-TnsA-REase	144	PTIM40_15	Cyanophage P-TIM40	GCA_001470935.1
AOO14201.1	000346	gp4-TnsA-REase	140	Sn110110_007	Cyanophage S-RIM14	GCA_002599065.1
AOO14853.1	000346	gp4-TnsA-REase	140	W1230910_007	Cyanophage S-RIM14	GCA_002599125.1
AMO43021.1	000346	gp4-TnsA-REase	162	R1080702_006	Cyanophage S-RIM32	GCA_001754165.1
AMO43252.1	000346	gp4-TnsA-REase	113	W270710_007	Cyanophage S-RIM44	GCA_002599145.1
AOO11489.1	000346	gp4-TnsA-REase	113	ES420910_007	Cyanophage S-RIM44	GCA_002599165.1
AOO11724.1	000346	gp4-TnsA-REase	113	Np050604_007	Cyanophage S-RIM44	GCA_002599185.1
AOO11954.1	000346	gp4-TnsA-REase	113	Np200711_007	Cyanophage S-RIM44	GCA_002599205.1
AOO12190.1	000346	gp4-TnsA-REase	113	Np420711_007	Cyanophage S-RIM44	GCA_002599225.1
AOO12425.1	000346	gp4-TnsA-REase	113	Sn080709_007	Cyanophage S-RIM44	GCA_002599245.1
AOO12655.1	000346	gp4-TnsA-REase	113	Sn130910_007	Cyanophage S-RIM44	GCA_002599265.1
AOO12890.1	000346	gp4-TnsA-REase	113	W2100709_007	Cyanophage S-RIM44	GCA_002599285.1
AGH07634.1	000346	gp4-TnsA-REase	152	CYVG_00191	Cyanophage S-SSM6a	GCA_002710385.1
AGG54363.1	000346	gp4-TnsA-REase	107	CYWG_00079	Cyanophage S-SSM6b	GCA_002710425.1
AIT14445.1	000346	gp4-TnsA-REase	142	PBI_121Q_555	Escherichia phage 121Q	GCA_000926855.1
QAY00503.1	000346	gp4-TnsA-REase	142	Ecwhy1_224	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34698.1	000346	gp4-TnsA-REase	142	ACQ29_gp018	Escherichia phage PBECO4	GCA_001041035.1
BBM62118.1	000346	gp4-TnsA-REase	142	EO157G_5290	Escherichia phage SP27	GCA_008033345.1
AXC36818.1	000346	gp4-TnsA-REase	142	-	Escherichia phage UB	GCA_003341455.1
ARM70709.1	000346	gp4-TnsA-REase	149	phiC120_c2	Escherichia phage phiC120	GCA_002621185.1
ARM70975.1	000346	gp4-TnsA-REase	149	phiC120_c270	Escherichia phage phiC120	GCA_002621185.1
QBO61857.1	000346	gp4-TnsA-REase	142	G17_00368	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13897.1	000346	gp4-TnsA-REase	142	vBEcoMphAPEC6_gp272c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80430.1	000346	gp4-TnsA-REase	142	PSLUR01_00453	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78724.1	000346	gp4-TnsA-REase	144	RB43ORF202c	Escherichia virus RB43	GCA_000863505.1
AFA44318.1	000346	gp4-TnsA-REase	148	RaK2_00045	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72828.1	000346	gp4-TnsA-REase	147	-	Myoviridae sp.	GCA_003657725.1
QHJ78974.1	000346	gp4-TnsA-REase	154	-	Myoviridae sp.	GCA_012593985.1
QIG65733.1	000346	gp4-TnsA-REase	146	phiOC_p068	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43773.1	000346	gp4-TnsA-REase	152	CBB_208	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26199.1	000346	gp4-TnsA-REase	144	CPMG_00098	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44390.1	000346	gp4-TnsA-REase	145	PSSM2_012	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12258.1	000346	gp4-TnsA-REase	145	PRTG_00103	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93394.1	000346	gp4-TnsA-REase	162	AVU42_gp008	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99110.1	000346	gp4-TnsA-REase	113	Syn1_008	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76081.1	000346	gp4-TnsA-REase	142	EST35_0200	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44467.1	000346	gp4-TnsA-REase	156	PBI_SCTP2_452	Salicola phage SCTP-2	GCA_002625545.1
QCW18921.1	000346	gp4-TnsA-REase	156	7t3_0400	Salmonella phage 7t3	GCA_006083215.1
AZU98178.1	000346	gp4-TnsA-REase	156	CPT_Munch_234	Salmonella phage Munch	GCA_004015485.1
QIG62806.1	000346	gp4-TnsA-REase	156	SEPL_193	Salmonella phage SE_PL	GCA_011067555.1
AQW88729.1	000346	gp4-TnsA-REase	152	BF_0204	Serratia phage BF	GCA_002619745.1
AGR47787.2	000346	gp4-TnsA-REase	154	SmphiM12_155	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13009.1	000346	gp4-TnsA-REase	154	PHIM19_103	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12649.1	000346	gp4-TnsA-REase	154	PHIM7_102	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13381.1	000346	gp4-TnsA-REase	154	PHIN3_116	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28132.1	000346	gp4-TnsA-REase	161	PAU_134	Sphingomonas phage PAU	GCA_000902455.1
AIX30481.1	000346	gp4-TnsA-REase	146	Syn7803US37_4	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54633.1	000346	gp4-TnsA-REase	146	b23_0005	Synechococcus phage B23	GCA_009745195.1
QGT54263.1	000346	gp4-TnsA-REase	146	b3_0005	Synechococcus phage B3	GCA_009745215.1
ASR76055.1	000346	gp4-TnsA-REase	103	PBI_BELLAMY_8	Synechococcus phage Bellamy	GCA_002627525.1
QCW22922.1	000346	gp4-TnsA-REase	159	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50637.1	000346	gp4-TnsA-REase	159	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59467.1	000346	gp4-TnsA-REase	157	S330809_006	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59229.1	000346	gp4-TnsA-REase	157	C440309_006	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59705.1	000346	gp4-TnsA-REase	157	N231010_006	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70445.1	000346	gp4-TnsA-REase	145	HOU04_gp046	Synechococcus phage S-T4	GCA_003443335.1
QJT70023.1	000346	gp4-TnsA-REase	114	SynMITS9220M01_007	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90393.1	000346	gp4-TnsA-REase	160	HYO65_gp001	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90701.1	000346	gp4-TnsA-REase	160	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV31391.1	000346	gp4-TnsA-REase	164	BPT24_176	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64400.1	000346	gp4-TnsA-REase	151	KVP40.0331	Vibrio phage KVP40	GCA_000843785.1
QIW90713.1	000346	gp4-TnsA-REase	151	GCAPEGMB_00394	Vibrio phage V07	GCA_012361095.1
QIW91084.1	000346	gp4-TnsA-REase	151	COHAPHLL_00221	Vibrio phage V09	GCA_012361135.1
QHJ74513.1	000346	gp4-TnsA-REase	151	VH12019_00213	Vibrio phage VH1_2019	GCA_009931825.1
QBX06142.1	000346	gp4-TnsA-REase	151	ValB1HC_188	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04541.1	000346	gp4-TnsA-REase	157	ValB1MD_254	Vibrio phage ValB1MD	GCA_004138815.1
AJT61154.1	000346	gp4-TnsA-REase	151	AVU32_gp313	Vibrio phage ValKK3	GCA_001501635.1
AGN30382.1	000346	gp4-TnsA-REase	151	VPFG_00385	Vibrio phage nt-1	GCA_000910195.2
ALP47127.1	000346	gp4-TnsA-REase	151	phiGrn1_0066	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47512.1	000346	gp4-TnsA-REase	151	phiST2_0197	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54767.1	000346	gp4-TnsA-REase	151	vBValMR10Z_227	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07102.1	000346	gp4-TnsA-REase	123	VmeM32_00115	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37563.1	000346	gp4-TnsA-REase	151	pp2_331	Vibriophage phi-pp2	GCA_002630725.1
BBA65496.1	000346	gp4-TnsA-REase	159	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96504.1	000346	gp4-TnsA-REase	130	Xoosp13_318	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59012.1	000346	gp4-TnsA-REase	152	g204	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58477.1	000346	gp4-TnsA-REase	152	g200	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prev15ph1000000245	000346	gp4-TnsA-REase	140	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44832.1	000347	gp4-TnsA-REase	268	SP15_033	Bacillus phage SP-15	GCA_001754685.1
AMM44822.1	000347	gp4-TnsA-REase	307	SP15_023	Bacillus phage SP-15	GCA_001754685.1
prevph1000000314	000348	gp4-TnsA-REase	58	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000244	000348	gp4-TnsA-REase	58	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
CCH63521.1	000000	gp4-TnsA-REase	115	CP21_059	Campylobacter virus CP21	GCA_000902535.1
prev15ph1000000420	000000	gp4-TnsA-REase	413	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01418.1	000349	gp45-clamp	230	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28809.1	000349	gp45-clamp	230	AP1_0102	Aeromonas phage AP1	GCA_014183365.1
ATI17480.1	000349	gp45-clamp	230	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00517.1	000349	gp45-clamp	230	HWB28_gp035	Aeromonas phage AS-zj	GCA_002627665.1
AUE22565.1	000349	gp45-clamp	225	Ah1_00024	Aeromonas phage Ah1	GCA_002957415.1
QAX98603.1	000349	gp45-clamp	225	ASfcp2_270	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97920.1	000349	gp45-clamp	230	ASswx1_277	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01230.1	000349	gp45-clamp	230	ASwh1_165	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39518.1	000349	gp45-clamp	230	CC2_255	Aeromonas phage CC2	GCA_000903495.1
ADQ52738.1	000349	gp45-clamp	225	PX29p019	Aeromonas phage PX29	GCA_000920195.1
ADM79991.1	000349	gp45-clamp	224	phiAS5_ORF0148	Aeromonas phage phiAS5	GCA_000887715.1
AAR90911.1	000349	gp45-clamp	230	65p027	Aeromonas virus 65	GCA_000893255.1
AAQ17676.1	000349	gp45-clamp	225	45	Aeromonas virus Aeh1	GCA_000843245.1
ANS05997.1	000349	gp45-clamp	221	ABCD_0043	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65043.1	000349	gp45-clamp	229	S13_246	Cronobacter phage S13	GCA_001503575.1
AON97053.1	000349	gp45-clamp	221	E_044	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56875.1	000349	gp45-clamp	226	CPXG_00072	Cyanophage P-RSM6	GCA_000906155.1
AJK27580.1	000349	gp45-clamp	243	PTIM40_153	Cyanophage P-TIM40	GCA_001470935.1
AOO14340.1	000349	gp45-clamp	217	Sn110110_146	Cyanophage S-RIM14	GCA_002599065.1
AOO14989.1	000349	gp45-clamp	217	W1230910_143	Cyanophage S-RIM14	GCA_002599125.1
AMO43159.1	000349	gp45-clamp	221	R1080702_150	Cyanophage S-RIM32	GCA_001754165.1
AMO43383.1	000349	gp45-clamp	221	W270710_139	Cyanophage S-RIM44	GCA_002599145.1
AOO11628.1	000349	gp45-clamp	221	ES420910_147	Cyanophage S-RIM44	GCA_002599165.1
AOO11855.1	000349	gp45-clamp	221	Np050604_139	Cyanophage S-RIM44	GCA_002599185.1
AOO12093.1	000349	gp45-clamp	221	Np200711_147	Cyanophage S-RIM44	GCA_002599205.1
AOO12329.1	000349	gp45-clamp	221	Np420711_147	Cyanophage S-RIM44	GCA_002599225.1
AOO12556.1	000349	gp45-clamp	221	Sn080709_139	Cyanophage S-RIM44	GCA_002599245.1
AOO12794.1	000349	gp45-clamp	221	Sn130910_147	Cyanophage S-RIM44	GCA_002599265.1
AOO13022.1	000349	gp45-clamp	221	W2100709_140	Cyanophage S-RIM44	GCA_002599285.1
AGH07480.1	000349	gp45-clamp	230	CYVG_00036	Cyanophage S-SSM6a	GCA_002710385.1
AGG54470.1	000349	gp45-clamp	219	CYWG_00186	Cyanophage S-SSM6b	GCA_002710425.1
ARM70875.1	000349	gp45-clamp	228	phiC120_c170	Escherichia phage phiC120	GCA_002621185.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAX78565.1	000349	gp45-clamp	213	RB43ORF043c	Escherichia virus RB43	GCA_000863505.1
QHJ78889.1	000349	gp45-clamp	228	-	Myoviridae sp.	GCA_012593985.1
QIG65676.1	000349	gp45-clamp	224	phiOC_p010	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AAX44535.1	000349	gp45-clamp	221	PSSM2_157	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12436.1	000349	gp45-clamp	221	PRTG_00286	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93467.1	000349	gp45-clamp	229	AVU42_gp129	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99241.1	000349	gp45-clamp	221	Syn1_140	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47673.1	000349	gp45-clamp	219	SmphiM12_041	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12936.1	000349	gp45-clamp	219	PHIM19_29	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12576.1	000349	gp45-clamp	219	PHIM7_28	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13308.1	000349	gp45-clamp	219	PHIN3_43	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30637.1	000349	gp45-clamp	222	Syn7803US37_160	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54910.1	000349	gp45-clamp	224	b23_0297	Synechococcus phage B23	GCA_009745195.1
QGT54545.1	000349	gp45-clamp	224	b3_0304	Synechococcus phage B3	GCA_009745215.1
ASR76195.1	000349	gp45-clamp	221	PBI_BELLAMY_150	Synechococcus phage Bellamy	GCA_002627525.1
QCW22905.1	000349	gp45-clamp	221	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50582.1	000349	gp45-clamp	221	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59607.1	000349	gp45-clamp	224	S330809_146	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59369.1	000349	gp45-clamp	224	C440309_146	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59845.1	000349	gp45-clamp	224	N231010_146	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70558.1	000349	gp45-clamp	224	HOU04_gp159	Synechococcus phage S-T4	GCA_003443335.1
QJT70140.1	000349	gp45-clamp	229	SynMITS9220M01_127	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64148.1	000349	gp45-clamp	221	KVP40.0077	Vibrio phage KVP40	GCA_000843785.1
QIW90471.1	000349	gp45-clamp	221	GCAPEGMB_00124	Vibrio phage V07	GCA_012361095.1
QIW90958.1	000349	gp45-clamp	221	COHAPHLL_00095	Vibrio phage V09	GCA_012361135.1
QHJ74260.1	000349	gp45-clamp	221	VH12019_00341	Vibrio phage VH1_2019	GCA_009931825.1
AGB07084.1	000349	gp45-clamp	221	CF80_gp297	Vibrio phage VH7D	GCA_000914495.1
QBX06011.1	000349	gp45-clamp	221	ValB1HC_057	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61024.1	000349	gp45-clamp	221	AVU32_gp183	Vibrio phage ValKK3	GCA_001501635.1
AGN30126.1	000349	gp45-clamp	220	VPFG_00124	Vibrio phage nt-1	GCA_000910195.2
ALP47058.1	000349	gp45-clamp	221	phiGrn1_0192	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47438.1	000349	gp45-clamp	221	phiST2_0323	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54636.1	000349	gp45-clamp	221	vBValMR10Z_95	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07129.1	000349	gp45-clamp	219	VmeM32_00142	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37308.1	000349	gp45-clamp	221	pp2_075	Vibriophage phi-pp2	GCA_002630725.1
AUZ95049.1	000350	gp45-clamp	248	FDI40_gp275	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21709.1	000350	gp45-clamp	243	GAP32_259	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14503.1	000350	gp45-clamp	243	PBI_121Q_613	Escherichia phage 121Q	GCA_000926855.1
QAY00446.1	000350	gp45-clamp	243	Ecwhy1_166	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35189.1	000350	gp45-clamp	243	ACQ29_gp509	Escherichia phage PBECO4	GCA_001041035.1
BBM62175.1	000350	gp45-clamp	243	EO157G_5860	Escherichia phage SP27	GCA_008033345.1
QBO61800.1	000350	gp45-clamp	243	G17_00311	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13844.1	000350	gp45-clamp	243	vBEcoMphAPEC6_gp215c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80487.1	000350	gp45-clamp	243	PSLUR01_00510	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44375.1	000350	gp45-clamp	247	RaK2_00102	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72733.1	000350	gp45-clamp	245	-	Myoviridae sp.	GCA_003657725.1
AMM43829.1	000350	gp45-clamp	243	CBB_265	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76195.1	000350	gp45-clamp	248	EST35_0314	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44193.1	000350	gp45-clamp	255	PBI_SCTP2_178	Salicola phage SCTP-2	GCA_002625545.1
QCW18988.1	000350	gp45-clamp	243	7t3_0467	Salmonella phage 7t3	GCA_006083215.1
AZU98236.1	000350	gp45-clamp	243	CPT_Munch_292	Salmonella phage Munch	GCA_004015485.1
QIG62748.1	000350	gp45-clamp	243	SEPL_135	Salmonella phage SE_PL	GCA_011067555.1
AQW88788.1	000350	gp45-clamp	243	BF_0263	Serratia phage BF	GCA_002619745.1
SOK59069.1	000350	gp45-clamp	243	g261	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58535.1	000350	gp45-clamp	243	g258	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BBA65490.1	000351	gp45-clamp	243	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96497.1	000351	gp45-clamp	243	Xoosp13_311	Xanthomonas phage Xoo-sp13	GCA_013364725.1
CCH63695.1	000352	gp45-clamp	195	CP21_235	Campylobacter virus CP21	GCA_000902535.1
QAU04519.1	000352	gp45-clamp	234	ValB1MD_198	Vibrio phage ValB1MD	GCA_004138815.1
APU01443.1	000353	gp59-hel-load	144	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28792.1	000353	gp59-hel-load	221	AP1_0085	Aeromonas phage AP1	GCA_014183365.1
ATI17456.1	000353	gp59-hel-load	221	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00140.1	000353	gp59-hel-load	221	HWB28_gp010	Aeromonas phage AS-zj	GCA_002627665.1
AUE22850.1	000353	gp59-hel-load	215	Ah1_00332	Aeromonas phage Ah1	GCA_002957415.1
QAX98561.1	000353	gp59-hel-load	215	ASfcp2_227	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97896.1	000353	gp59-hel-load	221	ASswx1_253	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01257.1	000353	gp59-hel-load	221	ASwh1_192	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39529.1	000353	gp59-hel-load	221	CC2_280	Aeromonas phage CC2	GCA_000903495.1
ADQ53026.1	000353	gp59-hel-load	215	PX29p307	Aeromonas phage PX29	GCA_000920195.1
ADM79950.1	000353	gp59-hel-load	216	phiAS5_ORF0107	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53063.1	000353	gp59-hel-load	144	65p053	Aeromonas virus 65	GCA_000893255.1
AAQ17979.1	000353	gp59-hel-load	215	59	Aeromonas virus Aeh1	GCA_000843245.1
ANS05998.1	000353	gp59-hel-load	221	ABCD_0046	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64813.1	000353	gp59-hel-load	219	S13_014	Cronobacter phage S13	GCA_001503575.1
AON97056.1	000353	gp59-hel-load	221	E_047	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AOO14195.1	000353	gp59-hel-load	191	Sn110110_001	Cyanophage S-RIM14	GCA_002599065.1
AOO14847.1	000353	gp59-hel-load	191	W1230910_001	Cyanophage S-RIM14	GCA_002599125.1
AGG54370.1	000353	gp59-hel-load	198	CYWG_00086	Cyanophage S-SSM6b	GCA_002710425.1
ARM70794.1	000353	gp59-hel-load	217	phiC120_c88	Escherichia phage phiC120	GCA_002621185.1
AAX78568.1	000353	gp59-hel-load	221	RB43ORF046c	Escherichia virus RB43	GCA_000863505.1
QHJ78851.1	000353	gp59-hel-load	221	-	Myoviridae sp.	GCA_012593985.1
AGH26213.1	000353	gp59-hel-load	194	CPMG_00112	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44384.1	000353	gp59-hel-load	198	PSSM2_006	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12264.1	000353	gp59-hel-load	191	PRTG_00109	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93388.1	000353	gp59-hel-load	202	AVU42_gp002	Prochlorococcus phage P-TIM68	GCA_001503075.1
AGR47818.1	000353	gp59-hel-load	202	SmphiM12_186	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13033.1	000353	gp59-hel-load	202	PHIM19_128	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12673.1	000353	gp59-hel-load	202	PHIM7_127	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13404.1	000353	gp59-hel-load	201	PHIN3_141	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30768.1	000353	gp59-hel-load	204	Syn7803US37_291	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54993.1	000353	gp59-hel-load	200	b23_0387	Synechococcus phage B23	GCA_009745195.1
QGT54628.1	000353	gp59-hel-load	200	b3_0393	Synechococcus phage B3	GCA_009745215.1
ASR76049.1	000353	gp59-hel-load	187	PBI_BELLAMY_2	Synechococcus phage Bellamy	GCA_002627525.1
QCW23066.1	000353	gp59-hel-load	203	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50686.1	000353	gp59-hel-load	203	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70017.1	000353	gp59-hel-load	196	SynMITS9220M01_001	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64075.1	000353	gp59-hel-load	216	KVP40.0004	Vibrio phage KVP40	GCA_000843785.1
QIW90401.1	000353	gp59-hel-load	216	GCAPEGMB_00054	Vibrio phage V07	GCA_012361095.1
QIW91028.1	000353	gp59-hel-load	216	COHAPHLL_00165	Vibrio phage V09	GCA_012361135.1
QHJ74187.1	000353	gp59-hel-load	216	VH12019_00268	Vibrio phage VH1_2019	GCA_009931825.1
AGB07011.1	000353	gp59-hel-load	209	CF80_gp224	Vibrio phage VH7D	GCA_000914495.1
QBX06085.1	000353	gp59-hel-load	186	ValB1HC_131	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61099.1	000353	gp59-hel-load	186	AVU32_gp258	Vibrio phage ValKK3	GCA_001501635.1
AGN30054.2	000353	gp59-hel-load	223	VPFG_00051	Vibrio phage nt-1	GCA_000910195.2
ALP47081.1	000353	gp59-hel-load	186	phiGrn1_0119	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47462.1	000353	gp59-hel-load	186	phiST2_0250	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54711.1	000353	gp59-hel-load	173	vBValMR10Z_170	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07091.1	000353	gp59-hel-load	222	VmeM32_00102	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37238.1	000353	gp59-hel-load	216	pp2_004	Vibriophage phi-pp2	GCA_002630725.1
QIG65750.1	000000	gp59-hel-load	208	phiOC_p085	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
APU01415.1	000354	gp62-Clloadss	195	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28807.1	000354	gp62-Clloadss	192	AP1_0100	Aeromonas phage AP1	GCA_014183365.1
ATI17482.1	000354	gp62-Clloadss	192	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00515.1	000354	gp62-Clloadss	192	HWB28_gp037	Aeromonas phage AS-zj	GCA_002627665.1
AUE22563.1	000354	gp62-Clloadss	193	Ah1_00022	Aeromonas phage Ah1	GCA_002957415.1
QAX98601.1	000354	gp62-Clloadss	192	ASfcp2_268	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97922.1	000354	gp62-Clloadss	192	ASswx1_279	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01227.1	000354	gp62-Clloadss	192	ASwh1_162	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39516.1	000354	gp62-Clloadss	192	CC2_252	Aeromonas phage CC2	GCA_000903495.1
ADQ52736.1	000354	gp62-Clloadss	192	PX20p017	Aeromonas phage PX29	GCA_000920195.1
ADM79989.1	000354	gp62-Clloadss	193	phiAS5_ORF0146	Aeromonas phage phiAS5	GCA_000887715.1
AAR90914.2	000354	gp62-Clloadss	195	65p024	Aeromonas virus 65	GCA_000893255.1
AAQ17674.1	000354	gp62-Clloadss	193	62	Aeromonas virus Aeh1	GCA_000843245.1
ANS06017.1	000354	gp62-Clloadss	190	ABCD_0041	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65045.1	000354	gp62-Clloadss	197	S13_248	Cronobacter phage S13	GCA_001503575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AON97051.1	000354	gp62-Clloadss	190	E_042	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56869.1	000354	gp62-Clloadss	130	CPXG_00066	Cyanophage P-RSM6	GCA_000906155.1
AJK27587.1	000354	gp62-Clloadss	130	PTIM40_160	Cyanophage P-TIM40	GCA_001470935.1
AOO14346.1	000354	gp62-Clloadss	123	Sn110110_152	Cyanophage S-RIM14	GCA_002599065.1
AOO14995.1	000354	gp62-Clloadss	123	W1230910_149	Cyanophage S-RIM14	GCA_002599125.1
AMO43165.1	000354	gp62-Clloadss	128	R1080702_156	Cyanophage S-RIM32	GCA_001754165.1
AMO43390.1	000354	gp62-Clloadss	128	W270710_146	Cyanophage S-RIM44	GCA_002599145.1
AOO11635.1	000354	gp62-Clloadss	128	ES420910_154	Cyanophage S-RIM44	GCA_002599165.1
AOO11862.1	000354	gp62-Clloadss	128	Np050604_146	Cyanophage S-RIM44	GCA_002599185.1
AOO12100.1	000354	gp62-Clloadss	128	Np200711_154	Cyanophage S-RIM44	GCA_002599205.1
AOO12336.1	000354	gp62-Clloadss	128	Np420711_154	Cyanophage S-RIM44	GCA_002599225.1
AOO12563.1	000354	gp62-Clloadss	128	Sn080709_146	Cyanophage S-RIM44	GCA_002599245.1
AOO12801.1	000354	gp62-Clloadss	128	Sn130910_154	Cyanophage S-RIM44	GCA_002599265.1
AOO13029.1	000354	gp62-Clloadss	128	W2100709_147	Cyanophage S-RIM44	GCA_002599285.1
AGH07489.1	000354	gp62-Clloadss	127	CYVG_00045	Cyanophage S-SSM6a	GCA_002710385.1
AGG54463.1	000354	gp62-Clloadss	138	CYWG_00179	Cyanophage S-SSM6b	GCA_002710425.1
ARM70873.1	000354	gp62-Clloadss	187	phiC120_c168	Escherichia phage phiC120	GCA_002621185.1
AAX78563.1	000354	gp62-Clloadss	190	RB43ORF041c	Escherichia virus RB43	GCA_000863505.1
QHJ78887.1	000354	gp62-Clloadss	198	-	Myoviridae sp.	GCA_012593985.1
QIG65674.1	000354	gp62-Clloadss	132	phiOC_p008	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26296.1	000354	gp62-Clloadss	126	CPMG_00196	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44549.2	000354	gp62-Clloadss	82	PSSM2_171	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12422.1	000354	gp62-Clloadss	126	PRTG_00271	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93478.1	000354	gp62-Clloadss	128	AVU42_gp141	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99248.1	000354	gp62-Clloadss	128	Syn1_147	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47668.1	000354	gp62-Clloadss	132	SmphiM12_036	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12932.1	000354	gp62-Clloadss	132	PHIM19_25	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12572.1	000354	gp62-Clloadss	132	PHIM7_24	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13304.2	000354	gp62-Clloadss	132	PHIN3_39	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30642.1	000354	gp62-Clloadss	136	Syn7803US37_165	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54912.1	000354	gp62-Clloadss	124	b23_0299	Synechococcus phage B23	GCA_009745195.1
QGT54547.1	000354	gp62-Clloadss	124	b3_0306	Synechococcus phage B3	GCA_009745215.1
ASR76201.1	000354	gp62-Clloadss	122	PBI_BELLAMY_156	Synechococcus phage Bellamy	GCA_002627525.1
QCW23084.1	000354	gp62-Clloadss	126	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50575.1	000354	gp62-Clloadss	126	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59615.1	000354	gp62-Clloadss	127	S330809_154	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59377.1	000354	gp62-Clloadss	127	C440309_154	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59853.1	000354	gp62-Clloadss	127	N231010_154	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70550.1	000354	gp62-Clloadss	126	HOU04_gp151	Synechococcus phage S-T4	GCA_003443335.1
QJT70150.1	000354	gp62-Clloadss	122	SynMITS9220M01_137	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64150.1	000354	gp62-Clloadss	162	KVP40.0079	Vibrio phage KVP40	GCA_000843785.1
QIW90474.1	000354	gp62-Clloadss	162	GCAPEGMB_00127	Vibrio phage V07	GCA_012361095.1
QIW90955.1	000354	gp62-Clloadss	162	COHAPHLL_00092	Vibrio phage V09	GCA_012361135.1
QHJ74262.1	000354	gp62-Clloadss	162	VH12019_00343	Vibrio phage VH1_2019	GCA_009931825.1
AGB07086.1	000354	gp62-Clloadss	163	CF80_gp299	Vibrio phage VH7D	GCA_000914495.1
QBX06009.1	000354	gp62-Clloadss	163	ValB1HC_055	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04485.1	000354	gp62-Clloadss	127	ValB1MD_113	Vibrio phage ValB1MD	GCA_004138815.1
AJT61022.1	000354	gp62-Clloadss	163	AVU32_gp181	Vibrio phage ValKK3	GCA_001501635.1
AGN30128.2	000354	gp62-Clloadss	162	VPFG_00126	Vibrio phage nt-1	GCA_000910195.2
ALP47110.1	000354	gp62-Clloadss	163	phiGrn1_0194	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47492.1	000354	gp62-Clloadss	163	phiST2_0325	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54634.1	000354	gp62-Clloadss	163	vBValMR10Z_93	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07131.1	000354	gp62-Clloadss	195	VmeM32_00144	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37310.1	000354	gp62-Clloadss	162	pp2_077	Vibriophage phi-pp2	GCA_002630725.1
CCH63614.1	000000	gp62-Clloadss	110	CP21_152	Campylobacter virus CP21	GCA_000902535.1
APU01473.1	000355	Portal_protein	524	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28787.1	000355	Portal_protein	525	AP1_0080	Aeromonas phage AP1	GCA_014183365.1
ATI17424.1	000355	Portal_protein	525	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00171.1	000355	Portal_protein	525	HWB28_gp381	Aeromonas phage AS-zj	GCA_002627665.1
AUE22756.1	000355	Portal_protein	521	Ah1_00238	Aeromonas phage Ah1	GCA_002957415.1
QAX98473.1	000355	Portal_protein	521	ASfcp2_134	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97864.1	000355	Portal_protein	525	ASswx1_221	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01286.1	000355	Portal_protein	526	ASwh1_223	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39540.1	000355	Portal_protein	525	CC2_313	Aeromonas phage CC2	GCA_000903495.1
ADQ52934.1	000355	Portal_protein	521	PX29p215	Aeromonas phage PX29	GCA_000920195.1
ADM79857.1	000355	Portal_protein	521	phiAS5_ORF0014	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53096.1	000355	Portal_protein	524	65p086	Aeromonas virus 65	GCA_000893255.1
AAQ17881.1	000355	Portal_protein	521	20	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94980.1	000355	Portal_protein	584	FDI40_gp198	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMM44826.1	000355	Portal_protein	504	SP15_027	Bacillus phage SP-15	GCA_001754685.1
CCH63625.1	000355	Portal_protein	275	CP21_163	Campylobacter virus CP21	GCA_000902535.1
ANS05943.1	000355	Portal_protein	524	ABCD_0211	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64884.1	000355	Portal_protein	514	S13_085	Cronobacter phage S13	GCA_001503575.1
AFC21695.1	000355	Portal_protein	580	GAP32_245	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97226.1	000355	Portal_protein	524	E_218	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56903.1	000355	Portal_protein	540	CPXG_00100	Cyanophage P-RSM6	GCA_000906155.1
AJK27559.1	000355	Portal_protein	542	PTIM40_132	Cyanophage P-TIM40	GCA_001470935.1
AOO14309.1	000355	Portal_protein	549	Sn110110_115	Cyanophage S-RIM14	GCA_002599065.1
AOO14958.1	000355	Portal_protein	549	W1230910_112	Cyanophage S-RIM14	GCA_002599125.1
AMO43137.1	000355	Portal_protein	559	R1080702_128	Cyanophage S-RIM32	GCA_001754165.1
AMO43363.1	000355	Portal_protein	559	W270710_119	Cyanophage S-RIM44	GCA_002599145.1
AOO11607.1	000355	Portal_protein	559	ES420910_126	Cyanophage S-RIM44	GCA_002599165.1
AOO11835.1	000355	Portal_protein	559	Np050604_119	Cyanophage S-RIM44	GCA_002599185.1
AOO12072.1	000355	Portal_protein	559	Np200711_126	Cyanophage S-RIM44	GCA_002599205.1
AOO12308.1	000355	Portal_protein	559	Np420711_126	Cyanophage S-RIM44	GCA_002599225.1
AOO12536.1	000355	Portal_protein	559	Sn080709_119	Cyanophage S-RIM44	GCA_002599245.1
AOO12773.1	000355	Portal_protein	559	Sn130910_126	Cyanophage S-RIM44	GCA_002599265.1
AOO13002.1	000355	Portal_protein	559	W2100709_120	Cyanophage S-RIM44	GCA_002599285.1
AGH07457.1	000355	Portal_protein	563	CYVG_00013	Cyanophage S-SSM6a	GCA_002710385.1
AGG54494.1	000355	Portal_protein	538	CYWG_00210	Cyanophage S-SSM6b	GCA_002710425.1
AIT14488.1	000355	Portal_protein	573	PBI_121Q_598	Escherichia phage 121Q	GCA_000926855.1
QAY00461.1	000355	Portal_protein	578	Ecwhy1_181	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35203.1	000355	Portal_protein	535	ACQ29_gp523	Escherichia phage PBECO4	GCA_001041035.1
BBM62160.1	000355	Portal_protein	579	EO157G_5710	Escherichia phage SP27	GCA_008033345.1
AXC36775.1	000355	Portal_protein	535	-	Escherichia phage UB	GCA_003341455.1
ARM70729.1	000355	Portal_protein	523	phiC120_c22	Escherichia phage phiC120	GCA_002621185.1
QBO61815.1	000355	Portal_protein	579	G17_00326	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13859.1	000355	Portal_protein	579	vBEcoMphAPEC6_gp230c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80472.1	000355	Portal_protein	579	PSLUR01_00495	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78744.1	000355	Portal_protein	524	RB43ORF222w	Escherichia virus RB43	GCA_000863505.1
AFA44362.1	000355	Portal_protein	577	RaK2_00089	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72821.1	000355	Portal_protein	584	-	Myoviridae sp.	GCA_003657725.1
QHJ79055.1	000355	Portal_protein	515	-	Myoviridae sp.	GCA_012593985.1
QIG65700.1	000355	Portal_protein	584	phiOC_p034	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43817.1	000355	Portal_protein	578	CBB_252	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26107.1	000355	Portal_protein	560	CPMG_00006	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44509.1	000355	Portal_protein	558	PSSM2_131	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12457.1	000355	Portal_protein	558	PRTG_00310	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93443.1	000355	Portal_protein	552	AVU42_gp104	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99221.1	000355	Portal_protein	559	Syn1_120	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76031.1	000355	Portal_protein	571	EST35_0149	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44105.1	000355	Portal_protein	564	PBI_SCTP2_90	Salicola phage SCTP-2	GCA_002625545.1
QCW18972.1	000355	Portal_protein	575	7t3_0451	Salmonella phage 7t3	GCA_006083215.1
AZU98222.1	000355	Portal_protein	575	CPT_Munch_278	Salmonella phage Munch	GCA_004015485.1
QIG62763.1	000355	Portal_protein	581	SEPL_150	Salmonella phage SE_PL	GCA_011067555.1
AQW88775.1	000355	Portal_protein	575	BF_0250	Serratia phage BF	GCA_002619745.1
AGR47703.1	000355	Portal_protein	540	SmphiM12_071	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12961.1	000355	Portal_protein	540	PHIM19_54	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12601.1	000355	Portal_protein	540	PHIM7_53	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13334.1	000355	Portal_protein	540	PHIN3_69	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28145.1	000355	Portal_protein	584	PAU_147	Sphingomonas phage PAU	GCA_000902455.1
AIX30612.1	000355	Portal_protein	586	Syn7803US37_135	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54884.1	000355	Portal_protein	557	b23_0270	Synechococcus phage B23	GCA_009745195.1
QGT54519.1	000355	Portal_protein	557	b3_0277	Synechococcus phage B3	GCA_009745215.1
ASR76173.1	000355	Portal_protein	555	PBI_BELLAMY_128	Synechococcus phage Bellamy	GCA_002627525.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW22883.1	000355	Portal_protein	560	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50474.1	000355	Portal_protein	560	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59587.1	000355	Portal_protein	567	S330809_126	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59349.1	000355	Portal_protein	567	C440309_126	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59825.1	000355	Portal_protein	567	N231010_126	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70579.1	000355	Portal_protein	550	HOU04_gp180	Synechococcus phage S-T4	GCA_003443335.1
QJT70115.1	000355	Portal_protein	556	SynMITS9220M01_102	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90690.1	000355	Portal_protein	577	HYO65_gp298	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90997.1	000355	Portal_protein	577	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25556.1	000355	Portal_protein	548	BPT24_143	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64427.1	000355	Portal_protein	511	KVP40.0358	Vibrio phage KVP40	GCA_000843785.1
QIW90372.1	000355	Portal_protein	515	GCAPEGMB_00025	Vibrio phage V07	GCA_012361095.1
QIW91057.1	000355	Portal_protein	515	COHAPHLL_00194	Vibrio phage V09	GCA_012361135.1
QHJ74541.1	000355	Portal_protein	515	VH12019_00241	Vibrio phage VH1_2019	GCA_009931825.1
AGB06999.1	000355	Portal_protein	516	CF80_gp212	Vibrio phage VH7D	GCA_000914495.1
QBX06115.1	000355	Portal_protein	516	ValB1HC_161	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04543.1	000355	Portal_protein	500	ValB1MD_256	Vibrio phage ValB1MD	GCA_004138815.1
AJT61127.1	000355	Portal_protein	516	AVU32_gp286	Vibrio phage ValKK3	GCA_001501635.1
AGN30031.1	000355	Portal_protein	515	VPFG_00023	Vibrio phage nt-1	GCA_000910195.2
ALP46975.1	000355	Portal_protein	516	phiGrn1_0092	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47358.1	000355	Portal_protein	516	phiST2_0224	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54740.1	000355	Portal_protein	516	vBValMR10Z_200	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07001.1	000355	Portal_protein	517	VmeM32_00005	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37590.1	000355	Portal_protein	515	pp2_358	Vibriophage phi-pp2	GCA_002630725.1
BBA65449.1	000355	Portal_protein	579	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96464.1	000355	Portal_protein	588	Xoosp13_278	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59056.1	000355	Portal_protein	577	g248	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58522.1	000355	Portal_protein	577	g245	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prev15ph1000000463	000355	Portal_protein	629	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70289.1	000356	Portal_protein	953	CF8_0121	Aeromonas phage CF8	GCA_006384595.2
QDJ97266.1	000356	Portal_protein	1085	D6_0106	Aeromonas phage D6	GCA_007051205.2
QDH47015.1	000356	Portal_protein	1087	LAh10_38	Aeromonas phage LAh10	GCA_006863975.1
QDJ96880.1	000356	Portal_protein	975	PS1_0121	Aeromonas phage PS1	GCA_007051165.2
QFR59512.1	000356	Portal_protein	975	PS2_0121	Aeromonas phage PS2	GCA_009388305.2
AFO71295.1	000356	Portal_protein	912	CR5_075	Cronobacter phage CR5	GCA_000910235.1
QBZ70652.1	000356	Portal_protein	974	pETSU_071	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59731.1	000356	Portal_protein	739	SEGD1_082	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07504.1	000356	Portal_protein	928	DERBICUS_78	Erwinia phage Derbicus	GCA_004521655.1
AHI60156.1	000356	Portal_protein	951	Ea357_006	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49731.1	000356	Portal_protein	912	MACHINA_93	Erwinia phage Machina	GCA_002758035.1
AGX01930.1	000356	Portal_protein	925	CF95_gp208	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07114.1	000356	Portal_protein	951	REBECCA_6	Erwinia phage Rebecca	GCA_004521635.1
AXF51231.1	000356	Portal_protein	917	WELLINGTON_101	Erwinia phage Wellington	GCA_003344985.1
AFQ96550.1	000356	Portal_protein	907	G173_gp005	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48110.1	000356	Portal_protein	913	ASESINO_97	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85794.1	000356	Portal_protein	951	BOSOLAPHORUS_6	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48385.1	000356	Portal_protein	925	CAITLIN_90	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48657.1	000356	Portal_protein	922	CHRISDB_95	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52104.1	000356	Portal_protein	951	DM_6	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86114.1	000356	Portal_protein	951	DESERTFOX_6	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48928.1	000356	Portal_protein	913	EARLPHILLIPIV_78	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49176.1	000356	Portal_protein	912	HUXLEY_94	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03827.1	000356	Portal_protein	998	JOAD_88	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49452.1	000356	Portal_protein	917	KWAN_100	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86434.1	000356	Portal_protein	952	MADMEL_6	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86755.1	000356	Portal_protein	952	MORTIMER_6	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50004.1	000356	Portal_protein	912	PARSHIK_95	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50268.1	000356	Portal_protein	910	PHOBOS_78	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51787.1	000356	Portal_protein	951	RAY_6	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03582.1	000356	Portal_protein	999	RISINGSUN_88	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51468.1	000356	Portal_protein	951	SIMMY50_6	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64816.1	000356	Portal_protein	952	SPECIALG_6	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50524.1	000356	Portal_protein	913	STRATTON_99	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85921.1	000356	Portal_protein	914	ACEC001_0830	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63829.1	000356	Portal_protein	969	Goslar_00036	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71968.1	000356	Portal_protein	962	N1M2_105	Klebsiella phage N1M2	GCA_010092605.1
QGZ14442.1	000356	Portal_protein	973	HWC77_gp079	Photobacterium phage PDCC-1	GCA_009800445.1
QMP23998.1	000356	Portal_protein	953	-	Proteus phage 10	GCA_014071245.1
ABY63043.1	000356	Portal_protein	917	201phi2-1p214	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27197.1	000356	Portal_protein	990	PPEV_gp103	Pseudomonas phage EL	GCA_000866825.1
ANM44922.1	000356	Portal_protein	893	KTN4_164	Pseudomonas phage KTN4	GCA_002607225.1
ARV77301.1	000356	Portal_protein	924	NOXIFER_132	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89569.1	000356	Portal_protein	961	OBP_132	Pseudomonas phage OBP	GCA_000896635.1
QBX32309.1	000356	Portal_protein	899	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76832.1	000356	Portal_protein	894	PHABIO_201	Pseudomonas phage Phabio	GCA_002624965.1
AEH03571.1	000356	Portal_protein	827	148	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02708.1	000356	Portal_protein	909	PSA21_182	Pseudomonas phage Psa21	GCA_004340405.1
ATN94792.1	000356	Portal_protein	893	SL2_215	Pseudomonas phage SL2	GCA_002956015.1
QJB22800.1	000356	Portal_protein	893	fnug_157	Pseudomonas phage fnug	GCA_012837215.1
QEM41882.1	000356	Portal_protein	898	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83030.1	000356	Portal_protein	896	PHIKZ129	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19063.1	000356	Portal_protein	934	FDH28_gp089	Ralstonia phage RP12	GCA_002617345.1
BAW19348.1	000356	Portal_protein	934	-	Ralstonia phage RP31	GCA_002617365.1
BAS04893.1	000356	Portal_protein	1002	AVU11_gp101	Ralstonia phage RSF1	GCA_001500875.1
BAQ02620.1	000356	Portal_protein	1007	AVU38_gp092	Ralstonia phage RSL2	GCA_001503055.1
QNI20791.1	000356	Portal_protein	914	-	Salmonella phage JN03	GCA_014319805.1
AWN09020.1	000356	Portal_protein	918	MLDJOKPK_00078	Salmonella phage SPAsTU	GCA_003183805.1
AEP83914.1	000356	Portal_protein	913	SPN3US_0081	Salmonella phage SPN3US	GCA_001042275.1
QKE54320.1	000356	Portal_protein	1167	ACSA002_0060	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65379.1	000356	Portal_protein	299	2050HW_00044	Serratia phage 2050HW	GCA_002628125.1
ATA65381.1	000356	Portal_protein	501	2050HW_00046	Serratia phage 2050HW	GCA_002628125.1
QDB71163.1	000356	Portal_protein	932	CPT_Moabite_133	Serratia phage Moabite	GCA_006384735.1
QFP93046.1	000356	Portal_protein	942	-	Serratia phage PCH45	GCA_009187865.1
QAU04292.1	000356	Portal_protein	970	HWC03_gp137	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23285.1	000356	Portal_protein	965	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80917.1	000356	Portal_protein	968	Aphrodite1_0060	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70862.1	000356	Portal_protein	866	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47443.1	000356	Portal_protein	965	HWC35_gp049	Vibrio phage USC-1	GCA_006864065.1
BAW98264.1	000356	Portal_protein	947	FDH33_gp055	Vibrio phage pTD1	GCA_002618825.1
AQT27958.1	000356	Portal_protein	921	pVa21_016	Vibrio phage pVa-21	GCA_002619305.1
QAX96627.1	000356	Portal_protein	792	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96945.1	000356	Portal_protein	792	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95991.1	000356	Portal_protein	792	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96309.1	000356	Portal_protein	792	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21114.1	000356	Portal_protein	921	-	Vibrio phage vB_pir03	GCA_014319855.1
AMS01212.1	000357	Portal_protein	731	AR9_g128	Bacillus phage AR9	GCA_001743835.1
ALN97883.1	000357	Portal_protein	739	Bp8pS_204	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99837.1	000357	Portal_protein	731	PBI_PBS1_15	Bacillus virus PBS1	GCA_002601325.1
CCE26184.1	000357	Portal_protein	878	g160	Yersinia phage phiR1-37	GCA_000895615.1
CCH63626.1	000000	Portal_protein	182	CP21_164	Campylobacter virus CP21	GCA_000902535.1
prevph1000000650	000000	Portal_protein	158	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QHJ85990.1	000000	Portal_protein	553	KKIINIFJ_00078	Pseudomonas phage PN05	GCA_009931935.1
ATA65380.1	000000	Portal_protein	116	2050HW_00045	Serratia phage 2050HW	GCA_002628125.1
QMV29141.1	000000	Portal_protein	176	AP1_0438	Aeromonas phage AP1	GCA_014183365.1
QHJ86099.1	000000	Portal_protein	317	KKIINIFJ_00187	Pseudomonas phage PN05	GCA_009931935.1
AUE22619.1	000358	Portal_protein	231	Ah1_00078	Aeromonas phage Ah1	GCA_002957415.1
ADQ52803.1	000358	Portal_protein	231	PX29p084	Aeromonas phage PX29	GCA_000920195.1
ADM80059.1	000358	Portal_protein	234	phiAS5_ORF0216	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17746.1	000358	Portal_protein	231	Aeh1ORF085c	Aeromonas virus Aeh1	GCA_000843245.1
AJT61170.1	000359	Portal_protein	72	AVU32_gp329	Vibrio phage ValKK3	GCA_001501635.1
ALP47284.1	000359	Portal_protein	72	phiGrn1_0051	Vibrio phage phi-Grn1	GCA_002757115.1
AIR93445.1	000360	prohead-Peptidase_S77	216	AVU42_gp107	Prochlorococcus phage P-TIM68	GCA_001503075.1
AMO43365.1	000360	prohead-Peptidase_S77	214	W270710_121	Cyanophage S-RIM44	GCA_002599145.1
APU01470.1	000360	prohead-Peptidase_S77	241	-	Aeromonas phage 65.2	GCA_002618145.1
CCE26103.1	000360	prohead-Peptidase_S77	266	g079	Yersinia phage phiR1-37	GCA_000895615.1

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ADO99223.1	000360	prohead-Peptidase_S77	214	Syn1_122	Prochlorococcus phage Syn1	GCA_000892495.1
QNJ54737.1	000360	prohead-Peptidase_S77	213	vBValMR10Z_197	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QIW91054.1	000360	prohead-Peptidase_S77	213	COHAPHLL_00191	Vibrio phage V09	GCA_012361135.1
AGN12455.1	000360	prohead-Peptidase_S77	216	PRTG_00308	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOO11609.1	000360	prohead-Peptidase_S77	214	ES420910_128	Cyanophage S-RIM44	GCA_002599165.1
ALP47442.1	000360	prohead-Peptidase_S77	213	phiST2_0227	Vibrio phage phi-ST2	GCA_002757135.1
QMV28784.1	000360	prohead-Peptidase_S77	241	AP1_0077	Aeromonas phage AP1	GCA_014183365.1
AZU98225.1	000360	prohead-Peptidase_S77	207	CPT_Munch_281	Salmonella phage Munch	GCA_004015485.1
AGR47700.1	000360	prohead-Peptidase_S77	222	SmphiM12_068	Sinorhizobium phage phiM12	GCA_001023565.1
QIW90375.1	000360	prohead-Peptidase_S77	213	GCAPEGMB_00028	Vibrio phage V07	GCA_012361095.1
AOO11837.1	000360	prohead-Peptidase_S77	214	Np050604_121	Cyanophage S-RIM44	GCA_002599185.1
AOO12074.1	000360	prohead-Peptidase_S77	214	Np200711_128	Cyanophage S-RIM44	GCA_002599205.1
AAX44511.1	000360	prohead-Peptidase_S77	216	PSSM2_133	Prochlorococcus phage P-SSM2	GCA_000859585.1
AKF12958.1	000360	prohead-Peptidase_S77	222	PHIM19_51	Sinorhizobium phage phiM19	GCA_002605865.1
AQW88778.1	000360	prohead-Peptidase_S77	209	BF_0253	Serratia phage BF	GCA_002619745.1
AOO12310.1	000360	prohead-Peptidase_S77	214	Np420711_128	Cyanophage S-RIM44	GCA_002599225.1
AAQ64430.1	000360	prohead-Peptidase_S77	213	KVP40.0361	Vibrio phage KVP40	GCA_000843785.1
AKF12598.1	000360	prohead-Peptidase_S77	222	PHIM7_50	Sinorhizobium phage phiM7	GCA_002622405.1
AGH26105.1	000360	prohead-Peptidase_S77	215	CPMG_00004	Prochlorococcus phage MED4-213	GCA_000904535.1
ANS06004.1	000360	prohead-Peptidase_S77	215	ABCD_0214	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AOO12538.1	000360	prohead-Peptidase_S77	214	Sn080709_121	Cyanophage S-RIM44	GCA_002599245.1
AOO12775.1	000360	prohead-Peptidase_S77	214	Sn130910_128	Cyanophage S-RIM44	GCA_002599265.1
AKF13331.1	000360	prohead-Peptidase_S77	222	PHIN3_66	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28149.1	000360	prohead-Peptidase_S77	246	PAU_151	Sphingomonas phage PAU	GCA_000902455.1
SOK58525.1	000360	prohead-Peptidase_S77	209	g248	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIX30615.1	000360	prohead-Peptidase_S77	216	Syn7803US37_138	Synechococcus phage ACG-2014f	GCA_002594065.1
ALY07004.1	000360	prohead-Peptidase_S77	211	VmeM32_00008	Vibrio phage vB_VmeM-32	GCA_002608825.1
AOO13004.1	000360	prohead-Peptidase_S77	214	W2100709_122	Cyanophage S-RIM44	GCA_002599285.1
AIA64881.1	000360	prohead-Peptidase_S77	209	S13_082	Cronobacter phage S13	GCA_001503575.1
AQW88641.1	000360	prohead-Peptidase_S77	154	BF_0116	Serratia phage BF	GCA_002619745.1
ALP47062.1	000360	prohead-Peptidase_S77	213	phiGrn1_0095	Vibrio phage phi-Grn1	GCA_002757115.1
AMM44169.1	000360	prohead-Peptidase_S77	209	CBB_255	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH07459.1	000360	prohead-Peptidase_S77	244	CYVG_00015	Cyanophage S-SSM6a	GCA_002710385.1
QAX97867.1	000360	prohead-Peptidase_S77	241	ASswx1_224	Aeromonas phage Asswx_1	GCA_004146865.1
BAV39266.1	000360	prohead-Peptidase_S77	527	BPT24_140	Tenacibaculum phage pT24	GCA_002611925.1
QGT54890.1	000360	prohead-Peptidase_S77	216	b23_0277	Synechococcus phage B23	GCA_009745195.1
AGG54492.1	000360	prohead-Peptidase_S77	215	CYWG_00208	Cyanophage S-SSM6b	GCA_002710425.1
QIG65698.1	000360	prohead-Peptidase_S77	220	phiOC_p032	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BBI90999.1	000360	prohead-Peptidase_S77	564	-	Tenacibaculum phage PTm5	GCA_009730715.1
AMO43139.1	000360	prohead-Peptidase_S77	214	R1080702_130	Cyanophage S-RIM32	GCA_001754165.1
QGT54525.1	000360	prohead-Peptidase_S77	216	b3_0284	Synechococcus phage B3	GCA_009745215.1
QHJ79058.1	000360	prohead-Peptidase_S77	208	-	Myoviridae sp.	GCA_012593985.1
BBI90692.1	000360	prohead-Peptidase_S77	564	HYO65_gp300	Tenacibaculum phage PTm1	GCA_009730695.1
AXH72822.1	000360	prohead-Peptidase_S77	211	-	Myoviridae sp.	GCA_003657725.1
ASR76176.1	000360	prohead-Peptidase_S77	216	PBI_BELLAMY_131	Synechococcus phage Bellamy	GCA_002627525.1
AFA44365.1	000360	prohead-Peptidase_S77	206	RaK2_00092	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QJT70118.1	000360	prohead-Peptidase_S77	216	SynMITS9220M01_105	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAX78747.1	000360	prohead-Peptidase_S77	215	RB43ORF225w	Escherichia virus RB43	GCA_000863505.1
SCA80475.1	000360	prohead-Peptidase_S77	207	PSLUR01_00498	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
CCH63585.1	000360	prohead-Peptidase_S77	251	CP21_123	Campylobacter virus CP21	GCA_000902535.1
QHJ74544.1	000360	prohead-Peptidase_S77	213	VH12019_00244	Vibrio phage VH1_2019	GCA_009931825.1
ADQ52937.1	000360	prohead-Peptidase_S77	216	PX29p218	Aeromonas phage PX29	GCA_000920195.1
AOO14960.1	000360	prohead-Peptidase_S77	214	W1230910_114	Cyanophage S-RIM14	GCA_002599125.1
QDF13856.1	000360	prohead-Peptidase_S77	207	vBEcoMphAPEC6_gp227c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
BBA65445.1	000360	prohead-Peptidase_S77	208	-	Xanthomonas phage XacN1	GCA_003173815.1
ADM79860.1	000360	prohead-Peptidase_S77	206	phiAS5_ORF0017	Aeromonas phage phiAS5	GCA_000887715.1
QAY01283.1	000360	prohead-Peptidase_S77	226	ASwh1_220	Aeromonas phage Aswh_1	GCA_004146945.1
AFC21698.1	000360	prohead-Peptidase_S77	210	GAP32_248	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ASU00132.1	000360	prohead-Peptidase_S77	193	PBI_PBS1_310	Bacillus virus PBS1	GCA_002601325.1
QAX98475.1	000360	prohead-Peptidase_S77	216	ASfcp2_137	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53093.1	000360	prohead-Peptidase_S77	241	65p083	Aeromonas virus 65	GCA_000893255.1
AXQ70576.1	000360	prohead-Peptidase_S77	216	HOU04_gp177	Synechococcus phage S-T4	GCA_003443335.1
AOO14311.1	000360	prohead-Peptidase_S77	214	Sn110110_117	Cyanophage S-RIM14	GCA_002599065.1
AGB07002.1	000360	prohead-Peptidase_S77	213	CF80_gp215	Vibrio phage VH7D	GCA_000914495.1
QBX06112.1	000360	prohead-Peptidase_S77	213	ValB1HC_158	Vibrio phage ValB1 HC	GCA_004771355.1
SOK59059.1	000360	prohead-Peptidase_S77	209	g251	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58921.1	000360	prohead-Peptidase_S77	144	g113	Yersinia phage fHe-Yen9-03	GCA_002990515.1
ARM70732.1	000360	prohead-Peptidase_S77	213	phiC120_c25	Escherichia phage phiC120	GCA_002621185.1
QCW18975.1	000360	prohead-Peptidase_S77	207	7t3_0454	Salmonella phage 7t3	GCA_006083215.1
AXC36772.1	000360	prohead-Peptidase_S77	207	-	Escherichia phage UB	GCA_003341455.1
ATI17427.1	000360	prohead-Peptidase_S77	241	-	Aeromonas phage AS-szw	GCA_002743635.1
ALN97868.1	000360	prohead-Peptidase_S77	92	Bp8pS_189	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
BBM62163.1	000360	prohead-Peptidase_S77	207	EO157G_5740	Escherichia phage SP27	GCA_008033345.1
AFN37593.1	000360	prohead-Peptidase_S77	213	pp2_361	Vibriophage phi-pp2	GCA_002630725.1
AOV59827.1	000360	prohead-Peptidase_S77	214	N231010_128	Synechococcus phage S-CAM4	GCA_002922155.1
AGC35200.1	000360	prohead-Peptidase_S77	207	ACQ29_gp520	Escherichia phage PBECO4	GCA_001041035.1
ASV44108.1	000360	prohead-Peptidase_S77	212	PBI_SCTP2_93	Salicola phage SCTP-2	GCA_002625545.1
QIG62760.1	000360	prohead-Peptidase_S77	207	SEPL_147	Salmonella phage SE_PL	GCA_011067555.1
AUE22759.1	000360	prohead-Peptidase_S77	209	Ah1_00241	Aeromonas phage Ah1	GCA_002957415.1
AON97229.1	000360	prohead-Peptidase_S77	219	E_221	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
QAY00458.1	000360	prohead-Peptidase_S77	206	Ecwhy1_178	Escherichia phage Ecwhy_1	GCA_004146585.1
QCW22886.1	000360	prohead-Peptidase_S77	216	-	Synechococcus phage S-B05	GCA_006083695.1
AIT14491.1	000360	prohead-Peptidase_S77	207	PBI_121Q_601	Escherichia phage 121Q	GCA_000926855.1
QCG76034.1	000360	prohead-Peptidase_S77	210	EST35_0152	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AOV59351.1	000360	prohead-Peptidase_S77	214	C440309_128	Synechococcus phage S-CAM4	GCA_002922145.1
QBO61812.1	000360	prohead-Peptidase_S77	207	G17_00323	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QAU04550.1	000360	prohead-Peptidase_S77	232	ValB1MD_266	Vibrio phage ValB1MD	GCA_004138815.1
AUZ94986.1	000360	prohead-Peptidase_S77	210	FDI40_gp204	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGH56901.1	000360	prohead-Peptidase_S77	214	CPXG_00098	Cyanophage P-RSM6	GCA_000906155.1
AIE13785.1	000360	prohead-Peptidase_S77	213	VPFG_00026	Vibrio phage nt-1	GCA_000910195.2
QDJ96461.1	000360	prohead-Peptidase_S77	211	Xoosp13_275	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AJT61124.1	000360	prohead-Peptidase_S77	213	AVU32_gp283	Vibrio phage ValKK3	GCA_001501635.1
ASU00168.1	000360	prohead-Peptidase_S77	241	HWB28_gp384	Aeromonas phage AS-zj	GCA_002627665.1
AJK27561.1	000360	prohead-Peptidase_S77	215	PTIM40_134	Cyanophage P-TIM40	GCA_001470935.1
AAQ17884.1	000360	prohead-Peptidase_S77	209	21	Aeromonas virus Aeh1	GCA_000843245.1
AMS01198.1	000360	prohead-Peptidase_S77	268	AR9_g114	Bacillus phage AR9	GCA_001743835.1
AFN39539.1	000360	prohead-Peptidase_S77	241	CC2_310	Aeromonas phage CC2	GCA_000903495.1
QDH50471.1	000360	prohead-Peptidase_S77	216	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59589.1	000360	prohead-Peptidase_S77	214	S330809_128	Synechococcus phage S-CAM4	GCA_002366065.1
SOK58386.1	000360	prohead-Peptidase_S77	144	g109	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMM44830.1	000360	prohead-Peptidase_S77	568	SP15_031	Bacillus phage SP-15	GCA_001754685.1
prevph1000000782	000360	prohead-Peptidase_S77	204	-	Prevotella_phage_Lak-B8	GCA_004379655.1
ALN97870.1	000361	prohead-Peptidase_S77	83	Bp8pS_191	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00134.1	000361	prohead-Peptidase_S77	90	PBI_PBS1_312	Bacillus virus PBS1	GCA_002601325.1
QHJ85988.1	000000	prohead-Peptidase_S77	714	KKIINIFJ_00076	Pseudomonas phage PN05	GCA_009931935.1
AQT28026.1	000000	prohead-Peptidase_S77	143	pVa21_085	Vibrio phage pVa-21	GCA_002619305.1
prev15ph1000000533	000000	prohead-Peptidase_S77	582	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70402.1	000362	prohead-Peptidase_S77	284	CF8_0233	Aeromonas phage CF8	GCA_006384595.2
QDJ97399.1	000362	prohead-Peptidase_S77	281	D6_0240	Aeromonas phage D6	GCA_007051205.2
QDH47100.1	000362	prohead-Peptidase_S77	281	LAh10_153	Aeromonas phage LAh10	GCA_006863975.1
QDJ96747.1	000362	prohead-Peptidase_S77	284	PS1_0236	Aeromonas phage PS1	GCA_007051165.2
QFR59380.1	000362	prohead-Peptidase_S77	284	PS2_0238	Aeromonas phage PS2	GCA_009388305.2
AFO71433.1	000362	prohead-Peptidase_S77	268	CR5_213	Cronobacter phage CR5	GCA_000910235.1
QBZ70785.1	000362	prohead-Peptidase_S77	283	pETSU_204	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59897.1	000362	prohead-Peptidase_S77	267	SEGD1_250	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07646.1	000362	prohead-Peptidase_S77	271	DERBICUS_220	Erwinia phage Derbicus	GCA_004521655.1
AHI60320.1	000362	prohead-Peptidase_S77	262	Ea357_169	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49769.1	000362	prohead-Peptidase_S77	158	MACHINA_131	Erwinia phage Machina	GCA_002758035.1
ANZ49896.1	000362	prohead-Peptidase_S77	268	MACHINA_258	Erwinia phage Machina	GCA_002758035.1
AGX01861.1	000362	prohead-Peptidase_S77	254	CF95_gp139	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07279.1	000362	prohead-Peptidase_S77	262	REBECCA_172	Erwinia phage Rebecca	GCA_004521635.1
AXF51397.1	000362	prohead-Peptidase_S77	271	WELLINGTON_271	Erwinia phage Wellington	GCA_003344985.1
AFQ96710.1	000362	prohead-Peptidase_S77	267	G173_gp165	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96585.1	000362	prohead-Peptidase_S77	153	G173_gp040	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48145.1	000362	prohead-Peptidase_S77	154	ASESINO_132	Erwinia phage vB_EamM_Asesino	GCA_001744335.2

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ANZ48280.1	000362	prohead-Peptidase_S77	267	ASESINO_267	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85959.1	000362	prohead-Peptidase_S77	262	BOSOLAPHORUS_172	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48424.1	000362	prohead-Peptidase_S77	156	CAITLIN_129	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48552.1	000362	prohead-Peptidase_S77	267	CAITLIN_257	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48696.1	000362	prohead-Peptidase_S77	157	CHRISDB_134	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48830.1	000362	prohead-Peptidase_S77	267	CHRISDB_268	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52274.1	000362	prohead-Peptidase_S77	262	DM_176	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86278.1	000362	prohead-Peptidase_S77	262	DESERTFOX_171	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49070.1	000362	prohead-Peptidase_S77	267	EARLPHILLIPIV_221	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49214.1	000362	prohead-Peptidase_S77	157	HUXLEY_132	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49339.1	000362	prohead-Peptidase_S77	268	HUXLEY_257	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03678.1	000362	prohead-Peptidase_S77	284	JOAD_237	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49623.1	000362	prohead-Peptidase_S77	271	KWAN_271	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86600.1	000362	prohead-Peptidase_S77	262	MADMEL_172	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86924.1	000362	prohead-Peptidase_S77	262	MORTIMER_175	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50042.1	000362	prohead-Peptidase_S77	157	PARSHIK_133	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50167.1	000362	prohead-Peptidase_S77	268	PARSHIK_258	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50417.1	000362	prohead-Peptidase_S77	268	PHOBOS_227	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51951.1	000362	prohead-Peptidase_S77	262	RAY_170	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03435.1	000362	prohead-Peptidase_S77	284	RISINGSUN_235	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51635.1	000362	prohead-Peptidase_S77	262	SIMMY50_173	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64982.1	000362	prohead-Peptidase_S77	262	SPECIALG_172	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50561.1	000362	prohead-Peptidase_S77	153	STRATTON_136	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50692.1	000362	prohead-Peptidase_S77	267	STRATTON_267	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86086.1	000362	prohead-Peptidase_S77	267	ACEC001_2430	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64015.1	000362	prohead-Peptidase_S77	268	Goslar_00223	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72091.1	000362	prohead-Peptidase_S77	282	N1M2_228	Klebsiella phage N1M2	GCA_010092605.1
QGZ14520.1	000362	prohead-Peptidase_S77	298	HWC77_gp157	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24101.1	000362	prohead-Peptidase_S77	275	-	Proteus phage 10	GCA_014071245.1
ABY63096.1	000362	prohead-Peptidase_S77	280	201phi2-1p268	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27286.1	000362	prohead-Peptidase_S77	287	PPEV_gp192	Pseudomonas phage EL	GCA_000866825.1
ANM44973.1	000362	prohead-Peptidase_S77	270	KTN4_215	Pseudomonas phage KTN4	GCA_002607225.1
ARV77360.1	000362	prohead-Peptidase_S77	259	NOXIFER_191	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89720.1	000362	prohead-Peptidase_S77	283	OBP_283	Pseudomonas phage OBP	GCA_000896635.1
QBX32363.1	000362	prohead-Peptidase_S77	277	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76889.1	000362	prohead-Peptidase_S77	275	PHABIO_258	Pseudomonas phage Phabio	GCA_002624965.1
AEH03628.1	000362	prohead-Peptidase_S77	277	205	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02765.1	000362	prohead-Peptidase_S77	276	PSA21_239	Pseudomonas phage Psa21	GCA_004340405.1
ATN94741.1	000362	prohead-Peptidase_S77	270	SL2_164	Pseudomonas phage SL2	GCA_002956015.1
QJB22851.1	000362	prohead-Peptidase_S77	270	fnug_208	Pseudomonas phage fnug	GCA_012837215.1
QEM41937.1	000362	prohead-Peptidase_S77	277	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83076.1	000362	prohead-Peptidase_S77	270	PHIKZ175	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19011.1	000362	prohead-Peptidase_S77	257	FDH28_gp037	Ralstonia phage RP12	GCA_002617345.1
BAW19297.1	000362	prohead-Peptidase_S77	257	-	Ralstonia phage RP31	GCA_002617365.1
BAS04828.1	000362	prohead-Peptidase_S77	260	AVU11_gp036	Ralstonia phage RSF1	GCA_001500875.1
BAQ02561.1	000362	prohead-Peptidase_S77	260	AVU38_gp033	Ralstonia phage RSL2	GCA_001503055.1
QNI20929.1	000362	prohead-Peptidase_S77	267	-	Salmonella phage JN03	GCA_014319805.1
AXF51068.1	000362	prohead-Peptidase_S77	148	MLDJOKPK_00038	Salmonella phage SPAsTU	GCA_003183805.1
AWN09108.1	000362	prohead-Peptidase_S77	267	MLDJOKPK_00195	Salmonella phage SPAsTU	GCA_003183805.1
AEP84078.1	000362	prohead-Peptidase_S77	267	SPN3US_0245	Salmonella phage SPN3US	GCA_001042275.1
QKE54477.1	000362	prohead-Peptidase_S77	260	ACSA002_1630	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65443.1	000362	prohead-Peptidase_S77	249	2050HW_00108	Serratia phage 2050HW	GCA_002628125.1
QDB71213.1	000362	prohead-Peptidase_S77	249	CPT_Moabite_183	Serratia phage Moabite	GCA_006384735.1
QFP93126.1	000362	prohead-Peptidase_S77	258	-	Serratia phage PCH45	GCA_009187865.1
QFP93194.1	000362	prohead-Peptidase_S77	159	-	Serratia phage PCH45	GCA_009187865.1
QAU04214.1	000362	prohead-Peptidase_S77	298	HWC03_gp059	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23146.1	000362	prohead-Peptidase_S77	297	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80994.1	000362	prohead-Peptidase_S77	297	Aphrodite1_0194	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70771.1	000362	prohead-Peptidase_S77	256	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47581.1	000362	prohead-Peptidase_S77	297	HWC35_gp187	Vibrio phage USC-1	GCA_006864065.1
BAW98396.1	000362	prohead-Peptidase_S77	298	FDH33_gp187	Vibrio phage pTD1	GCA_002618825.1
AQT28112.1	000362	prohead-Peptidase_S77	261	pVa21_171	Vibrio phage pVa-21	GCA_002619305.1
QAX96757.1	000362	prohead-Peptidase_S77	268	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97076.1	000362	prohead-Peptidase_S77	268	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96122.1	000362	prohead-Peptidase_S77	268	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96440.1	000362	prohead-Peptidase_S77	268	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20987.1	000362	prohead-Peptidase_S77	273	-	Vibrio phage vB_pir03	GCA_014319855.1
AMR59768.1	000363	prohead-Peptidase_S77	161	SEGD1_121	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49768.1	000363	prohead-Peptidase_S77	230	MACHINA_130	Erwinia phage Machina	GCA_002758035.1
AXF51274.1	000363	prohead-Peptidase_S77	145	WELLINGTON_144	Erwinia phage Wellington	GCA_003344985.1
ANZ48423.1	000363	prohead-Peptidase_S77	258	CAITLIN_128	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48695.1	000363	prohead-Peptidase_S77	258	CHRISDB_133	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49496.1	000363	prohead-Peptidase_S77	143	KWAN_144	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50560.1	000363	prohead-Peptidase_S77	164	STRATTON_135	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXF51071.1	000363	prohead-Peptidase_S77	161	MLDJOKPK_00041	Salmonella phage SPAsTU	GCA_003183805.1
AEP83950.1	000363	prohead-Peptidase_S77	161	SPN3US_0117	Salmonella phage SPN3US	GCA_001042275.1
AFO71330.1	000364	prohead-Peptidase_S77	243	CR5_110	Cronobacter phage CR5	GCA_000910235.1
QBP07539.1	000364	prohead-Peptidase_S77	238	DERBICUS_113	Erwinia phage Derbicus	GCA_004521655.1
ANZ48962.1	000364	prohead-Peptidase_S77	238	EARLPHILLIPIV_113	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50304.1	000364	prohead-Peptidase_S77	243	PHOBOS_114	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QBX32302.1	000365	prohead-Peptidase_S77	136	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03566.1	000365	prohead-Peptidase_S77	136	143	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41875.1	000365	prohead-Peptidase_S77	136	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BBI90550.1	000366	prohead-Peptidase_S77	101	HYO65_gp158	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90858.1	000366	prohead-Peptidase_S77	101	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBO63802.1	000000	prohead-Peptidase_S77	391	Goslar_00009	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ABY63035.1	000000	prohead-Peptidase_S77	145	201phi2-1p206	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76824.1	000000	prohead-Peptidase_S77	137	PHABIO_193	Pseudomonas phage Phabio	GCA_002624965.1
ARV76972.1	000000	prohead-Peptidase_S77	124	PHABIO_341	Pseudomonas phage Phabio	GCA_002624965.1
ARV76973.1	000000	prohead-Peptidase_S77	128	PHABIO_342	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02836.1	000000	prohead-Peptidase_S77	144	PSA21_310	Pseudomonas phage Psa21	GCA_004340405.1
QKE54345.1	000000	prohead-Peptidase_S77	146	ACSA002_0310	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AXH70927.1	000000	prohead-Peptidase_S77	137	-	Vibrio phage BONAISHI	GCA_003441475.1
ABY63039.1	000000	prohead-Peptidase_S77	125	201phi2-1p210	Pseudomonas phage 201phi2-1	GCA_000875305.1
AEV89618.1	000000	prohead-Peptidase_S77	152	OBP_181	Pseudomonas phage OBP	GCA_000896635.1
QHJ86097.1	000000	prohead-Peptidase_S77	441	KKIINIFJ_00185	Pseudomonas phage PN05	GCA_009931935.1
QBZ70787.1	000367	prohead-Peptidase_S77	190	pETSU_206	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89723.1	000367	prohead-Peptidase_S77	256	OBP_286	Pseudomonas phage OBP	GCA_000896635.1
AND75236.1	000368	R2A-GHKL	779	ME3_75	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01392.1	000368	R2A-GHKL	744	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28877.1	000368	R2A-GHKL	281	AP1_0170	Aeromonas phage AP1	GCA_014183365.1
ATI17503.1	000368	R2A-GHKL	745	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00494.1	000368	R2A-GHKL	744	HWB28_gp058	Aeromonas phage AS-zj	GCA_002627665.1
AUE22542.1	000368	R2A-GHKL	732	Ah1_00001	Aeromonas phage Ah1	GCA_002957415.1
QAX97942.1	000368	R2A-GHKL	744	ASswx1_300	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01205.1	000368	R2A-GHKL	760	ASwh1_140	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39392.1	000368	R2A-GHKL	744	CC2_231	Aeromonas phage CC2	GCA_000903495.1
ADQ52720.1	000368	R2A-GHKL	734	PX29p001	Aeromonas phage PX29	GCA_000920195.1
ADM79972.1	000368	R2A-GHKL	732	phiAS5_ORF0129	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53050.1	000368	R2A-GHKL	744	65p001	Aeromonas virus 65	GCA_000893255.1
AAQ17656.1	000368	R2A-GHKL	732	rIIA	Aeromonas virus Aeh1	GCA_000843245.1
ARB13665.1	000368	R2A-GHKL	750	Ccr10_gp136c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14010.1	000368	R2A-GHKL	750	Ccr2_gp135c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14698.1	000368	R2A-GHKL	707	Ccr29_gp142	Caulobacter phage Ccr29	GCA_002619485.1
ARB15052.1	000368	R2A-GHKL	707	Ccr32_gp134	Caulobacter phage Ccr32	GCA_002619505.1
ARB15385.1	000368	R2A-GHKL	707	Ccr34_gp143	Caulobacter phage Ccr34	GCA_002619525.1
ARB14353.1	000368	R2A-GHKL	707	Ccr5_gp134c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68334.1	000368	R2A-GHKL	707	CcrBL10_gp130c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88049.1	000368	R2A-GHKL	720	CcrColossus_gp179	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68726.1	000368	R2A-GHKL	674	CcrPW_gp187c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87657.1	000368	R2A-GHKL	707	CcrKarma_gp140	Caulobacter virus Karma	GCA_000901575.1
AFU87306.1	000368	R2A-GHKL	707	CcrMagneto_gp136	Caulobacter virus Magneto	GCA_000903095.1
AFU86618.1	000368	R2A-GHKL	707	CcrRogue_gp136	Caulobacter virus Rogue	GCA_000900555.1
AFU88453.1	000368	R2A-GHKL	707	CcrSwift_gp135	Caulobacter virus Swift	GCA_000899655.1
AFU86970.1	000368	R2A-GHKL	707	CbK_gp138	Caulobacter virus phiCbK	GCA_000900535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANS05928.1	000368	R2A-GHKL	749	ABCD_0002	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS05929.1	000368	R2A-GHKL	749	ABCD_0003	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65061.1	000368	R2A-GHKL	715	S13_264	Cronobacter phage S13	GCA_001503575.1
AON97011.1	000368	R2A-GHKL	749	E_002	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70821.1	000368	R2A-GHKL	737	phiC120_c115	Escherichia phage phiC120	GCA_002621185.1
QIG57929.1	000368	R2A-GHKL	729	SEA_PAULODIABOLI_244	Microbacterium phage PauloDiaboli	GCA_011067425.1
QHJ78869.1	000368	R2A-GHKL	722	-	Myoviridae sp.	GCA_012593985.1
QCG76067.1	000368	R2A-GHKL	727	EST35_0186	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAQ64213.1	000368	R2A-GHKL	689	KVP40.0143	Vibrio phage KVP40	GCA_000843785.1
QIW90528.1	000368	R2A-GHKL	689	GCAPEGMB_00181	Vibrio phage V07	GCA_012361095.1
QIW90894.1	000368	R2A-GHKL	689	COHAPHLL_00031	Vibrio phage V09	GCA_012361135.1
QHJ74324.1	000368	R2A-GHKL	689	VH12019_00405	Vibrio phage VH1_2019	GCA_009931825.1
AGB06818.1	000368	R2A-GHKL	689	CF80_gp031	Vibrio phage VH7D	GCA_000914495.1
QBX06329.1	000368	R2A-GHKL	689	ValB1HC_376	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60959.1	000368	R2A-GHKL	689	AVU32_gp118	Vibrio phage ValKK3	GCA_001501635.1
AGN30190.2	000368	R2A-GHKL	694	VPFG_00190	Vibrio phage nt-1	GCA_000910195.2
ALP46966.1	000368	R2A-GHKL	689	phiGrn1_0254	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47346.1	000368	R2A-GHKL	689	phiST2_0009	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54572.1	000368	R2A-GHKL	689	vBValMR10Z_31	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07200.1	000368	R2A-GHKL	747	VmeM32_00214	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37374.1	000368	R2A-GHKL	689	pp2_141	Vibriophage phi-pp2	GCA_002630725.1
BBA65271.1	000368	R2A-GHKL	735	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65730.1	000368	R2A-GHKL	735	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96310.1	000368	R2A-GHKL	734	Xoosp13_123	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QMV28956.1	000368	R2A-GHKL	468	AP1_0249	Aeromonas phage AP1	GCA_014183365.1
AAX78523.1	000369	R2A-GHKL+R2B-HTH	1049	RB43ORF001c	Escherichia virus RB43	GCA_000863505.1
prevph1000000232	000370	R2A-GHKL	659	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000182	000370	R2A-GHKL	679	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBQ74450.1	000371	Uri-nuclease+HTH	323	BcepSauron_070	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06483.1	000371	Uri-nuclease+HTH	323	BcepSaruman_070	Burkholderia phage BcepSaruman	GCA_004771375.1
AND75235.1	000372	R2B-HTH	273	ME3_74	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01801.1	000372	R2B-HTH	411	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28955.1	000372	R2B-HTH	397	AP1_0248	Aeromonas phage AP1	GCA_014183365.1
ATI17504.1	000372	R2B-HTH	397	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00493.1	000372	R2B-HTH	397	HWB28_gp059	Aeromonas phage AS-zj	GCA_002627665.1
AUE22873.1	000372	R2B-HTH	438	Ah1_00355	Aeromonas phage Ah1	GCA_002957415.1
QAX98584.1	000372	R2B-HTH	433	ASfcp2_250	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97943.1	000372	R2B-HTH	397	ASswx1_301	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01204.1	000372	R2B-HTH	414	ASwh1_139	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39391.1	000372	R2B-HTH	397	CC2_230	Aeromonas phage CC2	GCA_000903495.1
ADQ53049.1	000372	R2B-HTH	439	PX29p332	Aeromonas phage PX29	GCA_000920195.1
ADM79971.1	000372	R2B-HTH	432	phiAS5_ORF0128	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53445.1	000372	R2B-HTH	411	65p439	Aeromonas virus 65	GCA_000893255.1
AAQ18002.1	000372	R2B-HTH	438	rIIB	Aeromonas virus Aeh1	GCA_000843245.1
ARB13664.1	000372	R2B-HTH	542	Ccr10_gp135c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14009.1	000372	R2B-HTH	542	Ccr2_gp134c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14697.1	000372	R2B-HTH	542	Ccr29_gp141	Caulobacter phage Ccr29	GCA_002619485.1
ARB15051.1	000372	R2B-HTH	542	Ccr32_gp133	Caulobacter phage Ccr32	GCA_002619505.1
ARB15384.1	000372	R2B-HTH	542	Ccr34_gp142	Caulobacter phage Ccr34	GCA_002619525.1
ARB14352.1	000372	R2B-HTH	538	Ccr5_gp133c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68333.1	000372	R2B-HTH	519	CcrBL10_gp129c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88048.1	000372	R2B-HTH	431	CcrColossus_gp178	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68725.1	000372	R2B-HTH	433	CcrPW_gp186c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87656.1	000372	R2B-HTH	542	CcrKarma_gp139	Caulobacter virus Karma	GCA_000901575.1
AFU87305.1	000372	R2B-HTH	542	CcrMagneto_gp135	Caulobacter virus Magneto	GCA_000903095.1
AFU86617.1	000372	R2B-HTH	540	CcrRogue_gp135	Caulobacter virus Rogue	GCA_000900555.1
AFU88452.1	000372	R2B-HTH	542	CcrSwift_gp134	Caulobacter virus Swift	GCA_000899655.1
AFU86969.1	000372	R2B-HTH	542	CbK_gp137	Caulobacter virus phiCbK	GCA_000900535.1
ANS05976.1	000372	R2B-HTH	299	ABCD_0001	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65062.1	000372	R2B-HTH	342	S13_265	Cronobacter phage S13	GCA_001503575.1
AON97010.1	000372	R2B-HTH	299	E_001	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70820.1	000372	R2B-HTH	311	phiC120_c114	Escherichia phage phiC120	GCA_002621185.1
QIG57930.1	000372	R2B-HTH	364	SEA_PAULODIABOLI_245	Microbacterium phage PauloDiaboli	GCA_011067425.1
QHJ78868.1	000372	R2B-HTH	346	-	Myoviridae sp.	GCA_012593985.1
QCG76068.1	000372	R2B-HTH	247	EST35_0187	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAQ64214.1	000372	R2B-HTH	345	KVP40.0144	Vibrio phage KVP40	GCA_000843785.1
QIW90529.1	000372	R2B-HTH	345	GCAPEGMB_00182	Vibrio phage V07	GCA_012361095.1
QIW90893.1	000372	R2B-HTH	345	COHAPHLL_00030	Vibrio phage V09	GCA_012361135.1
QHJ74325.1	000372	R2B-HTH	345	VH12019_00406	Vibrio phage VH1_2019	GCA_009931825.1
AGB06819.1	000372	R2B-HTH	346	CF80_gp032	Vibrio phage VH7D	GCA_000914495.1
QBX06328.1	000372	R2B-HTH	346	ValB1HC_375	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60958.1	000372	R2B-HTH	343	AVU32_gp117	Vibrio phage ValKK3	GCA_001501635.1
AGN30191.1	000372	R2B-HTH	343	VPFG_00191	Vibrio phage nt-1	GCA_000910195.2
ALP47006.1	000372	R2B-HTH	346	phiGrn1_0255	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47392.1	000372	R2B-HTH	328	phiST2_0010	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54571.1	000372	R2B-HTH	346	vBValMR10Z_30	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07201.1	000372	R2B-HTH	316	VmeM32_00215	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37375.1	000372	R2B-HTH	345	pp2_142	Vibriophage phi-pp2	GCA_002630725.1
BBA65729.1	000372	R2B-HTH	333	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65270.1	000372	R2B-HTH	333	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96309.1	000372	R2B-HTH	359	Xoosp13_122	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXQ68225.1	000373	HTH	152	CcrBL10_gp021	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86507.1	000373	HTH	152	CcrRogue_gp025	Caulobacter virus Rogue	GCA_000900555.1
AEO93797.1	000374	SIG+Rot_TROVE+VWA	543	G_540	Bacillus virus G	GCA_000917535.1
AFU88009.1	000374	SIG+Rot_TROVE+VWA	469	CcrColossus_gp139	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68685.1	000374	SIG+Rot_TROVE+VWA	469	CcrPW_gp146c	Caulobacter phage CcrPW	GCA_003443275.1
AYD81304.1	000374	SIG+Rot_TROVE+VWA	554	SEA_JUSTBECAUSE_135	Streptomyces phage JustBecause	GCA_003613775.1
QJD53707.1	000374	SIG+Rot_TROVE+VWA	554	SEA_KELA_136	Streptomyces phage Kela	GCA_012934305.1
QBZ72034.1	000374	SIG+Rot_TROVE+VWA	537	SEA_KRADAL_136	Streptomyces phage Kradal	GCA_004799925.1
AXH66297.1	000374	SIG+Rot_TROVE+VWA	537	SEA_SATIS_136	Streptomyces phage Satis	GCA_003366315.1
ASV44713.1	000375	SIG+Rot_TROVE+VWA	551	FDI40_gp128	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG57882.1	000375	SIG+Rot_TROVE+VWA	566	SEA_PAULODIABOLI_194	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH70790.1	000375	SIG+Rot_TROVE+VWA	539	-	Vibrio phage BONAISHI	GCA_003441475.1
QAU04459.1	000000	Rot_TROVE+VWA	502	ValB1MD_045	Vibrio phage ValB1MD	GCA_004138815.1
AND75374.1	000376	SIG+VWA	481	ME3_213	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUE22691.1	000376	SIG+VWA	478	Ah1_00150	Aeromonas phage Ah1	GCA_002957415.1
QAX98416.1	000376	SIG+VWA	480	ASfcp2_72	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52871.1	000376	SIG+VWA	476	PX29p152	Aeromonas phage PX29	GCA_000920195.1
ADM80133.1	000376	SIG+VWA	477	phiAS5_ORF0290	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17819.1	000376	SIG+VWA	526	Aeh1ORF154c	Aeromonas virus Aeh1	GCA_000843245.1
AIA64993.1	000376	SIG+VWA	467	S13_196	Cronobacter phage S13	GCA_001503575.1
AFC21626.1	000376	SIG+VWA	504	GAP32_176	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QHJ78939.1	000376	SIG+VWA	461	-	Myoviridae sp.	GCA_012593985.1
QIG65818.1	000376	SIG+VWA	467	phiOC_p153	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43748.1	000376	SIG+VWA	504	CBB_183	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18897.1	000376	SIG+VWA	505	7t3_0376	Salmonella phage 7t3	GCA_006083215.1
AZU98154.1	000376	SIG+VWA	505	CPT_Munch_210	Salmonella phage Munch	GCA_004015485.1
QIG62829.1	000376	SIG+VWA	505	SEPL_216	Salmonella phage SE_PL	GCA_011067555.1
AQW88705.1	000376	SIG+VWA	508	BF_0180	Serratia phage BF	GCA_002619745.1
AGR47874.1	000376	SIG+VWA	470	SmphiM12_242	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13076.1	000376	SIG+VWA	470	PHIM19_171	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12716.1	000376	SIG+VWA	470	PHIM7_171	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13446.1	000376	SIG+VWA	470	PHIN3_183	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54949.1	000376	SIG+VWA	491	b23_0339	Synechococcus phage B23	GCA_009745195.1
QGT54584.1	000376	SIG+VWA	491	b3_0345	Synechococcus phage B3	GCA_009745215.1
AAQ64370.1	000376	SIG+VWA	478	KVP40.0300	Vibrio phage KVP40	GCA_000843785.1
QIW90686.1	000376	SIG+VWA	478	GCAPEGMB_00339	Vibrio phage V07	GCA_012361095.1
QIW91112.1	000376	SIG+VWA	478	COHAPHLL_00276	Vibrio phage V09	GCA_012361135.1
QHJ74481.1	000376	SIG+VWA	479	VH12019_00154	Vibrio phage VH1_2019	GCA_009931825.1
QBX06168.1	000376	SIG+VWA	478	ValB1HC_215	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61185.1	000376	SIG+VWA	478	AVU32_gp344	Vibrio phage ValKK3	GCA_001501635.1
AGN30348.2	000376	SIG+VWA	478	VPFG_00351	Vibrio phage nt-1	GCA_000910195.2
ALP46983.1	000376	SIG+VWA	478	phiGrn1_0037	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47366.1	000376	SIG+VWA	478	phiST2_0169	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54794.1	000376	SIG+VWA	478	vBValMR10Z_254	Vibrio phage vB_ValM_R10Z	GCA_014337545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN37532.1	000376	SIG+VWA	478	pp2_299	Vibriophage phi-pp2	GCA_002630725.1
SOK58987.1	000376	SIG+VWA	508	g179	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58453.1	000376	SIG+VWA	508	g176	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56879.1	000377	MPTase+VWA	736	CPXG_00076	Cyanophage P-RSM6	GCA_000906155.1
AJK27576.1	000377	MPTase+VWA	736	PTIM40_149	Cyanophage P-TIM40	GCA_001470935.1
AOO14336.1	000377	MPTase+VWA	708	Sn110110_142	Cyanophage S-RIM14	GCA_002599065.1
AOO14985.1	000377	MPTase+VWA	708	W1230910_139	Cyanophage S-RIM14	GCA_002599125.1
AMO43155.1	000377	MPTase+VWA	712	R1080702_146	Cyanophage S-RIM32	GCA_001754165.1
AMO43379.1	000377	MPTase+VWA	711	W270710_135	Cyanophage S-RIM44	GCA_002599145.1
AOO11623.1	000377	MPTase+VWA	711	ES420910_142	Cyanophage S-RIM44	GCA_002599165.1
AOO11851.1	000377	MPTase+VWA	711	Np050604_135	Cyanophage S-RIM44	GCA_002599185.1
AOO12088.1	000377	MPTase+VWA	711	Np200711_142	Cyanophage S-RIM44	GCA_002599205.1
AOO12324.1	000377	MPTase+VWA	711	Np420711_142	Cyanophage S-RIM44	GCA_002599225.1
AOO12552.1	000377	MPTase+VWA	711	Sn080709_135	Cyanophage S-RIM44	GCA_002599245.1
AOO12789.1	000377	MPTase+VWA	711	Sn130910_142	Cyanophage S-RIM44	GCA_002599265.1
AOO13018.1	000377	MPTase+VWA	711	W2100709_136	Cyanophage S-RIM44	GCA_002599285.1
AGH07475.1	000377	MPTase+VWA	751	CYVG_00031	Cyanophage S-SSM6a	GCA_002710385.1
AGG54479.1	000377	MPTase+VWA	747	CYWG_00195	Cyanophage S-SSM6b	GCA_002710425.1
QIG65680.1	000377	MPTase+VWA	699	phiOC_p014	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26306.1	000377	MPTase+VWA	741	CPMG_00207	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44528.1	000377	MPTase+VWA	737	PSSM2_150	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12441.1	000377	MPTase+VWA	737	PRTG_00292	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93458.1	000377	MPTase+VWA	732	AVU42_gp121	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99237.1	000377	MPTase+VWA	711	Syn1_136	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30634.1	000377	MPTase+VWA	714	Syn7803US37_157	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76191.1	000377	MPTase+VWA	706	PBI_BELLAMY_146	Synechococcus phage Bellamy	GCA_002627525.1
QCW22902.1	000377	MPTase+VWA	706	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50585.1	000377	MPTase+VWA	706	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59603.1	000377	MPTase+VWA	710	S330809_142	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59365.1	000377	MPTase+VWA	710	C440309_142	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59841.1	000377	MPTase+VWA	710	N231010_142	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70563.1	000377	MPTase+VWA	720	HOU04_gp164	Synechococcus phage S-T4	GCA_003443335.1
QJT70136.1	000377	MPTase+VWA	691	SynMITS9220M01_123	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASV44728.2	000378	VWA	429	FDI40_gp263	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01114.1	000378	VWA	474	AR9_g029	Bacillus phage AR9	GCA_001743835.1
ALN97763.1	000378	VWA	521	Bp8pS_084	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93821.1	000378	VWA	392	G_576	Bacillus virus G	GCA_000917535.1
ASU00036.1	000378	VWA	471	PBI_PBS1_214	Bacillus virus PBS1	GCA_002601325.1
AFC21661.1	000378	VWA	451	GAP32_211	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14454.1	000378	VWA	474	PBI_121Q_564	Escherichia phage 121Q	GCA_000926855.1
QAY00494.1	000378	VWA	469	Ecwhy1_215	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34689.1	000378	VWA	474	ACQ29_gp009	Escherichia phage PBECO4	GCA_001041035.1
BBM62127.1	000378	VWA	474	EO157G_5380	Escherichia phage SP27	GCA_008033345.1
AXC36809.1	000378	VWA	474	-	Escherichia phage UB	GCA_003341455.1
QBO61848.1	000378	VWA	474	G17_00359	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13889.1	000378	VWA	474	vBEcoMphAPEC6_gp264c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80439.1	000378	VWA	474	PSLUR01_00462	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44327.1	000378	VWA	461	RaK2_00054	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72919.1	000378	VWA	438	-	Myoviridae sp.	GCA_003657725.1
AMM43782.1	000378	VWA	450	CBB_217	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76221.1	000378	VWA	394	EST35_0340	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44184.1	000378	VWA	431	PBI_SCTP2_169	Salicola phage SCTP-2	GCA_002625545.1
QCW18931.1	000378	VWA	473	7t3_0410	Salmonella phage 7t3	GCA_006083215.1
AZU98187.1	000378	VWA	475	CPT_Munch_243	Salmonella phage Munch	GCA_004015485.1
QIG62797.1	000378	VWA	473	SEPL_184	Salmonella phage SE_PL	GCA_011067555.1
AQW88738.1	000378	VWA	446	BF_0213	Serratia phage BF	GCA_002619745.1
QAU04573.1	000378	VWA	444	ValB1MD_297	Vibrio phage ValB1MD	GCA_004138815.1
SOK59021.1	000378	VWA	438	g213	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58486.1	000378	VWA	438	g209	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26328.1	000378	VWA	611	g305	Yersinia phage phiR1-37	GCA_000895615.1
AND75454.1	000379	VWA	229	ME3_293	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXQ69275.1	000379	VWA	248	CcrBL9_gp251c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88091.1	000379	VWA	234	CcrColossus_gp221	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68767.1	000379	VWA	234	CcrPW_gp228c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69832.1	000379	VWA	248	CcrSC_gp250c	Caulobacter phage CcrSC	GCA_003443315.1
ANS05930.1	000380	VWA	739	ABCD_0118	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97129.1	000380	VWA	748	E_121	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78641.1	000380	VWA	739	RB43ORF119c	Escherichia virus RB43	GCA_000863505.1
ALY07060.1	000380	VWA	725	VmeM32_00069	Vibrio phage vB_VmeM-32	GCA_002608825.1
AYD81320.1	000381	VWA	367	SEA_JUSTBECAUSE_155	Streptomyces phage JustBecause	GCA_003613775.1
QJD53723.1	000381	VWA	367	SEA_KELA_153	Streptomyces phage Kela	GCA_012934305.1
QBZ72052.1	000381	VWA	363	SEA_KRADAL_156	Streptomyces phage Kradal	GCA_004799925.1
AXH66315.1	000381	VWA	363	SEA_SATIS_156	Streptomyces phage Satis	GCA_003366315.1
AMS01152.1	000382	SIG+VWA	749	AR9_g068	Bacillus phage AR9	GCA_001743835.1
ALN97822.1	000382	SIG+VWA	740	Bp8pS_143	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00081.1	000382	SIG+VWA	749	PBI_PBS1_259	Bacillus virus PBS1	GCA_002601325.1
prevph1000000107	000383	SIG+VWA	855	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000077	000383	SIG+VWA	855	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000077	000384	VWA	452	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000062	000384	VWA	452	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ95446.1	000385	VWA	226	FDI40_gp707	Agrobacterium phage Atu_ph07	GCA_002628245.1
BBA65561.1	000385	VWA	216	-	Xanthomonas phage XacN1	GCA_003173815.1
AUZ94934.1	000386	VWA	144	FDI40_gp152	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95300.1	000386	VWA	150	FDI40_gp541	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83623.1	000000	VWA	553	0305phi8-36p063	Bacillus phage 0305phi8-36	GCA_000871045.1
AUZ95440.1	000000	Lysozyme	205	FDI40_gp701	Agrobacterium phage Atu_ph07	GCA_002628245.1
SBV38463.1	000000	Lysozyme	240	BN7874_259	Phage NCTB	GCA_900092385.1
prev15ph1000000162	000387	Lysozyme	347	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXG67172.1	000388	Lysozyme	879	AD1_128	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79922.1	000388	Lysozyme	930	JA11_117	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66521.1	000388	Lysozyme	930	JA13_118	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66846.1	000388	Lysozyme	932	JA29_120	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67491.1	000388	Lysozyme	930	JA33_117	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08405.1	000388	Lysozyme	888	Alexandra_133	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58769.1	000388	Lysozyme	892	Y3_129	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28608.1	000388	Lysozyme	913	YOLOSWAG_127	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXH72838.1	000388	Lysozyme	290	-	Myoviridae sp.	GCA_003657725.1
AFH14556.1	000388	Lysozyme	202	Lu11_0025	Pseudomonas phage Lu11	GCA_000897175.1
QHJ85968.1	000388	Lysozyme	714	KKIINIFJ_00056	Pseudomonas phage PN05	GCA_009931935.1
AGS81955.1	000388	Lysozyme	1176	PaBG_00071	Pseudomonas phage PaBG	GCA_000912555.1
AXG67237.1	000389	Lysozyme+PG_binding	190	AD1_193	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79987.1	000389	Lysozyme+PG_binding	191	JA11_182	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66585.1	000389	Lysozyme+PG_binding	191	JA13_182	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66910.1	000389	Lysozyme+PG_binding	191	JA29_184	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67556.1	000389	Lysozyme+PG_binding	191	JA33_182	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMR59806.1	000389	Lysozyme+PG_binding	196	SEGD1_159	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49807.1	000389	Lysozyme+PG_binding	199	MACHINA_169	Erwinia phage Machina	GCA_002758035.1
AXF51304.1	000389	Lysozyme+PG_binding	194	WELLINGTON_175	Erwinia phage Wellington	GCA_003344985.1
AFQ96620.1	000389	Lysozyme+PG_binding	199	G173_gp075	Erwinia phage phiEaH2	GCA_000902915.1
AWY08467.1	000389	Lysozyme+PG_binding	190	Alexandra_203	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48184.1	000389	Lysozyme+PG_binding	199	ASESINO_171	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48463.1	000389	Lysozyme+PG_binding	200	CAITLIN_168	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48742.1	000389	Lysozyme+PG_binding	200	CHRISDB_180	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49251.1	000389	Lysozyme+PG_binding	199	HUXLEY_169	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49528.1	000389	Lysozyme+PG_binding	194	KWAN_176	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50079.1	000389	Lysozyme+PG_binding	199	PARSHIK_170	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50597.1	000389	Lysozyme+PG_binding	199	STRATTON_172	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARW58837.1	000389	Lysozyme+PG_binding	189	Y3_197	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28667.1	000389	Lysozyme+PG_binding	190	YOLOSWAG_188	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QKN85994.1	000389	Lysozyme+PG_binding	205	ACEC001_1550	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63817.1	000389	Lysozyme+PG_binding	211	Goslar_00024	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
AGS81928.1	000389	Lysozyme+PG_binding	207	PaBG_00044	Pseudomonas phage PaBG	GCA_000912555.1
QNI20854.1	000389	Lysozyme+PG_binding	196	-	Salmonella phage JN03	GCA_014319805.1
AWN09175.2	000389	Lysozyme+PG_binding	205	MLDJOKPK_00289	Salmonella phage SPAsTU	GCA_003183805.1
AEP83989.1	000389	Lysozyme+PG_binding	205	SPN3US_0156	Salmonella phage SPN3US	GCA_001042275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQT28060.1	000389	Lysozyme+PG_binding	210	pVa21_119	Vibrio phage pVa-21	GCA_002619305.1
QIG63366.1	000390	SIG+Lysozyme	169	DAC16_133	Bacteroides phage DAC16	GCA_013387695.1
QIG63631.1	000390	SIG+Lysozyme	169	DAC19_140	Bacteroides phage DAC19	GCA_013387715.1
QIG63892.1	000390	SIG+Lysozyme	169	DAC20_139	Bacteroides phage DAC20	GCA_013387725.1
QIG64155.1	000390	SIG+Lysozyme	169	DAC22_141	Bacteroides phage DAC22	GCA_013387735.1
QIG64412.1	000390	SIG+Lysozyme	169	DAC23_134	Bacteroides phage DAC23	GCA_013387745.1
AFF28215.1	000390	SIG+Lysozyme	211	PAU_217	Sphingomonas phage PAU	GCA_000902455.1
AHI60220.1	000391	SIG+Lysozyme	458	Ea357_069	Erwinia phage Ea35-70	GCA_000914635.1
QBP07179.1	000391	SIG+Lysozyme	473	REBECCA_71	Erwinia phage Rebecca	GCA_004521635.1
AUG85858.1	000391	SIG+Lysozyme	473	BOSOLAPHORUS_70	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52170.1	000391	SIG+Lysozyme	473	DM_72	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86177.1	000391	SIG+Lysozyme	473	DESERTFOX_69	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86499.1	000391	SIG+Lysozyme	473	MADMEL_71	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86820.1	000391	SIG+Lysozyme	473	MORTIMER_71	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51850.2	000391	SIG+Lysozyme	473	RAY_69	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51534.2	000391	SIG+Lysozyme	473	SIMMY50_72	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64882.1	000391	SIG+Lysozyme	473	SPECIALG_72	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMS01110.1	000392	SIG+Lysozyme	265	AR9_g025	Bacillus phage AR9	GCA_001743835.1
ALN97772.1	000392	SIG+Lysozyme	265	Bp8pS_093	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93833.1	000392	SIG+Lysozyme	256	G_588	Bacillus virus G	GCA_000917535.1
ASU00032.1	000392	SIG+Lysozyme	265	PBI_PBS1_210	Bacillus virus PBS1	GCA_002601325.1
AEO93443.1	000000	Lysozyme+PTSEIIA1	2893	G_183	Bacillus virus G	GCA_000917535.1
AEO93294.1	000393	Amidase_3+LysM+Lysozyme	556	G_23	Bacillus virus G	GCA_000917535.1
BAE47806.1	000000	Lysozyme+SH3	242	CST108	Clostridium phage c-st	GCA_000865225.1
APU01546.1	000394	Gp5_OB+Lysozyme	166	-	Aeromonas phage 65.2	GCA_002618145.1
APU01497.1	000394	Gp5_OB+Lysozyme	612	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28959.1	000394	Gp5_OB+Lysozyme	612	AP1_0252	Aeromonas phage AP1	GCA_014183365.1
QMV29040.1	000394	Gp5_OB+Lysozyme	166	AP1_0333	Aeromonas phage AP1	GCA_014183365.1
ATI17368.1	000394	Gp5_OB+Lysozyme	166	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17400.1	000394	Gp5_OB+Lysozyme	612	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00226.1	000394	Gp5_OB+Lysozyme	166	HWB28_gp326	Aeromonas phage AS-zj	GCA_002627665.1
ASU00195.1	000394	Gp5_OB+Lysozyme	612	HWB28_gp357	Aeromonas phage AS-zj	GCA_002627665.1
AUE22730.1	000394	Gp5_OB+Lysozyme	604	Ah1_00212	Aeromonas phage Ah1	GCA_002957415.1
AUE22861.1	000394	Gp5_OB+Lysozyme	165	Ah1_00343	Aeromonas phage Ah1	GCA_002957415.1
QAX98451.1	000394	Gp5_OB+Lysozyme	604	ASfcp2_109	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98571.1	000394	Gp5_OB+Lysozyme	165	ASfcp2_237	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97809.1	000394	Gp5_OB+Lysozyme	166	ASswx1_165	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97840.1	000394	Gp5_OB+Lysozyme	612	ASswx1_197	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01312.1	000394	Gp5_OB+Lysozyme	606	ASwh1_249	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01356.1	000394	Gp5_OB+Lysozyme	166	ASwh1_296	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39557.1	000394	Gp5_OB+Lysozyme	612	CC2_338	Aeromonas phage CC2	GCA_000903495.1
AFN39567.1	000394	Gp5_OB+Lysozyme	166	CC2_371	Aeromonas phage CC2	GCA_000903495.1
ADQ52909.1	000394	Gp5_OB+Lysozyme	604	PX29p190	Aeromonas phage PX29	GCA_000920195.1
ADQ53036.1	000394	Gp5_OB+Lysozyme	165	PX29p319	Aeromonas phage PX29	GCA_000920195.1
ADM79960.1	000394	Gp5_OB+Lysozyme	165	phiAS5_ORF0117	Aeromonas phage phiAS5	GCA_000887715.1
ADM80176.1	000394	Gp5_OB+Lysozyme	606	phiAS5_ORF0333	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53118.1	000394	Gp5_OB+Lysozyme	529	65p110	Aeromonas virus 65	GCA_000893255.1
ADQ53168.1	000394	Gp5_OB+Lysozyme	166	65p160	Aeromonas virus 65	GCA_000893255.1
AAQ17861.1	000394	Gp5_OB+Lysozyme	604	5	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17989.1	000394	Gp5_OB+Lysozyme	165	e	Aeromonas virus Aeh1	GCA_000843245.1
ASV44767.1	000394	Gp5_OB+Lysozyme	865	FDI40_gp699	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63502.1	000394	Gp5_OB+Lysozyme	294	CP21_040	Campylobacter virus CP21	GCA_000902535.1
ANS05938.1	000394	Gp5_OB+Lysozyme	586	ABCD_0194	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64956.1	000394	Gp5_OB+Lysozyme	597	S13_157	Cronobacter phage S13	GCA_001503575.1
AIA64987.1	000394	Gp5_OB+Lysozyme	164	S13_190	Cronobacter phage S13	GCA_001503575.1
AFC21630.1	000394	Gp5_OB+Lysozyme	310	GAP32_180	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21683.1	000394	Gp5_OB+Lysozyme	162	GAP32_233	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21684.1	000394	Gp5_OB+Lysozyme	894	GAP32_234	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97208.1	000394	Gp5_OB+Lysozyme	586	E_200	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14422.1	000394	Gp5_OB+Lysozyme	308	PBI_121Q_532	Escherichia phage 121Q	GCA_000926855.1
AIT14476.1	000394	Gp5_OB+Lysozyme	162	PBI_121Q_586	Escherichia phage 121Q	GCA_000926855.1
AIT14477.1	000394	Gp5_OB+Lysozyme	887	PBI_121Q_587	Escherichia phage 121Q	GCA_000926855.1
QAY00471.1	000394	Gp5_OB+Lysozyme	887	Ecwhy1_192	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00472.1	000394	Gp5_OB+Lysozyme	162	Ecwhy1_193	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00528.1	000394	Gp5_OB+Lysozyme	308	Ecwhy1_249	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35215.1	000394	Gp5_OB+Lysozyme	162	ACQ29_gp535	Escherichia phage PBECO4	GCA_001041035.1
AGC34720.1	000394	Gp5_OB+Lysozyme	308	ACQ29_gp040	Escherichia phage PBECO4	GCA_001041035.1
AGC35214.1	000394	Gp5_OB+Lysozyme	887	ACQ29_gp534	Escherichia phage PBECO4	GCA_001041035.1
BBM62094.1	000394	Gp5_OB+Lysozyme	308	EO157G_5050	Escherichia phage SP27	GCA_008033345.1
BBM62148.1	000394	Gp5_OB+Lysozyme	162	EO157G_5590	Escherichia phage SP27	GCA_008033345.1
BBM62149.1	000394	Gp5_OB+Lysozyme	887	EO157G_5600	Escherichia phage SP27	GCA_008033345.1
AXC36787.1	000394	Gp5_OB+Lysozyme	162	-	Escherichia phage UB	GCA_003341455.1
AXC36838.1	000394	Gp5_OB+Lysozyme	308	-	Escherichia phage UB	GCA_003341455.1
AXC36786.1	000394	Gp5_OB+Lysozyme	887	-	Escherichia phage UB	GCA_003341455.1
ARM70945.1	000394	Gp5_OB+Lysozyme	162	phiC120_c240	Escherichia phage phiC120	GCA_002621185.1
ARM70977.1	000394	Gp5_OB+Lysozyme	577	phiC120_c272	Escherichia phage phiC120	GCA_002621185.1
ARM70711.1	000394	Gp5_OB+Lysozyme	577	phiC120_c4	Escherichia phage phiC120	GCA_002621185.1
QBO61826.1	000394	Gp5_OB+Lysozyme	887	G17_00337	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61827.1	000394	Gp5_OB+Lysozyme	162	G17_00338	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61879.1	000394	Gp5_OB+Lysozyme	308	G17_00390	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13870.1	000394	Gp5_OB+Lysozyme	887	vBEcoMphAPEC6_gp241	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13871.1	000394	Gp5_OB+Lysozyme	162	vBEcoMphAPEC6_gp242	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13918.1	000394	Gp5_OB+Lysozyme	308	vBEcoMphAPEC6_gp293c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80408.1	000394	Gp5_OB+Lysozyme	308	PSLUR01_00431	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80460.1	000394	Gp5_OB+Lysozyme	162	PSLUR01_00483	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80461.1	000394	Gp5_OB+Lysozyme	887	PSLUR01_00484	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78726.1	000394	Gp5_OB+Lysozyme	589	RB43ORF204w	Escherichia virus RB43	GCA_000863505.1
AFA44346.1	000394	Gp5_OB+Lysozyme	162	RaK2_00073	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44351.1	000394	Gp5_OB+Lysozyme	886	RaK2_00078	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44302.1	000394	Gp5_OB+Lysozyme	300	RaK2_00029	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78947.1	000394	Gp5_OB+Lysozyme	162	-	Myoviridae sp.	GCA_012593985.1
QHJ78978.1	000394	Gp5_OB+Lysozyme	596	-	Myoviridae sp.	GCA_012593985.1
AMM43752.1	000394	Gp5_OB+Lysozyme	311	CBB_187	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43804.1	000394	Gp5_OB+Lysozyme	162	CBB_239	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43805.1	000394	Gp5_OB+Lysozyme	894	CBB_240	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18901.1	000394	Gp5_OB+Lysozyme	307	7t3_0380	Salmonella phage 7t3	GCA_006083215.1
QCW18956.1	000394	Gp5_OB+Lysozyme	162	7t3_0435	Salmonella phage 7t3	GCA_006083215.1
QCW18957.1	000394	Gp5_OB+Lysozyme	889	7t3_0436	Salmonella phage 7t3	GCA_006083215.1
AZU98158.1	000394	Gp5_OB+Lysozyme	307	CPT_Munch_214	Salmonella phage Munch	GCA_004015485.1
AZU98209.1	000394	Gp5_OB+Lysozyme	162	CPT_Munch_265	Salmonella phage Munch	GCA_004015485.1
AZU98210.1	000394	Gp5_OB+Lysozyme	889	CPT_Munch_266	Salmonella phage Munch	GCA_004015485.1
QIG62774.1	000394	Gp5_OB+Lysozyme	889	SEPL_161	Salmonella phage SE_PL	GCA_011067555.1
QIG62775.1	000394	Gp5_OB+Lysozyme	162	SEPL_162	Salmonella phage SE_PL	GCA_011067555.1
QIG62826.1	000394	Gp5_OB+Lysozyme	307	SEPL_213	Salmonella phage SE_PL	GCA_011067555.1
AQW88710.1	000394	Gp5_OB+Lysozyme	311	BF_0185	Serratia phage BF	GCA_002619745.1
AQW88763.1	000394	Gp5_OB+Lysozyme	162	BF_0238	Serratia phage BF	GCA_002619745.1
AQW88764.1	000394	Gp5_OB+Lysozyme	893	BF_0239	Serratia phage BF	GCA_002619745.1
AGR47778.3	000394	Gp5_OB+Lysozyme	537	SmphiM12_146	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13005.1	000394	Gp5_OB+Lysozyme	537	PHIM19_99	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12645.1	000394	Gp5_OB+Lysozyme	537	PHIM7_98	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13377.2	000394	Gp5_OB+Lysozyme	537	PHIN3_112	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64404.1	000394	Gp5_OB+Lysozyme	421	KVP40.0335	Vibrio phage KVP40	GCA_000843785.1
QIW90349.1	000394	Gp5_OB+Lysozyme	421	GCAPEGMB_00002	Vibrio phage V07	GCA_012361095.1
QIW91080.1	000394	Gp5_OB+Lysozyme	421	COHAPHLL_00217	Vibrio phage V09	GCA_012361135.1
QHJ74517.1	000394	Gp5_OB+Lysozyme	421	VH12019_00217	Vibrio phage VH1_2019	GCA_009931825.1
AGB06978.1	000394	Gp5_OB+Lysozyme	405	CF80_gp191	Vibrio phage VH7D	GCA_000914495.1
QBX06138.1	000394	Gp5_OB+Lysozyme	405	ValB1HC_184	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61150.1	000394	Gp5_OB+Lysozyme	403	AVU32_gp309	Vibrio phage ValKK3	GCA_001501635.1
AGN30386.1	000394	Gp5_OB+Lysozyme	389	VPFG_00389	Vibrio phage nt-1	GCA_000910195.2
ALP46994.1	000394	Gp5_OB+Lysozyme	403	phiGrn1_0069	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47375.1	000394	Gp5_OB+Lysozyme	403	phiST2_0201	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54763.1	000394	Gp5_OB+Lysozyme	403	vBValMR10Z_223	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07248.1	000394	Gp5_OB+Lysozyme	601	VmeM32_00262	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37567.1	000394	Gp5_OB+Lysozyme	419	pp2_335	Vibriophage phi-pp2	GCA_002630725.1
SOK58992.1	000394	Gp5_OB+Lysozyme	311	g184	Yersinia phage fHe-Yen9-03	GCA_002990515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK59044.1	000394	Gp5_OB+Lysozyme	162	g236c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59045.1	000394	Gp5_OB+Lysozyme	893	g237c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58457.1	000394	Gp5_OB+Lysozyme	311	g180	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58509.1	000394	Gp5_OB+Lysozyme	162	g232c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58510.1	000394	Gp5_OB+Lysozyme	893	g233c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMM44850.1	000395	Gp5_OB	424	SP15_051	Bacillus phage SP-15	GCA_001754685.1
AXH72914.1	000395	Gp5_OB	587	-	Myoviridae sp.	GCA_003657725.1
AGH26191.1	000395	Gp5_OB	289	CPMG_00090	Prochlorococcus phage MED4-213	GCA_000904535.1
QCG76015.1	000395	Gp5_OB	477	EST35_0133	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44204.1	000395	Gp5_OB	476	PBI_SCTP2_189	Salicola phage SCTP-2	GCA_002625545.1
QAU04563.1	000395	Gp5_OB	335	ValB1MD_282	Vibrio phage ValB1MD	GCA_004138815.1
APU01492.1	000396	Lysozyme-GPW_gp25	142	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28801.1	000396	Lysozyme-GPW_gp25	142	AP1_0094	Aeromonas phage AP1	GCA_014183365.1
ATI17405.1	000396	Lysozyme-GPW_gp25	142	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00190.1	000396	Lysozyme-GPW_gp25	142	HWB28_gp362	Aeromonas phage AS-zj	GCA_002627665.1
AUE22733.1	000396	Lysozyme-GPW_gp25	140	Ah1_00215	Aeromonas phage Ah1	GCA_002957415.1
QAX98454.1	000396	Lysozyme-GPW_gp25	140	ASfcp2_112	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97845.1	000396	Lysozyme-GPW_gp25	142	ASswx1_202	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01307.1	000396	Lysozyme-GPW_gp25	142	ASwh1_244	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39555.1	000396	Lysozyme-GPW_gp25	142	CC2_333	Aeromonas phage CC2	GCA_000903495.1
ADQ52912.1	000396	Lysozyme-GPW_gp25	140	PX29p193	Aeromonas phage PX29	GCA_000920195.1
ADM80179.1	000396	Lysozyme-GPW_gp25	140	phiAS5_ORF0336	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53113.1	000396	Lysozyme-GPW_gp25	142	65p105	Aeromonas virus 65	GCA_000893255.1
AAQ17864.1	000396	Lysozyme-GPW_gp25	140	25	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94964.1	000396	Lysozyme-GPW_gp25	129	FDI40_gp182	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63635.1	000396	Lysozyme-GPW_gp25	120	CP21_173	Campylobacter virus CP21	GCA_000902535.1
ANS06066.1	000396	Lysozyme-GPW_gp25	130	ABCD_0109	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64902.1	000396	Lysozyme-GPW_gp25	141	S13_103	Cronobacter phage S13	GCA_001503575.1
AFC21682.1	000396	Lysozyme-GPW_gp25	129	GAP32_232	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97119.1	000396	Lysozyme-GPW_gp25	130	E_111	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56933.1	000396	Lysozyme-GPW_gp25	137	CPXG_00130	Cyanophage P-RSM6	GCA_000906155.1
AJK27524.1	000396	Lysozyme-GPW_gp25	136	PTIM40_97	Cyanophage P-TIM40	GCA_001470935.1
AOO14283.1	000396	Lysozyme-GPW_gp25	145	Sn110110_089	Cyanophage S-RIM14	GCA_002599065.1
AOO14932.1	000396	Lysozyme-GPW_gp25	145	W1230910_086	Cyanophage S-RIM14	GCA_002599125.1
AMO43108.1	000396	Lysozyme-GPW_gp25	130	R1080702_099	Cyanophage S-RIM32	GCA_001754165.1
AMO43335.1	000396	Lysozyme-GPW_gp25	130	W270710_091	Cyanophage S-RIM44	GCA_002599145.1
AOO11568.1	000396	Lysozyme-GPW_gp25	130	ES420910_087	Cyanophage S-RIM44	GCA_002599165.1
AOO11807.1	000396	Lysozyme-GPW_gp25	130	Np050604_091	Cyanophage S-RIM44	GCA_002599185.1
AOO12033.1	000396	Lysozyme-GPW_gp25	130	Np200711_087	Cyanophage S-RIM44	GCA_002599205.1
AOO12269.1	000396	Lysozyme-GPW_gp25	130	Np420711_087	Cyanophage S-RIM44	GCA_002599225.1
AOO12508.1	000396	Lysozyme-GPW_gp25	130	Sn080709_091	Cyanophage S-RIM44	GCA_002599245.1
AOO12734.1	000396	Lysozyme-GPW_gp25	130	Sn130910_087	Cyanophage S-RIM44	GCA_002599265.1
AOO12974.1	000396	Lysozyme-GPW_gp25	130	W2100709_092	Cyanophage S-RIM44	GCA_002599285.1
AGH07716.1	000396	Lysozyme-GPW_gp25	138	CYVG_00273	Cyanophage S-SSM6a	GCA_002710385.1
AGG54301.1	000396	Lysozyme-GPW_gp25	139	CYWG_00017	Cyanophage S-SSM6b	GCA_002710425.1
AXG67157.1	000396	Lysozyme-GPW_gp25	140	AD1_113	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79906.1	000396	Lysozyme-GPW_gp25	137	JA11_101	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66505.1	000396	Lysozyme-GPW_gp25	137	JA13_102	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66830.1	000396	Lysozyme-GPW_gp25	137	JA29_104	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67475.1	000396	Lysozyme-GPW_gp25	137	JA33_101	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08390.1	000396	Lysozyme-GPW_gp25	140	Alexandra_118	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58754.1	000396	Lysozyme-GPW_gp25	139	Y3_114	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28588.1	000396	Lysozyme-GPW_gp25	116	YOLO5WAG_106	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14475.1	000396	Lysozyme-GPW_gp25	131	PBI_121Q_585	Escherichia phage 121Q	GCA_000926855.1
QAY00473.1	000396	Lysozyme-GPW_gp25	131	Ecwhy1_194	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35216.1	000396	Lysozyme-GPW_gp25	131	ACQ29_gp536	Escherichia phage PBECO4	GCA_001041035.1
BBM62147.1	000396	Lysozyme-GPW_gp25	131	EO157G_5580	Escherichia phage SP27	GCA_008033345.1
AXC36788.1	000396	Lysozyme-GPW_gp25	131	-	Escherichia phage UB	GCA_003341455.1
ARM70747.1	000396	Lysozyme-GPW_gp25	132	phiC120_c40	Escherichia phage phiC120	GCA_002621185.1
QBO61828.1	000396	Lysozyme-GPW_gp25	131	G17_00339	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13872.1	000396	Lysozyme-GPW_gp25	131	vBEcoMphAPEC6_gp243	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80459.1	000396	Lysozyme-GPW_gp25	131	PSLUR01_00482	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78631.1	000396	Lysozyme-GPW_gp25	130	RB43ORF109w	Escherichia virus RB43	GCA_000863505.1
AFA44345.1	000396	Lysozyme-GPW_gp25	129	RaK2_00072	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72685.1	000396	Lysozyme-GPW_gp25	123	-	Myoviridae sp.	GCA_003657725.1
QHJ79037.1	000396	Lysozyme-GPW_gp25	144	-	Myoviridae sp.	GCA_012593985.1
QIG65718.1	000396	Lysozyme-GPW_gp25	138	phiOC_p052	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43803.1	000396	Lysozyme-GPW_gp25	129	CBB_238	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38309.1	000396	Lysozyme-GPW_gp25	166	BN7874_140	Phage NCTB	GCA_900092385.1
AGH26138.1	000396	Lysozyme-GPW_gp25	129	CPMG_00037	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44487.1	000396	Lysozyme-GPW_gp25	133	PSSM2_109	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12161.1	000396	Lysozyme-GPW_gp25	133	PRTG_00003	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93627.1	000396	Lysozyme-GPW_gp25	133	AVU42_gp084	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99193.1	000396	Lysozyme-GPW_gp25	130	Syn1_092	Prochlorococcus phage Syn1	GCA_000892495.1
AFH14762.1	000396	Lysozyme-GPW_gp25	129	Lu11_0225	Pseudomonas phage Lu11	GCA_000897175.1
QHJ85935.1	000396	Lysozyme-GPW_gp25	144	KKIINIFJ_00023	Pseudomonas phage PN05	GCA_009931935.1
QHJ86084.1	000396	Lysozyme-GPW_gp25	122	KKIINIFJ_00172	Pseudomonas phage PN05	GCA_009931935.1
AGS82113.1	000396	Lysozyme-GPW_gp25	132	PaBG_00239	Pseudomonas phage PaBG	GCA_000912555.1
QCG76012.1	000396	Lysozyme-GPW_gp25	130	EST35_0130	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44253.1	000396	Lysozyme-GPW_gp25	124	PBI_SCTP2_238	Salicola phage SCTP-2	GCA_002625545.1
QCW18955.1	000396	Lysozyme-GPW_gp25	130	7t3_0434	Salmonella phage 7t3	GCA_006083215.1
AZU98208.1	000396	Lysozyme-GPW_gp25	130	CPT_Munch_264	Salmonella phage Munch	GCA_004015485.1
QIG62776.1	000396	Lysozyme-GPW_gp25	130	SEPL_163	Salmonella phage SE_PL	GCA_011067555.1
AQW88762.1	000396	Lysozyme-GPW_gp25	129	BF_0237	Serratia phage BF	GCA_002619745.1
AGR47774.1	000396	Lysozyme-GPW_gp25	134	SmphiM12_142	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13002.1	000396	Lysozyme-GPW_gp25	134	PHIM19_96	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12642.1	000396	Lysozyme-GPW_gp25	134	PHIM7_95	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13374.1	000396	Lysozyme-GPW_gp25	134	PHIN3_109	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30593.1	000396	Lysozyme-GPW_gp25	134	Syn7803US37_116	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54869.1	000396	Lysozyme-GPW_gp25	130	b23_0255	Synechococcus phage B23	GCA_009745195.1
QGT54504.1	000396	Lysozyme-GPW_gp25	130	b3_0262	Synechococcus phage B3	GCA_009745215.1
ASR76154.1	000396	Lysozyme-GPW_gp25	119	PBI_BELLAMY_109	Synechococcus phage Bellamy	GCA_002627525.1
QCW22833.1	000396	Lysozyme-GPW_gp25	133	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50592.1	000396	Lysozyme-GPW_gp25	130	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50499.1	000396	Lysozyme-GPW_gp25	133	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59548.1	000396	Lysozyme-GPW_gp25	130	S330809_087	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59310.1	000396	Lysozyme-GPW_gp25	130	C440309_087	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59786.1	000396	Lysozyme-GPW_gp25	130	N231010_087	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70598.1	000396	Lysozyme-GPW_gp25	133	HOU04_gp199	Synechococcus phage S-T4	GCA_003443335.1
QJT70094.1	000396	Lysozyme-GPW_gp25	133	SynMITS9220M01_081	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64409.1	000396	Lysozyme-GPW_gp25	139	KVP40.0340	Vibrio phage KVP40	GCA_000843785.1
QIW90354.1	000396	Lysozyme-GPW_gp25	139	GCAPEGMB_00007	Vibrio phage V07	GCA_012361095.1
QIW91075.1	000396	Lysozyme-GPW_gp25	139	COHAPHLL_00212	Vibrio phage V09	GCA_012361135.1
QHJ74522.1	000396	Lysozyme-GPW_gp25	139	VH12019_00222	Vibrio phage VH1_2019	GCA_009931825.1
AGB06981.1	000396	Lysozyme-GPW_gp25	139	CF80_gp194	Vibrio phage VH7D	GCA_000914495.1
QBX06133.1	000396	Lysozyme-GPW_gp25	139	ValB1HC_179	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04564.1	000396	Lysozyme-GPW_gp25	118	ValB1MD_284	Vibrio phage ValB1MD	GCA_004138815.1
AJT61145.1	000396	Lysozyme-GPW_gp25	139	AVU32_gp304	Vibrio phage ValKK3	GCA_001501635.1
AGN30013.1	000396	Lysozyme-GPW_gp25	139	VPFG_00005	Vibrio phage nt-1	GCA_000910195.2
ALP47140.1	000396	Lysozyme-GPW_gp25	139	phiGrn1_0074	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47527.1	000396	Lysozyme-GPW_gp25	139	phiST2_0206	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54758.1	000396	Lysozyme-GPW_gp25	139	vBValMR10Z_218	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07049.1	000396	Lysozyme-GPW_gp25	142	VmeM32_00058	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37572.1	000396	Lysozyme-GPW_gp25	139	pp2_340	Vibriophage phi-pp2	GCA_002630725.1
BBA65471.1	000396	Lysozyme-GPW_gp25	125	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96480.1	000396	Lysozyme-GPW_gp25	79	Xoosp13_294	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59043.1	000396	Lysozyme-GPW_gp25	129	g235c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58508.1	000396	Lysozyme-GPW_gp25	129	g231c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70305.1	000397	SIG+Lysozyme	251	CF8_0137	Aeromonas phage CF8	GCA_006384595.2
QDJ97282.1	000397	SIG+Lysozyme	252	D6_0122	Aeromonas phage D6	GCA_007051205.2
QDH47107.1	000397	SIG+Lysozyme	252	LAh10_54	Aeromonas phage LAh10	GCA_006863975.1
QDJ96899.1	000397	SIG+Lysozyme	255	PS1_0140	Aeromonas phage PS1	GCA_007051165.2
QFR59529.1	000397	SIG+Lysozyme	255	PS2_0138	Aeromonas phage PS2	GCA_009388305.2
AFO71398.1	000397	SIG+Lysozyme	284	CR5_178	Cronobacter phage CR5	GCA_000910235.1
QBZ70670.1	000397	SIG+Lysozyme	264	pETSU_089	Edwardsiella virus pEt-SU	GCA_004800915.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMR59848.1	000397	SIG+Lysozyme	240	SEGD1_201	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07610.1	000397	SIG+Lysozyme	285	DERBICUS_184	Erwinia phage Derbicus	GCA_004521655.1
AHI60179.1	000397	SIG+Lysozyme	255	Ea357_029	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49846.1	000397	SIG+Lysozyme	254	MACHINA_208	Erwinia phage Machina	GCA_002758035.1
AGX01767.1	000397	SIG+Lysozyme	232	CF95_gp045	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07137.1	000397	SIG+Lysozyme	255	REBECCA_29	Erwinia phage Rebecca	GCA_004521635.1
AXF51348.1	000397	SIG+Lysozyme	235	WELLINGTON_222	Erwinia phage Wellington	GCA_003344985.1
AFQ96665.1	000397	SIG+Lysozyme	238	G173_gp120	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48231.1	000397	SIG+Lysozyme	239	ASESINO_218	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85817.1	000397	SIG+Lysozyme	255	BOSOLAPHORUS_29	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48503.1	000397	SIG+Lysozyme	256	CAITLIN_208	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48781.1	000397	SIG+Lysozyme	256	CHRISDB_219	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52127.1	000397	SIG+Lysozyme	255	DM_29	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86137.1	000397	SIG+Lysozyme	255	DESERTFOX_29	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49034.1	000397	SIG+Lysozyme	285	EARLPHILLIPIV_185	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49290.1	000397	SIG+Lysozyme	254	HUXLEY_208	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03811.1	000397	SIG+Lysozyme	232	JOAD_104	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49575.1	000397	SIG+Lysozyme	235	KWAN_223	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86457.1	000397	SIG+Lysozyme	255	MADMEL_29	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86778.1	000397	SIG+Lysozyme	255	MORTIMER_29	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50118.1	000397	SIG+Lysozyme	254	PARSHIK_209	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50382.1	000397	SIG+Lysozyme	283	PHOBOS_192	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51810.1	000397	SIG+Lysozyme	255	RAY_29	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03566.1	000397	SIG+Lysozyme	232	RISINGSUN_104	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51492.1	000397	SIG+Lysozyme	255	SIMMY50_30	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64839.1	000397	SIG+Lysozyme	255	SPECIALG_29	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50645.1	000397	SIG+Lysozyme	238	STRATTON_220	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86039.1	000397	SIG+Lysozyme	240	ACEC001_1960	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QGH71985.1	000397	SIG+Lysozyme	269	N1M2_122	Klebsiella phage N1M2	GCA_010092605.1
QMP24020.1	000397	SIG+Lysozyme	253	-	Proteus phage 10	GCA_014071245.1
ANM44938.1	000397	SIG+Lysozyme	260	KTN4_180	Pseudomonas phage KTN4	GCA_002607225.1
AEV89586.1	000397	SIG+Lysozyme	255	OBP_149	Pseudomonas phage OBP	GCA_000896635.1
QBX32324.1	000397	SIG+Lysozyme	259	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03586.1	000397	SIG+Lysozyme	266	163	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02724.1	000397	SIG+Lysozyme	258	PSA21_198	Pseudomonas phage Psa21	GCA_004340405.1
ATN94776.1	000397	SIG+Lysozyme	260	SL2_199	Pseudomonas phage SL2	GCA_002956015.1
QJB22816.1	000397	SIG+Lysozyme	260	fnug_173	Pseudomonas phage fnug	GCA_012837215.1
QEM41897.1	000397	SIG+Lysozyme	259	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83045.1	000397	SIG+Lysozyme	260	PHIKZ144	Pseudomonas virus phiKZ	GCA_000842965.1
QNI20887.1	000397	SIG+Lysozyme	240	-	Salmonella phage JN03	GCA_014319805.1
AWN09144.1	000397	SIG+Lysozyme	242	MLDJOKPK_00242	Salmonella phage SPAsTU	GCA_003183805.1
AEP84031.1	000397	SIG+Lysozyme	240	SPN3US_0198	Salmonella phage SPN3US	GCA_001042275.1
QKE54343.1	000397	SIG+Lysozyme	260	ACSA002_0290	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65620.1	000397	SIG+Lysozyme	123	2050HW_00285	Serratia phage 2050HW	GCA_002628125.1
QDB71048.1	000397	SIG+Lysozyme	222	CPT_Moabite_016	Serratia phage Moabite	GCA_006384735.1
QFP93147.1	000397	SIG+Lysozyme	219	-	Serratia phage PCH45	GCA_009187865.1
AQT28075.1	000397	SIG+Lysozyme	295	pVa21_134	Vibrio phage pVa-21	GCA_002619305.1
AND75168.1	000398	PG_binding+Muraidase	237	ME3_7	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABY63058.1	000398	PG_binding+Muraidase	262	201phi2-1p229	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77309.1	000398	PG_binding+Muraidase	281	NOXIFER_140	Pseudomonas phage Noxifer	GCA_002625005.1
ARV76848.1	000398	PG_binding+Muraidase	270	PHABIO_217	Pseudomonas phage Phabio	GCA_002624965.1
BAW19239.1	000398	PG_binding+Muraidase	281	FDH28_gp156	Ralstonia phage RP12	GCA_002617345.1
BAW19525.1	000398	PG_binding+Muraidase	281	-	Ralstonia phage RP31	GCA_002617365.1
BAS04883.1	000398	PG_binding+Muraidase	264	AVU11_gp091	Ralstonia phage RSF1	GCA_001500875.1
BAQ02612.1	000398	PG_binding+Muraidase	264	AVU38_gp084	Ralstonia phage RSL2	GCA_001503055.1
ATA65621.1	000398	PG_binding+Muraidase	85	2050HW_00286	Serratia phage 2050HW	GCA_002628125.1
APU01498.1	000399	Base-plate-Lysozyme	415	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28958.1	000399	Base-plate-Lysozyme	412	AP1_0251	Aeromonas phage AP1	GCA_014183365.1
ATI17399.1	000399	Base-plate-Lysozyme	412	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00196.1	000399	Base-plate-Lysozyme	412	HWB28_gp356	Aeromonas phage AS-zj	GCA_002627665.1
AUE22728.1	000399	Base-plate-Lysozyme	156	Ah1_00210	Aeromonas phage Ah1	GCA_002957415.1
AUE22729.1	000399	Base-plate-Lysozyme	252	Ah1_00211	Aeromonas phage Ah1	GCA_002957415.1
AFN39427.1	000399	Base-plate-Lysozyme	412	CC2_339	Aeromonas phage CC2	GCA_000903495.1
ADQ52908.1	000399	Base-plate-Lysozyme	387	PX29p189	Aeromonas phage PX29	GCA_000920195.1
ADM80175.1	000399	Base-plate-Lysozyme	408	phiAS5_ORF0332	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53119.1	000399	Base-plate-Lysozyme	366	65p111	Aeromonas virus 65	GCA_000893255.1
AAQ17860.1	000399	Base-plate-Lysozyme	408	Aeh1ORF194w	Aeromonas virus Aeh1	GCA_000843245.1
AIA64957.1	000399	Base-plate-Lysozyme	385	S13_158	Cronobacter phage S13	GCA_001503575.1
AGH57006.1	000399	Base-plate-Lysozyme	542	CPXG_00203	Cyanophage P-RSM6	GCA_000906155.1
AJK27449.1	000399	Base-plate-Lysozyme	468	PTIM40_22	Cyanophage P-TIM40	GCA_001470935.1
AOO14207.1	000399	Base-plate-Lysozyme	596	Sn110110_013	Cyanophage S-RIM14	GCA_002599065.1
AOO14859.1	000399	Base-plate-Lysozyme	596	W1230910_013	Cyanophage S-RIM14	GCA_002599125.1
AMO43027.1	000399	Base-plate-Lysozyme	464	R1080702_012	Cyanophage S-RIM32	GCA_001754165.1
AMO43258.1	000399	Base-plate-Lysozyme	465	W270710_013	Cyanophage S-RIM44	GCA_002599145.1
AOO11495.1	000399	Base-plate-Lysozyme	465	ES420910_013	Cyanophage S-RIM44	GCA_002599165.1
AOO11730.1	000399	Base-plate-Lysozyme	465	Np050604_013	Cyanophage S-RIM44	GCA_002599185.1
AOO11960.1	000399	Base-plate-Lysozyme	465	Np200711_013	Cyanophage S-RIM44	GCA_002599205.1
AOO12196.1	000399	Base-plate-Lysozyme	465	Np420711_013	Cyanophage S-RIM44	GCA_002599225.1
AOO12431.1	000399	Base-plate-Lysozyme	465	Sn080709_013	Cyanophage S-RIM44	GCA_002599245.1
AOO12661.1	000399	Base-plate-Lysozyme	465	Sn130910_013	Cyanophage S-RIM44	GCA_002599265.1
AOO12896.1	000399	Base-plate-Lysozyme	465	W2100709_013	Cyanophage S-RIM44	GCA_002599285.1
AGH07640.1	000399	Base-plate-Lysozyme	470	CYVG_00197	Cyanophage S-SSM6a	GCA_002710385.1
AGG54358.1	000399	Base-plate-Lysozyme	446	CYWG_00074	Cyanophage S-SSM6b	GCA_002710425.1
QHJ78977.1	000399	Base-plate-Lysozyme	410	-	Myoviridae sp.	GCA_012593985.1
QIG65730.1	000399	Base-plate-Lysozyme	546	phiOC_p065	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AAX44396.1	000399	Base-plate-Lysozyme	420	PSSM2_018	Prochlorococcus phage P-SSM2	GCA_000859585.1
AIR93400.1	000399	Base-plate-Lysozyme	461	AVU42_gp014	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99116.1	000399	Base-plate-Lysozyme	465	Syn1_014	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47782.1	000399	Base-plate-Lysozyme	416	SmphiM12_150	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13006.1	000399	Base-plate-Lysozyme	416	PHIM19_100	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12646.1	000399	Base-plate-Lysozyme	416	PHIM7_99	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13378.1	000399	Base-plate-Lysozyme	416	PHIN3_113	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30489.1	000399	Base-plate-Lysozyme	449	Syn7803US37_12	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54639.1	000399	Base-plate-Lysozyme	442	b23_0011	Synechococcus phage B23	GCA_009745195.1
QGT54269.1	000399	Base-plate-Lysozyme	442	b3_0011	Synechococcus phage B3	GCA_009745215.1
ASR76061.1	000399	Base-plate-Lysozyme	449	PBI_BELLAMY_14	Synechococcus phage Bellamy	GCA_002627525.1
QCW22917.1	000399	Base-plate-Lysozyme	438	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59471.1	000399	Base-plate-Lysozyme	472	S330809_010	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59233.1	000399	Base-plate-Lysozyme	472	C440309_010	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59709.1	000399	Base-plate-Lysozyme	472	N231010_010	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70439.1	000399	Base-plate-Lysozyme	420	HOU04_gp040	Synechococcus phage S-T4	GCA_003443335.1
QJT70029.1	000399	Base-plate-Lysozyme	446	SynMITS9220M01_013	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64403.1	000399	Base-plate-Lysozyme	423	KVP40.0334	Vibrio phage KVP40	GCA_000843785.1
QIW90348.1	000399	Base-plate-Lysozyme	423	GCAPEGMB_00001	Vibrio phage V07	GCA_012361095.1
QIW91081.1	000399	Base-plate-Lysozyme	423	COHAPHLL_00218	Vibrio phage V09	GCA_012361135.1
QHJ74516.1	000399	Base-plate-Lysozyme	423	VH12019_00216	Vibrio phage VH1_2019	GCA_009931825.1
AGB06977.1	000399	Base-plate-Lysozyme	423	CF80_gp190	Vibrio phage VH7D	GCA_000914495.1
QBX06139.1	000399	Base-plate-Lysozyme	423	ValB1HC_185	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61151.1	000399	Base-plate-Lysozyme	423	AVU32_gp310	Vibrio phage ValKK3	GCA_001501635.1
AGN30385.1	000399	Base-plate-Lysozyme	423	VPFG_00388	Vibrio phage nt-1	GCA_000910195.2
ALP46991.1	000399	Base-plate-Lysozyme	423	phiGrn1_0380	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47372.1	000399	Base-plate-Lysozyme	423	phiST2_0200	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54764.1	000399	Base-plate-Lysozyme	423	vBValMR10Z_224	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07249.1	000399	Base-plate-Lysozyme	404	VmeM32_00263	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37566.1	000399	Base-plate-Lysozyme	423	pp2_334	Vibriophage phi-pp2	GCA_002630725.1
QDH83648.1	000400	Lysozyme+PG-binding	498	H1O15_gp140	Achromobacter phage Motura	GCA_006964305.1
QDH83710.1	000400	Lysozyme+PG-binding	216	H1O15_gp118	Achromobacter phage Motura	GCA_006964305.1
QDB70398.1	000400	Lysozyme+PG-binding	317	CF8_0229	Aeromonas phage CF8	GCA_006384595.2
QDJ97395.1	000400	Lysozyme+PG-binding	290	D6_0236	Aeromonas phage D6	GCA_007051205.2
QDH47097.1	000400	Lysozyme+PG-binding	290	LAh10_150	Aeromonas phage LAh10	GCA_006863975.1
QDJ96743.1	000400	Lysozyme+PG-binding	289	PS1_0232	Aeromonas phage PS1	GCA_007051165.2
QFR59376.1	000400	Lysozyme+PG-binding	289	PS2_0234	Aeromonas phage PS2	GCA_009388305.2
QBX06695.1	000400	Lysozyme+PG-binding	223	BcepSaruman_282	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74663.1	000400	Lysozyme+PG-binding	223	BcepSauron_283	Burkholderia phage BcepSauron	GCA_005394215.1
AFO71304.1	000400	Lysozyme+PG-binding	224	CR5_084	Cronobacter phage CR5	GCA_000910235.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBZ70781.1	000400	Lysozyme+PG-binding	289	pETSU_200	Edwardsiella virus pEt-SU	GCA_004800915.1
QBP07513.1	000400	Lysozyme+PG-binding	226	DERBICUS_87	Erwinia phage Derbicus	GCA_004521655.1
AHI60315.1	000400	Lysozyme+PG-binding	237	Ea357_164	Erwinia phage Ea35-70	GCA_000914635.1
AGX01799.1	000400	Lysozyme+PG-binding	225	CF95_gp077	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07274.1	000400	Lysozyme+PG-binding	237	REBECCA_167	Erwinia phage Rebecca	GCA_004521635.1
AUG85954.1	000400	Lysozyme+PG-binding	237	BOSOLAPHORUS_167	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52269.2	000400	Lysozyme+PG-binding	237	DM_171	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86273.1	000400	Lysozyme+PG-binding	237	DESERTFOX_166	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49091.1	000400	Lysozyme+PG-binding	224	EARLPHILLIPIV_87	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ASU03682.1	000400	Lysozyme+PG-binding	290	JOAD_233	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86595.1	000400	Lysozyme+PG-binding	237	MADMEL_167	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86919.1	000400	Lysozyme+PG-binding	237	MORTIMER_170	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50277.1	000400	Lysozyme+PG-binding	224	PHOBOS_87	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51946.1	000400	Lysozyme+PG-binding	237	RAY_165	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03439.1	000400	Lysozyme+PG-binding	294	RISINGSUN_231	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51630.1	000400	Lysozyme+PG-binding	237	SIMMY50_168	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64977.2	000400	Lysozyme+PG-binding	237	SPECIALG_167	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGH72087.1	000400	Lysozyme+PG-binding	288	N1M2_224	Klebsiella phage N1M2	GCA_010092605.1
QIG65812.1	000400	Lysozyme+PG-binding	427	phiOC_p147	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QGZ14516.1	000400	Lysozyme+PG-binding	284	HWC77_gp153	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27282.1	000400	Lysozyme+PG-binding	292	PPEV_gp188	Pseudomonas phage EL	GCA_000866825.1
AEV89716.1	000400	Lysozyme+PG-binding	328	OBP_279	Pseudomonas phage OBP	GCA_000896635.1
QHJ85920.1	000400	Lysozyme+PG-binding	212	KKIINIFJ_00008	Pseudomonas phage PN05	GCA_009931935.1
BAG41629.1	000400	Lysozyme+PG-binding	225	RSL1_ORF181	Ralstonia phage phiRSL1	GCA_000879455.1
QKE54472.1	000400	Lysozyme+PG-binding	240	ACSA002_1580	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65600.1	000400	Lysozyme+PG-binding	223	2050HW_00265	Serratia phage 2050HW	GCA_002628125.1
QDB71364.1	000400	Lysozyme+PG-binding	223	CPT_Moabite_334	Serratia phage Moabite	GCA_006384735.1
QFP93127.1	000400	Lysozyme+PG-binding	249	-	Serratia phage PCH45	GCA_009187865.1
AGR48034.1	000400	Lysozyme+PG-binding	210	SmphiM12_402	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13216.1	000400	Lysozyme+PG-binding	210	PHIM19_311	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12857.1	000400	Lysozyme+PG-binding	210	PHIM7_311	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13579.1	000400	Lysozyme+PG-binding	210	PHIN3_316	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54932.1	000400	Lysozyme+PG-binding	420	b23_0319	Synechococcus phage B23	GCA_009745195.1
QGT54567.1	000400	Lysozyme+PG-binding	420	b3_0326	Synechococcus phage B3	GCA_009745215.1
QAU04218.1	000400	Lysozyme+PG-binding	286	HWC03_gp063	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23142.1	000400	Lysozyme+PG-binding	284	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80998.1	000400	Lysozyme+PG-binding	284	Aphrodite1_0198	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70879.1	000400	Lysozyme+PG-binding	303	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47585.1	000400	Lysozyme+PG-binding	284	HWC35_gp191	Vibrio phage USC-1	GCA_006864065.1
QAU04575.1	000400	Lysozyme+PG-binding	288	ValB1MD_316	Vibrio phage ValB1MD	GCA_004138815.1
BAW98400.1	000400	Lysozyme+PG-binding	284	FDH33_gp191	Vibrio phage pTD1	GCA_002618825.1
QAX96928.1	000400	Lysozyme+PG-binding	294	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97233.1	000400	Lysozyme+PG-binding	294	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96292.1	000400	Lysozyme+PG-binding	294	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96610.1	000400	Lysozyme+PG-binding	294	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21129.1	000400	Lysozyme+PG-binding	304	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65420.1	000400	Lysozyme+PG-binding	211	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96442.1	000400	Lysozyme+PG-binding	213	Xoosp13_256	Xanthomonas phage Xoo-sp13	GCA_013364725.1
APU01783.1	000401	SIG+Lysozyme	175	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29100.1	000401	SIG+Lysozyme	175	AP1_0393	Aeromonas phage AP1	GCA_014183365.1
ATI17519.1	000401	SIG+Lysozyme	175	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00478.1	000401	SIG+Lysozyme	175	HWB28_gp074	Aeromonas phage AS-zj	GCA_002627665.1
AUE22807.1	000401	SIG+Lysozyme	174	Ah1_00289	Aeromonas phage Ah1	GCA_002957415.1
QAX98522.1	000401	SIG+Lysozyme	173	ASfcp2_186	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97959.1	000401	SIG+Lysozyme	175	ASswx1_317	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01184.1	000401	SIG+Lysozyme	169	ASwh1_119	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39489.1	000401	SIG+Lysozyme	175	CC2_214	Aeromonas phage CC2	GCA_000903495.1
ADQ52985.1	000401	SIG+Lysozyme	173	PX29p266	Aeromonas phage PX29	GCA_000920195.1
ADM79909.1	000401	SIG+Lysozyme	173	phiAS5_ORF0066	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53426.1	000401	SIG+Lysozyme	175	65p420	Aeromonas virus 65	GCA_000893255.1
AAQ17934.1	000401	SIG+Lysozyme	174	vs.1	Aeromonas virus Aeh1	GCA_000843245.1
ANS06003.1	000401	SIG+Lysozyme	215	ABCD_0148	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64828.1	000401	SIG+Lysozyme	178	S13_029	Cronobacter phage S13	GCA_001503575.1
AON97159.1	000401	SIG+Lysozyme	170	E_151	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70932.1	000401	SIG+Lysozyme	180	phiC120_c227	Escherichia phage phiC120	GCA_002621185.1
AAX78675.1	000401	SIG+Lysozyme	211	RB43ORF153c	Escherichia virus RB43	GCA_000863505.1
QHJ78834.1	000401	SIG+Lysozyme	172	-	Myoviridae sp.	GCA_012593985.1
AAQ64349.1	000401	SIG+Lysozyme	208	KVP40.0279.1	Vibrio phage KVP40	GCA_000843785.1
QIW90663.1	000401	SIG+Lysozyme	190	GCAPEGMB_00316	Vibrio phage V07	GCA_012361095.1
QIW91135.1	000401	SIG+Lysozyme	190	COHAPHLL_00299	Vibrio phage V09	GCA_012361135.1
QHJ74458.1	000401	SIG+Lysozyme	190	VH12019_00131	Vibrio phage VH1_2019	GCA_009931825.1
AGB06952.1	000401	SIG+Lysozyme	190	CF80_gp165	Vibrio phage VH7D	GCA_000914495.1
QBX06193.1	000401	SIG+Lysozyme	190	ValB1HC_240	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61210.1	000401	SIG+Lysozyme	190	AVU32_gp369	Vibrio phage ValKK3	GCA_001501635.1
AGN30326.1	000401	SIG+Lysozyme	186	VPFG_00328	Vibrio phage nt-1	GCA_000910195.2
ALP47078.1	000401	SIG+Lysozyme	190	phiGrn1_0012	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47458.1	000401	SIG+Lysozyme	190	phiST2_0144	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54818.1	000401	SIG+Lysozyme	190	vBValMR10Z_278	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07227.1	000401	SIG+Lysozyme	174	VmeM32_00241	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37510.1	000401	SIG+Lysozyme	190	pp2_277	Vibriophage phi-pp2	GCA_002630725.1
QDB70393.1	000402	Lysozyme+Neuromodulin	2354	CF8_0224	Aeromonas phage CF8	GCA_006384595.2
QDJ97392.1	000402	Lysozyme+Neuromodulin	2353	D6_0233	Aeromonas phage D6	GCA_007051205.2
QDH47008.1	000402	Lysozyme+Neuromodulin	2353	LAh10_147	Aeromonas phage LAh10	GCA_006863975.1
QDJ96737.1	000402	Lysozyme+Neuromodulin	2347	PS1_0226	Aeromonas phage PS1	GCA_007051165.2
QFR59370.1	000402	Lysozyme+Neuromodulin	2347	PS2_0228	Aeromonas phage PS2	GCA_009388305.2
QBZ70778.1	000402	Lysozyme+Neuromodulin	2433	pETSU_197	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60312.1	000402	Lysozyme+Neuromodulin	2238	Ea357_161	Erwinia phage Ea35-70	GCA_000914635.1
QBP07271.1	000402	Lysozyme+Neuromodulin	2234	REBECCA_164	Erwinia phage Rebecca	GCA_004521635.1
AUG85951.1	000402	Lysozyme+Neuromodulin	2234	BOSOLAPHORUS_164	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52266.1	000402	Lysozyme+Neuromodulin	2239	DM_168	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86270.1	000402	Lysozyme+Neuromodulin	2238	DESERTFOX_163	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03685.1	000402	Lysozyme+Neuromodulin	2561	JOAD_230	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86592.1	000402	Lysozyme+Neuromodulin	2236	MADMEL_164	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86916.1	000402	Lysozyme+Neuromodulin	2239	MORTIMER_167	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51943.1	000402	Lysozyme+Neuromodulin	2239	RAY_162	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03442.1	000402	Lysozyme+Neuromodulin	2561	RISINGSUN_228	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51627.1	000402	Lysozyme+Neuromodulin	2235	SIMMY50_165	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64974.1	000402	Lysozyme+Neuromodulin	2238	SPECIALG_164	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBO64023.1	000402	Lysozyme+Neuromodulin	2252	Goslar_00232	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72084.1	000402	Lysozyme+Neuromodulin	2395	N1M2_221	Klebsiella phage N1M2	GCA_010092605.1
QGZ14511.1	000402	Lysozyme+Neuromodulin	2356	HWC77_gp148	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24093.1	000402	Lysozyme+Neuromodulin	2034	-	Proteus phage 10	GCA_014071245.1
CAG27277.1	000402	Lysozyme+Neuromodulin	2543	PPEV_gp183	Pseudomonas phage EL	GCA_000866825.1
AEV89713.1	000402	Lysozyme+Neuromodulin	2432	OBP_276	Pseudomonas phage OBP	GCA_000896635.1
QKE54469.1	000402	Lysozyme+Neuromodulin	2216	ACSA002_1550	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QAU04223.1	000402	Lysozyme+Neuromodulin	2326	HWC03_gp068	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23139.1	000402	Lysozyme+Neuromodulin	2326	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80910.1	000402	Lysozyme+Neuromodulin	2351	Aphrodite1_0201	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47588.1	000402	Lysozyme+Neuromodulin	2326	HWC35_gp194	Vibrio phage USC-1	GCA_006864065.1
BAW98403.1	000402	Lysozyme+Neuromodulin	2324	FDH33_gp194	Vibrio phage pTD1	GCA_002618825.1
AFO71427.1	000403	Lysozyme	2474	CR5_207	Cronobacter phage CR5	GCA_000910235.1
AMR59891.1	000403	Lysozyme	2124	SEGD1_244	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07640.1	000403	Lysozyme	2479	DERBICUS_214	Erwinia phage Derbicus	GCA_004521655.1
ANZ49890.1	000403	Lysozyme	2463	MACHINA_252	Erwinia phage Machina	GCA_002758035.1
AXF51391.1	000403	Lysozyme	2434	WELLINGTON_265	Erwinia phage Wellington	GCA_003344985.1
AFQ96704.1	000403	Lysozyme	2382	G173_gp159	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48274.1	000403	Lysozyme	2379	ASESINO_261	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48546.1	000403	Lysozyme	2457	CAITLIN_251	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48824.1	000403	Lysozyme	2461	CHRISDB_262	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49064.1	000403	Lysozyme	2479	EARLPHILLIPIV_215	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49333.1	000403	Lysozyme	2463	HUXLEY_251	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49617.1	000403	Lysozyme	2434	KWAN_265	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50161.1	000403	Lysozyme	2463	PARSHIK_252	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50411.1	000403	Lysozyme	2470	PHOBOS_221	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50686.1	000403	Lysozyme	2381	STRATTON_261	Erwinia phage vB_EamM_Stratton	GCA_002600675.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QKN86080.1	000403	Lysozyme	2324	ACEC001_2370	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20924.1	000403	Lysozyme	2373	-	Salmonella phage JN03	GCA_014319805.1
AWN09113.2	000403	Lysozyme	2377	MLDJOKPK_00201	Salmonella phage SPAsTU	GCA_003183805.1
AEP84072.1	000403	Lysozyme	2372	SPN3US_0239	Salmonella phage SPN3US	GCA_001042275.1
AQT28106.1	000403	Lysozyme	2329	pVa21_165	Vibrio phage pVa-21	GCA_002619305.1
AMO43025.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	864	R1080702_010	Cyanophage S-RIM32	GCA_001754165.1
AMO43256.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	861	W270710_011	Cyanophage S-RIM44	GCA_002599145.1
AOO11493.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	870	ES420910_011	Cyanophage S-RIM44	GCA_002599165.1
AOO11728.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	861	Np050604_011	Cyanophage S-RIM44	GCA_002599185.1
AOO11958.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	855	Np200711_011	Cyanophage S-RIM44	GCA_002599205.1
AOO12194.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	855	Np420711_011	Cyanophage S-RIM44	GCA_002599225.1
AOO12429.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	861	Sn080709_011	Cyanophage S-RIM44	GCA_002599245.1
AOO12659.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	870	Sn130910_011	Cyanophage S-RIM44	GCA_002599265.1
AOO12894.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	861	W2100709_011	Cyanophage S-RIM44	GCA_002599285.1
ADO99114.1	000404	SIG+Gly-zipper_Omp+Phage_lysozyme	868	Syn1_012	Prochlorococcus phage Syn1	GCA_000892495.1
AJK27463.1	000405	SIG+Lysozyme	162	PTIM40_36	Cyanophage P-TIM40	GCA_001470935.1
AOO14395.1	000405	SIG+Lysozyme	189	Sn110110_202	Cyanophage S-RIM14	GCA_002599065.1
AOO15043.1	000405	SIG+Lysozyme	189	W1230910_198	Cyanophage S-RIM14	GCA_002599125.1
AMO43204.1	000405	SIG+Lysozyme	234	R1080702_195	Cyanophage S-RIM32	GCA_001754165.1
AMO43434.1	000405	SIG+Lysozyme	194	W270710_190	Cyanophage S-RIM44	GCA_002599145.1
AOO11678.1	000405	SIG+Lysozyme	199	ES420910_197	Cyanophage S-RIM44	GCA_002599165.1
AOO11906.1	000405	SIG+Lysozyme	194	Np050604_190	Cyanophage S-RIM44	GCA_002599185.1
AOO12144.1	000405	SIG+Lysozyme	198	Np200711_198	Cyanophage S-RIM44	GCA_002599205.1
AOO12379.1	000405	SIG+Lysozyme	196	Np420711_197	Cyanophage S-RIM44	GCA_002599225.1
AOO12607.1	000405	SIG+Lysozyme	194	Sn080709_190	Cyanophage S-RIM44	GCA_002599245.1
AOO12844.1	000405	SIG+Lysozyme	196	Sn130910_197	Cyanophage S-RIM44	GCA_002599265.1
AOO13073.1	000405	SIG+Lysozyme	194	W2100709_191	Cyanophage S-RIM44	GCA_002599285.1
AGG54394.1	000405	SIG+Lysozyme	185	CYWG_00110	Cyanophage S-SSM6b	GCA_002710425.1
ADO99293.1	000405	SIG+Lysozyme	229	Syn1_191	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30691.1	000405	SIG+Lysozyme	214	Syn7803US37_214	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23017.1	000405	SIG+Lysozyme	201	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50526.1	000405	SIG+Lysozyme	201	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70526.1	000405	SIG+Lysozyme	201	HOU04_gp127	Synechococcus phage S-T4	GCA_003443335.1
QJT70222.1	000405	SIG+Lysozyme	190	SynMITS9220M01_216	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG67168.1	000406	Lysozyme	631	AD1_124	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79917.1	000406	Lysozyme	627	JA11_112	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66516.1	000406	Lysozyme	627	JA13_113	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66841.1	000406	Lysozyme	627	JA29_115	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67486.1	000406	Lysozyme	627	JA33_112	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08401.1	000406	Lysozyme	631	Alexandra_129	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58765.1	000406	Lysozyme	631	Y3_125	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28603.1	000406	Lysozyme	629	YOLOSWAG_122	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38378.1	000406	Lysozyme	667	BN7874_206	Phage NCTB	GCA_900092385.1
ABY63103.1	000407	Lysozyme	2337	201phi2-1p276	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44979.1	000407	Lysozyme	2237	KTN4_221	Pseudomonas phage KTN4	GCA_002607225.1
ARV77366.1	000407	Lysozyme	2318	NOXIFER_197	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32370.1	000407	Lysozyme	1566	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32369.1	000407	Lysozyme	703	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76896.1	000407	Lysozyme	2326	PHABIO_265	Pseudomonas phage Phabio	GCA_002624965.1
AEH03636.1	000407	Lysozyme	2319	213	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02772.1	000407	Lysozyme	2336	PSA21_246	Pseudomonas phage Psa21	GCA_004340405.1
ATN94735.1	000407	Lysozyme	2237	SL2_158	Pseudomonas phage SL2	GCA_002956015.1
QJB22857.1	000407	Lysozyme	2237	fnug_214	Pseudomonas phage fnug	GCA_012837215.1
QEM41943.1	000407	Lysozyme	2256	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83082.1	000407	Lysozyme	2237	PHIKZ181	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67167.1	000408	Lysozyme	262	AD1_123	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79916.1	000408	Lysozyme	261	JA11_111	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66515.1	000408	Lysozyme	260	JA13_112	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66840.1	000408	Lysozyme	262	JA29_114	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67485.1	000408	Lysozyme	261	JA33_111	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08400.1	000408	Lysozyme	262	Alexandra_128	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58764.1	000408	Lysozyme	262	Y3_124	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28602.1	000408	Lysozyme	262	YOLOSWAG_121	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38376.1	000408	Lysozyme	275	BN7874_205	Phage NCTB	GCA_900092385.1
AFH14724.1	000408	Lysozyme	262	Lu11_0187	Pseudomonas phage Lu11	GCA_000897175.1
QHJ86083.1	000408	Lysozyme	197	KKIINIFJ_00171	Pseudomonas phage PN05	GCA_009931935.1
QKE11206.1	000408	Lysozyme	269	PaBG_00099	Pseudomonas phage PaBG	GCA_000912555.1
AGX01869.1	000409	Lysozyme	2222	CF95_gp147	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65431.1	000409	Lysozyme	2213	2050HW_00096	Serratia phage 2050HW	GCA_002628125.1
QDB71206.1	000409	Lysozyme	2213	CPT_Moabite_176	Serratia phage Moabite	GCA_006384735.1
QFP93041.1	000409	Lysozyme	2274	-	Serratia phage PCH45	GCA_009187865.1
AMO43029.1	000410	Lysozyme	363	R1080702_014	Cyanophage S-RIM32	GCA_001754165.1
AMO43260.1	000410	Lysozyme	359	W270710_015	Cyanophage S-RIM44	GCA_002599145.1
AOO11497.1	000410	Lysozyme	359	ES420910_015	Cyanophage S-RIM44	GCA_002599165.1
AOO11732.1	000410	Lysozyme	359	Np050604_015	Cyanophage S-RIM44	GCA_002599185.1
AOO11962.1	000410	Lysozyme	359	Np200711_015	Cyanophage S-RIM44	GCA_002599205.1
AOO12198.1	000410	Lysozyme	359	Np420711_015	Cyanophage S-RIM44	GCA_002599225.1
AOO12433.1	000410	Lysozyme	359	Sn080709_015	Cyanophage S-RIM44	GCA_002599245.1
AOO12663.1	000410	Lysozyme	359	Sn130910_015	Cyanophage S-RIM44	GCA_002599265.1
AOO12898.1	000410	Lysozyme	359	W2100709_015	Cyanophage S-RIM44	GCA_002599285.1
ADO99118.1	000410	Lysozyme	359	Syn1_016	Prochlorococcus phage Syn1	GCA_000892495.1
AYD80088.1	000411	SIG+Lysozyme	172	JA11_283	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66689.1	000411	SIG+Lysozyme	172	JA13_286	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67009.1	000411	SIG+Lysozyme	172	JA29_283	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67658.1	000411	SIG+Lysozyme	172	JA33_284	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08566.1	000411	SIG+Lysozyme	226	Alexandra_313	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58941.1	000411	SIG+Lysozyme	225	Y3_301	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28766.1	000411	SIG+Lysozyme	223	YOLOSWAG_296	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QGT54637.1	000412	TM+TM+Lysozyme	940	b23_0009	Synechococcus phage B23	GCA_009745195.1
QGT54267.1	000412	TM+TM+Lysozyme	938	b3_0009	Synechococcus phage B3	GCA_009745215.1
AGH57002.1	000413	Gp5_OB+Lysozyme	910	CPXG_00199	Cyanophage P-RSM6	GCA_000906155.1
AJK27459.1	000413	Gp5_OB+Lysozyme	865	PTIM40_32	Cyanophage P-TIM40	GCA_001470935.1
AOO14210.1	000413	Gp5_OB+Lysozyme	827	Sn110110_016	Cyanophage S-RIM14	GCA_002599065.1
AOO14862.1	000413	Gp5_OB+Lysozyme	827	W1230910_016	Cyanophage S-RIM14	GCA_002599125.1
AGG54355.1	000413	Gp5_OB+Lysozyme	830	CYWG_00071	Cyanophage S-SSM6b	GCA_002710425.1
AOO14206.1	000414	TM	1123	Sn110110_012	Cyanophage S-RIM14	GCA_002599065.1
ANS05959.1	000415	SIG+Phage-tail+Lysozyme	367	ABCD_0102	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97112.1	000415	SIG+Phage-tail+Lysozyme	367	E_104	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70750.1	000415	SIG+Phage-tail+Lysozyme	390	phiC120_c44	Escherichia phage phiC120	GCA_002621185.1
AAX78623.1	000415	SIG+Phage-tail+Lysozyme	367	RB43ORF101c	Escherichia virus RB43	GCA_000863505.1
AYD81263.1	000416	SIG+Lysozyme	212	SEA_JUSTBECAUSE_94	Streptomyces phage JustBecause	GCA_003613775.1
QJD53666.1	000416	SIG+Lysozyme	212	SEA_KELA_95	Streptomyces phage Kela	GCA_012934305.1
QBZ71995.1	000416	SIG+Lysozyme	210	SEA_KRADAL_97	Streptomyces phage Kradal	GCA_004799925.1
AXH66258.1	000416	SIG+Lysozyme	210	SEA_SATIS_97	Streptomyces phage Satis	GCA_003366315.1
AMS01316.1	000417	Lysozyme	141	AR9_g232	Bacillus phage AR9	GCA_001743835.1
ALN97966.1	000417	Lysozyme	139	Bp8pS_287	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99945.1	000417	Lysozyme	141	PBL_PBS1_123	Bacillus virus PBS1	GCA_002601325.1
CCE26263.1	000417	Lysozyme	155	g240	Yersinia phage phiR1-37	GCA_000895615.1
QDH83677.1	000418	GPW_gp25-Lysozyme	139	H1O15_gp134	Achromobacter phage Motura	GCA_006964305.1
QBX06674.1	000418	GPW_gp25-Lysozyme	142	BcepSaruman_261	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74644.1	000418	GPW_gp25-Lysozyme	142	BcepSauron_264	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41648.1	000418	GPW_gp25-Lysozyme	150	RSL1_ORF199	Ralstonia phage phiRSL1	GCA_000879455.1
AMS01288.1	000419	Lysozyme	1925	AR9_g204	Bacillus phage AR9	GCA_001743835.1
ALN97942.1	000419	Lysozyme	1797	Bp8pS_263	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99917.1	000419	Lysozyme	1925	PBL_PBS1_95	Bacillus virus PBS1	GCA_002601325.1
BAW19017.1	000420	OmpH+Lysozyme	2500	FDH28_gp043	Ralstonia phage RP12	GCA_002617345.1
BAW19303.1	000420	OmpH+Lysozyme	2502	-	Ralstonia phage RP31	GCA_002617365.1
BAS04834.2	000421	SIG+LPD14+ATPgrasp+TM+TM+Lysozyme	2123	AVU11_agp11	Ralstonia phage RSF1	GCA_001500875.1
BAQ02567.1	000421	SIG+LPD14+ATPgrasp+TM+TM+Lysozyme	2039	AVU38_gp039	Ralstonia phage RSL2	GCA_001503055.1
AOO14205.1	000422	TM+TM+TM+TM	1083	Sn110110_011	Cyanophage S-RIM14	GCA_002599065.1
AOO14857.1	000422	TM+TM+TM+TM	1083	W1230910_011	Cyanophage S-RIM14	GCA_002599125.1
QGT54638.1	000423	TM+TM+Lysozyme+PTSEIIA1	900	b23_0010	Synechococcus phage B23	GCA_009745195.1
QGT54268.1	000423	TM+TM+Lysozyme+PTSEIIA1	900	b3_0010	Synechococcus phage B3	GCA_009745215.1
BAW19140.1	000424	SIG+Lysozyme	219	FDH28_gp255	Ralstonia phage RP12	GCA_002617345.1
BAW19426.1	000424	SIG+Lysozyme	219	-	Ralstonia phage RP31	GCA_002617365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAS04847.2	000425	Lysozyme	143	AVU11_agp14	Ralstonia phage RSF1	GCA_001500875.1
BAQ02580.1	000425	Lysozyme	120	AVU38_gp052	Ralstonia phage RSL2	GCA_001503055.1
CCE26107.1	000000	SIG+Lysozyme	2553	g083	Yersinia phage phiR1-37	GCA_000895615.1
CCE26354.1	000000	SIG+Lysozyme	238	g331	Yersinia phage phiR1-37	GCA_000895615.1
AFH14587.1	000000	VanY+Lysozyme	1168	Lu11_0056	Pseudomonas phage Lu11	GCA_000897175.1
AMM44852.1	000000	GPW_gp25+Lysozyme	139	SP15_053	Bacillus phage SP-15	GCA_001754685.1
prev15ph1000000404	000000	GPW_gp25+Lysozyme	125	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG65729.1	000000	Peptidase-M15+Lysozyme	808	phiOC_p064	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AND75198.1	000000	Thermonuclease+PTSEIIA1+Lysozyme	2329	ME3_37	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QHJ86109.1	000000	SIG+Lysozyme	894	KKIINIFJ_00198	Pseudomonas phage PN05	GCA_009931935.1
QMV29166.1	000000	Lysozyme	94	AP1_0468	Aeromonas phage AP1	GCA_014183665.1
AGH26193.1	000000	Lysozyme	415	CPMG_00092	Prochlorococcus phage MED4-213	GCA_000904535.1
QHJ86082.1	000000	Lysozyme	103	KKIINIFJ_00170	Pseudomonas phage PN05	GCA_009931935.1
QDH50540.1	000000	Lysozyme	123	-	Synechococcus phage S-B43	GCA_006869725.1
QIW90818.1	000000	Lysozyme	254	GCAPEGMB_00503	Vibrio phage V07	GCA_012361095.1
prevph1000000199	000000	Lysozyme	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000221	000000	Lysozyme	405	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB71301.1	000000	Lysozyme	118	CPT_Moabite_271	Serratia phage Moabite	GCA_006384735.1
QIG65719.1	000000	Lysozyme	96	phiOC_p053	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMO43026.1	000426	Peptidase_M23	751	R1080702_011	Cyanophage S-RIM32	GCA_001754165.1
AMO43257.1	000426	Peptidase_M23	718	W270710_012	Cyanophage S-RIM44	GCA_002599145.1
AOO11494.1	000426	Peptidase_M23	720	ES420910_012	Cyanophage S-RIM44	GCA_002599165.1
AOO11729.1	000426	Peptidase_M23	718	Np050604_012	Cyanophage S-RIM44	GCA_002599185.1
AOO11959.1	000426	Peptidase_M23	720	Np200711_012	Cyanophage S-RIM44	GCA_002599205.1
AOO12195.1	000426	Peptidase_M23	720	Np420711_012	Cyanophage S-RIM44	GCA_002599225.1
AOO12430.1	000426	Peptidase_M23	718	Sn080709_012	Cyanophage S-RIM44	GCA_002599245.1
AOO12660.1	000426	Peptidase_M23	720	Sn130910_012	Cyanophage S-RIM44	GCA_002599265.1
AOO12895.1	000426	Peptidase_M23	718	W2100709_012	Cyanophage S-RIM44	GCA_002599285.1
ADO99115.1	000426	Peptidase_M23	721	Syn1_013	Prochlorococcus phage Syn1	GCA_000892495.1
QDH83674.1	000427	Cluster612_1clades	374	H1O15_gp137	Achromobacter phage Motura	GCA_006964305.1
QBX06672.1	000427	Cluster612_1clades	373	BcepSaruman_259	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74642.1	000427	Cluster612_1clades	373	BcepSauron_262	Burkholderia phage BcepSauron	GCA_005394215.1
AFH14584.1	000427	Cluster612_1clades	421	Lu11_0053	Pseudomonas phage Lu11	GCA_000897175.1
QHJ85965.1	000427	Cluster612_1clades	373	KKIINIFJ_00053	Pseudomonas phage PN05	GCA_009931935.1
AGS81952.1	000427	Cluster612_1clades	824	PaBG_00068	Pseudomonas phage PaBG	GCA_000912555.1
BAG41650.1	000427	Cluster612_1clades	373	RSL1_ORF201	Ralstonia phage phiRSL1	GCA_000879455.1
AXH70764.1	000428	Peptidase_M23	1905	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96768.1	000428	Peptidase_M23	1830	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97087.1	000428	Peptidase_M23	1830	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96133.1	000428	Peptidase_M23	1830	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96451.1	000428	Peptidase_M23	1830	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20973.1	000428	Peptidase_M23	1919	-	Vibrio phage vB_pir03	GCA_014319855.1
AIR93398.1	000429	TM+TM	623	AVU42_gp012	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76059.1	000429	TM+TM	799	PBI_BELLAMY_12	Synechococcus phage Bellamy	GCA_002627525.1
QCW22919.1	000429	TM+TM	831	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70027.1	000429	TM+TM	659	SynMITS9220M01_011	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH57007.1	000430	TM	779	CPXG_00204	Cyanophage P-RSM6	GCA_000906155.1
AOO14858.1	000430	TM	1205	W1230910_012	Cyanophage S-RIM14	GCA_002599125.1
AGG54359.1	000430	TM	809	CYWG_00075	Cyanophage S-SSM6b	GCA_002710425.1
QGY75133.1	000431	DDRP-beta	359	CF8_0228	Aeromonas phage CF8	GCA_006384595.2
QDJ97394.1	000431	DDRP-beta	1452	D6_0235	Aeromonas phage D6	GCA_007051205.2
QDH47010.1	000431	DDRP-beta	1452	LAh10_149	Aeromonas phage LAh10	GCA_006863975.1
QDJ96742.1	000431	DDRP-beta	370	PS1_0231	Aeromonas phage PS1	GCA_007051165.2
QFR59375.1	000431	DDRP-beta	370	PS2_0233	Aeromonas phage PS2	GCA_009388305.2
AMS01273.1	000431	DDRP-beta	1398	AR9_g189	Bacillus phage AR9	GCA_001743835.1
ALN97924.1	000431	DDRP-beta	256	Bp8pS_245	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99900.1	000431	DDRP-beta	348	PBI_PBS1_78	Bacillus virus PBS1	GCA_002601325.1
AFO71429.1	000431	DDRP-beta	1385	CR5_209	Cronobacter phage CR5	GCA_000910235.1
QBZ70780.1	000431	DDRP-beta	1441	pETSU_199	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59893.1	000431	DDRP-beta	1401	SEGD1_246	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07642.1	000431	DDRP-beta	1385	DERBICUS_216	Erwinia phage Derbicus	GCA_004521655.1
AHI60314.1	000431	DDRP-beta	1527	Ea357_163	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49892.1	000431	DDRP-beta	1395	MACHINA_254	Erwinia phage Machina	GCA_002758035.1
AGX01867.1	000431	DDRP-beta	1504	CF95_gp145	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07273.1	000431	DDRP-beta	1527	REBECCA_166	Erwinia phage Rebecca	GCA_004521635.1
AXF51393.1	000431	DDRP-beta	1390	WELLINGTON_267	Erwinia phage Wellington	GCA_003344985.1
AFQ96706.1	000431	DDRP-beta	1388	G173_gp161	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48276.1	000431	DDRP-beta	1387	ASESINO_263	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85953.1	000431	DDRP-beta	1527	BOSOLAPHORUS_166	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48548.1	000431	DDRP-beta	1389	CAITLIN_253	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48826.1	000431	DDRP-beta	1391	CHRISDB_264	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52268.1	000431	DDRP-beta	1527	DM_170	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86272.1	000431	DDRP-beta	1527	DESERTFOX_165	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49066.1	000431	DDRP-beta	1385	EARLPHILLIPIV_217	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49335.1	000431	DDRP-beta	1395	HUXLEY_253	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03683.1	000431	DDRP-beta	1438	JOAD_232	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49619.1	000431	DDRP-beta	1390	KWAN_267	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86594.1	000431	DDRP-beta	1527	MADMEL_166	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86918.1	000431	DDRP-beta	1527	MORTIMER_169	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50163.1	000431	DDRP-beta	1395	PARSHIK_254	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50413.1	000431	DDRP-beta	1385	PHOBOS_223	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51945.1	000431	DDRP-beta	1527	RAY_164	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03440.1	000431	DDRP-beta	1438	RISINGSUN_230	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51629.1	000431	DDRP-beta	1527	SIMMY50_167	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64976.1	000431	DDRP-beta	1527	SPECIALG_166	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50688.1	000431	DDRP-beta	1388	STRATTON_263	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86082.1	000431	DDRP-beta	1401	ACEC001_2390	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64020.1	000431	DDRP-beta	1448	Goslar_00228	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72086.1	000431	DDRP-beta	1446	N1M2_223	Klebsiella phage N1M2	GCA_010092605.1
QGZ14515.1	000431	DDRP-beta	1453	HWC77_gp152	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24095.1	000431	DDRP-beta	1542	-	Proteus phage 10	GCA_014071245.1
ABY63101.1	000431	DDRP-beta	1500	201phi2-1p273/274	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27281.1	000431	DDRP-beta	357	PPEV_gp187	Pseudomonas phage EL	GCA_000866825.1
ANM44977.1	000431	DDRP-beta	1451	KTN4_219	Pseudomonas phage KTN4	GCA_002607225.1
ARV77364.1	000431	DDRP-beta	1454	NOXIFER_195	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89715.1	000431	DDRP-beta	1450	OBP_278	Pseudomonas phage OBP	GCA_000896635.1
QBX32367.1	000431	DDRP-beta	1453	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76894.1	000431	DDRP-beta	1469	PHABIO_263	Pseudomonas phage Phabio	GCA_002624965.1
AEH03632.1	000431	DDRP-beta	379	209	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02770.1	000431	DDRP-beta	1492	PSA21_244	Pseudomonas phage Psa21	GCA_004340405.1
ATN94737.1	000431	DDRP-beta	1451	SL2_160	Pseudomonas phage SL2	GCA_002956015.1
QJB22855.1	000431	DDRP-beta	1451	fnug_212	Pseudomonas phage fnug	GCA_012837215.1
QEM41941.1	000431	DDRP-beta	1453	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83079.1	000431	DDRP-beta	1451	PHIKZ178	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19015.1	000431	DDRP-beta	1483	FDH28_gp041	Ralstonia phage RP12	GCA_002617345.1
BAW19301.1	000431	DDRP-beta	1482	-	Ralstonia phage RP31	GCA_002617365.1
BAS04832.1	000431	DDRP-beta	1473	AVU11_gp040	Ralstonia phage RSF1	GCA_001500875.1
BAQ02565.2	000431	DDRP-beta	1464	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20926.1	000431	DDRP-beta	1401	-	Salmonella phage JN03	GCA_014319805.1
AWN09111.1	000431	DDRP-beta	1390	MLDJOKPK_00199	Salmonella phage SPAsTU	GCA_003183805.1
AEP84074.1	000431	DDRP-beta	1401	SPN3US_0241	Salmonella phage SPN3US	GCA_001042275.1
QKE54471.1	000431	DDRP-beta	1565	ACSA002_1570	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65437.1	000431	DDRP-beta	363	2050HW_00102	Serratia phage 2050HW	GCA_002628125.1
QDB71208.1	000431	DDRP-beta	1503	CPT_Moabite_178	Serratia phage Moabite	GCA_006384735.1
QFP93043.1	000431	DDRP-beta	1536	-	Serratia phage PCH45	GCA_009187865.1
QAU04219.1	000431	DDRP-beta	1453	HWC03_gp064	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23141.1	000431	DDRP-beta	1449	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80913.1	000431	DDRP-beta	1449	Aphrodite1_0199	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70767.1	000431	DDRP-beta	375	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47586.1	000431	DDRP-beta	1449	HWC35_gp192	Vibrio phage USC-1	GCA_006864065.1
BAW98401.1	000431	DDRP-beta	1451	FDH33_gp192	Vibrio phage pTD1	GCA_002618825.1
AQT28108.1	000431	DDRP-beta	1384	pVa21_167	Vibrio phage pVa-21	GCA_002619305.1
QAX96761.1	000431	DDRP-beta	846	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97080.1	000431	DDRP-beta	846	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96126.1	000431	DDRP-beta	846	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96444.1	000431	DDRP-beta	846	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20983.1	000431	DDRP-beta	854	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26123.1	000431	DDRP-beta	1393	g099	Yersinia phage phiR1-37	GCA_000895615.1
QDB70396.1	000432	DDRP-beta	1079	CF8_0227	Aeromonas phage CF8	GCA_006384595.2
QDJ96740.1	000432	DDRP-beta	1084	PS1_0229	Aeromonas phage PS1	GCA_007051165.2
QFR59373.1	000432	DDRP-beta	1084	PS2_0231	Aeromonas phage PS2	GCA_009388305.2
ALN97929.1	000432	DDRP-beta	933	Bp8pS_250	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99902.1	000432	DDRP-beta	921	PBI_PBS1_80	Bacillus virus PBS1	GCA_002601325.1
CAG27280.1	000432	DDRP-beta	1067	PPEV_gp186	Pseudomonas phage EL	GCA_000866825.1
AEH03634.1	000432	DDRP-beta	1096	211	Pseudomonas phage PhiPA3	GCA_001502095.1
ATA65435.1	000432	DDRP-beta	1120	2050HW_00100	Serratia phage 2050HW	GCA_002628125.1
AXH70766.1	000432	DDRP-beta	964	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96764.1	000432	DDRP-beta	462	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97083.1	000432	DDRP-beta	462	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96129.1	000432	DDRP-beta	462	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96447.1	000432	DDRP-beta	462	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20979.1	000432	DDRP-beta	461	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70480.1	000433	DDRP-beta	704	CF8_0069	Aeromonas phage CF8	GCA_006384595.2
QDJ97220.1	000433	DDRP-beta	696	D6_0060	Aeromonas phage D6	GCA_007051205.2
QDH47028.1	000433	DDRP-beta	696	LAh10_225	Aeromonas phage LAh10	GCA_006863975.1
QDJ96828.1	000433	DDRP-beta	700	PS1_0069	Aeromonas phage PS1	GCA_007051165.2
QFR59458.1	000433	DDRP-beta	700	PS2_0067	Aeromonas phage PS2	GCA_009388305.2
AFO71255.1	000433	DDRP-beta	737	CR5_035	Cronobacter phage CR5	GCA_000910235.1
QBZ70598.1	000433	DDRP-beta	698	pETSU_017	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59686.1	000433	DDRP-beta	745	SEGD1_037	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07462.1	000433	DDRP-beta	737	DERBICUS_36	Erwinia phage Derbicus	GCA_004521655.1
AHI60398.1	000433	DDRP-beta	703	Ea357_245	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49688.1	000433	DDRP-beta	737	MACHINA_50	Erwinia phage Machina	GCA_002758035.1
AGX01730.1	000433	DDRP-beta	765	CF95_gp008	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07354.1	000433	DDRP-beta	731	REBECCA_249	Erwinia phage Rebecca	GCA_004521635.1
AXF51177.1	000433	DDRP-beta	739	WELLINGTON_46	Erwinia phage Wellington	GCA_003344985.1
AFQ96761.1	000433	DDRP-beta	746	G173_gp216	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48064.1	000433	DDRP-beta	746	ASESINO_51	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86036.1	000433	DDRP-beta	703	BOSOLAPHORUS_250	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48339.1	000433	DDRP-beta	737	CAITLIN_44	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48612.1	000433	DDRP-beta	737	CHRISDB_50	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52353.1	000433	DDRP-beta	703	DM_254	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86356.1	000433	DDRP-beta	703	DESERTFOX_249	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48886.1	000433	DDRP-beta	737	EARLPHILLIPIV_36	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49133.1	000433	DDRP-beta	737	HUXLEY_51	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03872.1	000433	DDRP-beta	703	JOAD_43	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49398.1	000433	DDRP-beta	739	KWAN_46	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86678.1	000433	DDRP-beta	703	MADMEL_251	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87002.1	000433	DDRP-beta	669	MORTIMER_254	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49961.1	000433	DDRP-beta	737	PARSHIK_52	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50226.1	000433	DDRP-beta	737	PHOBOS_36	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52028.1	000433	DDRP-beta	703	RAY_248	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03627.1	000433	DDRP-beta	703	RISINGSUN_43	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51711.1	000433	DDRP-beta	703	SIMMY50_253	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65063.1	000433	DDRP-beta	703	SPECIALG_252	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50474.1	000433	DDRP-beta	746	STRATTON_49	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85875.1	000433	DDRP-beta	745	ACEC001_0370	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63964.1	000433	DDRP-beta	722	Goslar_00171	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71914.1	000433	DDRP-beta	702	N1M2_51	Klebsiella phage N1M2	GCA_010092605.1
QGZ14383.1	000433	DDRP-beta	700	HWC77_gp020	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24165.1	000433	DDRP-beta	702	-	Proteus phage 10	GCA_014071245.1
ABY62961.1	000433	DDRP-beta	703	201phi2-1p129	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27132.1	000433	DDRP-beta	768	PPEV_gp038	Pseudomonas phage EL	GCA_000866825.1
ANM44853.1	000433	DDRP-beta	394	KTN4_095	Pseudomonas phage KTN4	GCA_002607225.1
ANM44854.1	000433	DDRP-beta	300	KTN4_096	Pseudomonas phage KTN4	GCA_002607225.1
ARV77236.1	000433	DDRP-beta	712	NOXIFER_65	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89510.1	000433	DDRP-beta	706	OBP_073	Pseudomonas phage OBP	GCA_000896635.1
QBX32220.1	000433	DDRP-beta	703	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76743.1	000433	DDRP-beta	729	PHABIO_112	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02604.1	000433	DDRP-beta	712	PSA21_75	Pseudomonas phage Psa21	GCA_004340405.1
ATN94859.1	000433	DDRP-beta	300	SL2_282	Pseudomonas phage SL2	GCA_002956015.1
ATN94860.1	000433	DDRP-beta	394	SL2_283	Pseudomonas phage SL2	GCA_002956015.1
QJB22730.1	000433	DDRP-beta	394	fnug_87	Pseudomonas phage fnug	GCA_012837215.1
QJB22731.1	000433	DDRP-beta	295	fnug_88	Pseudomonas phage fnug	GCA_012837215.1
QEM41798.1	000433	DDRP-beta	703	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82974.2	000433	DDRP-beta	295	PHIKZ073	Pseudomonas virus phiKZ	GCA_000842965.1
AAL82972.1	000433	DDRP-beta	394	PHIKZ071	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19249.1	000433	DDRP-beta	767	FDH28_gp146	Ralstonia phage RP12	GCA_002617345.1
BAW19535.1	000433	DDRP-beta	767	-	Ralstonia phage RP31	GCA_002617365.1
BAS05007.2	000433	DDRP-beta	723	AVU11_gp215	Ralstonia phage RSF1	GCA_001500875.1
BAQ02737.2	000433	DDRP-beta	720	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20750.1	000433	DDRP-beta	745	-	Salmonella phage JN03	GCA_014319805.1
AWN09061.1	000433	DDRP-beta	745	MLDJOKPK_00131	Salmonella phage SPAsTU	GCA_003183805.1
AEP83867.1	000433	DDRP-beta	745	SPN3US_0034	Salmonella phage SPN3US	GCA_001042275.1
QKE54573.1	000433	DDRP-beta	704	ACSA002_2570	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65662.1	000433	DDRP-beta	749	2050HW_00327	Serratia phage 2050HW	GCA_002628125.1
QDB71086.1	000433	DDRP-beta	749	CPT_Moabite_054	Serratia phage Moabite	GCA_006384735.1
QFP93054.1	000433	DDRP-beta	721	-	Serratia phage PCH45	GCA_009187865.1
QAU04353.1	000433	DDRP-beta	700	HWC03_gp198	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23223.1	000433	DDRP-beta	700	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80928.1	000433	DDRP-beta	700	Aphrodite1_0122	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70824.1	000433	DDRP-beta	688	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47505.1	000433	DDRP-beta	700	HWC35_gp111	Vibrio phage USC-1	GCA_006864065.1
BAW98324.1	000433	DDRP-beta	700	FDH33_gp115	Vibrio phage pTD1	GCA_002618825.1
AQT28161.1	000433	DDRP-beta	676	pVa21_220	Vibrio phage pVa-21	GCA_002619305.1
QAX96673.1	000433	DDRP-beta	690	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96991.1	000433	DDRP-beta	690	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96037.1	000433	DDRP-beta	690	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96355.1	000433	DDRP-beta	690	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21069.1	000433	DDRP-beta	735	-	Vibrio phage vB_pir03	GCA_014319855.1
AMS01173.1	000434	DDRP-beta	665	AR9_g089	Bacillus phage AR9	GCA_001743835.1
ALN97834.1	000434	DDRP-beta	394	Bp8pS_155	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97837.1	000434	DDRP-beta	250	Bp8pS_158	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00106.1	000434	DDRP-beta	665	PBI_PBS1_284	Bacillus virus PBS1	GCA_002601325.1
CCE26284.1	000434	DDRP-beta	658	g261	Yersinia phage phiR1-37	GCA_000895615.1
ASU03741.1	000435	DDRP-beta	232	JOAD_174	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03497.1	000435	DDRP-beta	232	RISINGSUN_173	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QKE54555.1	000000	DDRP-beta	164	ACSA002_2390	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QMV29133.1	000000	DDRP-beta	152	AP1_0430	Aeromonas phage AP1	GCA_014183365.1
ALN97927.1	000000	DDRP-beta	83	Bp8pS_248	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
APU01786.1	000436	ALP	169	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29106.1	000436	ALP	171	AP1_0399	Aeromonas phage AP1	GCA_014183365.1
ATI17517.1	000436	ALP	169	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00479.1	000436	ALP	171	HWB28_gp073	Aeromonas phage AS-zj	GCA_002627665.1
QAX97957.1	000436	ALP	171	ASswx1_315	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01187.1	000436	ALP	169	ASwh1_122	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39382.1	000436	ALP	171	CC2_217	Aeromonas phage CC2	GCA_000903495.1
ADQ53429.1	000436	ALP	139	65p423	Aeromonas virus 65	GCA_000893255.1
AIA64827.1	000436	ALP	175	S13_028	Cronobacter phage S13	GCA_001503575.1
ARM70782.1	000436	ALP	166	phiC120_c76	Escherichia phage phiC120	GCA_002621185.1
QHJ78835.1	000436	ALP	178	-	Myoviridae sp.	GCA_012593985.1
AAQ64131.1	000436	ALP	208	KVP40.0060	Vibrio phage KVP40	GCA_000843785.1
QIW90454.1	000436	ALP	208	GCAPEGMB_00107	Vibrio phage V07	GCA_012361095.1
QIW90975.1	000436	ALP	208	COHAPHLL_00112	Vibrio phage V09	GCA_012361135.1
QHJ74243.1	000436	ALP	208	VH12019_00324	Vibrio phage VH1_2019	GCA_009931825.1
AGB07067.1	000436	ALP	167	CF80_gp280	Vibrio phage VH7D	GCA_000914495.1
QBX06028.1	000436	ALP	167	ValB1HC_074	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04468.1	000436	ALP	168	ValB1MD_066	Vibrio phage ValB1MD	GCA_004138815.1
AJT61042.1	000436	ALP	167	AVU32_gp201	Vibrio phage ValKK3	GCA_001501635.1
AGN30109.1	000436	ALP	184	VPFG_00107	Vibrio phage nt-1	GCA_000910195.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALP47101.1	000436	ALP	168	phiGrn1_0175	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47482.1	000436	ALP	168	phiST2_0306	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54653.1	000436	ALP	167	vBValMR10Z_112	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37291.1	000436	ALP	167	pp2_058	Vibriophage phi-pp2	GCA_002630725.1
CCH63509.1	000437	ALP_N	328	CP21_047	Campylobacter virus CP21	GCA_000902535.1
QHJ86180.1	000437	ALP_N	131	KKIINIFJ_00270	Pseudomonas phage PN05	GCA_009931935.1
QAU04518.1	000437	ALP_N	320	ValB1MD_190	Vibrio phage ValB1MD	GCA_004138815.1
ABS83765.1	000438	ALP_N	330	0305phi8-36p207	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93764.1	000438	ALP_N	371	G_506	Bacillus virus G	GCA_000917535.1
APU01467.1	000439	Gp23	407	-	Aeromonas phage 65.2	GCA_002618145.1
APU01468.1	000439	Gp23	560	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28951.1	000439	Gp23	409	AP1_0244	Aeromonas phage AP1	GCA_014183365.1
QMV28952.1	000439	Gp23	560	AP1_0245	Aeromonas phage AP1	GCA_014183365.1
ATI17430.1	000439	Gp23	409	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17429.1	000439	Gp23	560	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00165.1	000439	Gp23	409	HWB28_gp387	Aeromonas phage AS-zj	GCA_002627665.1
ASU00166.1	000439	Gp23	560	HWB28_gp386	Aeromonas phage AS-zj	GCA_002627665.1
AUE22762.1	000439	Gp23	431	Ah1_00244	Aeromonas phage Ah1	GCA_002957415.1
AUE22763.1	000439	Gp23	392	Ah1_00245	Aeromonas phage Ah1	GCA_002957415.1
QAX98477.1	000439	Gp23	535	ASfcp2_139	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98478.1	000439	Gp23	392	ASfcp2_140	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97869.1	000439	Gp23	560	ASswx1_226	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97870.1	000439	Gp23	409	ASswx1_227	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01280.1	000439	Gp23	410	ASwh1_217	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01281.1	000439	Gp23	560	ASwh1_218	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39536.1	000439	Gp23	409	CC2_307	Aeromonas phage CC2	GCA_000903495.1
AFN39537.1	000439	Gp23	560	CC2_308	Aeromonas phage CC2	GCA_000903495.1
ADQ52939.1	000439	Gp23	535	PX29p220	Aeromonas phage PX29	GCA_000920195.1
ADQ52940.1	000439	Gp23	392	PX29p221	Aeromonas phage PX29	GCA_000920195.1
ADM79862.1	000439	Gp23	534	phiAS5_ORF0019	Aeromonas phage phiAS5	GCA_000887715.1
ADM79863.1	000439	Gp23	392	phiAS5_ORF0020	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53090.1	000439	Gp23	560	65p080	Aeromonas virus 65	GCA_000893255.1
ADQ53089.1	000439	Gp23	407	65p079	Aeromonas virus 65	GCA_000893255.1
AAF61695.2	000439	Gp23	534	23	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17886.1	000439	Gp23	392	24	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94997.1	000439	Gp23	409	FDI40_gp215	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMM44831.1	000439	Gp23	468	SP15_032	Bacillus phage SP-15	GCA_001754685.1
AMM44833.1	000439	Gp23	197	SP15_034	Bacillus phage SP-15	GCA_001754685.1
CCH63541.1	000439	Gp23	414	CP21_079	Campylobacter virus CP21	GCA_000902535.1
ANS05944.1	000439	Gp23	524	ABCD_0216	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS05953.1	000439	Gp23	432	ABCD_0217	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64878.1	000439	Gp23	425	S13_079	Cronobacter phage S13	GCA_001503575.1
AIA64879.1	000439	Gp23	515	S13_080	Cronobacter phage S13	GCA_001503575.1
AFC21700.1	000439	Gp23	391	GAP32_250	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97231.1	000439	Gp23	524	E_223	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97233.1	000439	Gp23	432	E_225	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56899.1	000439	Gp23	448	CPXG_00096	Cyanophage P-RSM6	GCA_000906155.1
AJK27563.1	000439	Gp23	448	PTIM40_136	Cyanophage P-TIM40	GCA_001470935.1
AOO14313.1	000439	Gp23	465	Sn110110_119	Cyanophage S-RIM14	GCA_002599065.1
AOO14962.1	000439	Gp23	465	W1230910_116	Cyanophage S-RIM14	GCA_002599125.1
AMO43141.1	000439	Gp23	471	R1080702_132	Cyanophage S-RIM32	GCA_001754165.1
AMO43367.1	000439	Gp23	468	W270710_123	Cyanophage S-RIM44	GCA_002599145.1
AOO11611.1	000439	Gp23	468	ES420910_130	Cyanophage S-RIM44	GCA_002599165.1
AOO11839.1	000439	Gp23	468	Np050604_123	Cyanophage S-RIM44	GCA_002599185.1
AOO12076.1	000439	Gp23	468	Np200711_130	Cyanophage S-RIM44	GCA_002599205.1
AOO12312.1	000439	Gp23	468	Np420711_130	Cyanophage S-RIM44	GCA_002599225.1
AOO12540.1	000439	Gp23	468	Sn080709_123	Cyanophage S-RIM44	GCA_002599245.1
AOO12777.1	000439	Gp23	468	Sn130910_130	Cyanophage S-RIM44	GCA_002599265.1
AOO13006.1	000439	Gp23	468	W2100709_124	Cyanophage S-RIM44	GCA_002599285.1
AGH07461.1	000439	Gp23	468	CYVG_00017	Cyanophage S-SSM6a	GCA_002710385.1
AGG54490.1	000439	Gp23	462	CYWG_00206	Cyanophage S-SSM6b	GCA_002710425.1
AIT14493.1	000439	Gp23	391	PBI_121Q_603	Escherichia phage 121Q	GCA_000926855.1
QAY00456.1	000439	Gp23	391	Ecwhy1_176	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35198.1	000439	Gp23	391	ACQ29_gp518	Escherichia phage PBECO4	GCA_001041035.1
BBM62165.1	000439	Gp23	391	EO157G_5760	Escherichia phage SP27	GCA_008033345.1
AXC36770.1	000439	Gp23	391	-	Escherichia phage UB	GCA_003341455.1
ARM70734.1	000439	Gp23	522	phiC120_c27	Escherichia phage phiC120	GCA_002621185.1
ARM70736.1	000439	Gp23	426	phiC120_c29	Escherichia phage phiC120	GCA_002621185.1
QBO61810.1	000439	Gp23	391	G17_00321	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13854.1	000439	Gp23	391	vBEcoMphAPEC6_gp225c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80477.1	000439	Gp23	391	PSLUR01_00500	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78749.1	000439	Gp23	524	RB43ORF227w	Escherichia virus RB43	GCA_000863505.1
AAX78750.1	000439	Gp23	440	RB43ORF228w	Escherichia virus RB43	GCA_000863505.1
AFA44367.1	000439	Gp23	393	RaK2_00094	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72823.1	000439	Gp23	407	-	Myoviridae sp.	GCA_003657725.1
QHJ79061.1	000439	Gp23	429	-	Myoviridae sp.	GCA_012593985.1
QHJ79060.1	000439	Gp23	521	-	Myoviridae sp.	GCA_012593985.1
QIG65696.1	000439	Gp23	447	phiOC_p030	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43821.1	000439	Gp23	391	CBB_257	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26103.1	000439	Gp23	455	CPMG_00002	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44513.1	000439	Gp23	470	PSSM2_135	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12453.1	000439	Gp23	468	PRTG_00306	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93447.1	000439	Gp23	480	AVU42_gp109	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99225.1	000439	Gp23	468	Syn1_124	Prochlorococcus phage Syn1	GCA_000892495.1
QHJ85987.1	000439	Gp23	471	KKIINIFJ_00075	Pseudomonas phage PN05	GCA_009931935.1
QCG76036.1	000439	Gp23	395	EST35_0154	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44110.1	000439	Gp23	394	PBI_SCTP2_95	Salicola phage SCTP-2	GCA_002625545.1
QCW18977.1	000439	Gp23	391	7t3_0456	Salmonella phage 7t3	GCA_006083215.1
AZU98227.1	000439	Gp23	391	CPT_Munch_283	Salmonella phage Munch	GCA_004015485.1
QIG62758.1	000439	Gp23	391	SEPL_145	Salmonella phage SE_PL	GCA_011067555.1
AQW88780.1	000439	Gp23	391	BF_0255	Serratia phage BF	GCA_002619745.1
AGR47697.1	000439	Gp23	434	SmphiM12_065	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12956.1	000439	Gp23	434	PHIM19_49	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12596.1	000439	Gp23	434	PHIM7_48	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13329.1	000439	Gp23	434	PHIN3_64	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30617.1	000439	Gp23	467	Syn7803US37_140	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54892.1	000439	Gp23	465	b23_0279	Synechococcus phage B23	GCA_009745195.1
QGT54527.1	000439	Gp23	465	b3_0286	Synechococcus phage B3	GCA_009745215.1
ASR76178.1	000439	Gp23	475	PBI_BELLAMY_133	Synechococcus phage Bellamy	GCA_002627525.1
QCW22888.1	000439	Gp23	476	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50469.1	000439	Gp23	476	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59591.1	000439	Gp23	471	S330809_130	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59353.1	000439	Gp23	471	C440309_130	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59829.1	000439	Gp23	471	N231010_130	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70574.1	000439	Gp23	474	HOU04_gp175	Synechococcus phage S-T4	GCA_003443335.1
QJT70120.1	000439	Gp23	475	SynMITS9220M01_107	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64432.1	000439	Gp23	514	KVP40.0363	Vibrio phage KVP40	GCA_000843785.1
AAQ64134.1	000439	Gp23	298	KVP40.0063	Vibrio phage KVP40	GCA_000843785.1
QIW90377.1	000439	Gp23	514	GCAPEGMB_00030	Vibrio phage V07	GCA_012361095.1
QIW90457.1	000439	Gp23	298	GCAPEGMB_00110	Vibrio phage V07	GCA_012361095.1
QIW90972.1	000439	Gp23	298	COHAPHLL_00109	Vibrio phage V09	GCA_012361135.1
QIW91052.1	000439	Gp23	514	COHAPHLL_00189	Vibrio phage V09	GCA_012361135.1
QHJ74546.1	000439	Gp23	514	VH12019_00246	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74246.1	000439	Gp23	298	VH12019_00327	Vibrio phage VH1_2019	GCA_009931825.1
AGB07070.1	000439	Gp23	299	CF80_gp283	Vibrio phage VH7D	GCA_000914495.1
AGB07004.1	000439	Gp23	514	CF80_gp217	Vibrio phage VH7D	GCA_000914495.1
QBX06025.1	000439	Gp23	299	ValB1HC_071	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06110.1	000439	Gp23	514	ValB1HC_156	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04552.1	000439	Gp23	455	ValB1MD_268	Vibrio phage ValB1MD	GCA_004138815.1
AJT61039.1	000439	Gp23	299	AVU32_gp198	Vibrio phage ValKK3	GCA_001501635.1
AJT61122.1	000439	Gp23	514	AVU32_gp281	Vibrio phage ValKK3	GCA_001501635.1
AGN30034.1	000439	Gp23	516	VPFG_00028	Vibrio phage nt-1	GCA_000910195.2
AGN30112.1	000439	Gp23	297	VPFG_00110	Vibrio phage nt-1	GCA_000910195.2
ALP46976.1	000439	Gp23	514	phiGrn1_0097	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47025.1	000439	Gp23	299	phiGrn1_0178	Vibrio phage phi-Grn1	GCA_002757115.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALP47359.1	000439	Gp23	514	phiST2_0229	Vibrio phage phi-ST2	GCA_002757135.1
ALP47404.1	000439	Gp23	299	phiST2_0309	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54650.1	000439	Gp23	299	vBValMR10Z_109	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54735.1	000439	Gp23	514	vBValMR10Z_195	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07017.1	000439	Gp23	382	VmeM32_00023	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37294.1	000439	Gp23	298	pp2_061	Vibriophage phi-pp2	GCA_002630725.1
AFN37595.1	000439	Gp23	514	pp2_363	Vibriophage phi-pp2	GCA_002630725.1
BBA65422.1	000439	Gp23	463	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96429.1	000439	Gp23	380	Xoosp13_243	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96443.1	000439	Gp23	463	Xoosp13_257	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59061.1	000439	Gp23	391	g253	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58527.1	000439	Gp23	391	g250	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22708.1	000440	SIG+Gp23	129	Ah1_00182	Aeromonas phage Ah1	GCA_002957415.1
QAX98435.1	000440	SIG+Gp23	140	ASfcp2_91	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52889.1	000440	SIG+Gp23	140	PX29p170	Aeromonas phage PX29	GCA_000920195.1
ADM80154.1	000440	SIG+Gp23	141	phiAS5_ORF0311	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17842.1	000440	SIG+Gp23	140	Aeh1ORF176c	Aeromonas virus Aeh1	GCA_000843245.1
QHJ78959.1	000440	SIG+Gp23	129	-	Myoviridae sp.	GCA_012593985.1
AIA64973.1	000440	SIG+Gp23	88	S13_174	Cronobacter phage S13	GCA_001503575.1
AFF28154.1	000441	SIG+Gp23+TM	585	PAU_156	Sphingomonas phage PAU	GCA_000902455.1
BBI90693.1	000441	SIG+Gp23+TM	616	HYO65_gp301	Tenacibaculum phage PTm1	GCA_009730695.1
BBI91000.1	000441	SIG+Gp23+TM	616	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39265.1	000441	SIG+Gp23+TM	590	BPT24_139	Tenacibaculum phage pT24	GCA_002611925.1
prevph1000000074	000441	SIG+Gp23+TM	617	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000059	000441	SIG+Gp23+TM	668	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMS01201.1	000442	Gp23	531	AR9_g117	Bacillus phage AR9	GCA_001743835.1
ALN97876.1	000442	Gp23	540	Bp8pS_197	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99825.1	000442	Gp23	531	PBI_PBS1_3	Bacillus virus PBS1	GCA_002601325.1
CCE26159.1	000442	Gp23	518	g135	Yersinia phage phiR1-37	GCA_000895615.1
CCH63670.1	000443	Gp23	304	CP21_208	Campylobacter virus CP21	GCA_000902535.1
QAU04525.1	000443	Gp23	303	ValB1MD_207	Vibrio phage ValB1MD	GCA_004138815.1
AUE22761.1	000000	SIG+Gp23+TM	116	Ah1_00243	Aeromonas phage Ah1	GCA_002957415.1
BBA65409.1	000000	Gp23	261	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65599.1	000000	Gp23	74	-	Xanthomonas phage XacN1	GCA_003173815.1
AKF13314.1	000000	Gp23	105	PHIN3_49	Sinorhizobium phage phiN3	GCA_001501175.1
QHJ86096.1	000000	Gp23	471	KKIINIFJ_00184	Pseudomonas phage PN05	GCA_009931935.1
AXH72435.1	000444	Gp23	250	-	Myoviridae sp.	GCA_003657725.1
AXH72430.1	000444	Gp23	328	-	Myoviridae sp.	GCA_003657725.1
QMV29135.1	000445	RpobetaC	229	AP1_0432	Aeromonas phage AP1	GCA_014183365.1
QDB70385.1	000445	RpobetaC	223	CF8_0216	Aeromonas phage CF8	GCA_006384595.2
QDJ97384.1	000445	RpobetaC	226	D6_0225	Aeromonas phage D6	GCA_007051205.2
QDH47130.1	000445	RpobetaC	226	LAh10_139	Aeromonas phage LAh10	GCA_006863975.1
QDJ96727.1	000445	RpobetaC	225	PS1_0216	Aeromonas phage PS1	GCA_007051165.2
QFR59360.1	000445	RpobetaC	225	PS2_0218	Aeromonas phage PS2	GCA_009388305.2
AMS01162.1	000445	RpobetaC	516	AR9_g078	Bacillus phage AR9	GCA_001743835.1
ALN97827.1	000445	RpobetaC	371	Bp8pS_148	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00091.1	000445	RpobetaC	423	PBI_PBS1_269	Bacillus virus PBS1	GCA_002601325.1
AFO71413.1	000445	RpobetaC	223	CR5_193	Cronobacter phage CR5	GCA_000910235.1
QBZ70770.1	000445	RpobetaC	225	pETSU_189	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59870.1	000445	RpobetaC	222	SEGD1_223	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07626.1	000445	RpobetaC	223	DERBICUS_200	Erwinia phage Derbicus	GCA_004521655.1
AHI60304.1	000445	RpobetaC	224	Ea357_153	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49869.1	000445	RpobetaC	222	MACHINA_231	Erwinia phage Machina	GCA_002758035.1
AGX01894.1	000445	RpobetaC	214	CF95_gp171	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07262.1	000445	RpobetaC	224	REBECCA_155	Erwinia phage Rebecca	GCA_004521635.1
AXF51372.1	000445	RpobetaC	223	WELLINGTON_246	Erwinia phage Wellington	GCA_003344985.1
AFQ96685.1	000445	RpobetaC	105	G173_gp140	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48253.1	000445	RpobetaC	222	ASESINO_240	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85942.1	000445	RpobetaC	224	BOSOLAPHORUS_155	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48526.1	000445	RpobetaC	222	CAITLIN_231	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48803.1	000445	RpobetaC	222	CHRISDB_241	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52257.1	000445	RpobetaC	224	DM_159	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86261.1	000445	RpobetaC	224	DESERTFOX_154	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49050.1	000445	RpobetaC	223	EARLPHILLIPIV_201	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49313.1	000445	RpobetaC	222	HUXLEY_231	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03693.1	000445	RpobetaC	226	JOAD_222	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49598.1	000445	RpobetaC	223	KWAN_246	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86583.1	000445	RpobetaC	224	MADMEL_155	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86907.1	000445	RpobetaC	224	MORTIMER_158	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50141.1	000445	RpobetaC	222	PARSHIK_232	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50397.1	000445	RpobetaC	223	PHOBOS_207	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51935.1	000445	RpobetaC	224	RAY_154	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03450.1	000445	RpobetaC	226	RISINGSUN_220	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51619.1	000445	RpobetaC	224	SIMMY50_157	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64966.1	000445	RpobetaC	224	SPECIALG_156	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50666.1	000445	RpobetaC	222	STRATTON_241	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86059.1	000445	RpobetaC	222	ACEC001_2160	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64031.1	000445	RpobetaC	224	Goslar_00240	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72076.1	000445	RpobetaC	225	N1M2_213	Klebsiella phage N1M2	GCA_010092605.1
QGZ14502.1	000445	RpobetaC	226	HWC77_gp139	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24083.1	000445	RpobetaC	222	-	Proteus phage 10	GCA_014071245.1
ABY63062.1	000445	RpobetaC	224	201phi2-1p233	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27269.1	000445	RpobetaC	225	PPEV_gp175	Pseudomonas phage EL	GCA_000866825.1
ANM44943.1	000445	RpobetaC	224	KTN4_185	Pseudomonas phage KTN4	GCA_002607225.1
ARV77327.1	000445	RpobetaC	222	NOXIFER_158	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89705.1	000445	RpobetaC	226	OBP_268	Pseudomonas phage OBP	GCA_000896635.1
QBX32330.1	000445	RpobetaC	212	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76852.1	000445	RpobetaC	225	PHABIO_221	Pseudomonas phage Phabio	GCA_002624965.1
AEH03595.1	000445	RpobetaC	224	172	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02731.1	000445	RpobetaC	222	PSA21_205	Pseudomonas phage Psa21	GCA_004340405.1
ATN94771.1	000445	RpobetaC	224	SL2_194	Pseudomonas phage SL2	GCA_002956015.1
QJB22821.1	000445	RpobetaC	224	fnug_178	Pseudomonas phage fnug	GCA_012837215.1
QEM41903.1	000445	RpobetaC	224	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83050.1	000445	RpobetaC	224	PHIKZ149	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19029.1	000445	RpobetaC	224	FDH28_gp055	Ralstonia phage RP12	GCA_002617345.1
BAW19314.1	000445	RpobetaC	224	-	Ralstonia phage RP31	GCA_002617365.1
BAS04843.2	000445	RpobetaC	215	AVU11_gp051	Ralstonia phage RSF1	GCA_001500875.1
BAQ02576.1	000445	RpobetaC	227	AVU38_gp048	Ralstonia phage RSL2	GCA_001503055.1
QNI20905.1	000445	RpobetaC	222	-	Salmonella phage JN03	GCA_014319805.1
AWN09130.1	000445	RpobetaC	222	MLDJOKPK_00222	Salmonella phage SPAsTU	GCA_003183805.1
AEP84051.1	000445	RpobetaC	222	SPN3US_0218	Salmonella phage SPN3US	GCA_001042275.1
QKE54458.1	000445	RpobetaC	222	ACSA002_1440	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65415.1	000445	RpobetaC	199	2050HW_00080	Serratia phage 2050HW	GCA_002628125.1
QDB71194.1	000445	RpobetaC	146	CPT_Moabite_164	Serratia phage Moabite	GCA_006384735.1
QFP93142.1	000445	RpobetaC	225	-	Serratia phage PCH45	GCA_009187865.1
QAU04232.1	000445	RpobetaC	226	HWC03_gp077	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23131.1	000445	RpobetaC	226	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81025.1	000445	RpobetaC	210	Aphrodite1_0209	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70756.1	000445	RpobetaC	221	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47596.1	000445	RpobetaC	226	HWC35_gp202	Vibrio phage USC-1	GCA_006864065.1
BAW98411.1	000445	RpobetaC	229	FDH33_gp202	Vibrio phage pTD1	GCA_002618825.1
AQT28092.1	000445	RpobetaC	217	pVa21_151	Vibrio phage pVa-21	GCA_002619305.1
QAX96778.1	000445	RpobetaC	221	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97097.1	000445	RpobetaC	221	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96143.1	000445	RpobetaC	221	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96461.1	000445	RpobetaC	221	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20965.1	000445	RpobetaC	256	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26226.1	000445	RpobetaC	248	g203	Yersinia phage phiR1-37	GCA_000895615.1
ALN97829.1	000446	RpobetaC	88	Bp8pS_150	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00094.1	000446	RpobetaC	67	PBI_PBS1_272	Bacillus virus PBS1	GCA_002601325.1
AND75472.1	000447	DPRA-HTH	206	ME3_311	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01465.1	000447	DPRA-HTH	183	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28949.1	000447	DPRA-HTH	186	AP1_0242	Aeromonas phage AP1	GCA_014183365.1
ATI17432.1	000447	DPRA-HTH	186	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00163.1	000447	DPRA-HTH	186	HWB28_gp389	Aeromonas phage AS-zj	GCA_002627665.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22766.1	000447	DPRA-HTH	185	Ah1_00248	Aeromonas phage Ah1	GCA_002957415.1
QAX98481.1	000447	DPRA-HTH	181	ASfcp2_143	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97872.1	000447	DPRA-HTH	186	ASswx1_229	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01277.1	000447	DPRA-HTH	167	ASwh1_214	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39420.1	000447	DPRA-HTH	186	CC2_305	Aeromonas phage CC2	GCA_000903495.1
ADQ52943.1	000447	DPRA-HTH	181	PX29p224	Aeromonas phage PX29	GCA_000920195.1
ADM79865.1	000447	DPRA-HTH	145	phiAS5_ORF0022	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17889.1	000447	DPRA-HTH	185	Aeh1ORF228c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06013.1	000447	DPRA-HTH	194	ABCD_0236	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFO71306.1	000447	DPRA-HTH	172	CR5_086	Cronobacter phage CR5	GCA_000910235.1
AIA64877.1	000447	DPRA-HTH	159	S13_078	Cronobacter phage S13	GCA_001503575.1
AON97254.1	000447	DPRA-HTH	193	E_246	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AMR59745.1	000447	DPRA-HTH	199	SEGD1_096	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07515.1	000447	DPRA-HTH	198	DERBICUS_89	Erwinia phage Derbicus	GCA_004521655.1
ANZ49741.1	000447	DPRA-HTH	200	MACHINA_103	Erwinia phage Machina	GCA_002758035.1
AXF51242.1	000447	DPRA-HTH	188	WELLINGTON_112	Erwinia phage Wellington	GCA_003344985.1
AFQ96561.1	000447	DPRA-HTH	198	G173_gp016	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48121.1	000447	DPRA-HTH	198	ASESINO_108	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48395.1	000447	DPRA-HTH	199	CAITLIN_100	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48667.1	000447	DPRA-HTH	199	CHRISDB_105	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48938.1	000447	DPRA-HTH	198	EARLPHILLIPIV_89	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49186.1	000447	DPRA-HTH	200	HUXLEY_104	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49463.1	000447	DPRA-HTH	188	KWAN_111	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50014.1	000447	DPRA-HTH	200	PARSHIK_105	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50279.1	000447	DPRA-HTH	198	PHOBOS_89	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50535.1	000447	DPRA-HTH	198	STRATTON_110	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85932.1	000447	DPRA-HTH	199	ACEC001_0940	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AAX78772.1	000447	DPRA-HTH	144	RB43ORF250w	Escherichia virus RB43	GCA_000863505.1
QHJ79062.1	000447	DPRA-HTH	180	-	Myoviridae sp.	GCA_012593985.1
ABY63146.1	000447	DPRA-HTH	219	201phi2-1p321	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45007.1	000447	DPRA-HTH	217	KTN4_249	Pseudomonas phage KTN4	GCA_002607225.1
ARV77398.1	000447	DPRA-HTH	229	NOXIFER_233	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32405.1	000447	DPRA-HTH	212	-	Pseudomonas phage PA1C	GCA_004785505.1
QKE11203.1	000447	DPRA-HTH	213	PaBG_00052	Pseudomonas phage PaBG	GCA_000912555.1
ARV76951.1	000447	DPRA-HTH	213	PHABIO_320	Pseudomonas phage Phabio	GCA_002624965.1
AEH03672.1	000447	DPRA-HTH	217	249	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02806.1	000447	DPRA-HTH	215	PSA21_280	Pseudomonas phage Psa21	GCA_004340405.1
ATN94707.1	000447	DPRA-HTH	217	SL2_130	Pseudomonas phage SL2	GCA_002956015.1
QJB22885.1	000447	DPRA-HTH	217	fnug_242	Pseudomonas phage fnug	GCA_012837215.1
QEM41975.1	000447	DPRA-HTH	212	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83108.1	000447	DPRA-HTH	217	PHIKZ207	Pseudomonas virus phiKZ	GCA_000842965.1
ASV44324.1	000447	DPRA-HTH	189	PBI_SCTP2_309	Salicola phage SCTP-2	GCA_002625545.1
QNI20802.1	000447	DPRA-HTH	199	-	Salmonella phage JN03	GCA_014319805.1
AWN09011.1	000447	DPRA-HTH	198	MLDJOKPK_00067	Salmonella phage SPAsTU	GCA_003183805.1
AEP83925.1	000447	DPRA-HTH	199	SPN3US_0092	Salmonella phage SPN3US	GCA_001042275.1
ATA65695.1	000447	DPRA-HTH	179	2050HW_00360	Serratia phage 2050HW	GCA_002628125.1
QDB71122.1	000447	DPRA-HTH	214	CPT_Moabite_092	Serratia phage Moabite	GCA_006384735.1
QFP93172.1	000447	DPRA-HTH	187	-	Serratia phage PCH45	GCA_009187865.1
AGR47938.1	000447	DPRA-HTH	177	SmphiM12_306	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13135.1	000447	DPRA-HTH	177	PHIM19_230	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12774.1	000447	DPRA-HTH	177	PHIM7_229	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13503.1	000447	DPRA-HTH	177	PHIN3_240	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28139.1	000447	DPRA-HTH	165	PAU_141	Sphingomonas phage PAU	GCA_000902455.1
AXH70900.1	000447	DPRA-HTH	314	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT27977.1	000447	DPRA-HTH	220	pVa21_035	Vibrio phage pVa-21	GCA_002619305.1
ALY07063.1	000447	DPRA-HTH	157	VmeM32_00072	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96875.1	000447	DPRA-HTH	177	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97180.1	000447	DPRA-HTH	177	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96239.1	000447	DPRA-HTH	177	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96557.1	000447	DPRA-HTH	177	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21141.1	000447	DPRA-HTH	203	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65434.1	000447	DPRA-HTH	150	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96451.1	000447	DPRA-HTH	158	Xoosp13_265	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ADQ53087.1	000447	DPRA-HTH	39	65p077	Aeromonas virus 65	GCA_000893255.1
ASV44715.1	000448	DPRA-HTH	185	FDI40_gp133	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21665.1	000448	DPRA-HTH	195	GAP32_215	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14457.1	000448	DPRA-HTH	197	PBI_121Q_567	Escherichia phage 121Q	GCA_000926855.1
QAY00491.1	000448	DPRA-HTH	198	Ecwhy1_212	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34686.1	000448	DPRA-HTH	197	ACQ29_gp006	Escherichia phage PBECO4	GCA_001041035.1
BBM62130.1	000448	DPRA-HTH	197	EO157G_5410	Escherichia phage SP27	GCA_008033345.1
AXC36806.1	000448	DPRA-HTH	197	-	Escherichia phage UB	GCA_003341455.1
QBO61845.1	000448	DPRA-HTH	197	G17_00356	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80442.1	000448	DPRA-HTH	197	PSLUR01_00465	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44331.1	000448	DPRA-HTH	196	RaK2_00058	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72471.1	000448	DPRA-HTH	190	-	Myoviridae sp.	GCA_003657725.1
AMM43786.1	000448	DPRA-HTH	195	CBB_221	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18936.1	000448	DPRA-HTH	209	7t3_0415	Salmonella phage 7t3	GCA_006083215.1
AZU98191.1	000448	DPRA-HTH	195	CPT_Munch_247	Salmonella phage Munch	GCA_004015485.1
QIG62793.1	000448	DPRA-HTH	195	SEPL_180	Salmonella phage SE_PL	GCA_011067555.1
AQW88742.1	000448	DPRA-HTH	195	BF_0217	Serratia phage BF	GCA_002619745.1
SOK59025.1	000448	DPRA-HTH	195	g217	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58490.1	000448	DPRA-HTH	195	g213	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDF13885.1	000448	DPRA-HTH	65	vBEcoMphAPEC6_gp260c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ABS83657.1	000449	YpsA-like	188	0305phi8-36p097	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01089.1	000449	YpsA-like	182	AR9_g004	Bacillus phage AR9	GCA_001743835.1
AMM44800.1	000449	YpsA-like	199	SP15_002	Bacillus phage SP-15	GCA_001754685.1
AEO93337.1	000449	YpsA-like	177	G_66	Bacillus virus G	GCA_000917535.1
ASU00011.1	000449	YpsA-like	182	PBI_PBS1_189	Bacillus virus PBS1	GCA_002601325.1
AXG67231.1	000449	YpsA-like	168	AD1_187	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79980.1	000449	YpsA-like	174	JA11_175	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66578.1	000449	YpsA-like	174	JA13_175	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66903.1	000449	YpsA-like	133	JA29_177	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67549.1	000449	YpsA-like	174	JA33_175	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08459.1	000449	YpsA-like	172	Alexandra_193	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58828.1	000449	YpsA-like	175	Y3_188	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28662.1	000449	YpsA-like	169	YOLOSWAG_183	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38222.1	000449	YpsA-like	130	BN7874_053	Phage NCTB	GCA_900092385.1
QHJ86171.1	000449	YpsA-like	160	KKIINIFJ_00261	Pseudomonas phage PN05	GCA_009931935.1
BAV39382.1	000449	YpsA-like	167	BPT24_264	Tenacibaculum phage pT24	GCA_002611925.1
QDH83605.1	000450	2H	175	H1O15_gp183	Achromobacter phage Motura	GCA_006964305.1
AUE22716.1	000450	2H	164	Ah1_00198	Aeromonas phage Ah1	GCA_002957415.1
QAX98440.1	000450	2H	164	ASfcp2_97	Aeromonas phage AsFcp_2	GCA_004146885.1
QDB70470.1	000450	2H	159	CF8_0057	Aeromonas phage CF8	GCA_006384595.2
QDJ97209.1	000450	2H	161	D6_0049	Aeromonas phage D6	GCA_007051205.2
QDH47172.1	000450	2H	161	LAh10_216	Aeromonas phage LAh10	GCA_006863975.1
QDJ96816.1	000450	2H	162	PS1_0057	Aeromonas phage PS1	GCA_007051165.2
QFR59445.1	000450	2H	162	PS2_0054	Aeromonas phage PS2	GCA_009388305.2
ADQ52896.1	000450	2H	165	PX29p177	Aeromonas phage PX29	GCA_000920195.1
ADM80163.1	000450	2H	165	phiAS5_ORF0320	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17849.1	000450	2H	164	57B	Aeromonas virus Aeh1	GCA_000843245.1
QBX06679.1	000450	2H	170	BcepSaruman_266	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74649.1	000450	2H	170	BcepSauron_269	Burkholderia phage BcepSauron	GCA_005394215.1
ANS06006.1	000450	2H	207	ABCD_0186	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64968.1	000450	2H	160	S13_169	Cronobacter phage S13	GCA_001503575.1
AFC21566.1	000450	2H	148	GAP32_118	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97200.1	000450	2H	207	E_192	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXG67279.1	000450	2H	155	AD1_235	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80023.1	000450	2H	149	JA11_218	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66622.1	000450	2H	149	JA13_219	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66946.1	000450	2H	149	JA29_220	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67593.1	000450	2H	149	JA33_219	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBZ70587.1	000450	2H	153	pETSU_006	Edwardsiella virus pEt-SU	GCA_004800915.1
AWY08504.1	000450	2H	155	Alexandra_244	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ASU03795.1	000450	2H	144	JOAD_120	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03550.1	000450	2H	144	RISINGSUN_120	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARW58879.1	000450	2H	155	Y3_239	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28712.1	000450	2H	156	YOLOSWAG_234	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ARM70970.1	000450	2H	151	phiC120_c265	Escherichia phage phiC120	GCA_002621185.1
AAX78718.1	000450	2H	207	RB43ORF196c	Escherichia virus RB43	GCA_000863505.1
QGH71903.1	000450	2H	154	N1M2_40	Klebsiella phage N1M2	GCA_010092605.1
QHJ78966.1	000450	2H	159	-	Myoviridae sp.	GCA_012593985.1
QIG66049.1	000450	2H	157	phiOC_p407	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43683.1	000450	2H	148	CBB_118	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38350.1	000450	2H	142	BN7874_181	Phage NCTB	GCA_900092385.1
QGZ14466.1	000450	2H	156	HWC77_gp103	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27220.1	000450	2H	141	PPEV_gp126	Pseudomonas phage EL	GCA_000866825.1
AEV89498.1	000450	2H	153	OBP_061	Pseudomonas phage OBP	GCA_000896635.1
AGS82103.1	000450	2H	177	PaBG_00228	Pseudomonas phage PaBG	GCA_000912555.1
ASV44173.1	000450	2H	172	PBI_SCTP2_158	Salicola phage SCTP-2	GCA_002625545.1
QCW18821.1	000450	2H	148	7t3_0300	Salmonella phage 7t3	GCA_006083215.1
AZU98085.1	000450	2H	148	CPT_Munch_141	Salmonella phage Munch	GCA_004015485.1
QIG62897.1	000450	2H	148	SEPL_284	Salmonella phage SE_PL	GCA_011067555.1
AQW88635.1	000450	2H	148	BF_0110	Serratia phage BF	GCA_002619745.1
AKF13101.1	000450	2H	164	PHIM19_196	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12741.1	000450	2H	164	PHIM7_196	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13471.1	000450	2H	164	PHIN3_208	Sinorhizobium phage phiN3	GCA_001501175.1
QAU04268.1	000450	2H	156	HWC03_gp113	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23097.1	000450	2H	163	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81047.1	000450	2H	163	Aphrodite1_0036	Vibrio phage Aphrodite1	GCA_002958015.1
AAQ64392.1	000450	2H	151	KVP40.0322	Vibrio phage KVP40	GCA_000843785.1
QDH47419.1	000450	2H	163	HWC35_gp025	Vibrio phage USC-1	GCA_006864065.1
QIW90704.1	000450	2H	151	GCAPEGMB_00385	Vibrio phage V07	GCA_012361095.1
QIW91093.1	000450	2H	151	COHAPHLL_00230	Vibrio phage V09	GCA_012361135.1
QHJ74504.1	000450	2H	151	VH12019_00204	Vibrio phage VH1_2019	GCA_009931825.1
QBX06151.1	000450	2H	151	ValB1HC_197	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04489.1	000450	2H	177	ValB1MD_126	Vibrio phage ValB1MD	GCA_004138815.1
AJT61163.1	000450	2H	151	AVU32_gp322	Vibrio phage ValKK3	GCA_001501635.1
AGN30373.1	000450	2H	151	VPFG_00376	Vibrio phage nt-1	GCA_000910195.2
BAW98239.1	000450	2H	160	FDH33_gp030	Vibrio phage pTD1	GCA_002618825.1
ALP47128.1	000450	2H	151	phiGrn1_0056	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47513.1	000450	2H	151	phiST2_0188	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54776.1	000450	2H	151	vBValMR10Z_236	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07111.1	000450	2H	164	VmeM32_00124	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37554.1	000450	2H	151	pp2_322	Vibriophage phi-pp2	GCA_002630725.1
BBA65333.1	000450	2H	190	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96371.1	000450	2H	185	Xoosp13_184	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58914.1	000450	2H	148	g106	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58379.1	000450	2H	148	g102	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BBI90673.1	000451	2H	188	HYO65_gp281	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90980.1	000451	2H	188	-	Tenacibaculum phage PTm5	GCA_009730715.1
AEO93499.1	000000	2H	189	G_240	Bacillus virus G	GCA_000917535.1
AXH72583.1	000000	2H	146	-	Myoviridae sp.	GCA_003657725.1
QHJ86174.1	000000	2H	166	KKIINIFJ_00264	Pseudomonas phage PN05	GCA_009931935.1
QIG57912.1	000000	2H	179	SEA_PAULODIABOLI_227	Microbacterium phage PauloDiaboli	GCA_011067425.1
AYD81233.1	000452	AEprimase+SFIII-Helicase+ZDNA-HTH	761	SEA_JUSTBECAUSE_64	Streptomyces phage JustBecause	GCA_003613775.1
QJD53636.1	000452	AEprimase+SFIII-Helicase+ZDNA-HTH	761	SEA_KELA_65	Streptomyces phage Kela	GCA_012934305.1
QBZ71967.1	000452	AEprimase+SFIII-Helicase+ZDNA-HTH	761	SEA_KRADAL_69	Streptomyces phage Kradal	GCA_004799925.1
AXH66230.1	000452	AEprimase+SFIII-Helicase+ZDNA-HTH	761	SEA_SATIS_69	Streptomyces phage Satis	GCA_003366315.1
APU01447.1	000453	ATP-LIGASE+OB	518	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28932.1	000453	ATP-LIGASE+OB	517	AP1_0225	Aeromonas phage AP1	GCA_014183665.1
ATI17452.1	000453	ATP-LIGASE+OB	517	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00144.1	000453	ATP-LIGASE+OB	517	HWB28_gp006	Aeromonas phage AS-zj	GCA_002627665.1
AUE22786.1	000453	ATP-LIGASE+OB	495	Ah1_00268	Aeromonas phage Ah1	GCA_002957415.1
QAX98500.1	000453	ATP-LIGASE+OB	495	ASfcp2_164	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97892.1	000453	ATP-LIGASE+OB	517	ASswx1_249	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01260.1	000453	ATP-LIGASE+OB	521	ASwh1_196	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39532.1	000453	ATP-LIGASE+OB	517	CC2_284	Aeromonas phage CC2	GCA_000903495.1
ADQ52963.1	000453	ATP-LIGASE+OB	495	PX29p244	Aeromonas phage PX29	GCA_000920195.1
ADM79889.1	000453	ATP-LIGASE+OB	495	phiAS5_ORF0046	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53067.1	000453	ATP-LIGASE+OB	518	65p057	Aeromonas virus 65	GCA_000893255.1
AAQ17911.1	000453	ATP-LIGASE+OB	495	30	Aeromonas virus Aeh1	GCA_000843245.1
CCH63629.1	000453	ATP-LIGASE+OB	296	CP21_167	Campylobacter virus CP21	GCA_000902535.1
ANS05945.1	000453	ATP-LIGASE+OB	507	ABCD_0095	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64845.1	000453	ATP-LIGASE+OB	476	S13_046	Cronobacter phage S13	GCA_001503575.1
AFC21547.1	000453	ATP-LIGASE+OB	471	GAP32_099	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97107.1	000453	ATP-LIGASE+OB	507	E_099	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14350.1	000453	ATP-LIGASE+OB	472	PBI_121Q_460	Escherichia phage 121Q	GCA_000926855.1
QAY00594.1	000453	ATP-LIGASE+OB	472	Ecwhy1_317	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34789.1	000453	ATP-LIGASE+OB	472	ACQ29_gp109	Escherichia phage PBECO4	GCA_001041035.1
BBM62021.1	000453	ATP-LIGASE+OB	472	EO157G_4320	Escherichia phage SP27	GCA_008033345.1
AXC36905.1	000453	ATP-LIGASE+OB	472	-	Escherichia phage UB	GCA_003341455.1
ARM70758.1	000453	ATP-LIGASE+OB	497	phiC120_c52	Escherichia phage phiC120	GCA_002621185.1
QBO61954.1	000453	ATP-LIGASE+OB	472	G17_00465	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13981.1	000453	ATP-LIGASE+OB	472	vBEcoMphAPEC6_gp357c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80337.1	000453	ATP-LIGASE+OB	472	PSLUR01_00360	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78617.1	000453	ATP-LIGASE+OB	507	RB43ORF095w	Escherichia virus RB43	GCA_000863505.1
AFA44759.1	000453	ATP-LIGASE+OB	467	RaK2_00486	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78818.1	000453	ATP-LIGASE+OB	475	-	Myoviridae sp.	GCA_012593985.1
AMM43665.1	000453	ATP-LIGASE+OB	471	CBB_100	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QHJ86010.1	000453	ATP-LIGASE+OB	432	KKIINIFJ_00098	Pseudomonas phage PN05	GCA_009931935.1
QCG76148.1	000453	ATP-LIGASE+OB	456	EST35_0267	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44551.1	000453	ATP-LIGASE+OB	451	PBI_SCTP2_536	Salicola phage SCTP-2	GCA_002625545.1
QCW18801.1	000453	ATP-LIGASE+OB	476	7t3_0280	Salmonella phage 7t3	GCA_006083215.1
AZU98066.1	000453	ATP-LIGASE+OB	476	CPT_Munch_122	Salmonella phage Munch	GCA_004015485.1
QIG62916.1	000453	ATP-LIGASE+OB	476	SEPL_303	Salmonella phage SE_PL	GCA_011067555.1
AQW88618.1	000453	ATP-LIGASE+OB	471	BF_0093	Serratia phage BF	GCA_002619745.1
AAQ64128.1	000453	ATP-LIGASE+OB	447	KVP40.0057	Vibrio phage KVP40	GCA_000843785.1
QIW90451.1	000453	ATP-LIGASE+OB	447	GCAPEGMB_00104	Vibrio phage V07	GCA_012361095.1
QIW90978.1	000453	ATP-LIGASE+OB	447	COHAPHLL_00115	Vibrio phage V09	GCA_012361135.1
QHJ74240.1	000453	ATP-LIGASE+OB	447	VH12019_00321	Vibrio phage VH1_2019	GCA_009931825.1
AGB07065.1	000453	ATP-LIGASE+OB	445	CF80_gp278	Vibrio phage VH7D	GCA_000914495.1
QBX06031.1	000453	ATP-LIGASE+OB	445	ValB1HC_077	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04535.1	000453	ATP-LIGASE+OB	482	ValB1MD_241	Vibrio phage ValB1MD	GCA_004138815.1
AJT61045.1	000453	ATP-LIGASE+OB	445	AVU32_gp204	Vibrio phage ValKK3	GCA_001501635.1
AGN30106.1	000453	ATP-LIGASE+OB	444	VPFG_00104	Vibrio phage nt-1	GCA_000910195.2
ALP46988.1	000453	ATP-LIGASE+OB	445	phiGrn1_0172	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47369.1	000453	ATP-LIGASE+OB	445	phiST2_0303	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54656.1	000453	ATP-LIGASE+OB	445	vBValMR10Z_115	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07196.1	000453	ATP-LIGASE+OB	494	VmeM32_00210	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37616.1	000453	ATP-LIGASE+OB	447	pp2_055	Vibriophage phi-pp2	GCA_002630725.1
SOK58894.1	000453	ATP-LIGASE+OB	471	g086	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58359.1	000453	ATP-LIGASE+OB	471	g082	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13677.1	000454	SIG+ATP-LIGASE+OB	353	Ccr10_gp148c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14022.1	000454	SIG+ATP-LIGASE+OB	353	Ccr2_gp147c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14710.1	000454	SIG+ATP-LIGASE+OB	353	Ccr29_gp154	Caulobacter phage Ccr29	GCA_002619485.1
ARB15065.1	000454	SIG+ATP-LIGASE+OB	353	Ccr32_gp147	Caulobacter phage Ccr32	GCA_002619505.1
ARB15399.1	000454	SIG+ATP-LIGASE+OB	353	Ccr34_gp157	Caulobacter phage Ccr34	GCA_002619525.1
ARB14365.1	000454	SIG+ATP-LIGASE+OB	354	Ccr5_gp146c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68348.1	000454	SIG+ATP-LIGASE+OB	357	CcrBL10_gp144c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87670.1	000454	SIG+ATP-LIGASE+OB	356	CcrKarma_gp153	Caulobacter virus Karma	GCA_000901575.1
AFU87319.1	000454	SIG+ATP-LIGASE+OB	356	CcrMagneto_gp149	Caulobacter virus Magneto	GCA_000903095.1
AFU86632.1	000454	SIG+ATP-LIGASE+OB	357	CcrRogue_gp150	Caulobacter virus Rogue	GCA_000900555.1
AFU88466.1	000454	SIG+ATP-LIGASE+OB	356	CcrSwift_gp148	Caulobacter virus Swift	GCA_000899655.1
AFU86983.1	000454	SIG+ATP-LIGASE+OB	353	CbK_gp151	Caulobacter virus phiCbK	GCA_000900535.1
QGT54756.1	000454	SIG+ATP-LIGASE+OB	290	b23_0141	Synechococcus phage B23	GCA_009745195.1
QGT54386.1	000454	SIG+ATP-LIGASE+OB	290	b3_0142	Synechococcus phage B3	GCA_009745215.1
QIW90736.1	000454	SIG+ATP-LIGASE+OB	353	GCAPEGMB_00417	Vibrio phage V07	GCA_012361095.1
AND75238.1	000455	ATP-LIGASE+OB	367	ME3_77	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXQ69248.1	000455	ATP-LIGASE+OB	394	CcrBL9_gp224	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88061.1	000455	ATP-LIGASE+OB	395	CcrColossus_gp191	Caulobacter phage CcrColossus	GCA_000899635.1

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AXQ68739.1	000455	ATP-LIGASE+OB	395	CcrPW_gp200c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69803.1	000455	ATP-LIGASE+OB	394	CcrSC_gp221	Caulobacter phage CcrSC	GCA_003443315.1
QIG65871.1	000455	ATP-LIGASE+OB	381	phiOC_p206	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR48050.2	000455	ATP-LIGASE+OB	379	SmphiM12_418	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13231.1	000455	ATP-LIGASE+OB	379	PHIM19_326	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12871.1	000455	ATP-LIGASE+OB	379	PHIM7_326	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13594.1	000455	ATP-LIGASE+OB	379	PHIN3_331	Sinorhizobium phage phiN3	GCA_001501175.1
AFU88099.1	000456	AlkB-2OGFEDO	200	CcrColossus_gp229	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68776.1	000456	AlkB-2OGFEDO	200	CcrPW_gp237	Caulobacter phage CcrPW	GCA_003443275.1
ASV44332.1	000456	AlkB-2OGFEDO	197	PBI_SCTP2_317	Salicola phage SCTP-2	GCA_002625545.1
BBA65348.1	000456	AlkB-2OGFEDO	184	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96382.1	000456	AlkB-2OGFEDO	184	Xoosp13_196	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGH07631.1	000457	Base-wedge	251	CYVG_00188	Cyanophage S-SSM6a	GCA_002710385.1
AXQ70448.1	000457	Base-wedge	214	HOU04_gp049	Synechococcus phage S-T4	GCA_003443335.1
AGH26202.1	000457	Base-wedge	205	CPMG_00101	Prochlorococcus phage MED4-213	GCA_000904535.1
AON97207.1	000457	Base-wedge	184	E_199	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAQ17859.1	000457	Base-wedge	188	53	Aeromonas virus Aeh1	GCA_000843245.1
AOV59226.1	000457	Base-wedge	209	C440309_003	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59702.1	000457	Base-wedge	209	N231010_003	Synechococcus phage S-CAM4	GCA_002922155.1
ASU00197.1	000457	Base-wedge	188	HWB28_gp355	Aeromonas phage AS-zj	GCA_002627665.1
QBX06140.1	000457	Base-wedge	192	ValB1HC_186	Vibrio phage ValB1 HC	GCA_004771355.1
AFN39558.1	000457	Base-wedge	188	CC2_340	Aeromonas phage CC2	GCA_000903495.1
ATI17398.1	000457	Base-wedge	188	-	Aeromonas phage AS-szw	GCA_002743635.1
ARM70976.1	000457	Base-wedge	191	phiC120_c271	Escherichia phage phiC120	GCA_002621185.1
AOO14199.1	000457	Base-wedge	314	Sn110110_005	Cyanophage S-RIM14	GCA_002599065.1
QCW23072.1	000457	Base-wedge	168	-	Synechococcus phage S-B05	GCA_006083695.1
QMV28957.1	000457	Base-wedge	158	AP1_0250	Aeromonas phage AP1	GCA_014183365.1
QAY01313.1	000457	Base-wedge	188	ASwh1_251	Aeromonas phage Aswh_1	GCA_004146945.1
ARM70710.1	000457	Base-wedge	191	phiC120_c3	Escherichia phage phiC120	GCA_002621185.1
AFN37565.1	000457	Base-wedge	192	pp2_333	Vibriophage phi-pp2	GCA_002630725.1
QAX98450.1	000457	Base-wedge	188	ASfcp2_107	Aeromonas phage AsFcp_2	GCA_004146885.1
AUE22727.1	000457	Base-wedge	188	Ah1_00209	Aeromonas phage Ah1	GCA_002957415.1
AOO14851.1	000457	Base-wedge	323	W1230910_005	Cyanophage S-RIM14	GCA_002599125.1
QJT70020.1	000457	Base-wedge	230	SynMITS9220M01_004	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ADM80174.1	000457	Base-wedge	186	phiAS5_ORF0331	Aeromonas phage phiAS5	GCA_000887715.1
ASR76052.1	000457	Base-wedge	221	PBI_BELLAMY_5	Synechococcus phage Bellamy	GCA_002627525.1
AGB06976.1	000457	Base-wedge	192	CF80_gp189	Vibrio phage VH7D	GCA_000914495.1
ADQ52907.1	000457	Base-wedge	188	PX29p188	Aeromonas phage PX29	GCA_000920195.1
ADQ53120.1	000457	Base-wedge	187	65p112	Aeromonas virus 65	GCA_000893255.1
AAX78725.1	000457	Base-wedge	184	RB43ORF203w	Escherichia virus RB43	GCA_000863505.1
AMO43018.1	000457	Base-wedge	219	R1080702_003	Cyanophage S-RIM32	GCA_001754165.1
QHJ78976.1	000457	Base-wedge	184	-	Myoviridae sp.	GCA_012593985.1
AIA64958.1	000457	Base-wedge	184	S13_159	Cronobacter phage S13	GCA_001503575.1
QGT54260.1	000457	Base-wedge	242	b3_0002	Synechococcus phage B3	GCA_009745215.1
AGH57015.1	000457	Base-wedge	285	CPXG_00212	Cyanophage P-RSM6	GCA_000906155.1
QIG65731.1	000457	Base-wedge	187	phiOC_p066	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGG54365.1	000457	Base-wedge	326	CYWG_00081	Cyanophage S-SSM6b	GCA_002710425.1
QAX97839.1	000457	Base-wedge	188	ASswx1_195	Aeromonas phage Asswx_1	GCA_004146865.1
QGT54630.1	000457	Base-wedge	242	b23_0002	Synechococcus phage B23	GCA_009745195.1
QHJ74515.1	000457	Base-wedge	192	VH12019_00215	Vibrio phage VH1_2019	GCA_009931825.1
AIX30484.1	000457	Base-wedge	219	Syn7803US37_7	Synechococcus phage ACG-2014f	GCA_002594065.1
ALY07104.1	000457	Base-wedge	183	VmeM32_00117	Vibrio phage vB_VmeM-32	GCA_002608825.1
AOO12887.1	000457	Base-wedge	219	W2100709_004	Cyanophage S-RIM44	GCA_002599285.1
ALP47455.1	000457	Base-wedge	192	phiST2_0199	Vibrio phage phi-ST2	GCA_002757135.1
AOO12652.1	000457	Base-wedge	219	Sn130910_004	Cyanophage S-RIM44	GCA_002599265.1
AKF13379.1	000457	Base-wedge	190	PHIN3_114	Sinorhizobium phage phiN3	GCA_001501175.1
AOO12422.1	000457	Base-wedge	219	Sn080709_004	Cyanophage S-RIM44	GCA_002599245.1
APU01499.1	000457	Base-wedge	187	-	Aeromonas phage 65.2	GCA_002618145.1
AKF12647.1	000457	Base-wedge	190	PHIM7_100	Sinorhizobium phage phiM7	GCA_002622405.1
AAQ64402.1	000457	Base-wedge	192	KVP40.0333	Vibrio phage KVP40	GCA_000843785.1
AJK27440.1	000457	Base-wedge	365	PTIM40_13	Cyanophage P-TIM40	GCA_001470935.1
AOO12187.1	000457	Base-wedge	219	Np420711_004	Cyanophage S-RIM44	GCA_002599225.1
AKF13007.1	000457	Base-wedge	190	PHIM19_101	Sinorhizobium phage phiM19	GCA_002605865.1
AOO11951.1	000457	Base-wedge	219	Np200711_004	Cyanophage S-RIM44	GCA_002599205.1
AGR47784.1	000457	Base-wedge	190	SmphiM12_152	Sinorhizobium phage phiM12	GCA_001023565.1
AAX44387.1	000457	Base-wedge	241	PSSM2_009	Prochlorococcus phage P-SSM2	GCA_000859585.1
AOO11721.1	000457	Base-wedge	219	Np050604_004	Cyanophage S-RIM44	GCA_002599185.1
ADO99107.1	000457	Base-wedge	219	Syn1_005	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59464.1	000457	Base-wedge	209	S330809_003	Synechococcus phage S-CAM4	GCA_002366065.1
QIW90715.1	000457	Base-wedge	192	GCAPEGMB_00396	Vibrio phage V07	GCA_012361095.1
ALP47075.1	000457	Base-wedge	192	phiGrn1_0068	Vibrio phage phi-Grn1	GCA_002757115.1
AGN12261.1	000457	Base-wedge	241	PRTG_00106	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOO11486.1	000457	Base-wedge	219	ES420910_004	Cyanophage S-RIM44	GCA_002599165.1
ANS06022.1	000457	Base-wedge	184	ABCD_0193	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
QNJ54765.1	000457	Base-wedge	192	vBValMR10Z_225	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AMO43249.1	000457	Base-wedge	219	W270710_004	Cyanophage S-RIM44	GCA_002599145.1
QIW91082.1	000457	Base-wedge	192	COHAPHLL_00219	Vibrio phage V09	GCA_012361135.1
AJT61152.1	000457	Base-wedge	192	AVU32_gp311	Vibrio phage ValKK3	GCA_001501635.1
AGN30384.1	000457	Base-wedge	192	VPFG_00387	Vibrio phage nt-1	GCA_000910195.2
AIR93391.1	000457	Base-wedge	224	AVU42_gp005	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASV44766.1	000458	Base-wedge	104	FDI40_gp697	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21686.1	000458	Base-wedge	104	GAP32_236	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14479.1	000458	Base-wedge	104	PBI_121Q_589	Escherichia phage 121Q	GCA_000926855.1
QAY00469.1	000458	Base-wedge	104	Ecwhy1_190	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35212.1	000458	Base-wedge	104	ACQ29_gp532	Escherichia phage PBECO4	GCA_001041035.1
BBM62151.1	000458	Base-wedge	104	EO157G_5620	Escherichia phage SP27	GCA_008033345.1
AXC36784.1	000458	Base-wedge	104	-	Escherichia phage UB	GCA_003341455.1
QBO61824.1	000458	Base-wedge	104	G17_00335	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13868.1	000458	Base-wedge	104	vBEcoMphAPEC6_gp239	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80463.1	000458	Base-wedge	104	PSLUR01_00486	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44353.1	000458	Base-wedge	108	RaK2_00080	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72727.1	000458	Base-wedge	104	-	Myoviridae sp.	GCA_003657725.1
AMM43807.1	000458	Base-wedge	104	CBB_242	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76017.1	000458	Base-wedge	99	EST35_0135	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44202.1	000458	Base-wedge	97	PBI_SCTP2_187	Salicola phage SCTP-2	GCA_002625545.1
QCW18959.1	000458	Base-wedge	104	7t3_0438	Salmonella phage 7t3	GCA_006083215.1
AZU98212.1	000458	Base-wedge	104	CPT_Munch_268	Salmonella phage Munch	GCA_004015485.1
QIG62772.1	000458	Base-wedge	104	SEPL_159	Salmonella phage SE_PL	GCA_011067555.1
AQW88766.1	000458	Base-wedge	104	BF_0241	Serratia phage BF	GCA_002619745.1
SOK59047.1	000458	Base-wedge	104	g239c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58512.1	000458	Base-wedge	104	g235c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67170.1	000459	Base-wedge	97	AD1_126	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79920.1	000459	Base-wedge	97	JA11_115	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66519.1	000459	Base-wedge	97	JA13_116	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66844.1	000459	Base-wedge	97	JA29_118	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67489.1	000459	Base-wedge	53	JA33_115	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08403.1	000459	Base-wedge	97	Alexandra_131	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58767.1	000459	Base-wedge	96	Y3_127	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28606.1	000459	Base-wedge	96	YOLOSWAG_125	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFH14585.1	000459	Base-wedge	108	Lu11_0054	Pseudomonas phage Lu11	GCA_000897175.1
AGS81953.1	000459	Base-wedge	111	PaBG_00069	Pseudomonas phage PaBG	GCA_000912555.1
AFF28126.1	000460	Base-wedge	145	PAU_128	Sphingomonas phage PAU	GCA_000902455.1
BBI90637.1	000460	Base-wedge	143	HYO65_gp245	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90944.1	000460	Base-wedge	143	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39300.1	000460	Base-wedge	157	BPT24_174	Tenacibaculum phage pT24	GCA_002611925.1
QDH83673.1	000461	Base-wedge	111	H1O15_gp138	Achromobacter phage Motura	GCA_006964305.1
QBX06671.1	000461	Base-wedge	116	BcepSaruman_258	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74641.1	000461	Base-wedge	116	BcepSauron_261	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41651.1	000461	Base-wedge	114	RSL1_ORF202	Ralstonia phage phiRSL1	GCA_000879455.1
AMS01095.1	000462	Base-wedge	848	AR9_g010	Bacillus phage AR9	GCA_001743835.1
ALN97728.1	000462	Base-wedge	818	Bp8pS_049	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00017.1	000462	Base-wedge	848	PBI_PBS1_195	Bacillus virus PBS1	GCA_002601325.1
prevph1000000463	000463	Base-wedge	93	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000355	000463	Base-wedge	245	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000464	000463	Base-wedge	114	-	Prevotella_phage_Lak-B8	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANS06110.1	000464	SIG+LysM	93	ABCD_0021	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97029.1	000464	SIG+LysM	93	E_020	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78542.1	000464	SIG+LysM	93	RB43ORF020c	Escherichia virus RB43	GCA_000863505.1
BBA65467.1	000465	Base-wedge	119	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96476.1	000465	Base-wedge	108	Xoosp13_290	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AMM44848.1	000000	Base-wedge	122	SP15_049	Bacillus phage SP-15	GCA_001754685.1
SBV38380.1	000000	Base-wedge	47	BN7874_207	Phage NCTB	GCA_900092385.1
QHJ85966.1	000000	Base-wedge	113	KKIINIFJ_00054	Pseudomonas phage PN05	GCA_009931935.1
QHJ86159.1	000000	Base-wedge	125	KKIINIFJ_00249	Pseudomonas phage PN05	GCA_009931935.1
CCE26071.1	000000	Base-wedge	154	g047	Yersinia phage phiR1-37	GCA_000895615.1
APU01659.1	000466	CYTH	155	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29108.1	000466	CYTH	158	AP1_0401	Aeromonas phage AP1	GCA_014183365.1
ATI17227.1	000466	CYTH	158	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00360.1	000466	CYTH	158	HWB28_gp192	Aeromonas phage AS-zj	GCA_002627665.1
AUE22545.1	000466	CYTH	162	Ah1_00004	Aeromonas phage Ah1	GCA_002957415.1
QAX98586.1	000466	CYTH	161	ASfcp2_253	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97670.1	000466	CYTH	158	ASswx1_24	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01071.1	000466	CYTH	157	ASwh1_3	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39493.1	000466	CYTH	158	CC2_091	Aeromonas phage CC2	GCA_000903495.1
QDB70356.1	000466	CYTH	178	CF8_0187	Aeromonas phage CF8	GCA_006384595.2
QDJ97336.1	000466	CYTH	504	D6_0177	Aeromonas phage D6	GCA_007051205.2
QDH47048.1	000466	CYTH	504	LAh10_96	Aeromonas phage LAh10	GCA_006863975.1
ADQ52722.1	000466	CYTH	161	PX29p003	Aeromonas phage PX29	GCA_000920195.1
ADM79974.1	000466	CYTH	156	phiAS5_ORF0131	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53290.1	000466	CYTH	155	65p282	Aeromonas virus 65	GCA_000893255.1
AAQ17659.1	000466	CYTH	162	Aeh1ORF004c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64305.1	000467	CYTH	285	KVP40.0236	Vibrio phage KVP40	GCA_000843785.1
QIW90621.1	000467	CYTH	274	GCAPEGMB_00274	Vibrio phage V07	GCA_012361095.1
QIW91178.1	000467	CYTH	274	COHAPHLL_00342	Vibrio phage V09	GCA_012361135.1
QHJ74416.1	000467	CYTH	274	VH12019_00089	Vibrio phage VH1_2019	GCA_009931825.1
AGB06924.1	000467	CYTH	274	CF80_gp137	Vibrio phage VH7D	GCA_000914495.1
QBX06222.1	000467	CYTH	274	ValB1HC_269	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60848.1	000467	CYTH	274	AVU32_gp007	Vibrio phage ValKK3	GCA_001501635.1
AGN30293.2	000467	CYTH	270	VPFG_00294	Vibrio phage nt-1	GCA_000910195.2
ALP47035.1	000467	CYTH	274	phiGrn1_0360	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47416.1	000467	CYTH	274	phiST2_0115	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54847.1	000467	CYTH	274	vBValMR10Z_307	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37466.1	000467	CYTH	274	pp2_233	Vibriophage phi-pp2	GCA_002630725.1
AXH72872.1	000000	CYTH	181	-	Myoviridae sp.	GCA_003657725.1
AYD81192.1	000468	Capsid-protease	361	SEA_JUSTBECAUSE_23	Streptomyces phage JustBecause	GCA_003613775.1
QJD53594.1	000468	Capsid-protease	361	SEA_KELA_23	Streptomyces phage Kela	GCA_012934305.1
QBZ71926.1	000468	Capsid-protease	361	SEA_KRADAL_27	Streptomyces phage Kradal	GCA_004799925.1
AXH66188.1	000468	Capsid-protease	361	SEA_SATIS_27	Streptomyces phage Satis	GCA_003366315.1
QDH83395.1	000469	Clamp-RFC-AAA	365	H1O15_gp067	Achromobacter phage Motura	GCA_006964305.1
APU01416.1	000469	Clamp-RFC-AAA	326	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28808.1	000469	Clamp-RFC-AAA	326	AP1_0101	Aeromonas phage AP1	GCA_014183365.1
ATI17481.1	000469	Clamp-RFC-AAA	326	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00516.1	000469	Clamp-RFC-AAA	326	HWB28_gp036	Aeromonas phage AS-zj	GCA_002627665.1
AUE22564.1	000469	Clamp-RFC-AAA	321	Ah1_00023	Aeromonas phage Ah1	GCA_002957415.1
QAX98602.1	000469	Clamp-RFC-AAA	323	ASfcp2_269	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97921.1	000469	Clamp-RFC-AAA	326	ASswx1_278	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01228.1	000469	Clamp-RFC-AAA	326	ASwh1_163	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39517.1	000469	Clamp-RFC-AAA	326	CC2_253	Aeromonas phage CC2	GCA_000903495.1
ADQ52737.1	000469	Clamp-RFC-AAA	323	PX29p018	Aeromonas phage PX29	GCA_000920195.1
ADM79990.1	000469	Clamp-RFC-AAA	322	phiAS5_ORF0147	Aeromonas phage phiAS5	GCA_000887715.1
AAR90913.1	000469	Clamp-RFC-AAA	326	65p025	Aeromonas virus 65	GCA_000893255.1
AAQ17675.1	000469	Clamp-RFC-AAA	321	44	Aeromonas virus Aeh1	GCA_000843245.1
ASV44741.1	000469	Clamp-RFC-AAA	315	FDI40_gp312	Agrobacterium phage Atu_ph07	GCA_002628245.1
QBX06708.1	000469	Clamp-RFC-AAA	384	BcepSaruman_295	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74676.1	000469	Clamp-RFC-AAA	384	BcepSauron_296	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63600.1	000469	Clamp-RFC-AAA	304	CP21_138	Campylobacter virus CP21	GCA_000902535.1
ANS05965.1	000469	Clamp-RFC-AAA	332	ABCD_0042	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65044.1	000469	Clamp-RFC-AAA	322	S13_247	Cronobacter phage S13	GCA_001503575.1
AFC21777.1	000469	Clamp-RFC-AAA	318	GAP32_327	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97052.1	000469	Clamp-RFC-AAA	332	E_043	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56872.1	000469	Clamp-RFC-AAA	313	CPXG_00069	Cyanophage P-RSM6	GCA_000906155.1
AJK27581.1	000469	Clamp-RFC-AAA	313	PTIM40_154	Cyanophage P-TIM40	GCA_001470935.1
AOO14343.1	000469	Clamp-RFC-AAA	313	Sn110110_149	Cyanophage S-RIM14	GCA_002599065.1
AOO14992.1	000469	Clamp-RFC-AAA	313	W1230910_146	Cyanophage S-RIM14	GCA_002599125.1
AMO43160.1	000469	Clamp-RFC-AAA	313	R1080702_151	Cyanophage S-RIM32	GCA_001754165.1
AMO43384.1	000469	Clamp-RFC-AAA	313	W270710_140	Cyanophage S-RIM44	GCA_002599145.1
AOO11629.1	000469	Clamp-RFC-AAA	313	ES420910_148	Cyanophage S-RIM44	GCA_002599165.1
AOO11856.1	000469	Clamp-RFC-AAA	313	Np050604_140	Cyanophage S-RIM44	GCA_002599185.1
AOO12094.1	000469	Clamp-RFC-AAA	313	Np200711_148	Cyanophage S-RIM44	GCA_002599205.1
AOO12330.1	000469	Clamp-RFC-AAA	313	Np420711_148	Cyanophage S-RIM44	GCA_002599225.1
AOO12557.1	000469	Clamp-RFC-AAA	313	Sn080709_140	Cyanophage S-RIM44	GCA_002599245.1
AOO12795.1	000469	Clamp-RFC-AAA	313	Sn130910_148	Cyanophage S-RIM44	GCA_002599265.1
AOO13023.1	000469	Clamp-RFC-AAA	313	W2100709_141	Cyanophage S-RIM44	GCA_002599285.1
AGH07486.1	000469	Clamp-RFC-AAA	315	CYVG_00042	Cyanophage S-SSM6a	GCA_002710385.1
AGG54468.1	000469	Clamp-RFC-AAA	314	CYWG_00184	Cyanophage S-SSM6b	GCA_002710425.1
AXG67249.1	000469	Clamp-RFC-AAA	429	AD1_205	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79997.1	000469	Clamp-RFC-AAA	406	JA11_192	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66595.1	000469	Clamp-RFC-AAA	406	JA13_192	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66920.1	000469	Clamp-RFC-AAA	406	JA29_194	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67566.1	000469	Clamp-RFC-AAA	406	JA33_192	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08479.1	000469	Clamp-RFC-AAA	426	Alexandra_215	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58849.1	000469	Clamp-RFC-AAA	430	Y3_209	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28679.1	000469	Clamp-RFC-AAA	430	YOLOSWAG_201	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT13957.1	000469	Clamp-RFC-AAA	317	PBI_121Q_60	Escherichia phage 121Q	GCA_000926855.1
QAY00380.1	000469	Clamp-RFC-AAA	317	Ecwhy1_99	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35125.1	000469	Clamp-RFC-AAA	317	ACQ29_gp445	Escherichia phage PBECO4	GCA_001041035.1
BBM61649.1	000469	Clamp-RFC-AAA	317	EO157G_0600	Escherichia phage SP27	GCA_008033345.1
AXC36699.1	000469	Clamp-RFC-AAA	317	-	Escherichia phage UB	GCA_003341455.1
ARM70874.1	000469	Clamp-RFC-AAA	320	phiC120_c169	Escherichia phage phiC120	GCA_002621185.1
QBO61736.1	000469	Clamp-RFC-AAA	317	G17_00247	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13781.1	000469	Clamp-RFC-AAA	317	vBEcoMphAPEC6_gp152c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80551.1	000469	Clamp-RFC-AAA	317	PSLUR01_00574	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78564.1	000469	Clamp-RFC-AAA	332	RB43ORF042c	Escherichia virus RB43	GCA_000863505.1
AFA44439.1	000469	Clamp-RFC-AAA	319	RaK2_00166	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72813.1	000469	Clamp-RFC-AAA	313	-	Myoviridae sp.	GCA_003657725.1
QHJ78888.1	000469	Clamp-RFC-AAA	320	-	Myoviridae sp.	GCA_012593985.1
QIG65675.1	000469	Clamp-RFC-AAA	315	phiOC_p009	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43895.1	000469	Clamp-RFC-AAA	317	CBB_332	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38537.1	000469	Clamp-RFC-AAA	430	BN7874_295	Phage NCTB	GCA_900092385.1
AGH26301.1	000469	Clamp-RFC-AAA	313	CPMG_00201	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44539.1	000469	Clamp-RFC-AAA	313	PSSM2_161	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12432.1	000469	Clamp-RFC-AAA	313	PRTG_00282	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93473.1	000469	Clamp-RFC-AAA	313	AVU42_gp136	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99242.1	000469	Clamp-RFC-AAA	313	Syn1_141	Prochlorococcus phage Syn1	GCA_000892495.1
AFH14652.1	000469	Clamp-RFC-AAA	373	Lu11_0120	Pseudomonas phage Lu11	GCA_000897175.1
AGS82061.1	000469	Clamp-RFC-AAA	379	PaBG_00185	Pseudomonas phage PaBG	GCA_000912555.1
QCG76172.1	000469	Clamp-RFC-AAA	309	EST35_0291	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41613.1	000469	Clamp-RFC-AAA	362	RSL1_ORF166	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44309.1	000469	Clamp-RFC-AAA	312	PBI_SCTP2_294	Salicola phage SCTP-2	GCA_002625545.1
QCW19054.1	000469	Clamp-RFC-AAA	318	7t3_0534	Salmonella phage 7t3	GCA_006083215.1
AZU98301.1	000469	Clamp-RFC-AAA	318	CPT_Munch_357	Salmonella phage Munch	GCA_004015485.1
QIG62683.1	000469	Clamp-RFC-AAA	318	SEPL_070	Salmonella phage SE_PL	GCA_011067555.1
AQW88855.1	000469	Clamp-RFC-AAA	317	BF_0330	Serratia phage BF	GCA_002619745.1
AGR47671.1	000469	Clamp-RFC-AAA	312	SmphiM12_039	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12934.1	000469	Clamp-RFC-AAA	312	PHIM19_27	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12574.1	000469	Clamp-RFC-AAA	312	PHIM7_26	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13306.1	000469	Clamp-RFC-AAA	312	PHIN3_41	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28074.1	000469	Clamp-RFC-AAA	314	PAU_76	Sphingomonas phage PAU	GCA_000902455.1
AIX30639.1	000469	Clamp-RFC-AAA	316	Syn7803US37_162	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54911.1	000469	Clamp-RFC-AAA	311	b23_0298	Synechococcus phage B23	GCA_009745195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54546.1	000469	Clamp-RFC-AAA	311	b3_0305	Synechococcus phage B3	GCA_009745215.1
ASR76198.1	000469	Clamp-RFC-AAA	316	PBI_BELLAMY_153	Synechococcus phage Bellamy	GCA_002627525.1
QDH50578.1	000469	Clamp-RFC-AAA	315	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59610.1	000469	Clamp-RFC-AAA	314	S330809_149	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59372.1	000469	Clamp-RFC-AAA	314	C440309_149	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59848.1	000469	Clamp-RFC-AAA	314	N231010_149	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70554.1	000469	Clamp-RFC-AAA	314	HOU04_gp155	Synechococcus phage S-T4	GCA_003443335.1
QJT70146.1	000469	Clamp-RFC-AAA	314	SynMITS9220M01_133	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90664.1	000469	Clamp-RFC-AAA	322	HYO65_gp272	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90969.1	000469	Clamp-RFC-AAA	322	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39207.1	000469	Clamp-RFC-AAA	338	BPT24_082	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64149.1	000469	Clamp-RFC-AAA	318	KVP40.0078	Vibrio phage KVP40	GCA_000843785.1
QIW90473.1	000469	Clamp-RFC-AAA	318	GCAPEGMB_00126	Vibrio phage V07	GCA_012361095.1
QIW90956.1	000469	Clamp-RFC-AAA	318	COHAPHLL_00093	Vibrio phage V09	GCA_012361135.1
QHJ74261.1	000469	Clamp-RFC-AAA	318	VH12019_00342	Vibrio phage VH1_2019	GCA_009931825.1
AGB07085.1	000469	Clamp-RFC-AAA	316	CF80_gp298	Vibrio phage VH7D	GCA_000914495.1
QBX06010.1	000469	Clamp-RFC-AAA	316	ValB1HC_056	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04480.1	000469	Clamp-RFC-AAA	310	ValB1MD_095	Vibrio phage ValB1MD	GCA_004138815.1
AJT61023.1	000469	Clamp-RFC-AAA	316	AVU32_gp182	Vibrio phage ValKK3	GCA_001501635.1
AGN30127.1	000469	Clamp-RFC-AAA	317	VPFG_00125	Vibrio phage nt-1	GCA_000910195.2
ALP47015.1	000469	Clamp-RFC-AAA	316	phiGrn1_0193	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47395.1	000469	Clamp-RFC-AAA	316	phiST2_0324	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54635.1	000469	Clamp-RFC-AAA	316	vBValMR10Z_94	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07130.1	000469	Clamp-RFC-AAA	324	VmeM32_00143	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37309.1	000469	Clamp-RFC-AAA	318	pp2_076	Vibriophage phi-pp2	GCA_002630725.1
BBA65389.1	000469	Clamp-RFC-AAA	310	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96417.1	000469	Clamp-RFC-AAA	311	Xoosp13_231	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59139.1	000469	Clamp-RFC-AAA	316	g331	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58605.1	000469	Clamp-RFC-AAA	316	g328	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000521	000469	Clamp-RFC-AAA	329	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000395	000469	Clamp-RFC-AAA	329	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM45019.1	000470	Clamp-RFC-AAA	429	SP15_218	Bacillus phage SP-15	GCA_001754685.1
AEO93341.1	000470	Clamp-RFC-AAA	442	G_70	Bacillus virus G	GCA_000917535.1
QDB70366.1	000471	CLP_protease	255	CF8_0198	Aeromonas phage CF8	GCA_006384595.2
QDJ97366.1	000471	CLP_protease	240	D6_0207	Aeromonas phage D6	GCA_007051205.2
QDH47118.1	000471	CLP_protease	240	LAh10_121	Aeromonas phage LAh10	GCA_006863975.1
QDJ96709.1	000471	CLP_protease	243	PS1_0198	Aeromonas phage PS1	GCA_007051165.2
QFR59342.1	000471	CLP_protease	243	PS2_0200	Aeromonas phage PS2	GCA_009388305.2
ASV44753.1	000471	CLP_protease	204	FDI40_gp676	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93516.1	000471	CLP_protease	200	G_257	Bacillus virus G	GCA_000917535.1
CCH63658.1	000471	CLP_protease	266	CP21_196	Campylobacter virus CP21	GCA_000902535.1
AFC21551.1	000471	CLP_protease	230	GAP32_103	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14354.1	000471	CLP_protease	231	PBI_121Q_464	Escherichia phage 121Q	GCA_000926855.1
QAY00590.1	000471	CLP_protease	231	Ecwhy1_313	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34785.1	000471	CLP_protease	231	ACQ29_gp105	Escherichia phage PBECO4	GCA_001041035.1
BBM62025.1	000471	CLP_protease	231	EO157G_4360	Escherichia phage SP27	GCA_008033345.1
AXC36901.1	000471	CLP_protease	231	-	Escherichia phage UB	GCA_003341455.1
QBO61950.1	000471	CLP_protease	231	G17_00461	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13977.1	000471	CLP_protease	231	vBEcoMphAPEC6_gp353c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80341.1	000471	CLP_protease	231	PSLUR01_00364	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QGH72055.1	000471	CLP_protease	215	N1M2_192	Klebsiella phage N1M2	GCA_010092605.1
AFA44591.1	000471	CLP_protease	210	RaK2_00318	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44762.1	000471	CLP_protease	249	RaK2_00489	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72920.1	000471	CLP_protease	200	-	Myoviridae sp.	GCA_003657725.1
AMM43669.1	000471	CLP_protease	230	CBB_104	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AEV89681.1	000471	CLP_protease	218	OBP_244	Pseudomonas phage OBP	GCA_000896635.1
QCG76153.1	000471	CLP_protease	223	EST35_0272	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44137.1	000471	CLP_protease	198	PBI_SCTP2_122	Salicola phage SCTP-2	GCA_002625545.1
QCW18804.1	000471	CLP_protease	225	7t3_0283	Salmonella phage 7t3	GCA_006083215.1
AZU98069.1	000471	CLP_protease	225	CPT_Munch_125	Salmonella phage Munch	GCA_004015485.1
QIG62913.1	000471	CLP_protease	225	SEPL_300	Salmonella phage SE_PL	GCA_011067555.1
AQW88622.1	000471	CLP_protease	219	BF_0097	Serratia phage BF	GCA_002619745.1
AQW88975.1	000471	CLP_protease	228	BF_0450	Serratia phage BF	GCA_002619745.1
AXH70828.1	000471	CLP_protease	163	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64078.1	000471	CLP_protease	239	KVP40.0007	Vibrio phage KVP40	GCA_000843785.1
QIW90404.1	000471	CLP_protease	242	GCAPEGMB_00057	Vibrio phage V07	GCA_012361095.1
QIW91025.1	000471	CLP_protease	239	COHAPHLL_00162	Vibrio phage V09	GCA_012361135.1
QHJ74190.1	000471	CLP_protease	239	VH12019_00271	Vibrio phage VH1_2019	GCA_009931825.1
AGB07014.1	000471	CLP_protease	238	CF80_gp227	Vibrio phage VH7D	GCA_000914495.1
QBX06082.1	000471	CLP_protease	238	ValB1HC_128	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04467.1	000471	CLP_protease	194	ValB1MD_065	Vibrio phage ValB1MD	GCA_004138815.1
AJT61096.1	000471	CLP_protease	238	AVU32_gp255	Vibrio phage ValKK3	GCA_001501635.1
AGN30057.1	000471	CLP_protease	244	VPFG_00054	Vibrio phage nt-1	GCA_000910195.2
ALP47048.1	000471	CLP_protease	238	phiGrn1_0122	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47427.1	000471	CLP_protease	238	phiST2_0253	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54708.1	000471	CLP_protease	238	vBValMR10Z_167	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QAX96665.1	000471	CLP_protease	170	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96983.1	000471	CLP_protease	170	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96029.1	000471	CLP_protease	170	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96347.1	000471	CLP_protease	170	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21074.1	000471	CLP_protease	164	-	Vibrio phage vB_pir03	GCA_014319855.1
AFN37241.1	000471	CLP_protease	239	pp2_007	Vibriophage phi-pp2	GCA_002630725.1
BBA65325.1	000471	CLP_protease	237	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96364.1	000471	CLP_protease	236	Xoosp13_177	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58898.1	000471	CLP_protease	219	g090	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58363.1	000471	CLP_protease	219	g086	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26121.1	000471	CLP_protease	219	g097	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000750	000471	CLP_protease	227	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000502	000471	CLP_protease	227	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AIT14363.1	000472	CLP_protease	202	PBI_121Q_473	Escherichia phage 121Q	GCA_000926855.1
AGC34777.1	000472	CLP_protease	202	ACQ29_gp097	Escherichia phage PBECO4	GCA_001041035.1
BBM62033.1	000472	CLP_protease	202	EO157G_4440	Escherichia phage SP27	GCA_008033345.1
AXC36893.1	000472	CLP_protease	202	-	Escherichia phage UB	GCA_003341455.1
QBO61942.1	000472	CLP_protease	202	G17_00453	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13970.1	000472	CLP_protease	202	vBEcoMphAPEC6_gp346c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80349.1	000472	CLP_protease	202	PSLUR01_00372	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44770.1	000472	CLP_protease	198	RaK2_00497	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
prevph1000000807	000473	CLP_protease	113	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000553	000473	CLP_protease	203	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFC21764.1	000474	ClpS	177	GAP32_314	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13945.1	000474	ClpS	181	PBI_121Q_48	Escherichia phage 121Q	GCA_000926855.1
QAY00392.1	000474	ClpS	181	Ecwhy1_111	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35137.1	000474	ClpS	181	ACQ29_gp457	Escherichia phage PBECO4	GCA_001041035.1
BBM61637.1	000474	ClpS	181	EO157G_0480	Escherichia phage SP27	GCA_008033345.1
AXC36711.1	000474	ClpS	181	-	Escherichia phage UB	GCA_003341455.1
QBO61748.1	000474	ClpS	181	G17_00259	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13793.1	000474	ClpS	181	vBEcoMphAPEC6_gp164c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80539.1	000474	ClpS	181	PSLUR01_00562	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44427.1	000474	ClpS	179	RaK2_00154	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43882.1	000474	ClpS	177	CBB_319	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19042.1	000474	ClpS	183	7t3_0522	Salmonella phage 7t3	GCA_006083215.1
AZU98289.1	000474	ClpS	183	CPT_Munch_345	Salmonella phage Munch	GCA_004015485.1
QIG62695.1	000474	ClpS	183	SEPL_082	Salmonella phage SE_PL	GCA_011067555.1
AQW88842.1	000474	ClpS	173	BF_0317	Serratia phage BF	GCA_002619745.1
SOK59126.1	000474	ClpS	175	g318	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58592.1	000474	ClpS	175	g315	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95447.1	000475	ClpS	100	FDI40_gp708	Agrobacterium phage Atu_ph07	GCA_002628245.1
QCG76141.1	000475	ClpS	100	EST35_0260	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44207.1	000475	ClpS	100	PBI_SCTP2_192	Salicola phage SCTP-2	GCA_002625545.1
AXH72843.1	000000	ClpS	105	-	Myoviridae sp.	GCA_003657725.1
ARB15038.1	000476	DCMethylase	323	Ccr32_gp120	Caulobacter phage Ccr32	GCA_002619505.1
ARB14339.1	000476	DCMethylase	352	Ccr5_gp121c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68319.1	000476	DCMethylase	357	CcrBL10_gp115c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69211.1	000476	DCMethylase	328	CcrBL9_gp187	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88029.1	000476	DCMethylase	346	CcrColossus_gp159	Caulobacter phage CcrColossus	GCA_000899635.1

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AXQ68706.1	000476	DCMethylase	346	CcrPW_gp167c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69765.1	000476	DCMethylase	328	CcrSC_gp183	Caulobacter phage CcrSC	GCA_003443315.1
AFU87643.1	000476	DCMethylase	352	CcrKarma_gp126	Caulobacter virus Karma	GCA_000901575.1
AFU87292.1	000476	DCMethylase	352	CcrMagneto_gp122	Caulobacter virus Magneto	GCA_000903095.1
AFU86603.1	000476	DCMethylase	357	CcrRogue_gp121	Caulobacter virus Rogue	GCA_000900555.1
AFU88439.1	000476	DCMethylase	352	CcrSwift_gp121	Caulobacter virus Swift	GCA_000899655.1
AFU86956.1	000476	DCMethylase	352	CbK_gp124	Caulobacter virus phiCbK	GCA_000900535.1
ANS05975.1	000476	DCMethylase	303	ABCD_0126	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47742.1	000476	DCMethylase	370	CST044	Clostridium phage c-st	GCA_000865225.1
AFC21842.1	000476	DCMethylase	288	GAP32_390	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97137.1	000476	DCMethylase	307	E_129	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXG67092.1	000476	DCMethylase	709	AD1_048	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08326.1	000476	DCMethylase	709	Alexandra_46	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58690.1	000476	DCMethylase	709	Y3_050	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28528.1	000476	DCMethylase	702	YOLOSWAG_43	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT13988.1	000476	DCMethylase	286	PBI_121Q_91	Escherichia phage 121Q	GCA_000926855.1
QAY00350.1	000476	DCMethylase	286	Ecwhy1_69	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35096.1	000476	DCMethylase	286	ACQ29_gp416	Escherichia phage PBECO4	GCA_001041035.1
BBM61679.1	000476	DCMethylase	286	EO157G_0900	Escherichia phage SP27	GCA_008033345.1
AXC36673.1	000476	DCMethylase	286	-	Escherichia phage UB	GCA_003341455.1
QBO61705.1	000476	DCMethylase	286	G17_00216	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13752.1	000476	DCMethylase	286	vBEcoMphAPEC6_gp123c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79992.1	000476	DCMethylase	286	PSLUR01_00008	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78649.1	000476	DCMethylase	302	RB43ORF127c	Escherichia virus RB43	GCA_000863505.1
AFA44467.1	000476	DCMethylase	297	RaK2_00194	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72851.1	000476	DCMethylase	356	-	Myoviridae sp.	GCA_003657725.1
AMM43962.1	000476	DCMethylase	286	CBB_399	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGS82053.1	000476	DCMethylase	335	PaBG_00177	Pseudomonas phage PaBG	GCA_000912555.1
QCW22935.1	000476	DCMethylase	372	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50620.1	000476	DCMethylase	372	-	Synechococcus phage S-B43	GCA_006869725.1
ARB13650.1	000477	DCMethylase	69	Ccr10_gp121c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13995.1	000477	DCMethylase	69	Ccr2_gp120c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14683.1	000477	DCMethylase	69	Ccr29_gp127	Caulobacter phage Ccr29	GCA_002619485.1
ARB15370.1	000477	DCMethylase	69	Ccr34_gp128	Caulobacter phage Ccr34	GCA_002619525.1
AEO93560.1	000000	DCMethylase	426	G_301	Bacillus virus G	GCA_000917535.1
AND75286.1	000478	DHH	287	ME3_125	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ARB13588.1	000478	DHH	352	Ccr10_gp060	Caulobacter phage Ccr10	GCA_002619445.1
ARB13934.1	000478	DHH	352	Ccr2_gp059	Caulobacter phage Ccr2	GCA_002619465.1
ARB14623.1	000478	DHH	352	Ccr29_gp066	Caulobacter phage Ccr29	GCA_002619485.1
ARB14979.1	000478	DHH	352	Ccr32_gp060	Caulobacter phage Ccr32	GCA_002619505.1
ARB15310.1	000478	DHH	352	Ccr34_gp061	Caulobacter phage Ccr34	GCA_002619525.1
ARB14277.1	000478	DHH	352	Ccr5_gp059	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68261.1	000478	DHH	311	CcrBL10_gp057	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87940.1	000478	DHH	309	CcrColossus_gp070	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68612.1	000478	DHH	309	CcrPW_gp073	Caulobacter phage CcrPW	GCA_003443275.1
AFU87578.1	000478	DHH	352	CcrKarma_gp061	Caulobacter virus Karma	GCA_000901575.1
AFU87228.1	000478	DHH	352	CcrMagneto_gp058	Caulobacter virus Magneto	GCA_000903095.1
AFU86544.1	000478	DHH	349	CcrRogue_gp062	Caulobacter virus Rogue	GCA_000900555.1
AFU88376.1	000478	DHH	352	CcrSwift_gp058	Caulobacter virus Swift	GCA_000899655.1
AFU86892.1	000478	DHH	352	CbK_gp060	Caulobacter virus phiCbK	GCA_000900535.1
AGX01811.1	000478	DHH	321	CF95_gp089	Erwinia phage PhiEaH1	GCA_000914555.1
CAG27219.1	000478	DHH	412	PPEV_gp125	Pseudomonas phage EL	GCA_000866825.1
ARV77405.1	000478	DHH	336	NOXIFER_240	Pseudomonas phage Noxifer	GCA_002625005.1
AGS82064.1	000478	DHH	283	PaBG_00188	Pseudomonas phage PaBG	GCA_000912555.1
BAW19142.1	000478	DHH	336	FDH28_gp253	Ralstonia phage RP12	GCA_002617345.1
BAW19428.1	000478	DHH	336	-	Ralstonia phage RP31	GCA_002617365.1
ATA65596.1	000478	DHH	310	2050HW_00261	Serratia phage 2050HW	GCA_002628125.1
QDB71360.1	000478	DHH	310	CPT_Moabite_330	Serratia phage Moabite	GCA_006384735.1
QFP93105.1	000478	DHH	324	-	Serratia phage PCH45	GCA_009187865.1
AXG67202.1	000479	DHH	361	AD1_158	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79953.1	000479	DHH	348	JA11_148	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66552.1	000479	DHH	348	JA13_149	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66877.1	000479	DHH	348	JA29_151	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67522.1	000479	DHH	348	JA33_148	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08435.1	000479	DHH	366	Alexandra_163	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58799.1	000479	DHH	347	Y3_159	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28637.1	000479	DHH	371	YOLOSWAG_157	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AMS01241.1	000480	DHH	296	AR9_g157	Bacillus phage AR9	GCA_001743835.1
AST99867.1	000480	DHH	296	PBI_PBS1_45	Bacillus virus PBS1	GCA_002601325.1
ALN97901.1	000480	DHH	298	Bp8pS_222	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
prevph1000000208	000481	DHH	322	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000164	000481	DHH	322	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83639.1	000000	DHH	577	0305phi8-36p079	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44898.1	000000	DHH	307	SP15_099	Bacillus phage SP-15	GCA_001754685.1
AEO93519.1	000000	DHH	323	G_260	Bacillus virus G	GCA_000917535.1
QAU04488.1	000000	DHH	307	ValB1MD_121	Vibrio phage ValB1MD	GCA_004138815.1
QIG57860.1	000000	DHH	99	SEA_PAULODIABOLI_144	Microbacterium phage PauloDiaboli	GCA_011067425.1
SBV38335.1	000000	DHH	296	BN7874_166	Phage NCTB	GCA_900092385.1
SBV38518.1	000000	DHH	319	BN7874_287	Phage NCTB	GCA_900092385.1
APU01503.1	000482	DNA-end-protector	331	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28988.1	000482	DNA-end-protector	332	AP1_0281	Aeromonas phage AP1	GCA_014183365.1
ATI17395.1	000482	DNA-end-protector	332	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00200.1	000482	DNA-end-protector	332	HWB28_gp352	Aeromonas phage AS-zj	GCA_002627665.1
AUE22724.1	000482	DNA-end-protector	332	Ah1_00206	Aeromonas phage Ah1	GCA_002957415.1
QAX98447.1	000482	DNA-end-protector	332	ASfcp2_104	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97836.1	000482	DNA-end-protector	332	ASswx1_192	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01316.1	000482	DNA-end-protector	332	ASwh1_254	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39561.1	000482	DNA-end-protector	332	CC2_343	Aeromonas phage CC2	GCA_000903495.1
ADQ52904.1	000482	DNA-end-protector	332	PX29p185	Aeromonas phage PX29	GCA_000920195.1
ADM80171.1	000482	DNA-end-protector	332	phiAS5_ORF0328	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53124.1	000482	DNA-end-protector	331	65p116	Aeromonas virus 65	GCA_000893255.1
AAQ17856.1	000482	DNA-end-protector	332	2	Aeromonas virus Aeh1	GCA_000843245.1
CCH63528.1	000482	DNA-end-protector	166	CP21_066	Campylobacter virus CP21	GCA_000902535.1
ANS05982.1	000482	DNA-end-protector	284	ABCD_0191	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64961.1	000482	DNA-end-protector	331	S13_162	Cronobacter phage S13	GCA_001503575.1
AON97205.1	000482	DNA-end-protector	284	E_197	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH57012.1	000482	DNA-end-protector	158	CPXG_00209	Cyanophage P-RSM6	GCA_000906155.1
AJK27443.1	000482	DNA-end-protector	156	PTIM40_16	Cyanophage P-TIM40	GCA_001470935.1
AMO43020.1	000482	DNA-end-protector	220	R1080702_005	Cyanophage S-RIM32	GCA_001754165.1
AMO43251.1	000482	DNA-end-protector	220	W270710_006	Cyanophage S-RIM44	GCA_002599145.1
AOO11488.1	000482	DNA-end-protector	220	ES420910_006	Cyanophage S-RIM44	GCA_002599165.1
AOO11723.1	000482	DNA-end-protector	220	Np050604_006	Cyanophage S-RIM44	GCA_002599185.1
AOO11953.1	000482	DNA-end-protector	220	Np200711_006	Cyanophage S-RIM44	GCA_002599205.1
AOO12189.1	000482	DNA-end-protector	220	Np420711_006	Cyanophage S-RIM44	GCA_002599225.1
AOO12424.1	000482	DNA-end-protector	220	Sn080709_006	Cyanophage S-RIM44	GCA_002599245.1
AOO12654.1	000482	DNA-end-protector	220	Sn130910_006	Cyanophage S-RIM44	GCA_002599265.1
AOO12889.1	000482	DNA-end-protector	220	W2100709_006	Cyanophage S-RIM44	GCA_002599285.1
AGH07633.1	000482	DNA-end-protector	164	CYVG_00190	Cyanophage S-SSM6a	GCA_002710385.1
ARM70974.1	000482	DNA-end-protector	273	phiC120_c269	Escherichia phage phiC120	GCA_002621185.1
AAX78723.1	000482	DNA-end-protector	284	RB43ORF201c	Escherichia virus RB43	GCA_000863505.1
QHJ78973.1	000482	DNA-end-protector	332	-	Myoviridae sp.	GCA_012593985.1
QIG65734.1	000482	DNA-end-protector	219	phiOC_p069	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26200.1	000482	DNA-end-protector	154	CPMG_00099	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99109.1	000482	DNA-end-protector	220	Syn1_007	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47789.2	000482	DNA-end-protector	200	SmphiM12_157	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13010.1	000482	DNA-end-protector	200	PHIM19_104	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12650.1	000482	DNA-end-protector	200	PHIM7_103	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13382.2	000482	DNA-end-protector	200	PHIN3_117	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28137.1	000482	DNA-end-protector	249	PAU_139	Sphingomonas phage PAU	GCA_000902455.1
AOV59466.1	000482	DNA-end-protector	229	S330809_005	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59228.1	000482	DNA-end-protector	229	C440309_005	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59704.1	000482	DNA-end-protector	229	N231010_005	Synechococcus phage S-CAM4	GCA_002922155.1
BBI90689.1	000482	DNA-end-protector	215	HYO65_gp297	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90996.1	000482	DNA-end-protector	243	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39270.1	000482	DNA-end-protector	248	BPT24_144	Tenacibaculum phage pT24	GCA_002611925.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW90712.1	000482	DNA-end-protector	198	GCAPEGMB_00393	Vibrio phage V07	GCA_012361095.1
QIW91085.1	000482	DNA-end-protector	198	COHAPHLL_00222	Vibrio phage V09	GCA_012361135.1
QHJ74512.1	000482	DNA-end-protector	198	VH12019_00212	Vibrio phage VH1_2019	GCA_009931825.1
QBX06143.1	000482	DNA-end-protector	198	ValB1HC_189	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04549.1	000482	DNA-end-protector	182	ValB1MD_264	Vibrio phage ValB1MD	GCA_004138815.1
AJT61155.1	000482	DNA-end-protector	198	AVU32_gp314	Vibrio phage ValKK3	GCA_001501635.1
AGN30381.1	000482	DNA-end-protector	198	VPFG_00384	Vibrio phage nt-1	GCA_000910195.2
ALP47070.1	000482	DNA-end-protector	198	phiGrn1_0064	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47449.1	000482	DNA-end-protector	198	phiST2_0196	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54768.1	000482	DNA-end-protector	198	vBValMR10Z_228	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37562.1	000482	DNA-end-protector	137	pp2_330	Vibriophage phi-pp2	GCA_002630725.1
AAX44389.1	000483	DNA-end-protector	115	PSSM2_011	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12259.1	000483	DNA-end-protector	115	PRTG_00104	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93393.1	000483	DNA-end-protector	125	AVU42_gp007	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30480.1	000483	DNA-end-protector	126	Syn7803US37_3	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54632.1	000483	DNA-end-protector	192	b23_0004	Synechococcus phage B23	GCA_009745195.1
QGT54262.1	000483	DNA-end-protector	192	b3_0004	Synechococcus phage B3	GCA_009745215.1
ASR76054.1	000483	DNA-end-protector	116	PBI_BELLAMY_7	Synechococcus phage Bellamy	GCA_002627525.1
QCW22925.1	000483	DNA-end-protector	129	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50640.1	000483	DNA-end-protector	129	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70446.1	000483	DNA-end-protector	129	HOU04_gp047	Synechococcus phage S-T4	GCA_003443335.1
QJT70022.1	000483	DNA-end-protector	114	SynMITS9220M01_006	Synechococcus phage SynMITS9220M01	GCA_013187275.1
prevph1000000564	000484	DNA-end-protector	145	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000411	000484	DNA-end-protector	233	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01510.1	000485	DNAJ	337	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29084.1	000485	DNAJ	337	AP1_0377	Aeromonas phage AP1	GCA_014183365.1
ATI17386.1	000485	DNAJ	337	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00207.1	000485	DNAJ	337	HWB28_gp345	Aeromonas phage AS-zj	GCA_002627665.1
QAX97828.1	000485	DNAJ	337	ASswx1_184	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01324.1	000485	DNAJ	337	ASwh1_262	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39483.1	000485	DNAJ	337	CC2_351	Aeromonas phage CC2	GCA_000903495.1
ADQ53132.1	000485	DNAJ	244	65p124	Aeromonas virus 65	GCA_000893255.1
ANS05941.1	000485	DNAJ	565	ABCD_0057	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97069.1	000485	DNAJ	566	E_060	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78579.1	000485	DNAJ	237	RB43ORF057w	Escherichia virus RB43	GCA_000863505.1
ALY07140.1	000485	DNAJ	350	VmeM32_00154	Vibrio phage vB_VmeM-32	GCA_002608825.1
AAX78580.1	000485	DNAJ	305	RB43ORF058w	Escherichia virus RB43	GCA_000863505.1
AUZ95062.1	000486	DNAJ+DnaJ_C	268	FDI40_gp293	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72816.1	000486	DNAJ+DnaJ_C	260	-	Myoviridae sp.	GCA_003657725.1
prevph1000000625	000486	DNAJ+DnaJ_C	359	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000444	000486	DNAJ+DnaJ_C	363	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDH83459.1	000487	DnaJ	223	H1O15_gp051	Achromobacter phage Motura	GCA_006964305.1
QBX06589.1	000487	DnaJ	248	BcepSaruman_176	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74554.1	000487	DnaJ	248	BcepSauron_174	Burkholderia phage BcepSauron	GCA_005394215.1
AXH72849.1	000000	SIG+DNAJ	259	-	Myoviridae sp.	GCA_003657725.1
QCG76178.1	000000	DnaJ+DnaJ_C	229	EST35_0297	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ANS06041.1	000488	EndoV	161	ABCD_0017	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFC21957.1	000488	EndoV	146	GAP32_498	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14107.1	000488	EndoV	171	PBI_121Q_217	Escherichia phage 121Q	GCA_000926855.1
QAY00814.1	000488	EndoV	171	Ecwhy1_541	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34989.1	000488	EndoV	144	ACQ29_gp309	Escherichia phage PBECO4	GCA_001041035.1
BBM61789.1	000488	EndoV	171	EO157G_2000	Escherichia phage SP27	GCA_008033345.1
AXC36568.1	000488	EndoV	171	-	Escherichia phage UB	GCA_003341455.1
ARM70943.1	000488	EndoV	137	phiC120_c238	Escherichia phage phiC120	GCA_002621185.1
QBO61592.1	000488	EndoV	171	G17_00096	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13653.1	000488	EndoV	144	vBEcoMphAPEC6_gp022c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80101.1	000488	EndoV	144	PSLUR01_00124	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78538.1	000488	EndoV	161	RB43ORF016c	Escherichia virus RB43	GCA_000863505.1
AFA44564.1	000488	EndoV	147	RaK2_00291	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44082.1	000488	EndoV	144	CBB_519	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AAQ64274.1	000488	EndoV	138	KVP40.0205	Vibrio phage KVP40	GCA_000843785.1
QIW90590.1	000488	EndoV	138	GCAPEGMB_00243	Vibrio phage V07	GCA_012361095.1
QIW91209.1	000488	EndoV	138	COHAPHLL_00373	Vibrio phage V09	GCA_012361135.1
QHJ74386.1	000488	EndoV	138	VH12019_00059	Vibrio phage VH1_2019	GCA_009931825.1
AGB06891.1	000488	EndoV	134	CF80_gp104	Vibrio phage VH7D	GCA_000914495.1
QBX06255.1	000488	EndoV	140	ValB1HC_302	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60881.1	000488	EndoV	140	AVU32_gp040	Vibrio phage ValKK3	GCA_001501635.1
AGN30264.1	000488	EndoV	140	VPFG_00265	Vibrio phage nt-1	GCA_000910195.2
ALP47148.1	000488	EndoV	134	phiGrn1_0329	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47535.1	000488	EndoV	134	phiST2_0084	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54882.1	000488	EndoV	140	vBValMR10Z_342	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37434.1	000488	EndoV	138	pp2_201	Vibriophage phi-pp2	GCA_002630725.1
APU01440.1	000489	5_3_exonuc_N+RNaseH_C	306	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28795.1	000489	5_3_exonuc_N+RNaseH_C	311	AP1_0088	Aeromonas phage AP1	GCA_014183365.1
ATI17459.1	000489	5_3_exonuc_N+RNaseH_C	311	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00137.1	000489	5_3_exonuc_N+RNaseH_C	311	HWB28_gp013	Aeromonas phage AS-zj	GCA_002627665.1
AUE22853.1	000489	5_3_exonuc_N+RNaseH_C	306	Ah1_00335	Aeromonas phage Ah1	GCA_002957415.1
QAX98564.1	000489	5_3_exonuc_N+RNaseH_C	306	ASfcp2_230	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97899.1	000489	5_3_exonuc_N+RNaseH_C	311	ASswx1_256	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01254.1	000489	5_3_exonuc_N+RNaseH_C	307	ASwh1_189	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39528.1	000489	5_3_exonuc_N+RNaseH_C	311	CC2_277	Aeromonas phage CC2	GCA_000903495.1
ADQ53029.1	000489	5_3_exonuc_N+RNaseH_C	300	PX29p310	Aeromonas phage PX29	GCA_000920195.1
ADM79953.1	000489	5_3_exonuc_N+RNaseH_C	306	phiAS5_ORF0110	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53060.1	000489	5_3_exonuc_N+RNaseH_C	306	65p050	Aeromonas virus 65	GCA_000893255.1
AAQ17982.1	000489	5_3_exonuc_N+RNaseH_C	306	rnh	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95046.1	000489	5_3_exonuc_N+RNaseH_C	353	FDI40_gp271	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63601.1	000489	5_3_exonuc_N+RNaseH_C	352	CP21_139	Campylobacter virus CP21	GCA_000902535.1
ANS05971.1	000489	5_3_exonuc_N+RNaseH_C	311	ABCD_0049	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64810.1	000489	5_3_exonuc_N+RNaseH_C	302	S13_011	Cronobacter phage S13	GCA_001503575.1
AFC21716.1	000489	5_3_exonuc_N+RNaseH_C	328	GAP32_266	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97059.1	000489	5_3_exonuc_N+RNaseH_C	311	E_050	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AMO43230.1	000489	5_3_exonuc_N+RNaseH_C	287	R1080702_225	Cyanophage S-RIM32	GCA_001754165.1
AMO43462.1	000489	5_3_exonuc_N+RNaseH_C	287	W270710_223	Cyanophage S-RIM44	GCA_002599145.1
AOO11702.1	000489	5_3_exonuc_N+RNaseH_C	287	ES420910_225	Cyanophage S-RIM44	GCA_002599165.1
AOO11934.1	000489	5_3_exonuc_N+RNaseH_C	287	Np050604_223	Cyanophage S-RIM44	GCA_002599185.1
AOO12168.1	000489	5_3_exonuc_N+RNaseH_C	287	Np200711_226	Cyanophage S-RIM44	GCA_002599205.1
AOO12403.1	000489	5_3_exonuc_N+RNaseH_C	287	Np420711_225	Cyanophage S-RIM44	GCA_002599225.1
AOO12635.1	000489	5_3_exonuc_N+RNaseH_C	287	Sn080709_223	Cyanophage S-RIM44	GCA_002599245.1
AOO12868.1	000489	5_3_exonuc_N+RNaseH_C	287	Sn130910_225	Cyanophage S-RIM44	GCA_002599265.1
AOO13101.1	000489	5_3_exonuc_N+RNaseH_C	287	W2100709_224	Cyanophage S-RIM44	GCA_002599285.1
AIT13898.1	000489	5_3_exonuc_N+RNaseH_C	345	PBI_121Q_1	Escherichia phage 121Q	GCA_000926855.1
QAY00440.1	000489	5_3_exonuc_N+RNaseH_C	328	Ecwhy1_160	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35183.1	000489	5_3_exonuc_N+RNaseH_C	298	ACQ29_gp503	Escherichia phage PBECO4	GCA_001041035.1
BBM61590.1	000489	5_3_exonuc_N+RNaseH_C	328	EO157G_0010	Escherichia phage SP27	GCA_008033345.1
AXC36755.1	000489	5_3_exonuc_N+RNaseH_C	281	-	Escherichia phage UB	GCA_003341455.1
ARM70797.1	000489	5_3_exonuc_N+RNaseH_C	305	phiC120_c91	Escherichia phage phiC120	GCA_002621185.1
QBO61794.1	000489	5_3_exonuc_N+RNaseH_C	328	G17_00305	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13838.1	000489	5_3_exonuc_N+RNaseH_C	281	vBEcoMphAPEC6_gp209c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80493.1	000489	5_3_exonuc_N+RNaseH_C	328	PSLUR01_00516	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78571.1	000489	5_3_exonuc_N+RNaseH_C	311	RB43ORF049c	Escherichia virus RB43	GCA_000863505.1
AFA44381.1	000489	5_3_exonuc_N+RNaseH_C	328	RaK2_00108	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72917.1	000489	5_3_exonuc_N+RNaseH_C	360	-	Myoviridae sp.	GCA_003657725.1
QHJ78854.1	000489	5_3_exonuc_N+RNaseH_C	302	-	Myoviridae sp.	GCA_012593985.1
QIG65757.1	000489	5_3_exonuc_N+RNaseH_C	270	phiOC_p092	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43836.1	000489	5_3_exonuc_N+RNaseH_C	328	CBB_272	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ADO99323.1	000489	5_3_exonuc_N+RNaseH_C	287	Syn1_227	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76206.1	000489	5_3_exonuc_N+RNaseH_C	328	EST35_0325	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44191.1	000489	5_3_exonuc_N+RNaseH_C	355	PBI_SCTP2_176	Salicola phage SCTP-2	GCA_002625545.1
QCW18995.1	000489	5_3_exonuc_N+RNaseH_C	335	7t3_0475	Salmonella phage 7t3	GCA_006083215.1
AZU98243.1	000489	5_3_exonuc_N+RNaseH_C	328	CPT_Munch_299	Salmonella phage Munch	GCA_004015485.1
QIG62741.1	000489	5_3_exonuc_N+RNaseH_C	335	SEPL_128	Salmonella phage SE_PL	GCA_011067555.1
AQW88795.1	000489	5_3_exonuc_N+RNaseH_C	328	BF_0270	Serratia phage BF	GCA_002619745.1
AGR47893.1	000489	5_3_exonuc_N+RNaseH_C	281	SmphiM12_261	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13093.1	000489	5_3_exonuc_N+RNaseH_C	281	PHIM19_188	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12733.1	000489	5_3_exonuc_N+RNaseH_C	281	PHIM7_188	Sinorhizobium phage phiM7	GCA_002622405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF13463.1	000489	5_3_exonuc_N+RNaseH_C	281	PHIN3_200	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64072.1	000489	5_3_exonuc_N+RNaseH_C	310	KVP40.0001	Vibrio phage KVP40	GCA_000843785.1
QIW90398.1	000489	5_3_exonuc_N+RNaseH_C	310	GCAPEGMB_00051	Vibrio phage V07	GCA_012361095.1
QIW91031.1	000489	5_3_exonuc_N+RNaseH_C	310	COHAPHLL_00168	Vibrio phage V09	GCA_012361135.1
QHJ74184.1	000489	5_3_exonuc_N+RNaseH_C	310	VH12019_00265	Vibrio phage VH1_2019	GCA_009931825.1
AGB07008.1	000489	5_3_exonuc_N+RNaseH_C	310	CF80_gp221	Vibrio phage VH7D	GCA_000914495.1
QBX06088.1	000489	5_3_exonuc_N+RNaseH_C	310	ValB1HC_134	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04521.1	000489	5_3_exonuc_N+RNaseH_C	355	ValB1MD_200	Vibrio phage ValB1MD	GCA_004138815.1
AJT61102.1	000489	5_3_exonuc_N+RNaseH_C	310	AVU32_gp261	Vibrio phage ValKK3	GCA_001501635.1
AIE13790.1	000489	5_3_exonuc_N+RNaseH_C	238	VPFG_00048	Vibrio phage nt-1	GCA_000910195.2
ALP47017.1	000489	5_3_exonuc_N+RNaseH_C	310	phiGrn1_0116	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47396.1	000489	5_3_exonuc_N+RNaseH_C	310	phiST2_0247	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54714.1	000489	5_3_exonuc_N+RNaseH_C	310	vBValMR10Z_173	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07094.1	000489	5_3_exonuc_N+RNaseH_C	318	VmeM32_00105	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37235.1	000489	5_3_exonuc_N+RNaseH_C	310	pp2_001	Vibriophage phi-pp2	GCA_002630725.1
BBA65488.1	000489	5_3_exonuc_N+RNaseH_C	316	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96495.1	000489	5_3_exonuc_N+RNaseH_C	316	Xoosp13_309	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59077.1	000489	5_3_exonuc_N+RNaseH_C	328	g269	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58542.1	000489	5_3_exonuc_N+RNaseH_C	328	g265	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000717	000489	5_3_exonuc_N+RNaseH_C	359	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000486	000489	5_3_exonuc_N+RNaseH_C	400	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDH83385.1	000490	5_3_exonuc_N+5_3_exonuc	288	H1O15_gp078	Achromobacter phage Motura	GCA_006964305.1
AEO93933.1	000490	5_3_exonuc_N+5_3_exonuc	291	G_690	Bacillus virus G	GCA_000917535.1
QBX06699.1	000490	5_3_exonuc_N+5_3_exonuc	304	BcepSaruman_286	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74667.1	000490	5_3_exonuc_N+5_3_exonuc	304	BcepSauron_287	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67055.1	000490	5_3_exonuc_N+5_3_exonuc	342	AD1_011	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79814.1	000490	5_3_exonuc_N+5_3_exonuc	345	JA11_009	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66412.1	000490	5_3_exonuc_N+5_3_exonuc	345	JA13_009	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66735.1	000490	5_3_exonuc_N+5_3_exonuc	345	JA29_009	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67383.1	000490	5_3_exonuc_N+5_3_exonuc	345	JA33_009	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08292.1	000490	5_3_exonuc_N+5_3_exonuc	342	Alexandra_11	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58651.1	000490	5_3_exonuc_N+5_3_exonuc	323	Y3_011	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28498.1	000490	5_3_exonuc_N+5_3_exonuc	345	YOLOSWAG_11	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38272.1	000490	5_3_exonuc_N+5_3_exonuc	343	BN7874_103	Phage NCTB	GCA_900092385.1
AFH14684.1	000490	5_3_exonuc_N+5_3_exonuc	281	Lu11_0151	Pseudomonas phage Lu11	GCA_000897175.1
AGS82019.1	000490	5_3_exonuc_N+5_3_exonuc	293	PaBG_00137	Pseudomonas phage PaBG	GCA_000912555.1
BAG41625.1	000490	5_3_exonuc_N+5_3_exonuc	250	RSL1_ORF177	Ralstonia phage phiRSL1	GCA_000879455.1
AFF28081.1	000491	5_3_exonuc_N	436	PAU_83	Sphingomonas phage PAU	GCA_000902455.1
BAV39285.1	000491	5_3_exonuc_N	524	BPT24_159	Tenacibaculum phage pT24	GCA_002611925.1
BBI90675.1	000492	5_3_exonuc_N	480	HYO65_gp283	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90982.1	000492	5_3_exonuc_N	480	-	Tenacibaculum phage PTm5	GCA_009730715.1
AMM44903.1	000000	5_3_exonuc_N	322	SP15_104	Bacillus phage SP-15	GCA_001754685.1
QHJ86057.1	000000	5_3_exonuc_N	288	KKIINIFJ_00145	Pseudomonas phage PN05	GCA_009931935.1
QHJ86020.1	000000	5_3_exonuc_N	332	KKIINIFJ_00108	Pseudomonas phage PN05	GCA_009931935.1
AND75246.1	000000	5_3_exonuc_N	298	ME3_85	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QIW90852.1	000000	5_3_exonuc	282	GCAPEGMB_00537	Vibrio phage V07	GCA_012361095.1
BAG41624.1	000000	5_3_exonuc	81	RSL1_ORF176	Ralstonia phage phiRSL1	GCA_000879455.1
QDH83438.1	000493	GTP_cyclohydroI	219	H1O15_gp030	Achromobacter phage Motura	GCA_006964305.1
CCH63693.1	000493	GTP_cyclohydroI	251	CP21_233	Campylobacter virus CP21	GCA_000902535.1
SBV38459.1	000493	GTP_cyclohydroI	238	BN7874_256	Phage NCTB	GCA_900092385.1
QCG76134.1	000493	GTP_cyclohydroI	229	EST35_0253	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAQ64192.1	000493	GTP_cyclohydroI	222	KVP40.0121	Vibrio phage KVP40	GCA_000843785.1
QIW90772.1	000493	GTP_cyclohydroI	207	GCAPEGMB_00453	Vibrio phage V07	GCA_012361095.1
QIW90835.1	000493	GTP_cyclohydroI	222	GCAPEGMB_00520	Vibrio phage V07	GCA_012361095.1
QIW90914.1	000493	GTP_cyclohydroI	222	COHAPHLL_00051	Vibrio phage V09	GCA_012361135.1
QHJ74304.1	000493	GTP_cyclohydroI	222	VH12019_00385	Vibrio phage VH1_2019	GCA_009931825.1
AGB06798.1	000493	GTP_cyclohydroI	222	CF80_gp011	Vibrio phage VH7D	GCA_000914495.1
QBX05968.1	000493	GTP_cyclohydroI	222	ValB1HC_014	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60980.1	000493	GTP_cyclohydroI	222	AVU32_gp139	Vibrio phage ValKK3	GCA_001501635.1
AGN30172.1	000493	GTP_cyclohydroI	224	VPFG_00170	Vibrio phage nt-1	GCA_000910195.2
ALP47057.1	000493	GTP_cyclohydroI	222	phiGrn1_0233	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47437.1	000493	GTP_cyclohydroI	224	phiST2_0368	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54593.1	000493	GTP_cyclohydroI	222	vBValMR10Z_52	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37351.1	000493	GTP_cyclohydroI	224	pp2_118	Vibriophage phi-pp2	GCA_002630725.1
QDB70412.1	000494	HD-GYP	242	CF8_0243	Aeromonas phage CF8	GCA_006384595.2
QDJ97418.1	000494	HD-GYP	240	D6_0259	Aeromonas phage D6	GCA_007051205.2
QDH47119.1	000494	HD-GYP	240	LAh10_169	Aeromonas phage LAh10	GCA_006863975.1
QDJ96757.1	000494	HD-GYP	241	PS1_0246	Aeromonas phage PS1	GCA_007051165.2
QFR59390.1	000494	HD-GYP	241	PS2_0248	Aeromonas phage PS2	GCA_009388305.2
AFO71437.1	000494	HD-GYP	219	CR5_217	Cronobacter phage CR5	GCA_000910235.1
QBZ70805.1	000494	HD-GYP	245	pETSU_224	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59903.1	000494	HD-GYP	223	SEGD1_256	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07650.1	000494	HD-GYP	222	DERBICUS_224	Erwinia phage Derbicus	GCA_004521655.1
AHI60224.1	000494	HD-GYP	249	Ea357_073	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49901.1	000494	HD-GYP	225	MACHINA_263	Erwinia phage Machina	GCA_002758035.1
QBP07183.1	000494	HD-GYP	249	REBECCA_75	Erwinia phage Rebecca	GCA_004521635.1
AXF51401.1	000494	HD-GYP	225	WELLINGTON_275	Erwinia phage Wellington	GCA_003344985.1
AFQ96715.1	000494	HD-GYP	223	G173_gp170	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48285.1	000494	HD-GYP	223	ASESINO_272	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85862.1	000494	HD-GYP	249	BOSOLAPHORUS_74	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48557.1	000494	HD-GYP	224	CAITLIN_262	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48834.1	000494	HD-GYP	223	CHRISDB_272	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52174.1	000494	HD-GYP	249	DM_76	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86181.1	000494	HD-GYP	249	DESERTFOX_73	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49074.1	000494	HD-GYP	222	EARLPHILLIPIV_225	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49344.1	000494	HD-GYP	225	HUXLEY_262	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03675.1	000494	HD-GYP	231	JOAD_240	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49627.1	000494	HD-GYP	225	KWAN_275	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86503.1	000494	HD-GYP	249	MADMEL_75	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86824.1	000494	HD-GYP	249	MORTIMER_75	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50172.1	000494	HD-GYP	225	PARSHIK_263	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50421.1	000494	HD-GYP	225	PHOBOS_231	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51854.1	000494	HD-GYP	249	RAY_73	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03432.1	000494	HD-GYP	231	RISINGSUN_238	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51538.1	000494	HD-GYP	249	SIMMY50_76	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64886.1	000494	HD-GYP	249	SPECIALG_76	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50697.1	000494	HD-GYP	223	STRATTON_272	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86092.1	000494	HD-GYP	223	ACEC001_2490	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63952.1	000494	HD-GYP	228	Goslar_00159	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72105.1	000494	HD-GYP	234	N1M2_242	Klebsiella phage N1M2	GCA_010092605.1
QGZ14530.1	000494	HD-GYP	263	HWC77_gp167	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24041.1	000494	HD-GYP	260	-	Proteus phage 10	GCA_014071245.1
ARV77419.1	000494	HD-GYP	200	NOXIFER_254	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89744.1	000494	HD-GYP	233	OBP_307	Pseudomonas phage OBP	GCA_000896635.1
QNI20935.1	000494	HD-GYP	223	-	Salmonella phage JN03	GCA_014319805.1
AWN09102.1	000494	HD-GYP	223	MLDJOKPK_00189	Salmonella phage SPAsTU	GCA_003183805.1
AEP84084.1	000494	HD-GYP	223	SPN3US_0251	Salmonella phage SPN3US	GCA_001042275.1
QKE54381.1	000494	HD-GYP	268	ACSA002_0670	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFP93128.1	000494	HD-GYP	248	-	Serratia phage PCH45	GCA_009187865.1
QAU04204.1	000494	HD-GYP	263	HWC03_gp049	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23156.1	000494	HD-GYP	262	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81003.1	000494	HD-GYP	262	Aphrodite1_0184	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70785.1	000494	HD-GYP	199	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47572.1	000494	HD-GYP	262	HWC35_gp178	Vibrio phage USC-1	GCA_006864065.1
BAW98386.1	000494	HD-GYP	264	FDH33_gp177	Vibrio phage pTD1	GCA_002618825.1
ARB13585.1	000495	HD-GYP	226	Ccr10_gp057	Caulobacter phage Ccr10	GCA_002619445.1
ARB13931.1	000495	HD-GYP	226	Ccr2_gp056	Caulobacter phage Ccr2	GCA_002619465.1
ARB14620.1	000495	HD-GYP	226	Ccr29_gp063	Caulobacter phage Ccr29	GCA_002619485.1
ARB14976.1	000495	HD-GYP	226	Ccr32_gp057	Caulobacter phage Ccr32	GCA_002619505.1
ARB15307.1	000495	HD-GYP	226	Ccr34_gp058	Caulobacter phage Ccr34	GCA_002619525.1
ARB14274.1	000495	HD-GYP	227	Ccr5_gp056	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68258.1	000495	HD-GYP	232	CcrBL10_gp054	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87931.1	000495	HD-GYP	389	CcrColossus_gp061	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68603.1	000495	HD-GYP	396	CcrPW_gp064	Caulobacter phage CcrPW	GCA_003443275.1
AFU87575.1	000495	HD-GYP	226	CcrKarma_gp058	Caulobacter virus Karma	GCA_000901575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU87225.1	000495	HD-GYP	226	CcrMagneto_gp055	Caulobacter virus Magneto	GCA_000903095.1
AFU86540.1	000495	HD-GYP	226	CcrRogue_gp058	Caulobacter virus Rogue	GCA_000900555.1
AFU88373.1	000495	HD-GYP	226	CcrSwift_gp055	Caulobacter virus Swift	GCA_000899655.1
AFU86889.1	000495	HD-GYP	226	CbK_gp057	Caulobacter virus phiCbK	GCA_000900535.1
QIG65782.1	000495	HD-GYP	181	phiOC_p117	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QDB70438.1	000496	HD-GYP	223	CF8_0026	Aeromonas phage CF8	GCA_006384595.2
QDJ96673.1	000496	HD-GYP	222	PS1_0162	Aeromonas phage PS1	GCA_007051165.2
QFR59307.1	000496	HD-GYP	222	PS2_0166	Aeromonas phage PS2	GCA_009388305.2
AUE22587.1	000497	HJR-EndoVII	161	Ah1_00046	Aeromonas phage Ah1	GCA_002957415.1
QAX98624.1	000497	HJR-EndoVII	161	ASfcp2_291	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52764.1	000497	HJR-EndoVII	161	PX29p045	Aeromonas phage PX29	GCA_000920195.1
ADM80019.1	000497	HJR-EndoVII	161	phiAS5_ORF0176	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17709.1	000497	HJR-EndoVII	161	49	Aeromonas virus Aeh1	GCA_000843245.1
CCH63622.1	000497	HJR-EndoVII	79	CP21_160	Campylobacter virus CP21	GCA_000902535.1
ANS06043.1	000497	HJR-EndoVII	160	ABCD_0244	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65030.1	000497	HJR-EndoVII	159	S13_233	Cronobacter phage S13	GCA_001503575.1
AFC21691.1	000497	HJR-EndoVII	164	GAP32_241	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14484.1	000497	HJR-EndoVII	163	PBI_121Q_594	Escherichia phage 121Q	GCA_000926855.1
QAY00465.1	000497	HJR-EndoVII	163	Ecwhy1_185	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35207.1	000497	HJR-EndoVII	163	ACQ29_gp527	Escherichia phage PBECO4	GCA_001041035.1
BBM62156.1	000497	HJR-EndoVII	163	EO157G_5670	Escherichia phage SP27	GCA_008033345.1
AXC36779.1	000497	HJR-EndoVII	163	-	Escherichia phage UB	GCA_003341455.1
ARM70901.1	000497	HJR-EndoVII	157	phiC120_c196	Escherichia phage phiC120	GCA_002621185.1
QBO61819.1	000497	HJR-EndoVII	163	G17_00330	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13863.1	000497	HJR-EndoVII	163	vBEcoMphAPEC6_gp234	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80468.1	000497	HJR-EndoVII	163	PSLUR01_00491	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78781.1	000497	HJR-EndoVII	160	RB43ORF259w	Escherichia virus RB43	GCA_000863505.1
AFA44359.1	000497	HJR-EndoVII	164	RaK2_00086	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78902.1	000497	HJR-EndoVII	158	-	Myoviridae sp.	GCA_012593985.1
AMM43813.1	000497	HJR-EndoVII	158	CBB_248	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18964.1	000497	HJR-EndoVII	164	7t3_0443	Salmonella phage 7t3	GCA_006083215.1
AZU98217.1	000497	HJR-EndoVII	163	CPT_Munch_273	Salmonella phage Munch	GCA_004015485.1
QIG62767.1	000497	HJR-EndoVII	164	SEPL_154	Salmonella phage SE_PL	GCA_011067555.1
AQW88771.1	000497	HJR-EndoVII	160	BF_0246	Serratia phage BF	GCA_002619745.1
AAQ64202.1	000497	HJR-EndoVII	151	KVP40.0131	Vibrio phage KVP40	GCA_000843785.1
QIW90517.1	000497	HJR-EndoVII	169	GCAPEGMB_00170	Vibrio phage V07	GCA_012361095.1
QIW90905.1	000497	HJR-EndoVII	169	COHAPHLL_00042	Vibrio phage V09	GCA_012361135.1
QHJ74313.1	000497	HJR-EndoVII	169	VH12019_00394	Vibrio phage VH1_2019	GCA_009931825.1
QBX05958.1	000497	HJR-EndoVII	168	ValB1HC_004	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04571.1	000497	HJR-EndoVII	179	ValB1MD_293	Vibrio phage ValB1MD	GCA_004138815.1
AJT60970.1	000497	HJR-EndoVII	168	AVU32_gp129	Vibrio phage ValKK3	GCA_001501635.1
AGN30181.2	000497	HJR-EndoVII	168	VPFG_00179	Vibrio phage nt-1	GCA_000910195.2
ALP47218.1	000497	HJR-EndoVII	95	phiGrn1_0243	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47524.1	000497	HJR-EndoVII	142	phiST2_0381	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54583.1	000497	HJR-EndoVII	168	vBValMR10Z_42	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37362.1	000497	HJR-EndoVII	169	pp2_129	Vibriophage phi-pp2	GCA_002630725.1
SOK59052.1	000497	HJR-EndoVII	164	g244c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58517.1	000497	HJR-EndoVII	164	g240c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMS01292.1	000498	HJR-RusA	199	AR9_g208	Bacillus phage AR9	GCA_001743835.1
ALN97944.1	000498	HJR-RusA	209	Bp8pS_265	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99921.1	000498	HJR-RusA	199	PBI_PBS1_99	Bacillus virus PBS1	GCA_002601325.1
CCE26110.1	000498	HJR-RusA	178	g086	Yersinia phage phiR1-37	GCA_000895615.1
QHJ86061.1	000000	RusA	146	KKIINIFJ_00149	Pseudomonas phage PN05	GCA_009931935.1
BAE47800.1	000000	SIG+RusA	215	CST102	Clostridium phage c-st	GCA_000865225.1
AFO71314.1	000499	GNAT	158	CR5_094	Cronobacter phage CR5	GCA_000910235.1
AMR59748.1	000499	GNAT	106	SEGD1_099	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07523.1	000499	GNAT	158	DERBICUS_97	Erwinia phage Derbicus	GCA_004521655.1
ANZ49745.1	000499	GNAT	158	MACHINA_107	Erwinia phage Machina	GCA_002758035.1
AGX01959.1	000499	GNAT	175	CF95_gp237	Erwinia phage PhiEaH1	GCA_000914555.1
AXF51246.1	000499	GNAT	155	WELLINGTON_116	Erwinia phage Wellington	GCA_003344985.1
AFQ96565.1	000499	GNAT	154	G173_gp020	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48124.1	000499	GNAT	154	ASESINO_111	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48398.1	000499	GNAT	155	CAITLIN_103	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48671.1	000499	GNAT	155	CHRISDB_109	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48946.1	000499	GNAT	158	EARLPHILLIPIV_97	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49190.1	000499	GNAT	158	HUXLEY_108	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49467.1	000499	GNAT	155	KWAN_115	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50018.1	000499	GNAT	158	PARSHIK_109	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50287.1	000499	GNAT	157	PHOBOS_97	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50539.1	000499	GNAT	154	STRATTON_114	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85935.1	000499	GNAT	164	ACEC001_0970	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85936.1	000499	GNAT	154	ACEC001_0980	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63906.1	000499	GNAT	177	Goslar_00113	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QNI20804.1	000499	GNAT	153	-	Salmonella phage JN03	GCA_014319805.1
QNI20805.1	000499	GNAT	154	-	Salmonella phage JN03	GCA_014319805.1
AWN09009.2	000499	GNAT	165	MLDJOKPK_00063	Salmonella phage SPAsTU	GCA_003183805.1
AEP83928.1	000499	GNAT	154	SPN3US_0095	Salmonella phage SPN3US	GCA_001042275.1
ATA65687.1	000499	GNAT	49	2050HW_00352	Serratia phage 2050HW	GCA_002628125.1
QDB71114.1	000499	GNAT	158	CPT_Moabite_084	Serratia phage Moabite	GCA_006384735.1
AFO71302.1	000500	GNAT	158	CR5_082	Cronobacter phage CR5	GCA_000910235.1
AMR59741.1	000500	GNAT	160	SEGD1_092	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07511.1	000500	GNAT	158	DERBICUS_85	Erwinia phage Derbicus	GCA_004521655.1
ANZ49738.1	000500	GNAT	158	MACHINA_100	Erwinia phage Machina	GCA_002758035.1
AXF51238.1	000500	GNAT	159	WELLINGTON_108	Erwinia phage Wellington	GCA_003344985.1
AFQ96557.1	000500	GNAT	122	G173_gp012	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48117.1	000500	GNAT	159	ASESINO_104	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48392.1	000500	GNAT	159	CAITLIN_97	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48664.1	000500	GNAT	159	CHRISDB_102	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48935.1	000500	GNAT	158	EARLPHILLIPIV_85	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49183.1	000500	GNAT	158	HUXLEY_101	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49459.1	000500	GNAT	159	KWAN_107	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50011.1	000500	GNAT	158	PARSHIK_102	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50275.1	000500	GNAT	161	PHOBOS_85	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50531.1	000500	GNAT	159	STRATTON_106	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85928.1	000500	GNAT	160	ACEC001_0900	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20798.1	000500	GNAT	160	-	Salmonella phage JN03	GCA_014319805.1
AWN09014.1	000500	GNAT	160	MLDJOKPK_00071	Salmonella phage SPAsTU	GCA_003183805.1
AEP83921.1	000500	GNAT	160	SPN3US_0088	Salmonella phage SPN3US	GCA_001042275.1
AFO71319.1	000501	GNAT	285	CR5_099	Cronobacter phage CR5	GCA_000910235.1
QBP07528.1	000501	GNAT	323	DERBICUS_102	Erwinia phage Derbicus	GCA_004521655.1
ANZ49754.1	000501	GNAT	335	MACHINA_116	Erwinia phage Machina	GCA_002758035.1
AXF51262.1	000501	GNAT	317	WELLINGTON_132	Erwinia phage Wellington	GCA_003344985.1
ANZ48410.1	000501	GNAT	314	CAITLIN_115	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48682.1	000501	GNAT	315	CHRISDB_120	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48951.1	000501	GNAT	285	EARLPHILLIPIV_102	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49198.1	000501	GNAT	335	HUXLEY_116	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49483.1	000501	GNAT	317	KWAN_131	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50026.1	000501	GNAT	335	PARSHIK_117	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50292.1	000501	GNAT	285	PHOBOS_102	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QKN85945.1	000501	GNAT	332	ACEC001_1070	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20813.1	000501	GNAT	332	-	Salmonella phage JN03	GCA_014319805.1
AXF51074.1	000501	GNAT	333	MLDJOKPK_00053	Salmonella phage SPAsTU	GCA_003183805.1
AEP83937.1	000501	GNAT	332	SPN3US_0104	Salmonella phage SPN3US	GCA_001042275.1
AMR59843.1	000502	GNAT	162	SEGD1_196	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49840.1	000502	GNAT	161	MACHINA_202	Erwinia phage Machina	GCA_002758035.1
AXF51341.1	000502	GNAT	160	WELLINGTON_215	Erwinia phage Wellington	GCA_003344985.1
AFQ96659.1	000502	GNAT	163	G173_gp114	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48225.1	000502	GNAT	163	ASESINO_212	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48496.1	000502	GNAT	159	CAITLIN_201	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48776.1	000502	GNAT	159	CHRISDB_214	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49284.1	000502	GNAT	161	HUXLEY_202	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49568.1	000502	GNAT	160	KWAN_216	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50112.1	000502	GNAT	161	PARSHIK_203	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50638.1	000502	GNAT	163	STRATTON_213	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86033.1	000502	GNAT	162	ACEC001_1900	Escherichia phage vB_EcoM_EC001	GCA_014131305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNI20883.1	000502	GNAT	162	-	Salmonella phage JN03	GCA_014319805.1
AWN09147.1	000502	GNAT	164	MLDJOKPK_00248	Salmonella phage SPAsTU	GCA_003183805.1
AEP84024.1	000502	GNAT	162	SPN3US_0191	Salmonella phage SPN3US	GCA_001042275.1
AHI60185.1	000503	GNAT	139	Ea357_035	Erwinia phage Ea35-70	GCA_000914635.1
QBP07143.1	000503	GNAT	158	REBECCA_35	Erwinia phage Rebecca	GCA_004521635.1
AUG85823.1	000503	GNAT	158	BOSOLAPHORUS_35	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52134.1	000503	GNAT	158	DM_36	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86143.1	000503	GNAT	158	DESERTFOX_35	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86463.1	000503	GNAT	158	MADMEL_35	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86784.1	000503	GNAT	158	MORTIMER_35	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51816.2	000503	GNAT	158	RAY_35	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51498.2	000503	GNAT	158	SIMMY50_36	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64845.1	000503	GNAT	158	SPECIALG_35	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24021.1	000503	GNAT	161	-	Proteus phage 10	GCA_014071245.1
AXH72808.1	000504	GNAT	152	-	Myoviridae sp.	GCA_003657725.1
QMP24042.1	000504	GNAT	147	-	Proteus phage 10	GCA_014071245.1
ABY63038.1	000504	GNAT	149	201phi2-1p209	Pseudomonas phage 201phi2-1	GCA_000875305.1
BAW19245.1	000504	GNAT	144	FDH28_gp150	Ralstonia phage RP12	GCA_002617345.1
BAW19531.1	000504	GNAT	144	-	Ralstonia phage RP31	GCA_002617365.1
BAS04813.2	000504	GNAT	144	AVU11_agp09	Ralstonia phage RSF1	GCA_001500875.1
BAQ02548.2	000504	GNAT	143	-	Ralstonia phage RSL2	GCA_001503055.1
ABY63198.1	000505	GNAT	199	201phi2-1p373	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63199.1	000505	GNAT	181	201phi2-1p374	Pseudomonas phage 201phi2-1	GCA_000875305.1
AFH14873.1	000505	GNAT	187	Lu11_0335	Pseudomonas phage Lu11	GCA_000897175.1
QBX32467.1	000505	GNAT	166	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77002.1	000505	GNAT	198	PHABIO_371	Pseudomonas phage Phabio	GCA_002624965.1
QEM42039.1	000505	GNAT	166	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AFC21865.1	000506	GNAT	147	GAP32_412	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43988.1	000506	GNAT	146	CBB_425	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88945.1	000506	GNAT	146	BF_0420	Serratia phage BF	GCA_002619745.1
SOK59233.1	000506	GNAT	144	g425	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58699.1	000506	GNAT	144	g422	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14185.1	000507	GNAT	118	PBI_121Q_295	Escherichia phage 121Q	GCA_000926855.1
QAY00753.1	000507	GNAT	118	Ecwhy1_479	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61859.1	000507	GNAT	118	EO157G_2700	Escherichia phage SP27	GCA_008033345.1
AXC37036.1	000507	GNAT	118	-	Escherichia phage UB	GCA_003341455.1
QDF14135.1	000507	GNAT	118	vBEcoMphAPEC6_gp512c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QAX98348.1	000508	ABC-ATPase+GNAT	392	ASfcp2_2	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52804.1	000508	ABC-ATPase+GNAT	392	PX29p085	Aeromonas phage PX29	GCA_000920195.1
BAV39160.1	000508	ABC-ATPase+GNAT	253	BPT24_038	Tenacibaculum phage pT24	GCA_002611925.1
ALY07058.1	000509	GNAT	387	VmeM32_00067	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFO71320.1	000510	GNAT	285	CR5_100	Cronobacter phage CR5	GCA_000910235.1
QBP07529.1	000510	GNAT	289	DERBICUS_103	Erwinia phage Derbicus	GCA_004521655.1
ANZ48952.1	000510	GNAT	289	EARLPHILLIPIV_103	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50293.1	000510	GNAT	288	PHOBOS_103	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ABY62875.1	000511	GNAT	127	201phi2-1p042	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32169.1	000511	GNAT	127	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76657.1	000511	GNAT	130	PHABIO_26	Pseudomonas phage Phabio	GCA_002624965.1
QEM41749.1	000511	GNAT	128	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65367.1	000512	GNAT	181	2050HW_00032	Serratia phage 2050HW	GCA_002628125.1
QDB71152.1	000512	GNAT	184	CPT_Moabite_122	Serratia phage Moabite	GCA_006384735.1
AEO93766.1	000513	GNAT	175	G_508	Bacillus virus G	GCA_000917535.1
AEO93873.1	000513	GNAT	172	G_628	Bacillus virus G	GCA_000917535.1
ATA65343.1	000514	GNAT	171	2050HW_00008	Serratia phage 2050HW	GCA_002628125.1
QDB71131.1	000514	GNAT	171	CPT_Moabite_101	Serratia phage Moabite	GCA_006384735.1
ATA65668.1	000515	GNAT	163	2050HW_00333	Serratia phage 2050HW	GCA_002628125.1
QDB71090.1	000515	GNAT	163	CPT_Moabite_058	Serratia phage Moabite	GCA_006384735.1
ASU03789.1	000516	GNAT	152	JOAD_126	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03545.1	000516	GNAT	162	RISINGSUN_125	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QDJ96707.1	000517	GNAT	161	PS1_0196	Aeromonas phage PS1	GCA_007051165.2
QFR59340.1	000517	GNAT	161	PS2_0198	Aeromonas phage PS2	GCA_009388305.2
AXF51340.1	000518	GNAT	151	WELLINGTON_214	Erwinia phage Wellington	GCA_003344985.1
ANZ49567.1	000518	GNAT	129	KWAN_215	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QAX97775.1	000519	GNAT	150	ASswx1_130	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01378.1	000519	GNAT	132	ASwh1_318	Aeromonas phage Aswh_1	GCA_004146945.1
BBA65671.1	000520	GNAT	149	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65212.1	000520	GNAT	149	-	Xanthomonas phage XacN1	GCA_003173815.1
BAS04815.1	000521	GNAT	140	AVU11_gp023	Ralstonia phage RSF1	GCA_001500875.1
BAU71403.1	000521	GNAT	135	-	Ralstonia phage RSL2	GCA_001503055.1
BBI90546.1	000522	GNAT	116	HYO65_gp154	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90854.1	000522	GNAT	116	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000494	000523	GNAT	113	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000375	000523	GNAT	113	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXG66440.1	000524	GNAT	83	JA13_037	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66764.1	000524	GNAT	103	JA29_038	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
QDB70363.1	000000	GNAT	168	CF8_0195	Aeromonas phage CF8	GCA_006384595.2
QBZ70740.1	000000	GNAT	342	pETSU_159	Edwardsiella virus pEt-SU	GCA_004800915.1
AQT28750.1	000000	GNAT	141	YOLOSWAG_278	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
CAG27231.1	000000	GNAT	160	PPEV_gp137	Pseudomonas phage EL	GCA_000866825.1
CAG27246.1	000000	GNAT	166	PPEV_gp152	Pseudomonas phage EL	GCA_000866825.1
AFH14741.1	000000	GNAT	119	Lu11_0204	Pseudomonas phage Lu11	GCA_000897175.1
AEV89677.1	000000	GNAT	160	OBP_240	Pseudomonas phage OBP	GCA_000896635.1
AXH70943.1	000000	GNAT	106	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT27968.1	000000	GNAT	157	pVa21_026	Vibrio phage pVa-21	GCA_002619305.1
QNI21172.1	000000	GNAT	140	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65355.1	000000	GNAT	165	-	Xanthomonas phage XacN1	GCA_003173815.1
AEO93921.1	000000	GNAT	537	G_678	Bacillus virus G	GCA_000917535.1
AFH14903.1	000000	GNAT	138	Lu11_0365	Pseudomonas phage Lu11	GCA_000897175.1
AMM44963.1	000000	GNAT	177	SP15_165	Bacillus phage SP-15	GCA_001754685.1
AEO93856.1	000000	GNAT	118	G_611	Bacillus virus G	GCA_000917535.1
AEO93903.1	000000	GNAT	128	G_660	Bacillus virus G	GCA_000917535.1
AIA64953.1	000000	GNAT	134	S13_154	Cronobacter phage S13	GCA_001503575.1
AXH72541.1	000000	GNAT	109	-	Myoviridae sp.	GCA_003657725.1
AFH14866.1	000000	GNAT	160	Lu11_0328	Pseudomonas phage Lu11	GCA_000897175.1
AGS81894.1	000000	GNAT	121	PaBG_00010	Pseudomonas phage PaBG	GCA_000912555.1
BAV39159.1	000000	GNAT	113	BPT24_037	Tenacibaculum phage pT24	GCA_002611925.1
BBA65321.1	000000	GNAT	134	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96238.1	000000	GNAT	139	Xoosp13_51	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXG67304.1	000525	GNAT	146	AD1_260	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08530.1	000525	GNAT	146	Alexandra_273	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58909.1	000525	GNAT	146	Y3_269	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28809.1	000525	GNAT	161	YOLOSWAG_258	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD80043.1	000526	GNAT	171	JA11_238	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66642.1	000526	GNAT	171	JA13_239	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66966.1	000526	GNAT	171	JA29_240	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67613.1	000526	GNAT	171	JA33_239	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ASV44323.1	000000	GNAT	153	PBI_SCTP2_308	Salicola phage SCTP-2	GCA_002625545.1
AEO93900.1	000000	GNAT	182	G_657	Bacillus virus G	GCA_000917535.1
QDB70294.1	000527	HJR-RuvC	195	CF8_0126	Aeromonas phage CF8	GCA_006384595.2
QDJ97271.1	000527	HJR-RuvC	195	D6_0111	Aeromonas phage D6	GCA_007051205.2
QDH47148.1	000527	HJR-RuvC	195	LAh10_43	Aeromonas phage LAh10	GCA_006863975.1
QDJ96886.1	000527	HJR-RuvC	190	PS1_0127	Aeromonas phage PS1	GCA_007051165.2
QFR59518.1	000527	HJR-RuvC	190	PS2_0127	Aeromonas phage PS2	GCA_009388305.2
AFO71299.1	000527	HJR-RuvC	221	CR5_079	Cronobacter phage CR5	GCA_000910235.1
QBZ70657.1	000527	HJR-RuvC	191	pETSU_076	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59738.1	000527	HJR-RuvC	216	SEGD1_089	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07508.1	000527	HJR-RuvC	221	DERBICUS_82	Erwinia phage Derbicus	GCA_004521655.1
AHI60162.1	000527	HJR-RuvC	201	Ea357_012	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49735.1	000527	HJR-RuvC	216	MACHINA_97	Erwinia phage Machina	GCA_002758035.1
AGX01924.1	000527	HJR-RuvC	192	CF95_gp202	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07120.1	000527	HJR-RuvC	214	REBECCA_12	Erwinia phage Rebecca	GCA_004521635.1
AXF51235.1	000527	HJR-RuvC	217	WELLINGTON_105	Erwinia phage Wellington	GCA_003344985.1
AFQ96554.1	000527	HJR-RuvC	191	G173_gp009	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48114.1	000527	HJR-RuvC	217	ASESINO_101	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85800.1	000527	HJR-RuvC	214	BOSOLAPHORUS_12	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48389.1	000527	HJR-RuvC	219	CAITLIN_94	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48661.1	000527	HJR-RuvC	219	CHRISDB_99	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52110.1	000527	HJR-RuvC	214	DM_12	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86120.1	000527	HJR-RuvC	214	DESERTFOX_12	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48932.1	000527	HJR-RuvC	221	EARLPHILLIPIV_82	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49180.1	000527	HJR-RuvC	216	HUXLEY_98	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03822.1	000527	HJR-RuvC	208	JOAD_93	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49456.1	000527	HJR-RuvC	217	KWAN_104	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86440.1	000527	HJR-RuvC	201	MADMEL_12	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86761.1	000527	HJR-RuvC	214	MORTIMER_12	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50008.1	000527	HJR-RuvC	216	PARSHIK_99	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50272.1	000527	HJR-RuvC	220	PHOBOS_82	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51793.2	000527	HJR-RuvC	214	RAY_12	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03577.1	000527	HJR-RuvC	208	RISINGSUN_93	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51475.1	000527	HJR-RuvC	214	SIMMY50_13	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64822.1	000527	HJR-RuvC	201	SPECIALG_12	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50528.1	000527	HJR-RuvC	217	STRATTON_103	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85925.1	000527	HJR-RuvC	216	ACEC001_0870	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63803.1	000527	HJR-RuvC	204	Goslar_00010	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71973.1	000527	HJR-RuvC	197	N1M2_110	Klebsiella phage N1M2	GCA_010092605.1
QGZ14445.1	000527	HJR-RuvC	200	HWC77_gp082	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24004.1	000527	HJR-RuvC	200	-	Proteus phage 10	GCA_014071245.1
ABY63054.1	000527	HJR-RuvC	187	201phi2-1p225	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27202.1	000527	HJR-RuvC	174	PPEV_gp108	Pseudomonas phage EL	GCA_000866825.1
ANM44933.1	000527	HJR-RuvC	187	KTN4_175	Pseudomonas phage KTN4	GCA_002607225.1
ARV77314.1	000527	HJR-RuvC	190	NOXIFER_145	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89574.1	000527	HJR-RuvC	188	OBP_137	Pseudomonas phage OBP	GCA_000896635.1
QBX32320.1	000527	HJR-RuvC	188	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76843.1	000527	HJR-RuvC	187	PHABIO_212	Pseudomonas phage Phabio	GCA_002624965.1
AEH03582.1	000527	HJR-RuvC	187	159	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02719.1	000527	HJR-RuvC	217	PSA21_193	Pseudomonas phage Psa21	GCA_004340405.1
ATN94781.1	000527	HJR-RuvC	187	SL2_204	Pseudomonas phage SL2	GCA_002956015.1
QJB22811.1	000527	HJR-RuvC	187	fnug_168	Pseudomonas phage fnug	GCA_012837215.1
QEM41893.1	000527	HJR-RuvC	188	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83041.1	000527	HJR-RuvC	187	PHIKZ140	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19060.1	000527	HJR-RuvC	197	FDH28_gp086	Ralstonia phage RP12	GCA_002617345.1
BAW19345.1	000527	HJR-RuvC	197	-	Ralstonia phage RP31	GCA_002617365.1
BAS04890.2	000527	HJR-RuvC	148	AVU11_agp21	Ralstonia phage RSF1	GCA_001500875.1
BAQ02617.1	000527	HJR-RuvC	193	AVU38_gp089	Ralstonia phage RSL2	GCA_001503055.1
QNI20795.1	000527	HJR-RuvC	216	-	Salmonella phage JN03	GCA_014319805.1
AWN09016.1	000527	HJR-RuvC	214	MLDJOKPK_00074	Salmonella phage SPAsTU	GCA_003183805.1
AEP83918.1	000527	HJR-RuvC	216	SPN3US_0085	Salmonella phage SPN3US	GCA_001042275.1
QKE54326.1	000527	HJR-RuvC	207	ACSA002_0120	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65388.1	000527	HJR-RuvC	214	2050HW_00053	Serratia phage 2050HW	GCA_002628125.1
QDB71169.1	000527	HJR-RuvC	214	CPT_Moabite_139	Serratia phage Moabite	GCA_006384735.1
QFP93162.1	000527	HJR-RuvC	199	-	Serratia phage PCH45	GCA_009187865.1
QAU04289.1	000527	HJR-RuvC	200	HWC03_gp134	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23288.1	000527	HJR-RuvC	200	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81036.1	000527	HJR-RuvC	178	Aphrodite1_0057	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70859.1	000527	HJR-RuvC	186	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47440.1	000527	HJR-RuvC	200	HWC35_gp046	Vibrio phage USC-1	GCA_006864065.1
BAW98261.1	000527	HJR-RuvC	177	FDH33_gp052	Vibrio phage pTD1	GCA_002618825.1
AQT27962.1	000527	HJR-RuvC	216	pVa21_020	Vibrio phage pVa-21	GCA_002619305.1
QAX96630.1	000527	HJR-RuvC	193	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96948.1	000527	HJR-RuvC	193	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95994.1	000527	HJR-RuvC	193	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96312.1	000527	HJR-RuvC	193	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21111.1	000527	HJR-RuvC	197	-	Vibrio phage vB_pir03	GCA_014319855.1
ARB13850.1	000528	HJR-RuvC	171	Ccr10_gp320	Caulobacter phage Ccr10	GCA_002619445.1
ARB14195.1	000528	HJR-RuvC	171	Ccr2_gp319	Caulobacter phage Ccr2	GCA_002619465.1
ARB14889.1	000528	HJR-RuvC	171	Ccr29_gp333	Caulobacter phage Ccr29	GCA_002619485.1
ARB15227.1	000528	HJR-RuvC	171	Ccr32_gp309	Caulobacter phage Ccr32	GCA_002619505.1
ARB15561.1	000528	HJR-RuvC	171	Ccr34_gp319	Caulobacter phage Ccr34	GCA_002619525.1
ARB14535.1	000528	HJR-RuvC	171	Ccr5_gp315	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68519.1	000528	HJR-RuvC	171	CcrBL10_gp315	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69533.1	000528	HJR-RuvC	172	CcrBL9_gp509	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88314.1	000528	HJR-RuvC	168	CcrColossus_gp444	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68985.1	000528	HJR-RuvC	168	CcrPW_gp446	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70076.1	000528	HJR-RuvC	172	CcrSC_gp494	Caulobacter phage CcrSC	GCA_003443315.1
AFU87846.1	000528	HJR-RuvC	171	CcrKarma_gp329	Caulobacter virus Karma	GCA_000901575.1
AFU87494.1	000528	HJR-RuvC	171	CcrMagneto_gp324	Caulobacter virus Magneto	GCA_000903095.1
AFU86809.1	000528	HJR-RuvC	171	CcrRogue_gp327	Caulobacter virus Rogue	GCA_000900555.1
AFU88639.1	000528	HJR-RuvC	171	CcrSwift_gp321	Caulobacter virus Swift	GCA_000899655.1
AFU87146.1	000528	HJR-RuvC	171	CbK_gp314	Caulobacter virus phiCbK	GCA_000900535.1
QDH83638.1	000529	HJR-RuvC	203	H1O15_gp150	Achromobacter phage Motura	GCA_006964305.1
QBX06658.1	000529	HJR-RuvC	208	BcepSaruman_245	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74626.1	000529	HJR-RuvC	208	BcepSauron_246	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67261.1	000529	HJR-RuvC	182	AD1_217	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80008.1	000529	HJR-RuvC	182	JA11_203	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66606.1	000529	HJR-RuvC	182	JA13_203	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66931.1	000529	HJR-RuvC	182	JA29_205	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67578.1	000529	HJR-RuvC	182	JA33_204	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08490.1	000529	HJR-RuvC	182	Alexandra_227	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58862.1	000529	HJR-RuvC	182	Y3_222	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28694.1	000529	HJR-RuvC	182	YOLOSWAG_216	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38174.1	000529	HJR-RuvC	194	BN7874_005	Phage NCTB	GCA_900092385.1
AFH14667.1	000529	HJR-RuvC	208	Lu11_0133	Pseudomonas phage Lu11	GCA_000897175.1
AGS82039.1	000529	HJR-RuvC	212	PaBG_00156	Pseudomonas phage PaBG	GCA_000912555.1
BAG41664.1	000529	HJR-RuvC	200	RSL1_ORF215	Ralstonia phage phiRSL1	GCA_000879455.1
ABS83750.1	000000	HJR-RuvC	177	0305phi8-36p192	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93608.1	000000	HJR-RuvC	208	G_349	Bacillus virus G	GCA_000917535.1
BAV39239.1	000000	HJR-RuvC	195	BPT24_114	Tenacibaculum phage pT24	GCA_002611925.1
APU01764.1	000530	Hsp10	124	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28982.1	000530	Hsp10	125	AP1_0275	Aeromonas phage AP1	GCA_014183365.1
ATI17533.1	000530	Hsp10	125	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00463.1	000530	Hsp10	125	HWB28_gp089	Aeromonas phage AS-zj	GCA_002627665.1
AUE22798.1	000530	Hsp10	136	Ah1_00280	Aeromonas phage Ah1	GCA_002957415.1
QAX98513.1	000530	Hsp10	136	ASfcp2_177	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97974.1	000530	Hsp10	125	ASswx1_333	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01166.1	000530	Hsp10	125	ASwh1_100	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39377.1	000530	Hsp10	125	CC2_200	Aeromonas phage CC2	GCA_000903495.1
ADQ52975.1	000530	Hsp10	155	PX29p256	Aeromonas phage PX29	GCA_000920195.1
ADM79901.1	000530	Hsp10	115	phiAS5_ORF0058	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53407.1	000530	Hsp10	124	65p400	Aeromonas virus 65	GCA_000893255.1
AAQ17925.1	000530	Hsp10	136	31	Aeromonas virus Aeh1	GCA_000843245.1
ANS06074.1	000530	Hsp10	118	ABCD_0074	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64837.1	000530	Hsp10	106	S13_038	Cronobacter phage S13	GCA_001503575.1
AON97088.1	000530	Hsp10	118	E_079	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70768.1	000530	Hsp10	110	phiC120_c62	Escherichia phage phiC120	GCA_002621185.1
AAX78598.1	000530	Hsp10	114	RB43ORF076w	Escherichia virus RB43	GCA_000863505.1
QHJ78825.1	000530	Hsp10	115	-	Myoviridae sp.	GCA_012593985.1
AAQ64200.1	000530	Hsp10	112	KVP40.0129	Vibrio phage KVP40	GCA_000843785.1
QIW90515.1	000530	Hsp10	112	GCAPEGMB_00168	Vibrio phage V07	GCA_012361095.1
QIW90907.1	000530	Hsp10	112	COHAPHLL_00044	Vibrio phage V09	GCA_012361135.1
QHJ74311.1	000530	Hsp10	112	VH12019_00392	Vibrio phage VH1_2019	GCA_009931825.1
AGB06806.1	000530	Hsp10	112	CF80_gp019	Vibrio phage VH7D	GCA_000914495.1
QBX05960.1	000530	Hsp10	112	ValB1HC_006	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60972.1	000530	Hsp10	112	AVU32_gp131	Vibrio phage ValKK3	GCA_001501635.1
AGN30179.1	000530	Hsp10	110	VPFG_00177	Vibrio phage nt-1	GCA_000910195.2
ALP47177.1	000530	Hsp10	112	phiGrn1_0241	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47563.1	000530	Hsp10	112	phiST2_0379	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54585.1	000530	Hsp10	112	vBValMR10Z_44	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07221.1	000530	Hsp10	117	VmeM32_00235	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37360.1	000530	Hsp10	112	pp2_127	Vibriophage phi-pp2	GCA_002630725.1
ASV44742.1	000531	SIG+Hsp10	111	FDI40_gp314	Agrobacterium phage Atu_ph07	GCA_002628245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21775.1	000531	SIG+Hsp10	106	GAP32_325	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13955.1	000531	SIG+Hsp10	108	PBI_121Q_58	Escherichia phage 121Q	GCA_000926855.1
QAY00382.1	000531	SIG+Hsp10	108	Ecwhy1_101	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35127.1	000531	SIG+Hsp10	108	ACQ29_gp447	Escherichia phage PBECO4	GCA_001041035.1
BBM61647.1	000531	SIG+Hsp10	108	EO157G_0580	Escherichia phage SP27	GCA_008033345.1
AXC36701.1	000531	SIG+Hsp10	108	-	Escherichia phage UB	GCA_003341455.1
QBO61738.1	000531	SIG+Hsp10	108	G17_00249	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13783.1	000531	SIG+Hsp10	108	vBEcoMphAPEC6_gp154c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80549.1	000531	SIG+Hsp10	108	PSLUR01_00572	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44437.1	000531	SIG+Hsp10	110	RaK2_00164	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72550.1	000531	SIG+Hsp10	134	-	Myoviridae sp.	GCA_003657725.1
AMM43893.1	000531	SIG+Hsp10	106	CBB_330	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76171.1	000531	SIG+Hsp10	108	EST35_0290	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44308.1	000531	SIG+Hsp10	104	PBI_SCTP2_293	Salicola phage SCTP-2	GCA_002625545.1
QCW19052.1	000531	SIG+Hsp10	107	7t3_0532	Salmonella phage 7t3	GCA_006083215.1
AZU98299.1	000531	SIG+Hsp10	107	CPT_Munch_355	Salmonella phage Munch	GCA_004015485.1
QIG62685.1	000531	SIG+Hsp10	107	SEPL_072	Salmonella phage SE_PL	GCA_011067555.1
AQW88853.1	000531	SIG+Hsp10	106	BF_0328	Serratia phage BF	GCA_002619745.1
SOK59137.1	000531	SIG+Hsp10	106	g329	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58603.1	000531	SIG+Hsp10	106	g326	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21712.1	000532	Hsp10	95	GAP32_262	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14505.1	000532	Hsp10	99	PBI_121Q_615	Escherichia phage 121Q	GCA_000926855.1
QAY00444.1	000532	Hsp10	100	Ecwhy1_164	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35187.1	000532	Hsp10	111	ACQ29_gp507	Escherichia phage PBECO4	GCA_001041035.1
BBM62177.1	000532	Hsp10	99	EO157G_5880	Escherichia phage SP27	GCA_008033345.1
AXC36759.1	000532	Hsp10	99	-	Escherichia phage UB	GCA_003341455.1
QBO61798.1	000532	Hsp10	99	G17_00309	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13842.1	000532	Hsp10	99	vBEcoMphAPEC6_gp213c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80489.1	000532	Hsp10	99	PSLUR01_00512	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44377.1	000532	Hsp10	99	RaK2_00104	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43832.1	000532	Hsp10	99	CBB_268	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18991.1	000532	Hsp10	96	7t3_0470	Salmonella phage 7t3	GCA_006083215.1
AZU98239.1	000532	Hsp10	96	CPT_Munch_295	Salmonella phage Munch	GCA_004015485.1
QIG62745.1	000532	Hsp10	96	SEPL_132	Salmonella phage SE_PL	GCA_011067555.1
AQW88791.1	000532	Hsp10	95	BF_0266	Serratia phage BF	GCA_002619745.1
SOK59072.1	000532	Hsp10	95	g264	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58538.1	000532	Hsp10	95	g261	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21580.1	000533	Hsp10	93	GAP32_130	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43696.1	000533	Hsp10	93	CBB_131	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88649.1	000533	Hsp10	92	BF_0124	Serratia phage BF	GCA_002619745.1
SOK58929.1	000533	Hsp10	89	g121	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58394.1	000533	Hsp10	89	g117	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63490.1	000534	Hsp10	87	DAC16_261	Bacteroides phage DAC16	GCA_013387695.1
QIG63752.1	000534	Hsp10	87	DAC19_265	Bacteroides phage DAC19	GCA_013387715.1
QIG64013.1	000534	Hsp10	87	DAC20_264	Bacteroides phage DAC20	GCA_013387725.1
QIG64277.1	000534	Hsp10	87	DAC22_267	Bacteroides phage DAC22	GCA_013387735.1
QIG64534.1	000534	Hsp10	87	DAC23_260	Bacteroides phage DAC23	GCA_013387745.1
ABS83602.1	000535	Hsp10	104	0305phi8-36p041	Bacillus phage 0305phi8-36	GCA_000871045.1
QBX06624.1	000535	Hsp10	93	BcepSaruman_211	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74592.1	000535	Hsp10	93	BcepSauron_212	Burkholderia phage BcepSauron	GCA_005394215.1
AXH72881.1	000535	Hsp10	99	-	Myoviridae sp.	GCA_003657725.1
BBA65391.1	000536	Hsp10	103	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96419.1	000536	Hsp10	103	Xoosp13_233	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65430.1	000537	Hsp10	99	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96448.1	000537	Hsp10	103	Xoosp13_262	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDH83429.1	000000	Hsp10	91	H1O15_gp021	Achromobacter phage Motura	GCA_006964305.1
AMM44814.1	000000	Hsp10	99	SP15_015	Bacillus phage SP-15	GCA_001754685.1
CCH63565.1	000000	Hsp10	90	CP21_103	Campylobacter virus CP21	GCA_000902535.1
QAU04538.1	000000	SIG+Hsp10	101	ValB1MD_249	Vibrio phage ValB1MD	GCA_004138815.1
ASV44185.1	000000	Hsp10	92	PBI_SCTP2_170	Salicola phage SCTP-2	GCA_002625545.1
AUZ95449.1	000538	HSP20	133	FDI40_gp710	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGH56859.1	000538	HSP20	143	CPXG_00056	Cyanophage P-RSM6	GCA_000906155.1
AJK27597.1	000538	HSP20	148	PTIM40_170	Cyanophage P-TIM40	GCA_001470935.1
AOO14353.1	000538	HSP20	176	Sn110110_159	Cyanophage S-RIM14	GCA_002599065.1
AOO15002.1	000538	HSP20	166	W1230910_156	Cyanophage S-RIM14	GCA_002599125.1
AMO43167.1	000538	HSP20	135	R1080702_158	Cyanophage S-RIM32	GCA_001754165.1
AMO43393.1	000538	HSP20	135	W270710_149	Cyanophage S-RIM44	GCA_002599145.1
AOO11637.1	000538	HSP20	135	ES420910_156	Cyanophage S-RIM44	GCA_002599165.1
AOO11865.1	000538	HSP20	135	Np050604_149	Cyanophage S-RIM44	GCA_002599185.1
AOO12103.1	000538	HSP20	135	Np200711_157	Cyanophage S-RIM44	GCA_002599205.1
AOO12338.1	000538	HSP20	135	Np420711_156	Cyanophage S-RIM44	GCA_002599225.1
AOO12566.1	000538	HSP20	135	Sn080709_149	Cyanophage S-RIM44	GCA_002599245.1
AOO12803.1	000538	HSP20	135	Sn130910_156	Cyanophage S-RIM44	GCA_002599265.1
AOO13032.1	000538	HSP20	135	W2100709_150	Cyanophage S-RIM44	GCA_002599285.1
AGH07491.1	000538	HSP20	143	CYVG_00047	Cyanophage S-SSM6a	GCA_002710385.1
AGG54455.1	000538	HSP20	160	CYWG_00171	Cyanophage S-SSM6b	GCA_002710425.1
AXH72862.1	000538	HSP20	132	-	Myoviridae sp.	GCA_003657725.1
AGH26293.1	000538	HSP20	139	CPMG_00193	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44552.1	000538	HSP20	152	PSSM2_174	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12419.1	000538	HSP20	152	PRTG_00268	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93480.1	000538	HSP20	142	AVU42_gp143	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99252.1	000538	HSP20	135	Syn1_151	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76140.1	000538	HSP20	143	EST35_0259	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44452.1	000538	HSP20	173	PBI_SCTP2_437	Salicola phage SCTP-2	GCA_002625545.1
AIX30644.1	000538	HSP20	147	Syn7803US37_167	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76203.1	000538	HSP20	143	PBI_BELLAMY_158	Synechococcus phage Bellamy	GCA_002627525.1
QCW23082.1	000538	HSP20	141	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50573.1	000538	HSP20	141	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59617.1	000538	HSP20	134	S330809_156	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59379.1	000538	HSP20	134	C440309_156	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59855.1	000538	HSP20	134	N231010_156	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70548.1	000538	HSP20	119	HOU04_gp149	Synechococcus phage S-T4	GCA_003443335.1
QJT70153.1	000538	HSP20	144	SynMITS9220M01_140	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QIG65672.1	000000	HSP20	202	phiOC_p006	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QDB70367.1	000539	Hsp60	539	CF8_0199	Aeromonas phage CF8	GCA_006384595.2
QDJ97367.1	000539	Hsp60	542	D6_0208	Aeromonas phage D6	GCA_007051205.2
QDH47037.1	000539	Hsp60	542	LAh10_122	Aeromonas phage LAh10	GCA_006863975.1
QDJ96710.1	000539	Hsp60	517	PS1_0199	Aeromonas phage PS1	GCA_007051165.2
QFR59343.1	000539	Hsp60	517	PS2_0201	Aeromonas phage PS2	GCA_009388305.2
AMS01312.1	000539	Hsp60	562	AR9_g228	Bacillus phage AR9	GCA_001743835.1
ALN97962.1	000539	Hsp60	565	Bp8pS_283	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99941.1	000539	Hsp60	562	PBI_PBS1_119	Bacillus virus PBS1	GCA_002601325.1
QIG63491.1	000539	Hsp60	540	DAC16_262	Bacteroides phage DAC16	GCA_013387695.1
QIG63753.1	000539	Hsp60	540	DAC19_266	Bacteroides phage DAC19	GCA_013387715.1
QIG64014.1	000539	Hsp60	540	DAC20_265	Bacteroides phage DAC20	GCA_013387725.1
QIG64278.1	000539	Hsp60	540	DAC22_268	Bacteroides phage DAC22	GCA_013387735.1
QIG64535.1	000539	Hsp60	540	DAC23_261	Bacteroides phage DAC23	GCA_013387745.1
QBZ70750.1	000539	Hsp60	526	pETSU_169	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03723.1	000539	Hsp60	559	JOAD_192	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03480.1	000539	Hsp60	559	RISINGSUN_190	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72057.1	000539	Hsp60	519	N1M2_194	Klebsiella phage N1M2	GCA_010092605.1
QGZ14469.1	000539	Hsp60	519	HWC77_gp106	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27240.1	000539	Hsp60	558	PPEV_gp146	Pseudomonas phage EL	GCA_000866825.1
AEV89683.1	000539	Hsp60	520	OBP_246	Pseudomonas phage OBP	GCA_000896635.1
QAU04265.1	000539	Hsp60	519	HWC03_gp110	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23100.1	000539	Hsp60	519	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80941.1	000539	Hsp60	519	Aphrodite1_0033	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47416.1	000539	Hsp60	519	HWC35_gp022	Vibrio phage USC-1	GCA_006864065.1
QAU04545.1	000539	Hsp60	526	ValB1MD_259	Vibrio phage ValB1MD	GCA_004138815.1
BAW98236.1	000539	Hsp60	519	FDH33_gp027	Vibrio phage pTD1	GCA_002618825.1
CCE26266.1	000539	Hsp60	574	g243	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000624	000540	HSP70	444	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000443	000540	HSP70	444	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000623	000541	HSP70	210	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000441	000541	HSP70	210	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ94813.1	000542	Alba	167	FDI40_gp001	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21763.1	000542	Alba	168	GAP32_313	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13944.1	000542	Alba	167	PBI_121Q_47	Escherichia phage 121Q	GCA_000926855.1
QAY00393.1	000542	Alba	167	Ecwhy1_112	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35138.1	000542	Alba	167	ACQ29_gp458	Escherichia phage PBECO4	GCA_001041035.1
BBM61636.1	000542	Alba	167	EO157G_0470	Escherichia phage SP27	GCA_008033345.1
AXC36712.1	000542	Alba	167	-	Escherichia phage UB	GCA_003341455.1
QBO61749.1	000542	Alba	167	G17_00260	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13794.1	000542	Alba	167	vBEcoMphAPEC6_gp165c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80538.1	000542	Alba	167	PSLUR01_00561	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44426.1	000542	Alba	169	RaK2_00153	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72841.1	000542	Alba	138	-	Myoviridae sp.	GCA_003657725.1
AMM43881.1	000542	Alba	168	CBB_318	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19041.1	000542	Alba	168	7t3_0521	Salmonella phage 7t3	GCA_006083215.1
AZU98288.1	000542	Alba	168	CPT_Munch_344	Salmonella phage Munch	GCA_004015485.1
QIG62696.1	000542	Alba	168	SEPL_083	Salmonella phage SE_PL	GCA_011067555.1
AQW88841.1	000542	Alba	168	BF_0316	Serratia phage BF	GCA_002619745.1
SOK59125.1	000542	Alba	168	g317	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58591.1	000542	Alba	168	g314	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21765.1	000543	KTSC	177	GAP32_315	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13946.1	000543	KTSC	181	PBI_121Q_49	Escherichia phage 121Q	GCA_000926855.1
QAY00391.1	000543	KTSC	181	Ecwhy1_110	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35136.1	000543	KTSC	181	ACQ29_gp456	Escherichia phage PBECO4	GCA_001041035.1
BBM61638.1	000543	KTSC	181	EO157G_0490	Escherichia phage SP27	GCA_008033345.1
AXC36710.1	000543	KTSC	181	-	Escherichia phage UB	GCA_003341455.1
QBO61747.1	000543	KTSC	181	G17_00258	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13792.1	000543	KTSC	181	vBEcoMphAPEC6_gp163c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80540.1	000543	KTSC	181	PSLUR01_00563	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44428.1	000543	KTSC	186	RaK2_00155	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43883.1	000543	KTSC	177	CBB_320	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19043.1	000543	KTSC	177	7t3_0523	Salmonella phage 7t3	GCA_006083215.1
AZU98290.1	000543	KTSC	177	CPT_Munch_346	Salmonella phage Munch	GCA_004015485.1
QIG62694.1	000543	KTSC	177	SEPL_081	Salmonella phage SE_PL	GCA_011067555.1
AQW88843.1	000543	KTSC	177	BF_0318	Serratia phage BF	GCA_002619745.1
SOK59127.1	000543	KTSC	177	g319	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58593.1	000543	KTSC	177	g316	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFH14720.1	000544	KTSC	436	Lu11_0183	Pseudomonas phage Lu11	GCA_000897175.1
AGS81992.1	000544	KTSC	184	PaBG_00107	Pseudomonas phage PaBG	GCA_000912555.1
AFH14538.1	000000	SIG+KTSC	463	Lu11_0007	Pseudomonas phage Lu11	GCA_000897175.1
QCG76056.1	000000	KTSC	70	EST35_0175	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44487.1	000000	KTSC	123	PBI_SCTP2_472	Salicola phage SCTP-2	GCA_002625545.1
AEO93539.1	000545	KptA_PTS_2-RNA	186	G_280	Bacillus virus G	GCA_000917535.1
AXG67309.1	000545	KptA_PTS_2-RNA	177	AD1_265	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80067.1	000545	KptA_PTS_2-RNA	180	JA11_262	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66668.1	000545	KptA_PTS_2-RNA	180	JA13_265	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66989.1	000545	KptA_PTS_2-RNA	180	JA29_263	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67637.1	000545	KptA_PTS_2-RNA	180	JA33_263	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AHI60233.1	000545	KptA_PTS_2-RNA	193	Ea357_082	Erwinia phage Ea35-70	GCA_000914635.1
QBP07192.1	000545	KptA_PTS_2-RNA	193	REBECCA_84	Erwinia phage Rebecca	GCA_004521635.1
AWY08534.1	000545	KptA_PTS_2-RNA	177	Alexandra_277	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AUG85871.1	000545	KptA_PTS_2-RNA	193	BOSOLAPHORUS_83	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52183.1	000545	KptA_PTS_2-RNA	193	DM_85	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86190.1	000545	KptA_PTS_2-RNA	193	DESERTFOX_82	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86512.1	000545	KptA_PTS_2-RNA	193	MADMEL_84	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86833.1	000545	KptA_PTS_2-RNA	193	MORTIMER_84	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51863.1	000545	KptA_PTS_2-RNA	193	RAY_82	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51547.1	000545	KptA_PTS_2-RNA	193	SIMMY50_85	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64895.1	000545	KptA_PTS_2-RNA	193	SPECIALG_85	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARW58912.1	000545	KptA_PTS_2-RNA	181	Y3_272	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXH72870.1	000545	KptA_PTS_2-RNA	185	-	Myoviridae sp.	GCA_003657725.1
AMO43110.1	000546	SIG+YHYH	3411	R1080702_101	Cyanophage S-RIM32	GCA_001754165.1
AMO43337.1	000546	SIG+YHYH	3274	W270710_093	Cyanophage S-RIM44	GCA_002599145.1
AOO11570.1	000546	SIG+YHYH	3328	ES420910_089	Cyanophage S-RIM44	GCA_002599165.1
AOO11809.1	000546	SIG+YHYH	3274	Np050604_093	Cyanophage S-RIM44	GCA_002599185.1
AOO12035.1	000546	SIG+YHYH	3328	Np200711_089	Cyanophage S-RIM44	GCA_002599205.1
AOO12271.1	000546	SIG+YHYH	3328	Np420711_089	Cyanophage S-RIM44	GCA_002599225.1
AOO12510.1	000546	SIG+YHYH	3274	Sn080709_093	Cyanophage S-RIM44	GCA_002599245.1
AOO12736.1	000546	SIG+YHYH	3328	Sn130910_089	Cyanophage S-RIM44	GCA_002599265.1
AOO12976.1	000546	SIG+YHYH	3274	W2100709_094	Cyanophage S-RIM44	GCA_002599285.1
ADO99195.1	000546	SIG+YHYH	3274	Syn1_094	Prochlorococcus phage Syn1	GCA_000892495.1
QDH50594.1	000546	SIG+YHYH	2162	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59550.1	000546	SIG+YHYH	3494	S330809_089	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59312.1	000546	SIG+YHYH	3494	C440309_089	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59788.1	000546	SIG+YHYH	3494	N231010_089	Synechococcus phage S-CAM4	GCA_002922155.1
QDH50589.1	000547	KVP40.0284	1390	-	Synechococcus phage S-B43	GCA_006869725.1
AGH07718.1	000548	YHYH	3007	CYVG_00275	Cyanophage S-SSM6a	GCA_002710385.1
AAX44489.1	000548	YHYH	5195	PSSM2_111	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12159.1	000548	YHYH	4108	PRTG_00001	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93427.1	000548	YHYH	4307	AVU42_gp086	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30595.1	000548	YHYH	4225	Syn7803US37_118	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54871.1	000548	YHYH	2845	b23_0257	Synechococcus phage B23	GCA_009745195.1
QGT54506.1	000548	YHYH	2845	b3_0264	Synechococcus phage B3	GCA_009745215.1
ASR76156.1	000548	YHYH	4067	PBI_BELLAMY_111	Synechococcus phage Bellamy	GCA_002627525.1
QCW22831.1	000548	YHYH	4024	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50497.1	000548	YHYH	4337	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70596.1	000548	YHYH	4749	HOU04_gp197	Synechococcus phage S-T4	GCA_003443335.1
QJT70096.1	000548	YHYH	4067	SynMITS9220M01_083	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AOO14288.1	000549	YHYH+YHYH	1184	Sn110110_094	Cyanophage S-RIM14	GCA_002599065.1
AOO14937.1	000549	YHYH+YHYH	1184	W1230910_091	Cyanophage S-RIM14	GCA_002599125.1
AGG54296.1	000549	YHYH+YHYH	1154	CYWG_00012	Cyanophage S-SSM6b	GCA_002710425.1
AGH56928.1	000550	CPXG_00125	614	CPXG_00125	Cyanophage P-RSM6	GCA_000906155.1
AJK27529.1	000550	CPXG_00125	614	PTIM40_102	Cyanophage P-TIM40	GCA_001470935.1
AGH56930.1	000551	YHYH	531	CPXG_00127	Cyanophage P-RSM6	GCA_000906155.1
AJK27527.1	000551	YHYH	526	PTIM40_100	Cyanophage P-TIM40	GCA_001470935.1
AOO14286.1	000551	YHYH	573	Sn110110_092	Cyanophage S-RIM14	GCA_002599065.1
AOO14935.1	000551	YHYH	573	W1230910_089	Cyanophage S-RIM14	GCA_002599125.1
AGG54298.1	000551	YHYH	590	CYWG_00014	Cyanophage S-SSM6b	GCA_002710425.1
AGH56931.1	000552	YHYH+DUF3221+Laminin_G+Laminin_G	8573	CPXG_00128	Cyanophage P-RSM6	GCA_000906155.1
AJK27526.1	000552	YHYH+DUF3221+Laminin_G+Laminin_G	7351	PTIM40_99	Cyanophage P-TIM40	GCA_001470935.1
AOO14285.1	000552	YHYH+DUF3221+Laminin_G+Laminin_G	6198	Sn110110_091	Cyanophage S-RIM14	GCA_002599065.1
AOO14934.1	000552	YHYH+DUF3221+Laminin_G+Laminin_G	6198	W1230910_088	Cyanophage S-RIM14	GCA_002599125.1
AGG54299.1	000000	YHYH+Laminin_G+Laminin_G	6932	CYWG_00015	Cyanophage S-SSM6b	GCA_002710425.1
AGH26136.1	000000	SIG+YHYH	4458	CPMG_00035	Prochlorococcus phage MED4-213	GCA_000904535.1
BBA65498.1	000553	Laminin_G	654	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96517.1	000553	Laminin_G	636	Xoosp13_331	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGH07449.1	000554	T4_neck-protein+Laminin_G	762	CYVG_00005	Cyanophage S-SSM6a	GCA_002710385.1
ARB13604.1	000555	Laminin_G	2797	Ccr10_gp076	Caulobacter phage Ccr10	GCA_002619445.1
ARB13950.1	000555	Laminin_G	2797	Ccr2_gp075	Caulobacter phage Ccr2	GCA_002619465.1
ARB14640.1	000555	Laminin_G	2517	Ccr29_gp083	Caulobacter phage Ccr29	GCA_002619485.1
ARB14996.1	000555	Laminin_G	2799	Ccr32_gp077	Caulobacter phage Ccr32	GCA_002619505.1
ARB15326.1	000555	Laminin_G	1630	Ccr34_gp081	Caulobacter phage Ccr34	GCA_002619525.1
ARB14293.1	000555	Laminin_G	2796	Ccr5_gp075	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68278.1	000555	Laminin_G	2384	CcrBL10_gp074	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69161.1	000555	Laminin_G	2748	CcrBL9_gp137	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87961.1	000555	Laminin_G	2750	CcrColossus_gp091	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68637.1	000555	Laminin_G	2765	CcrPW_gp098	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69716.1	000555	Laminin_G	2756	CcrSC_gp134	Caulobacter phage CcrSC	GCA_003443315.1
AFU87594.1	000555	Laminin_G	2797	CcrKarma_gp077	Caulobacter virus Karma	GCA_000901575.1
AFU87244.1	000555	Laminin_G	2798	CcrMagneto_gp074	Caulobacter virus Magneto	GCA_000903095.1
AFU86560.1	000555	Laminin_G	2805	CcrRogue_gp078	Caulobacter virus Rogue	GCA_000900555.1
AFU88392.1	000555	Laminin_G	2797	CcrSwift_gp074	Caulobacter virus Swift	GCA_000899655.1
AFU86908.1	000555	Laminin_G	2799	CbK_gp076	Caulobacter virus phiCbK	GCA_000900535.1
ARB14641.1	000555	Laminin_G	1052	Ccr29_gp084	Caulobacter phage Ccr29	GCA_002619485.1
ARB15327.1	000555	Laminin_G	406	Ccr34_gp083	Caulobacter phage Ccr34	GCA_002619525.1
AXG67129.1	000556	Laminin_G	362	AD1_085	Dickeya phage vB_DsoM_AD1	GCA_003568515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AWY08365.1	000556	Laminin_G	362	Alexandra_89	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58728.1	000556	Laminin_G	361	Y3_088	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28560.1	000556	Laminin_G	351	YOLOSWAG_77	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67130.1	000556	Laminin_G	318	AD1_086	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79884.1	000556	Laminin_G	339	JA11_079	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79885.1	000556	Laminin_G	524	JA11_080	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66483.1	000556	Laminin_G	339	JA13_080	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66484.1	000556	Laminin_G	524	JA13_081	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66808.1	000556	Laminin_G	339	JA29_082	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66809.1	000556	Laminin_G	524	JA29_083	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67453.1	000556	Laminin_G	339	JA33_079	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67454.1	000556	Laminin_G	524	JA33_080	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08366.1	000556	Laminin_G	318	Alexandra_90	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58729.1	000556	Laminin_G	314	Y3_089	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28561.1	000556	Laminin_G	322	YOLOSWAG_78	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AHI60264.1	000557	Laminin_G	238	Ea357_113	Erwinia phage Ea35-70	GCA_000914635.1
AGX01918.1	000557	Laminin_G	235	CF95_gp196	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07222.1	000557	Laminin_G	238	REBECCA_115	Erwinia phage Rebecca	GCA_004521635.1
AUG85902.1	000557	Laminin_G	238	BOSOLAPHORUS_115	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52217.1	000557	Laminin_G	238	DM_119	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86221.1	000557	Laminin_G	238	DESERTFOX_114	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86543.1	000557	Laminin_G	238	MADMEL_115	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86867.1	000557	Laminin_G	238	MORTIMER_118	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51895.1	000557	Laminin_G	238	RAY_114	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51579.1	000557	Laminin_G	238	SIMMY50_117	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64926.1	000557	Laminin_G	238	SPECIALG_116	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARV77376.1	000557	Laminin_G	255	NOXIFER_207	Pseudomonas phage Noxifer	GCA_002625005.1
QBJ02930.1	000557	Laminin_G	235	PSA21_408	Pseudomonas phage Psa21	GCA_004340405.1
QFP93136.1	000557	Laminin_G	233	-	Serratia phage PCH45	GCA_009187865.1
AMO43220.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1362	R1080702_215	Cyanophage S-RIM32	GCA_001754165.1
AMO43453.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1357	W270710_214	Cyanophage S-RIM44	GCA_002599145.1
AOO11694.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1331	ES420910_217	Cyanophage S-RIM44	GCA_002599165.1
AOO11925.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1357	Np050604_214	Cyanophage S-RIM44	GCA_002599185.1
AOO12160.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1331	Np200711_218	Cyanophage S-RIM44	GCA_002599205.1
AOO12395.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1286	Np420711_217	Cyanophage S-RIM44	GCA_002599225.1
AOO12626.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1357	Sn080709_214	Cyanophage S-RIM44	GCA_002599245.1
AOO12860.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1331	Sn130910_217	Cyanophage S-RIM44	GCA_002599265.1
AOO13092.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1358	W2100709_215	Cyanophage S-RIM44	GCA_002599285.1
ADO99313.1	000558	BetaPropeller+Laminin_G+Laminin_G+Laminin_G	1357	Syn1_217	Prochlorococcus phage Syn1	GCA_000892495.1
AFC21991.1	000559	Laminin_G	217	GAP32_530	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXG67135.1	000559	Laminin_G	211	AD1_091	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AMM44111.1	000559	Laminin_G	217	CBB_548	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAS04882.1	000559	Laminin_G	220	AVU11_gp090	Ralstonia phage RSF1	GCA_001500875.1
QCW18641.1	000559	Laminin_G	215	7t3_0120	Salmonella phage 7t3	GCA_006083215.1
AZU98466.1	000559	Laminin_G	215	CPT_Munch_534	Salmonella phage Munch	GCA_004015485.1
QIG63048.1	000559	Laminin_G	215	SEPL_435	Salmonella phage SE_PL	GCA_011067555.1
QFP93152.1	000559	Laminin_G	214	-	Serratia phage PCH45	GCA_009187865.1
QBX06171.1	000560	Laminin_G	1152	ValB1HC_218	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61188.1	000560	Laminin_G	1152	AVU32_gp347	Vibrio phage ValKK3	GCA_001501635.1
ALP46960.1	000560	Laminin_G	1152	phiGrn1_0034	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47340.1	000560	Laminin_G	1152	phiST2_0166	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54797.1	000560	Laminin_G	1152	vBValMR10Z_257	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AGS82143.2	000561	Laminin_G+Laminin_G	1029	PaBG_00270	Pseudomonas phage PaBG	GCA_000912555.1
AGS82144.2	000561	Laminin_G+Laminin_G	1231	PaBG_00271	Pseudomonas phage PaBG	GCA_000912555.1
QCG76190.1	000561	Laminin_G+Laminin_G	636	EST35_0309	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW23080.1	000562	SIG+Laminin_G	893	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50631.1	000562	SIG+Laminin_G	919	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70047.1	000562	SIG+Laminin_G	782	SynMITS9220M01_034	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QGT54649.1	000563	Laminin_G+IG+IG+IG	1909	b23_0021	Synechococcus phage B23	GCA_009745195.1
QGT54279.1	000563	Laminin_G+IG+IG+IG	1909	b3_0021	Synechococcus phage B3	GCA_009745215.1
AGH26128.1	000564	SIG+Laminin_G	1324	CPMG_00027	Prochlorococcus phage MED4-213	GCA_000904535.1
AIX30748.1	000564	SIG+Laminin_G	1560	Syn7803US37_271	Synechococcus phage ACG-2014f	GCA_002594065.1
AGX01920.1	000565	Laminin_G	256	CF95_gp198	Erwinia phage PhiEaH1	GCA_000914555.1
AMM43812.1	000565	Laminin_G	244	CBB_247	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44114.1	000000	Laminin_G	234	CBB_551	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAU71414.1	000000	Laminin_G	190	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02621.1	000000	Laminin_G	128	AVU38_gp093	Ralstonia phage RSL2	GCA_001503055.1
QKE54423.1	000000	Laminin_G	215	ACSA002_1090	Salmonella phage vB_SalM_SA002	GCA_014131285.1
BAX25557.1	000000	Laminin_G	552	BPT24_146	Tenacibaculum phage pT24	GCA_002611925.1
AEO93449.1	000000	Laminin_G	1109	G_189	Bacillus virus G	GCA_000917535.1
BAE47808.1	000000	Laminin_G	288	CST110	Clostridium phage c-st	GCA_000865225.1
QBJ02617.1	000000	Laminin_G	232	PSA21_89	Pseudomonas phage Psa21	GCA_004340405.1
QIW90758.1	000000	Laminin_G	897	GCAPEGMB_00439	Vibrio phage V07	GCA_012361095.1
AEO93470.1	000000	Laminin_G	1178	G_211	Bacillus virus G	GCA_000917535.1
AGX01837.1	000000	Laminin_G	235	CF95_gp115	Erwinia phage PhiEaH1	GCA_000914555.1
QCW23022.1	000000	Laminin_G	851	-	Synechococcus phage S-B05	GCA_006083695.1
AWY08600.1	000000	SIG+Laminin_G	222	Alexandra_77	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BAQ02611.1	000000	SIG+Laminin_G	234	AVU38_gp083	Ralstonia phage RSL2	GCA_001503055.1
AOV59892.1	000000	Laminin_G	775	N231010_193	Synechococcus phage S-CAM4	GCA_002922155.1
ALY07146.1	000000	Laminin_G	803	VmeM32_00160	Vibrio phage vB_VmeM-32	GCA_002608825.1
BAE47784.1	000000	Tox-HopH1+Laminin_G	1291	CST086	Clostridium phage c-st	GCA_000865225.1
BAS04881.2	000000	Laminin_G	160	AVU11_agp19	Ralstonia phage RSF1	GCA_001500875.1
ASV44155.1	000000	LamininG	3807	PBI_SCTP2_140	Salicola phage SCTP-2	GCA_002625545.1
AFH14782.1	000000	LamininG	626	Lu11_0246	Pseudomonas phage Lu11	GCA_000897175.1
QIG63403.1	000566	YAcAr	144	DAC16_173	Bacteroides phage DAC16	GCA_013387695.1
QIG63667.1	000566	YAcAr	144	DAC19_179	Bacteroides phage DAC19	GCA_013387715.1
QIG63928.1	000566	YAcAr	144	DAC20_178	Bacteroides phage DAC20	GCA_013387725.1
QIG64192.1	000566	YAcAr	144	DAC22_181	Bacteroides phage DAC22	GCA_013387735.1
QIG64448.1	000566	YAcAr	144	DAC23_173	Bacteroides phage DAC23	GCA_013387745.1
ARB13678.1	000566	YAcAr	150	Ccr10_gp149c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14023.1	000566	YAcAr	150	Ccr2_gp148c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14711.1	000566	YAcAr	150	Ccr29_gp155	Caulobacter phage Ccr29	GCA_002619485.1
ARB15066.1	000566	YAcAr	150	Ccr32_gp148	Caulobacter phage Ccr32	GCA_002619505.1
ARB15400.1	000566	YAcAr	150	Ccr34_gp158	Caulobacter phage Ccr34	GCA_002619525.1
ARB14366.1	000566	YAcAr	150	Ccr5_gp147c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68349.1	000566	YAcAr	144	CcrBL10_gp145c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69247.1	000566	YAcAr	151	CcrBL9_gp223	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88062.1	000566	YAcAr	135	CcrColossus_gp192	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68740.1	000566	YAcAr	135	CcrPW_gp201c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69802.1	000566	YAcAr	143	CcrSC_gp220	Caulobacter phage CcrSC	GCA_003443315.1
AFU87671.1	000566	YAcAr	150	CcrKarma_gp154	Caulobacter virus Karma	GCA_000901575.1
AFU87320.1	000566	YAcAr	150	CcrMagneto_gp150	Caulobacter virus Magneto	GCA_000903095.1
AFU86633.1	000566	YAcAr	153	CcrRogue_gp151	Caulobacter virus Rogue	GCA_000900555.1
AFU88467.1	000566	YAcAr	150	CcrSwift_gp149	Caulobacter virus Swift	GCA_000899655.1
AFU86984.1	000566	YAcAr	150	CbK_gp152	Caulobacter virus phiCbK	GCA_000900535.1
BAE47744.1	000566	YAcAr	305	CST046	Clostridium phage c-st	GCA_000865225.1
AHI60303.1	000566	YAcAr	293	Ea357_152	Erwinia phage Ea35-70	GCA_000914635.1
AGX01893.1	000566	YAcAr	148	CF95_gp172	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07261.1	000566	YAcAr	293	REBECCA_154	Erwinia phage Rebecca	GCA_004521635.1
AUG85941.1	000566	YAcAr	293	BOSOLAPHORUS_154	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52256.1	000566	YAcAr	293	DM_158	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86260.1	000566	YAcAr	293	DESERTFOX_153	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86582.1	000566	YAcAr	293	MADMEL_154	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86906.1	000566	YAcAr	293	MORTIMER_157	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51934.1	000566	YAcAr	293	RAY_153	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51618.1	000566	YAcAr	293	SIMMY50_156	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64965.1	000566	YAcAr	293	SPECIALG_155	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBO64032.1	000566	YAcAr	108	Goslar_00241	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QIG57933.1	000566	YAcAr	128	SEA_PAULODIABOLI_248	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72889.1	000566	YAcAr	123	-	Myoviridae sp.	GCA_003657725.1
QIG65720.1	000566	YAcAr	118	phiOC_p054	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QCG76130.1	000566	YAcAr	122	EST35_0249	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAW19030.1	000566	YAcAr	95	FDH28_gp056	Ralstonia phage RP12	GCA_002617345.1
BAW19315.1	000566	YAcAr	95	-	Ralstonia phage RP31	GCA_002617365.1
BAS04844.1	000566	YAcAr	157	AVU11_gp052	Ralstonia phage RSF1	GCA_001500875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAQ02577.2	000566	YAcAr	182	-	Ralstonia phage RSL2	GCA_001503055.1
ATA65414.1	000566	YAcAr	164	2050HW_00079	Serratia phage 2050HW	GCA_002628125.1
QDB71193.1	000566	YAcAr	164	CPT_Moabite_163	Serratia phage Moabite	GCA_006384735.1
AYD81281.1	000566	YAcAr	154	SEA_JUSTBECAUSE_112	Streptomyces phage JustBecause	GCA_003613775.1
QJD53684.1	000566	YAcAr	154	SEA_KELA_113	Streptomyces phage Kela	GCA_012934305.1
QBZ72011.1	000566	YAcAr	155	SEA_KRADAL_113	Streptomyces phage Kradal	GCA_004799925.1
AXH66274.1	000566	YAcAr	155	SEA_SATIS_113	Streptomyces phage Satis	GCA_003366315.1
AAQ64224.1	000566	YAcAr	123	KVP40.0155	Vibrio phage KVP40	GCA_000843785.1
QIW90538.1	000566	YAcAr	124	GCAPEGMB_00191	Vibrio phage V07	GCA_012361095.1
QIW90767.1	000566	YAcAr	117	GCAPEGMB_00448	Vibrio phage V07	GCA_012361095.1
QIW90884.1	000566	YAcAr	124	COHAPHLL_00021	Vibrio phage V09	GCA_012361135.1
QHJ74336.1	000566	YAcAr	124	VH12019_00009	Vibrio phage VH1_2019	GCA_009931825.1
AGB06829.1	000566	YAcAr	89	CF80_gp042	Vibrio phage VH7D	GCA_000914495.1
QBX06317.1	000566	YAcAr	89	ValB1HC_364	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04446.1	000566	YAcAr	119	ValB1MD_021	Vibrio phage ValB1MD	GCA_004138815.1
AJT60948.1	000566	YAcAr	124	AVU32_gp107	Vibrio phage ValKK3	GCA_001501635.1
AGN30202.1	000566	YAcAr	124	VPFG_00202	Vibrio phage nt-1	GCA_000910195.2
ALP47235.1	000566	YAcAr	89	phiGrn1_0266	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47621.1	000566	YAcAr	89	phiST2_0025	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54560.1	000566	YAcAr	123	vBValMR10Z_19	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37383.1	000566	YAcAr	124	pp2_150	Vibriophage phi-pp2	GCA_002630725.1
AHI60303.1	000567	NADAR+YAcAr	293	Ea357_152	Erwinia phage Ea35-70	GCA_000914635.1
QBP07261.1	000567	NADAR+YAcAr	293	REBECCA_154	Erwinia phage Rebecca	GCA_004521635.1
AUG85941.1	000567	NADAR+YAcAr	293	BOSOLAPHORUS_154	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52256.1	000567	NADAR+YAcAr	293	DM_158	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86260.1	000567	NADAR+YAcAr	293	DESERTFOX_153	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86582.1	000567	NADAR+YAcAr	293	MADMEL_154	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86906.1	000567	NADAR+YAcAr	293	MORTIMER_157	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51934.1	000567	NADAR+YAcAr	293	RAY_153	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51618.1	000567	NADAR+YAcAr	293	SIMMY50_156	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64965.1	000567	NADAR+YAcAr	293	SPECIALG_155	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AFO71419.1	000568	NADAR	338	CR5_199	Cronobacter phage CR5	GCA_000910235.1
AFC21792.1	000568	NADAR	161	GAP32_342	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMR59875.1	000568	NADAR	283	SEGD1_228	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07632.1	000568	NADAR	338	DERBICUS_206	Erwinia phage Derbicus	GCA_004521655.1
ANZ49876.1	000568	NADAR	339	MACHINA_238	Erwinia phage Machina	GCA_002758035.1
AXF51378.1	000568	NADAR	346	WELLINGTON_252	Erwinia phage Wellington	GCA_003344985.1
AFQ96690.1	000568	NADAR	292	G173_gp145	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48259.1	000568	NADAR	292	ASESINO_246	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48533.1	000568	NADAR	335	CAITLIN_238	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48809.1	000568	NADAR	331	CHRISDB_247	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49056.1	000568	NADAR	338	EARLPHILLIPIV_207	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49319.1	000568	NADAR	339	HUXLEY_237	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49604.1	000568	NADAR	346	KWAN_252	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50147.1	000568	NADAR	339	PARSHIK_238	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50403.1	000568	NADAR	334	PHOBOS_213	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50672.1	000568	NADAR	292	STRATTON_247	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AIT13970.1	000568	NADAR	163	PBI_121Q_73	Escherichia phage 121Q	GCA_000926855.1
QAY00367.1	000568	NADAR	163	Ecwhy1_86	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35112.1	000568	NADAR	163	ACQ29_gp432	Escherichia phage PBECO4	GCA_001041035.1
BBM61662.1	000568	NADAR	163	EO157G_0730	Escherichia phage SP27	GCA_008033345.1
AXC36686.1	000568	NADAR	163	-	Escherichia phage UB	GCA_003341455.1
QKN86065.1	000568	NADAR	283	ACEC001_2220	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61721.1	000568	NADAR	71	G17_00232	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61722.1	000568	NADAR	92	G17_00233	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13768.1	000568	NADAR	163	vBEcoMphAPEC6_gp139c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80564.1	000568	NADAR	163	PSLUR01_00587	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44452.1	000568	NADAR	178	RaK2_00179	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43911.1	000568	NADAR	161	CBB_348	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QHJ86054.1	000568	NADAR	162	KKIINIFJ_00142	Pseudomonas phage PN05	GCA_009931935.1
BAW19021.1	000568	NADAR	182	FDH28_gp047	Ralstonia phage RP12	GCA_002617345.1
BAW19307.1	000568	NADAR	182	-	Ralstonia phage RP31	GCA_002617365.1
BAS04837.2	000568	NADAR	170	AVU11_gp045	Ralstonia phage RSF1	GCA_001500875.1
BAQ02570.2	000568	NADAR	172	-	Ralstonia phage RSL2	GCA_001503055.1
QCW19069.1	000568	NADAR	164	7t3_0549	Salmonella phage 7t3	GCA_006083215.1
QNI20911.1	000568	NADAR	283	-	Salmonella phage JN03	GCA_014319805.1
AZU98315.1	000568	NADAR	164	CPT_Munch_371	Salmonella phage Munch	GCA_004015485.1
QIG62669.1	000568	NADAR	164	SEPL_056	Salmonella phage SE_PL	GCA_011067555.1
AWN09126.1	000568	NADAR	282	MLDJOKPK_00216	Salmonella phage SPAsTU	GCA_003183805.1
AEP84057.1	000568	NADAR	283	SPN3US_0224	Salmonella phage SPN3US	GCA_001042275.1
ATA65474.1	000568	NADAR	166	2050HW_00139	Serratia phage 2050HW	GCA_002628125.1
AQW88872.1	000568	NADAR	161	BF_0347	Serratia phage BF	GCA_002619745.1
QDB71244.1	000568	NADAR	166	CPT_Moabite_214	Serratia phage Moabite	GCA_006384735.1
AXH71013.1	000568	NADAR	172	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT28101.1	000568	NADAR	183	pVa21_160	Vibrio phage pVa-21	GCA_002619305.1
QAX96840.1	000568	NADAR	298	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97145.1	000568	NADAR	298	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96204.1	000568	NADAR	298	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96522.1	000568	NADAR	298	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
SOK59156.1	000568	NADAR	161	g348	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58622.1	000568	NADAR	161	g345	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67297.1	000569	NADAR	161	AD1_253	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80035.1	000569	NADAR	213	JA11_230	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66634.1	000569	NADAR	210	JA13_231	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66958.1	000569	NADAR	213	JA29_232	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67605.1	000569	NADAR	213	JA33_231	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08522.1	000569	NADAR	210	Alexandra_265	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58900.1	000569	NADAR	161	Y3_260	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BAG41532.1	000569	NADAR	215	RSL1_ORF086	Ralstonia phage phiRSL1	GCA_000879455.1
AHI60301.1	000570	YAcAr	139	Ea357_150	Erwinia phage Ea35-70	GCA_000914635.1
QBP07259.1	000570	YAcAr	139	REBECCA_152	Erwinia phage Rebecca	GCA_004521635.1
AUG85939.1	000570	YAcAr	139	BOSOLAPHORUS_152	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52254.1	000570	YAcAr	139	DM_156	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86258.1	000570	YAcAr	139	DESERTFOX_151	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86580.1	000570	YAcAr	139	MADMEL_152	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86904.1	000570	YAcAr	139	MORTIMER_155	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51932.1	000570	YAcAr	139	RAY_151	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51616.1	000570	YAcAr	139	SIMMY50_154	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64963.1	000570	YAcAr	139	SPECIALG_153	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24081.1	000570	YAcAr	138	-	Proteus phage 10	GCA_014071245.1
QKE54455.1	000570	YAcAr	138	ACSA002_1410	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AXF51097.1	000571	YAcAr	141	MLDJOKPK_00141	Salmonella phage SPAsTU	GCA_003183805.1
AQT28091.1	000571	YAcAr	310	pVa21_150	Vibrio phage pVa-21	GCA_002619305.1
AND75405.1	000000	YAcAr	149	ME3_244	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QMV28731.1	000572	NADAR-gp30	149	AP1_0013	Aeromonas phage AP1	GCA_014183365.1
ATI17561.1	000572	NADAR-gp30	149	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00436.1	000572	NADAR-gp30	149	HWB28_gp116	Aeromonas phage AS-zj	GCA_002627665.1
QAX98508.1	000572	NADAR-gp30	154	ASfcp2_172	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98001.1	000572	NADAR-gp30	149	ASswx1_361	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01140.1	000572	NADAR-gp30	152	ASwh1_74	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39502.1	000572	NADAR-gp30	149	CC2_174	Aeromonas phage CC2	GCA_000903495.1
ADQ52970.1	000572	NADAR-gp30	154	PX29p251	Aeromonas phage PX29	GCA_000920195.1
ADM79896.1	000572	NADAR-gp30	158	phiAS5_ORF0053	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53380.1	000572	NADAR-gp30	149	65p372	Aeromonas virus 65	GCA_000893255.1
AAQ17919.1	000572	NADAR-gp30	154	30.3	Aeromonas virus Aeh1	GCA_000843245.1
AFU88039.1	000572	NADAR-gp30	153	CcrColossus_gp169	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68716.1	000572	NADAR-gp30	153	CcrPW_gp177c	Caulobacter phage CcrPW	GCA_003443275.1
ANS06049.1	000572	NADAR-gp30	146	ABCD_0090	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64840.1	000572	NADAR-gp30	148	S13_041	Cronobacter phage S13	GCA_001503575.1
AON97103.1	000572	NADAR-gp30	146	E_095	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70761.1	000572	NADAR-gp30	152	phiC120_c55	Escherichia phage phiC120	GCA_002621185.1
AAX78612.1	000572	NADAR-gp30	146	RB43ORF090w	Escherichia virus RB43	GCA_000863505.1
QHJ78822.1	000572	NADAR-gp30	148	-	Myoviridae sp.	GCA_012593985.1
AGR47984.2	000572	NADAR-gp30	151	SmphiM12_352	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13170.1	000572	NADAR-gp30	151	PHIM19_265	Sinorhizobium phage phiM19	GCA_002605865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF12810.1	000572	NADAR-gp30	151	PHIM7_265	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13533.1	000572	NADAR-gp30	151	PHIN3_270	Sinorhizobium phage phiN3	GCA_001501175.1
BAV39184.1	000572	NADAR-gp30	292	BPT24_061	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64141.1	000572	NADAR-gp30	154	KVP40.0070	Vibrio phage KVP40	GCA_000843785.1
QIW90464.1	000572	NADAR-gp30	154	GCAPEGMB_00117	Vibrio phage V07	GCA_012361095.1
QIW90965.1	000572	NADAR-gp30	154	COHAPHLL_00102	Vibrio phage V09	GCA_012361135.1
QHJ74253.1	000572	NADAR-gp30	154	VH12019_00334	Vibrio phage VH1_2019	GCA_009931825.1
AGB07077.1	000572	NADAR-gp30	154	CF80_gp290	Vibrio phage VH7D	GCA_000914495.1
QBX06018.1	000572	NADAR-gp30	154	ValB1HC_064	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61032.1	000572	NADAR-gp30	154	AVU32_gp191	Vibrio phage ValKK3	GCA_001501635.1
AGN30119.1	000572	NADAR-gp30	154	VPFG_00117	Vibrio phage nt-1	GCA_000910195.2
ALP47120.1	000572	NADAR-gp30	154	phiGrn1_0185	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47504.1	000572	NADAR-gp30	154	phiST2_0316	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54643.1	000572	NADAR-gp30	154	vBValMR10Z_102	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07174.1	000572	NADAR-gp30	148	VmeM32_00188	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37301.1	000572	NADAR-gp30	154	pp2_068	Vibriophage phi-pp2	GCA_002630725.1
AND75377.1	000573	NADAR-YbiA	166	ME3_216	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ASV44752.1	000573	NADAR-YbiA	178	FDI40_gp673	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83792.1	000573	NADAR-YbiA	155	0305phi8-36p234	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01224.1	000573	NADAR-YbiA	139	AR9_g140	Bacillus phage AR9	GCA_001743835.1
AST99849.1	000573	NADAR-YbiA	140	PBI_PBS1_27	Bacillus virus PBS1	GCA_002601325.1
QBX06850.1	000573	NADAR-YbiA	198	BcepSaruman_437	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74819.1	000573	NADAR-YbiA	198	BcepSauron_439	Burkholderia phage BcepSauron	GCA_005394215.1
QIG57958.1	000573	NADAR-YbiA	149	SEA_PAULODIABOLI_274	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72804.1	000573	NADAR-YbiA	168	-	Myoviridae sp.	GCA_003657725.1
QIG65850.1	000573	NADAR-YbiA	146	phiOC_p185	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43736.1	000573	NADAR-YbiA	167	CBB_171	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFH14826.1	000573	NADAR-YbiA	175	Lu11_0288	Pseudomonas phage Lu11	GCA_000897175.1
QHJ86175.1	000573	NADAR-YbiA	165	KKIINIFJ_00265	Pseudomonas phage PN05	GCA_009931935.1
QKE11208.1	000573	NADAR-YbiA	183	PaBG_00104	Pseudomonas phage PaBG	GCA_000912555.1
AQW88694.1	000573	NADAR-YbiA	168	BF_0169	Serratia phage BF	GCA_002619745.1
QGT54675.1	000573	NADAR-YbiA	176	b23_0047	Synechococcus phage B23	GCA_009745195.1
QGT54305.1	000573	NADAR-YbiA	176	b3_0047	Synechococcus phage B3	GCA_009745215.1
QAU04453.1	000573	NADAR-YbiA	216	ValB1MD_035	Vibrio phage ValB1MD	GCA_004138815.1
QNI21225.1	000573	NADAR-YbiA	167	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65437.1	000573	NADAR-YbiA	146	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65361.1	000573	NADAR-YbiA	195	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96454.1	000573	NADAR-YbiA	97	Xoosp13_268	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58975.1	000573	NADAR-YbiA	162	g167	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58441.1	000573	NADAR-YbiA	162	g164	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000359	000573	NADAR-YbiA	179	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000285	000573	NADAR-YbiA	179	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AND75457.1	000574	MACRODOMAIN	208	ME3_296	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01542.1	000574	MACRODOMAIN	163	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29050.1	000574	MACRODOMAIN	164	AP1_0343	Aeromonas phage AP1	GCA_014183365.1
ATI17364.1	000574	MACRODOMAIN	164	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00230.1	000574	MACRODOMAIN	164	HWB28_gp322	Aeromonas phage AS-zj	GCA_002627665.1
AUE22812.1	000574	MACRODOMAIN	199	Ah1_00294	Aeromonas phage Ah1	GCA_002957415.1
QAX98525.1	000574	MACRODOMAIN	202	ASfcp2_189	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97805.1	000574	MACRODOMAIN	164	ASswx1_161	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01351.1	000574	MACRODOMAIN	165	ASwh1_291	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39568.1	000574	MACRODOMAIN	164	CC2_375	Aeromonas phage CC2	GCA_000903495.1
ADQ52988.1	000574	MACRODOMAIN	202	PX29p269	Aeromonas phage PX29	GCA_000920195.1
ADM79913.1	000574	MACRODOMAIN	207	phiAS5_ORF0070	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53164.1	000574	MACRODOMAIN	163	65p156	Aeromonas virus 65	GCA_000893255.1
AAQ17939.1	000574	MACRODOMAIN	202	tk.4	Aeromonas virus Aeh1	GCA_000843245.1
ASV44750.1	000574	MACRODOMAIN	145	FDI40_gp670	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASU00109.1	000574	MACRODOMAIN	175	PBI_PBS1_287	Bacillus virus PBS1	GCA_002601325.1
ANS06040.1	000574	MACRODOMAIN	162	ABCD_0144	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFO71397.1	000574	MACRODOMAIN	165	CR5_177	Cronobacter phage CR5	GCA_000910235.1
AIA64822.1	000574	MACRODOMAIN	167	S13_023	Cronobacter phage S13	GCA_001503575.1
AFC21642.1	000574	MACRODOMAIN	165	GAP32_192	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97154.1	000574	MACRODOMAIN	163	E_146	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
QBP07609.1	000574	MACRODOMAIN	165	DERBICUS_183	Erwinia phage Derbicus	GCA_004521655.1
AHI60302.1	000574	MACRODOMAIN	148	Ea357_151	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49845.1	000574	MACRODOMAIN	161	MACHINA_207	Erwinia phage Machina	GCA_002758035.1
AGX01726.1	000574	MACRODOMAIN	154	CF95_gp004	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07260.1	000574	MACRODOMAIN	148	REBECCA_153	Erwinia phage Rebecca	GCA_004521635.1
AXF51347.1	000574	MACRODOMAIN	163	WELLINGTON_221	Erwinia phage Wellington	GCA_003344985.1
AFQ96664.1	000574	MACRODOMAIN	166	G173_gp119	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48230.1	000574	MACRODOMAIN	166	ASESINO_217	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85940.1	000574	MACRODOMAIN	148	BOSOLAPHORUS_153	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48501.1	000574	MACRODOMAIN	161	CAITLIN_206	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48780.1	000574	MACRODOMAIN	161	CHRISDB_218	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52255.1	000574	MACRODOMAIN	148	DM_157	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86259.1	000574	MACRODOMAIN	148	DESERTFOX_152	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49033.1	000574	MACRODOMAIN	165	EARLPHILLIPIV_184	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49289.1	000574	MACRODOMAIN	161	HUXLEY_207	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49574.1	000574	MACRODOMAIN	163	KWAN_222	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86581.1	000574	MACRODOMAIN	148	MADMEL_153	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86905.1	000574	MACRODOMAIN	148	MORTIMER_156	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50117.1	000574	MACRODOMAIN	161	PARSHIK_208	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50381.1	000574	MACRODOMAIN	165	PHOBOS_191	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51933.1	000574	MACRODOMAIN	148	RAY_152	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51617.1	000574	MACRODOMAIN	148	SIMMY50_155	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64964.1	000574	MACRODOMAIN	148	SPECIALG_154	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50644.1	000574	MACRODOMAIN	166	STRATTON_219	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AIT14434.1	000574	MACRODOMAIN	158	PBI_121Q_544	Escherichia phage 121Q	GCA_000926855.1
QAY00514.1	000574	MACRODOMAIN	159	Ecwhy1_235	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34708.1	000574	MACRODOMAIN	158	ACQ29_gp028	Escherichia phage PBECO4	GCA_001041035.1
BBM62106.1	000574	MACRODOMAIN	158	EO157G_5170	Escherichia phage SP27	GCA_008033345.1
AXC36827.1	000574	MACRODOMAIN	158	-	Escherichia phage UB	GCA_003341455.1
ARM70930.1	000574	MACRODOMAIN	155	phiC120_c225	Escherichia phage phiC120	GCA_002621185.1
QKN86038.1	000574	MACRODOMAIN	166	ACEC001_1950	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61867.1	000574	MACRODOMAIN	158	G17_00378	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO63876.1	000574	MACRODOMAIN	186	Goslar_00083	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13908.1	000574	MACRODOMAIN	158	vBEcoMphAPEC6_gp283c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80420.1	000574	MACRODOMAIN	158	PSLUR01_00443	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78669.1	000574	MACRODOMAIN	132	RB43ORF147c	Escherichia virus RB43	GCA_000863505.1
AFA44308.1	000574	MACRODOMAIN	159	RaK2_00035	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57866.1	000574	MACRODOMAIN	153	SEA_PAULODIABOLI_171	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72858.1	000574	MACRODOMAIN	153	-	Myoviridae sp.	GCA_003657725.1
QHJ78840.1	000574	MACRODOMAIN	160	-	Myoviridae sp.	GCA_012593985.1
AMM43763.1	000574	MACRODOMAIN	166	CBB_198	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ABY62997.1	000574	MACRODOMAIN	160	201phi2-1p167	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44890.1	000574	MACRODOMAIN	162	KTN4_132	Pseudomonas phage KTN4	GCA_002607225.1
ARV77274.1	000574	MACRODOMAIN	157	NOXIFER_105	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32267.1	000574	MACRODOMAIN	157	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76782.1	000574	MACRODOMAIN	161	PHABIO_151	Pseudomonas phage Phabio	GCA_002624965.1
AEH03532.1	000574	MACRODOMAIN	160	108	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02651.1	000574	MACRODOMAIN	158	PSA21_123	Pseudomonas phage Psa21	GCA_004340405.1
ATN94823.1	000574	MACRODOMAIN	162	SL2_246	Pseudomonas phage SL2	GCA_002956015.1
QJB22767.1	000574	MACRODOMAIN	162	fnug_124	Pseudomonas phage fnug	GCA_012837215.1
QCG75995.1	000574	MACRODOMAIN	124	EST35_0113	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM41841.1	000574	MACRODOMAIN	157	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83005.1	000574	MACRODOMAIN	162	PHIKZ104	Pseudomonas virus phiKZ	GCA_000842965.1
QCW18912.1	000574	MACRODOMAIN	157	7t3_0391	Salmonella phage 7t3	GCA_006083215.1
QNI20886.1	000574	MACRODOMAIN	166	-	Salmonella phage JN03	GCA_014319805.1
AZU98169.1	000574	MACRODOMAIN	157	CPT_Munch_225	Salmonella phage Munch	GCA_004015485.1
QIG62815.1	000574	MACRODOMAIN	157	SEPL_202	Salmonella phage SE_PL	GCA_011067555.1
AXF51121.1	000574	MACRODOMAIN	166	MLDJOKPK_00243	Salmonella phage SPAsTU	GCA_003183805.1
AEP84029.1	000574	MACRODOMAIN	166	SPN3US_0196	Salmonella phage SPN3US	GCA_001042275.1
ATA65669.1	000574	MACRODOMAIN	146	2050HW_00334	Serratia phage 2050HW	GCA_002628125.1
AQW88719.1	000574	MACRODOMAIN	166	BF_0194	Serratia phage BF	GCA_002619745.1
QDB71091.1	000574	MACRODOMAIN	151	CPT_Moabite_059	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGR47919.1	000574	MACRODOMAIN	157	SmphiM12_287	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13122.1	000574	MACRODOMAIN	157	PHIM19_217	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12762.1	000574	MACRODOMAIN	157	PHIM7_217	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13492.1	000574	MACRODOMAIN	157	PHIN3_229	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28293.1	000574	MACRODOMAIN	142	PAU_296	Sphingomonas phage PAU	GCA_000902455.1
AYD81421.1	000574	MACRODOMAIN	151	SEA_JUSTBECAUSE_266	Streptomyces phage JustBecause	GCA_003613775.1
QJD53826.1	000574	MACRODOMAIN	151	SEA_KELA_266	Streptomyces phage Kela	GCA_012934305.1
QBZ72152.1	000574	MACRODOMAIN	151	SEA_KRADAL_266	Streptomyces phage Kradal	GCA_004799925.1
AXH66415.1	000574	MACRODOMAIN	151	SEA_SATIS_266	Streptomyces phage Satis	GCA_003366315.1
QGT54739.1	000574	MACRODOMAIN	167	b23_0124	Synechococcus phage B23	GCA_009745195.1
QGT54369.1	000574	MACRODOMAIN	167	b3_0125	Synechococcus phage B3	GCA_009745215.1
AXH70994.1	000574	MACRODOMAIN	218	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64163.1	000574	MACRODOMAIN	170	KVP40.0092	Vibrio phage KVP40	GCA_000843785.1
QIW90487.1	000574	MACRODOMAIN	170	GCAPEGMB_00140	Vibrio phage V07	GCA_012361095.1
QIW90942.1	000574	MACRODOMAIN	170	COHAPHLL_00079	Vibrio phage V09	GCA_012361135.1
QHJ74275.1	000574	MACRODOMAIN	170	VH12019_00356	Vibrio phage VH1_2019	GCA_009931825.1
AGB07100.1	000574	MACRODOMAIN	170	CF80_gp313	Vibrio phage VH7D	GCA_000914495.1
QBX05996.1	000574	MACRODOMAIN	170	ValB1HC_042	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61009.1	000574	MACRODOMAIN	170	AVU32_gp168	Vibrio phage ValKK3	GCA_001501635.1
AGN30142.2	000574	MACRODOMAIN	171	VPFG_00140	Vibrio phage nt-1	GCA_000910195.2
AQT28074.1	000574	MACRODOMAIN	85	pVa21_133	Vibrio phage pVa-21	GCA_002619305.1
ALP47098.1	000574	MACRODOMAIN	170	phiGrn1_0207	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47479.1	000574	MACRODOMAIN	170	phiST2_0340	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54620.1	000574	MACRODOMAIN	170	vBValMR10Z_79	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07150.1	000574	MACRODOMAIN	149	VmeM32_00164	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96685.1	000574	MACRODOMAIN	155	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97003.1	000574	MACRODOMAIN	155	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96049.1	000574	MACRODOMAIN	155	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96367.1	000574	MACRODOMAIN	155	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFN37323.1	000574	MACRODOMAIN	170	pp2_090	Vibriophage phi-pp2	GCA_002630725.1
BBA65315.1	000574	MACRODOMAIN	148	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96350.1	000574	MACRODOMAIN	124	Xoosp13_163	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59001.1	000574	MACRODOMAIN	165	g193	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58466.1	000574	MACRODOMAIN	165	g189	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QKE54456.1	000575	NADAR+MACRODOMAIN	290	ACSA002_1420	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54457.1	000576	NADAR+MACRODOMAIN+YAcAr	326	ACSA002_1430	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QIG63401.1	000577	MACRODOMAIN+YAcAr	272	DAC16_171	Bacteroides phage DAC16	GCA_013387695.1
QIG63665.1	000577	MACRODOMAIN+YAcAr	272	DAC19_177	Bacteroides phage DAC19	GCA_013387715.1
QIG63926.1	000577	MACRODOMAIN+YAcAr	272	DAC20_176	Bacteroides phage DAC20	GCA_013387725.1
QIG64190.1	000577	MACRODOMAIN+YAcAr	272	DAC22_179	Bacteroides phage DAC22	GCA_013387735.1
QIG64446.1	000577	MACRODOMAIN+YAcAr	272	DAC23_171	Bacteroides phage DAC23	GCA_013387745.1
QMP24082.1	000577	MACRODOMAIN+YAcAr	276	-	Proteus phage 10	GCA_014071245.1
QHJ86018.1	000577	MACRODOMAIN+YAcAr	237	KKIINIFJ_00106	Pseudomonas phage PN05	GCA_009931935.1
ARV77446.1	000578	MACRODOMAIN	215	NOXIFER_281	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32427.1	000578	MACRODOMAIN	251	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03694.1	000578	MACRODOMAIN	250	271	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41998.1	000578	MACRODOMAIN	251	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAG41500.1	000578	MACRODOMAIN	178	RSL1_ORF054	Ralstonia phage phiRSL1	GCA_000879455.1
AGR47871.1	000578	MACRODOMAIN	187	SmphiM12_239	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13073.1	000578	MACRODOMAIN	187	PHIM19_168	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12713.1	000578	MACRODOMAIN	187	PHIM7_168	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13443.1	000578	MACRODOMAIN	187	PHIN3_180	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67057.1	000579	MACRODOMAIN	197	AD1_013	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79816.1	000579	MACRODOMAIN	195	JA11_011	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66414.1	000579	MACRODOMAIN	195	JA13_011	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66737.1	000579	MACRODOMAIN	194	JA29_011	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67385.1	000579	MACRODOMAIN	195	JA33_011	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08294.1	000579	MACRODOMAIN	197	Alexandra_13	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58653.1	000579	MACRODOMAIN	194	Y3_013	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28500.1	000579	MACRODOMAIN	194	YOLOSWAG_13	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AMM44914.1	000000	MACRODOMAIN	156	SP15_116	Bacillus phage SP-15	GCA_001754685.1
AEO93384.1	000000	MACRODOMAIN	159	G_122	Bacillus virus G	GCA_000917535.1
AEO93695.1	000000	MACRODOMAIN	144	G_437	Bacillus virus G	GCA_000917535.1
QIG65767.1	000000	MACRODOMAIN	175	phiOC_p102	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
SBV38275.1	000000	SIG+MACRODOMAIN	184	BN7874_106	Phage NCTB	GCA_900092385.1
ASV44729.1	000580	MoxR-AAA	417	FDI40_gp264	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01113.1	000580	MoxR-AAA	399	AR9_g028	Bacillus phage AR9	GCA_001743835.1
ALN97762.1	000580	MoxR-AAA	399	Bp8pS_083	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93812.1	000580	MoxR-AAA	357	G_566	Bacillus virus G	GCA_000917535.1
ASU00035.1	000580	MoxR-AAA	399	PBI_PBS1_213	Bacillus virus PBS1	GCA_002601325.1
AFC21660.1	000580	MoxR-AAA	447	GAP32_210	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14453.1	000580	MoxR-AAA	441	PBI_121Q_563	Escherichia phage 121Q	GCA_000926855.1
QAY00495.1	000580	MoxR-AAA	442	Ecwhy1_216	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34690.1	000580	MoxR-AAA	441	ACQ29_gp010	Escherichia phage PBECO4	GCA_001041035.1
BBM62126.1	000580	MoxR-AAA	441	EO157G_5370	Escherichia phage SP27	GCA_008033345.1
AXC36810.1	000580	MoxR-AAA	441	-	Escherichia phage UB	GCA_003341455.1
QBO61849.1	000580	MoxR-AAA	441	G17_00360	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13890.1	000580	MoxR-AAA	441	vBEcoMphAPEC6_gp265c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80438.1	000580	MoxR-AAA	441	PSLUR01_00461	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44326.1	000580	MoxR-AAA	424	RaK2_00053	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72918.1	000580	MoxR-AAA	423	-	Myoviridae sp.	GCA_003657725.1
AMM43781.1	000580	MoxR-AAA	447	CBB_216	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76216.1	000580	MoxR-AAA	371	EST35_0335	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44187.1	000580	MoxR-AAA	452	PBI_SCTP2_172	Salicola phage SCTP-2	GCA_002625545.1
QCW18930.1	000580	MoxR-AAA	440	7t3_0409	Salmonella phage 7t3	GCA_006083215.1
AZU98186.1	000580	MoxR-AAA	440	CPT_Munch_242	Salmonella phage Munch	GCA_004015485.1
QIG62798.1	000580	MoxR-AAA	440	SEPL_185	Salmonella phage SE_PL	GCA_011067555.1
AQW88737.1	000580	MoxR-AAA	443	BF_0212	Serratia phage BF	GCA_002619745.1
QAU04463.1	000580	MoxR-AAA	369	ValB1MD_057	Vibrio phage ValB1MD	GCA_004138815.1
SOK59020.1	000580	MoxR-AAA	466	g212	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58485.1	000580	MoxR-AAA	443	g208	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26327.1	000580	MoxR-AAA	430	g304	Yersinia phage phiR1-37	GCA_000895615.1
BAG41536.1	000580	MoxR-AAA	419	RSL1_ORF091	Ralstonia phage phiRSL1	GCA_000879455.1
prev15ph1000000078	000581	MoxR-AAA	930	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000108	000581	MoxR-AAA	345	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AGH56878.1	000582	MoxR-AAA	383	CPXG_00075	Cyanophage P-RSM6	GCA_000906155.1
AJK27578.1	000582	MoxR-AAA	364	PTIM40_151	Cyanophage P-TIM40	GCA_001470935.1
AOO14338.1	000582	MoxR-AAA	352	Sn110110_144	Cyanophage S-RIM14	GCA_002599065.1
AOO14987.1	000582	MoxR-AAA	352	W1230910_141	Cyanophage S-RIM14	GCA_002599125.1
AMO43157.1	000582	MoxR-AAA	367	R1080702_148	Cyanophage S-RIM32	GCA_001754165.1
AMO43380.1	000582	MoxR-AAA	365	W270710_136	Cyanophage S-RIM44	GCA_002599145.1
AOO11625.1	000582	MoxR-AAA	365	ES420910_144	Cyanophage S-RIM44	GCA_002599165.1
AOO11852.1	000582	MoxR-AAA	365	Np050604_136	Cyanophage S-RIM44	GCA_002599185.1
AOO12090.1	000582	MoxR-AAA	365	Np200711_144	Cyanophage S-RIM44	GCA_002599205.1
AOO12326.1	000582	MoxR-AAA	365	Np420711_144	Cyanophage S-RIM44	GCA_002599225.1
AOO12553.1	000582	MoxR-AAA	365	Sn080709_136	Cyanophage S-RIM44	GCA_002599245.1
AOO12791.1	000582	MoxR-AAA	365	Sn130910_144	Cyanophage S-RIM44	GCA_002599265.1
AOO13019.1	000582	MoxR-AAA	365	W2100709_137	Cyanophage S-RIM44	GCA_002599285.1
AGH07476.1	000582	MoxR-AAA	371	CYVG_00032	Cyanophage S-SSM6a	GCA_002710385.1
AGG54472.1	000582	MoxR-AAA	361	CYWG_00188	Cyanophage S-SSM6b	GCA_002710425.1
QIG65679.1	000582	MoxR-AAA	312	phiOC_p013	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26305.1	000582	MoxR-AAA	354	CPMG_00206	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44532.1	000582	MoxR-AAA	364	PSSM2_154	Prochlorococcus phage P-SSM2	GCA_000859585.1
AIR93465.1	000582	MoxR-AAA	369	AVU42_gp127	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99238.1	000582	MoxR-AAA	376	Syn1_137	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30635.1	000582	MoxR-AAA	377	Syn7803US37_158	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76193.1	000582	MoxR-AAA	358	PBI_BELLAMY_148	Synechococcus phage Bellamy	GCA_002627525.1
QCW22903.1	000582	MoxR-AAA	362	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50584.1	000582	MoxR-AAA	362	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59604.1	000582	MoxR-AAA	366	S330809_143	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59366.1	000582	MoxR-AAA	366	C440309_143	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59842.1	000582	MoxR-AAA	366	N231010_143	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70562.1	000582	MoxR-AAA	357	HOU04_gp163	Synechococcus phage S-T4	GCA_003443335.1
QJT70138.1	000582	MoxR-AAA	363	SynMITS9220M01_125	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QIG57928.1	000000	MoxR-AAA	350	SEA_PAULODIABOLI_243	Microbacterium phage PauloDiaboli	GCA_011067425.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ABS83626.1	000000	SIG+MoxR-AAA	471	0305phi8-36p066	Bacillus phage 0305phi8-36	GCA_000871045.1
QDH83545.1	000583	NAD-LIGASE+BRCT	638	H1O15_gp243	Achromobacter phage Motura	GCA_006964305.1
QDB70308.1	000583	NAD-LIGASE+BRCT	646	CF8_0140	Aeromonas phage CF8	GCA_006384595.2
QDJ97286.1	000583	NAD-LIGASE+BRCT	659	D6_0126	Aeromonas phage D6	GCA_007051205.2
QDH47032.1	000583	NAD-LIGASE+BRCT	658	LAh10_56	Aeromonas phage LAh10	GCA_006863975.1
QDJ96656.1	000583	NAD-LIGASE+BRCT	645	PS1_0145	Aeromonas phage PS1	GCA_007051165.2
QFR59533.1	000583	NAD-LIGASE+BRCT	645	PS2_0142	Aeromonas phage PS2	GCA_009388305.2
AUZ95054.1	000583	NAD-LIGASE+BRCT	664	FDI40_gp282	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMS01179.1	000583	NAD-LIGASE+BRCT	671	AR9_g095	Bacillus phage AR9	GCA_001743835.1
AMM44941.1	000583	NAD-LIGASE+BRCT	619	SP15_143	Bacillus phage SP-15	GCA_001754685.1
ALN97842.1	000583	NAD-LIGASE+BRCT	676	Bp8pS_163	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93495.1	000583	NAD-LIGASE+BRCT	680	G_236	Bacillus virus G	GCA_000917535.1
ASU00113.1	000583	NAD-LIGASE+BRCT	681	PBI_PBS1_291	Bacillus virus PBS1	GCA_002601325.1
QIG63463.1	000583	NAD-LIGASE+BRCT	636	DAC16_234	Bacteroides phage DAC16	GCA_013387695.1
QIG63726.1	000583	NAD-LIGASE+BRCT	636	DAC19_239	Bacteroides phage DAC19	GCA_013387715.1
QIG63987.1	000583	NAD-LIGASE+BRCT	636	DAC20_238	Bacteroides phage DAC20	GCA_013387725.1
QIG64251.1	000583	NAD-LIGASE+BRCT	636	DAC22_241	Bacteroides phage DAC22	GCA_013387735.1
QIG64507.1	000583	NAD-LIGASE+BRCT	636	DAC23_233	Bacteroides phage DAC23	GCA_013387745.1
QBX06530.1	000583	NAD-LIGASE+BRCT	632	BcepSaruman_117	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74496.1	000583	NAD-LIGASE+BRCT	632	BcepSauron_116	Burkholderia phage BcepSauron	GCA_005394215.1
BAE47730.1	000583	NAD-LIGASE+BRCT	649	CST032	Clostridium phage c-st	GCA_000865225.1
AXG67191.1	000583	NAD-LIGASE+BRCT	648	AD1_147	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79941.1	000583	NAD-LIGASE+BRCT	656	JA11_136	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66540.1	000583	NAD-LIGASE+BRCT	656	JA13_137	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66865.1	000583	NAD-LIGASE+BRCT	656	JA29_139	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67510.1	000583	NAD-LIGASE+BRCT	656	JA33_136	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBZ70673.1	000583	NAD-LIGASE+BRCT	655	pETSU_092	Edwardsiella virus pEt-SU	GCA_004800915.1
AWY08424.1	000583	NAD-LIGASE+BRCT	647	Alexandra_152	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ASU03807.1	000583	NAD-LIGASE+BRCT	643	JOAD_108	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03562.1	000583	NAD-LIGASE+BRCT	643	RISINGSUN_108	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ARW58788.1	000583	NAD-LIGASE+BRCT	648	Y3_148	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28626.1	000583	NAD-LIGASE+BRCT	650	YOLOSWAG_146	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QBO63914.1	000583	NAD-LIGASE+BRCT	691	Goslar_00121	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71988.1	000583	NAD-LIGASE+BRCT	657	N1M2_125	Klebsiella phage N1M2	GCA_010092605.1
AXH72915.1	000583	NAD-LIGASE+BRCT	647	-	Myoviridae sp.	GCA_003657725.1
SBV38428.1	000583	NAD-LIGASE+BRCT	671	BN7874_237	Phage NCTB	GCA_900092385.1
QGZ14459.1	000583	NAD-LIGASE+BRCT	654	HWC77_gp096	Photobacterium phage PDCC-1	GCA_009800445.1
ABY63157.1	000583	NAD-LIGASE+BRCT	308	201phi2-1p332	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63158.1	000583	NAD-LIGASE+BRCT	695	201phi2-1p333	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27216.1	000583	NAD-LIGASE+BRCT	656	PPEV_gp122	Pseudomonas phage EL	GCA_000866825.1
AFH14608.1	000583	NAD-LIGASE+BRCT	652	Lu11_0076	Pseudomonas phage Lu11	GCA_000897175.1
ARV77482.1	000583	NAD-LIGASE+BRCT	717	NOXIFER_317	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89590.1	000583	NAD-LIGASE+BRCT	657	OBP_153	Pseudomonas phage OBP	GCA_000896635.1
QBX32411.1	000583	NAD-LIGASE+BRCT	680	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ86130.1	000583	NAD-LIGASE+BRCT	622	KKIINIFJ_00219	Pseudomonas phage PN05	GCA_009931935.1
AGS82093.2	000583	NAD-LIGASE+BRCT	646	PaBG_00218	Pseudomonas phage PaBG	GCA_000912555.1
ARV76962.1	000583	NAD-LIGASE+BRCT	332	PHABIO_331	Pseudomonas phage Phabio	GCA_002624965.1
ARV76963.1	000583	NAD-LIGASE+BRCT	678	PHABIO_332	Pseudomonas phage Phabio	GCA_002624965.1
AEH03680.1	000583	NAD-LIGASE+BRCT	680	257	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02811.1	000583	NAD-LIGASE+BRCT	684	PSA21_285	Pseudomonas phage Psa21	GCA_004340405.1
QEM41982.1	000583	NAD-LIGASE+BRCT	680	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAW19135.1	000583	NAD-LIGASE+BRCT	653	FDH28_gp260	Ralstonia phage RP12	GCA_002617345.1
BAW19421.1	000583	NAD-LIGASE+BRCT	653	-	Ralstonia phage RP31	GCA_002617365.1
BAS04897.1	000583	NAD-LIGASE+BRCT	685	AVU11_gp105	Ralstonia phage RSF1	GCA_001500875.1
BAQ02623.2	000583	NAD-LIGASE+BRCT	672	-	Ralstonia phage RSL2	GCA_001503055.1
BAG41511.1	000583	NAD-LIGASE+BRCT	625	lig	Ralstonia phage phiRSL1	GCA_000879455.1
ATA65594.1	000583	NAD-LIGASE+BRCT	535	2050HW_00259	Serratia phage 2050HW	GCA_002628125.1
QDB71358.1	000583	NAD-LIGASE+BRCT	682	CPT_Moabite_328	Serratia phage Moabite	GCA_006384735.1
AFF28204.1	000583	NAD-LIGASE+BRCT	624	PAU_206	Sphingomonas phage PAU	GCA_000902455.1
BBI90571.1	000583	NAD-LIGASE+BRCT	274	HYO65_gp179	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90552.1	000583	NAD-LIGASE+BRCT	370	HYO65_gp160	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90879.1	000583	NAD-LIGASE+BRCT	274	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90860.1	000583	NAD-LIGASE+BRCT	370	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39128.1	000583	NAD-LIGASE+BRCT	634	BPT24_006	Tenacibaculum phage pT24	GCA_002611925.1
QAU04275.1	000583	NAD-LIGASE+BRCT	654	HWC03_gp120	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23302.1	000583	NAD-LIGASE+BRCT	653	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80933.1	000583	NAD-LIGASE+BRCT	653	Aphrodite1_0043	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70939.1	000583	NAD-LIGASE+BRCT	671	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47426.1	000583	NAD-LIGASE+BRCT	653	HWC35_gp032	Vibrio phage USC-1	GCA_006864065.1
BAW98247.1	000583	NAD-LIGASE+BRCT	654	FDH33_gp038	Vibrio phage pTD1	GCA_002618825.1
QAX96911.1	000583	NAD-LIGASE+BRCT	669	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97216.1	000583	NAD-LIGASE+BRCT	669	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96275.1	000583	NAD-LIGASE+BRCT	669	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96593.1	000583	NAD-LIGASE+BRCT	669	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21222.1	000583	NAD-LIGASE+BRCT	645	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65326.1	000583	NAD-LIGASE+BRCT	637	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96365.1	000583	NAD-LIGASE+BRCT	638	Xoosp13_178	Xanthomonas phage Xoo-sp13	GCA_013364725.1
CCE26290.1	000583	NAD-LIGASE+BRCT	697	g267	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000374	000583	NAD-LIGASE+BRCT	712	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000300	000583	NAD-LIGASE+BRCT	712	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65592.1	000000	NAD-LIGASE	65	2050HW_00257	Serratia phage 2050HW	GCA_002628125.1
ATA65593.1	000000	NAD-LIGASE	59	2050HW_00258	Serratia phage 2050HW	GCA_002628125.1
AXF51090.1	000584	DNA_ligase_aden	134	MLDJOKPK_00098	Salmonella phage SPAsTU	GCA_003183805.1
ANZ48702.1	000584	DNA_ligase_aden	131	CHRISDB_140	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50296.1	000584	DNA_ligase_aden	131	PHOBOS_106	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QMP24057.1	000584	DNA_ligase_aden	88	-	Proteus phage 10	GCA_014071245.1
QKE54429.1	000584	DNA_ligase_aden	204	ACSA002_1150	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60270.1	000584	DNA_ligase_aden	205	Ea357_119	Erwinia phage Ea35-70	GCA_000914635.1
ANJ64932.1	000584	DNA_ligase_aden	205	SPECIALG_122	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANH51585.1	000584	DNA_ligase_aden	205	SIMMY50_123	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
AUG86549.1	000584	DNA_ligase_aden	205	MADMEL_121	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86227.1	000584	DNA_ligase_aden	205	DESERTFOX_120	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANH52223.1	000584	DNA_ligase_aden	205	DM_125	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
QBP07228.1	000584	DNA_ligase_aden	205	REBECCA_121	Erwinia phage Rebecca	GCA_004521635.1
AUG85908.1	000584	DNA_ligase_aden	205	BOSOLAPHORUS_121	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH51901.1	000584	DNA_ligase_aden	205	RAY_120	Erwinia phage vB_EamM_RAY	GCA_002624345.1
AUG86873.1	000584	DNA_ligase_aden	205	MORTIMER_124	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AEO93552.1	000585	NAD-synth-Kinase	190	G_293	Bacillus virus G	GCA_000917535.1
AXQ69166.1	000585	NAD-synth-Kinase	168	CcrBL9_gp142	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69721.1	000585	NAD-synth-Kinase	170	CcrSC_gp139	Caulobacter phage CcrSC	GCA_003443315.1
AFC21586.1	000585	NAD-synth-Kinase	183	GAP32_136	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXH72494.1	000585	NAD-synth-Kinase	184	-	Myoviridae sp.	GCA_003657725.1
AMM43705.1	000585	NAD-synth-Kinase	183	CBB_140	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18844.1	000585	NAD-synth-Kinase	185	7t3_0323	Salmonella phage 7t3	GCA_006083215.1
AZU98106.1	000585	NAD-synth-Kinase	185	CPT_Munch_162	Salmonella phage Munch	GCA_004015485.1
QIG62876.1	000585	NAD-synth-Kinase	185	SEPL_263	Salmonella phage SE_PL	GCA_011067555.1
AQW88657.1	000585	NAD-synth-Kinase	184	BF_0132	Serratia phage BF	GCA_002619745.1
SOK58939.1	000585	NAD-synth-Kinase	184	g131	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58405.1	000585	NAD-synth-Kinase	184	g128	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000344	000585	NAD-synth-Kinase	106	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000272	000585	NAD-synth-Kinase	282	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG63352.1	000586	NAD-synth-Kinase	184	DAC16_119	Bacteroides phage DAC16	GCA_013387695.1
QIG63617.1	000586	NAD-synth-Kinase	184	DAC19_126	Bacteroides phage DAC19	GCA_013387715.1
QIG63878.1	000586	NAD-synth-Kinase	184	DAC20_125	Bacteroides phage DAC20	GCA_013387725.1
QIG64141.1	000586	NAD-synth-Kinase	184	DAC22_127	Bacteroides phage DAC22	GCA_013387735.1
QIG64398.1	000586	NAD-synth-Kinase	184	DAC23_120	Bacteroides phage DAC23	GCA_013387745.1
AUZ95020.1	000587	NUDIX	165	FDI40_gp238	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93532.1	000587	NUDIX	251	G_273	Bacillus virus G	GCA_000917535.1
AND75325.1	000588	CTP_transf_like+NUDIX	176	ME3_164	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUE22819.1	000588	CTP_transf_like+NUDIX	351	Ah1_00301	Aeromonas phage Ah1	GCA_002957415.1
QAX98534.1	000588	CTP_transf_like+NUDIX	351	ASfcp2_198	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52997.1	000588	CTP_transf_like+NUDIX	351	PX29p278	Aeromonas phage PX29	GCA_000920195.1
ADM79920.1	000588	CTP_transf_like+NUDIX	350	phiAS5_ORF0077	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17949.1	000588	CTP_transf_like+NUDIX	351	Aeh1ORF282c	Aeromonas virus Aeh1	GCA_000843245.1
QBX06528.1	000588	CTP_transf_like+NUDIX	368	BcepSaruman_115	Burkholderia phage BcepSaruman	GCA_004771375.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBQ74494.1	000588	CTP_transf_like+NUDIX	368	BcepSauron_114	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13689.1	000588	CTP_transf_like+NUDIX	413	Ccr10_gp159c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14034.1	000588	CTP_transf_like+NUDIX	413	Ccr2_gp158c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14721.1	000588	CTP_transf_like+NUDIX	413	Ccr29_gp165	Caulobacter phage Ccr29	GCA_002619485.1
ARB15076.1	000588	CTP_transf_like+NUDIX	413	Ccr32_gp158	Caulobacter phage Ccr32	GCA_002619505.1
ARB15410.1	000588	CTP_transf_like+NUDIX	413	Ccr34_gp168	Caulobacter phage Ccr34	GCA_002619525.1
ARB14377.1	000588	CTP_transf_like+NUDIX	413	Ccr5_gp157c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68359.1	000588	CTP_transf_like+NUDIX	405	CcrBL10_gp155c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69259.1	000588	CTP_transf_like+NUDIX	362	CcrBL9_gp235c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88074.1	000588	CTP_transf_like+NUDIX	389	CcrColossus_gp204	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68751.1	000588	CTP_transf_like+NUDIX	389	CcrPW_gp212c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69816.1	000588	CTP_transf_like+NUDIX	390	CcrSC_gp234c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87682.1	000588	CTP_transf_like+NUDIX	413	CcrKarma_gp165	Caulobacter virus Karma	GCA_000901575.1
AFU87331.1	000588	CTP_transf_like+NUDIX	413	CcrMagneto_gp161	Caulobacter virus Magneto	GCA_000903095.1
AFU86642.1	000588	CTP_transf_like+NUDIX	411	CcrRogue_gp160	Caulobacter virus Rogue	GCA_000900555.1
AFU88478.1	000588	CTP_transf_like+NUDIX	413	CcrSwift_gp160	Caulobacter virus Swift	GCA_000899655.1
AFU86995.1	000588	CTP_transf_like+NUDIX	413	CbK_gp163	Caulobacter virus phiCbK	GCA_000900535.1
ANS05961.1	000588	CTP_transf_like+NUDIX	352	ABCD_0137	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65004.1	000588	CTP_transf_like+NUDIX	351	S13_207	Cronobacter phage S13	GCA_001503575.1
AFC21560.1	000588	CTP_transf_like+NUDIX	365	GAP32_112	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97145.1	000588	CTP_transf_like+NUDIX	351	E_137	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78660.1	000588	CTP_transf_like+NUDIX	352	RB43ORF138c	Escherichia virus RB43	GCA_000863505.1
AFA44771.1	000588	CTP_transf_like+NUDIX	354	RaK2_00498	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72854.1	000588	CTP_transf_like+NUDIX	190	-	Myoviridae sp.	GCA_003657725.1
QHJ78927.1	000588	CTP_transf_like+NUDIX	351	-	Myoviridae sp.	GCA_012593985.1
QIG65797.1	000588	CTP_transf_like+NUDIX	371	phiOC_p132	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43678.1	000588	CTP_transf_like+NUDIX	365	CBB_113	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAG41548.1	000588	CTP_transf_like+NUDIX	371	RSL1_ORF104	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44118.1	000588	CTP_transf_like+NUDIX	357	PBI_SCTP2_103	Salicola phage SCTP-2	GCA_002625545.1
QCW18814.1	000588	CTP_transf_like+NUDIX	371	7t3_0293	Salmonella phage 7t3	GCA_006083215.1
AZU98078.1	000588	CTP_transf_like+NUDIX	371	CPT_Munch_134	Salmonella phage Munch	GCA_004015485.1
QIG62904.1	000588	CTP_transf_like+NUDIX	371	SEPL_291	Salmonella phage SE_PL	GCA_011067555.1
AQW88631.1	000588	CTP_transf_like+NUDIX	355	BF_0106	Serratia phage BF	GCA_002619745.1
AGR47911.1	000588	CTP_transf_like+NUDIX	357	SmphiM12_279	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13115.1	000588	CTP_transf_like+NUDIX	357	PHIM19_210	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12755.1	000588	CTP_transf_like+NUDIX	357	PHIM7_210	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13485.1	000588	CTP_transf_like+NUDIX	357	PHIN3_222	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54674.1	000588	CTP_transf_like+NUDIX	341	b23_0046	Synechococcus phage B23	GCA_009745195.1
QGT54304.1	000588	CTP_transf_like+NUDIX	341	b3_0046	Synechococcus phage B3	GCA_009745215.1
AXH70917.1	000588	CTP_transf_like+NUDIX	372	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64231.1	000588	CTP_transf_like+NUDIX	341	KVP40.0162	Vibrio phage KVP40	GCA_000843785.1
QIW90545.1	000588	CTP_transf_like+NUDIX	341	GCAPEGMB_00198	Vibrio phage V07	GCA_012361095.1
QIW90877.1	000588	CTP_transf_like+NUDIX	341	COHAPHLL_00014	Vibrio phage V09	GCA_012361135.1
QHJ74343.1	000588	CTP_transf_like+NUDIX	341	VH12019_00016	Vibrio phage VH1_2019	GCA_009931825.1
AGB06836.1	000588	CTP_transf_like+NUDIX	341	CF80_gp049	Vibrio phage VH7D	GCA_000914495.1
QBX06310.1	000588	CTP_transf_like+NUDIX	341	ValB1HC_357	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60941.1	000588	CTP_transf_like+NUDIX	341	AVU32_gp100	Vibrio phage ValKK3	GCA_001501635.1
AGN30209.2	000588	CTP_transf_like+NUDIX	343	VPFG_00209	Vibrio phage nt-1	GCA_000910195.2
ALP47007.1	000588	CTP_transf_like+NUDIX	341	phiGrn1_0273	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47387.1	000588	CTP_transf_like+NUDIX	341	phiST2_0032	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54553.1	000588	CTP_transf_like+NUDIX	341	vBValMR10Z_12	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07151.1	000588	CTP_transf_like+NUDIX	352	VmeM32_00165	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37390.1	000588	CTP_transf_like+NUDIX	341	pp2_157	Vibriophage phi-pp2	GCA_002630725.1
BBA65364.1	000588	CTP_transf_like+NUDIX	367	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96392.1	000588	CTP_transf_like+NUDIX	302	Xoosp13_206	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58908.1	000588	CTP_transf_like+NUDIX	357	g100	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58373.1	000588	CTP_transf_like+NUDIX	357	g096	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95346.1	000589	NAD-synth-Ploop	341	FDI40_gp587	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69368.1	000589	NAD-synth-Ploop	346	CcrBL9_gp344	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69928.1	000589	NAD-synth-Ploop	346	CcrSC_gp346	Caulobacter phage CcrSC	GCA_003443315.1
AFC21803.1	000589	NAD-synth-Ploop	348	GAP32_353	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG57953.1	000589	NAD-synth-Ploop	355	SEA_PAULODIABOLI_269	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG65784.1	000589	NAD-synth-Ploop	362	phiOC_p119	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43924.1	000589	NAD-synth-Ploop	349	CBB_361	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88884.1	000589	NAD-synth-Ploop	352	BF_0359	Serratia phage BF	GCA_002619745.1
AGR48041.2	000589	NAD-synth-Ploop	343	SmphiM12_409	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13225.1	000589	NAD-synth-Ploop	343	PHIM19_320	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12865.1	000589	NAD-synth-Ploop	343	PHIM7_320	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13588.1	000589	NAD-synth-Ploop	343	PHIN3_325	Sinorhizobium phage phiN3	GCA_001501175.1
AXH70913.1	000589	NAD-synth-Ploop	549	-	Vibrio phage BONAISHI	GCA_003441475.1
SOK59170.1	000589	NAD-synth-Ploop	295	g362	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58637.1	000589	NAD-synth-Ploop	354	g360	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000041	000589	NAD-synth-Ploop	386	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000032	000589	NAD-synth-Ploop	386	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAQ64280.1	000590	CTP_transf_like+NAD-synth-Ploop	326	KVP40.0211	Vibrio phage KVP40	GCA_000843785.1
QIW90596.1	000590	CTP_transf_like+NAD-synth-Ploop	326	GCAPEGMB_00249	Vibrio phage V07	GCA_012361095.1
QIW91202.1	000590	CTP_transf_like+NAD-synth-Ploop	324	COHAPHLL_00366	Vibrio phage V09	GCA_012361135.1
QHJ74392.1	000590	CTP_transf_like+NAD-synth-Ploop	326	VH12019_00065	Vibrio phage VH1_2019	GCA_009931825.1
AGB06898.1	000590	CTP_transf_like+NAD-synth-Ploop	326	CF80_gp111	Vibrio phage VH7D	GCA_000914495.1
QBX06248.1	000590	CTP_transf_like+NAD-synth-Ploop	326	ValB1HC_295	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60874.1	000590	CTP_transf_like+NAD-synth-Ploop	326	AVU32_gp033	Vibrio phage ValKK3	GCA_001501635.1
AGN30272.1	000590	CTP_transf_like+NAD-synth-Ploop	324	VPFG_00273	Vibrio phage nt-1	GCA_000910195.2
ALP47012.1	000590	CTP_transf_like+NAD-synth-Ploop	326	phiGrn1_0336	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47393.1	000590	CTP_transf_like+NAD-synth-Ploop	326	phiST2_0091	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54874.1	000590	CTP_transf_like+NAD-synth-Ploop	326	vBValMR10Z_334	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37441.1	000590	CTP_transf_like+NAD-synth-Ploop	326	pp2_208	Vibriophage phi-pp2	GCA_002630725.1
APU01434.1	000591	ATP-cone+NRDD	613	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28766.1	000591	ATP-cone+NRDD	609	AP1_0048	Aeromonas phage AP1	GCA_014183365.1
ATI17465.1	000591	ATP-cone+NRDD	609	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00532.1	000591	ATP-cone+NRDD	609	HWB28_gp020	Aeromonas phage AS-zj	GCA_002627665.1
AUE22581.1	000591	ATP-cone+NRDD	704	Ah1_00040	Aeromonas phage Ah1	GCA_002957415.1
QAX98616.1	000591	ATP-cone+NRDD	704	ASfcp2_283	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97905.1	000591	ATP-cone+NRDD	609	ASswx1_262	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01247.1	000591	ATP-cone+NRDD	613	ASwh1_182	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39524.1	000591	ATP-cone+NRDD	609	CC2_270	Aeromonas phage CC2	GCA_000903495.1
ADQ52754.1	000591	ATP-cone+NRDD	704	PX29p035	Aeromonas phage PX29	GCA_000920195.1
ADM80010.1	000591	ATP-cone+NRDD	703	phiAS5_ORF0167	Aeromonas phage phiAS5	GCA_000887715.1
AAR90895.2	000591	ATP-cone+NRDD	613	65p043	Aeromonas virus 65	GCA_000893255.1
AAQ17696.1	000591	ATP-cone+NRDD	704	nrdD	Aeromonas virus Aeh1	GCA_000843245.1
ANS05931.1	000591	ATP-cone+NRDD	705	ABCD_0245	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFC21588.1	000591	ATP-cone+NRDD	600	GAP32_138	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97265.1	000591	ATP-cone+NRDD	703	E_257	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14386.1	000591	ATP-cone+NRDD	601	PBI_121Q_496	Escherichia phage 121Q	GCA_000926855.1
QAY00562.1	000591	ATP-cone+NRDD	601	Ecwhy1_283	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34756.1	000591	ATP-cone+NRDD	622	ACQ29_gp076	Escherichia phage PBECO4	GCA_001041035.1
BBM62057.1	000591	ATP-cone+NRDD	601	EO157G_4680	Escherichia phage SP27	GCA_008033345.1
AXC36871.1	000591	ATP-cone+NRDD	601	-	Escherichia phage UB	GCA_003341455.1
ARM70900.1	000591	ATP-cone+NRDD	605	phiC120_c195	Escherichia phage phiC120	GCA_002621185.1
QBO61916.1	000591	ATP-cone+NRDD	601	G17_00427	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13950.1	000591	ATP-cone+NRDD	601	vBEcoMphAPEC6_gp326c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80375.1	000591	ATP-cone+NRDD	601	PSLUR01_00398	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78783.1	000591	ATP-cone+NRDD	707	RB43ORF261w	Escherichia virus RB43	GCA_000863505.1
AFA44793.1	000591	ATP-cone+NRDD	601	RaK2_00520	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43706.1	000591	ATP-cone+NRDD	611	CBB_141	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18849.1	000591	ATP-cone+NRDD	601	7t3_0328	Salmonella phage 7t3	GCA_006083215.1
AZU98110.1	000591	ATP-cone+NRDD	601	CPT_Munch_166	Salmonella phage Munch	GCA_004015485.1
QIG62872.1	000591	ATP-cone+NRDD	601	SEPL_259	Salmonella phage SE_PL	GCA_011067555.1
AQW88658.1	000591	ATP-cone+NRDD	607	BF_0133	Serratia phage BF	GCA_002619745.1
AAQ64083.1	000591	ATP-cone+NRDD	611	KVP40.0012	Vibrio phage KVP40	GCA_000843785.1
QIW90407.1	000591	ATP-cone+NRDD	611	GCAPEGMB_00060	Vibrio phage V07	GCA_012361095.1
QIW91022.1	000591	ATP-cone+NRDD	611	COHAPHLL_00159	Vibrio phage V09	GCA_012361135.1
QHJ74195.1	000591	ATP-cone+NRDD	611	VH12019_00276	Vibrio phage VH1_2019	GCA_009931825.1
AGB07019.1	000591	ATP-cone+NRDD	611	CF80_gp232	Vibrio phage VH7D	GCA_000914495.1
QBX06077.1	000591	ATP-cone+NRDD	611	ValB1HC_123	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61091.1	000591	ATP-cone+NRDD	611	AVU32_gp250	Vibrio phage ValKK3	GCA_001501635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN30062.1	000591	ATP-cone+NRDD	611	VPFG_00059	Vibrio phage nt-1	GCA_000910195.2
ALP46970.1	000591	ATP-cone+NRDD	611	phiGrn1_0127	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47350.1	000591	ATP-cone+NRDD	611	phiST2_0257	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54703.1	000591	ATP-cone+NRDD	611	vBValMR10Z_162	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07115.1	000591	ATP-cone+NRDD	711	VmeM32_00128	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37246.1	000591	ATP-cone+NRDD	611	pp2_012	Vibriophage phi-pp2	GCA_002630725.1
SOK58941.1	000591	ATP-cone+NRDD	606	g133	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58407.1	000591	ATP-cone+NRDD	606	g130	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BAE47774.1	000592	NRDD	978	CST076	Clostridium phage c-st	GCA_000865225.1
AIA65032.1	000592	NRDD	610	S13_235	Cronobacter phage S13	GCA_001503575.1
QHJ78900.1	000592	NRDD	611	-	Myoviridae sp.	GCA_012593985.1
QAU04448.1	000592	NRDD	601	ValB1MD_028	Vibrio phage ValB1MD	GCA_004138815.1
prevph1000000224	000593	ATPcone+NRDD	292	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000174	000593	ATPcone+NRDD	373	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000215	000594	NRDD	156	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000169	000594	NRDD	129	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000212	000000	NRDD	93	-	Prevotella_phage_Lak-B8	GCA_004379655.1
APU01433.1	000595	NTP-Riboreductase-small	156	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28765.1	000595	NTP-Riboreductase-small	157	AP1_0047	Aeromonas phage AP1	GCA_014183365.1
ATI17466.1	000595	NTP-Riboreductase-small	157	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00531.1	000595	NTP-Riboreductase-small	157	HWB28_gp021	Aeromonas phage AS-zj	GCA_002627665.1
AUE22580.1	000595	NTP-Riboreductase-small	160	Ah1_00039	Aeromonas phage Ah1	GCA_002957415.1
QAX97906.1	000595	NTP-Riboreductase-small	157	ASswx1_263	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01246.1	000595	NTP-Riboreductase-small	157	ASwh1_181	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39523.1	000595	NTP-Riboreductase-small	157	CC2_269	Aeromonas phage CC2	GCA_000903495.1
ADQ52753.1	000595	NTP-Riboreductase-small	166	PX29p034	Aeromonas phage PX29	GCA_000920195.1
ADM80009.1	000595	NTP-Riboreductase-small	159	phiAS5_ORF0166	Aeromonas phage phiAS5	GCA_000887715.1
AAR90896.1	000595	NTP-Riboreductase-small	156	65p042	Aeromonas virus 65	GCA_000893255.1
AAQ17695.1	000595	NTP-Riboreductase-small	159	nrdG	Aeromonas virus Aeh1	GCA_000843245.1
ANS06039.1	000595	NTP-Riboreductase-small	163	ABCD_0254	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47773.1	000595	NTP-Riboreductase-small	176	CST075	Clostridium phage c-st	GCA_000865225.1
AFC21591.1	000595	NTP-Riboreductase-small	157	GAP32_141	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97272.1	000595	NTP-Riboreductase-small	163	E_264	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14388.1	000595	NTP-Riboreductase-small	156	PBI_121Q_498	Escherichia phage 121Q	GCA_000926855.1
QAY00560.1	000595	NTP-Riboreductase-small	156	Ecwhy1_281	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34754.1	000595	NTP-Riboreductase-small	156	ACQ29_gp074	Escherichia phage PBECO4	GCA_001041035.1
BBM62059.1	000595	NTP-Riboreductase-small	156	EO157G_4700	Escherichia phage SP27	GCA_008033345.1
AXC36869.1	000595	NTP-Riboreductase-small	156	-	Escherichia phage UB	GCA_003341455.1
ARM70899.1	000595	NTP-Riboreductase-small	156	phiC120_c194	Escherichia phage phiC120	GCA_002621185.1
QBO61914.1	000595	NTP-Riboreductase-small	156	G17_00425	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13948.1	000595	NTP-Riboreductase-small	111	vBEcoMphAPEC6_gp324c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80377.1	000595	NTP-Riboreductase-small	156	PSLUR01_00400	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78794.1	000595	NTP-Riboreductase-small	148	RB43ORF272w	Escherichia virus RB43	GCA_000863505.1
AFA44806.1	000595	NTP-Riboreductase-small	156	RaK2_00523	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43710.1	000595	NTP-Riboreductase-small	157	CBB_145	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18851.1	000595	NTP-Riboreductase-small	156	7t3_0330	Salmonella phage 7t3	GCA_006083215.1
AZU98112.1	000595	NTP-Riboreductase-small	156	CPT_Munch_168	Salmonella phage Munch	GCA_004015485.1
QIG62870.1	000595	NTP-Riboreductase-small	156	SEPL_257	Salmonella phage SE_PL	GCA_011067555.1
AQW88664.1	000595	NTP-Riboreductase-small	157	BF_0139	Serratia phage BF	GCA_002619745.1
AAQ64086.1	000595	NTP-Riboreductase-small	158	KVP40.0015	Vibrio phage KVP40	GCA_000843785.1
QHJ74198.1	000595	NTP-Riboreductase-small	158	VH12019_00279	Vibrio phage VH1_2019	GCA_009931825.1
AGB07022.1	000595	NTP-Riboreductase-small	158	CF80_gp235	Vibrio phage VH7D	GCA_000914495.1
QBX06074.1	000595	NTP-Riboreductase-small	158	ValB1HC_120	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61088.1	000595	NTP-Riboreductase-small	158	AVU32_gp247	Vibrio phage ValKK3	GCA_001501635.1
AGN30066.2	000595	NTP-Riboreductase-small	140	VPFG_00063	Vibrio phage nt-1	GCA_000910195.2
ALP47116.1	000595	NTP-Riboreductase-small	158	phiGrn1_0130	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47498.1	000595	NTP-Riboreductase-small	158	phiST2_0260	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54700.1	000595	NTP-Riboreductase-small	158	vBValMR10Z_159	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07116.1	000595	NTP-Riboreductase-small	161	VmeM32_00129	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96852.1	000595	NTP-Riboreductase-small	154	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97157.1	000595	NTP-Riboreductase-small	154	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96216.1	000595	NTP-Riboreductase-small	154	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96534.1	000595	NTP-Riboreductase-small	154	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFN37249.1	000595	NTP-Riboreductase-small	158	pp2_015	Vibriophage phi-pp2	GCA_002630725.1
SOK58946.1	000595	NTP-Riboreductase-small	157	g138	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58412.1	000595	NTP-Riboreductase-small	157	g135	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QAU04449.1	000596	NTP-Riboreductase-small	147	ValB1MD_029	Vibrio phage ValB1MD	GCA_004138815.1
prevph1000000120	000596	NTP-Riboreductase-small	174	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000089	000596	NTP-Riboreductase-small	174	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDH83582.1	000597	NUDIX	270	H1O15_gp206	Achromobacter phage Motura	GCA_006964305.1
QBX06513.1	000597	NUDIX	185	BcepSaruman_100	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74479.1	000597	NUDIX	185	BcepSauron_099	Burkholderia phage BcepSauron	GCA_005394215.1
AFC21676.1	000597	NUDIX	155	GAP32_226	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14468.1	000597	NUDIX	154	PBI_121Q_578	Escherichia phage 121Q	GCA_000926855.1
QAY00479.1	000597	NUDIX	154	Ecwhy1_200	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35222.1	000597	NUDIX	154	ACQ29_gp542	Escherichia phage PBECO4	GCA_001041035.1
BBM62141.1	000597	NUDIX	154	EO157G_5520	Escherichia phage SP27	GCA_008033345.1
AXC36794.1	000597	NUDIX	154	-	Escherichia phage UB	GCA_003341455.1
QBO61834.1	000597	NUDIX	154	G17_00345	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13878.1	000597	NUDIX	154	vBEcoMphAPEC6_gp249	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80453.1	000597	NUDIX	154	PSLUR01_00476	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44339.1	000597	NUDIX	157	RaK2_00066	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43797.1	000597	NUDIX	155	CBB_232	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76043.1	000597	NUDIX	105	EST35_0161	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41553.1	000597	NUDIX	167	RSL1_ORF109	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44257.1	000597	NUDIX	175	PBI_SCTP2_242	Salicola phage SCTP-2	GCA_002625545.1
ASV44280.1	000597	NUDIX	143	PBI_SCTP2_265	Salicola phage SCTP-2	GCA_002625545.1
QCW18948.1	000597	NUDIX	153	7t3_0427	Salmonella phage 7t3	GCA_006083215.1
AZU98202.1	000597	NUDIX	153	CPT_Munch_258	Salmonella phage Munch	GCA_004015485.1
QIG62782.1	000597	NUDIX	153	SEPL_169	Salmonella phage SE_PL	GCA_011067555.1
AQW88756.1	000597	NUDIX	155	BF_0231	Serratia phage BF	GCA_002619745.1
SOK59037.1	000597	NUDIX	155	g229c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58502.1	000597	NUDIX	155	g225c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06057.1	000598	NUDIX	137	ABCD_0178	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFC21637.1	000598	NUDIX	142	GAP32_187	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97191.1	000598	NUDIX	137	E_183	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14430.1	000598	NUDIX	132	PBI_121Q_540	Escherichia phage 121Q	GCA_000926855.1
QAY00518.1	000598	NUDIX	136	Ecwhy1_239	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34712.1	000598	NUDIX	132	ACQ29_gp032	Escherichia phage PBECO4	GCA_001041035.1
BBM62102.1	000598	NUDIX	132	EO157G_5130	Escherichia phage SP27	GCA_008033345.1
AXC36831.1	000598	NUDIX	132	-	Escherichia phage UB	GCA_003341455.1
ARM70946.1	000598	NUDIX	151	phiC120_c241	Escherichia phage phiC120	GCA_002621185.1
QBO61871.1	000598	NUDIX	132	G17_00382	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13911.1	000598	NUDIX	132	vBEcoMphAPEC6_gp286c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80416.1	000598	NUDIX	132	PSLUR01_00439	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78708.1	000598	NUDIX	137	RB43ORF186c	Escherichia virus RB43	GCA_000863505.1
AFA44305.1	000598	NUDIX	144	RaK2_00032	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43758.1	000598	NUDIX	140	CBB_193	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18908.1	000598	NUDIX	146	7t3_0387	Salmonella phage 7t3	GCA_006083215.1
AZU98165.1	000598	NUDIX	143	CPT_Munch_221	Salmonella phage Munch	GCA_004015485.1
QIG62819.1	000598	NUDIX	143	SEPL_206	Salmonella phage SE_PL	GCA_011067555.1
AQW88714.1	000598	NUDIX	141	BF_0189	Serratia phage BF	GCA_002619745.1
SOK58996.1	000598	NUDIX	141	g188	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58461.1	000598	NUDIX	141	g184	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDH83484.1	000599	NUDIX	141	H1O15_gp322	Achromobacter phage Motura	GCA_006964305.1
AXG67163.1	000599	NUDIX	152	AD1_119	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79913.1	000599	NUDIX	150	JA11_108	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66512.1	000599	NUDIX	150	JA13_109	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66837.1	000599	NUDIX	150	JA29_111	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67482.1	000599	NUDIX	150	JA33_108	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08396.1	000599	NUDIX	152	Alexandra_124	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58760.1	000599	NUDIX	152	Y3_120	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28598.1	000599	NUDIX	148	YOLOSWAG_116	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38203.1	000599	NUDIX	150	BN7874_034	Phage NCTB	GCA_900092385.1
AFH14799.1	000599	NUDIX	166	Lu11_0262	Pseudomonas phage Lu11	GCA_000897175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFH14845.1	000599	NUDIX	162	Lu11_0307	Pseudomonas phage Lu11	GCA_000897175.1
AGS81914.2	000599	NUDIX	147	PaBG_00030	Pseudomonas phage PaBG	GCA_000912555.1
AGS82152.1	000599	NUDIX	241	PaBG_00279	Pseudomonas phage PaBG	GCA_000912555.1
BAW18976.1	000600	NUDIX	140	FDH28_gp002	Ralstonia phage RP12	GCA_002617345.1
BAW19264.1	000600	NUDIX	140	-	Ralstonia phage RP31	GCA_002617365.1
AYD81339.1	000600	NUDIX	149	SEA_JUSTBECAUSE_174	Streptomyces phage JustBecause	GCA_003613775.1
QJD53742.1	000600	NUDIX	149	SEA_KELA_172	Streptomyces phage Kela	GCA_012934305.1
QBZ72068.1	000600	NUDIX	150	SEA_KRADAL_172	Streptomyces phage Kradal	GCA_004799925.1
AXH66331.1	000600	NUDIX	150	SEA_SATIS_172	Streptomyces phage Satis	GCA_003366315.1
QGZ14538.1	000601	NUDIX	130	HWC77_gp175	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04196.1	000601	NUDIX	129	HWC03_gp041	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23164.1	000601	NUDIX	130	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81075.1	000601	NUDIX	129	Aphrodite1_0177	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47564.1	000601	NUDIX	130	HWC35_gp170	Vibrio phage USC-1	GCA_006864065.1
BAW98381.1	000601	NUDIX	130	FDH33_gp172	Vibrio phage pTD1	GCA_002618825.1
QIG63429.1	000602	NUDIX	226	DAC16_200	Bacteroides phage DAC16	GCA_013387695.1
QIG63693.1	000602	NUDIX	226	DAC19_206	Bacteroides phage DAC19	GCA_013387715.1
QIG63954.1	000602	NUDIX	226	DAC20_205	Bacteroides phage DAC20	GCA_013387725.1
QIG64218.1	000602	NUDIX	226	DAC22_208	Bacteroides phage DAC22	GCA_013387735.1
QIG64474.1	000602	NUDIX	226	DAC23_200	Bacteroides phage DAC23	GCA_013387745.1
ASV44256.1	000603	NUDIX	139	PBI_SCTP2_241	Salicola phage SCTP-2	GCA_002625545.1
ASV44340.1	000603	NUDIX	176	PBI_SCTP2_325	Salicola phage SCTP-2	GCA_002625545.1
BBA65485.1	000603	NUDIX	143	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96492.1	000603	NUDIX	130	Xoosp13_306	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AMS01158.1	000604	NUDIX	186	AR9_g074	Bacillus phage AR9	GCA_001743835.1
ALN97824.1	000604	NUDIX	169	Bp8pS_145	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00087.1	000604	NUDIX	186	PBI_PBS1_265	Bacillus virus PBS1	GCA_002601325.1
AXQ69340.1	000605	NUDIX	211	CcrBL9_gp316	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69900.1	000605	NUDIX	211	CcrSC_gp318	Caulobacter phage CcrSC	GCA_003443315.1
AUZ95156.1	000606	NUDIX	181	FDI40_gp397	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72894.1	000606	NUDIX	179	-	Myoviridae sp.	GCA_003657725.1
QBX06545.1	000607	NUDIX	153	BcepSaruman_132	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74511.1	000607	NUDIX	153	BcepSauron_131	Burkholderia phage BcepSauron	GCA_005394215.1
AND75375.1	000000	NUDIX	146	ME3_214	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ95036.1	000000	NUDIX	148	FDI40_gp257	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72852.1	000000	NUDIX	230	-	Myoviridae sp.	GCA_003657725.1
CAG27292.1	000000	NUDIX	272	PPEV_gp198	Pseudomonas phage EL	GCA_000866825.1
AQT28007.1	000000	NUDIX	299	pVa21_065	Vibrio phage pVa-21	GCA_002619305.1
CCE26084.1	000000	NUDIX	145	g060	Yersinia phage phiR1-37	GCA_000895615.1
BAV39203.1	000000	SIG+NUDIX	182	BPT24_078	Tenacibaculum phage pT24	GCA_002611925.1
APU01446.1	000608	PTH2	194	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28931.1	000608	PTH2	153	AP1_0224	Aeromonas phage AP1	GCA_014183365.1
ATI17453.1	000608	PTH2	153	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00143.1	000608	PTH2	153	HWB28_gp007	Aeromonas phage AS-zj	GCA_002627665.1
AUE22788.1	000608	PTH2	132	Ah1_00270	Aeromonas phage Ah1	GCA_002957415.1
QAX98502.1	000608	PTH2	132	ASfcp2_166	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97893.1	000608	PTH2	153	ASswx1_250	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01259.1	000608	PTH2	127	ASwh1_195	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39408.1	000608	PTH2	120	CC2_283	Aeromonas phage CC2	GCA_000903495.1
ADQ52965.1	000608	PTH2	132	PX29p246	Aeromonas phage PX29	GCA_000920195.1
ADM79891.1	000608	PTH2	136	phiAS5_ORF0048	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53066.1	000608	PTH2	194	65p056	Aeromonas virus 65	GCA_000893255.1
AAQ17913.1	000608	PTH2	132	Aeh1ORF251c	Aeromonas virus Aeh1	GCA_000843245.1
AIA64874.1	000608	PTH2	180	S13_075	Cronobacter phage S13	GCA_001503575.1
AFC21545.1	000608	PTH2	152	GAP32_097	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14348.1	000608	PTH2	139	PBI_121Q_458	Escherichia phage 121Q	GCA_000926855.1
QAY00596.1	000608	PTH2	137	Ecwhy1_319	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34791.1	000608	PTH2	139	ACQ29_gp111	Escherichia phage PBECO4	GCA_001041035.1
BBM62019.1	000608	PTH2	137	EO157G_4300	Escherichia phage SP27	GCA_008033345.1
AXC36907.1	000608	PTH2	139	-	Escherichia phage UB	GCA_003341455.1
QBO61956.1	000608	PTH2	137	G17_00467	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13983.1	000608	PTH2	137	vBEcoMphAPEC6_gp359c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80335.1	000608	PTH2	137	PSLUR01_00358	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44756.1	000608	PTH2	145	RaK2_00483	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ79065.1	000608	PTH2	194	-	Myoviridae sp.	GCA_012593985.1
AMM43663.1	000608	PTH2	152	CBB_98	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18798.1	000608	PTH2	151	7t3_0277	Salmonella phage 7t3	GCA_006083215.1
AZU98063.1	000608	PTH2	151	CPT_Munch_119	Salmonella phage Munch	GCA_004015485.1
QIG62919.1	000608	PTH2	151	SEPL_306	Salmonella phage SE_PL	GCA_011067555.1
AQW88616.1	000608	PTH2	160	BF_0091	Serratia phage BF	GCA_002619745.1
AAQ64099.1	000608	PTH2	147	KVP40.0028	Vibrio phage KVP40	GCA_000843785.1
QIW90422.1	000608	PTH2	81	GCAPEGMB_00075	Vibrio phage V07	GCA_012361095.1
QIW91007.1	000608	PTH2	81	COHAPHLL_00144	Vibrio phage V09	GCA_012361135.1
QHJ74211.1	000608	PTH2	148	VH12019_00292	Vibrio phage VH1_2019	GCA_009931825.1
AGB07035.1	000608	PTH2	147	CF80_gp248	Vibrio phage VH7D	GCA_000914495.1
QBX06061.1	000608	PTH2	147	ValB1HC_107	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04504.1	000608	PTH2	164	ValB1MD_154	Vibrio phage ValB1MD	GCA_004138815.1
AJT61074.1	000608	PTH2	148	AVU32_gp233	Vibrio phage ValKK3	GCA_001501635.1
AGN30078.1	000608	PTH2	149	VPFG_00076	Vibrio phage nt-1	GCA_000910195.2
ALP47134.1	000608	PTH2	147	phiGrn1_0143	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47518.1	000608	PTH2	147	phiST2_0273	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54687.1	000608	PTH2	147	vBValMR10Z_146	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37262.1	000608	PTH2	147	pp2_028	Vibriophage phi-pp2	GCA_002630725.1
SOK58892.1	000608	PTH2	160	g084	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58355.1	000608	PTH2	160	g078	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44756.1	000609	PTH2	155	FDI40_gp680	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21834.1	000609	PTH2	142	GAP32_382	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44461.1	000609	PTH2	137	RaK2_00188	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43955.1	000609	PTH2	142	CBB_392	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44341.1	000609	PTH2	130	PBI_SCTP2_326	Salicola phage SCTP-2	GCA_002625545.1
QCW19093.1	000609	PTH2	129	7t3_0575	Salmonella phage 7t3	GCA_006083215.1
AZU98332.1	000609	PTH2	148	CPT_Munch_390	Salmonella phage Munch	GCA_004015485.1
QIG62651.1	000609	PTH2	104	SEPL_038	Salmonella phage SE_PL	GCA_011067555.1
AQW88916.1	000609	PTH2	143	BF_0391	Serratia phage BF	GCA_002619745.1
AGR48002.1	000609	PTH2	156	SmphiM12_370	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13188.1	000609	PTH2	156	PHIM19_283	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12828.1	000609	PTH2	156	PHIM7_283	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13550.1	000609	PTH2	156	PHIN3_287	Sinorhizobium phage phiN3	GCA_001501175.1
BBA65443.1	000609	PTH2	138	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96459.1	000609	PTH2	92	Xoosp13_273	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59206.1	000609	PTH2	133	g398	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58671.1	000609	PTH2	133	g394	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13691.1	000610	PTH2	157	Ccr10_gp161c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14036.1	000610	PTH2	157	Ccr2_gp160c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14723.1	000610	PTH2	157	Ccr29_gp167	Caulobacter phage Ccr29	GCA_002619485.1
ARB15078.1	000610	PTH2	157	Ccr32_gp160	Caulobacter phage Ccr32	GCA_002619505.1
ARB15412.1	000610	PTH2	157	Ccr34_gp170	Caulobacter phage Ccr34	GCA_002619525.1
ARB14379.1	000610	PTH2	157	Ccr5_gp159c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68361.1	000610	PTH2	158	CcrBL10_gp157c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69414.1	000610	PTH2	243	CcrBL9_gp390	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69971.1	000610	PTH2	136	CcrSC_gp389	Caulobacter phage CcrSC	GCA_003443315.1
AFU87684.1	000610	PTH2	143	CcrKarma_gp167	Caulobacter virus Karma	GCA_000901575.1
AFU87333.1	000610	PTH2	157	CcrMagneto_gp163	Caulobacter virus Magneto	GCA_000903095.1
AFU86644.1	000610	PTH2	144	CcrRogue_gp162	Caulobacter virus Rogue	GCA_000900555.1
AFU88480.1	000610	PTH2	143	CcrSwift_gp162	Caulobacter virus Swift	GCA_000899655.1
AFU86997.1	000610	PTH2	143	CbK_gp165	Caulobacter virus phiCbK	GCA_000900535.1
AND75355.1	000611	PTH2	187	ME3_194	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75356.1	000611	PTH2	99	ME3_195	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AFA44489.1	000611	PTH2	107	RaK2_00216	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
BAV39355.1	000611	PTH2	272	BPT24_235	Tenacibaculum phage pT24	GCA_002611925.1
BBA65512.1	000611	PTH2	279	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96513.1	000611	PTH2	280	Xoosp13_327	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ASV44721.1	000612	PTH2	139	FDI40_gp145	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69394.1	000612	PTH2	151	CcrBL9_gp370	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88174.1	000612	PTH2	136	CcrColossus_gp304	Caulobacter phage CcrColossus	GCA_000899635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ68851.1	000612	PTH2	136	CcrPW_gp312	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69953.1	000612	PTH2	151	CcrSC_gp371	Caulobacter phage CcrSC	GCA_003443315.1
AXH72542.1	000612	PTH2	153	-	Myoviridae sp.	GCA_003657725.1
AGR47918.1	000612	PTH2	140	SmphiM12_286	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13120.1	000612	PTH2	140	PHIM19_215	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12760.1	000612	PTH2	140	PHIM7_215	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13490.1	000612	PTH2	140	PHIN3_227	Sinorhizobium phage phiN3	GCA_001501175.1
AUZ95035.1	000000	PTH2	110	FDI40_gp256	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93584.1	000000	PTH2	119	G_325	Bacillus virus G	GCA_000917535.1
QIG57855.1	000000	PTH2	126	SEA_PAULODIABOLI_137	Microbacterium phage PauloDiaboli	GCA_011067425.1
AFC21644.1	000613	PTH2	120	GAP32_194	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14436.1	000613	PTH2	125	PBI_121Q_546	Escherichia phage 121Q	GCA_000926855.1
QAY00512.1	000613	PTH2	125	Ecwhy1_233	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34706.1	000613	PTH2	125	ACQ29_gp026	Escherichia phage PBECO4	GCA_001041035.1
BBM62108.1	000613	PTH2	125	EO157G_5190	Escherichia phage SP27	GCA_008033345.1
AXC36825.1	000613	PTH2	125	-	Escherichia phage UB	GCA_003341455.1
QBO61865.1	000613	PTH2	125	G17_00376	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13906.1	000613	PTH2	125	vBEcoMphAPEC6_gp281c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80422.1	000613	PTH2	125	PSLUR01_00445	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44310.1	000613	PTH2	126	RaK2_00037	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43765.1	000613	PTH2	120	CBB_200	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18914.1	000613	PTH2	125	7t3_0393	Salmonella phage 7t3	GCA_006083215.1
AZU98171.1	000613	PTH2	125	CPT_Munch_227	Salmonella phage Munch	GCA_004015485.1
QIG62813.1	000613	PTH2	125	SEPL_200	Salmonella phage SE_PL	GCA_011067555.1
AQW88721.1	000613	PTH2	120	BF_0196	Serratia phage BF	GCA_002619745.1
SOK59003.1	000613	PTH2	120	g195	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58468.1	000613	PTH2	120	g191	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXH72886.1	000000	PTH1	185	-	Myoviridae sp.	GCA_003657725.1
QDB70461.1	000614	Polass-SH3	140	CF8_0048	Aeromonas phage CF8	GCA_006384595.2
QDH47192.1	000614	Polass-SH3	140	LAh10_208	Aeromonas phage LAh10	GCA_006863975.1
QDJ96803.1	000614	Polass-SH3	140	PS1_0044	Aeromonas phage PS1	GCA_007051165.2
QFR59434.1	000614	Polass-SH3	140	PS2_0043	Aeromonas phage PS2	GCA_009388305.2
AFO71237.1	000614	Polass-SH3	134	CR5_017	Cronobacter phage CR5	GCA_000910235.1
QBZ70864.1	000614	Polass-SH3	139	pETSU_283	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59667.1	000614	Polass-SH3	136	SEGD1_016	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07443.1	000614	Polass-SH3	135	DERBICUS_17	Erwinia phage Derbicus	GCA_004521655.1
AHI60369.1	000614	Polass-SH3	139	Ea357_216	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49670.1	000614	Polass-SH3	134	MACHINA_32	Erwinia phage Machina	GCA_002758035.1
AGX01747.1	000614	Polass-SH3	151	CF95_gp025	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07326.1	000614	Polass-SH3	139	REBECCA_221	Erwinia phage Rebecca	GCA_004521635.1
AXF51158.1	000614	Polass-SH3	136	WELLINGTON_27	Erwinia phage Wellington	GCA_003344985.1
AFQ96744.1	000614	Polass-SH3	136	G173_gp199	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48047.1	000614	Polass-SH3	136	ASESINO_34	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86007.1	000614	Polass-SH3	139	BOSOLAPHORUS_221	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48321.1	000614	Polass-SH3	135	CAITLIN_26	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48594.1	000614	Polass-SH3	153	CHRISDB_32	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52324.2	000614	Polass-SH3	139	DM_224	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86326.1	000614	Polass-SH3	139	DESERTFOX_219	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48867.1	000614	Polass-SH3	135	EARLPHILLIPIV_17	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49115.1	000614	Polass-SH3	134	HUXLEY_33	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03891.1	000614	Polass-SH3	136	JOAD_24	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49379.1	000614	Polass-SH3	136	KWAN_27	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86649.1	000614	Polass-SH3	139	MADMEL_221	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86972.1	000614	Polass-SH3	139	MORTIMER_224	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49943.1	000614	Polass-SH3	134	PARSHIK_34	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50207.1	000614	Polass-SH3	132	PHOBOS_17	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51999.1	000614	Polass-SH3	139	RAY_219	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03646.1	000614	Polass-SH3	136	RISINGSUN_24	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51683.1	000614	Polass-SH3	139	SIMMY50_224	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65033.2	000614	Polass-SH3	139	SPECIALG_222	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50457.1	000614	Polass-SH3	136	STRATTON_32	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85855.1	000614	Polass-SH3	136	ACEC001_0180	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63984.1	000614	Polass-SH3	137	Goslar_00192	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71896.1	000614	Polass-SH3	143	N1M2_33	Klebsiella phage N1M2	GCA_010092605.1
QGZ14577.1	000614	Polass-SH3	135	HWC77_gp214	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24142.1	000614	Polass-SH3	136	-	Proteus phage 10	GCA_014071245.1
ABY62914.1	000614	Polass-SH3	134	201phi2-1p081	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27114.1	000614	Polass-SH3	140	PPEV_gp020	Pseudomonas phage EL	GCA_000866825.1
ANM44825.1	000614	Polass-SH3	138	KTN4_067	Pseudomonas phage KTN4	GCA_002607225.1
ARV77214.1	000614	Polass-SH3	138	NOXIFER_43	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89491.1	000614	Polass-SH3	140	OBP_054	Pseudomonas phage OBP	GCA_000896635.1
QBX32199.1	000614	Polass-SH3	135	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76697.1	000614	Polass-SH3	135	PHABIO_66	Pseudomonas phage Phabio	GCA_002624965.1
AEH03473.1	000614	Polass-SH3	136	046	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02575.1	000614	Polass-SH3	138	PSA21_45	Pseudomonas phage Psa21	GCA_004340405.1
ATN94887.1	000614	Polass-SH3	138	SL2_310	Pseudomonas phage SL2	GCA_002956015.1
QJB22703.1	000614	Polass-SH3	138	fnug_60	Pseudomonas phage fnug	GCA_012837215.1
QEM41776.1	000614	Polass-SH3	135	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82950.1	000614	Polass-SH3	138	PHIKZ049	Pseudomonas virus phiKZ	GCA_000842965.1
BAW18980.1	000614	Polass-SH3	135	FDH28_gp006	Ralstonia phage RP12	GCA_002617345.1
BAW19268.1	000614	Polass-SH3	135	-	Ralstonia phage RP31	GCA_002617365.1
BAS04796.1	000614	Polass-SH3	133	AVU11_gp004	Ralstonia phage RSF1	GCA_001500875.1
BAQ02532.1	000614	Polass-SH3	141	AVU38_gp004	Ralstonia phage RSL2	GCA_001503055.1
QNI20735.1	000614	Polass-SH3	136	-	Salmonella phage JN03	GCA_014319805.1
AWN09077.1	000614	Polass-SH3	136	MLDJOKPK_00150	Salmonella phage SPAsTU	GCA_003183805.1
AEP83850.1	000614	Polass-SH3	136	SPN3US_0017	Salmonella phage SPN3US	GCA_001042275.1
QKE54543.1	000614	Polass-SH3	136	ACSA002_2270	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65641.1	000614	Polass-SH3	141	2050HW_00306	Serratia phage 2050HW	GCA_002628125.1
QDB71069.1	000614	Polass-SH3	141	CPT_Moabite_037	Serratia phage Moabite	GCA_006384735.1
QFP93209.1	000614	Polass-SH3	138	-	Serratia phage PCH45	GCA_009187865.1
QAU04156.1	000614	Polass-SH3	135	HWC03_gp001	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23202.1	000614	Polass-SH3	135	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81068.1	000614	Polass-SH3	135	Aphrodite1_0142	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70809.1	000614	Polass-SH3	135	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47526.1	000614	Polass-SH3	135	HWC35_gp132	Vibrio phage USC-1	GCA_006864065.1
BAW98343.1	000614	Polass-SH3	136	FDH33_gp134	Vibrio phage pTD1	GCA_002618825.1
AQT28146.1	000614	Polass-SH3	139	pVa21_205	Vibrio phage pVa-21	GCA_002619305.1
QAX96701.1	000614	Polass-SH3	138	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97019.1	000614	Polass-SH3	138	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96065.1	000614	Polass-SH3	138	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96383.1	000614	Polass-SH3	138	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21044.1	000614	Polass-SH3	138	-	Vibrio phage vB_pir03	GCA_014319855.1
AMO43210.1	000615	Phd-YefM	70	R1080702_204	Cyanophage S-RIM32	GCA_001754165.1
AMO43439.1	000615	Phd-YefM	67	W270710_199	Cyanophage S-RIM44	GCA_002599145.1
AOO11682.1	000615	Phd-YefM	67	ES420910_204	Cyanophage S-RIM44	GCA_002599165.1
AOO11911.1	000615	Phd-YefM	67	Np050604_199	Cyanophage S-RIM44	GCA_002599185.1
AOO12148.1	000615	Phd-YefM	67	Np200711_205	Cyanophage S-RIM44	GCA_002599205.1
AOO12383.1	000615	Phd-YefM	67	Np420711_204	Cyanophage S-RIM44	GCA_002599225.1
AOO12612.1	000615	Phd-YefM	67	Sn080709_199	Cyanophage S-RIM44	GCA_002599245.1
AOO12848.1	000615	Phd-YefM	67	Sn130910_204	Cyanophage S-RIM44	GCA_002599265.1
AOO13078.1	000615	Phd-YefM	67	W2100709_200	Cyanophage S-RIM44	GCA_002599285.1
ADO99298.1	000615	Phd-YefM	67	Syn1_201	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59645.1	000615	Phd-YefM	67	S330809_184	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59407.1	000615	Phd-YefM	67	C440309_184	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59883.1	000615	Phd-YefM	67	N231010_184	Synechococcus phage S-CAM4	GCA_002922155.1
ASR76231.1	000616	Phd-YefM	63	PBI_BELLAMY_194	Synechococcus phage Bellamy	GCA_002627525.1
QCW23023.1	000616	Phd-YefM	57	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70189.1	000616	Phd-YefM	56	SynMITS9220M01_182	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH07557.1	000000	Phd-YefM	66	CYVG_00113	Cyanophage S-SSM6a	GCA_002710385.1
AGH26256.1	000000	Phd-YefM	58	CPMG_00155	Prochlorococcus phage MED4-213	GCA_000904535.1
AFO71291.1	000617	PhiKZ-Major-Capsid	751	CR5_071	Cronobacter phage CR5	GCA_000910235.1
AMR59724.1	000617	PhiKZ-Major-Capsid	688	SEGD1_075	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07499.1	000617	PhiKZ-Major-Capsid	751	DERBICUS_73	Erwinia phage Derbicus	GCA_004521655.1
AHI60467.1	000617	PhiKZ-Major-Capsid	755	Ea357_313	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49724.1	000617	PhiKZ-Major-Capsid	773	MACHINA_86	Erwinia phage Machina	GCA_002758035.1

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AGX01937.1	000617	PhiKZ-Major-Capsid	787	CF95_gp215	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07424.1	000617	PhiKZ-Major-Capsid	755	REBECCA_319	Erwinia phage Rebecca	GCA_004521635.1
AXF51219.1	000617	PhiKZ-Major-Capsid	769	WELLINGTON_89	Erwinia phage Wellington	GCA_003344985.1
AFQ96806.1	000617	PhiKZ-Major-Capsid	691	G173_gp261	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48104.1	000617	PhiKZ-Major-Capsid	769	ASESINO_91	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86106.1	000617	PhiKZ-Major-Capsid	755	BOSOLAPHORUS_320	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48377.1	000617	PhiKZ-Major-Capsid	766	CAITLIN_82	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48650.1	000617	PhiKZ-Major-Capsid	767	CHRISDB_88	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52422.1	000617	PhiKZ-Major-Capsid	755	DM_323	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86426.1	000617	PhiKZ-Major-Capsid	755	DESERTFOX_319	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48923.1	000617	PhiKZ-Major-Capsid	751	EARLPHILLIPIV_73	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49169.1	000617	PhiKZ-Major-Capsid	773	HUXLEY_87	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49440.1	000617	PhiKZ-Major-Capsid	768	KWAN_88	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86747.1	000617	PhiKZ-Major-Capsid	755	MADMEL_320	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87072.1	000617	PhiKZ-Major-Capsid	755	MORTIMER_324	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49997.1	000617	PhiKZ-Major-Capsid	770	PARSHIK_88	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50264.1	000617	PhiKZ-Major-Capsid	754	PHOBOS_74	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52097.1	000617	PhiKZ-Major-Capsid	755	RAY_317	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51780.1	000617	PhiKZ-Major-Capsid	755	SIMMY50_322	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65132.1	000617	PhiKZ-Major-Capsid	755	SPECIALG_321	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50518.1	000617	PhiKZ-Major-Capsid	769	STRATTON_93	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85915.1	000617	PhiKZ-Major-Capsid	766	ACEC001_0770	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63834.1	000617	PhiKZ-Major-Capsid	740	Goslar_00041	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24226.1	000617	PhiKZ-Major-Capsid	755	-	Proteus phage 10	GCA_014071245.1
ABY63029.1	000617	PhiKZ-Major-Capsid	746	201phi2-1p200	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44913.1	000617	PhiKZ-Major-Capsid	747	KTN4_155	Pseudomonas phage KTN4	GCA_002607225.1
ARV77291.1	000617	PhiKZ-Major-Capsid	738	NOXIFER_122	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32297.1	000617	PhiKZ-Major-Capsid	741	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76818.1	000617	PhiKZ-Major-Capsid	742	PHABIO_187	Pseudomonas phage Phabio	GCA_002624965.1
ARV76905.1	000617	PhiKZ-Major-Capsid	315	PHABIO_274	Pseudomonas phage Phabio	GCA_002624965.1
AEH03559.1	000617	PhiKZ-Major-Capsid	747	136	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02697.1	000617	PhiKZ-Major-Capsid	740	PSA21_170	Pseudomonas phage Psa21	GCA_004340405.1
ATN94801.1	000617	PhiKZ-Major-Capsid	747	SL2_224	Pseudomonas phage SL2	GCA_002956015.1
QJB22791.1	000617	PhiKZ-Major-Capsid	747	fnug_148	Pseudomonas phage fnug	GCA_012837215.1
QEM41871.1	000617	PhiKZ-Major-Capsid	741	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83021.1	000617	PhiKZ-Major-Capsid	747	PHIKZ120	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19068.1	000617	PhiKZ-Major-Capsid	719	FDH28_gp094	Ralstonia phage RP12	GCA_002617345.1
BAW19353.1	000617	PhiKZ-Major-Capsid	719	-	Ralstonia phage RP31	GCA_002617365.1
BAS04916.1	000617	PhiKZ-Major-Capsid	758	AVU11_gp124	Ralstonia phage RSF1	GCA_001500875.1
BAQ02645.1	000617	PhiKZ-Major-Capsid	758	AVU38_gp117	Ralstonia phage RSL2	GCA_001503055.1
QNI20786.1	000617	PhiKZ-Major-Capsid	766	-	Salmonella phage JN03	GCA_014319805.1
AXF51086.1	000617	PhiKZ-Major-Capsid	765	MLDJOKPK_00087	Salmonella phage SPAsTU	GCA_003183805.1
AEP83908.1	000617	PhiKZ-Major-Capsid	766	SPN3US_0075	Salmonella phage SPN3US	GCA_001042275.1
QKE54648.1	000617	PhiKZ-Major-Capsid	740	ACSA002_3310	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65374.1	000617	PhiKZ-Major-Capsid	762	2050HW_00039	Serratia phage 2050HW	GCA_002628125.1
QDB71158.1	000617	PhiKZ-Major-Capsid	764	CPT_Moabite_128	Serratia phage Moabite	GCA_006384735.1
QFP93055.1	000617	PhiKZ-Major-Capsid	777	-	Serratia phage PCH45	GCA_009187865.1
AXH70854.1	000617	PhiKZ-Major-Capsid	730	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT27953.1	000617	PhiKZ-Major-Capsid	755	pVa21_011	Vibrio phage pVa-21	GCA_002619305.1
QAX96636.1	000617	PhiKZ-Major-Capsid	707	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96954.1	000617	PhiKZ-Major-Capsid	707	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96000.1	000617	PhiKZ-Major-Capsid	707	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96318.1	000617	PhiKZ-Major-Capsid	707	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21103.1	000617	PhiKZ-Major-Capsid	721	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70284.1	000618	PhiKZ-Major-Capsid	723	CF8_0116	Aeromonas phage CF8	GCA_006384595.2
QDJ97261.1	000618	PhiKZ-Major-Capsid	722	D6_0101	Aeromonas phage D6	GCA_007051205.2
QDH47025.1	000618	PhiKZ-Major-Capsid	722	LAh10_33	Aeromonas phage LAh10	GCA_006863975.1
QDJ96875.1	000618	PhiKZ-Major-Capsid	724	PS1_0116	Aeromonas phage PS1	GCA_007051165.2
QFR59507.1	000618	PhiKZ-Major-Capsid	724	PS2_0116	Aeromonas phage PS2	GCA_009388305.2
QBZ70643.1	000618	PhiKZ-Major-Capsid	719	pETSU_062	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03832.1	000618	PhiKZ-Major-Capsid	727	JOAD_83	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03587.1	000618	PhiKZ-Major-Capsid	727	RISINGSUN_83	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71960.1	000618	PhiKZ-Major-Capsid	725	N1M2_97	Klebsiella phage N1M2	GCA_010092605.1
QGZ14434.1	000618	PhiKZ-Major-Capsid	730	HWC77_gp071	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27172.1	000618	PhiKZ-Major-Capsid	741	PPEV_gp078	Pseudomonas phage EL	GCA_000866825.1
AEV89561.1	000618	PhiKZ-Major-Capsid	719	OBP_124	Pseudomonas phage OBP	GCA_000896635.1
QAU04302.1	000618	PhiKZ-Major-Capsid	729	HWC03_gp147	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23276.1	000618	PhiKZ-Major-Capsid	731	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80923.1	000618	PhiKZ-Major-Capsid	731	Aphrodite1_0069	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47452.1	000618	PhiKZ-Major-Capsid	731	HWC35_gp058	Vibrio phage USC-1	GCA_006864065.1
BAW98274.1	000618	PhiKZ-Major-Capsid	731	FDH33_gp065	Vibrio phage pTD1	GCA_002618825.1
QBX32488.1	000619	PhiKZ-Major-Capsid-Cterm	146	-	Pseudomonas phage PA1C	GCA_004785505.1
QBJ02891.1	000619	PhiKZ-Major-Capsid-Cterm	153	PSA21_365	Pseudomonas phage Psa21	GCA_004340405.1
QEM42060.1	000619	PhiKZ-Major-Capsid-Cterm	146	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ABY63222.1	000619	PhiKZ-Major-Capsid-Cterm	150	201phi2-1p398	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45080.1	000619	PhiKZ-Major-Capsid-Cterm	143	KTN4_322	Pseudomonas phage KTN4	GCA_002607225.1
ARV77026.1	000619	PhiKZ-Major-Capsid-Cterm	149	PHABIO_395	Pseudomonas phage Phabio	GCA_002624965.1
AEH03749.1	000619	PhiKZ-Major-Capsid-Cterm	146	326	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94635.1	000619	PhiKZ-Major-Capsid-Cterm	143	SL2_058	Pseudomonas phage SL2	GCA_002956015.1
QJB22955.1	000619	PhiKZ-Major-Capsid-Cterm	143	fnug_312	Pseudomonas phage fnug	GCA_012837215.1
AAL83167.1	000619	PhiKZ-Major-Capsid-Cterm	143	PHIKZ266	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96691.1	000620	PhiKZ-Major-Capsid-Cterm	175	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97009.1	000620	PhiKZ-Major-Capsid-Cterm	175	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96055.1	000620	PhiKZ-Major-Capsid-Cterm	175	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96373.1	000620	PhiKZ-Major-Capsid-Cterm	175	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMR59784.1	000621	PhiKZ-Major-Capsid-Cterm	110	SEGD1_137	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ50572.1	000621	PhiKZ-Major-Capsid-Cterm	117	STRATTON_147	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AWN08984.1	000621	PhiKZ-Major-Capsid-Cterm	110	MLDJOKPK_00018	Salmonella phage SPAsTU	GCA_003183805.1
AEP83966.1	000621	PhiKZ-Major-Capsid-Cterm	110	SPN3US_0133	Salmonella phage SPN3US	GCA_001042275.1
QBZ70669.1	000622	PhiKZ-Major-Capsid-Cterm	185	pETSU_088	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71984.1	000622	PhiKZ-Major-Capsid-Cterm	185	N1M2_121	Klebsiella phage N1M2	GCA_010092605.1
AEV89585.1	000622	PhiKZ-Major-Capsid-Cterm	172	OBP_148	Pseudomonas phage OBP	GCA_000896635.1
BAW19188.1	000623	PhiKZ-Major-Capsid-Cterm	229	FDH28_gp207	Ralstonia phage RP12	GCA_002617345.1
BAW19474.1	000623	PhiKZ-Major-Capsid-Cterm	229	-	Ralstonia phage RP31	GCA_002617365.1
QBZ70677.1	000624	PhiKZ-Major-Capsid-Cterm	202	pETSU_096	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89597.1	000624	PhiKZ-Major-Capsid-Cterm	185	OBP_160	Pseudomonas phage OBP	GCA_000896635.1
AFQ96597.1	000625	PhiKZ-Major-Capsid-Cterm	114	G173_gp052	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48161.1	000625	PhiKZ-Major-Capsid-Cterm	115	ASESINO_148	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
QMV29128.1	000000	PhiKZ-Major-Capsid-Cterm	226	AP1_0425	Aeromonas phage AP1	GCA_014183365.1
QMV29131.1	000000	PhiKZ-Major-Capsid-Cterm	135	AP1_0428	Aeromonas phage AP1	GCA_014183365.1
QBZ70668.1	000000	PhiKZ-Major-Capsid-Cterm	188	pETSU_087	Edwardsiella virus pEt-SU	GCA_004800915.1
ABY62938.1	000000	PhiKZ-Major-Capsid-Cterm	188	201phi2-1p106	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63109.1	000000	PhiKZ-Major-Capsid-Cterm	406	201phi2-1p282	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76823.1	000000	PhiKZ-Major-Capsid-Cterm	139	PHABIO_192	Pseudomonas phage Phabio	GCA_002624965.1
AYD81305.1	000626	RNA_ligase	250	SEA_JUSTBECAUSE_136	Streptomyces phage JustBecause	GCA_003613775.1
QJD53708.1	000626	RNA_ligase	250	SEA_KELA_137	Streptomyces phage Kela	GCA_012934305.1
QDB70424.1	000627	Thymidylate_kin	223	CF8_0011	Aeromonas phage CF8	GCA_006384595.2
QDJ97429.1	000627	Thymidylate_kin	230	D6_0002	Aeromonas phage D6	GCA_007051205.2
QDH47126.1	000627	Thymidylate_kin	230	LAh10_176	Aeromonas phage LAh10	GCA_006863975.1
QDJ96770.1	000627	Thymidylate_kin	210	PS1_0012	Aeromonas phage PS1	GCA_007051165.2
QFR59403.1	000627	Thymidylate_kin	210	PS2_0012	Aeromonas phage PS2	GCA_009388305.2
AXG67161.1	000627	Thymidylate_kin	204	AD1_117	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79911.1	000627	Thymidylate_kin	197	JA11_106	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66510.1	000627	Thymidylate_kin	197	JA13_107	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66835.1	000627	Thymidylate_kin	197	JA29_109	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67480.1	000627	Thymidylate_kin	197	JA33_106	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBZ70814.1	000627	Thymidylate_kin	204	pETSU_233	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60461.1	000627	Thymidylate_kin	260	Ea357_307	Erwinia phage Ea35-70	GCA_000914635.1
AGX01923.1	000627	Thymidylate_kin	249	tmk	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07418.1	000627	Thymidylate_kin	260	REBECCA_313	Erwinia phage Rebecca	GCA_004521635.1
AWY08394.1	000627	Thymidylate_kin	204	Alexandra_122	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AUG86100.1	000627	Thymidylate_kin	254	BOSOLAPHORUS_314	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ASB43085.1	000627	Thymidylate_kin	254	DM_317	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86420.1	000627	Thymidylate_kin	254	DESERTFOX_313	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03909.1	000627	Thymidylate_kin	241	JOAD_6	Erwinia phage vB_EamM_Joad	GCA_002629065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86741.1	000627	Thymidylate_kin	254	MADMEL_314	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87066.1	000627	Thymidylate_kin	254	MORTIMER_318	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52091.1	000627	Thymidylate_kin	254	RAY_311	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03664.1	000627	Thymidylate_kin	241	RISINGSUN_6	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51774.2	000627	Thymidylate_kin	254	SIMMY50_316	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65126.2	000627	Thymidylate_kin	254	SPECIALG_315	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARW58758.1	000627	Thymidylate_kin	204	Y3_118	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28596.1	000627	Thymidylate_kin	209	YOLOSWAG_114	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QBO63801.1	000627	Thymidylate_kin	209	Goslar_00008	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72112.1	000627	Thymidylate_kin	208	N1M2_249	Klebsiella phage N1M2	GCA_010092605.1
SBV38344.1	000627	Thymidylate_kin	220	BN7874_175	Phage NCTB	GCA_900092385.1
QGZ14553.1	000627	Thymidylate_kin	207	HWC77_gp190	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24219.1	000627	Thymidylate_kin	206	-	Proteus phage 10	GCA_014071245.1
ABY63113.1	000627	Thymidylate_kin	357	201phi2-1p287	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27295.1	000627	Thymidylate_kin	215	PPEV_gp201	Pseudomonas phage EL	GCA_000866825.1
ANM44987.1	000627	Thymidylate_kin	352	KTN4_229	Pseudomonas phage KTN4	GCA_002607225.1
AFH14732.1	000627	Thymidylate_kin	216	Lu11_0195	Pseudomonas phage Lu11	GCA_000897175.1
ARV77371.1	000627	Thymidylate_kin	482	NOXIFER_202	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89445.1	000627	Thymidylate_kin	204	OBP_008	Pseudomonas phage OBP	GCA_000896635.1
QBX32377.1	000627	Thymidylate_kin	352	-	Pseudomonas phage PA1C	GCA_004785505.1
AGS81972.1	000627	Thymidylate_kin	209	PaBG_00087	Pseudomonas phage PaBG	GCA_000912555.1
ARV76909.1	000627	Thymidylate_kin	366	PHABIO_278	Pseudomonas phage Phabio	GCA_002624965.1
AEH03646.1	000627	Thymidylate_kin	362	223	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02783.1	000627	Thymidylate_kin	358	PSA21_257	Pseudomonas phage Psa21	GCA_004340405.1
ATN94727.1	000627	Thymidylate_kin	352	SL2_150	Pseudomonas phage SL2	GCA_002956015.1
QJB22865.1	000627	Thymidylate_kin	352	fnug_222	Pseudomonas phage fnug	GCA_012837215.1
QEM41950.1	000627	Thymidylate_kin	352	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83089.1	000627	Thymidylate_kin	352	PHIKZ188	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19195.1	000627	Thymidylate_kin	220	FDH28_gp200	Ralstonia phage RP12	GCA_002617345.1
BAW19481.1	000627	Thymidylate_kin	209	-	Ralstonia phage RP31	GCA_002617365.1
BAS04984.2	000627	Thymidylate_kin	242	AVU11_agp39	Ralstonia phage RSF1	GCA_001500875.1
BAQ02710.1	000627	Thymidylate_kin	231	AVU38_gp182	Ralstonia phage RSL2	GCA_001503055.1
QKE54641.1	000627	Thymidylate_kin	214	ACSA002_3240	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65389.1	000627	Thymidylate_kin	216	2050HW_00054	Serratia phage 2050HW	GCA_002628125.1
QDB71170.1	000627	Thymidylate_kin	216	CPT_Moabite_140	Serratia phage Moabite	GCA_006384735.1
QFP93141.1	000627	Thymidylate_kin	225	-	Serratia phage PCH45	GCA_009187865.1
QAU04181.1	000627	Thymidylate_kin	207	HWC03_gp026	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23178.1	000627	Thymidylate_kin	207	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81027.1	000627	Thymidylate_kin	207	Aphrodite1_0164	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47551.1	000627	Thymidylate_kin	207	HWC35_gp157	Vibrio phage USC-1	GCA_006864065.1
BAW98364.1	000627	Thymidylate_kin	212	FDH33_gp155	Vibrio phage pTD1	GCA_002618825.1
AQT28041.1	000627	Thymidylate_kin	311	pVa21_100	Vibrio phage pVa-21	GCA_002619305.1
QAX96897.1	000627	Thymidylate_kin	215	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97202.1	000627	Thymidylate_kin	215	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96261.1	000627	Thymidylate_kin	215	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96579.1	000627	Thymidylate_kin	215	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71318.1	000628	Thymidylate_kin	215	CR5_098	Cronobacter phage CR5	GCA_000910235.1
AMR59752.1	000628	Thymidylate_kin	207	SEGD1_103	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07527.1	000628	Thymidylate_kin	215	DERBICUS_101	Erwinia phage Derbicus	GCA_004521655.1
ANZ49751.1	000628	Thymidylate_kin	213	MACHINA_113	Erwinia phage Machina	GCA_002758035.1
AXF51250.1	000628	Thymidylate_kin	209	WELLINGTON_120	Erwinia phage Wellington	GCA_003344985.1
AFQ96570.1	000628	Thymidylate_kin	207	G173_gp025	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48130.1	000628	Thymidylate_kin	207	ASESINO_117	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48405.1	000628	Thymidylate_kin	220	CAITLIN_110	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48677.1	000628	Thymidylate_kin	221	CHRISDB_115	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48950.1	000628	Thymidylate_kin	215	EARLPHILLIPIV_101	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49195.1	000628	Thymidylate_kin	213	HUXLEY_113	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49471.1	000628	Thymidylate_kin	209	KWAN_119	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50023.1	000628	Thymidylate_kin	213	PARSHIK_114	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50291.1	000628	Thymidylate_kin	215	PHOBOS_101	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50545.1	000628	Thymidylate_kin	207	STRATTON_120	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85941.1	000628	Thymidylate_kin	207	ACEC001_1030	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20809.1	000628	Thymidylate_kin	207	-	Salmonella phage JN03	GCA_014319805.1
AWN09006.1	000628	Thymidylate_kin	207	MLDJOKPK_00058	Salmonella phage SPAsTU	GCA_003183805.1
AEP83933.1	000628	Thymidylate_kin	207	SPN3US_0100	Salmonella phage SPN3US	GCA_001042275.1
APU01531.1	000629	Thymidine_kinase	191	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29039.1	000629	Thymidine_kinase	191	AP1_0332	Aeromonas phage AP1	GCA_014183365.1
ATI17369.1	000629	Thymidine_kinase	191	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00225.1	000629	Thymidine_kinase	191	HWB28_gp327	Aeromonas phage AS-zj	GCA_002627665.1
AUE22692.1	000629	Thymidine_kinase	199	Ah1_00151	Aeromonas phage Ah1	GCA_002957415.1
QAX98417.1	000629	Thymidine_kinase	192	ASfcp2_73	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97810.1	000629	Thymidine_kinase	191	ASswx1_166	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01341.1	000629	Thymidine_kinase	189	ASwh1_280	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39566.1	000629	Thymidine_kinase	191	CC2_370	Aeromonas phage CC2	GCA_000903495.1
QDB70370.1	000629	Thymidine_kinase	230	CF8_0202	Aeromonas phage CF8	GCA_006384595.2
QDJ97368.1	000629	Thymidine_kinase	280	D6_0209	Aeromonas phage D6	GCA_007051205.2
QDH47099.1	000629	Thymidine_kinase	282	LAh10_123	Aeromonas phage LAh10	GCA_006863975.1
QDJ96712.1	000629	Thymidine_kinase	224	PS1_0201	Aeromonas phage PS1	GCA_007051165.2
QFR59345.1	000629	Thymidine_kinase	224	PS2_0203	Aeromonas phage PS2	GCA_009388305.2
ADQ52872.1	000629	Thymidine_kinase	192	PX29p153	Aeromonas phage PX29	GCA_000920195.1
ADM80134.1	000629	Thymidine_kinase	199	phiAS5_ORF0291	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53153.1	000629	Thymidine_kinase	191	65p145	Aeromonas virus 65	GCA_000893255.1
AAQ17820.1	000629	Thymidine_kinase	199	tk	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95448.1	000629	Thymidine_kinase	182	FDI40_gp709	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83754.1	000629	Thymidine_kinase	185	0305phi8-36p196	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93397.1	000629	Thymidine_kinase	184	G_135	Bacillus virus G	GCA_000917535.1
ANS06012.1	000629	Thymidine_kinase	194	ABCD_0142	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47793.1	000629	Thymidine_kinase	198	CST095	Clostridium phage c-st	GCA_000865225.1
AIA65001.1	000629	Thymidine_kinase	193	S13_204	Cronobacter phage S13	GCA_001503575.1
AFC21620.1	000629	Thymidine_kinase	189	GAP32_170	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97150.1	000629	Thymidine_kinase	194	E_142	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
QBZ70752.1	000629	Thymidine_kinase	196	pETSU_171	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60263.1	000629	Thymidine_kinase	192	Ea357_112	Erwinia phage Ea35-70	GCA_000914635.1
QBP07221.1	000629	Thymidine_kinase	192	REBECCA_114	Erwinia phage Rebecca	GCA_004521635.1
AUG85901.1	000629	Thymidine_kinase	192	BOSOLAPHORUS_114	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52216.1	000629	Thymidine_kinase	192	DM_118	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86220.1	000629	Thymidine_kinase	192	DESERTFOX_113	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03721.1	000629	Thymidine_kinase	195	JOAD_194	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86542.1	000629	Thymidine_kinase	192	MADMEL_114	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86866.1	000629	Thymidine_kinase	192	MORTIMER_117	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51894.1	000629	Thymidine_kinase	192	RAY_113	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03478.1	000629	Thymidine_kinase	195	RISINGSUN_192	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51578.1	000629	Thymidine_kinase	192	SIMMY50_116	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64925.1	000629	Thymidine_kinase	192	SPECIALG_115	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QAY00536.1	000629	Thymidine_kinase	194	Ecwhy1_257	Escherichia phage Ecwhy_1	GCA_004146585.1
ARM70926.1	000629	Thymidine_kinase	193	phiC120_c221	Escherichia phage phiC120	GCA_002621185.1
AAX78666.1	000629	Thymidine_kinase	193	RB43ORF144c	Escherichia virus RB43	GCA_000863505.1
QGH72059.1	000629	Thymidine_kinase	194	N1M2_196	Klebsiella phage N1M2	GCA_010092605.1
AFA44294.1	000629	Thymidine_kinase	191	RaK2_00021	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78930.1	000629	Thymidine_kinase	193	-	Myoviridae sp.	GCA_012593985.1
QIG65832.1	000629	Thymidine_kinase	195	phiOC_p167	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43738.1	000629	Thymidine_kinase	189	CBB_173	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QGZ14473.1	000629	Thymidine_kinase	198	HWC77_gp110	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24054.1	000629	Thymidine_kinase	182	-	Proteus phage 10	GCA_014071245.1
AEV89686.1	000629	Thymidine_kinase	206	OBP_249	Pseudomonas phage OBP	GCA_000896635.1
ASV44548.1	000629	Thymidine_kinase	198	PBI_SCTP2_533	Salicola phage SCTP-2	GCA_002625545.1
QCW18885.1	000629	Thymidine_kinase	189	7t3_0364	Salmonella phage 7t3	GCA_006083215.1
AZU98143.1	000629	Thymidine_kinase	189	CPT_Munch_199	Salmonella phage Munch	GCA_004015485.1
QIG62840.1	000629	Thymidine_kinase	189	SEPL_227	Salmonella phage SE_PL	GCA_011067555.1
QKE54421.1	000629	Thymidine_kinase	196	ACSA002_1070	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65544.1	000629	Thymidine_kinase	193	2050HW_00209	Serratia phage 2050HW	GCA_002628125.1
AQW88696.1	000629	Thymidine_kinase	193	BF_0171	Serratia phage BF	GCA_002619745.1
QDB71309.1	000629	Thymidine_kinase	193	CPT_Moabite_279	Serratia phage Moabite	GCA_006384735.1
QAU04261.1	000629	Thymidine_kinase	198	HWC03_gp106	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23102.1	000629	Thymidine_kinase	198	-	Vibrio phage 5 TSL-2019	GCA_006964265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUR81030.1	000629	Thymidine_kinase	198	Aphrodite1_0029	Vibrio phage Aphrodite1	GCA_002958015.1
AAQ64259.1	000629	Thymidine_kinase	194	KVP40.0190	Vibrio phage KVP40	GCA_000843785.1
QDH47414.1	000629	Thymidine_kinase	198	HWC35_gp020	Vibrio phage USC-1	GCA_006864065.1
QIW90575.1	000629	Thymidine_kinase	194	GCAPEGMB_00228	Vibrio phage V07	GCA_012361095.1
QIW91223.1	000629	Thymidine_kinase	194	COHAPHLL_00387	Vibrio phage V09	GCA_012361135.1
QHJ74373.1	000629	Thymidine_kinase	194	VH12019_00046	Vibrio phage VH1_2019	GCA_009931825.1
AGB06870.1	000629	Thymidine_kinase	189	CF80_gp083	Vibrio phage VH7D	GCA_000914495.1
QBX06276.1	000629	Thymidine_kinase	189	ValB1HC_323	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60902.1	000629	Thymidine_kinase	189	AVU32_gp061	Vibrio phage ValKK3	GCA_001501635.1
BAW98231.1	000629	Thymidine_kinase	197	FDH33_gp022	Vibrio phage pTD1	GCA_002618825.1
ALP47080.1	000629	Thymidine_kinase	189	phiGrn1_0309	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47460.1	000629	Thymidine_kinase	189	phiST2_0065	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54903.1	000629	Thymidine_kinase	189	vBValMR10Z_363	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37421.1	000629	Thymidine_kinase	194	pp2_188	Vibriophage phi-pp2	GCA_002630725.1
SOK58977.1	000629	Thymidine_kinase	190	g169	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58443.1	000629	Thymidine_kinase	190	g166	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56807.1	000630	DNA_ligase-DBD	144	CPXG_00004	Cyanophage P-RSM6	GCA_000906155.1
AJK27637.1	000630	DNA_ligase-DBD	147	PTIM40_233	Cyanophage P-TIM40	GCA_001470935.1
AOO14407.1	000630	DNA_ligase-DBD	154	Sn110110_214	Cyanophage S-RIM14	GCA_002599065.1
AOO15056.1	000630	DNA_ligase-DBD	154	W1230910_211	Cyanophage S-RIM14	GCA_002599125.1
AMO43231.1	000630	DNA_ligase-DBD	97	R1080702_226	Cyanophage S-RIM32	GCA_001754165.1
AMO43463.1	000630	DNA_ligase-DBD	133	W270710_224	Cyanophage S-RIM44	GCA_002599145.1
AOO11703.1	000630	DNA_ligase-DBD	133	ES420910_226	Cyanophage S-RIM44	GCA_002599165.1
AOO11935.1	000630	DNA_ligase-DBD	133	Np050604_224	Cyanophage S-RIM44	GCA_002599185.1
AOO12169.1	000630	DNA_ligase-DBD	133	Np200711_227	Cyanophage S-RIM44	GCA_002599205.1
AOO12404.1	000630	DNA_ligase-DBD	133	Np420711_226	Cyanophage S-RIM44	GCA_002599225.1
AOO12636.1	000630	DNA_ligase-DBD	133	Sn080709_224	Cyanophage S-RIM44	GCA_002599245.1
AOO12869.1	000630	DNA_ligase-DBD	133	Sn130910_226	Cyanophage S-RIM44	GCA_002599265.1
AOO13102.1	000630	DNA_ligase-DBD	133	W2100709_225	Cyanophage S-RIM44	GCA_002599285.1
AGH07617.1	000630	DNA_ligase-DBD	191	CYVG_00174	Cyanophage S-SSM6a	GCA_002710385.1
AGG54381.1	000630	DNA_ligase-DBD	150	CYWG_00097	Cyanophage S-SSM6b	GCA_002710425.1
QIG65756.1	000630	DNA_ligase-DBD	144	phiOC_p091	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26220.1	000630	DNA_ligase-DBD	151	CPMG_00119	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44695.1	000630	DNA_ligase-DBD	207	PSSM2_317	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12281.1	000630	DNA_ligase-DBD	207	PRTG_00128	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93571.1	000630	DNA_ligase-DBD	184	AVU42_gp238	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99324.1	000630	DNA_ligase-DBD	144	Syn1_228	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47894.1	000630	DNA_ligase-DBD	169	SmphiM12_262	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13094.1	000630	DNA_ligase-DBD	169	PHIM19_189	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12734.1	000630	DNA_ligase-DBD	169	PHIM7_189	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13464.1	000630	DNA_ligase-DBD	169	PHIN3_201	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30760.1	000630	DNA_ligase-DBD	168	Syn7803US37_283	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54981.1	000630	DNA_ligase-DBD	191	b23_0375	Synechococcus phage B23	GCA_009745195.1
QGT54616.1	000630	DNA_ligase-DBD	191	b3_0381	Synechococcus phage B3	GCA_009745215.1
ASR76303.1	000630	DNA_ligase-DBD	150	PBI_BELLAMY_267	Synechococcus phage Bellamy	GCA_002627525.1
QCW23054.1	000630	DNA_ligase-DBD	157	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50697.1	000630	DNA_ligase-DBD	157	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59685.1	000630	DNA_ligase-DBD	143	S330809_224	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59447.1	000630	DNA_ligase-DBD	143	C440309_224	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59922.1	000630	DNA_ligase-DBD	143	N231010_223	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70458.1	000630	DNA_ligase-DBD	150	HOU04_gp059	Synechococcus phage S-T4	GCA_003443335.1
QJT70250.1	000630	DNA_ligase-DBD	165	SynMITS9220M01_244	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01437.1	000631	novel-URI-nuclease	298	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28927.1	000631	novel-URI-nuclease	300	AP1_0220	Aeromonas phage AP1	GCA_014183365.1
ATI17462.1	000631	novel-URI-nuclease	300	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00535.1	000631	novel-URI-nuclease	300	HWB28_gp017	Aeromonas phage AS-zj	GCA_002627665.1
QAX97902.1	000631	novel-URI-nuclease	300	ASswx1_259	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01250.1	000631	novel-URI-nuclease	298	ASwh1_185	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39405.1	000631	novel-URI-nuclease	300	CC2_273	Aeromonas phage CC2	GCA_000903495.1
ADQ53056.1	000631	novel-URI-nuclease	298	65p046	Aeromonas virus 65	GCA_000893255.1
AON97263.1	000631	novel-URI-nuclease	359	E_255	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AOO14386.1	000631	novel-URI-nuclease	149	Sn110110_192	Cyanophage S-RIM14	GCA_002599065.1
AOO15034.1	000631	novel-URI-nuclease	149	W1230910_188	Cyanophage S-RIM14	GCA_002599125.1
AGH07551.1	000631	novel-URI-nuclease	145	CYVG_00107	Cyanophage S-SSM6a	GCA_002710385.1
AGG54404.1	000631	novel-URI-nuclease	107	CYWG_00120	Cyanophage S-SSM6b	GCA_002710425.1
QIG65990.1	000631	novel-URI-nuclease	157	phiOC_p348	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26261.1	000631	novel-URI-nuclease	155	CPMG_00160	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44595.1	000631	novel-URI-nuclease	145	PSSM2_218	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12375.1	000631	novel-URI-nuclease	145	PRTG_00222	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93507.1	000631	novel-URI-nuclease	144	AVU42_gp170	Prochlorococcus phage P-TIM68	GCA_001503075.1
AGR48033.1	000631	novel-URI-nuclease	137	SmphiM12_401	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13215.1	000631	novel-URI-nuclease	137	PHIM19_310	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12856.1	000631	novel-URI-nuclease	137	PHIM7_310	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13577.1	000631	novel-URI-nuclease	138	PHIN3_314	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30686.1	000631	novel-URI-nuclease	146	Syn7803US37_209	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54931.1	000631	novel-URI-nuclease	145	b23_0318	Synechococcus phage B23	GCA_009745195.1
QGT54566.1	000631	novel-URI-nuclease	145	b3_0325	Synechococcus phage B3	GCA_009745215.1
ASR76225.1	000631	novel-URI-nuclease	147	PBI_BELLAMY_182	Synechococcus phage Bellamy	GCA_002627525.1
QCW23016.1	000631	novel-URI-nuclease	140	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50527.1	000631	novel-URI-nuclease	140	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70179.1	000631	novel-URI-nuclease	143	SynMITS9220M01_167	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ALY07110.1	000631	novel-URI-nuclease	283	VmeM32_00123	Vibrio phage vB_VmeM-32	GCA_002608825.1
AEO93426.1	000632	ZnR-Bacillus_virus_G-expansion	106	G_166	Bacillus virus G	GCA_000917535.1
AEO93303.1	000632	ZnR-Bacillus_virus_G-expansion	117	G_32	Bacillus virus G	GCA_000917535.1
AEO93305.1	000632	ZnR-Bacillus_virus_G-expansion	118	G_34	Bacillus virus G	GCA_000917535.1
AEO93306.1	000632	ZnR-Bacillus_virus_G-expansion	107	G_35	Bacillus virus G	GCA_000917535.1
AEO93702.1	000632	ZnR-Bacillus_virus_G-expansion	221	G_444	Bacillus virus G	GCA_000917535.1
AEO93705.1	000632	ZnR-Bacillus_virus_G-expansion	216	G_447	Bacillus virus G	GCA_000917535.1
AEO93706.1	000632	ZnR-Bacillus_virus_G-expansion	205	G_448	Bacillus virus G	GCA_000917535.1
AEO93707.1	000632	ZnR-Bacillus_virus_G-expansion	212	G_449	Bacillus virus G	GCA_000917535.1
AEO93708.1	000632	ZnR-Bacillus_virus_G-expansion	204	G_450	Bacillus virus G	GCA_000917535.1
AEO93709.1	000632	ZnR-Bacillus_virus_G-expansion	217	G_451	Bacillus virus G	GCA_000917535.1
AEO93711.1	000632	ZnR-Bacillus_virus_G-expansion	222	G_453	Bacillus virus G	GCA_000917535.1
AEO93712.1	000632	ZnR-Bacillus_virus_G-expansion	223	G_454	Bacillus virus G	GCA_000917535.1
AEO93713.1	000632	ZnR-Bacillus_virus_G-expansion	219	G_455	Bacillus virus G	GCA_000917535.1
AEO93714.1	000632	ZnR-Bacillus_virus_G-expansion	196	G_456	Bacillus virus G	GCA_000917535.1
AEO93715.1	000632	ZnR-Bacillus_virus_G-expansion	197	G_457	Bacillus virus G	GCA_000917535.1
AEO93716.1	000632	ZnR-Bacillus_virus_G-expansion	213	G_458	Bacillus virus G	GCA_000917535.1
AEO93717.1	000632	ZnR-Bacillus_virus_G-expansion	203	G_459	Bacillus virus G	GCA_000917535.1
AEO93317.1	000632	ZnR-Bacillus_virus_G-expansion	100	G_46	Bacillus virus G	GCA_000917535.1
AEO93718.1	000632	ZnR-Bacillus_virus_G-expansion	201	G_460	Bacillus virus G	GCA_000917535.1
AEO93719.1	000632	ZnR-Bacillus_virus_G-expansion	208	G_461	Bacillus virus G	GCA_000917535.1
AEO93720.1	000632	ZnR-Bacillus_virus_G-expansion	209	G_462	Bacillus virus G	GCA_000917535.1
AEO93721.1	000632	ZnR-Bacillus_virus_G-expansion	212	G_463	Bacillus virus G	GCA_000917535.1
AEO93722.1	000632	ZnR-Bacillus_virus_G-expansion	204	G_464	Bacillus virus G	GCA_000917535.1
AEO93723.1	000632	ZnR-Bacillus_virus_G-expansion	187	G_465	Bacillus virus G	GCA_000917535.1
AEO93724.1	000632	ZnR-Bacillus_virus_G-expansion	188	G_466	Bacillus virus G	GCA_000917535.1
AEO93725.1	000632	ZnR-Bacillus_virus_G-expansion	190	G_467	Bacillus virus G	GCA_000917535.1
AEO93726.1	000632	ZnR-Bacillus_virus_G-expansion	182	G_468	Bacillus virus G	GCA_000917535.1
AEO93727.1	000632	ZnR-Bacillus_virus_G-expansion	181	G_469	Bacillus virus G	GCA_000917535.1
AEO93728.1	000632	ZnR-Bacillus_virus_G-expansion	198	G_470	Bacillus virus G	GCA_000917535.1
AEO93729.1	000632	ZnR-Bacillus_virus_G-expansion	197	G_471	Bacillus virus G	GCA_000917535.1
AEO93730.1	000632	ZnR-Bacillus_virus_G-expansion	197	G_472	Bacillus virus G	GCA_000917535.1
AEO93731.1	000632	ZnR-Bacillus_virus_G-expansion	196	G_473	Bacillus virus G	GCA_000917535.1
AEO93732.1	000632	ZnR-Bacillus_virus_G-expansion	183	G_474	Bacillus virus G	GCA_000917535.1
ARB13593.1	000633	3′-5′-exoribonuclease	146	Ccr10_gp065	Caulobacter phage Ccr10	GCA_002619445.1
ARB13939.1	000633	3′-5′-exoribonuclease	146	Ccr2_gp064	Caulobacter phage Ccr2	GCA_002619465.1
ARB14628.1	000633	3′-5′-exoribonuclease	146	Ccr29_gp071	Caulobacter phage Ccr29	GCA_002619485.1
ARB14984.1	000633	3′-5′-exoribonuclease	146	Ccr32_gp065	Caulobacter phage Ccr32	GCA_002619505.1
ARB15315.1	000633	3′-5′-exoribonuclease	146	Ccr34_gp066	Caulobacter phage Ccr34	GCA_002619525.1
ARB14282.1	000633	3′-5′-exoribonuclease	146	Ccr5_gp064	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68266.1	000633	3′-5′-exoribonuclease	147	CcrBL10_gp062	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69382.1	000633	3′-5′-exoribonuclease	149	CcrBL9_gp358	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87948.1	000633	3′-5′-exoribonuclease	156	CcrColossus_gp078	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68621.1	000633	3′-5′-exoribonuclease	156	CcrPW_gp082	Caulobacter phage CcrPW	GCA_003443275.1

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AXQ69942.1	000633	3′-5′-exoribonuclease	150	CcrSC_gp360	Caulobacter phage CcrSC	GCA_003443315.1
AFU87583.1	000633	3′-5′-exoribonuclease	146	CcrKarma_gp066	Caulobacter virus Karma	GCA_000901575.1
AFU87233.1	000633	3′-5′-exoribonuclease	146	CcrMagneto_gp063	Caulobacter virus Magneto	GCA_000903095.1
AFU86549.1	000633	3′-5′-exoribonuclease	147	CcrRogue_gp067	Caulobacter virus Rogue	GCA_000900555.1
AFU88381.1	000633	3′-5′-exoribonuclease	146	CcrSwift_gp063	Caulobacter virus Swift	GCA_000899655.1
AFU86897.1	000633	3′-5′-exoribonuclease	146	CbK_gp065	Caulobacter virus phiCbK	GCA_000900535.1
ABY63122.1	000633	3′-5′-exoribonuclease	143	201phi2-1p296	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44998.1	000633	3′-5′-exoribonuclease	143	KTN4_240	Pseudomonas phage KTN4	GCA_002607225.1
ARV77392.1	000633	3′-5′-exoribonuclease	143	NOXIFER_227	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77428.1	000633	3′-5′-exoribonuclease	263	NOXIFER_263	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32383.1	000633	3′-5′-exoribonuclease	143	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76923.1	000633	3′-5′-exoribonuclease	142	PHABIO_292	Pseudomonas phage Phabio	GCA_002624965.1
AEH03654.1	000633	3′-5′-exoribonuclease	144	231	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02790.1	000633	3′-5′-exoribonuclease	159	PSA21_264	Pseudomonas phage Psa21	GCA_004340405.1
ATN94716.1	000633	3′-5′-exoribonuclease	143	SL2_139	Pseudomonas phage SL2	GCA_002956015.1
QJB22876.1	000633	3′-5′-exoribonuclease	143	fnug_233	Pseudomonas phage fnug	GCA_012837215.1
QEM41956.1	000633	3′-5′-exoribonuclease	143	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83100.1	000633	3′-5′-exoribonuclease	143	PHIKZ199	Pseudomonas virus phiKZ	GCA_000842965.1
BAS04905.1	000633	3′-5′-exoribonuclease	433	AVU11_gp113	Ralstonia phage RSF1	GCA_001500875.1
BAQ02632.1	000633	3′-5′-exoribonuclease	409	AVU38_gp104	Ralstonia phage RSL2	GCA_001503055.1
QGT54670.1	000633	3′-5′-exoribonuclease	156	b23_0042	Synechococcus phage B23	GCA_009745195.1
QGT54300.1	000633	3′-5′-exoribonuclease	156	b3_0042	Synechococcus phage B3	GCA_009745215.1
APU01428.1	000634	REase-MmcB-like	190	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28761.1	000634	REase-MmcB-like	201	AP1_0043	Aeromonas phage AP1	GCA_014183365.1
ATI17470.1	000634	REase-MmcB-like	201	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00527.1	000634	REase-MmcB-like	201	HWB28_gp025	Aeromonas phage AS-zj	GCA_002627665.1
AUE22576.1	000634	REase-MmcB-like	166	Ah1_00035	Aeromonas phage Ah1	GCA_002957415.1
QAX98612.1	000634	REase-MmcB-like	166	ASfcp2_279	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97910.1	000634	REase-MmcB-like	201	ASswx1_267	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01240.1	000634	REase-MmcB-like	198	ASwh1_175	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39402.1	000634	REase-MmcB-like	201	CC2_265	Aeromonas phage CC2	GCA_000903495.1
ADQ52749.1	000634	REase-MmcB-like	166	PX29p030	Aeromonas phage PX29	GCA_000920195.1
ADM80005.1	000634	REase-MmcB-like	168	phiAS5_ORF0162	Aeromonas phage phiAS5	GCA_000887715.1
AAR90901.1	000634	REase-MmcB-like	190	65p037	Aeromonas virus 65	GCA_000893255.1
AAQ17691.1	000634	REase-MmcB-like	166	Aeh1ORF033c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64206.1	000634	REase-MmcB-like	182	KVP40.0135	Vibrio phage KVP40	GCA_000843785.1
QIW90520.1	000634	REase-MmcB-like	182	GCAPEGMB_00173	Vibrio phage V07	GCA_012361095.1
QIW90902.1	000634	REase-MmcB-like	182	COHAPHLL_00039	Vibrio phage V09	GCA_012361135.1
QHJ74316.1	000634	REase-MmcB-like	182	VH12019_00397	Vibrio phage VH1_2019	GCA_009931825.1
AGB06810.1	000634	REase-MmcB-like	183	CF80_gp023	Vibrio phage VH7D	GCA_000914495.1
QBX05955.1	000634	REase-MmcB-like	183	ValB1HC_001	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60967.1	000634	REase-MmcB-like	183	AVU32_gp126	Vibrio phage ValKK3	GCA_001501635.1
AGN30183.1	000634	REase-MmcB-like	179	VPFG_00183	Vibrio phage nt-1	GCA_000910195.2
ALP47084.1	000634	REase-MmcB-like	183	phiGrn1_0246	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47466.1	000634	REase-MmcB-like	183	phiST2_0001	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54580.1	000634	REase-MmcB-like	183	vBValMR10Z_39	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07120.1	000634	REase-MmcB-like	176	VmeM32_00133	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37366.1	000634	REase-MmcB-like	179	pp2_133	Vibriophage phi-pp2	GCA_002630725.1
APU01712.1	000635	Uri-nuclease-RE_Eco29kI	122	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28911.1	000635	Uri-nuclease-RE_Eco29kI	121	AP1_0204	Aeromonas phage AP1	GCA_014183365.1
ATI17584.1	000635	Uri-nuclease-RE_Eco29kI	121	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00413.1	000635	Uri-nuclease-RE_Eco29kI	121	HWB28_gp139	Aeromonas phage AS-zj	GCA_002627665.1
AUE22840.1	000635	Uri-nuclease-RE_Eco29kI	145	Ah1_00322	Aeromonas phage Ah1	GCA_002957415.1
QAX98553.1	000635	Uri-nuclease-RE_Eco29kI	145	ASfcp2_218	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98023.1	000635	Uri-nuclease-RE_Eco29kI	121	ASswx1_383	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39496.1	000635	Uri-nuclease-RE_Eco29kI	121	CC2_149	Aeromonas phage CC2	GCA_000903495.1
ADQ53017.1	000635	Uri-nuclease-RE_Eco29kI	145	PX29p298	Aeromonas phage PX29	GCA_000920195.1
ADM79941.1	000635	Uri-nuclease-RE_Eco29kI	145	phiAS5_ORF0098	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53351.1	000635	Uri-nuclease-RE_Eco29kI	122	65p343	Aeromonas virus 65	GCA_000893255.1
AAQ17970.1	000635	Uri-nuclease-RE_Eco29kI	145	denA	Aeromonas virus Aeh1	GCA_000843245.1
ANS06058.1	000635	Uri-nuclease-RE_Eco29kI	136	ABCD_0066	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64820.1	000635	Uri-nuclease-RE_Eco29kI	121	S13_021	Cronobacter phage S13	GCA_001503575.1
AON97078.1	000635	Uri-nuclease-RE_Eco29kI	128	E_069	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70784.1	000635	Uri-nuclease-RE_Eco29kI	136	phiC120_c78	Escherichia phage phiC120	GCA_002621185.1
AAX78589.1	000635	Uri-nuclease-RE_Eco29kI	135	RB43ORF067w	Escherichia virus RB43	GCA_000863505.1
QHJ78843.1	000635	Uri-nuclease-RE_Eco29kI	149	-	Myoviridae sp.	GCA_012593985.1
ALY07153.1	000635	Uri-nuclease-RE_Eco29kI	123	VmeM32_00167	Vibrio phage vB_VmeM-32	GCA_002608825.1
AOO14365.1	000636	AbrB-family-half-barrel	111	Sn110110_171	Cyanophage S-RIM14	GCA_002599065.1
AOO15013.1	000636	AbrB-family-half-barrel	111	W1230910_167	Cyanophage S-RIM14	GCA_002599125.1
AMO43448.1	000636	AbrB-family-half-barrel	120	W270710_209	Cyanophage S-RIM44	GCA_002599145.1
AOO11689.1	000636	AbrB-family-half-barrel	95	ES420910_212	Cyanophage S-RIM44	GCA_002599165.1
AOO11920.1	000636	AbrB-family-half-barrel	120	Np050604_209	Cyanophage S-RIM44	GCA_002599185.1
AOO12155.1	000636	AbrB-family-half-barrel	95	Np200711_213	Cyanophage S-RIM44	GCA_002599205.1
AOO12390.1	000636	AbrB-family-half-barrel	95	Np420711_212	Cyanophage S-RIM44	GCA_002599225.1
AOO12621.1	000636	AbrB-family-half-barrel	120	Sn080709_209	Cyanophage S-RIM44	GCA_002599245.1
AOO12855.1	000636	AbrB-family-half-barrel	95	Sn130910_212	Cyanophage S-RIM44	GCA_002599265.1
AOO13087.1	000636	AbrB-family-half-barrel	120	W2100709_210	Cyanophage S-RIM44	GCA_002599285.1
ADO99308.1	000636	AbrB-family-half-barrel	120	Syn1_212	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30620.1	000636	AbrB-family-half-barrel	86	Syn7803US37_143	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76120.1	000636	AbrB-family-half-barrel	100	PBI_BELLAMY_75	Synechococcus phage Bellamy	GCA_002627525.1
QCW22897.1	000636	AbrB-family-half-barrel	105	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50663.1	000636	AbrB-family-half-barrel	105	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59668.1	000636	AbrB-family-half-barrel	116	S330809_207	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59430.1	000636	AbrB-family-half-barrel	116	C440309_207	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59905.1	000636	AbrB-family-half-barrel	116	N231010_206	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70500.1	000636	AbrB-family-half-barrel	116	HOU04_gp101	Synechococcus phage S-T4	GCA_003443335.1
AFC21584.1	000637	DEAM	119	GAP32_134	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14380.1	000637	DEAM	122	PBI_121Q_490	Escherichia phage 121Q	GCA_000926855.1
QAY00568.1	000637	DEAM	122	Ecwhy1_289	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34760.1	000637	DEAM	122	ACQ29_gp080	Escherichia phage PBECO4	GCA_001041035.1
BBM62051.1	000637	DEAM	122	EO157G_4620	Escherichia phage SP27	GCA_008033345.1
AXC36875.1	000637	DEAM	108	-	Escherichia phage UB	GCA_003341455.1
QBO61922.1	000637	DEAM	122	G17_00433	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13954.1	000637	DEAM	122	vBEcoMphAPEC6_gp330c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80369.1	000637	DEAM	122	PSLUR01_00392	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44791.1	000637	DEAM	122	RaK2_00518	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43700.1	000637	DEAM	121	CBB_135	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ANM45072.1	000637	DEAM	119	KTN4_314	Pseudomonas phage KTN4	GCA_002607225.1
ATN94643.1	000637	DEAM	119	SL2_066	Pseudomonas phage SL2	GCA_002956015.1
QJB22947.1	000637	DEAM	119	fnug_304	Pseudomonas phage fnug	GCA_012837215.1
AAL83161.1	000637	DEAM	119	PHIKZ260	Pseudomonas virus phiKZ	GCA_000842965.1
ASV44125.1	000637	DEAM	125	PBI_SCTP2_110	Salicola phage SCTP-2	GCA_002625545.1
QCW18841.1	000637	DEAM	124	7t3_0320	Salmonella phage 7t3	GCA_006083215.1
AZU98103.1	000637	DEAM	124	CPT_Munch_159	Salmonella phage Munch	GCA_004015485.1
QIG62879.1	000637	DEAM	124	SEPL_266	Salmonella phage SE_PL	GCA_011067555.1
AQW88656.1	000637	DEAM	129	BF_0131	Serratia phage BF	GCA_002619745.1
AIX30521.1	000637	DEAM	122	Syn7803US37_44	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54807.1	000637	DEAM	141	b23_0192	Synechococcus phage B23	GCA_009745195.1
QGT54437.1	000637	DEAM	141	b3_0194	Synechococcus phage B3	GCA_009745215.1
SOK58937.1	000637	DEAM	121	g129	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58402.1	000637	DEAM	122	g125	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44751.1	000638	35exo	263	FDI40_gp671	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21725.1	000638	35exo	281	GAP32_275	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13906.1	000638	35exo	272	PBI_121Q_9	Escherichia phage 121Q	GCA_000926855.1
QAY00431.1	000638	35exo	272	Ecwhy1_151	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35175.1	000638	35exo	272	ACQ29_gp495	Escherichia phage PBECO4	GCA_001041035.1
BBM61598.1	000638	35exo	272	EO157G_0090	Escherichia phage SP27	GCA_008033345.1
AXC36747.1	000638	35exo	272	-	Escherichia phage UB	GCA_003341455.1
QBO61786.1	000638	35exo	272	G17_00297	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13830.1	000638	35exo	272	vBEcoMphAPEC6_gp201c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80501.1	000638	35exo	272	PSLUR01_00524	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44390.1	000638	35exo	273	RaK2_00117	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43844.1	000638	35exo	281	CBB_280	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76151.1	000638	35exo	257	EST35_0270	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW19003.1	000638	35exo	272	7t3_0483	Salmonella phage 7t3	GCA_006083215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AZU98250.1	000638	35exo	272	CPT_Munch_306	Salmonella phage Munch	GCA_004015485.1
QIG62734.1	000638	35exo	272	SEPL_121	Salmonella phage SE_PL	GCA_011067555.1
AQW88803.1	000638	35exo	290	BF_0278	Serratia phage BF	GCA_002619745.1
SOK59086.1	000638	35exo	279	g278	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58550.1	000638	35exo	279	g273	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13733.1	000639	HNH	207	Ccr10_gp203c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13841.1	000639	HNH	206	Ccr10_gp311	Caulobacter phage Ccr10	GCA_002619445.1
ARB14078.1	000639	HNH	207	Ccr2_gp202c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14186.1	000639	HNH	206	Ccr2_gp310	Caulobacter phage Ccr2	GCA_002619465.1
ARB14767.1	000639	HNH	207	Ccr29_gp211	Caulobacter phage Ccr29	GCA_002619485.1
ARB14880.1	000639	HNH	206	Ccr29_gp324	Caulobacter phage Ccr29	GCA_002619485.1
ARB15111.1	000639	HNH	207	Ccr32_gp193	Caulobacter phage Ccr32	GCA_002619505.1
ARB15218.1	000639	HNH	206	Ccr32_gp300	Caulobacter phage Ccr32	GCA_002619505.1
ARB15445.1	000639	HNH	207	Ccr34_gp203	Caulobacter phage Ccr34	GCA_002619525.1
ARB15552.1	000639	HNH	206	Ccr34_gp310	Caulobacter phage Ccr34	GCA_002619525.1
ARB14420.1	000639	HNH	244	Ccr5_gp200c	Caulobacter phage Ccr5	GCA_002619545.1
ARB14527.1	000639	HNH	206	Ccr5_gp307	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68400.1	000639	HNH	184	CcrBL10_gp196c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68507.1	000639	HNH	206	CcrBL10_gp303	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87726.1	000639	HNH	244	CcrKarma_gp209	Caulobacter virus Karma	GCA_000901575.1
AFU87838.1	000639	HNH	206	CcrKarma_gp321	Caulobacter virus Karma	GCA_000901575.1
AFU87375.1	000639	HNH	244	CcrMagneto_gp205	Caulobacter virus Magneto	GCA_000903095.1
AFU87485.1	000639	HNH	206	CcrMagneto_gp315	Caulobacter virus Magneto	GCA_000903095.1
AFU86686.1	000639	HNH	221	CcrRogue_gp204	Caulobacter virus Rogue	GCA_000900555.1
AFU86795.1	000639	HNH	207	CcrRogue_gp313	Caulobacter virus Rogue	GCA_000900555.1
AFU88522.1	000639	HNH	244	CcrSwift_gp204	Caulobacter virus Swift	GCA_000899655.1
AFU88630.1	000639	HNH	206	CcrSwift_gp312	Caulobacter virus Swift	GCA_000899655.1
AFU87030.1	000639	HNH	244	CbK_gp198	Caulobacter virus phiCbK	GCA_000900535.1
AFU87137.1	000639	HNH	206	CbK_gp305	Caulobacter virus phiCbK	GCA_000900535.1
ASV44726.1	000640	HNH	185	FDI40_gp252	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83799.2	000640	HNH	169	0305phi8-36p239	Bacillus phage 0305phi8-36	GCA_000871045.1
QIG57862.1	000640	HNH	157	SEA_PAULODIABOLI_157	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57913.1	000640	HNH	138	SEA_PAULODIABOLI_228	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57981.1	000640	HNH	154	SEA_PAULODIABOLI_297	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72848.1	000640	HNH	177	-	Myoviridae sp.	GCA_003657725.1
AXH72922.1	000640	HNH	182	-	Myoviridae sp.	GCA_003657725.1
AXH72896.1	000640	HNH	226	-	Myoviridae sp.	GCA_003657725.1
QIG65829.1	000640	HNH	185	phiOC_p164	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AAX44669.1	000640	HNH	123	PSSM2_292	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12308.1	000640	HNH	123	PRTG_00155	Prochlorococcus phage P-SSM5	GCA_002991095.1
QCG76227.1	000640	HNH	200	EST35_0346	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44375.1	000640	HNH	186	PBI_SCTP2_360	Salicola phage SCTP-2	GCA_002625545.1
AGR48044.2	000640	HNH	99	SmphiM12_412	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13228.1	000640	HNH	99	PHIM19_323	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12868.1	000640	HNH	99	PHIM7_323	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13591.1	000640	HNH	119	PHIN3_328	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30744.1	000640	HNH	124	Syn7803US37_267	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54656.1	000640	HNH	158	b23_0028	Synechococcus phage B23	GCA_009745195.1
QGT54286.1	000640	HNH	158	b3_0028	Synechococcus phage B3	GCA_009745215.1
AUZ95224.1	000641	Tox-HNH	202	FDI40_gp465	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44700.1	000641	Tox-HNH	220	FDI40_gp090	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95219.1	000641	Tox-HNH	254	FDI40_gp460	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83771.1	000641	Tox-HNH	139	0305phi8-36p213	Bacillus phage 0305phi8-36	GCA_000871045.1
AFC21824.1	000641	Tox-HNH	229	GAP32_373	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG65914.1	000641	Tox-HNH	231	phiOC_p261	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QBX32539.1	000641	Tox-HNH	185	-	Pseudomonas phage PA1C	GCA_004785505.1
QBJ02936.1	000641	Tox-HNH	188	PSA21_414	Pseudomonas phage Psa21	GCA_004340405.1
AAL83197.1	000641	Tox-HNH	160	PHIKZ296	Pseudomonas virus phiKZ	GCA_000842965.1
ASV44380.1	000641	Tox-HNH	229	PBI_SCTP2_365	Salicola phage SCTP-2	GCA_002625545.1
ASV44508.1	000641	Tox-HNH	283	PBI_SCTP2_493	Salicola phage SCTP-2	GCA_002625545.1
QCW18564.1	000641	Tox-HNH	270	7t3_043	Salmonella phage 7t3	GCA_006083215.1
QCW19103.1	000641	Tox-HNH	172	7t3_0586	Salmonella phage 7t3	GCA_006083215.1
AZU98393.1	000641	Tox-HNH	270	CPT_Munch_461	Salmonella phage Munch	GCA_004015485.1
QIG62642.1	000641	Tox-HNH	172	SEPL_029	Salmonella phage SE_PL	GCA_011067555.1
QIG63120.1	000641	Tox-HNH	270	SEPL_507	Salmonella phage SE_PL	GCA_011067555.1
SOK59248.1	000641	Tox-HNH	210	g440	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58672.1	000641	Tox-HNH	160	g395	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58713.1	000641	Tox-HNH	210	g436	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ94996.1	000642	KptA-ART	414	FDI40_gp214	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21699.1	000642	KptA-ART	375	GAP32_249	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14492.1	000642	KptA-ART	371	PBI_121Q_602	Escherichia phage 121Q	GCA_000926855.1
QAY00457.1	000642	KptA-ART	371	Ecwhy1_177	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35199.1	000642	KptA-ART	371	ACQ29_gp519	Escherichia phage PBECO4	GCA_001041035.1
BBM62164.1	000642	KptA-ART	371	EO157G_5750	Escherichia phage SP27	GCA_008033345.1
AXC36771.1	000642	KptA-ART	371	-	Escherichia phage UB	GCA_003341455.1
QBO61811.1	000642	KptA-ART	371	G17_00322	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13855.1	000642	KptA-ART	371	vBEcoMphAPEC6_gp226c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80476.1	000642	KptA-ART	371	PSLUR01_00499	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44366.1	000642	KptA-ART	370	RaK2_00093	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72800.1	000642	KptA-ART	464	-	Myoviridae sp.	GCA_003657725.1
AMM43820.1	000642	KptA-ART	374	CBB_256	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76035.1	000642	KptA-ART	368	EST35_0153	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44109.1	000642	KptA-ART	448	PBI_SCTP2_94	Salicola phage SCTP-2	GCA_002625545.1
QCW18976.1	000642	KptA-ART	372	7t3_0455	Salmonella phage 7t3	GCA_006083215.1
AZU98226.1	000642	KptA-ART	372	CPT_Munch_282	Salmonella phage Munch	GCA_004015485.1
QIG62759.1	000642	KptA-ART	372	SEPL_146	Salmonella phage SE_PL	GCA_011067555.1
AQW88779.1	000642	KptA-ART	374	BF_0254	Serratia phage BF	GCA_002619745.1
BBA65423.1	000642	KptA-ART	318	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96444.1	000642	KptA-ART	318	Xoosp13_258	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59060.1	000642	KptA-ART	374	g252	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58526.1	000642	KptA-ART	374	g249	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21754.1	000643	MazG-Phage	238	GAP32_304	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13934.1	000643	MazG-Phage	245	PBI_121Q_37	Escherichia phage 121Q	GCA_000926855.1
QAY00403.1	000643	MazG-Phage	244	Ecwhy1_122	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35147.1	000643	MazG-Phage	243	ACQ29_gp467	Escherichia phage PBECO4	GCA_001041035.1
BBM61626.1	000643	MazG-Phage	243	EO157G_0370	Escherichia phage SP27	GCA_008033345.1
AXC36720.1	000643	MazG-Phage	243	-	Escherichia phage UB	GCA_003341455.1
QBO61759.1	000643	MazG-Phage	243	G17_00270	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13803.1	000643	MazG-Phage	243	vBEcoMphAPEC6_gp174c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80528.1	000643	MazG-Phage	243	PSLUR01_00551	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44417.1	000643	MazG-Phage	246	RaK2_00144	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43872.1	000643	MazG-Phage	238	CBB_309	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19031.1	000643	MazG-Phage	230	7t3_0511	Salmonella phage 7t3	GCA_006083215.1
AZU98278.1	000643	MazG-Phage	230	CPT_Munch_334	Salmonella phage Munch	GCA_004015485.1
QIG62706.1	000643	MazG-Phage	230	SEPL_093	Salmonella phage SE_PL	GCA_011067555.1
AQW88831.1	000643	MazG-Phage	234	BF_0306	Serratia phage BF	GCA_002619745.1
SOK59115.1	000643	MazG-Phage	234	g307	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58581.1	000643	MazG-Phage	234	g304	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44744.2	000644	pyrophosphatase_MazG	135	FDI40_gp319	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83581.1	000644	pyrophosphatase_MazG	117	0305phi8-36p016	Bacillus phage 0305phi8-36	GCA_000871045.1
AGH56849.1	000644	pyrophosphatase_MazG	180	CPXG_00046	Cyanophage P-RSM6	GCA_000906155.1
AJK27644.1	000644	pyrophosphatase_MazG	223	PTIM40_179	Cyanophage P-TIM40	GCA_001470935.1
AOO14363.1	000644	pyrophosphatase_MazG	133	Sn110110_169	Cyanophage S-RIM14	GCA_002599065.1
AOO15012.1	000644	pyrophosphatase_MazG	133	W1230910_166	Cyanophage S-RIM14	GCA_002599125.1
AMO43173.1	000644	pyrophosphatase_MazG	135	R1080702_164	Cyanophage S-RIM32	GCA_001754165.1
AMO43399.1	000644	pyrophosphatase_MazG	135	W270710_155	Cyanophage S-RIM44	GCA_002599145.1
AOO11643.1	000644	pyrophosphatase_MazG	135	ES420910_162	Cyanophage S-RIM44	GCA_002599165.1
AOO11871.1	000644	pyrophosphatase_MazG	135	Np050604_155	Cyanophage S-RIM44	GCA_002599185.1
AOO12109.1	000644	pyrophosphatase_MazG	135	Np200711_163	Cyanophage S-RIM44	GCA_002599205.1
AOO12344.1	000644	pyrophosphatase_MazG	135	Np420711_162	Cyanophage S-RIM44	GCA_002599225.1
AOO12572.1	000644	pyrophosphatase_MazG	135	Sn080709_155	Cyanophage S-RIM44	GCA_002599245.1
AOO12809.1	000644	pyrophosphatase_MazG	135	Sn130910_162	Cyanophage S-RIM44	GCA_002599265.1
AOO13038.1	000644	pyrophosphatase_MazG	135	W2100709_156	Cyanophage S-RIM44	GCA_002599285.1
AGH07504.1	000644	pyrophosphatase_MazG	134	CYVG_00060	Cyanophage S-SSM6a	GCA_002710385.1
AGG54446.1	000644	pyrophosphatase_MazG	154	CYWG_00162	Cyanophage S-SSM6b	GCA_002710425.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH26283.1	000644	pyrophosphatase_MazG	136	CPMG_00183	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44566.1	000644	pyrophosphatase_MazG	138	PSSM2_188	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12407.1	000644	pyrophosphatase_MazG	138	PRTG_00254	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93491.1	000644	pyrophosphatase_MazG	136	AVU42_gp154	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99258.1	000644	pyrophosphatase_MazG	135	Syn1_157	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76159.1	000644	pyrophosphatase_MazG	135	EST35_0278	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AIX30656.1	000644	pyrophosphatase_MazG	134	Syn7803US37_179	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54919.1	000644	pyrophosphatase_MazG	135	b23_0306	Synechococcus phage B23	GCA_009745195.1
QGT54554.1	000644	pyrophosphatase_MazG	135	b3_0313	Synechococcus phage B3	GCA_009745215.1
ASR76211.1	000644	pyrophosphatase_MazG	134	PBI_BELLAMY_167	Synechococcus phage Bellamy	GCA_002627525.1
QCW22931.1	000644	pyrophosphatase_MazG	135	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50616.1	000644	pyrophosphatase_MazG	135	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59625.1	000644	pyrophosphatase_MazG	134	S330809_164	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59387.1	000644	pyrophosphatase_MazG	134	C440309_164	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59863.1	000644	pyrophosphatase_MazG	134	N231010_164	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70540.1	000644	pyrophosphatase_MazG	135	HOU04_gp141	Synechococcus phage S-T4	GCA_003443335.1
QJT70164.1	000644	pyrophosphatase_MazG	136	SynMITS9220M01_151	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFC21552.1	000645	MazG-Cluster592_1clades	95	GAP32_104	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14355.1	000645	MazG-Cluster592_1clades	96	PBI_121Q_465	Escherichia phage 121Q	GCA_000926855.1
QAY00589.1	000645	MazG-Cluster592_1clades	96	Ecwhy1_312	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34784.1	000645	MazG-Cluster592_1clades	96	ACQ29_gp104	Escherichia phage PBECO4	GCA_001041035.1
BBM62026.1	000645	MazG-Cluster592_1clades	96	EO157G_4370	Escherichia phage SP27	GCA_008033345.1
AXC36900.1	000645	MazG-Cluster592_1clades	96	-	Escherichia phage UB	GCA_003341455.1
QBO61949.1	000645	MazG-Cluster592_1clades	96	G17_00460	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13976.1	000645	MazG-Cluster592_1clades	96	vBEcoMphAPEC6_gp352c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80342.1	000645	MazG-Cluster592_1clades	96	PSLUR01_00365	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44763.1	000645	MazG-Cluster592_1clades	93	RaK2_00490	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43670.1	000645	MazG-Cluster592_1clades	95	CBB_105	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18805.1	000645	MazG-Cluster592_1clades	97	7t3_0284	Salmonella phage 7t3	GCA_006083215.1
AZU98070.1	000645	MazG-Cluster592_1clades	97	CPT_Munch_126	Salmonella phage Munch	GCA_004015485.1
QIG62912.1	000645	MazG-Cluster592_1clades	97	SEPL_299	Salmonella phage SE_PL	GCA_011067555.1
AQW88623.1	000645	MazG-Cluster592_1clades	95	BF_0098	Serratia phage BF	GCA_002619745.1
SOK58899.1	000645	MazG-Cluster592_1clades	95	g091	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58364.1	000645	MazG-Cluster592_1clades	95	g087	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67088.1	000646	MazG	216	AD1_044	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79832.1	000646	MazG	215	JA11_027	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66431.1	000646	MazG	215	JA13_028	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66755.1	000646	MazG	215	JA29_029	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67401.1	000646	MazG	215	JA33_027	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08322.1	000646	MazG	218	Alexandra_42	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58686.1	000646	MazG	215	Y3_046	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28524.1	000646	MazG	212	YOLOSWAG_39	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXH71027.1	000647	MazG-Phage	236	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96820.1	000647	MazG-Phage	239	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97139.1	000647	MazG-Phage	239	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96185.1	000647	MazG-Phage	239	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96503.1	000647	MazG-Phage	239	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21273.1	000647	MazG-Phage	242	-	Vibrio phage vB_pir03	GCA_014319855.1
AFC21579.1	000648	MazG	204	GAP32_129	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43695.1	000648	MazG	204	CBB_130	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88648.1	000648	MazG	204	BF_0123	Serratia phage BF	GCA_002619745.1
SOK58928.1	000648	MazG	91	g120	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58393.1	000648	MazG	91	g116	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AND75241.1	000649	MazG-Phage	168	ME3_80	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXH72811.1	000649	MazG-Phage	128	-	Myoviridae sp.	GCA_003657725.1
BBI90534.1	000649	MazG-Phage	150	HYO65_gp142	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90842.1	000649	MazG-Phage	150	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06514.1	000650	MazG-Phage	319	BcepSaruman_101	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74480.1	000650	MazG-Phage	332	BcepSauron_100	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41551.1	000650	MazG-Phage	276	RSL1_ORF107	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44488.1	000651	MazG	185	PBI_SCTP2_473	Salicola phage SCTP-2	GCA_002625545.1
BBA65343.1	000651	MazG	200	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96380.1	000651	MazG	207	Xoosp13_194	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXQ69115.1	000652	SIG+MazG	249	CcrBL9_gp091	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69669.1	000652	SIG+MazG	250	CcrSC_gp087	Caulobacter phage CcrSC	GCA_003443315.1
AYD81376.1	000653	MazG	137	SEA_JUSTBECAUSE_221	Streptomyces phage JustBecause	GCA_003613775.1
QJD53779.1	000653	MazG	137	SEA_KELA_219	Streptomyces phage Kela	GCA_012934305.1
AFC21753.1	000654	Cluster572_1clades	126	GAP32_303	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13933.1	000654	Cluster572_1clades	131	PBI_121Q_36	Escherichia phage 121Q	GCA_000926855.1
QAY00404.1	000654	Cluster572_1clades	131	Ecwhy1_123	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35148.1	000654	Cluster572_1clades	134	ACQ29_gp468	Escherichia phage PBECO4	GCA_001041035.1
BBM61625.1	000654	Cluster572_1clades	131	EO157G_0360	Escherichia phage SP27	GCA_008033345.1
AXC36721.1	000654	Cluster572_1clades	131	-	Escherichia phage UB	GCA_003341455.1
QBO61760.1	000654	Cluster572_1clades	131	G17_00271	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13804.1	000654	Cluster572_1clades	131	vBEcoMphAPEC6_gp175c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80527.1	000654	Cluster572_1clades	131	PSLUR01_00550	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44416.1	000654	Cluster572_1clades	127	RaK2_00143	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43871.1	000654	Cluster572_1clades	126	CBB_308	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19030.1	000654	Cluster572_1clades	130	7t3_0510	Salmonella phage 7t3	GCA_006083215.1
AZU98277.1	000654	Cluster572_1clades	130	CPT_Munch_333	Salmonella phage Munch	GCA_004015485.1
QIG62707.1	000654	Cluster572_1clades	130	SEPL_094	Salmonella phage SE_PL	GCA_011067555.1
AQW88830.1	000654	Cluster572_1clades	125	BF_0305	Serratia phage BF	GCA_002619745.1
SOK59114.1	000654	Cluster572_1clades	125	g306	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58580.1	000654	Cluster572_1clades	125	g303	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AEO93638.1	000655	MYB	255	G_379	Bacillus virus G	GCA_000917535.1
AEO93782.1	000655	MYB	342	G_524	Bacillus virus G	GCA_000917535.1
AEO93876.1	000655	MYB	185	G_631	Bacillus virus G	GCA_000917535.1
AEO93355.1	000655	MYB	191	G_84	Bacillus virus G	GCA_000917535.1
AEO93356.1	000655	MYB	121	G_85	Bacillus virus G	GCA_000917535.1
ABS83629.1	000655	MYB	177	0305phi8-36p069	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93544.1	000000	MYB+SWIM	233	G_285	Bacillus virus G	GCA_000917535.1
AEO93580.1	000000	MYB+Seadorna_VP6	201	G_321	Bacillus virus G	GCA_000917535.1
AEO93300.1	000000	SIG+ZNR	61	G_29	Bacillus virus G	GCA_000917535.1
AEO93701.1	000000	SIG+ZNR	74	G_443	Bacillus virus G	GCA_000917535.1
AFC21711.1	000656	Ruc-ZnR	69	GAP32_261	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14504.1	000656	Ruc-ZnR	68	PBI_121Q_614	Escherichia phage 121Q	GCA_000926855.1
QAY00445.1	000656	Ruc-ZnR	68	Ecwhy1_165	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35188.1	000656	Ruc-ZnR	68	ACQ29_gp508	Escherichia phage PBECO4	GCA_001041035.1
BBM62176.1	000656	Ruc-ZnR	68	EO157G_5870	Escherichia phage SP27	GCA_008033345.1
AXC36760.1	000656	Ruc-ZnR	68	-	Escherichia phage UB	GCA_003341455.1
QBO61799.1	000656	Ruc-ZnR	68	G17_00310	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13843.1	000656	Ruc-ZnR	68	vBEcoMphAPEC6_gp214c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80488.1	000656	Ruc-ZnR	68	PSLUR01_00511	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44376.1	000656	Ruc-ZnR	68	RaK2_00103	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43831.1	000656	Ruc-ZnR	69	CBB_267	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18990.1	000656	Ruc-ZnR	67	7t3_0469	Salmonella phage 7t3	GCA_006083215.1
AZU98238.1	000656	Ruc-ZnR	67	CPT_Munch_294	Salmonella phage Munch	GCA_004015485.1
QIG62746.1	000656	Ruc-ZnR	67	SEPL_133	Salmonella phage SE_PL	GCA_011067555.1
AQW88790.1	000656	Ruc-ZnR	69	BF_0265	Serratia phage BF	GCA_002619745.1
SOK59071.1	000656	Ruc-ZnR	69	g263	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58537.1	000656	Ruc-ZnR	69	g260	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21762.1	000657	Mrr_N	64	GAP32_312	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13943.1	000657	Mrr_N	64	PBI_121Q_46	Escherichia phage 121Q	GCA_000926855.1
QAY00394.1	000657	Mrr_N	64	Ecwhy1_113	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35139.1	000657	Mrr_N	64	ACQ29_gp459	Escherichia phage PBECO4	GCA_001041035.1
BBM61635.1	000657	Mrr_N	64	EO157G_0460	Escherichia phage SP27	GCA_008033345.1
AXC36713.1	000657	Mrr_N	64	-	Escherichia phage UB	GCA_003341455.1
QBO61750.1	000657	Mrr_N	64	G17_00261	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13795.1	000657	Mrr_N	64	vBEcoMphAPEC6_gp166c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80537.1	000657	Mrr_N	64	PSLUR01_00560	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44425.1	000657	Mrr_N	62	RaK2_00152	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43880.1	000657	Mrr_N	64	CBB_317	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19040.1	000657	Mrr_N	65	7t3_0520	Salmonella phage 7t3	GCA_006083215.1
AZU98287.1	000657	Mrr_N	65	CPT_Munch_343	Salmonella phage Munch	GCA_004015485.1
QIG62697.1	000657	Mrr_N	65	SEPL_084	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQW88840.1	000657	Mrr_N	64	BF_0315	Serratia phage BF	GCA_002619745.1
SOK59124.1	000657	Mrr_N	64	g316	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58590.1	000657	Mrr_N	64	g313	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBX06634.1	000658	HD	234	BcepSaruman_221	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74603.1	000658	HD	234	BcepSauron_223	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67340.1	000658	HD	313	AD1_296	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80092.1	000658	HD	235	JA11_287	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66693.1	000658	HD	235	JA13_290	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67012.1	000658	HD	235	JA29_286	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67662.1	000658	HD	235	JA33_288	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08568.1	000658	HD	313	Alexandra_315	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58943.1	000658	HD	313	Y3_303	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28768.1	000658	HD	256	YOLOSWAG_298	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFH14819.1	000658	HD	221	Lu11_0281	Pseudomonas phage Lu11	GCA_000897175.1
ARV77442.1	000658	HD	229	NOXIFER_277	Pseudomonas phage Noxifer	GCA_002625005.1
AGS81941.1	000658	HD	249	PaBG_00057	Pseudomonas phage PaBG	GCA_000912555.1
BAG41490.1	000658	HD	270	RSL1_ORF045	Ralstonia phage phiRSL1	GCA_000879455.1
prevph1000000779	000658	HD	227	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000532	000658	HD	227	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ARB13594.1	000659	Tox-HNH	159	Ccr10_gp066	Caulobacter phage Ccr10	GCA_002619445.1
ARB13940.1	000659	Tox-HNH	159	Ccr2_gp065	Caulobacter phage Ccr2	GCA_002619465.1
ARB14629.1	000659	Tox-HNH	159	Ccr29_gp072	Caulobacter phage Ccr29	GCA_002619485.1
ARB14985.1	000659	Tox-HNH	160	Ccr32_gp066	Caulobacter phage Ccr32	GCA_002619505.1
ARB15316.1	000659	Tox-HNH	160	Ccr34_gp067	Caulobacter phage Ccr34	GCA_002619525.1
ARB14283.1	000659	Tox-HNH	177	Ccr5_gp065	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68267.1	000659	Tox-HNH	58	CcrBL10_gp063	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69140.1	000659	Tox-HNH	152	CcrBL9_gp116	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87949.1	000659	Tox-HNH	179	CcrColossus_gp079	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ69694.1	000659	Tox-HNH	152	CcrSC_gp112	Caulobacter phage CcrSC	GCA_003443315.1
AFU87584.1	000659	Tox-HNH	102	CcrKarma_gp067	Caulobacter virus Karma	GCA_000901575.1
AFU87234.1	000659	Tox-HNH	159	CcrMagneto_gp064	Caulobacter virus Magneto	GCA_000903095.1
AFU86550.1	000659	Tox-HNH	160	CcrRogue_gp068	Caulobacter virus Rogue	GCA_000900555.1
AFU88382.1	000659	Tox-HNH	160	CcrSwift_gp064	Caulobacter virus Swift	GCA_000899655.1
AFU86898.1	000659	Tox-HNH	160	CbK_gp066	Caulobacter virus phiCbK	GCA_000900535.1
AXG67222.1	000660	HNH	121	AD1_178	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79972.1	000660	HNH	119	JA11_167	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66570.1	000660	HNH	119	JA13_167	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66895.1	000660	HNH	119	JA29_169	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67541.1	000660	HNH	119	JA33_167	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08451.1	000660	HNH	121	Alexandra_183	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58819.1	000660	HNH	121	Y3_179	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28653.1	000660	HNH	119	YOLOSWAG_174	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38489.1	000660	HNH	134	BN7874_275	Phage NCTB	GCA_900092385.1
AFH14634.1	000660	HNH	120	Lu11_0102	Pseudomonas phage Lu11	GCA_000897175.1
QKE11217.1	000660	HNH	124	PaBG_00199	Pseudomonas phage PaBG	GCA_000912555.1
QBO63911.1	000661	DUF2089-HTH	155	Goslar_00118	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63912.1	000661	DUF2089-HTH	106	Goslar_00119	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63908.1	000661	DUF2089-HTH	176	Goslar_00115	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63909.1	000661	DUF2089-HTH	167	Goslar_00116	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63910.1	000661	DUF2089-HTH	167	Goslar_00117	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63907.1	000661	DUF2089-HTH	147	Goslar_00114	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDB70302.1	000662	LRR	1306	CF8_0134	Aeromonas phage CF8	GCA_006384595.2
QDJ97279.1	000662	LRR	2042	D6_0119	Aeromonas phage D6	GCA_007051205.2
QDH47009.1	000662	LRR	2311	LAh10_51	Aeromonas phage LAh10	GCA_006863975.1
QDJ96896.1	000662	LRR	1174	PS1_0137	Aeromonas phage PS1	GCA_007051165.2
QFR59526.1	000662	LRR	1173	PS2_0135	Aeromonas phage PS2	GCA_009388305.2
QBZ70665.1	000662	LRR	1699	pETSU_084	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71981.1	000662	LRR	1965	N1M2_118	Klebsiella phage N1M2	GCA_010092605.1
AEV89582.1	000662	LRR	1713	OBP_145	Pseudomonas phage OBP	GCA_000896635.1
AFF28101.1	000662	LRR	1857	PAU_103	Sphingomonas phage PAU	GCA_000902455.1
QBO63815.1	000663	LRR	297	Goslar_00022	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63884.1	000663	LRR	175	Goslar_00091	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63886.1	000663	LRR	276	Goslar_00093	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63954.1	000663	LRR	483	Goslar_00161	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QFP93073.1	000663	LRR	491	-	Serratia phage PCH45	GCA_009187865.1
CCH63505.1	000664	LRR	178	CP21_043	Campylobacter virus CP21	GCA_000902535.1
AIX30756.1	000664	LRR	375	Syn7803US37_279	Synechococcus phage ACG-2014f	GCA_002594065.1
prev15ph1000000535	000664	LRR	492	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000786	000000	LRR	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QNI21234.1	000000	LRR	1227	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21147.1	000000	LRR	6417	-	Vibrio phage vB_pir03	GCA_014319855.1
QIG63319.1	000665	ImmLRR	2657	DAC16_86	Bacteroides phage DAC16	GCA_013387695.1
QIG63580.1	000665	ImmLRR	2657	DAC19_89	Bacteroides phage DAC19	GCA_013387715.1
QIG63841.1	000665	ImmLRR	2657	DAC20_88	Bacteroides phage DAC20	GCA_013387725.1
QIG64103.1	000665	ImmLRR	2657	DAC22_89	Bacteroides phage DAC22	GCA_013387735.1
QIG64363.1	000665	ImmLRR	2657	DAC23_85	Bacteroides phage DAC23	GCA_013387745.1
prevph1000000310	000666	ImmLRR	106	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000311	000666	ImmLRR	92	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000242	000666	ImmLRR	304	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000048	000667	ImmLRR	143	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000038	000667	ImmLRR	347	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBI90681.1	000668	LRR_8	98	HYO65_gp289	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90988.1	000668	LRR_8	55	-	Tenacibaculum phage PTm5	GCA_009730715.1
AEO93612.1	000000	IG+PTX+CotH-kinase+ImmLRR	2055	G_353	Bacillus virus G	GCA_000917535.1
APU01483.1	000669	Concanavalin-like	498	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28723.1	000669	Concanavalin-like	498	AP1_005	Aeromonas phage AP1	GCA_014183365.1
ATI17414.1	000669	Concanavalin-like	498	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00182.1	000669	Concanavalin-like	498	HWB28_gp370	Aeromonas phage AS-zj	GCA_002627665.1
AUE22744.1	000669	Concanavalin-like	523	Ah1_00226	Aeromonas phage Ah1	GCA_002957415.1
QAX98461.1	000669	Concanavalin-like	534	ASfcp2_121	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97854.1	000669	Concanavalin-like	498	ASswx1_211	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01296.1	000669	Concanavalin-like	499	ASwh1_233	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39424.1	000669	Concanavalin-like	498	CC2_323	Aeromonas phage CC2	GCA_000903495.1
ADQ52921.1	000669	Concanavalin-like	505	PX29p202	Aeromonas phage PX29	GCA_000920195.1
ADM79845.1	000669	Concanavalin-like	534	phiAS5_ORF0002	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53104.1	000669	Concanavalin-like	498	65p096	Aeromonas virus 65	GCA_000893255.1
AAP04360.1	000669	Concanavalin-like	534	Aeh1ORF207w	Aeromonas virus Aeh1	GCA_000843245.1
AIA64893.1	000669	Concanavalin-like	515	S13_094	Cronobacter phage S13	GCA_001503575.1
QHJ79046.1	000669	Concanavalin-like	517	-	Myoviridae sp.	GCA_012593985.1
ALY07236.1	000669	Concanavalin-like	416	VmeM32_00250	Vibrio phage vB_VmeM-32	GCA_002608825.1
QBX06685.1	000670	Concanavalin-like	372	BcepSaruman_272	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74655.1	000670	Concanavalin-like	149	BcepSauron_275	Burkholderia phage BcepSauron	GCA_005394215.1
QIG65831.1	000670	Concanavalin-like	591	phiOC_p166	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65968.1	000670	Concanavalin-like	547	phiOC_p326	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66001.1	000670	Concanavalin-like	322	phiOC_p359	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66003.1	000670	Concanavalin-like	355	phiOC_p361	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QHJ86107.1	000670	Concanavalin-like	506	KKIINIFJ_00196	Pseudomonas phage PN05	GCA_009931935.1
AND75264.1	000000	SIG+Concanavalin-like	1183	ME3_103	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AEO93678.1	000000	SIG+Concanavalin-like	2010	G_420	Bacillus virus G	GCA_000917535.1
QIG57832.1	000000	ASH-IG	1307	SEA_PAULODIABOLI_98	Microbacterium phage PauloDiaboli	GCA_011067425.1
BBA65346.1	000000	Concanavalin-like+SAM-methylase	429	-	Xanthomonas phage XacN1	GCA_003173815.1
AND75265.1	000000	PspA+Concanavalin-like	5419	ME3_104	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QDH83589.1	000671	dCMP_cyt_DEAM	181	H1O15_gp199	Achromobacter phage Motura	GCA_006964305.1
APU01767.1	000671	dCMP_cyt_DEAM	179	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28979.1	000671	dCMP_cyt_DEAM	174	AP1_0272	Aeromonas phage AP1	GCA_014183365.1
ATI17530.1	000671	dCMP_cyt_DEAM	174	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00466.1	000671	dCMP_cyt_DEAM	174	HWB28_gp086	Aeromonas phage AS-zj	GCA_002627665.1
AUE22801.1	000671	dCMP_cyt_DEAM	182	Ah1_00283	Aeromonas phage Ah1	GCA_002957415.1
QAX98516.1	000671	dCMP_cyt_DEAM	182	ASfcp2_180	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97972.1	000671	dCMP_cyt_DEAM	174	ASswx1_330	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01168.1	000671	dCMP_cyt_DEAM	174	ASwh1_102	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39506.1	000671	dCMP_cyt_DEAM	174	CC2_203	Aeromonas phage CC2	GCA_000903495.1
ADQ52979.1	000671	dCMP_cyt_DEAM	182	PX29p260	Aeromonas phage PX29	GCA_000920195.1
ADM79903.1	000671	dCMP_cyt_DEAM	182	phiAS5_ORF0060	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53410.1	000671	dCMP_cyt_DEAM	179	65p403	Aeromonas virus 65	GCA_000893255.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAQ17928.1	000671	dCMP_cyt_DEAM	182	cd	Aeromonas virus Aeh1	GCA_000843245.1
ABS83773.1	000671	dCMP_cyt_DEAM	255	0305phi8-36p215	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01305.1	000671	dCMP_cyt_DEAM	176	AR9_g221	Bacillus phage AR9	GCA_001743835.1
AMM45020.1	000671	dCMP_cyt_DEAM	144	SP15_219	Bacillus phage SP-15	GCA_001754685.1
ALN97955.1	000671	dCMP_cyt_DEAM	159	Bp8pS_276	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93576.1	000671	dCMP_cyt_DEAM	172	G_317	Bacillus virus G	GCA_000917535.1
AST99934.1	000671	dCMP_cyt_DEAM	176	PBI_PBS1_112	Bacillus virus PBS1	GCA_002601325.1
QIG63368.1	000671	dCMP_cyt_DEAM	145	DAC16_135	Bacteroides phage DAC16	GCA_013387695.1
QIG63633.1	000671	dCMP_cyt_DEAM	145	DAC19_142	Bacteroides phage DAC19	GCA_013387715.1
QIG63894.1	000671	dCMP_cyt_DEAM	145	DAC20_141	Bacteroides phage DAC20	GCA_013387725.1
QIG64157.1	000671	dCMP_cyt_DEAM	145	DAC22_143	Bacteroides phage DAC22	GCA_013387735.1
QIG64414.1	000671	dCMP_cyt_DEAM	145	DAC23_136	Bacteroides phage DAC23	GCA_013387745.1
QBX06511.1	000671	dCMP_cyt_DEAM	149	BcepSaruman_098	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74477.1	000671	dCMP_cyt_DEAM	149	BcepSauron_097	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13702.1	000671	dCMP_cyt_DEAM	127	Ccr10_gp172c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14047.1	000671	dCMP_cyt_DEAM	127	Ccr2_gp171c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14734.1	000671	dCMP_cyt_DEAM	127	Ccr29_gp178	Caulobacter phage Ccr29	GCA_002619485.1
ARB15089.1	000671	dCMP_cyt_DEAM	127	Ccr32_gp171	Caulobacter phage Ccr32	GCA_002619505.1
ARB15423.1	000671	dCMP_cyt_DEAM	127	Ccr34_gp181	Caulobacter phage Ccr34	GCA_002619525.1
ARB14390.1	000671	dCMP_cyt_DEAM	127	Ccr5_gp170c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68372.1	000671	dCMP_cyt_DEAM	131	CcrBL10_gp168c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69222.1	000671	dCMP_cyt_DEAM	83	CcrBL9_gp198	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88036.1	000671	dCMP_cyt_DEAM	122	CcrColossus_gp166	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88085.1	000671	dCMP_cyt_DEAM	129	CcrColossus_gp215	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68713.1	000671	dCMP_cyt_DEAM	130	CcrPW_gp174c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68761.1	000671	dCMP_cyt_DEAM	134	CcrPW_gp222c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69776.1	000671	dCMP_cyt_DEAM	113	CcrSC_gp194	Caulobacter phage CcrSC	GCA_003443315.1
AFU87695.1	000671	dCMP_cyt_DEAM	127	CcrKarma_gp178	Caulobacter virus Karma	GCA_000901575.1
AFU87344.1	000671	dCMP_cyt_DEAM	127	CcrMagneto_gp174	Caulobacter virus Magneto	GCA_000903095.1
AFU86655.1	000671	dCMP_cyt_DEAM	127	CcrRogue_gp173	Caulobacter virus Rogue	GCA_000900555.1
AFU88491.1	000671	dCMP_cyt_DEAM	127	CcrSwift_gp173	Caulobacter virus Swift	GCA_000899655.1
AFU87008.1	000671	dCMP_cyt_DEAM	127	CbK_gp176	Caulobacter virus phiCbK	GCA_000900535.1
ANS06031.1	000671	dCMP_cyt_DEAM	174	ABCD_0073	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64835.1	000671	dCMP_cyt_DEAM	170	S13_036	Cronobacter phage S13	GCA_001503575.1
AFC21557.1	000671	dCMP_cyt_DEAM	157	GAP32_109	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97087.1	000671	dCMP_cyt_DEAM	174	E_078	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXG67078.1	000671	dCMP_cyt_DEAM	173	AD1_034	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79827.1	000671	dCMP_cyt_DEAM	164	JA11_022	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66426.1	000671	dCMP_cyt_DEAM	164	JA13_023	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66748.1	000671	dCMP_cyt_DEAM	164	JA29_022	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67396.1	000671	dCMP_cyt_DEAM	164	JA33_022	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08311.1	000671	dCMP_cyt_DEAM	173	Alexandra_31	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58675.1	000671	dCMP_cyt_DEAM	172	Y3_035	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28517.1	000671	dCMP_cyt_DEAM	160	YOLOSWAG_32	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14359.1	000671	dCMP_cyt_DEAM	159	PBI_121Q_469	Escherichia phage 121Q	GCA_000926855.1
QAY00585.1	000671	dCMP_cyt_DEAM	157	Ecwhy1_308	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34779.1	000671	dCMP_cyt_DEAM	153	ACQ29_gp099	Escherichia phage PBECO4	GCA_001041035.1
BBM62030.1	000671	dCMP_cyt_DEAM	159	EO157G_4410	Escherichia phage SP27	GCA_008033345.1
AXC36895.1	000671	dCMP_cyt_DEAM	159	-	Escherichia phage UB	GCA_003341455.1
ARM70770.1	000671	dCMP_cyt_DEAM	193	phiC120_c64	Escherichia phage phiC120	GCA_002621185.1
QBO61945.1	000671	dCMP_cyt_DEAM	159	G17_00456	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80346.1	000671	dCMP_cyt_DEAM	159	PSLUR01_00369	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78597.1	000671	dCMP_cyt_DEAM	174	RB43ORF075w	Escherichia virus RB43	GCA_000863505.1
AFA44768.1	000671	dCMP_cyt_DEAM	156	RaK2_00495	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72814.1	000671	dCMP_cyt_DEAM	168	-	Myoviridae sp.	GCA_003657725.1
QHJ78827.1	000671	dCMP_cyt_DEAM	169	-	Myoviridae sp.	GCA_012593985.1
QIG65844.1	000671	dCMP_cyt_DEAM	148	phiOC_p179	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43675.1	000671	dCMP_cyt_DEAM	151	CBB_110	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38320.1	000671	dCMP_cyt_DEAM	274	BN7874_151	Phage NCTB	GCA_900092385.1
QCG76158.1	000671	dCMP_cyt_DEAM	158	EST35_0277	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41558.2	000671	dCMP_cyt_DEAM	145	RSL1_ORF113	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41722.1	000671	dCMP_cyt_DEAM	223	RSL1_ORF275	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44485.1	000671	dCMP_cyt_DEAM	286	PBI_SCTP2_470	Salicola phage SCTP-2	GCA_002625545.1
QCW18810.1	000671	dCMP_cyt_DEAM	157	7t3_0289	Salmonella phage 7t3	GCA_006083215.1
AZU98075.1	000671	dCMP_cyt_DEAM	157	CPT_Munch_131	Salmonella phage Munch	GCA_004015485.1
QIG62907.1	000671	dCMP_cyt_DEAM	151	SEPL_294	Salmonella phage SE_PL	GCA_011067555.1
AQW88628.1	000671	dCMP_cyt_DEAM	156	BF_0103	Serratia phage BF	GCA_002619745.1
AFF28035.1	000671	dCMP_cyt_DEAM	313	PAU_37	Sphingomonas phage PAU	GCA_000902455.1
AYD81368.1	000671	dCMP_cyt_DEAM	172	SEA_JUSTBECAUSE_213	Streptomyces phage JustBecause	GCA_003613775.1
QJD53771.1	000671	dCMP_cyt_DEAM	172	SEA_KELA_211	Streptomyces phage Kela	GCA_012934305.1
QBZ72100.1	000671	dCMP_cyt_DEAM	169	SEA_KRADAL_214	Streptomyces phage Kradal	GCA_004799925.1
AXH66361.1	000671	dCMP_cyt_DEAM	169	SEA_SATIS_212	Streptomyces phage Satis	GCA_003366315.1
AAQ64190.1	000671	dCMP_cyt_DEAM	150	KVP40.0119	Vibrio phage KVP40	GCA_000843785.1
QIW90833.1	000671	dCMP_cyt_DEAM	150	GCAPEGMB_00518	Vibrio phage V07	GCA_012361095.1
QIW90916.1	000671	dCMP_cyt_DEAM	150	COHAPHLL_00053	Vibrio phage V09	GCA_012361135.1
QHJ74302.1	000671	dCMP_cyt_DEAM	150	VH12019_00383	Vibrio phage VH1_2019	GCA_009931825.1
AGB06796.1	000671	dCMP_cyt_DEAM	150	CF80_gp009	Vibrio phage VH7D	GCA_000914495.1
QBX05970.1	000671	dCMP_cyt_DEAM	150	ValB1HC_016	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60982.1	000671	dCMP_cyt_DEAM	150	AVU32_gp141	Vibrio phage ValKK3	GCA_001501635.1
ALP47131.1	000671	dCMP_cyt_DEAM	150	phiGrn1_0231	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47515.1	000671	dCMP_cyt_DEAM	150	phiST2_0366	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54595.1	000671	dCMP_cyt_DEAM	150	vBValMR10Z_54	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07222.1	000671	dCMP_cyt_DEAM	179	VmeM32_00236	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37349.1	000671	dCMP_cyt_DEAM	150	pp2_116	Vibriophage phi-pp2	GCA_002630725.1
BBA65352.1	000671	dCMP_cyt_DEAM	244	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96384.1	000671	dCMP_cyt_DEAM	234	Xoosp13_198	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58904.1	000671	dCMP_cyt_DEAM	158	g096	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58369.1	000671	dCMP_cyt_DEAM	158	g092	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26127.1	000671	dCMP_cyt_DEAM	171	g103	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000160	000671	dCMP_cyt_DEAM	189	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000121	000671	dCMP_cyt_DEAM	189	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01709.1	000672	Zn-Binding-DUF4326	83	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28907.1	000672	Zn-Binding-DUF4326	101	AP1_0200	Aeromonas phage AP1	GCA_014183365.1
ATI17588.1	000672	Zn-Binding-DUF4326	101	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00409.1	000672	Zn-Binding-DUF4326	101	HWB28_gp143	Aeromonas phage AS-zj	GCA_002627665.1
AUE22841.1	000672	Zn-Binding-DUF4326	94	Ah1_00323	Aeromonas phage Ah1	GCA_002957415.1
QAX98554.1	000672	Zn-Binding-DUF4326	94	ASfcp2_219	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98027.1	000672	Zn-Binding-DUF4326	101	ASswx1_387	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01116.1	000672	Zn-Binding-DUF4326	101	ASwh1_48	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39473.1	000672	Zn-Binding-DUF4326	101	CC2_144	Aeromonas phage CC2	GCA_000903495.1
ADQ53018.1	000672	Zn-Binding-DUF4326	94	PX29p299	Aeromonas phage PX29	GCA_000920195.1
ADM79942.1	000672	Zn-Binding-DUF4326	94	phiAS5_ORF0099	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53348.1	000672	Zn-Binding-DUF4326	100	65p340	Aeromonas virus 65	GCA_000893255.1
AAQ17971.1	000672	Zn-Binding-DUF4326	94	nrdA.1	Aeromonas virus Aeh1	GCA_000843245.1
ASV44733.1	000672	Zn-Binding-DUF4326	82	FDI40_gp279	Agrobacterium phage Atu_ph07	GCA_002628245.1
ALN97849.1	000672	Zn-Binding-DUF4326	97	Bp8pS_170	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QBQ74671.1	000672	Zn-Binding-DUF4326	106	BcepSauron_291	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13744.1	000672	Zn-Binding-DUF4326	106	Ccr10_gp214c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14089.1	000672	Zn-Binding-DUF4326	106	Ccr2_gp213c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14778.1	000672	Zn-Binding-DUF4326	106	Ccr29_gp222	Caulobacter phage Ccr29	GCA_002619485.1
ARB15122.1	000672	Zn-Binding-DUF4326	106	Ccr32_gp204	Caulobacter phage Ccr32	GCA_002619505.1
ARB15456.1	000672	Zn-Binding-DUF4326	106	Ccr34_gp214	Caulobacter phage Ccr34	GCA_002619525.1
ARB14431.1	000672	Zn-Binding-DUF4326	88	Ccr5_gp211c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68410.1	000672	Zn-Binding-DUF4326	105	CcrBL10_gp206c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88110.1	000672	Zn-Binding-DUF4326	96	CcrColossus_gp240	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68787.1	000672	Zn-Binding-DUF4326	89	CcrPW_gp248	Caulobacter phage CcrPW	GCA_003443275.1
AFU87738.1	000672	Zn-Binding-DUF4326	106	CcrKarma_gp221	Caulobacter virus Karma	GCA_000901575.1
AFU87386.1	000672	Zn-Binding-DUF4326	106	CcrMagneto_gp216	Caulobacter virus Magneto	GCA_000903095.1
AFU86697.1	000672	Zn-Binding-DUF4326	105	CcrRogue_gp215	Caulobacter virus Rogue	GCA_000900555.1
AFU88534.1	000672	Zn-Binding-DUF4326	106	CcrSwift_gp216	Caulobacter virus Swift	GCA_000899655.1
AFU87041.1	000672	Zn-Binding-DUF4326	106	CbK_gp209	Caulobacter virus phiCbK	GCA_000900535.1
ANS06178.1	000672	Zn-Binding-DUF4326	59	ABCD_0065	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64819.1	000672	Zn-Binding-DUF4326	98	S13_020	Cronobacter phage S13	GCA_001503575.1
AFC21599.1	000672	Zn-Binding-DUF4326	100	GAP32_149	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXG67104.1	000672	Zn-Binding-DUF4326	141	AD1_060	Dickeya phage vB_DsoM_AD1	GCA_003568515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG66786.1	000672	Zn-Binding-DUF4326	113	JA29_060	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AWY08340.1	000672	Zn-Binding-DUF4326	133	Alexandra_60	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28803.1	000672	Zn-Binding-DUF4326	155	YOLOSWAG_58	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14387.1	000672	Zn-Binding-DUF4326	110	PBI_121Q_497	Escherichia phage 121Q	GCA_000926855.1
QAY00561.1	000672	Zn-Binding-DUF4326	108	Ecwhy1_282	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34755.1	000672	Zn-Binding-DUF4326	110	ACQ29_gp075	Escherichia phage PBECO4	GCA_001041035.1
BBM62058.1	000672	Zn-Binding-DUF4326	110	EO157G_4690	Escherichia phage SP27	GCA_008033345.1
AXC36870.1	000672	Zn-Binding-DUF4326	110	-	Escherichia phage UB	GCA_003414555.1
QBO61915.1	000672	Zn-Binding-DUF4326	110	G17_00426	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13949.1	000672	Zn-Binding-DUF4326	110	vBEcoMphAPEC6_gp325c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80376.1	000672	Zn-Binding-DUF4326	110	PSLUR01_00399	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44794.1	000672	Zn-Binding-DUF4326	115	Rak2_00522	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57849.1	000672	Zn-Binding-DUF4326	91	SEA_PAULODIABOLI_115	Microbacterium phage PauloDiaboli	GCA_011067425.1
QHJ78844.1	000672	Zn-Binding-DUF4326	98	-	Myoviridae sp.	GCA_012593985.1
AMM43719.1	000672	Zn-Binding-DUF4326	100	CBB_154	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QHJ86021.1	000672	Zn-Binding-DUF4326	94	KKIINIFJ_00109	Pseudomonas phage PN05	GCA_009931935.1
QCW18858.1	000672	Zn-Binding-DUF4326	102	7t3_0337	Salmonella phage 7t3	GCA_006083215.1
AZU98119.1	000672	Zn-Binding-DUF4326	102	CPT_Munch_175	Salmonella phage Munch	GCA_004015485.1
QIG62863.1	000672	Zn-Binding-DUF4326	102	SEPL_250	Salmonella phage SE_PL	GCA_011067555.1
AQW88673.1	000672	Zn-Binding-DUF4326	100	BF_0148	Serratia phage BF	GCA_002619745.1
AGR47862.1	000672	Zn-Binding-DUF4326	87	SmphiM12_230	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13065.1	000672	Zn-Binding-DUF4326	87	PHIM19_160	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12706.1	000672	Zn-Binding-DUF4326	87	PHIM7_160	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13435.1	000672	Zn-Binding-DUF4326	87	PHIN3_172	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64184.1	000672	Zn-Binding-DUF4326	94	KVP40.0113	Vibrio phage KVP40	GCA_000843785.1
QIW90507.1	000672	Zn-Binding-DUF4326	94	GCAPEGMB_00160	Vibrio phage V07	GCA_012361095.1
QIW90922.1	000672	Zn-Binding-DUF4326	94	COHAPHLL_00059	Vibrio phage V09	GCA_012361135.1
QHJ74296.1	000672	Zn-Binding-DUF4326	94	VH12019_00377	Vibrio phage VH1_2019	GCA_009931825.1
AGB06789.1	000672	Zn-Binding-DUF4326	83	CF80_gp002	Vibrio phage VH7D	GCA_000914495.1
QBX05977.1	000672	Zn-Binding-DUF4326	94	ValB1HC_023	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60990.1	000672	Zn-Binding-DUF4326	94	AVU32_gp149	Vibrio phage ValKK3	GCA_001501635.1
AGN30164.1	000672	Zn-Binding-DUF4326	94	VPFG_00162	Vibrio phage nt-1	GCA_000910195.2
ALP47222.1	000672	Zn-Binding-DUF4326	94	phiGrn1_0223	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47609.1	000672	Zn-Binding-DUF4326	94	phiST2_0358	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54602.1	000672	Zn-Binding-DUF4326	94	vBValMR10Z_61	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37342.1	000672	Zn-Binding-DUF4326	94	pp2_109	Vibriophage phi-pp2	GCA_002630725.1
BBA65542.1	000672	Zn-Binding-DUF4326	96	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK58955.1	000672	Zn-Binding-DUF4326	101	g147	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58421.1	000672	Zn-Binding-DUF4326	101	g144	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFH14796.1	000000	DUF4326	100	Lu11_0260A	Pseudomonas phage Lu11	GCA_000897175.1
APU01508.1	000673	dNMP-kinase	245	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29115.1	000673	dNMP-kinase	120	AP1_0412	Aeromonas phage AP1	GCA_014183365.1
QMV29145.1	000673	dNMP-kinase	145	AP1_0442	Aeromonas phage AP1	GCA_014183365.1
ATI17389.1	000673	dNMP-kinase	243	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00204.1	000673	dNMP-kinase	243	HWB28_gp348	Aeromonas phage AS-zj	GCA_002627665.1
AUE22718.1	000673	dNMP-kinase	228	Ah1_00200	Aeromonas phage Ah1	GCA_002957415.1
QAX98442.1	000673	dNMP-kinase	229	ASfcp2_99	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97831.1	000673	dNMP-kinase	243	ASswx1_187	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01321.1	000673	dNMP-kinase	245	ASwh1_259	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39565.1	000673	dNMP-kinase	243	CC2_348	Aeromonas phage CC2	GCA_000903495.1
ADQ52898.1	000673	dNMP-kinase	229	PX29p179	Aeromonas phage PX29	GCA_000920195.1
ADM80165.1	000673	dNMP-kinase	229	phiAS5_ORF0322	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53130.1	000673	dNMP-kinase	245	65p122	Aeromonas virus 65	GCA_000893255.1
AAQ17851.1	000673	dNMP-kinase	229	1	Aeromonas virus Aeh1	GCA_000843245.1
ASV44716.1	000673	dNMP-kinase	214	FDI40_gp134	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARB13643.1	000673	dNMP-kinase	178	Ccr10_gp114c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13988.1	000673	dNMP-kinase	178	Ccr2_gp113c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14676.1	000673	dNMP-kinase	178	Ccr29_gp120	Caulobacter phage Ccr29	GCA_002619485.1
ARB15031.1	000673	dNMP-kinase	178	Ccr32_gp113	Caulobacter phage Ccr32	GCA_002619505.1
ARB15363.1	000673	dNMP-kinase	178	Ccr34_gp121	Caulobacter phage Ccr34	GCA_002619525.1
ARB14332.1	000673	dNMP-kinase	178	Ccr5_gp114c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68312.1	000673	dNMP-kinase	178	CcrBL10_gp108c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69220.1	000673	dNMP-kinase	180	CcrBL9_gp196	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88022.1	000673	dNMP-kinase	194	CcrColossus_gp152	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68699.1	000673	dNMP-kinase	201	CcrPW_gp160c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69774.1	000673	dNMP-kinase	180	CcrSC_gp192	Caulobacter phage CcrSC	GCA_003443315.1
AFU87635.1	000673	dNMP-kinase	178	CcrKarma_gp118	Caulobacter virus Karma	GCA_000901575.1
AFU87284.1	000673	dNMP-kinase	178	CcrMagneto_gp114	Caulobacter virus Magneto	GCA_000903095.1
AFU86596.1	000673	dNMP-kinase	191	CcrRogue_gp114	Caulobacter virus Rogue	GCA_000900555.1
AFU88431.1	000673	dNMP-kinase	178	CcrSwift_gp113	Caulobacter virus Swift	GCA_000899655.1
AFU86949.1	000673	dNMP-kinase	178	CbK_gp117	Caulobacter virus phiCbK	GCA_000900535.1
ANS05999.1	000673	dNMP-kinase	220	ABCD_0188	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64966.1	000673	dNMP-kinase	224	S13_167	Cronobacter phage S13	GCA_001503575.1
AFC21647.1	000673	dNMP-kinase	228	GAP32_197	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97202.1	000673	dNMP-kinase	222	E_194	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14440.1	000673	dNMP-kinase	208	PBI_121Q_550	Escherichia phage 121Q	GCA_000926855.1
QAY00509.1	000673	dNMP-kinase	208	Ecwhy1_230	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34703.1	000673	dNMP-kinase	208	ACQ29_gp023	Escherichia phage PBECO4	GCA_001041035.1
BBM62111.1	000673	dNMP-kinase	208	EO157G_5220	Escherichia phage SP27	GCA_008033345.1
AXC36823.1	000673	dNMP-kinase	208	-	Escherichia phage UB	GCA_003414555.1
ARM70972.1	000673	dNMP-kinase	244	phiC120_c267	Escherichia phage phiC120	GCA_002621185.1
QBO61862.1	000673	dNMP-kinase	208	G17_00373	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13903.1	000673	dNMP-kinase	208	vBEcoMphAPEC6_gp278c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80425.1	000673	dNMP-kinase	208	PSLUR01_00448	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78720.1	000673	dNMP-kinase	220	RB43ORF198c	Escherichia virus RB43	GCA_000863505.1
AFA44313.1	000673	dNMP-kinase	208	RaK2_00040	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72826.1	000673	dNMP-kinase	225	-	Myoviridae sp.	GCA_003657725.1
QHJ78968.1	000673	dNMP-kinase	220	-	Myoviridae sp.	GCA_012593985.1
AMM43768.1	000673	dNMP-kinase	213	CBB_203	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76075.1	000673	dNMP-kinase	213	EST35_0194	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44491.1	000673	dNMP-kinase	217	PBI_SCTP2_476	Salicola phage SCTP-2	GCA_002625545.1
QCW18916.1	000673	dNMP-kinase	228	7t3_0395	Salmonella phage 7t3	GCA_006083215.1
AZU98173.1	000673	dNMP-kinase	214	CPT_Munch_229	Salmonella phage Munch	GCA_004015485.1
QIG62811.1	000673	dNMP-kinase	214	SEPL_198	Salmonella phage SE_PL	GCA_011067555.1
AQW88724.1	000673	dNMP-kinase	228	BF_0199	Serratia phage BF	GCA_002619745.1
AAQ64394.1	000673	dNMP-kinase	212	KVP40.0324	Vibrio phage KVP40	GCA_000843785.1
QIW90706.1	000673	dNMP-kinase	212	GCAPEGMB_00387	Vibrio phage V07	GCA_012361095.1
QIW91091.1	000673	dNMP-kinase	212	COHAPHLL_00228	Vibrio phage V09	GCA_012361135.1
QHJ74506.1	000673	dNMP-kinase	212	VH12019_00206	Vibrio phage VH1_2019	GCA_009931825.1
QBX06149.1	000673	dNMP-kinase	214	ValB1HC_195	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61161.1	000673	dNMP-kinase	214	AVU32_gp320	Vibrio phage ValKK3	GCA_001501635.1
AGN30375.1	000673	dNMP-kinase	212	VPFG_00378	Vibrio phage nt-1	GCA_000910195.2
ALP47061.1	000673	dNMP-kinase	214	phiGrn1_0058	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47441.1	000673	dNMP-kinase	214	phiST2_0190	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54774.1	000673	dNMP-kinase	214	vBValMR10Z_234	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07106.1	000673	dNMP-kinase	232	VmeM32_00119	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37556.1	000673	dNMP-kinase	212	pp2_324	Vibriophage phi-pp2	GCA_002630725.1
BBA65372.1	000673	dNMP-kinase	202	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96400.1	000673	dNMP-kinase	215	Xoosp13_214	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59006.1	000673	dNMP-kinase	213	g198	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58471.1	000673	dNMP-kinase	213	g194	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44764.1	000674	CTP_transf_like	184	FDI40_gp695	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21517.1	000674	CTP_transf_like	185	GAP32_069	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AGH56845.1	000674	CTP_transf_like	365	CPXG_00042	Cyanophage P-RSM6	GCA_000906155.1
AJK27651.1	000674	CTP_transf_like	357	PTIM40_183	Cyanophage P-TIM40	GCA_001470935.1
AOO14370.1	000674	CTP_transf_like	392	Sn1101l0_176	Cyanophage S-RIM14	GCA_002599065.1
AOO15018.1	000674	CTP_transf_like	392	W1230910_172	Cyanophage S-RIM14	GCA_002599125.1
AMO43178.1	000674	CTP_transf_like	187	R1080702_169	Cyanophage S-RIM32	GCA_001754165.1
AMO43403.1	000674	CTP_transf_like	161	W270710_159	Cyanophage S-RIM44	GCA_002599145.1
AOO11647.1	000674	CTP_transf_like	161	ES420910_166	Cyanophage S-RIM44	GCA_002599165.1
AOO11875.1	000674	CTP_transf_like	161	Np050604_159	Cyanophage S-RIM44	GCA_002599185.1
AOO12113.1	000674	CTP_transf_like	161	Np200711_167	Cyanophage S-RIM44	GCA_002599205.1
AOO12348.1	000674	CTP_transf_like	161	Np420711_166	Cyanophage S-RIM44	GCA_002599225.1
AOO12576.1	000674	CTP_transf_like	161	Sn080709_159	Cyanophage S-RIM44	GCA_002599245.1
AOO12813.1	000674	CTP_transf_like	161	Sn130910_166	Cyanophage S-RIM44	GCA_002599265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO13042.1	000674	CTP_transf_like	161	W2100709_160	Cyanophage S-RIM44	GCA_002599285.1
AGH07506.1	000674	CTP_transf_like	436	CYVG_00062	Cyanophage S-SSM6a	GCA_002710385.1
AGG54432.1	000674	CTP_transf_like	389	CYWG_00148	Cyanophage S-SSM6b	GCA_002710425.1
AIT14308.1	000674	CTP_transf_like	177	PBI_121Q_418	Escherichia phage 121Q	GCA_000926855.1
QAY00630.1	000674	CTP_transf_like	177	Ecwhy1_355	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34827.1	000674	CTP_transf_like	177	ACQ29_gp147	Escherichia phage PBECO4	GCA_001041035.1
BBM61982.1	000674	CTP_transf_like	177	EO157G_3930	Escherichia phage SP27	GCA_008033345.1
AXC36935.1	000674	CTP_transf_like	177	-	Escherichia phage UB	GCA_003341455.1
QBO61996.1	000674	CTP_transf_like	177	G17_00507	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14017.1	000674	CTP_transf_like	177	vBEcoMphAPEC6_gp393c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80295.1	000674	CTP_transf_like	177	PSLUR01_00318	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44721.1	000674	CTP_transf_like	178	RaK2_00448	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43638.1	000674	CTP_transf_like	179	CBB_73	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26279.1	000674	CTP_transf_like	188	CPMG_00179	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44572.1	000674	CTP_transf_like	424	PSSM2_194	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12401.1	000674	CTP_transf_like	424	PRTG_00248	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93495.1	000674	CTP_transf_like	401	AVU42_gp158	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99262.1	000674	CTP_transf_like	189	Syn1_161	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76188.1	000674	CTP_transf_like	190	EST35_0307	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44252.1	000674	CTP_transf_like	377	PBI_SCTP2_237	Salicola phage SCTP-2	GCA_002625545.1
QCW18769.1	000674	CTP_transf_like	178	7t3_0248	Salmonella phage 7t3	GCA_006083215.1
AZU98035.1	000674	CTP_transf_like	178	CPT_Munch_091	Salmonella phage Munch	GCA_004015485.1
QIG62945.1	000674	CTP_transf_like	178	SEPL_332	Salmonella phage SE_PL	GCA_011067555.1
AQW88589.1	000674	CTP_transf_like	172	BF_0064	Serratia phage BF	GCA_002619745.1
AIX30671.1	000674	CTP_transf_like	404	Syn7803US37_194	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54921.1	000674	CTP_transf_like	410	b23_0308	Synechococcus phage B23	GCA_009745195.1
QGT54556.1	000674	CTP_transf_like	410	b3_0315	Synechococcus phage B3	GCA_009745215.1
ASR76213.1	000674	CTP_transf_like	395	PBI_BELLAMY_170	Synechococcus phage Bellamy	GCA_002627525.1
QCW22944.1	000674	CTP_transf_like	432	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50538.1	000674	CTP_transf_like	432	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59628.1	000674	CTP_transf_like	187	S330809_167	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59390.1	000674	CTP_transf_like	187	C440309_167	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59866.1	000674	CTP_transf_like	187	N231010_167	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70536.1	000674	CTP_transf_like	350	HOU04_gp137	Synechococcus phage S-T4	GCA_003443335.1
QJT70167.1	000674	CTP_transf_like	408	SynMITS9220M01_155	Synechococcus phage SynMITS9220M01	GCA_013187275.1
SOK58865.1	000674	CTP_transf_like	183	g057	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58328.1	000674	CTP_transf_like	183	g051	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QNI21210.1	000675	TM+BCS1_N+BCS1-AAA	447	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB71291.1	000675	TM+BCS1_N+BCS1-AAA	413	CPT_Moabite_261	Serratia phage Moabite	GCA_006384735.1
QIG63113.1	000675	TM+BCS1_N+BCS1-AAA	411	SEPL_500	Salmonella phage SE_PL	GCA_011067555.1
AZU98400.1	000675	TM+BCS1_N+BCS1-AAA	411	CPT_Munch_468	Salmonella phage Munch	GCA_004015485.1
QCW18571.1	000675	TM+BCS1_N+BCS1-AAA	411	7t3_050	Salmonella phage 7t3	GCA_006083215.1
ASV44034.1	000675	TM+BCS1_N+BCS1-AAA	476	PBI_SCTP2_19	Salicola phage SCTP-2	GCA_002625545.1
BAQ02545.1	000675	TM+BCS1_N+BCS1-AAA	436	AVU38_gp017	Ralstonia phage RSL2	GCA_001503055.1
BAS04809.2	000675	TM+BCS1_N+BCS1-AAA	411	AVU11_gp017	Ralstonia phage RSF1	GCA_001500875.1
BAW19383.1	000675	TM+BCS1_N+BCS1-AAA	451	-	Ralstonia phage RP31	GCA_002617365.1
BAW19097.1	000675	TM+BCS1_N+BCS1-AAA	451	FDH28_gp123	Ralstonia phage RP12	GCA_002617345.1
AAL83187.1	000675	TM+BCS1_N+BCS1-AAA	508	PHIKZ286	Pseudomonas virus phiKZ	GCA_000842965.1
QEM42091.1	000675	TM+BCS1_N+BCS1-AAA	504	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATN94612.1	000675	TM+BCS1_N+BCS1-AAA	507	SL2_035	Pseudomonas phage SL2	GCA_002956015.1
QBJ02827.1	000675	TM+BCS1_N+BCS1-AAA	454	PSA21_301	Pseudomonas phage Psa21	GCA_004340405.1
AEH03770.1	000675	TM+BCS1_N+BCS1-AAA	508	347	Pseudomonas phage PhiPA3	GCA_001502095.1
QBX32518.1	000675	TM+BCS1_N+BCS1-AAA	504	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77480.1	000675	TM+BCS1_N+BCS1-AAA	446	NOXIFER_315	Pseudomonas phage Noxifer	GCA_002625005.1
ANM45102.1	000675	TM+BCS1_N+BCS1-AAA	508	KTN4_344	Pseudomonas phage KTN4	GCA_002607225.1
QJB22978.1	000675	TM+BCS1_N+BCS1-AAA	508	fnug_335	Pseudomonas phage fnug	GCA_012837215.1
AXH72859.1	000675	TM+BCS1_N+BCS1-AAA	411	-	Myoviridae sp.	GCA_003657725.1
ANZ50309.1	000675	TM+BCS1_N+BCS1-AAA	477	PHOBOS_119	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ48968.1	000675	TM+BCS1_N+BCS1-AAA	482	EARLPHILLIPIV_119	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
QBP07545.1	000675	TM+BCS1_N+BCS1-AAA	482	DERBICUS_119	Erwinia phage Derbicus	GCA_004521655.1
QBZ70687.1	000675	TM+BCS1_N+BCS1-AAA	417	pETSU_106	Edwardsiella virus pEt-SU	GCA_004800915.1
AFO71337.1	000675	TM+BCS1_N+BCS1-AAA	448	CR5_117	Cronobacter phage CR5	GCA_000910235.1
AXQ68782.1	000675	TM+BCS1_N+BCS1-AAA	408	CcrPW_gp243	Caulobacter phage CcrPW	GCA_003443275.1
AFU88105.1	000675	TM+BCS1_N+BCS1-AAA	408	CcrColossus_gp235	Caulobacter phage CcrColossus	GCA_000899635.1
ATA65526.1	000675	TM+BCS1_N+BCS1-AAA	125	2050HW_00191	Serratia phage 2050HW	GCA_002628125.1
AXH72875.1	000675	TM+BCS1_N+BCS1-AAA	542	-	Myoviridae sp.	GCA_003657725.1
ATA65527.1	000675	TM+BCS1_N+BCS1-AAA	291	2050HW_00192	Serratia phage 2050HW	GCA_002628125.1
QAX96847.1	000675	TM+BCS1_N+BCS1-AAA	427	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97152.1	000675	TM+BCS1_N+BCS1-AAA	427	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96211.1	000675	TM+BCS1_N+BCS1-AAA	427	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96529.1	000675	TM+BCS1_N+BCS1-AAA	427	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BAV39403.1	000675	TM+BCS1_N+BCS1-AAA	494	BPT24_286	Tenacibaculum phage pT24	GCA_002611925.1
BBI90452.1	000675	TM+BCS1_N+BCS1-AAA	450	HYO65_gp060	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90760.1	000675	TM+BCS1_N+BCS1-AAA	450	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAX96849.1	000676	BCS1_N+BCS1-AAA	456	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97154.1	000676	BCS1_N+BCS1-AAA	456	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96213.1	000676	BCS1_N+BCS1-AAA	456	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96531.1	000676	BCS1_N+BCS1-AAA	456	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ATN94706.1	000677	X+BCS1-AAA	366	SL2_129	Pseudomonas phage SL2	GCA_002956015.1
AAL83109.1	000677	X+BCS1-AAA	366	PHIKZ208	Pseudomonas virus phiKZ	GCA_000842965.1
QJB22886.1	000677	X+BCS1-AAA	366	fnug_243	Pseudomonas phage fnug	GCA_012837215.1
ANM45008.1	000677	X+BCS1-AAA	366	KTN4_250	Pseudomonas phage KTN4	GCA_002607225.1
QEM41968.1	000677	X+BCS1-AAA	366	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32398.1	000677	X+BCS1-AAA	366	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76939.1	000677	X+BCS1-AAA	400	PHABIO_308	Pseudomonas phage Phabio	GCA_002624965.1
AMM44093.1	000677	X+BCS1-AAA	356	CBB_530	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFC21970.1	000677	X+BCS1-AAA	403	GAP32_510	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
SOK58788.1	000677	X+BCS1-AAA	377	g511	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK59326.1	000677	X+BCS1-AAA	377	g518	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QJB22948.1	000677	X+BCS1-AAA	176	fnug_305	Pseudomonas phage fnug	GCA_012837215.1
ANM45073.1	000677	X+BCS1-AAA	176	KTN4_315	Pseudomonas phage KTN4	GCA_002607225.1
ATN94642.1	000677	X+BCS1-AAA	176	SL2_065	Pseudomonas phage SL2	GCA_002956015.1
BAW19466.1	000678	X+BCS1-AAA	455	-	Ralstonia phage RP31	GCA_002617365.1
BAW19180.1	000678	X+BCS1-AAA	455	FDH28_gp215	Ralstonia phage RP12	GCA_002617345.1
QCG76258.1	000679	X+BCS1-AAA	475	EST35_0378	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBA65554.1	000679	X+BCS1-AAA	389	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96549.1	000679	X+BCS1-AAA	389	Xoosp13_363	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AND75397.1	000680	X+BCS1-AAA	481	ME3_236	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXH71000.1	000681	X+BCS1-AAA	437	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70999.1	000682	X+BCS1-AAA	501	-	Vibrio phage BONAISHI	GCA_003441475.1
QAU04481.1	000683	X+BCS1-AAA	392	ValB1MD_100	Vibrio phage ValB1MD	GCA_004138815.1
QCG76147.1	000684	SIG+FtsH_ext+TM+BCS1-AAA+Peptidase_M41	576	EST35_0266	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AND75376.1	000685	Classical-AAA	366	ME3_215	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ASV44754.1	000685	Classical-AAA	374	FDI40_gp677	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21817.1	000685	Classical-AAA	405	GAP32_367	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG65783.1	000685	Classical-AAA	393	phiOC_p118	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43940.1	000685	Classical-AAA	396	CBB_377	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44399.1	000685	Classical-AAA	363	PBI_SCTP2_384	Salicola phage SCTP-2	GCA_002625545.1
AQW88900.1	000685	Classical-AAA	389	BF_0375	Serratia phage BF	GCA_002619745.1
SOK59188.1	000685	Classical-AAA	400	g380	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58652.1	000685	Classical-AAA	400	g375	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01400.1	000686	DexA-35exo	219	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28870.1	000686	DexA-35exo	217	AP1_0163	Aeromonas phage AP1	GCA_014183365.1
ATI17496.1	000686	DexA-35exo	217	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00501.1	000686	DexA-35exo	217	HWB28_gp051	Aeromonas phage AS-zj	GCA_002627665.1
AUE22551.1	000686	DexA-35exo	226	Ah1_00010	Aeromonas phage Ah1	GCA_002957415.1
QAX98591.1	000686	DexA-35exo	226	ASfcp2_258	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97935.1	000686	DexA-35exo	217	ASswx1_293	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01212.1	000686	DexA-35exo	220	ASwh1_147	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39510.1	000686	DexA-35exo	217	CC2_238	Aeromonas phage CC2	GCA_000903495.1
ADQ52727.1	000686	DexA-35exo	226	PX29p008	Aeromonas phage PX29	GCA_000920195.1
ADM79980.1	000686	DexA-35exo	226	phiAS5_ORF0137	Aeromonas phage phiAS5	GCA_000887715.1
AAR90930.1	000686	DexA-35exo	219	65p008	Aeromonas virus 65	GCA_000893255.1
AAQ17664.1	000686	DexA-35exo	226	dexA	Aeromonas virus Aeh1	GCA_000843245.1
ANS05996.1	000686	DexA-35exo	223	ABCD_0022	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIA65054.1	000686	DexA-35exo	225	S13_257	Cronobacter phage S13	GCA_001503575.1
AON97030.1	000686	DexA-35exo	223	E_021	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AHI60215.1	000686	DexA-35exo	236	Ea357_064	Erwinia phage Ea35-70	GCA_000914635.1
QBP07173.1	000686	DexA-35exo	250	REBECCA_65	Erwinia phage Rebecca	GCA_004521635.1
AUG85853.1	000686	DexA-35exo	250	BOSOLAPHORUS_65	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52165.1	000686	DexA-35exo	250	DM_67	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86172.1	000686	DexA-35exo	250	DESERTFOX_64	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86494.1	000686	DexA-35exo	250	MADMEL_66	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86815.1	000686	DexA-35exo	250	MORTIMER_66	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51845.2	000686	DexA-35exo	250	RAY_64	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51529.2	000686	DexA-35exo	250	SIMMY50_67	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64877.1	000686	DexA-35exo	250	SPECIALG_67	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARM70834.1	000686	DexA-35exo	225	phiC120_c128	Escherichia phage phiC120	GCA_002621185.1
QBO63940.1	000686	DexA-35exo	409	Goslar_00147	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
AAX78543.1	000686	DexA-35exo	224	RB43ORF021c	Escherichia virus RB43	GCA_000863505.1
QHJ78878.1	000686	DexA-35exo	223	-	Myoviridae sp.	GCA_012593985.1
QKE54368.1	000686	DexA-35exo	220	ACSA002_0540	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64094.1	000686	DexA-35exo	230	KVP40.0023	Vibrio phage KVP40	GCA_000843785.1
QIW90417.1	000686	DexA-35exo	230	GCAPEGMB_00070	Vibrio phage V07	GCA_012361095.1
QIW91012.1	000686	DexA-35exo	230	COHAPHLL_00149	Vibrio phage V09	GCA_012361135.1
QHJ74206.1	000686	DexA-35exo	230	VH12019_00287	Vibrio phage VH1_2019	GCA_009931825.1
AGB07030.1	000686	DexA-35exo	230	CF80_gp243	Vibrio phage VH7D	GCA_000914495.1
QBX06066.1	000686	DexA-35exo	230	ValB1HC_112	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61080.1	000686	DexA-35exo	230	AVU32_gp239	Vibrio phage ValKK3	GCA_001501635.1
AGN30074.1	000686	DexA-35exo	227	VPFG_00072	Vibrio phage nt-1	GCA_000910195.2
ALP47053.1	000686	DexA-35exo	230	phiGrn1_0138	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47434.1	000686	DexA-35exo	230	phiST2_0268	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54692.1	000686	DexA-35exo	230	vBValMR10Z_151	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07072.1	000686	DexA-35exo	225	VmeM32_00081	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37257.1	000686	DexA-35exo	230	pp2_023	Vibriophage phi-pp2	GCA_002630725.1
ARB13546.1	000687	wHTH	162	Ccr10_gp018	Caulobacter phage Ccr10	GCA_002619445.1
ARB13871.1	000687	wHTH	162	Ccr10_gp341	Caulobacter phage Ccr10	GCA_002619445.1
ARB13892.1	000687	wHTH	186	Ccr2_gp017	Caulobacter phage Ccr2	GCA_002619465.1
ARB14215.1	000687	wHTH	186	Ccr2_gp339	Caulobacter phage Ccr2	GCA_002619465.1
ARB14575.1	000687	wHTH	162	Ccr29_gp018	Caulobacter phage Ccr29	GCA_002619485.1
ARB14581.1	000687	wHTH	192	Ccr29_gp024	Caulobacter phage Ccr29	GCA_002619485.1
ARB14910.1	000687	wHTH	162	Ccr29_gp354	Caulobacter phage Ccr29	GCA_002619485.1
ARB14916.1	000687	wHTH	192	Ccr29_gp360	Caulobacter phage Ccr29	GCA_002619485.1
ARB14936.1	000687	wHTH	192	Ccr32_gp017	Caulobacter phage Ccr32	GCA_002619505.1
ARB15247.1	000687	wHTH	192	Ccr32_gp329	Caulobacter phage Ccr32	GCA_002619505.1
ARB15267.1	000687	wHTH	192	Ccr34_gp018	Caulobacter phage Ccr34	GCA_002619525.1
ARB15581.1	000687	wHTH	192	Ccr34_gp339	Caulobacter phage Ccr34	GCA_002619525.1
ARB14235.1	000687	wHTH	162	Ccr5_gp017	Caulobacter phage Ccr5	GCA_002619545.1
ARB14555.1	000687	wHTH	162	Ccr5_gp335	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68218.1	000687	wHTH	162	CcrBL10_gp014	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68536.1	000687	wHTH	162	CcrBL10_gp332	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69031.1	000687	wHTH	193	CcrBL9_gp007	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69043.1	000687	wHTH	235	CcrBL9_gp019	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69547.1	000687	wHTH	193	CcrBL9_gp523	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69559.1	000687	wHTH	235	CcrBL9_gp535	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87889.1	000687	wHTH	156	CcrColossus_gp019	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68559.1	000687	wHTH	174	CcrPW_gp020	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68560.1	000687	wHTH	159	CcrPW_gp021	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69008.1	000687	wHTH	174	CcrPW_gp469	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69009.1	000687	wHTH	159	CcrPW_gp470	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69592.1	000687	wHTH	196	CcrSC_gp010	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69603.1	000687	wHTH	243	CcrSC_gp021	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70092.1	000687	wHTH	196	CcrSC_gp510	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70103.1	000687	wHTH	243	CcrSC_gp521	Caulobacter phage CcrSC	GCA_003443315.1
AFU87533.1	000687	wHTH	192	CcrKarma_gp016	Caulobacter virus Karma	GCA_000901575.1
AFU87866.1	000687	wHTH	192	CcrKarma_gp349	Caulobacter virus Karma	GCA_000901575.1
AFU87186.1	000687	wHTH	189	CcrMagneto_gp016	Caulobacter virus Magneto	GCA_000903095.1
AFU87514.1	000687	wHTH	189	CcrMagneto_gp344	Caulobacter virus Magneto	GCA_000903095.1
AFU86498.1	000687	wHTH	239	CcrRogue_gp016	Caulobacter virus Rogue	GCA_000900555.1
AFU86829.1	000687	wHTH	239	CcrRogue_gp347	Caulobacter virus Rogue	GCA_000900555.1
AFU88333.1	000687	wHTH	236	CcrSwift_gp015	Caulobacter virus Swift	GCA_000899655.1
AFU88658.1	000687	wHTH	236	CcrSwift_gp340	Caulobacter virus Swift	GCA_000899655.1
AFU86849.1	000687	wHTH	192	CbK_gp017	Caulobacter virus phiCbK	GCA_000900535.1
AFU87167.1	000687	wHTH	192	CbK_gp335	Caulobacter virus phiCbK	GCA_000900535.1
AGH57019.1	000688	T4-gp33-HTH	81	CPXG_00216	Cyanophage P-RSM6	GCA_000906155.1
AJK27430.1	000688	T4-gp33-HTH	81	PTIM40_3	Cyanophage P-TIM40	GCA_001470935.1
AOO14414.1	000688	T4-gp33-HTH	83	Sn110110_221	Cyanophage S-RIM14	GCA_002599065.1
AOO15063.1	000688	T4-gp33-HTH	83	W1230910_218	Cyanophage S-RIM14	GCA_002599125.1
AMO43244.1	000688	T4-gp33-HTH	73	R1080702_239	Cyanophage S-RIM32	GCA_001754165.1
AMO43475.1	000688	T4-gp33-HTH	73	W270710_236	Cyanophage S-RIM44	GCA_002599145.1
AOO11717.1	000688	T4-gp33-HTH	73	ES420910_240	Cyanophage S-RIM44	GCA_002599165.1
AOO11947.1	000688	T4-gp33-HTH	73	Np050604_236	Cyanophage S-RIM44	GCA_002599185.1
AOO12183.1	000688	T4-gp33-HTH	73	Np200711_241	Cyanophage S-RIM44	GCA_002599205.1
AOO12418.1	000688	T4-gp33-HTH	73	Np420711_240	Cyanophage S-RIM44	GCA_002599225.1
AOO12648.1	000688	T4-gp33-HTH	73	Sn080709_236	Cyanophage S-RIM44	GCA_002599245.1
AOO12883.1	000688	T4-gp33-HTH	73	Sn130910_240	Cyanophage S-RIM44	GCA_002599265.1
AOO13114.1	000688	T4-gp33-HTH	73	W2100709_237	Cyanophage S-RIM44	GCA_002599285.1
AGH07627.1	000688	T4-gp33-HTH	84	CYVG_00184	Cyanophage S-SSM6a	GCA_002710385.1
AGG54371.1	000688	T4-gp33-HTH	84	CYWG_00087	Cyanophage S-SSM6b	GCA_002710425.1
AGH26214.1	000688	T4-gp33-HTH	85	CPMG_00113	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44379.1	000688	T4-gp33-HTH	86	PSSM2_001	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12268.1	000688	T4-gp33-HTH	86	PRTG_00114	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93582.1	000688	T4-gp33-HTH	89	AVU42_gp246	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99336.1	000688	T4-gp33-HTH	82	Syn1_240	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30767.1	000688	T4-gp33-HTH	87	Syn7803US37_290	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54992.1	000688	T4-gp33-HTH	90	b23_0386	Synechococcus phage B23	GCA_009745195.1
QGT54627.1	000688	T4-gp33-HTH	90	b3_0392	Synechococcus phage B3	GCA_009745215.1
ASR76048.1	000688	T4-gp33-HTH	53	PBI_BELLAMY_1	Synechococcus phage Bellamy	GCA_002627525.1
QCW23065.1	000688	T4-gp33-HTH	89	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50687.1	000688	T4-gp33-HTH	89	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59698.1	000688	T4-gp33-HTH	73	S330809_237	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59460.1	000688	T4-gp33-HTH	73	C440309_237	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59935.1	000688	T4-gp33-HTH	73	N231010_236	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70451.1	000688	T4-gp33-HTH	84	HOU04_gp052	Synechococcus phage S-T4	GCA_003443335.1
QJT70261.1	000688	T4-gp33-HTH	85	SynMITS9220M01_255	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01442.1	000689	T4-gp33-HTH	79	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28793.1	000689	T4-gp33-HTH	79	AP1_0086	Aeromonas phage AP1	GCA_014183365.1
ATI17457.1	000689	T4-gp33-HTH	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00139.1	000689	T4-gp33-HTH	79	HWB28_gp011	Aeromonas phage AS-zj	GCA_002627665.1
AUE22851.1	000689	T4-gp33-HTH	76	Ah1_00333	Aeromonas phage Ah1	GCA_002957415.1
QAX98562.1	000689	T4-gp33-HTH	76	ASfcp2_228	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97897.1	000689	T4-gp33-HTH	79	ASswx1_254	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01256.1	000689	T4-gp33-HTH	79	ASwh1_191	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39407.1	000689	T4-gp33-HTH	79	CC2_279	Aeromonas phage CC2	GCA_000903495.1
ADQ53027.1	000689	T4-gp33-HTH	76	PX29p308	Aeromonas phage PX29	GCA_000920195.1
ADM79951.1	000689	T4-gp33-HTH	80	phiAS5_ORF0108	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53062.1	000689	T4-gp33-HTH	61	65p052	Aeromonas virus 65	GCA_000893255.1
AAQ17980.1	000689	T4-gp33-HTH	76	33	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64074.1	000690	T4-gp33-HTH	98	KVP40.0003	Vibrio phage KVP40	GCA_000843785.1
QIW90400.1	000690	T4-gp33-HTH	97	GCAPEGMB_00053	Vibrio phage V07	GCA_012361095.1
QIW91029.1	000690	T4-gp33-HTH	97	COHAPHLL_00166	Vibrio phage V09	GCA_012361135.1
QHJ74186.1	000690	T4-gp33-HTH	97	VH12019_00267	Vibrio phage VH1_2019	GCA_009931825.1
AGB07010.1	000690	T4-gp33-HTH	98	CF80_gp223	Vibrio phage VH7D	GCA_000914495.1
QBX06086.1	000690	T4-gp33-HTH	100	ValB1HC_132	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61100.1	000690	T4-gp33-HTH	97	AVU32_gp259	Vibrio phage ValKK3	GCA_001501635.1
ALP47199.1	000690	T4-gp33-HTH	100	phiGrn1_0118	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47590.1	000690	T4-gp33-HTH	100	phiST2_0249	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54712.1	000690	T4-gp33-HTH	98	vBValMR10Z_171	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37237.1	000690	T4-gp33-HTH	97	pp2_003	Vibriophage phi-pp2	GCA_002630725.1
ANS06140.1	000691	Trans_coact	83	ABCD_0047	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AON97057.1	000691	Trans_coact	83	E_048	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70795.1	000691	Trans_coact	112	phiC120_c89	Escherichia phage phiC120	GCA_002621185.1
AAX78569.1	000691	Trans_coact	83	RB43ORF047c	Escherichia virus RB43	GCA_000863505.1
AGR47817.1	000692	T4-gp33-HTH	75	SmphiM12_185	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13032.1	000692	T4-gp33-HTH	75	PHIM19_127	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12672.1	000692	T4-gp33-HTH	75	PHIM7_126	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13403.1	000692	T4-gp33-HTH	75	PHIN3_140	Sinorhizobium phage phiN3	GCA_001501175.1
AIA64812.1	000693	T4-gp33-HTH	94	S13_013	Cronobacter phage S13	GCA_001503575.1
QHJ78852.1	000693	T4-gp33-HTH	83	-	Myoviridae sp.	GCA_012593985.1
QIG65751.1	000000	T4-gp33-HTH	76	phiOC_p086	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ALY07092.1	000000	T4-gp33-HTH	82	VmeM32_00103	Vibrio phage vB_VmeM-32	GCA_002608825.1
APU01778.1	000694	zf-dskA_traR	85	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29066.1	000694	zf-dskA_traR	85	AP1_0359	Aeromonas phage AP1	GCA_014183365.1
ATI17522.1	000694	zf-dskA_traR	85	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00474.1	000694	zf-dskA_traR	85	HWB28_gp078	Aeromonas phage AS-zj	GCA_002627665.1
QAX97964.1	000694	zf-dskA_traR	85	ASswx1_322	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39508.1	000694	zf-dskA_traR	85	CC2_210	Aeromonas phage CC2	GCA_000903495.1
ADQ53421.1	000694	zf-dskA_traR	85	65p414	Aeromonas virus 65	GCA_000893255.1
AIA64969.1	000694	zf-dskA_traR	87	S13_170	Cronobacter phage S13	GCA_001503575.1
AXG67315.1	000694	zf-dskA_traR	87	AD1_271	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80069.1	000694	zf-dskA_traR	85	JA11_264	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66670.1	000694	zf-dskA_traR	85	JA13_267	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66991.1	000694	zf-dskA_traR	85	JA29_265	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67639.1	000694	zf-dskA_traR	85	JA33_265	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08541.1	000694	zf-dskA_traR	87	Alexandra_285	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58919.1	000694	zf-dskA_traR	85	Y3_279	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28740.1	000694	zf-dskA_traR	85	YOLOSWAG_267	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14184.1	000694	zf-dskA_traR	85	PBI_121Q_294	Escherichia phage 121Q	GCA_000926855.1
QAY00754.1	000694	zf-dskA_traR	85	Ecwhy1_480	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61858.1	000694	zf-dskA_traR	85	EO157G_2690	Escherichia phage SP27	GCA_008033345.1
QBO61522.1	000694	zf-dskA_traR	85	G17_00026	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62128.1	000694	zf-dskA_traR	85	G17_00639	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14136.1	000694	zf-dskA_traR	85	vBEcoMphAPEC6_gp513c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80168.1	000694	zf-dskA_traR	85	PSLUR01_00191	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QHJ78965.1	000694	zf-dskA_traR	84	-	Myoviridae sp.	GCA_012593985.1
QCW18677.1	000694	zf-dskA_traR	86	7t3_0156	Salmonella phage 7t3	GCA_006083215.1
AZU97951.1	000694	zf-dskA_traR	86	CPT_Munch_007	Salmonella phage Munch	GCA_004015485.1
AQW89040.1	000694	zf-dskA_traR	86	BF_0515	Serratia phage BF	GCA_002619745.1
SOK59316.1	000694	zf-dskA_traR	86	g508	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58778.1	000694	zf-dskA_traR	86	g501	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCG76292.1	000000	zf-dskA_traR	76	EST35_0424	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AUZ95261.1	000695	R2K-ATP-GRASP	246	FDJ40_gp502	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95380.1	000695	R2K-ATP-GRASP	262	FDJ40_gp621	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFU88194.1	000695	R2K-ATP-GRASP	284	CcrColossus_gp324	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68871.1	000695	R2K-ATP-GRASP	284	CcrPW_gp332	Caulobacter phage CcrPW	GCA_003443275.1
AFC21815.1	000695	R2K-ATP-GRASP	274	GAP32_365	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21828.1	000695	R2K-ATP-GRASP	245	GAP32_376	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXH72536.1	000695	R2K-ATP-GRASP	273	-	Myoviridae sp.	GCA_003657725.1
AXH72453.1	000695	R2K-ATP-GRASP	243	-	Myoviridae sp.	GCA_003657725.1
AXH72803.1	000695	R2K-ATP-GRASP	249	-	Myoviridae sp.	GCA_003657725.1
QIG66010.1	000695	R2K-ATP-GRASP	274	phiOC_p368	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43938.1	000695	R2K-ATP-GRASP	262	CBB_375	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43949.1	000695	R2K-ATP-GRASP	263	CBB_386	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAG41784.1	000695	R2K-ATP-GRASP	265	RSL1_ORF336	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44292.1	000695	R2K-ATP-GRASP	296	PBI_SCTP2_277	Salicola phage SCTP-2	GCA_002625545.1
AQW88898.1	000695	R2K-ATP-GRASP	276	BF_0373	Serratia phage BF	GCA_002619745.1
AQW88908.1	000695	R2K-ATP-GRASP	262	BF_0383	Serratia phage BF	GCA_002619745.1
AKF13625.1	000695	R2K-ATP-GRASP	262	PHIN3_362	Sinorhizobium phage phiN3	GCA_001501175.1
BBA65568.1	000695	R2K-ATP-GRASP	271	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96575.1	000695	R2K-ATP-GRASP	270	Xoosp13_389	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59184.1	000695	R2K-ATP-GRASP	263	g376	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59198.1	000695	R2K-ATP-GRASP	264	g390	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58650.1	000695	R2K-ATP-GRASP	263	g373	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58662.1	000695	R2K-ATP-GRASP	264	g385	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AEO93670.1	000000	R2K-ATP-GRASP	235	G_412	Bacillus virus G	GCA_000917535.1
ARV77463.1	000000	R2K-ATP-GRASP	250	NOXIFER_298	Pseudomonas phage Noxifer	GCA_002625005.1
ASR76247.1	000000	Aldolase_II	197	PBI_BELLAMY_211	Synechococcus phage Bellamy	GCA_002627525.1
AAQ64368.1	000696	Phagesheath+T4_gp36+Phage-autopeptidase-S74	1094	KVP40.0298.1	Vibrio phage KVP40	GCA_000843785.1
QHJ74479.1	000696	Phagesheath+T4_gp36+Phage-autopeptidase-S74	1091	VH12019_00152	Vibrio phage VH1_2019	GCA_009931825.1
AFN37530.1	000696	Phagesheath+T4_gp36+Phage-autopeptidase-S74	1091	pp2_297	Vibriophage phi-pp2	GCA_002630725.1
QIW90684.1	000696	Phagesheath+T4_gp36+Phage-autopeptidase-S74	1091	GCAPEGMB_00337	Vibrio phage V07	GCA_012361095.1
QIW91114.1	000696	Phagesheath+T4_gp36+Phage-autopeptidase-S74	1091	COHAPHLL_00278	Vibrio phage V09	GCA_012361135.1
AGN30344.1	000697	Phage-autopeptidase-S74	1079	VPFG_00347	Vibrio phage nt-1	GCA_000910195.2
AJT61189.1	000697	Phage-autopeptidase-S74	576	AVU32_gp348	Vibrio phage ValKK3	GCA_001501635.1
AFN37529.1	000697	Phage-autopeptidase-S74	1109	pp2_296	Vibriophage phi-pp2	GCA_002630725.1
AJT61190.1	000697	Phage-autopeptidase-S74	1399	AVU32_gp349	Vibrio phage ValKK3	GCA_001501635.1
QBX06173.1	000697	Phage-autopeptidase-S74	1500	ValB1HC_220	Vibrio phage ValB1 HC	GCA_004771355.1
QCW22889.1	000697	Phage-autopeptidase-S74	535	-	Synechococcus phage S-B05	GCA_006083695.1
QBX06172.1	000697	Phage-autopeptidase-S74	552	ValB1HC_219	Vibrio phage ValB1 HC	GCA_004771355.1
ALP46957.1	000697	Phage-autopeptidase-S74	1399	phiGrn1_0031	Vibrio phage phi-Grn1	GCA_002757115.1
QBO63818.1	000697	Phage-autopeptidase-S74	682	Goslar_00025	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QHJ74478.1	000697	Phage-autopeptidase-S74	1109	VH12019_00151	Vibrio phage VH1_2019	GCA_009931825.1
ALP47036.1	000697	Phage-autopeptidase-S74	274	phiGrn1_0032	Vibrio phage phi-Grn1	GCA_002757115.1
SOK59064.1	000697	Phage-autopeptidase-S74	544	g256	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AFH14728.1	000697	Phage-autopeptidase-S74	268	Lu11_0191	Pseudomonas phage Lu11	GCA_000897175.1
ALY07238.1	000697	Phage-autopeptidase-S74	448	VmeM32_00252	Vibrio phage vB_VmeM-32	GCA_002608825.1
AIX30749.1	000697	Phage-autopeptidase-S74	356	Syn7803US37_272	Synechococcus phage ACG-2014f	GCA_002594065.1
ALY07145.1	000697	Phage-autopeptidase-S74	522	VmeM32_00159	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALP47337.1	000697	Phage-autopeptidase-S74	1337	phiST2_0164	Vibrio phage phi-ST2	GCA_002757135.1
ALP47353.1	000697	Phage-autopeptidase-S74	576	phiST2_0165	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54799.1	000697	Phage-autopeptidase-S74	1399	vBValMR10Z_259	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54798.1	000697	Phage-autopeptidase-S74	576	vBValMR10Z_258	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
SOK58530.1	000697	Phage-autopeptidase-S74	544	g253	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIW90683.1	000697	Phage-autopeptidase-S74	1085	GCAPEGMB_00336	Vibrio phage V07	GCA_012361095.1
AQW88783.1	000697	Phage-autopeptidase-S74	559	BF_0258	Serratia phage BF	GCA_002619745.1
QIW91115.1	000697	Phage-autopeptidase-S74	1085	COHAPHLL_00279	Vibrio phage V09	GCA_012361135.1
QFP93060.1	000697	Phage-autopeptidase-S74	576	-	Serratia phage PCH45	GCA_009187865.1
AIR93410.1	000697	Phage-autopeptidase-S74	974	AVU42_gp026	Prochlorococcus phage P-TIM68	GCA_001503075.1
QIG65712.1	000698	T4_gp36+Phage-autopeptidase-S74	552	phiOC_p046	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGN30345.1	000698	T4_gp36+Phage-autopeptidase-S74	1187	VPFG_00348	Vibrio phage nt-1	GCA_000910195.2
AGH07654.1	000699	Phage-autopeptidase-S74	2328	CYVG_00211	Cyanophage S-SSM6a	GCA_002710385.1
AAX44411.1	000699	Phage-autopeptidase-S74	1908	PSSM2_033	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12240.1	000699	Phage-autopeptidase-S74	1908	PRTG_00082	Prochlorococcus phage P-SSM5	GCA_002991095.1
ANS05926.1	000700	Phage-autopeptidase-S74	756	ABCD_0262	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS05924.1	000700	Phage-autopeptidase-S74	813	ABCD_0263	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64807.1	000700	Phage-autopeptidase-S74	851	S13_008	Cronobacter phage S13	GCA_001503575.1
AON97281.1	000700	Phage-autopeptidase-S74	739	E_273	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97282.1	000700	Phage-autopeptidase-S74	743	E_274	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70801.1	000700	Phage-autopeptidase-S74	1077	phiC120_c95	Escherichia phage phiC120	GCA_002621185.1
AAX78802.1	000700	Phage-autopeptidase-S74	742	RB43ORF280w	Escherichia virus RB43	GCA_000863505.1
AAX78803.1	000700	Phage-autopeptidase-S74	812	RB43ORF281w	Escherichia virus RB43	GCA_000863505.1
QHJ78857.1	000700	Phage-autopeptidase-S74	684	-	Myoviridae sp.	GCA_012593985.1
AIA64806.1	000700	Phage-autopeptidase-S74	763	S13_007	Cronobacter phage S13	GCA_001503575.1
AUE22856.1	000701	T4_gp36+Phage-autopeptidase-S74	1385	Ah1_00338	Aeromonas phage Ah1	GCA_002957415.1
QAX98567.1	000701	T4_gp36+Phage-autopeptidase-S74	1288	ASfcp2_233	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53031.1	000701	T4_gp36+Phage-autopeptidase-S74	1384	PX29p314	Aeromonas phage PX29	GCA_000920195.1
ADM79956.1	000701	T4_gp36+Phage-autopeptidase-S74	1313	phiAS5_ORF0113	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17985.1	000701	T4_gp36+Phage-autopeptidase-S74	1358	Aeh1ORF316w	Aeromonas virus Aeh1	GCA_000843245.1
AAX44675.1	000702	Phage-autopeptidase-S74	1094	PSSM2_298	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12301.1	000702	Phage-autopeptidase-S74	463	PRTG_00148	Prochlorococcus phage P-SSM5	GCA_002991095.1
BAG41619.2	000703	DUF3751+Phage-autopeptidase-S74	1224	RSL1_ORF171	Ralstonia phage phiRSL1	GCA_000879455.1
ATA65455.1	000704	Phage-autopeptidase-S74	1347	2050HW_00120	Serratia phage 2050HW	GCA_002628125.1
QDB71225.1	000704	Phage-autopeptidase-S74	1347	CPT_Moabite_195	Serratia phage Moabite	GCA_006384735.1
QCG76041.1	000705	Phage_fiber+Phage-autopeptidase-S74	1008	EST35_0159	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
prev15ph1000000406	000706	SIG+Phage-autopeptidase-S74+BZIP	406	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFA44801.1	000000	Phage-autopeptidase-S74	779	RaK2_00530	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG65967.1	000000	Phage-autopeptidase-S74	627	phiOC_p325	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66000.1	000000	Phage-autopeptidase-S74	663	phiOC_p358	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AIR93411.1	000000	Phage-autopeptidase-S74	730	AVU42_gp027	Prochlorococcus phage P-TIM68	GCA_001503075.1
QDH83636.1	000000	SIG+Collar+Phage-autopeptidase-S74	786	H1O15_gp152	Achromobacter phage Motura	GCA_006964305.1
QDH83431.1	000707	QueD	148	H1O15_gp023	Achromobacter phage Motura	GCA_006964305.1
CCH63508.1	000707	QueD	201	CP21_046	Campylobacter virus CP21	GCA_000902535.1
QCG76135.1	000707	QueD	172	EST35_0254	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76139.1	000707	QueD	156	EST35_0258	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QIW90774.1	000707	QueD	154	GCAPEGMB_00455	Vibrio phage V07	GCA_012361095.1
ANZ49651.1	000708	TerB	141	MACHINA_6	Erwinia phage Machina	GCA_002758035.1
ANZ48029.1	000708	TerB	141	ASESINO_6	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48305.1	000708	TerB	141	CAITLIN_5	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48577.1	000708	TerB	141	CHRISDB_6	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49095.1	000708	TerB	141	HUXLEY_6	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49924.1	000708	TerB	141	PARSHIK_6	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QBX06763.1	000709	Cluster7554_1clades	128	BcepSaruman_350	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74733.1	000709	Cluster7554_1clades	128	BcepSauron_353	Burkholderia phage BcepSauron	GCA_005394215.1
SBV38387.1	000710	Lu11_0058-structural-protein	258	BN7874_211	Phage NCTB	GCA_900092385.1
AFH14588.1	000710	Lu11_0058-structural-protein	324	Lu11_0057	Pseudomonas phage Lu11	GCA_000897175.1
AFH14589.1	000710	Lu11_0058-structural-protein	260	Lu11_0058	Pseudomonas phage Lu11	GCA_000897175.1
AGS81956.1	000710	Lu11_0058-structural-protein	315	PaBG_00072	Pseudomonas phage PaBG	GCA_000912555.1
AGS81957.1	000710	Lu11_0058-structural-protein	261	PaBG_00073	Pseudomonas phage PaBG	GCA_000912555.1
prevph1000000071	000711	METHYLASE	648	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000056	000711	METHYLASE	648	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBO63904.1	000712	METHYLASE	223	Goslar_00111	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QKE54396.1	000712	METHYLASE	221	ACSA002_0820	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAX44641.1	000713	METHYLASE	212	PSSM2_264	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12330.1	000713	METHYLASE	212	PRTG_00177	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFH14699.1	000000	SAM-methylase	230	Lu11_0165	Pseudomonas phage Lu11	GCA_000897175.1
QHJ86125.1	000000	SAM-methylase	154	KKIINIFJ_00214	Pseudomonas phage PN05	GCA_009931935.1
ASR76239.1	000000	SAM-methylase	226	PBI_BELLAMY_203	Synechococcus phage Bellamy	GCA_002627525.1
ASR76262.1	000000	SAM-methylase	259	PBI_BELLAMY_226	Synechococcus phage Bellamy	GCA_002627525.1
AXQ70513.1	000000	SAM-methylase	164	HOU04_gp114	Synechococcus phage S-T4	GCA_003443335.1
QJT70217.1	000000	SAM-methylase	206	SynMITS9220M01_211	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QAU04536.1	000000	SAM-methylase	201	ValB1MD_243	Vibrio phage ValB1MD	GCA_004138815.1
ADM80150.1	000000	METHYLASE	144	phiAS5_ORF0307	Aeromonas phage phiAS5	GCA_000887715.1
AUZ95404.1	000000	METHYLASE	254	FDI40_gp645	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIR93526.1	000000	METHYLASE	338	AVU42_gp189	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30668.1	000000	METHYLASE	301	Syn7803US37_191	Synechococcus phage ACG-2014f	GCA_002594065.1
BBA65301.1	000000	METHYLASE	251	-	Xanthomonas phage XacN1	GCA_003173815.1
AOO14241.1	000714	Methyltransf_24	547	Sn110110_047	Cyanophage S-RIM14	GCA_002599065.1
AOO14893.1	000714	Methyltransf_24	547	W1230910_047	Cyanophage S-RIM14	GCA_002599125.1
BAW19113.1	000714	Methyltransf_24	346	FDH28_gp282	Ralstonia phage RP12	GCA_002617345.1
BAW19399.1	000714	Methyltransf_24	346	-	Ralstonia phage RP31	GCA_002617365.1
AOV59564.1	000714	Methyltransf_24	527	S330809_103	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59326.1	000714	Methyltransf_24	527	C440309_103	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59802.1	000714	Methyltransf_24	527	N231010_103	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67060.1	000715	SAM-methylase	256	AD1_016	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08298.1	000715	SAM-methylase	256	Alexandra_17	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58657.1	000715	SAM-methylase	256	Y3_017	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28503.1	000715	SAM-methylase	257	YOLOSWAG_16	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGS82054.1	000715	SAM-methylase	258	PaBG_00178	Pseudomonas phage PaBG	GCA_000912555.1
QCW22933.1	000715	SAM-methylase	231	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50618.1	000715	SAM-methylase	231	-	Synechococcus phage S-B43	GCA_006869725.1
AFC21932.1	000716	SAM-methylase	180	GAP32_474	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44058.1	000716	SAM-methylase	179	CBB_495	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89012.1	000716	SAM-methylase	179	BF_0487	Serratia phage BF	GCA_002619745.1
BBA65350.1	000716	SAM-methylase	176	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK59293.1	000716	SAM-methylase	179	g485	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58758.1	000716	SAM-methylase	179	g481	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AAX44644.1	000717	Methyltransf_21	206	PSSM2_267	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12327.1	000717	Methyltransf_21	206	PRTG_00174	Prochlorococcus phage P-SSM5	GCA_002991095.1
QCW22975.1	000717	Methyltransf_21	237	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50555.1	000717	Methyltransf_21	237	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ69202.1	000718	SAM-methylase	175	CcrBL9_gp178	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88000.1	000718	SAM-methylase	134	CcrColossus_gp130	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68676.1	000718	SAM-methylase	168	CcrPW_gp137	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69755.1	000718	SAM-methylase	175	CcrSC_gp173	Caulobacter phage CcrSC	GCA_003443315.1
BBA65536.1	000719	SAM-methylase	192	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96533.1	000719	SAM-methylase	192	Xoosp13_347	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AIX30704.1	000000	SIG+SAM-methylase	207	Syn7803US37_227	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30504.1	000000	Methyltransf_24	184	Syn7803US37_27	Synechococcus phage ACG-2014f	GCA_002594065.1
AUZ94886.1	000720	zf_C2H2_6+C-term-domain	250	FDI40_gp077	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21730.1	000720	zf_C2H2_6+C-term-domain	239	GAP32_280	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13911.1	000720	zf_C2H2_6+C-term-domain	236	PBI_121Q_14	Escherichia phage 121Q	GCA_000926855.1
QAY00427.1	000720	zf_C2H2_6+C-term-domain	236	Ecwhy1_146	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35170.1	000720	zf_C2H2_6+C-term-domain	236	ACQ29_gp490	Escherichia phage PBECO4	GCA_001041035.1
BBM61603.1	000720	zf_C2H2_6+C-term-domain	236	EO157G_0140	Escherichia phage SP27	GCA_008033345.1
AXC36742.1	000720	zf_C2H2_6+C-term-domain	236	-	Escherichia phage UB	GCA_003341455.1
QBO61781.1	000720	zf_C2H2_6+C-term-domain	236	G17_00292	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13825.1	000720	zf_C2H2_6+C-term-domain	236	vBEcoMphAPEC6_gp196c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80506.1	000720	zf_C2H2_6+C-term-domain	236	PSLUR01_00529	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44395.1	000720	zf_C2H2_6+C-term-domain	248	RaK2_00122	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72768.1	000720	zf_C2H2_6+C-term-domain	239	-	Myoviridae sp.	GCA_003657725.1
AMM43849.1	000720	zf_C2H2_6+C-term-domain	239	CBB_285	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76100.1	000720	zf_C2H2_6+C-term-domain	235	EST35_0219	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44162.1	000720	zf_C2H2_6+C-term-domain	293	PBI_SCTP2_147	Salicola phage SCTP-2	GCA_002625545.1
QCW19008.1	000720	zf_C2H2_6+C-term-domain	236	7t3_0488	Salmonella phage 7t3	GCA_006083215.1
AZU98255.1	000720	zf_C2H2_6+C-term-domain	236	CPT_Munch_311	Salmonella phage Munch	GCA_004015485.1
QIG62729.1	000720	zf_C2H2_6+C-term-domain	236	SEPL_116	Salmonella phage SE_PL	GCA_011067555.1
AQW88808.1	000720	zf_C2H2_6+C-term-domain	239	BF_0283	Serratia phage BF	GCA_002619745.1
BBA65386.1	000720	zf_C2H2_6+C-term-domain	229	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96414.1	000720	zf_C2H2_6+C-term-domain	229	Xoosp13_228	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59091.1	000720	zf_C2H2_6+C-term-domain	239	g283	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58555.1	000720	zf_C2H2_6+C-term-domain	239	g278	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95251.1	000721	ClpABN-AAA+ClpABC-AAA	661	FDI40_gp492	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44736.1	000721	ClpABN-AAA+ClpABC-AAA	765	FDI40_gp292	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21679.1	000721	ClpABN-AAA+ClpABC-AAA	764	GAP32_229	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14471.1	000721	ClpABN-AAA+ClpABC-AAA	762	PBI_121Q_581	Escherichia phage 121Q	GCA_000926855.1
QAY00476.1	000721	ClpABN-AAA+ClpABC-AAA	762	Ecwhy1_197	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35219.1	000721	ClpABN-AAA+ClpABC-AAA	762	ACQ29_gp539	Escherichia phage PBECO4	GCA_001041035.1
BBM62144.1	000721	ClpABN-AAA+ClpABC-AAA	762	EO157G_5550	Escherichia phage SP27	GCA_008033345.1
AXC36792.1	000721	ClpABN-AAA+ClpABC-AAA	762	-	Escherichia phage UB	GCA_003341455.1
QBO61831.1	000721	ClpABN-AAA+ClpABC-AAA	762	G17_00342	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13875.1	000721	ClpABN-AAA+ClpABC-AAA	762	vBEcoMphAPEC6_gp246c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80456.1	000721	ClpABN-AAA+ClpABC-AAA	762	PSLUR01_00479	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44342.1	000721	ClpABN-AAA+ClpABC-AAA	769	RaK2_00069	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72817.1	000721	ClpABN-AAA+ClpABC-AAA	753	-	Myoviridae sp.	GCA_003657725.1
AMM43800.1	000721	ClpABN-AAA+ClpABC-AAA	765	CBB_235	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76179.1	000721	ClpABN-AAA+ClpABC-AAA	739	EST35_0298	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44085.1	000721	ClpABN-AAA+ClpABC-AAA	738	PBI_SCTP2_70	Salicola phage SCTP-2	GCA_002625545.1
QCW18952.1	000721	ClpABN-AAA+ClpABC-AAA	756	7t3_0431	Salmonella phage 7t3	GCA_006083215.1
AZU98205.1	000721	ClpABN-AAA+ClpABC-AAA	756	CPT_Munch_261	Salmonella phage Munch	GCA_004015485.1
QIG62779.1	000721	ClpABN-AAA+ClpABC-AAA	756	SEPL_166	Salmonella phage SE_PL	GCA_011067555.1
AQW88759.1	000721	ClpABN-AAA+ClpABC-AAA	764	BF_0234	Serratia phage BF	GCA_002619745.1
SOK59040.1	000721	ClpABN-AAA+ClpABC-AAA	765	g232	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58505.1	000721	ClpABN-AAA+ClpABC-AAA	765	g228	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70401.1	000722	virion_structural-Cluster73_1clades	250	CF8_0232	Aeromonas phage CF8	GCA_006384595.2
QDJ97398.1	000722	virion_structural-Cluster73_1clades	249	D6_0239	Aeromonas phage D6	GCA_007051205.2
QDH47111.1	000722	virion_structural-Cluster73_1clades	249	LAh10_152	Aeromonas phage LAh10	GCA_006863975.1
QDJ96746.1	000722	virion_structural-Cluster73_1clades	248	PS1_0235	Aeromonas phage PS1	GCA_007051165.2
QFR59379.1	000722	virion_structural-Cluster73_1clades	248	PS2_0237	Aeromonas phage PS2	GCA_009388305.2
AFO71432.1	000722	virion_structural-Cluster73_1clades	240	CR5_212	Cronobacter phage CR5	GCA_000910235.1
QBZ70784.1	000722	virion_structural-Cluster73_1clades	245	pETSU_203	Edwardsiella virus pEt-SU	GCA_004800915.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMR59896.1	000722	virion_structural-Cluster73_1clades	240	SEGD1_249	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07645.1	000722	virion_structural-Cluster73_1clades	240	DERBICUS_219	Erwinia phage Derbicus	GCA_004521655.1
AHI60318.1	000722	virion_structural-Cluster73_1clades	241	Ea357_167	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49895.1	000722	virion_structural-Cluster73_1clades	240	MACHINA_257	Erwinia phage Machina	GCA_002758035.1
AGX01864.1	000722	virion_structural-Cluster73_1clades	241	CF95_gp142	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07277.1	000722	virion_structural-Cluster73_1clades	241	REBECCA_170	Erwinia phage Rebecca	GCA_004521635.1
AXF51396.1	000722	virion_structural-Cluster73_1clades	240	WELLINGTON_270	Erwinia phage Wellington	GCA_003344985.1
AFQ96709.1	000722	virion_structural-Cluster73_1clades	242	G173_gp164	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48279.1	000722	virion_structural-Cluster73_1clades	242	ASESINO_266	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85957.1	000722	virion_structural-Cluster73_1clades	241	BOSOLAPHORUS_170	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48551.1	000722	virion_structural-Cluster73_1clades	240	CAITLIN_256	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48829.1	000722	virion_structural-Cluster73_1clades	240	CHRISDB_267	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52272.1	000722	virion_structural-Cluster73_1clades	241	DM_174	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86276.1	000722	virion_structural-Cluster73_1clades	241	DESERTFOX_169	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49069.1	000722	virion_structural-Cluster73_1clades	240	EARLPHILLIPIV_220	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49338.1	000722	virion_structural-Cluster73_1clades	240	HUXLEY_256	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03679.1	000722	virion_structural-Cluster73_1clades	241	JOAD_236	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49622.1	000722	virion_structural-Cluster73_1clades	240	KWAN_270	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86598.1	000722	virion_structural-Cluster73_1clades	241	MADMEL_170	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86922.1	000722	virion_structural-Cluster73_1clades	241	MORTIMER_173	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50166.1	000722	virion_structural-Cluster73_1clades	240	PARSHIK_257	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50416.1	000722	virion_structural-Cluster73_1clades	240	PHOBOS_226	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51949.1	000722	virion_structural-Cluster73_1clades	241	RAY_168	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03436.1	000722	virion_structural-Cluster73_1clades	241	RISINGSUN_234	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51633.1	000722	virion_structural-Cluster73_1clades	241	SIMMY50_171	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64980.1	000722	virion_structural-Cluster73_1clades	241	SPECIALG_170	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50691.1	000722	virion_structural-Cluster73_1clades	242	STRATTON_266	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86085.1	000722	virion_structural-Cluster73_1clades	240	ACEC001_2420	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64017.1	000722	virion_structural-Cluster73_1clades	236	Goslar_00225	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72090.1	000722	virion_structural-Cluster73_1clades	245	N1M2_227	Klebsiella phage N1M2	GCA_010092605.1
QGZ14519.1	000722	virion_structural-Cluster73_1clades	244	HWC77_gp156	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24099.1	000722	virion_structural-Cluster73_1clades	242	-	Proteus phage 10	GCA_014071245.1
ABY63097.1	000722	virion_structural-Cluster73_1clades	239	201phi2-1p269	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27285.1	000722	virion_structural-Cluster73_1clades	242	PPEV_gp191	Pseudomonas phage EL	GCA_000866825.1
ANM44974.1	000722	virion_structural-Cluster73_1clades	240	KTN4_216	Pseudomonas phage KTN4	GCA_002607225.1
ARV77361.1	000722	virion_structural-Cluster73_1clades	236	NOXIFER_192	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89719.1	000722	virion_structural-Cluster73_1clades	245	OBP_282	Pseudomonas phage OBP	GCA_000896635.1
QBX32364.1	000722	virion_structural-Cluster73_1clades	240	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76890.1	000722	virion_structural-Cluster73_1clades	240	PHABIO_259	Pseudomonas phage Phabio	GCA_002624965.1
AEH03629.1	000722	virion_structural-Cluster73_1clades	240	206	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02766.1	000722	virion_structural-Cluster73_1clades	237	PSA21_240	Pseudomonas phage Psa21	GCA_004340405.1
ATN94740.1	000722	virion_structural-Cluster73_1clades	240	SL2_163	Pseudomonas phage SL2	GCA_002956015.1
QJB22852.1	000722	virion_structural-Cluster73_1clades	240	fnug_209	Pseudomonas phage fnug	GCA_012837215.1
QEM41938.1	000722	virion_structural-Cluster73_1clades	240	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83077.1	000722	virion_structural-Cluster73_1clades	242	PHIKZ176	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19012.1	000722	virion_structural-Cluster73_1clades	240	FDH28_gp038	Ralstonia phage RP12	GCA_002617345.1
BAW19298.1	000722	virion_structural-Cluster73_1clades	240	-	Ralstonia phage RP31	GCA_002617365.1
BAS04829.1	000722	virion_structural-Cluster73_1clades	240	AVU11_gp037	Ralstonia phage RSF1	GCA_001500875.1
BAQ02562.1	000722	virion_structural-Cluster73_1clades	240	AVU38_gp034	Ralstonia phage RSL2	GCA_001503055.1
QNI20928.1	000722	virion_structural-Cluster73_1clades	133	-	Salmonella phage JN03	GCA_014319805.1
AXF51110.1	000722	virion_structural-Cluster73_1clades	240	MLDJOKPK_00196	Salmonella phage SPAsTU	GCA_003183805.1
AEP84077.1	000722	virion_structural-Cluster73_1clades	240	SPN3US_0244	Salmonella phage SPN3US	GCA_001042275.1
QKE54475.1	000722	virion_structural-Cluster73_1clades	241	ACSA002_1610	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65440.1	000722	virion_structural-Cluster73_1clades	241	2050HW_00105	Serratia phage 2050HW	GCA_002628125.1
QDB71211.1	000722	virion_structural-Cluster73_1clades	241	CPT_Moabite_181	Serratia phage Moabite	GCA_006384735.1
QFP93132.1	000722	virion_structural-Cluster73_1clades	241	-	Serratia phage PCH45	GCA_009187865.1
QAU04215.1	000722	virion_structural-Cluster73_1clades	244	HWC03_gp060	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23145.1	000722	virion_structural-Cluster73_1clades	244	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81009.1	000722	virion_structural-Cluster73_1clades	244	Aphrodite1_0195	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70770.1	000722	virion_structural-Cluster73_1clades	241	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47582.1	000722	virion_structural-Cluster73_1clades	244	HWC35_gp188	Vibrio phage USC-1	GCA_006864065.1
BAW98397.1	000722	virion_structural-Cluster73_1clades	244	FDH33_gp188	Vibrio phage pTD1	GCA_002618825.1
AQT28111.1	000722	virion_structural-Cluster73_1clades	240	pVa21_170	Vibrio phage pVa-21	GCA_002619305.1
QAX96758.1	000722	virion_structural-Cluster73_1clades	241	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97077.1	000722	virion_structural-Cluster73_1clades	241	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96123.1	000722	virion_structural-Cluster73_1clades	241	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96441.1	000722	virion_structural-Cluster73_1clades	241	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20986.1	000722	virion_structural-Cluster73_1clades	242	-	Vibrio phage vB_pir03	GCA_014319855.1
AFC21822.1	000723	Cluster543_1clades	186	GAP32_371	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13978.1	000723	Cluster543_1clades	183	PBI_121Q_81	Escherichia phage 121Q	GCA_000926855.1
QAY00359.1	000723	Cluster543_1clades	183	Ecwhy1_78	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35105.1	000723	Cluster543_1clades	183	ACQ29_gp425	Escherichia phage PBECO4	GCA_001041035.1
BBM61670.1	000723	Cluster543_1clades	183	EO157G_0810	Escherichia phage SP27	GCA_008033345.1
AXC36680.1	000723	Cluster543_1clades	183	-	Escherichia phage UB	GCA_003341455.1
QBO61714.1	000723	Cluster543_1clades	183	G17_00225	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13762.1	000723	Cluster543_1clades	183	vBEcoMphAPEC6_gp133c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80572.1	000723	Cluster543_1clades	183	PSLUR01_00595	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44458.1	000723	Cluster543_1clades	185	RaK2_00185	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43944.1	000723	Cluster543_1clades	184	CBB_381	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19084.1	000723	Cluster543_1clades	180	7t3_0565	Salmonella phage 7t3	GCA_006083215.1
AZU98325.1	000723	Cluster543_1clades	180	CPT_Munch_382	Salmonella phage Munch	GCA_004015485.1
QIG62658.1	000723	Cluster543_1clades	180	SEPL_045	Salmonella phage SE_PL	GCA_011067555.1
AQW88903.1	000723	Cluster543_1clades	184	BF_0378	Serratia phage BF	GCA_002619745.1
SOK59193.1	000723	Cluster543_1clades	184	g385	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58657.1	000723	Cluster543_1clades	184	g380	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21822.1	000724	Cluster543_1clades	186	GAP32_371	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13978.1	000724	Cluster543_1clades	183	PBI_121Q_81	Escherichia phage 121Q	GCA_000926855.1
QAY00359.1	000724	Cluster543_1clades	183	Ecwhy1_78	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35105.1	000724	Cluster543_1clades	183	ACQ29_gp425	Escherichia phage PBECO4	GCA_001041035.1
BBM61670.1	000724	Cluster543_1clades	183	EO157G_0810	Escherichia phage SP27	GCA_008033345.1
AXC36680.1	000724	Cluster543_1clades	183	-	Escherichia phage UB	GCA_003341455.1
QBO61714.1	000724	Cluster543_1clades	183	G17_00225	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13762.1	000724	Cluster543_1clades	183	vBEcoMphAPEC6_gp133c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80572.1	000724	Cluster543_1clades	183	PSLUR01_00595	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44458.1	000724	Cluster543_1clades	185	RaK2_00185	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43944.1	000724	Cluster543_1clades	184	CBB_381	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19084.1	000724	Cluster543_1clades	180	7t3_0565	Salmonella phage 7t3	GCA_006083215.1
AZU98325.1	000724	Cluster543_1clades	180	CPT_Munch_382	Salmonella phage Munch	GCA_004015485.1
QIG62658.1	000724	Cluster543_1clades	180	SEPL_045	Salmonella phage SE_PL	GCA_011067555.1
AQW88903.1	000724	Cluster543_1clades	184	BF_0378	Serratia phage BF	GCA_002619745.1
SOK59193.1	000724	Cluster543_1clades	184	g385	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58657.1	000724	Cluster543_1clades	184	g380	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21529.1	000725	Alpha-helical-Cluster767_1clades	78	GAP32_081	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14329.1	000725	Alpha-helical-Cluster767_1clades	84	PBI_121Q_439	Escherichia phage 121Q	GCA_000926855.1
QAY00612.1	000725	Alpha-helical-Cluster767_1clades	84	Ecwhy1_336	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34808.1	000725	Alpha-helical-Cluster767_1clades	84	ACQ29_gp128	Escherichia phage PBECO4	GCA_001041035.1
BBM62002.1	000725	Alpha-helical-Cluster767_1clades	84	EO157G_4130	Escherichia phage SP27	GCA_008033345.1
QBO61975.1	000725	Alpha-helical-Cluster767_1clades	84	G17_00486	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13999.1	000725	Alpha-helical-Cluster767_1clades	84	vBEcoMphAPEC6_gp375c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80316.1	000725	Alpha-helical-Cluster767_1clades	84	PSLUR01_00339	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43649.1	000725	Alpha-helical-Cluster767_1clades	78	CBB_84	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18784.1	000725	Alpha-helical-Cluster767_1clades	87	7t3_0263	Salmonella phage 7t3	GCA_006083215.1
AZU98049.1	000725	Alpha-helical-Cluster767_1clades	87	CPT_Munch_105	Salmonella phage Munch	GCA_004015485.1
QIG62931.1	000725	Alpha-helical-Cluster767_1clades	87	SEPL_318	Salmonella phage SE_PL	GCA_011067555.1
AQW88598.1	000725	Alpha-helical-Cluster767_1clades	78	BF_0073	Serratia phage BF	GCA_002619745.1
SOK58875.1	000725	Alpha-helical-Cluster767_1clades	78	g067	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58338.1	000725	Alpha-helical-Cluster767_1clades	78	g061	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QHJ86193.1	000000	-	63	KKIINIFJ_00283	Pseudomonas phage PN05	GCA_009931935.1
ARB13722.1	000726	PADR-HTH	82	Ccr10_gp192c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14067.1	000726	PADR-HTH	82	Ccr2_gp191c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14756.1	000726	PADR-HTH	114	Ccr29_gp200	Caulobacter phage Ccr29	GCA_002619485.1
ARB14410.1	000726	PADR-HTH	80	Ccr5_gp190c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68389.1	000726	PADR-HTH	110	CcrBL10_gp185c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69299.1	000726	PADR-HTH	129	CcrBL9_gp275c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69858.1	000726	PADR-HTH	129	CcrSC_gp276c	Caulobacter phage CcrSC	GCA_003443315.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU87715.1	000726	PADR-HTH	112	CcrKarma_gp198	Caulobacter virus Karma	GCA_000901575.1
AFU87364.1	000726	PADR-HTH	112	CcrMagneto_gp194	Caulobacter virus Magneto	GCA_000903095.1
AFU86675.1	000726	PADR-HTH	110	CcrRogue_gp193	Caulobacter virus Rogue	GCA_000900555.1
AFU88511.1	000726	PADR-HTH	112	CcrSwift_gp193	Caulobacter virus Swift	GCA_000899655.1
QDB70315.1	000727	HTH	117	CF8_0147	Aeromonas phage CF8	GCA_006384595.2
QDJ96661.1	000727	HTH	123	PS1_0150	Aeromonas phage PS1	GCA_007051165.2
QFR59295.1	000727	HTH	122	PS2_0154	Aeromonas phage PS2	GCA_009388305.2
AMR59753.1	000727	HTH	121	SEGD1_104	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49752.1	000727	HTH	116	MACHINA_114	Erwinia phage Machina	GCA_002758035.1
AGX01760.1	000727	HTH	118	CF95_gp038	Erwinia phage PhiEaH1	GCA_000914555.1
AXF51253.1	000727	HTH	116	WELLINGTON_123	Erwinia phage Wellington	GCA_003344985.1
AFQ96571.1	000727	HTH	123	G173_gp026	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48131.1	000727	HTH	123	ASESINO_118	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48407.1	000727	HTH	118	CAITLIN_112	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48679.1	000727	HTH	118	CHRISDB_117	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49196.1	000727	HTH	116	HUXLEY_114	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03734.1	000727	HTH	124	JOAD_181	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49474.1	000727	HTH	116	KWAN_122	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50024.1	000727	HTH	116	PARSHIK_115	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ASU03490.1	000727	HTH	124	RISINGSUN_180	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANZ50546.1	000727	HTH	123	STRATTON_121	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85942.1	000727	HTH	121	ACEC001_1040	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QGZ14420.1	000727	HTH	132	HWC77_gp057	Photobacterium phage PDCC-1	GCA_009800445.1
QNI20810.1	000727	HTH	121	-	Salmonella phage JN03	GCA_014319805.1
AWN09005.1	000727	HTH	123	MLDJOKPK_00056	Salmonella phage SPAsTU	GCA_003183805.1
AEP83934.1	000727	HTH	121	SPN3US_0101	Salmonella phage SPN3US	GCA_001042275.1
QAU04316.1	000727	HTH	132	HWC03_gp161	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23262.1	000727	HTH	132	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81071.1	000727	HTH	132	Aphrodite1_0083	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47466.1	000727	HTH	132	HWC35_gp072	Vibrio phage USC-1	GCA_006864065.1
BAW98287.1	000727	HTH	123	FDH33_gp078	Vibrio phage pTD1	GCA_002618825.1
ARB13635.1	000728	HTH+ColE7	266	Ccr10_gp106c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13980.1	000728	HTH+ColE7	266	Ccr2_gp105c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14668.1	000728	HTH+ColE7	266	Ccr29_gp112	Caulobacter phage Ccr29	GCA_002619485.1
ARB15023.1	000728	HTH+ColE7	266	Ccr32_gp105	Caulobacter phage Ccr32	GCA_002619505.1
ARB15355.1	000728	HTH+ColE7	266	Ccr34_gp113	Caulobacter phage Ccr34	GCA_002619525.1
ARB14324.1	000728	HTH+ColE7	266	Ccr5_gp106c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68304.1	000728	HTH+ColE7	264	CcrBL10_gp100c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69234.1	000728	HTH+ColE7	207	CcrBL9_gp210	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88010.1	000728	HTH+ColE7	242	CcrColossus_gp140	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68687.1	000728	HTH+ColE7	243	CcrPW_gp148c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69788.1	000728	HTH+ColE7	232	CcrSC_gp206	Caulobacter phage CcrSC	GCA_003443315.1
AFU87627.1	000728	HTH+ColE7	266	CcrKarma_gp110	Caulobacter virus Karma	GCA_000901575.1
AFU87276.1	000728	HTH+ColE7	266	CcrMagneto_gp106	Caulobacter virus Magneto	GCA_000903095.1
AFU86588.1	000728	HTH+ColE7	263	CcrRogue_gp106	Caulobacter virus Rogue	GCA_000900555.1
AFU88423.1	000728	HTH+ColE7	266	CcrSwift_gp105	Caulobacter virus Swift	GCA_000899655.1
AFU86941.1	000728	HTH+ColE7	266	CbK_gp109	Caulobacter virus phiCbK	GCA_000900535.1
ARB13674.1	000729	HTH	199	Ccr10_gp145	Caulobacter phage Ccr10	GCA_002619445.1
ARB14019.1	000729	HTH	199	Ccr2_gp144	Caulobacter phage Ccr2	GCA_002619465.1
ARB14707.1	000729	HTH	199	Ccr29_gp151	Caulobacter phage Ccr29	GCA_002619485.1
ARB15062.1	000729	HTH	199	Ccr32_gp144	Caulobacter phage Ccr32	GCA_002619505.1
ARB15396.1	000729	HTH	199	Ccr34_gp154	Caulobacter phage Ccr34	GCA_002619525.1
ARB14362.1	000729	HTH	199	Ccr5_gp143	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68344.1	000729	HTH	199	CcrBL10_gp140	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69251.1	000729	HTH	196	CcrBL9_gp227c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88056.1	000729	HTH	197	CcrColossus_gp186	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68735.1	000729	HTH	197	CcrPW_gp196	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69807.1	000729	HTH	195	CcrSC_gp225c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87667.1	000729	HTH	199	CcrKarma_gp150	Caulobacter virus Karma	GCA_000901575.1
AFU87316.1	000729	HTH	199	CcrMagneto_gp146	Caulobacter virus Magneto	GCA_000903095.1
AFU86628.1	000729	HTH	199	CcrRogue_gp146	Caulobacter virus Rogue	GCA_000900555.1
AFU88463.1	000729	HTH	199	CcrSwift_gp145	Caulobacter virus Swift	GCA_000899655.1
AFU86980.1	000729	HTH	199	CbK_gp148	Caulobacter virus phiCbK	GCA_000900535.1
ARB13751.1	000730	HTH	125	Ccr10_gp221c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14096.1	000730	HTH	125	Ccr2_gp220c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14785.1	000730	HTH	125	Ccr29_gp229	Caulobacter phage Ccr29	GCA_002619485.1
ARB15129.1	000730	HTH	125	Ccr32_gp211	Caulobacter phage Ccr32	GCA_002619505.1
ARB15463.1	000730	HTH	125	Ccr34_gp221	Caulobacter phage Ccr34	GCA_002619525.1
ARB14438.1	000730	HTH	125	Ccr5_gp218c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68418.1	000730	HTH	126	CcrBL10_gp214c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69261.1	000730	HTH	141	CcrBL9_gp237c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88122.1	000730	HTH	141	CcrColossus_gp252	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68800.1	000730	HTH	141	CcrPW_gp261	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69818.1	000730	HTH	141	CcrSC_gp236c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87745.1	000730	HTH	125	CcrKarma_gp228	Caulobacter virus Karma	GCA_000901575.1
AFU87393.1	000730	HTH	125	CcrMagneto_gp223	Caulobacter virus Magneto	GCA_000903095.1
AFU86704.1	000730	HTH	126	CcrRogue_gp222	Caulobacter virus Rogue	GCA_000900555.1
AFU88541.1	000730	HTH	125	CcrSwift_gp223	Caulobacter virus Swift	GCA_000899655.1
AFU87048.1	000730	HTH	125	CbK_gp216	Caulobacter virus phiCbK	GCA_000900535.1
ARB13647.1	000731	35exo	209	Ccr10_gp118c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13992.1	000731	35exo	209	Ccr2_gp117c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14680.1	000731	35exo	209	Ccr29_gp124	Caulobacter phage Ccr29	GCA_002619485.1
ARB15035.1	000731	35exo	209	Ccr32_gp117	Caulobacter phage Ccr32	GCA_002619505.1
ARB15367.1	000731	35exo	209	Ccr34_gp125	Caulobacter phage Ccr34	GCA_002619525.1
ARB14336.1	000731	35exo	209	Ccr5_gp118c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68316.1	000731	35exo	209	CcrBL10_gp112c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69214.1	000731	35exo	195	CcrBL9_gp190	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88026.1	000731	35exo	202	CcrColossus_gp156	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68703.1	000731	35exo	203	CcrPW_gp164c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69768.1	000731	35exo	195	CcrSC_gp186	Caulobacter phage CcrSC	GCA_003443315.1
AFU87640.1	000731	35exo	209	CcrKarma_gp123	Caulobacter virus Karma	GCA_000901575.1
AFU87289.1	000731	35exo	209	CcrMagneto_gp119	Caulobacter virus Magneto	GCA_000903095.1
AFU86600.1	000731	35exo	209	CcrRogue_gp118	Caulobacter virus Rogue	GCA_000900555.1
AFU88436.1	000731	35exo	209	CcrSwift_gp118	Caulobacter virus Swift	GCA_000899655.1
AFU86953.1	000731	35exo	209	CbK_gp121	Caulobacter virus phiCbK	GCA_000900535.1
ARB13569.1	000732	SIG+Peptidase_C93	248	Ccr10_gp041c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13915.1	000732	SIG+Peptidase_C93	248	Ccr2_gp040c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14604.1	000732	SIG+Peptidase_C93	129	Ccr29_gp047	Caulobacter phage Ccr29	GCA_002619485.1
ARB14960.1	000732	SIG+Peptidase_C93	129	Ccr32_gp041	Caulobacter phage Ccr32	GCA_002619505.1
ARB15291.1	000732	SIG+Peptidase_C93	248	Ccr34_gp042	Caulobacter phage Ccr34	GCA_002619525.1
ARB14258.1	000732	SIG+Peptidase_C93	248	Ccr5_gp040c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68245.1	000732	SIG+Peptidase_C93	246	CcrBL10_gp041c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87907.1	000732	SIG+Peptidase_C93	213	CcrColossus_gp037	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68576.1	000732	SIG+Peptidase_C93	149	CcrPW_gp037c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87559.1	000732	SIG+Peptidase_C93	248	CcrKarma_gp042	Caulobacter virus Karma	GCA_000901575.1
AFU87209.1	000732	SIG+Peptidase_C93	251	CcrMagneto_gp039	Caulobacter virus Magneto	GCA_000903095.1
AFU86526.1	000732	SIG+Peptidase_C93	246	CcrRogue_gp044	Caulobacter virus Rogue	GCA_000900555.1
AFU88357.1	000732	SIG+Peptidase_C93	248	CcrSwift_gp039	Caulobacter virus Swift	GCA_000899655.1
AFU86873.1	000732	SIG+Peptidase_C93	248	CbK_gp041	Caulobacter virus phiCbK	GCA_000900535.1
AOO14332.1	000733	SAICAR_synt	232	Sn110110_138	Cyanophage S-RIM14	GCA_002599065.1
AOO14981.1	000733	SAICAR_synt	232	W1230910_135	Cyanophage S-RIM14	GCA_002599125.1
AMO43268.1	000733	SAICAR_synt	232	W270710_023	Cyanophage S-RIM44	GCA_002599145.1
AOO11504.1	000733	SAICAR_synt	232	ES420910_022	Cyanophage S-RIM44	GCA_002599165.1
AOO11740.1	000733	SAICAR_synt	232	Np050604_023	Cyanophage S-RIM44	GCA_002599185.1
AOO11969.1	000733	SAICAR_synt	232	Np200711_022	Cyanophage S-RIM44	GCA_002599205.1
AOO12205.1	000733	SAICAR_synt	232	Np420711_022	Cyanophage S-RIM44	GCA_002599225.1
AOO12441.1	000733	SAICAR_synt	232	Sn080709_023	Cyanophage S-RIM44	GCA_002599245.1
AOO12670.1	000733	SAICAR_synt	232	Sn130910_022	Cyanophage S-RIM44	GCA_002599265.1
AOO12906.1	000733	SAICAR_synt	232	W2100709_023	Cyanophage S-RIM44	GCA_002599285.1
ADO99125.1	000733	SAICAR_synt	232	Syn1_023	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59677.1	000733	SAICAR_synt	243	S330809_216	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59439.1	000733	SAICAR_synt	240	C440309_216	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59914.1	000733	SAICAR_synt	232	N231010_215	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13569.1	000734	SIG+Peptidase_C93	248	Ccr10_gp041c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13915.1	000734	SIG+Peptidase_C93	248	Ccr2_gp040c	Caulobacter phage Ccr2	GCA_002619465.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB14604.1	000734	SIG+Peptidase_C93	129	Ccr29_gp047	Caulobacter phage Ccr29	GCA_002619485.1
ARB14960.1	000734	SIG+Peptidase_C93	129	Ccr32_gp041	Caulobacter phage Ccr32	GCA_002619505.1
ARB15291.1	000734	SIG+Peptidase_C93	248	Ccr34_gp042	Caulobacter phage Ccr34	GCA_002619525.1
ARB14258.1	000734	SIG+Peptidase_C93	248	Ccr5_gp040c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68245.1	000734	SIG+Peptidase_C93	246	CcrBL10_gp041c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87907.1	000734	SIG+Peptidase_C93	213	CcrColossus_gp037	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68576.1	000734	SIG+Peptidase_C93	149	CcrPW_gp037c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87559.1	000734	SIG+Peptidase_C93	248	CcrKarma_gp042	Caulobacter virus Karma	GCA_000901575.1
AFU87209.1	000734	SIG+Peptidase_C93	251	CcrMagneto_gp039	Caulobacter virus Magneto	GCA_000903095.1
AFU86526.1	000734	SIG+Peptidase_C93	246	CcrRogue_gp044	Caulobacter virus Rogue	GCA_000900555.1
AFU88357.1	000734	SIG+Peptidase_C93	248	CcrSwift_gp039	Caulobacter virus Swift	GCA_000899655.1
AFU86873.1	000734	SIG+Peptidase_C93	248	CbK_gp041	Caulobacter virus phiCbK	GCA_000900535.1
AOO14332.1	000735	SAICAR_synt	232	Sn110110_138	Cyanophage S-RIM14	GCA_002599065.1
AOO14981.1	000735	SAICAR_synt	232	W1230910_135	Cyanophage S-RIM14	GCA_002599125.1
AMO43268.1	000735	SAICAR_synt	232	W270710_023	Cyanophage S-RIM44	GCA_002599145.1
AOO11504.1	000735	SAICAR_synt	232	ES420910_022	Cyanophage S-RIM44	GCA_002599165.1
AOO11740.1	000735	SAICAR_synt	232	Np050604_023	Cyanophage S-RIM44	GCA_002599185.1
AOO11969.1	000735	SAICAR_synt	232	Np200711_022	Cyanophage S-RIM44	GCA_002599205.1
AOO12205.1	000735	SAICAR_synt	232	Np420711_022	Cyanophage S-RIM44	GCA_002599225.1
AOO12441.1	000735	SAICAR_synt	232	Sn080709_023	Cyanophage S-RIM44	GCA_002599245.1
AOO12670.1	000735	SAICAR_synt	232	Sn130910_022	Cyanophage S-RIM44	GCA_002599265.1
AOO12906.1	000735	SAICAR_synt	232	W2100709_023	Cyanophage S-RIM44	GCA_002599285.1
ADO99125.1	000735	SAICAR_synt	232	Syn1_023	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59677.1	000735	SAICAR_synt	243	S330809_216	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59439.1	000735	SAICAR_synt	240	C440309_216	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59914.1	000735	SAICAR_synt	232	N231010_215	Synechococcus phage S-CAM4	GCA_002922155.1
AIA65002.1	000736	RNaseH_like	158	S13_205	Cronobacter phage S13	GCA_001503575.1
QHJ78929.1	000736	RNaseH_like	155	-	Myoviridae sp.	GCA_012593985.1
AAQ64369.1	000736	RNaseH_like	176	KVP40.0299	Vibrio phage KVP40	GCA_000843785.1
QIW90685.1	000736	RNaseH_like	174	GCAPEGMB_00338	Vibrio phage V07	GCA_012361095.1
QIW91113.1	000736	RNaseH_like	174	COHAPHLL_00277	Vibrio phage V09	GCA_012361135.1
QHJ74480.1	000736	RNaseH_like	174	VH12019_00153	Vibrio phage VH1_2019	GCA_009931825.1
QBX06169.1	000736	RNaseH_like	174	ValB1HC_216	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04447.1	000736	RNaseH_like	153	ValB1MD_026	Vibrio phage ValB1MD	GCA_004138815.1
AJT61186.1	000736	RNaseH_like	174	AVU32_gp345	Vibrio phage ValKK3	GCA_001501635.1
AGN30347.1	000736	RNaseH_like	172	VPFG_00350	Vibrio phage nt-1	GCA_000910195.2
ALP47094.1	000736	RNaseH_like	174	phiGrn1_0036	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47474.1	000736	RNaseH_like	174	phiST2_0168	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54795.1	000736	RNaseH_like	174	vBValMR10Z_255	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37531.1	000736	RNaseH_like	174	pp2_298	Vibriophage phi-pp2	GCA_002630725.1
AEO93559.1	000000	Sigma70_r2	275	G_300	Bacillus virus G	GCA_000917535.1
AND75229.1	000000	REase	160	ME3_68	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75249.1	000000	REase	317	ME3_88	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83752.1	000000	REase	170	0305phi8-36p194	Bacillus phage 0305phi8-36	GCA_000871045.1
CCH63534.1	000000	REase	267	CP21_072	Campylobacter virus CP21	GCA_000902535.1
QCG76090.1	000000	REase	477	EST35_0209	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ALY07085.1	000000	REase	178	VmeM32_00096	Vibrio phage vB_VmeM-32	GCA_002608825.1
AMM45036.1	000737	Thermonuclease	191	SP15_233	Bacillus phage SP-15	GCA_001754685.1
AGH56908.1	000737	Thermonuclease	151	CPXG_00105	Cyanophage P-RSM6	GCA_000906155.1
AJK27548.1	000737	Thermonuclease	152	PTIM40_121	Cyanophage P-TIM40	GCA_001470935.1
AOO14304.1	000737	Thermonuclease	153	Sn110110_110	Cyanophage S-RIM14	GCA_002599065.1
AOO14953.1	000737	Thermonuclease	153	W1230910_107	Cyanophage S-RIM14	GCA_002599125.1
AMO43197.1	000737	Thermonuclease	136	R1080702_188	Cyanophage S-RIM32	GCA_001754165.1
AMO43425.1	000737	Thermonuclease	153	W270710_181	Cyanophage S-RIM44	GCA_002599145.1
AOO11669.1	000737	Thermonuclease	153	ES420910_188	Cyanophage S-RIM44	GCA_002599165.1
AOO11897.1	000737	Thermonuclease	153	Np050604_181	Cyanophage S-RIM44	GCA_002599185.1
AOO12135.1	000737	Thermonuclease	153	Np200711_189	Cyanophage S-RIM44	GCA_002599205.1
AOO12370.1	000737	Thermonuclease	153	Np420711_188	Cyanophage S-RIM44	GCA_002599225.1
AOO12598.1	000737	Thermonuclease	153	Sn080709_181	Cyanophage S-RIM44	GCA_002599245.1
AOO12835.1	000737	Thermonuclease	153	Sn130910_188	Cyanophage S-RIM44	GCA_002599265.1
AOO13064.1	000737	Thermonuclease	153	W2100709_182	Cyanophage S-RIM44	GCA_002599285.1
AGH07518.1	000737	Thermonuclease	138	CYVG_00074	Cyanophage S-SSM6a	GCA_002710385.1
AGG54500.1	000737	Thermonuclease	151	CYWG_00216	Cyanophage S-SSM6b	GCA_002710425.1
SBV38325.1	000737	Thermonuclease	123	BN7874_156	Phage NCTB	GCA_900092385.1
AGH26227.1	000737	Thermonuclease	138	CPMG_00126	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44610.1	000737	Thermonuclease	104	PSSM2_233	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12360.1	000737	Thermonuclease	133	PRTG_00207	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93547.1	000737	Thermonuclease	160	AVU42_gp213	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99284.1	000737	Thermonuclease	153	Syn1_183	Prochlorococcus phage Syn1	GCA_000892495.1
BAW19227.1	000737	Thermonuclease	120	FDH28_gp168	Ralstonia phage RP12	GCA_002617345.1
BAW19513.1	000737	Thermonuclease	120	-	Ralstonia phage RP31	GCA_002617365.1
ASR76288.1	000737	Thermonuclease	131	PBI_BELLAMY_252	Synechococcus phage Bellamy	GCA_002627525.1
QCW23037.1	000737	Thermonuclease	152	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50724.1	000737	Thermonuclease	77	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59582.1	000737	Thermonuclease	137	S330809_121	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59344.1	000737	Thermonuclease	137	C440309_121	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59820.1	000737	Thermonuclease	137	N231010_121	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70230.1	000737	Thermonuclease	152	SynMITS9220M01_224	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFA44551.1	000738	GxC-R	120	RaK2_00278	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44562.1	000738	GxC-R	143	RaK2_00289	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18607.1	000738	GxC-R	108	7t3_086	Salmonella phage 7t3	GCA_006083215.1
AZU98432.1	000738	GxC-R	108	CPT_Munch_500	Salmonella phage Munch	GCA_004015485.1
QIG63081.1	000738	GxC-R	108	SEPL_468	Salmonella phage SE_PL	GCA_011067555.1
AFC21454.1	000739	GxC-R	130	GAP32_007	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44122.1	000739	GxC-R	129	CBB_559	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43571.1	000739	GxC-R	129	CBB_6	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88530.1	000739	GxC-R	130	BF_0005	Serratia phage BF	GCA_002619745.1
SOK58812.1	000739	GxC-R	128	g004	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58280.1	000739	GxC-R	220	g003	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ABY63051.1	000740	2OG-FeII_Oxy_3	160	201phi2-1p222	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44930.1	000740	2OG-FeII_Oxy_3	148	KTN4_172	Pseudomonas phage KTN4	GCA_002607225.1
ARV77317.1	000740	2OG-FeII_Oxy_3	160	NOXIFER_148	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32317.1	000740	2OG-FeII_Oxy_3	160	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ85926.1	000740	2OG-FeII_Oxy_3	162	KKIINIFJ_00014	Pseudomonas phage PN05	GCA_009931935.1
ARV76840.1	000740	2OG-FeII_Oxy_3	151	PHABIO_209	Pseudomonas phage Phabio	GCA_002624965.1
AEH03579.1	000740	2OG-FeII_Oxy_3	105	156	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02716.1	000740	2OG-FeII_Oxy_3	150	PSA21_190	Pseudomonas phage Psa21	GCA_004340405.1
ATN94784.1	000740	2OG-FeII_Oxy_3	148	SL2_207	Pseudomonas phage SL2	GCA_002956015.1
QJB22808.1	000740	2OG-FeII_Oxy_3	160	fnug_165	Pseudomonas phage fnug	GCA_012837215.1
QEM41890.1	000740	2OG-FeII_Oxy_3	112	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83038.1	000740	2OG-FeII_Oxy_3	160	PHIKZ137	Pseudomonas virus phiKZ	GCA_000842965.1
AGH56821.1	000741	R3H-2OGFEDO	209	CPXG_00018	Cyanophage P-RSM6	GCA_000906155.1
AGH56822.1	000741	R3H-2OGFEDO	171	CPXG_00019	Cyanophage P-RSM6	GCA_000906155.1
AGH56851.1	000741	R3H-2OGFEDO	188	CPXG_00048	Cyanophage P-RSM6	GCA_000906155.1
AGH56877.1	000741	R3H-2OGFEDO	186	CPXG_00074	Cyanophage P-RSM6	GCA_000906155.1
AGH57004.1	000741	R3H-2OGFEDO	201	CPXG_00201	Cyanophage P-RSM6	GCA_000906155.1
AJK27642.1	000741	R3H-2OGFEDO	191	PTIM40_177	Cyanophage P-TIM40	GCA_001470935.1
AJK27655.1	000741	R3H-2OGFEDO	203	PTIM40_208	Cyanophage P-TIM40	GCA_001470935.1
AOO14317.1	000741	R3H-2OGFEDO	199	Sn110110_123	Cyanophage S-RIM14	GCA_002599065.1
AOO14341.1	000741	R3H-2OGFEDO	181	Sn110110_147	Cyanophage S-RIM14	GCA_002599065.1
AOO14361.1	000741	R3H-2OGFEDO	187	Sn110110_167	Cyanophage S-RIM14	GCA_002599065.1
AOO14966.1	000741	R3H-2OGFEDO	199	W1230910_120	Cyanophage S-RIM14	GCA_002599125.1
AOO14990.1	000741	R3H-2OGFEDO	181	W1230910_144	Cyanophage S-RIM14	GCA_002599125.1
AOO15010.1	000741	R3H-2OGFEDO	187	W1230910_164	Cyanophage S-RIM14	GCA_002599125.1
AMO43038.1	000741	R3H-2OGFEDO	199	R1080702_029	Cyanophage S-RIM32	GCA_001754165.1
AMO43046.1	000741	R3H-2OGFEDO	235	R1080702_037	Cyanophage S-RIM32	GCA_001754165.1
AMO43048.1	000741	R3H-2OGFEDO	231	R1080702_039	Cyanophage S-RIM32	GCA_001754165.1
AMO43056.1	000741	R3H-2OGFEDO	196	R1080702_047	Cyanophage S-RIM32	GCA_001754165.1
AMO43090.1	000741	R3H-2OGFEDO	204	R1080702_081	Cyanophage S-RIM32	GCA_001754165.1
AMO43278.1	000741	R3H-2OGFEDO	190	W270710_034	Cyanophage S-RIM44	GCA_002599145.1
AMO43286.1	000741	R3H-2OGFEDO	242	W270710_042	Cyanophage S-RIM44	GCA_002599145.1
AMO43288.1	000741	R3H-2OGFEDO	224	W270710_044	Cyanophage S-RIM44	GCA_002599145.1
AMO43319.1	000741	R3H-2OGFEDO	209	W270710_075	Cyanophage S-RIM44	GCA_002599145.1
AMO43446.1	000741	R3H-2OGFEDO	202	W270710_207	Cyanophage S-RIM44	GCA_002599145.1
AOO11512.1	000741	R3H-2OGFEDO	190	ES420910_031	Cyanophage S-RIM44	GCA_002599165.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO11520.1	000741	R3H-2OGFEDO	242	ES420910_039	Cyanophage S-RIM44	GCA_002599165.1
AOO11522.1	000741	R3H-2OGFEDO	224	ES420910_041	Cyanophage S-RIM44	GCA_002599165.1
AOO11552.1	000741	R3H-2OGFEDO	209	ES420910_071	Cyanophage S-RIM44	GCA_002599165.1
AOO11590.1	000741	R3H-2OGFEDO	197	ES420910_109	Cyanophage S-RIM44	GCA_002599165.1
AOO11750.1	000741	R3H-2OGFEDO	190	Np050604_034	Cyanophage S-RIM44	GCA_002599185.1
AOO11758.1	000741	R3H-2OGFEDO	242	Np050604_042	Cyanophage S-RIM44	GCA_002599185.1
AOO11760.1	000741	R3H-2OGFEDO	224	Np050604_044	Cyanophage S-RIM44	GCA_002599185.1
AOO11791.1	000741	R3H-2OGFEDO	209	Np050604_075	Cyanophage S-RIM44	GCA_002599185.1
AOO11918.1	000741	R3H-2OGFEDO	202	Np050604_207	Cyanophage S-RIM44	GCA_002599185.1
AOO11977.1	000741	R3H-2OGFEDO	190	Np200711_031	Cyanophage S-RIM44	GCA_002599205.1
AOO11985.1	000741	R3H-2OGFEDO	242	Np200711_039	Cyanophage S-RIM44	GCA_002599205.1
AOO11987.1	000741	R3H-2OGFEDO	224	Np200711_041	Cyanophage S-RIM44	GCA_002599205.1
AOO12017.1	000741	R3H-2OGFEDO	209	Np200711_071	Cyanophage S-RIM44	GCA_002599205.1
AOO12055.1	000741	R3H-2OGFEDO	197	Np200711_109	Cyanophage S-RIM44	GCA_002599205.1
AOO12213.1	000741	R3H-2OGFEDO	190	Np420711_031	Cyanophage S-RIM44	GCA_002599225.1
AOO12221.1	000741	R3H-2OGFEDO	242	Np420711_039	Cyanophage S-RIM44	GCA_002599225.1
AOO12223.1	000741	R3H-2OGFEDO	224	Np420711_041	Cyanophage S-RIM44	GCA_002599225.1
AOO12253.1	000741	R3H-2OGFEDO	209	Np420711_071	Cyanophage S-RIM44	GCA_002599225.1
AOO12291.1	000741	R3H-2OGFEDO	197	Np420711_109	Cyanophage S-RIM44	GCA_002599225.1
AOO12451.1	000741	R3H-2OGFEDO	190	Sn080709_034	Cyanophage S-RIM44	GCA_002599245.1
AOO12459.1	000741	R3H-2OGFEDO	242	Sn080709_042	Cyanophage S-RIM44	GCA_002599245.1
AOO12461.1	000741	R3H-2OGFEDO	224	Sn080709_044	Cyanophage S-RIM44	GCA_002599245.1
AOO12492.1	000741	R3H-2OGFEDO	209	Sn080709_075	Cyanophage S-RIM44	GCA_002599245.1
AOO12619.1	000741	R3H-2OGFEDO	202	Sn080709_207	Cyanophage S-RIM44	GCA_002599245.1
AOO12678.1	000741	R3H-2OGFEDO	190	Sn130910_031	Cyanophage S-RIM44	GCA_002599265.1
AOO12686.1	000741	R3H-2OGFEDO	242	Sn130910_039	Cyanophage S-RIM44	GCA_002599265.1
AOO12688.1	000741	R3H-2OGFEDO	224	Sn130910_041	Cyanophage S-RIM44	GCA_002599265.1
AOO12718.1	000741	R3H-2OGFEDO	209	Sn130910_071	Cyanophage S-RIM44	GCA_002599265.1
AOO12756.1	000741	R3H-2OGFEDO	197	Sn130910_109	Cyanophage S-RIM44	GCA_002599265.1
AOO12916.1	000741	R3H-2OGFEDO	190	W2100709_034	Cyanophage S-RIM44	GCA_002599285.1
AOO12924.1	000741	R3H-2OGFEDO	242	W2100709_042	Cyanophage S-RIM44	GCA_002599285.1
AOO12926.1	000741	R3H-2OGFEDO	224	W2100709_044	Cyanophage S-RIM44	GCA_002599285.1
AOO12957.1	000741	R3H-2OGFEDO	209	W2100709_075	Cyanophage S-RIM44	GCA_002599285.1
AOO13085.1	000741	R3H-2OGFEDO	202	W2100709_208	Cyanophage S-RIM44	GCA_002599285.1
AGH07445.1	000741	R3H-2OGFEDO	177	CYVG_00001	Cyanophage S-SSM6a	GCA_002710385.1
AGH07502.1	000741	R3H-2OGFEDO	180	CYVG_00058	Cyanophage S-SSM6a	GCA_002710385.1
AGH07561.1	000741	R3H-2OGFEDO	205	CYVG_00117	Cyanophage S-SSM6a	GCA_002710385.1
AGH07650.1	000741	R3H-2OGFEDO	195	CYVG_00207	Cyanophage S-SSM6a	GCA_002710385.1
AGH07657.1	000741	R3H-2OGFEDO	195	CYVG_00214	Cyanophage S-SSM6a	GCA_002710385.1
AGG54400.1	000741	R3H-2OGFEDO	214	CYWG_00116	Cyanophage S-SSM6b	GCA_002710425.1
AGG54421.1	000741	R3H-2OGFEDO	188	CYWG_00137	Cyanophage S-SSM6b	GCA_002710425.1
AGG54448.1	000741	R3H-2OGFEDO	201	CYWG_00164	Cyanophage S-SSM6b	GCA_002710425.1
ARW58660.1	000741	R3H-2OGFEDO	212	Y3_020	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28506.1	000741	R3H-2OGFEDO	213	YOLOSWAG_19	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38273.1	000741	R3H-2OGFEDO	208	BN7874_104	Phage NCTB	GCA_900092385.1
AAX44486.1	000741	R3H-2OGFEDO	197	PSSM2_108	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44547.1	000741	R3H-2OGFEDO	197	PSSM2_169	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44622.1	000741	R3H-2OGFEDO	191	PSSM2_245	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44409.1	000741	R3H-2OGFEDO	197	PSSM2_031	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12162.1	000741	R3H-2OGFEDO	209	PRTG_00004	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12242.1	000741	R3H-2OGFEDO	197	PRTG_00084	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12349.1	000741	R3H-2OGFEDO	191	PRTG_00196	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12424.1	000741	R3H-2OGFEDO	197	PRTG_00274	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99132.1	000741	R3H-2OGFEDO	190	Syn1_031	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99140.1	000741	R3H-2OGFEDO	242	Syn1_039	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99173.1	000741	R3H-2OGFEDO	215	Syn1_072	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99306.1	000741	R3H-2OGFEDO	202	Syn1_210	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99142.1	000741	R3H-2OGFEDO	224	Syn1_041	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30633.1	000741	R3H-2OGFEDO	240	Syn7803US37_156	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30654.1	000741	R3H-2OGFEDO	176	Syn7803US37_177	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30660.1	000741	R3H-2OGFEDO	238	Syn7803US37_183	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30661.1	000741	R3H-2OGFEDO	177	Syn7803US37_184	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30496.1	000741	R3H-2OGFEDO	197	Syn7803US37_19	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30687.1	000741	R3H-2OGFEDO	362	Syn7803US37_210	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30503.1	000741	R3H-2OGFEDO	190	Syn7803US37_26	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54917.1	000741	R3H-2OGFEDO	186	b23_0304	Synechococcus phage B23	GCA_009745195.1
QGT54552.1	000741	R3H-2OGFEDO	186	b3_0311	Synechococcus phage B3	GCA_009745215.1
ASR76091.1	000741	R3H-2OGFEDO	206	PBI_BELLAMY_46	Synechococcus phage Bellamy	GCA_002627525.1
ASR76092.1	000741	R3H-2OGFEDO	245	PBI_BELLAMY_47	Synechococcus phage Bellamy	GCA_002627525.1
QCW23092.1	000741	R3H-2OGFEDO	230	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50579.1	000741	R3H-2OGFEDO	228	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59495.1	000741	R3H-2OGFEDO	221	S330809_034	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59497.1	000741	R3H-2OGFEDO	158	S330809_036	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59545.1	000741	R3H-2OGFEDO	194	S330809_084	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59257.1	000741	R3H-2OGFEDO	221	C440309_034	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59259.1	000741	R3H-2OGFEDO	158	C440309_036	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59307.1	000741	R3H-2OGFEDO	194	C440309_084	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59733.1	000741	R3H-2OGFEDO	221	N231010_034	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59735.1	000741	R3H-2OGFEDO	158	N231010_036	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59783.1	000741	R3H-2OGFEDO	194	N231010_084	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70425.1	000741	R3H-2OGFEDO	204	HOU04_gp026	Synechococcus phage S-T4	GCA_003443335.1
AXQ70423.1	000741	R3H-2OGFEDO	226	HOU04_gp024	Synechococcus phage S-T4	GCA_003443335.1
AXQ70625.1	000741	R3H-2OGFEDO	226	HOU04_gp024	Synechococcus phage S-T4	GCA_003443335.1
AXQ70424.1	000741	R3H-2OGFEDO	285	HOU04_gp025	Synechococcus phage S-T4	GCA_003443335.1
AGH56978.1	000742	DNAglycofused-2OGFEDO	175	CPXG_00175	Cyanophage P-RSM6	GCA_000906155.1
AGH56981.1	000742	DNAglycofused-2OGFEDO	176	CPXG_00178	Cyanophage P-RSM6	GCA_000906155.1
AJK27478.1	000742	DNAglycofused-2OGFEDO	202	PTIM40_51	Cyanophage P-TIM40	GCA_001470935.1
AMO43034.1	000742	DNAglycofused-2OGFEDO	144	R1080702_019	Cyanophage S-RIM32	GCA_001754165.1
AOO11588.1	000742	DNAglycofused-2OGFEDO	211	ES420910_107	Cyanophage S-RIM44	GCA_002599165.1
AOO12053.1	000742	DNAglycofused-2OGFEDO	211	Np200711_107	Cyanophage S-RIM44	GCA_002599205.1
AOO12289.1	000742	DNAglycofused-2OGFEDO	211	Np420711_107	Cyanophage S-RIM44	GCA_002599225.1
AOO12754.1	000742	DNAglycofused-2OGFEDO	211	Sn130910_107	Cyanophage S-RIM44	GCA_002599265.1
AGH07621.1	000742	DNAglycofused-2OGFEDO	160	CYVG_00178	Cyanophage S-SSM6a	GCA_002710385.1
AGH07662.1	000742	DNAglycofused-2OGFEDO	174	CYVG_00219	Cyanophage S-SSM6a	GCA_002710385.1
AGH07740.1	000742	DNAglycofused-2OGFEDO	184	CYVG_00297	Cyanophage S-SSM6a	GCA_002710385.1
AAX44432.1	000742	DNAglycofused-2OGFEDO	182	PSSM2_054	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44702.1	000742	DNAglycofused-2OGFEDO	177	PSSM2_324	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44612.1	000742	DNAglycofused-2OGFEDO	182	PSSM2_235	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44482.1	000742	DNAglycofused-2OGFEDO	209	PSSM2_104	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12166.1	000742	DNAglycofused-2OGFEDO	209	PRTG_00008	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12273.1	000742	DNAglycofused-2OGFEDO	177	PRTG_00120	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12359.1	000742	DNAglycofused-2OGFEDO	182	PRTG_00206	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59609.1	000742	DNAglycofused-2OGFEDO	189	S330809_148	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59371.1	000742	DNAglycofused-2OGFEDO	189	C440309_148	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59847.1	000742	DNAglycofused-2OGFEDO	189	N231010_148	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70426.1	000742	DNAglycofused-2OGFEDO	187	HOU04_gp027	Synechococcus phage S-T4	GCA_003443335.1
QJT70141.1	000742	DNAglycofused-2OGFEDO	199	SynMITS9220M01_128	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27481.1	000743	2OG-FeII_Oxy_3	238	PTIM40_54	Cyanophage P-TIM40	GCA_001470935.1
AMO43049.1	000743	2OG-FeII_Oxy_3	167	R1080702_040	Cyanophage S-RIM32	GCA_001754165.1
AMO43289.1	000743	2OG-FeII_Oxy_3	171	W270710_045	Cyanophage S-RIM44	GCA_002599145.1
AOO11523.1	000743	2OG-FeII_Oxy_3	171	ES420910_042	Cyanophage S-RIM44	GCA_002599165.1
AOO11761.1	000743	2OG-FeII_Oxy_3	171	Np050604_045	Cyanophage S-RIM44	GCA_002599185.1
AOO11988.1	000743	2OG-FeII_Oxy_3	171	Np200711_042	Cyanophage S-RIM44	GCA_002599205.1
AOO12224.1	000743	2OG-FeII_Oxy_3	171	Np420711_042	Cyanophage S-RIM44	GCA_002599225.1
AOO12462.1	000743	2OG-FeII_Oxy_3	171	Sn080709_045	Cyanophage S-RIM44	GCA_002599245.1
AOO12689.1	000743	2OG-FeII_Oxy_3	171	Sn130910_042	Cyanophage S-RIM44	GCA_002599265.1
AOO12927.1	000743	2OG-FeII_Oxy_3	171	W2100709_045	Cyanophage S-RIM44	GCA_002599285.1
AGH07647.1	000743	2OG-FeII_Oxy_3	210	CYVG_00204	Cyanophage S-SSM6a	GCA_002710385.1
AGG54498.1	000743	2OG-FeII_Oxy_3	202	CYWG_00214	Cyanophage S-SSM6b	GCA_002710425.1
AAX44548.1	000743	2OG-FeII_Oxy_3	162	PSSM2_170	Prochlorococcus phage P-SSM2	GCA_000859585.1
ADO99143.1	000743	2OG-FeII_Oxy_3	171	Syn1_042	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30682.1	000743	2OG-FeII_Oxy_3	213	Syn7803US37_205	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23020.1	000743	2OG-FeII_Oxy_3	183	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50523.1	000743	2OG-FeII_Oxy_3	183	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59498.1	000743	2OG-FeII_Oxy_3	171	S330809_037	Synechococcus phage S-CAM4	GCA_002366065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59260.1	000743	2OG-FeII_Oxy_3	171	C440309_037	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59736.1	000743	2OG-FeII_Oxy_3	171	N231010_037	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70561.1	000743	2OG-FeII_Oxy_3	185	HOU04_gp162	Synechococcus phage S-T4	GCA_003443335.1
AMO43458.1	000744	2OG-FeII_Oxy_5	182	W270710_219	Cyanophage S-RIM44	GCA_002599145.1
AOO11698.1	000744	2OG-FeII_Oxy_5	185	ES420910_221	Cyanophage S-RIM44	GCA_002599165.1
AOO11930.1	000744	2OG-FeII_Oxy_5	182	Np050604_219	Cyanophage S-RIM44	GCA_002599185.1
AOO12164.1	000744	2OG-FeII_Oxy_5	185	Np200711_222	Cyanophage S-RIM44	GCA_002599205.1
AOO12399.1	000744	2OG-FeII_Oxy_5	185	Np420711_221	Cyanophage S-RIM44	GCA_002599225.1
AOO12631.1	000744	2OG-FeII_Oxy_5	182	Sn080709_219	Cyanophage S-RIM44	GCA_002599245.1
AOO12864.1	000744	2OG-FeII_Oxy_5	182	Sn130910_221	Cyanophage S-RIM44	GCA_002599265.1
AOO13097.1	000744	2OG-FeII_Oxy_5	182	W2100709_220	Cyanophage S-RIM44	GCA_002599285.1
AGH07492.1	000744	2OG-FeII_Oxy_5	192	CYVG_00048	Cyanophage S-SSM6a	GCA_002710385.1
AGH07538.1	000744	2OG-FeII_Oxy_5	165	CYVG_00094	Cyanophage S-SSM6a	GCA_002710385.1
AGH07738.1	000744	2OG-FeII_Oxy_5	155	CYVG_00295	Cyanophage S-SSM6a	GCA_002710385.1
AAX44691.1	000744	2OG-FeII_Oxy_5	165	PSSM2_314	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12285.1	000744	2OG-FeII_Oxy_5	165	PRTG_00132	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99319.1	000744	2OG-FeII_Oxy_5	182	Syn1_223	Prochlorococcus phage Syn1	GCA_000892495.1
AFH14887.1	000745	2OG-FeII_Oxy_3	122	Lu11_0349	Pseudomonas phage Lu11	GCA_000897175.1
ARV76976.1	000745	2OG-FeII_Oxy_3	148	PHABIO_345	Pseudomonas phage Phabio	GCA_002624965.1
BAW19100.1	000745	2OG-FeII_Oxy_3	116	FDH28_gp126	Ralstonia phage RP12	GCA_002617345.1
BAW19386.1	000745	2OG-FeII_Oxy_3	116	-	Ralstonia phage RP31	GCA_002617365.1
AOV59558.1	000746	2OG-FeII_Oxy_3	199	S330809_097	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59320.1	000746	2OG-FeII_Oxy_3	199	C440309_097	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59796.1	000746	2OG-FeII_Oxy_3	199	N231010_097	Synechococcus phage S-CAM4	GCA_002922155.1
AUZ95368.1	000000	2OG-FeII_Oxy_3	137	FDI40_gp609	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGG54313.1	000000	2OG-FeII_Oxy_3	227	CYWG_00029	Cyanophage S-SSM6b	GCA_002710425.1
AEO93293.1	000747	Amidase_3+LysM	248	G_22	Bacillus virus G	GCA_000917535.1
AJK27630.1	000748	Cluster304_1clades	229	PTIM40_224	Cyanophage P-TIM40	GCA_001470935.1
AOO14238.1	000748	Cluster304_1clades	224	Sn110110_044	Cyanophage S-RIM14	GCA_002599065.1
AOO14890.1	000748	Cluster304_1clades	224	W1230910_044	Cyanophage S-RIM14	GCA_002599125.1
AMO43062.1	000748	Cluster304_1clades	171	R1080702_053	Cyanophage S-RIM32	GCA_001754165.1
AMO43300.1	000748	Cluster304_1clades	223	W270710_056	Cyanophage S-RIM44	GCA_002599145.1
AOO11534.1	000748	Cluster304_1clades	223	ES420910_053	Cyanophage S-RIM44	GCA_002599165.1
AOO11772.1	000748	Cluster304_1clades	223	Np050604_056	Cyanophage S-RIM44	GCA_002599185.1
AOO11999.1	000748	Cluster304_1clades	223	Np200711_053	Cyanophage S-RIM44	GCA_002599205.1
AOO12235.1	000748	Cluster304_1clades	223	Np420711_053	Cyanophage S-RIM44	GCA_002599225.1
AOO12473.1	000748	Cluster304_1clades	223	Sn080709_056	Cyanophage S-RIM44	GCA_002599245.1
AOO12700.1	000748	Cluster304_1clades	223	Sn130910_053	Cyanophage S-RIM44	GCA_002599265.1
AOO12938.1	000748	Cluster304_1clades	223	W2100709_056	Cyanophage S-RIM44	GCA_002599285.1
AGH07494.1	000748	Cluster304_1clades	218	CYVG_00050	Cyanophage S-SSM6a	GCA_002710385.1
AGG54438.1	000748	Cluster304_1clades	226	CYWG_00154	Cyanophage S-SSM6b	GCA_002710425.1
ADO99154.1	000748	Cluster304_1clades	223	Syn1_053	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76276.1	000748	Cluster304_1clades	225	PBI_BELLAMY_240	Synechococcus phage Bellamy	GCA_002627525.1
QCW23003.1	000748	Cluster304_1clades	223	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50655.1	000748	Cluster304_1clades	330	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59525.1	000748	Cluster304_1clades	223	S330809_064	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59287.1	000748	Cluster304_1clades	223	C440309_064	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59763.1	000748	Cluster304_1clades	223	N231010_064	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70494.1	000748	Cluster304_1clades	186	HOU04_gp095	Synechococcus phage S-T4	GCA_003443335.1
QJT70225.1	000748	Cluster304_1clades	219	SynMITS9220M01_219	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QDH83424.1	000749	Cluster713_1clades	334	H1O15_gp016	Achromobacter phage Motura	GCA_006964305.1
QBX06643.1	000749	Cluster713_1clades	334	BcepSaruman_230	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74612.1	000749	Cluster713_1clades	337	BcepSauron_232	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67254.1	000749	Cluster713_1clades	324	AD1_210	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80000.1	000749	Cluster713_1clades	325	JA11_195	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66598.1	000749	Cluster713_1clades	325	JA13_195	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66923.1	000749	Cluster713_1clades	325	JA29_197	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67569.1	000749	Cluster713_1clades	325	JA33_195	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08484.1	000749	Cluster713_1clades	324	Alexandra_220	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58854.1	000749	Cluster713_1clades	323	Y3_214	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28685.1	000749	Cluster713_1clades	322	YOLOSWAG_207	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38550.1	000749	Cluster713_1clades	362	BN7874_300	Phage NCTB	GCA_900092385.1
AFH14654.1	000749	Cluster713_1clades	388	Lu11_0122	Pseudomonas phage Lu11	GCA_000897175.1
AGS82058.2	000749	Cluster713_1clades	321	PaBG_00182	Pseudomonas phage PaBG	GCA_000912555.1
BAG41696.1	000749	Cluster713_1clades	342	RSL1_ORF248	Ralstonia phage phiRSL1	GCA_000879455.1
AAQ64174.1	000750	MPTase	351	KVP40.0103	Vibrio phage KVP40	GCA_000843785.1
QIW90497.1	000750	MPTase	351	GCAPEGMB_00150	Vibrio phage V07	GCA_012361095.1
QIW90932.1	000750	MPTase	351	COHAPHLL_00069	Vibrio phage V09	GCA_012361135.1
QHJ74285.1	000750	MPTase	351	VH12019_00366	Vibrio phage VH1_2019	GCA_009931825.1
QBX05986.1	000750	MPTase	351	ValB1HC_032	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60999.1	000750	MPTase	351	AVU32_gp158	Vibrio phage ValKK3	GCA_001501635.1
AGN30152.1	000750	MPTase	351	VPFG_00150	Vibrio phage nt-1	GCA_000910195.2
ALP47004.1	000750	MPTase	351	phiGrn1_0216	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47385.1	000750	MPTase	351	phiST2_0349	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54611.1	000750	MPTase	351	vBValMR10Z_70	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37332.1	000750	MPTase	351	pp2_099	Vibriophage phi-pp2	GCA_002630725.1
ARB13727.1	000751	SIG+ArdCN+MPTase	343	Ccr10_gp197c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14072.1	000751	SIG+ArdCN+MPTase	343	Ccr2_gp196c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14761.1	000751	SIG+ArdCN+MPTase	343	Ccr29_gp205	Caulobacter phage Ccr29	GCA_002619485.1
ARB15106.1	000751	SIG+ArdCN+MPTase	343	Ccr32_gp188	Caulobacter phage Ccr32	GCA_002619505.1
ARB15440.1	000751	SIG+ArdCN+MPTase	343	Ccr34_gp198	Caulobacter phage Ccr34	GCA_002619525.1
ARB14415.1	000751	SIG+ArdCN+MPTase	343	Ccr5_gp195c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87720.1	000751	SIG+ArdCN+MPTase	343	CcrKarma_gp203	Caulobacter virus Karma	GCA_000901575.1
AFU87369.1	000751	SIG+ArdCN+MPTase	343	CcrMagneto_gp199	Caulobacter virus Magneto	GCA_000903095.1
AFU88516.1	000751	SIG+ArdCN+MPTase	343	CcrSwift_gp198	Caulobacter virus Swift	GCA_000899655.1
AFU87025.1	000751	SIG+ArdCN+MPTase	343	CbK_gp193	Caulobacter virus phiCbK	GCA_000900535.1
AXG67185.1	000752	Tox-ALFMPTase	375	AD1_141	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79935.1	000752	Tox-ALFMPTase	367	JA11_130	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66534.1	000752	Tox-ALFMPTase	348	JA13_131	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66859.1	000752	Tox-ALFMPTase	367	JA29_133	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67504.1	000752	Tox-ALFMPTase	367	JA33_130	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08418.1	000752	Tox-ALFMPTase	398	Alexandra_146	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58782.1	000752	Tox-ALFMPTase	370	Y3_142	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28620.1	000752	Tox-ALFMPTase	360	YOLOSWAG_140	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38410.1	000752	Tox-ALFMPTase	284	BN7874_226	Phage NCTB	GCA_900092385.1
AGH26173.1	000753	MPTase	145	CPMG_00072	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44452.2	000753	MPTase	165	PSSM2_074	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12202.1	000753	MPTase	111	PRTG_00044	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93587.1	000753	MPTase	114	AVU42_gp036	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22995.1	000753	MPTase	112	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50646.1	000753	MPTase	89	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70050.1	000753	MPTase	135	SynMITS9220M01_037	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QIG63299.1	000754	SIG+TM+TM	154	DAC16_66	Bacteroides phage DAC16	GCA_013387695.1
QIG63558.1	000754	SIG+TM+TM	154	DAC19_67	Bacteroides phage DAC19	GCA_013387715.1
QIG63819.1	000754	SIG+TM+TM	154	DAC20_66	Bacteroides phage DAC20	GCA_013387725.1
QIG64081.1	000754	SIG+TM+TM	154	DAC22_67	Bacteroides phage DAC22	GCA_013387735.1
QIG64344.1	000754	SIG+TM+TM	154	DAC23_66	Bacteroides phage DAC23	GCA_013387745.1
ARB13545.1	000755	MPTase	194	Ccr10_gp017	Caulobacter phage Ccr10	GCA_002619445.1
ARB13870.1	000755	MPTase	194	Ccr10_gp340	Caulobacter phage Ccr10	GCA_002619445.1
ARB14574.1	000755	MPTase	194	Ccr29_gp017	Caulobacter phage Ccr29	GCA_002619485.1
ARB14909.1	000755	MPTase	194	Ccr29_gp353	Caulobacter phage Ccr29	GCA_002619485.1
AGR47965.1	000756	Tox-Metpeptidase	166	SmphiM12_333	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13157.1	000756	Tox-Metpeptidase	166	PHIM19_252	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12796.1	000756	Tox-Metpeptidase	166	PHIM7_251	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13519.1	000756	Tox-Metpeptidase	167	PHIN3_256	Sinorhizobium phage phiN3	GCA_001501175.1
BBA65678.1	000757	Metallopeptidase	168	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65219.1	000757	Metallopeptidase	168	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96247.1	000757	Metallopeptidase	100	Xoosp13_60	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXG67086.1	000758	MPTase	116	AD1_042	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08320.1	000758	MPTase	114	Alexandra_40	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58684.1	000758	MPTase	101	Y3_044	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCG76260.1	000759	MPTase	250	EST35_0380	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76261.1	000759	MPTase	229	EST35_0381	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AMS01098.1	000760	MPTase	211	AR9_g013	Bacillus phage AR9	GCA_001743835.1
ASU00020.1	000760	MPTase	211	PBI_PBS1_198	Bacillus virus PBS1	GCA_002601325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW22865.1	000761	SIG+MPTase	183	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50716.1	000761	SIG+MPTase	183	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54943.1	000762	Tox-MPTase3	124	b23_0332	Synechococcus phage B23	GCA_009745195.1
QGT54578.1	000762	Tox-MPTase3	124	b3_0338	Synechococcus phage B3	GCA_009745215.1
BAE47822.1	000000	MPTase	173	CST124	Clostridium phage c-st	GCA_000865225.1
AXH72394.1	000000	MPTase	179	-	Myoviridae sp.	GCA_003657725.1
QIG65879.1	000000	MPTase	156	phiOC_p214	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ASV44123.1	000000	MPTase	365	PBI_SCTP2_108	Salicola phage SCTP-2	GCA_002625545.1
QCG76271.1	000000	SIG+MPTase	161	EST35_0391	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AIX30565.1	000000	SIG+MPTase	182	Syn7803US37_88	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76145.1	000000	SIG+MPTase	130	PBI_BELLAMY_100	Synechococcus phage Bellamy	GCA_002627525.1
BAG41483.1	000000	Tox-ALFMPTase	198	RSL1_ORF038	Ralstonia phage phiRSL1	GCA_000879455.1
BAV39322.1	000000	Tox-ALFMPTase	264	BPT24_198	Tenacibaculum phage pT24	GCA_002611925.1
QIG65902.1	000000	Metallopeptidase	161	phiOC_p241	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BAV39298.1	000000	Metallopeptidase	191	BPT24_172	Tenacibaculum phage pT24	GCA_002611925.1
QBO64004.1	000000	Tox-MPTase3	102	Goslar_00212	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
prev15ph1000000484	000763	SidE	2605	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000715	000763	SidE	823	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QDH47011.1	000764	Structural_Protein_Mix	1243	LAh10_50	Aeromonas phage LAh10	GCA_006863975.1
AUG85808.1	000764	Structural_Protein_Mix	1151	BOSOLAPHORUS_20	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
prev15ph1000000075	000764	Structural_Protein_Mix	736	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000105	000764	Structural_Protein_Mix	706	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QDH83445.1	000764	Structural_Protein_Mix	504	H1O15_gp037	Achromobacter phage Motura	GCA_006964305.1
QDH83477.1	000764	Structural_Protein_Mix	153	H1O15_gp329	Achromobacter phage Motura	GCA_006964305.1
CCE26158.1	000764	Structural_Protein_Mix	228	g134	Yersinia phage phiR1-37	GCA_000895615.1
QDH83637.1	000764	Structural_Protein_Mix	406	H1O15_gp151	Achromobacter phage Motura	GCA_006964305.1
QDH83708.1	000764	Structural_Protein_Mix	409	H1O15_gp120	Achromobacter phage Motura	GCA_006964305.1
QDH83702.1	000764	Structural_Protein_Mix	414	H1O15_gp128	Achromobacter phage Motura	GCA_006964305.1
AZU98224.1	000764	Structural_Protein_Mix	288	CPT_Munch_280	Salmonella phage Munch	GCA_004015485.1
CCE26157.1	000764	Structural_Protein_Mix	154	g133	Yersinia phage phiR1-37	GCA_000895615.1
AZU98115.1	000764	Structural_Protein_Mix	921	CPT_Munch_171	Salmonella phage Munch	GCA_004015485.1
CCE26153.1	000764	Structural_Protein_Mix	210	g129	Yersinia phage phiR1-37	GCA_000895615.1
APU01469.1	000764	Structural_Protein_Mix	279	-	Aeromonas phage 65.2	GCA_002618145.1
APU01485.1	000764	Structural_Protein_Mix	448	-	Aeromonas phage 65.2	GCA_002618145.1
CCE26125.1	000764	Structural_Protein_Mix	347	g101	Yersinia phage phiR1-37	GCA_000895615.1
APU01751.1	000764	Structural_Protein_Mix	252	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28725.1	000764	Structural_Protein_Mix	450	AP1_007	Aeromonas phage AP1	GCA_014183365.1
QMV28783.1	000764	Structural_Protein_Mix	277	AP1_0076	Aeromonas phage AP1	GCA_014183365.1
SOK58568.1	000764	Structural_Protein_Mix	216	g291	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58524.1	000764	Structural_Protein_Mix	279	g247	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV29056.1	000764	Structural_Protein_Mix	254	AP1_0349	Aeromonas phage AP1	GCA_014183365.1
SOK58495.1	000764	Structural_Protein_Mix	1545	g218c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ATI17412.1	000764	Structural_Protein_Mix	450	-	Aeromonas phage AS-szw	GCA_002743635.1
SOK58482.1	000764	Structural_Protein_Mix	325	g205	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ATI17545.1	000764	Structural_Protein_Mix	251	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17428.1	000764	Structural_Protein_Mix	277	-	Aeromonas phage AS-szw	GCA_002743635.1
SOK58416.1	000764	Structural_Protein_Mix	946	g139	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASU00184.1	000764	Structural_Protein_Mix	450	HWB28_gp368	Aeromonas phage AS-zj	GCA_002627665.1
SOK58415.1	000764	Structural_Protein_Mix	895	g138	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASU00452.1	000764	Structural_Protein_Mix	251	HWB28_gp100	Aeromonas phage AS-zj	GCA_002627665.1
ASU00167.1	000764	Structural_Protein_Mix	277	HWB28_gp385	Aeromonas phage AS-zj	GCA_002627665.1
AUE22741.1	000764	Structural_Protein_Mix	388	Ah1_00223	Aeromonas phage Ah1	GCA_002957415.1
SOK58414.1	000764	Structural_Protein_Mix	928	g137	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK59104.1	000764	Structural_Protein_Mix	216	g296	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AUE22760.1	000764	Structural_Protein_Mix	265	Ah1_00242	Aeromonas phage Ah1	GCA_002957415.1
SOK59058.1	000764	Structural_Protein_Mix	279	g250	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59030.1	000764	Structural_Protein_Mix	1545	g222c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QAX98476.1	000764	Structural_Protein_Mix	264	ASfcp2_138	Aeromonas phage AsFcp_2	GCA_004146885.1
SOK59017.1	000764	Structural_Protein_Mix	325	g209	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QAX97852.1	000764	Structural_Protein_Mix	450	ASswx1_209	Aeromonas phage Asswx_1	GCA_004146865.1
SOK58950.1	000764	Structural_Protein_Mix	946	g142	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QAX97868.1	000764	Structural_Protein_Mix	277	ASswx1_225	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97986.1	000764	Structural_Protein_Mix	251	ASswx1_345	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01282.1	000764	Structural_Protein_Mix	280	ASwh1_219	Aeromonas phage Aswh_1	GCA_004146945.1
SOK58949.1	000764	Structural_Protein_Mix	900	g141	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QAY01298.1	000764	Structural_Protein_Mix	452	ASwh1_235	Aeromonas phage Aswh_1	GCA_004146945.1
SOK58948.1	000764	Structural_Protein_Mix	928	g140	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QAY01154.1	000764	Structural_Protein_Mix	251	ASwh1_88	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39475.1	000764	Structural_Protein_Mix	249	CC2_190	Aeromonas phage CC2	GCA_000903495.1
AFN39538.1	000764	Structural_Protein_Mix	277	CC2_309	Aeromonas phage CC2	GCA_000903495.1
AZU98114.1	000764	Structural_Protein_Mix	195	CPT_Munch_170	Salmonella phage Munch	GCA_004015485.1
AFN39425.1	000764	Structural_Protein_Mix	451	CC2_325	Aeromonas phage CC2	GCA_000903495.1
QDJ96413.1	000764	Structural_Protein_Mix	417	Xoosp13_227	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDB70299.1	000764	Structural_Protein_Mix	254	CF8_0131	Aeromonas phage CF8	GCA_006384595.2
QDB70300.1	000764	Structural_Protein_Mix	1215	CF8_0132	Aeromonas phage CF8	GCA_006384595.2
QDB70301.1	000764	Structural_Protein_Mix	1306	CF8_0133	Aeromonas phage CF8	GCA_006384595.2
QDB70313.1	000764	Structural_Protein_Mix	337	CF8_0145	Aeromonas phage CF8	GCA_006384595.2
QDJ96412.1	000764	Structural_Protein_Mix	706	Xoosp13_226	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ97277.1	000764	Structural_Protein_Mix	1208	D6_0117	Aeromonas phage D6	GCA_007051205.2
QDJ97278.1	000764	Structural_Protein_Mix	1243	D6_0118	Aeromonas phage D6	GCA_007051205.2
QDJ97297.1	000764	Structural_Protein_Mix	521	D6_0137	Aeromonas phage D6	GCA_007051205.2
QDJ96411.1	000764	Structural_Protein_Mix	430	Xoosp13_225	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96410.1	000764	Structural_Protein_Mix	430	Xoosp13_224	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDH47012.1	000764	Structural_Protein_Mix	1208	LAh10_49	Aeromonas phage LAh10	GCA_006863975.1
QDJ96409.1	000764	Structural_Protein_Mix	210	Xoosp13_223	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96408.1	000764	Structural_Protein_Mix	528	Xoosp13_222	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96893.1	000764	Structural_Protein_Mix	253	PS1_0134	Aeromonas phage PS1	GCA_007051165.2
QDJ96894.1	000764	Structural_Protein_Mix	424	PS1_0135	Aeromonas phage PS1	GCA_007051165.2
QDJ96895.1	000764	Structural_Protein_Mix	862	PS1_0136	Aeromonas phage PS1	GCA_007051165.2
QDJ96657.1	000764	Structural_Protein_Mix	168	PS1_0146	Aeromonas phage PS1	GCA_007051165.2
QFR59523.1	000764	Structural_Protein_Mix	253	PS2_0132	Aeromonas phage PS2	GCA_009388305.2
QFR59524.1	000764	Structural_Protein_Mix	424	PS2_0133	Aeromonas phage PS2	GCA_009388305.2
QFR59525.1	000764	Structural_Protein_Mix	862	PS2_0134	Aeromonas phage PS2	GCA_009388305.2
QFR59534.1	000764	Structural_Protein_Mix	168	PS2_0143	Aeromonas phage PS2	GCA_009388305.2
QFR59294.1	000764	Structural_Protein_Mix	339	PS2_0153	Aeromonas phage PS2	GCA_009388305.2
ADQ52919.1	000764	Structural_Protein_Mix	436	PX29p200	Aeromonas phage PX29	GCA_000920195.1
QDJ96394.1	000764	Structural_Protein_Mix	377	Xoosp13_208	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ADQ52938.1	000764	Structural_Protein_Mix	264	PX29p219	Aeromonas phage PX29	GCA_000920195.1
QDJ96388.1	000764	Structural_Protein_Mix	332	Xoosp13_202	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65384.1	000764	Structural_Protein_Mix	746	-	Xanthomonas phage XacN1	GCA_003173815.1
ADM79861.1	000764	Structural_Protein_Mix	263	phiAS5_ORF0018	Aeromonas phage phiAS5	GCA_000887715.1
BBA65383.1	000764	Structural_Protein_Mix	434	-	Xanthomonas phage XacN1	GCA_003173815.1
ADM80186.1	000764	Structural_Protein_Mix	439	phiAS5_ORF0343	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53106.1	000764	Structural_Protein_Mix	448	65p098	Aeromonas virus 65	GCA_000893255.1
BBA65382.1	000764	Structural_Protein_Mix	431	-	Xanthomonas phage XacN1	GCA_003173815.1
ADQ53091.1	000764	Structural_Protein_Mix	239	65p081	Aeromonas virus 65	GCA_000893255.1
BBA65381.1	000764	Structural_Protein_Mix	430	-	Xanthomonas phage XacN1	GCA_003173815.1
ADQ53393.1	000764	Structural_Protein_Mix	252	65p386	Aeromonas virus 65	GCA_000893255.1
AAQ17871.1	000764	Structural_Protein_Mix	436	12	Aeromonas virus Aeh1	GCA_000843245.1
BBA65366.1	000764	Structural_Protein_Mix	418	-	Xanthomonas phage XacN1	GCA_003173815.1
AAQ17885.1	000764	Structural_Protein_Mix	264	22	Aeromonas virus Aeh1	GCA_000843245.1
BBA65385.1	000764	Structural_Protein_Mix	401	-	Xanthomonas phage XacN1	GCA_003173815.1
AZU98113.1	000764	Structural_Protein_Mix	897	CPT_Munch_169	Salmonella phage Munch	GCA_004015485.1
QNI20748.1	000764	Structural_Protein_Mix	455	-	Salmonella phage JN03	GCA_014319805.1
AUZ94995.1	000764	Structural_Protein_Mix	291	FDI40_gp213	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94982.1	000764	Structural_Protein_Mix	389	FDI40_gp200	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94856.1	000764	Structural_Protein_Mix	771	FDI40_gp044	Agrobacterium phage Atu_ph07	GCA_002628245.1
AZU98231.1	000764	Structural_Protein_Mix	531	CPT_Munch_287	Salmonella phage Munch	GCA_004015485.1
BBA65322.1	000764	Structural_Protein_Mix	586	-	Xanthomonas phage XacN1	GCA_003173815.1
ABS83595.1	000764	Structural_Protein_Mix	233	0305phi8-36p032	Bacillus phage 0305phi8-36	GCA_000871045.1
QCW19021.1	000764	Structural_Protein_Mix	210	7t3_0501	Salmonella phage 7t3	GCA_006083215.1
ABS83651.1	000764	Structural_Protein_Mix	240	0305phi8-36p091	Bacillus phage 0305phi8-36	GCA_000871045.1
QCW18983.1	000764	Structural_Protein_Mix	530	7t3_0462	Salmonella phage 7t3	GCA_006083215.1
BBA65517.1	000764	Structural_Protein_Mix	594	-	Xanthomonas phage XacN1	GCA_003173815.1
AMS01200.1	000764	Structural_Protein_Mix	213	AR9_g116	Bacillus phage AR9	GCA_001743835.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65359.1	000764	Structural_Protein_Mix	185	-	Xanthomonas phage XacN1	GCA_003173815.1
AMS01258.1	000764	Structural_Protein_Mix	154	AR9_g174	Bacillus phage AR9	GCA_001743835.1
AMS01372.1	000764	Structural_Protein_Mix	249	AR9_g288	Bacillus phage AR9	GCA_001743835.1
AZU98268.1	000764	Structural_Protein_Mix	210	CPT_Munch_324	Salmonella phage Munch	GCA_004015485.1
ALN97693.1	000764	Structural_Protein_Mix	150	Bp8pS_014	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AFN37580.1	000764	Structural_Protein_Mix	473	pp2_348	Vibriophage phi-pp2	GCA_002630725.1
AFN37579.1	000764	Structural_Protein_Mix	512	pp2_347	Vibriophage phi-pp2	GCA_002630725.1
QNI21279.1	000764	Structural_Protein_Mix	332	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20950.1	000764	Structural_Protein_Mix	329	-	Vibrio phage vB_pir03	GCA_014319855.1
QCW18974.1	000764	Structural_Protein_Mix	288	7t3_0453	Salmonella phage 7t3	GCA_006083215.1
QNI20949.1	000764	Structural_Protein_Mix	300	-	Vibrio phage vB_pir03	GCA_014319855.1
ASU00003.1	000764	Structural_Protein_Mix	249	PBI_PBS1_181	Bacillus virus PBS1	GCA_002601325.1
QCW18942.1	000764	Structural_Protein_Mix	1560	7t3_0421	Salmonella phage 7t3	GCA_006083215.1
AST99824.1	000764	Structural_Protein_Mix	213	PBI_PBS1_2	Bacillus virus PBS1	GCA_002601325.1
QAX96476.1	000764	Structural_Protein_Mix	332	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96482.1	000764	Structural_Protein_Mix	329	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AST99884.1	000764	Structural_Protein_Mix	154	PBI_PBS1_62	Bacillus virus PBS1	GCA_002601325.1
QAX96477.1	000764	Structural_Protein_Mix	308	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96329.1	000764	Structural_Protein_Mix	499	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96158.1	000764	Structural_Protein_Mix	332	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96164.1	000764	Structural_Protein_Mix	329	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96159.1	000764	Structural_Protein_Mix	308	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QBX06497.1	000764	Structural_Protein_Mix	568	BcepSaruman_084	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06500.1	000764	Structural_Protein_Mix	174	BcepSaruman_087	Burkholderia phage BcepSaruman	GCA_004771375.1
QAX96011.1	000764	Structural_Protein_Mix	499	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX97112.1	000764	Structural_Protein_Mix	332	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX97118.1	000764	Structural_Protein_Mix	329	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QBX06654.1	000764	Structural_Protein_Mix	512	BcepSaruman_241	Burkholderia phage BcepSaruman	GCA_004771375.1
AZU98476.1	000764	Structural_Protein_Mix	267	CPT_Munch_544	Salmonella phage Munch	GCA_004015485.1
QBX06686.1	000764	Structural_Protein_Mix	371	BcepSaruman_273	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06693.1	000764	Structural_Protein_Mix	431	BcepSaruman_280	Burkholderia phage BcepSaruman	GCA_004771375.1
QAX97113.1	000764	Structural_Protein_Mix	308	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QBQ74464.1	000764	Structural_Protein_Mix	568	BcepSauron_084	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74467.1	000764	Structural_Protein_Mix	175	BcepSauron_087	Burkholderia phage BcepSauron	GCA_005394215.1
QAX96965.1	000764	Structural_Protein_Mix	499	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96793.1	000764	Structural_Protein_Mix	332	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96799.1	000764	Structural_Protein_Mix	329	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QBQ74622.1	000764	Structural_Protein_Mix	511	BcepSauron_242	Burkholderia phage BcepSauron	GCA_005394215.1
QCW18854.1	000764	Structural_Protein_Mix	949	7t3_0333	Salmonella phage 7t3	GCA_006083215.1
QBQ74661.1	000764	Structural_Protein_Mix	431	BcepSauron_281	Burkholderia phage BcepSauron	GCA_005394215.1
QAX96794.1	000764	Structural_Protein_Mix	308	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
CCH63542.1	000764	Structural_Protein_Mix	250	CP21_080	Campylobacter virus CP21	GCA_000902535.1
QAX96647.1	000764	Structural_Protein_Mix	499	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
CCH63620.1	000764	Structural_Protein_Mix	276	CP21_158	Campylobacter virus CP21	GCA_000902535.1
ARB13626.1	000764	Structural_Protein_Mix	280	Ccr10_gp097	Caulobacter phage Ccr10	GCA_002619445.1
ARB13645.1	000764	Structural_Protein_Mix	362	Ccr10_gp116c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13971.1	000764	Structural_Protein_Mix	280	Ccr2_gp096	Caulobacter phage Ccr2	GCA_002619465.1
ARB13990.1	000764	Structural_Protein_Mix	362	Ccr2_gp115c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14660.1	000764	Structural_Protein_Mix	280	Ccr29_gp104	Caulobacter phage Ccr29	GCA_002619485.1
ARB14678.1	000764	Structural_Protein_Mix	362	Ccr29_gp122	Caulobacter phage Ccr29	GCA_002619485.1
ARB15015.1	000764	Structural_Protein_Mix	280	Ccr32_gp097	Caulobacter phage Ccr32	GCA_002619505.1
ARB15033.1	000764	Structural_Protein_Mix	359	Ccr32_gp115	Caulobacter phage Ccr32	GCA_002619505.1
ALY07005.1	000764	Structural_Protein_Mix	266	VmeM32_00009	Vibrio phage vB_VmeM-32	GCA_002608825.1
ARB15347.1	000764	Structural_Protein_Mix	280	Ccr34_gp105	Caulobacter phage Ccr34	GCA_002619525.1
ARB15365.1	000764	Structural_Protein_Mix	359	Ccr34_gp123	Caulobacter phage Ccr34	GCA_002619525.1
ARB14315.1	000764	Structural_Protein_Mix	280	Ccr5_gp097	Caulobacter phage Ccr5	GCA_002619545.1
ARB14334.1	000764	Structural_Protein_Mix	362	Ccr5_gp116c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68277.1	000764	Structural_Protein_Mix	391	CcrBL10_gp073	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68298.1	000764	Structural_Protein_Mix	281	CcrBL10_gp094	Caulobacter phage CcrBL10	GCA_003443255.1
QCW18853.1	000764	Structural_Protein_Mix	195	7t3_0332	Salmonella phage 7t3	GCA_006083215.1
AXQ69196.1	000764	Structural_Protein_Mix	276	CcrBL9_gp172	Caulobacter phage CcrBL9	GCA_003443295.1
QNJ54751.1	000764	Structural_Protein_Mix	512	vBValMR10Z_211	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFU87994.1	000764	Structural_Protein_Mix	277	CcrColossus_gp124	Caulobacter phage CcrColossus	GCA_000899635.1
QNJ54750.1	000764	Structural_Protein_Mix	475	vBValMR10Z_210	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AXQ68670.1	000764	Structural_Protein_Mix	277	CcrPW_gp131	Caulobacter phage CcrPW	GCA_003443275.1
QNJ54736.1	000764	Structural_Protein_Mix	282	vBValMR10Z_196	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AXQ69749.1	000764	Structural_Protein_Mix	276	CcrSC_gp167	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69770.1	000764	Structural_Protein_Mix	280	CcrSC_gp188	Caulobacter phage CcrSC	GCA_003443315.1
AFU87618.1	000764	Structural_Protein_Mix	280	CcrKarma_gp101	Caulobacter virus Karma	GCA_000901575.1
AFU87637.1	000764	Structural_Protein_Mix	362	CcrKarma_gp120	Caulobacter virus Karma	GCA_000901575.1
AFU87267.1	000764	Structural_Protein_Mix	280	CcrMagneto_gp097	Caulobacter virus Magneto	GCA_000903095.1
AFU87286.1	000764	Structural_Protein_Mix	362	CcrMagneto_gp116	Caulobacter virus Magneto	GCA_000903095.1
AFU86581.1	000764	Structural_Protein_Mix	281	CcrRogue_gp099	Caulobacter virus Rogue	GCA_000900555.1
AFU86598.1	000764	Structural_Protein_Mix	380	CcrRogue_gp116	Caulobacter virus Rogue	GCA_000900555.1
AFU88414.1	000764	Structural_Protein_Mix	280	CcrSwift_gp096	Caulobacter virus Swift	GCA_000899655.1
AFU88433.1	000764	Structural_Protein_Mix	362	CcrSwift_gp115	Caulobacter virus Swift	GCA_000899655.1
AFU86932.1	000764	Structural_Protein_Mix	280	CbK_gp100	Caulobacter virus phiCbK	GCA_000900535.1
AFU86951.1	000764	Structural_Protein_Mix	359	CbK_gp119	Caulobacter virus phiCbK	GCA_000900535.1
ALP47410.1	000764	Structural_Protein_Mix	282	phiST2_0228	Vibrio phage phi-ST2	GCA_002757135.1
QCW18852.1	000764	Structural_Protein_Mix	897	7t3_0331	Salmonella phage 7t3	GCA_006083215.1
ANS06144.1	000764	Structural_Protein_Mix	83	ABCD_0212	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ALP47367.1	000764	Structural_Protein_Mix	475	phiST2_0214	Vibrio phage phi-ST2	GCA_002757135.1
ANS05987.1	000764	Structural_Protein_Mix	263	ABCD_0215	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
QCW18653.1	000764	Structural_Protein_Mix	261	7t3_0132	Salmonella phage 7t3	GCA_006083215.1
AFO71253.1	000764	Structural_Protein_Mix	422	CR5_033	Cronobacter phage CR5	GCA_000910235.1
AFO71376.1	000764	Structural_Protein_Mix	69	CR5_156	Cronobacter phage CR5	GCA_000910235.1
ALP47360.1	000764	Structural_Protein_Mix	512	phiST2_0213	Vibrio phage phi-ST2	GCA_002757135.1
QIG62716.1	000764	Structural_Protein_Mix	210	SEPL_103	Salmonella phage SE_PL	GCA_011067555.1
AIA64880.1	000764	Structural_Protein_Mix	287	S13_081	Cronobacter phage S13	GCA_001503575.1
ALP47031.1	000764	Structural_Protein_Mix	282	phiGrn1_0096	Vibrio phage phi-Grn1	GCA_002757115.1
AIA64895.1	000764	Structural_Protein_Mix	436	S13_096	Cronobacter phage S13	GCA_001503575.1
ALP46984.1	000764	Structural_Protein_Mix	475	phiGrn1_0082	Vibrio phage phi-Grn1	GCA_002757115.1
AFC21593.1	000764	Structural_Protein_Mix	902	GAP32_143	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ALP46985.1	000764	Structural_Protein_Mix	474	phiGrn1_0081	Vibrio phage phi-Grn1	GCA_002757115.1
AFC21595.1	000764	Structural_Protein_Mix	916	GAP32_145	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21657.1	000764	Structural_Protein_Mix	318	GAP32_207	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21670.1	000764	Structural_Protein_Mix	1557	GAP32_220	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21697.1	000764	Structural_Protein_Mix	280	GAP32_247	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQT28159.1	000764	Structural_Protein_Mix	406	pVa21_218	Vibrio phage pVa-21	GCA_002619305.1
AFC21704.1	000764	Structural_Protein_Mix	539	GAP32_254	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21743.1	000764	Structural_Protein_Mix	215	GAP32_293	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG62753.1	000764	Structural_Protein_Mix	530	SEPL_140	Salmonella phage SE_PL	GCA_011067555.1
AFC21882.1	000764	Structural_Protein_Mix	139	GAP32_429	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
BAW98256.1	000764	Structural_Protein_Mix	816	FDH33_gp047	Vibrio phage pTD1	GCA_002618825.1
ASV44107.1	000764	Structural_Protein_Mix	180	PBI_SCTP2_92	Salicola phage SCTP-2	GCA_002625545.1
AON97227.1	000764	Structural_Protein_Mix	84	E_219	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
BAW98254.1	000764	Structural_Protein_Mix	730	FDH33_gp045	Vibrio phage pTD1	GCA_002618825.1
AON97230.1	000764	Structural_Protein_Mix	264	E_222	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56838.1	000764	Structural_Protein_Mix	274	CPXG_00035	Cyanophage P-RSM6	GCA_000906155.1
AGH56900.1	000764	Structural_Protein_Mix	346	CPXG_00097	Cyanophage P-RSM6	GCA_000906155.1
AGN30021.1	000764	Structural_Protein_Mix	473	VPFG_00013	Vibrio phage nt-1	GCA_000910195.2
AGN30020.1	000764	Structural_Protein_Mix	512	VPFG_00012	Vibrio phage nt-1	GCA_000910195.2
AGH56990.1	000764	Structural_Protein_Mix	267	CPXG_00187	Cyanophage P-RSM6	GCA_000906155.1
AGH56993.1	000764	Structural_Protein_Mix	285	CPXG_00190	Cyanophage P-RSM6	GCA_000906155.1
AJT61137.1	000764	Structural_Protein_Mix	475	AVU32_gp296	Vibrio phage ValKK3	GCA_001501635.1
AJT61123.1	000764	Structural_Protein_Mix	282	AVU32_gp282	Vibrio phage ValKK3	GCA_001501635.1
AJT61138.1	000764	Structural_Protein_Mix	512	AVU32_gp297	Vibrio phage ValKK3	GCA_001501635.1
QAU04551.1	000764	Structural_Protein_Mix	239	ValB1MD_267	Vibrio phage ValB1MD	GCA_004138815.1
AJK27562.1	000764	Structural_Protein_Mix	348	PTIM40_135	Cyanophage P-TIM40	GCA_001470935.1
AJK27662.1	000764	Structural_Protein_Mix	160	PTIM40_187	Cyanophage P-TIM40	GCA_001470935.1
AJK27661.1	000764	Structural_Protein_Mix	127	PTIM40_188	Cyanophage P-TIM40	GCA_001470935.1
AJK27467.1	000764	Structural_Protein_Mix	300	PTIM40_40	Cyanophage P-TIM40	GCA_001470935.1
AJK27469.1	000764	Structural_Protein_Mix	269	PTIM40_42	Cyanophage P-TIM40	GCA_001470935.1
AJK27470.1	000764	Structural_Protein_Mix	529	PTIM40_43	Cyanophage P-TIM40	GCA_001470935.1
QBX06126.1	000764	Structural_Protein_Mix	512	ValB1HC_172	Vibrio phage ValB1 HC	GCA_004771355.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06125.1	000764	Structural_Protein_Mix	475	ValB1HC_171	Vibrio phage ValB1 HC	GCA_004771355.1
AOO14223.1	000764	Structural_Protein_Mix	144	Sn110110_029	Cyanophage S-RIM14	GCA_002599065.1
AOO14225.1	000764	Structural_Protein_Mix	380	Sn110110_031	Cyanophage S-RIM14	GCA_002599065.1
QBX06111.1	000764	Structural_Protein_Mix	282	ValB1HC_157	Vibrio phage ValB1 HC	GCA_004771355.1
AGB06989.1	000764	Structural_Protein_Mix	475	CF80_gp202	Vibrio phage VH7D	GCA_000914495.1
AOO14312.1	000764	Structural_Protein_Mix	359	Sn110110_118	Cyanophage S-RIM14	GCA_002599065.1
AOO14374.1	000764	Structural_Protein_Mix	208	Sn110110_180	Cyanophage S-RIM14	GCA_002599065.1
AGB07003.1	000764	Structural_Protein_Mix	282	CF80_gp216	Vibrio phage VH7D	GCA_000914495.1
AOO14875.1	000764	Structural_Protein_Mix	144	W1230910_029	Cyanophage S-RIM14	GCA_002599125.1
AOO14877.1	000764	Structural_Protein_Mix	380	W1230910_031	Cyanophage S-RIM14	GCA_002599125.1
AGB06988.1	000764	Structural_Protein_Mix	512	CF80_gp201	Vibrio phage VH7D	GCA_000914495.1
AOO14961.1	000764	Structural_Protein_Mix	359	W1230910_115	Cyanophage S-RIM14	GCA_002599125.1
AOO15022.1	000764	Structural_Protein_Mix	208	W1230910_176	Cyanophage S-RIM14	GCA_002599125.1
QHJ74530.1	000764	Structural_Protein_Mix	473	VH12019_00230	Vibrio phage VH1_2019	GCA_009931825.1
AMO43042.1	000764	Structural_Protein_Mix	573	R1080702_033	Cyanophage S-RIM32	GCA_001754165.1
AMO43043.1	000764	Structural_Protein_Mix	600	R1080702_034	Cyanophage S-RIM32	GCA_001754165.1
AMO43044.1	000764	Structural_Protein_Mix	603	R1080702_035	Cyanophage S-RIM32	GCA_001754165.1
QHJ74529.1	000764	Structural_Protein_Mix	512	VH12019_00229	Vibrio phage VH1_2019	GCA_009931825.1
AMO43140.1	000764	Structural_Protein_Mix	394	R1080702_131	Cyanophage S-RIM32	GCA_001754165.1
AMO43183.1	000764	Structural_Protein_Mix	229	R1080702_174	Cyanophage S-RIM32	GCA_001754165.1
QIW91068.1	000764	Structural_Protein_Mix	512	COHAPHLL_00205	Vibrio phage V09	GCA_012361135.1
AMO43282.1	000764	Structural_Protein_Mix	616	W270710_038	Cyanophage S-RIM44	GCA_002599145.1
AMO43283.1	000764	Structural_Protein_Mix	884	W270710_039	Cyanophage S-RIM44	GCA_002599145.1
AMO43284.1	000764	Structural_Protein_Mix	589	W270710_040	Cyanophage S-RIM44	GCA_002599145.1
QIW91067.1	000764	Structural_Protein_Mix	473	COHAPHLL_00204	Vibrio phage V09	GCA_012361135.1
AMO43366.1	000764	Structural_Protein_Mix	391	W270710_122	Cyanophage S-RIM44	GCA_002599145.1
AMO43408.1	000764	Structural_Protein_Mix	285	W270710_164	Cyanophage S-RIM44	GCA_002599145.1
AOO11516.1	000764	Structural_Protein_Mix	603	ES420910_035	Cyanophage S-RIM44	GCA_002599165.1
AOO11517.1	000764	Structural_Protein_Mix	486	ES420910_036	Cyanophage S-RIM44	GCA_002599165.1
AOO11518.1	000764	Structural_Protein_Mix	589	ES420910_037	Cyanophage S-RIM44	GCA_002599165.1
AOO11578.1	000764	Structural_Protein_Mix	252	ES420910_097	Cyanophage S-RIM44	GCA_002599165.1
AOO11579.1	000764	Structural_Protein_Mix	254	ES420910_098	Cyanophage S-RIM44	GCA_002599165.1
AOO11580.1	000764	Structural_Protein_Mix	254	ES420910_099	Cyanophage S-RIM44	GCA_002599165.1
QIG62761.1	000764	Structural_Protein_Mix	288	SEPL_148	Salmonella phage SE_PL	GCA_011067555.1
AOO11610.1	000764	Structural_Protein_Mix	391	ES420910_129	Cyanophage S-RIM44	GCA_002599165.1
AOO11652.1	000764	Structural_Protein_Mix	190	ES420910_171	Cyanophage S-RIM44	GCA_002599165.1
AOO11754.1	000764	Structural_Protein_Mix	616	Np050604_038	Cyanophage S-RIM44	GCA_002599185.1
AOO11755.1	000764	Structural_Protein_Mix	884	Np050604_039	Cyanophage S-RIM44	GCA_002599185.1
AOO11756.1	000764	Structural_Protein_Mix	589	Np050604_040	Cyanophage S-RIM44	GCA_002599185.1
QIW90362.1	000764	Structural_Protein_Mix	473	GCAPEGMB_00015	Vibrio phage V07	GCA_012361095.1
AOO11838.1	000764	Structural_Protein_Mix	394	Np050604_122	Cyanophage S-RIM44	GCA_002599185.1
AOO11880.1	000764	Structural_Protein_Mix	285	Np050604_164	Cyanophage S-RIM44	GCA_002599185.1
QIW90361.1	000764	Structural_Protein_Mix	512	GCAPEGMB_00014	Vibrio phage V07	GCA_012361095.1
AOO11981.1	000764	Structural_Protein_Mix	603	Np200711_035	Cyanophage S-RIM44	GCA_002599205.1
AOO11982.1	000764	Structural_Protein_Mix	407	Np200711_036	Cyanophage S-RIM44	GCA_002599205.1
AOO11983.1	000764	Structural_Protein_Mix	589	Np200711_037	Cyanophage S-RIM44	GCA_002599205.1
AOO12043.1	000764	Structural_Protein_Mix	252	Np200711_097	Cyanophage S-RIM44	GCA_002599205.1
AOO12044.1	000764	Structural_Protein_Mix	254	Np200711_098	Cyanophage S-RIM44	GCA_002599205.1
AOO12045.1	000764	Structural_Protein_Mix	254	Np200711_099	Cyanophage S-RIM44	GCA_002599205.1
QDH47433.1	000764	Structural_Protein_Mix	736	HWC35_gp039	Vibrio phage USC-1	GCA_006864065.1
AOO12075.1	000764	Structural_Protein_Mix	391	Np200711_129	Cyanophage S-RIM44	GCA_002599205.1
AOO12118.1	000764	Structural_Protein_Mix	190	Np200711_172	Cyanophage S-RIM44	GCA_002599205.1
QDH47435.1	000764	Structural_Protein_Mix	713	HWC35_gp041	Vibrio phage USC-1	GCA_006864065.1
AOO12217.1	000764	Structural_Protein_Mix	603	Np420711_035	Cyanophage S-RIM44	GCA_002599225.1
AOO12218.1	000764	Structural_Protein_Mix	486	Np420711_036	Cyanophage S-RIM44	GCA_002599225.1
AOO12219.1	000764	Structural_Protein_Mix	589	Np420711_037	Cyanophage S-RIM44	GCA_002599225.1
AOO12279.1	000764	Structural_Protein_Mix	252	Np420711_097	Cyanophage S-RIM44	GCA_002599225.1
AOO12280.1	000764	Structural_Protein_Mix	254	Np420711_098	Cyanophage S-RIM44	GCA_002599225.1
AOO12281.1	000764	Structural_Protein_Mix	254	Np420711_099	Cyanophage S-RIM44	GCA_002599225.1
AOO12311.1	000764	Structural_Protein_Mix	391	Np420711_129	Cyanophage S-RIM44	GCA_002599225.1
AOO12353.1	000764	Structural_Protein_Mix	190	Np420711_171	Cyanophage S-RIM44	GCA_002599225.1
AAQ64417.1	000764	Structural_Protein_Mix	473	KVP40.0348	Vibrio phage KVP40	GCA_000843785.1
AOO12455.1	000764	Structural_Protein_Mix	616	Sn080709_038	Cyanophage S-RIM44	GCA_002599245.1
AOO12456.1	000764	Structural_Protein_Mix	884	Sn080709_039	Cyanophage S-RIM44	GCA_002599245.1
AOO12457.1	000764	Structural_Protein_Mix	589	Sn080709_040	Cyanophage S-RIM44	GCA_002599245.1
AAQ64416.1	000764	Structural_Protein_Mix	512	KVP40.0347	Vibrio phage KVP40	GCA_000843785.1
AOO12539.1	000764	Structural_Protein_Mix	391	Sn080709_122	Cyanophage S-RIM44	GCA_002599245.1
AOO12581.1	000764	Structural_Protein_Mix	285	Sn080709_164	Cyanophage S-RIM44	GCA_002599245.1
AXH71036.1	000764	Structural_Protein_Mix	333	-	Vibrio phage BONAISHI	GCA_003441475.1
AOO12682.1	000764	Structural_Protein_Mix	603	Sn130910_035	Cyanophage S-RIM44	GCA_002599265.1
AOO12683.1	000764	Structural_Protein_Mix	486	Sn130910_036	Cyanophage S-RIM44	GCA_002599265.1
AOO12684.1	000764	Structural_Protein_Mix	589	Sn130910_037	Cyanophage S-RIM44	GCA_002599265.1
AOO12744.1	000764	Structural_Protein_Mix	252	Sn130910_097	Cyanophage S-RIM44	GCA_002599265.1
AOO12745.1	000764	Structural_Protein_Mix	254	Sn130910_098	Cyanophage S-RIM44	GCA_002599265.1
AOO12746.1	000764	Structural_Protein_Mix	254	Sn130910_099	Cyanophage S-RIM44	GCA_002599265.1
AXH71041.1	000764	Structural_Protein_Mix	327	-	Vibrio phage BONAISHI	GCA_003441475.1
AOO12776.1	000764	Structural_Protein_Mix	391	Sn130910_129	Cyanophage S-RIM44	GCA_002599265.1
AOO12818.1	000764	Structural_Protein_Mix	190	Sn130910_171	Cyanophage S-RIM44	GCA_002599265.1
AXH71040.1	000764	Structural_Protein_Mix	305	-	Vibrio phage BONAISHI	GCA_003441475.1
AOO12920.1	000764	Structural_Protein_Mix	616	W2100709_038	Cyanophage S-RIM44	GCA_002599285.1
AOO12921.1	000764	Structural_Protein_Mix	884	W2100709_039	Cyanophage S-RIM44	GCA_002599285.1
AOO12922.1	000764	Structural_Protein_Mix	589	W2100709_040	Cyanophage S-RIM44	GCA_002599285.1
AUR80925.1	000764	Structural_Protein_Mix	713	Aphrodite1_0052	Vibrio phage Aphrodite1	GCA_002958015.1
AOO13005.1	000764	Structural_Protein_Mix	391	W2100709_123	Cyanophage S-RIM44	GCA_002599285.1
AOO13047.1	000764	Structural_Protein_Mix	285	W2100709_165	Cyanophage S-RIM44	GCA_002599285.1
AUR80922.1	000764	Structural_Protein_Mix	736	Aphrodite1_0050	Vibrio phage Aphrodite1	GCA_002958015.1
QCW23295.1	000764	Structural_Protein_Mix	736	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23293.1	000764	Structural_Protein_Mix	713	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AGH07543.1	000764	Structural_Protein_Mix	244	CYVG_00099	Cyanophage S-SSM6a	GCA_002710385.1
AGH07545.1	000764	Structural_Protein_Mix	853	CYVG_00101	Cyanophage S-SSM6a	GCA_002710385.1
AGH07659.1	000764	Structural_Protein_Mix	526	CYVG_00216	Cyanophage S-SSM6a	GCA_002710385.1
QAU04282.1	000764	Structural_Protein_Mix	738	HWC03_gp127	Vibrio phage 2 TSL-2019	GCA_006964105.1
AGG54342.1	000764	Structural_Protein_Mix	154	CYWG_00058	Cyanophage S-SSM6b	GCA_002710425.1
QAU04284.1	000764	Structural_Protein_Mix	713	HWC03_gp129	Vibrio phage 2 TSL-2019	GCA_006964105.1
AGG54491.1	000764	Structural_Protein_Mix	355	CYWG_00207	Cyanophage S-SSM6b	GCA_002710425.1
BBI90840.1	000764	Structural_Protein_Mix	156	-	Tenacibaculum phage PTm5	GCA_009730715.1
AXG67136.1	000764	Structural_Protein_Mix	193	AD1_092	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
ASV44453.1	000764	Structural_Protein_Mix	1038	PBI_SCTP2_438	Salicola phage SCTP-2	GCA_002625545.1
AXG67150.1	000764	Structural_Protein_Mix	163	AD1_106	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
QIG62788.1	000764	Structural_Protein_Mix	1560	SEPL_175	Salmonella phage SE_PL	GCA_011067555.1
BAG41579.1	000764	Structural_Protein_Mix	542	RSL1_ORF134	Ralstonia phage phiRSL1	GCA_000879455.1
BBI90532.1	000764	Structural_Protein_Mix	156	HYO65_gp140	Tenacibaculum phage PTm1	GCA_009730695.1
AXG67192.1	000764	Structural_Protein_Mix	619	AD1_148	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67203.1	000764	Structural_Protein_Mix	288	AD1_159	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
QJT70119.1	000764	Structural_Protein_Mix	353	SynMITS9220M01_106	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG67271.1	000764	Structural_Protein_Mix	154	AD1_227	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67282.1	000764	Structural_Protein_Mix	424	AD1_238	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67356.1	000764	Structural_Protein_Mix	543	AD1_312	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
QJT70046.1	000764	Structural_Protein_Mix	473	SynMITS9220M01_033	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70044.1	000764	Structural_Protein_Mix	336	SynMITS9220M01_031	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BAG41672.1	000764	Structural_Protein_Mix	490	RSL1_ORF222	Ralstonia phage phiRSL1	GCA_000879455.1
QIG62867.1	000764	Structural_Protein_Mix	921	SEPL_254	Salmonella phage SE_PL	GCA_011067555.1
BAG41575.1	000764	Structural_Protein_Mix	174	RSL1_ORF130	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41775.1	000764	Structural_Protein_Mix	162	RSL1_ORF329	Ralstonia phage phiRSL1	GCA_000879455.1
QJT70043.1	000764	Structural_Protein_Mix	413	SynMITS9220M01_030	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXQ70467.1	000764	Structural_Protein_Mix	225	HOU04_gp068	Synechococcus phage S-T4	GCA_003443335.1
AXQ70465.1	000764	Structural_Protein_Mix	384	HOU04_gp066	Synechococcus phage S-T4	GCA_003443335.1
AYD80016.1	000764	Structural_Protein_Mix	133	JA11_211	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80026.1	000764	Structural_Protein_Mix	401	JA11_221	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80078.1	000764	Structural_Protein_Mix	649	JA11_273	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80108.1	000764	Structural_Protein_Mix	537	JA11_303	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80116.1	000764	Structural_Protein_Mix	263	JA11_311	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80118.1	000764	Structural_Protein_Mix	172	JA11_313	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
BAG41582.1	000764	Structural_Protein_Mix	162	RSL1_ORF137	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41790.1	000764	Structural_Protein_Mix	177	RSL1_ORF342	Ralstonia phage phiRSL1	GCA_000879455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAQ02686.1	000764	Structural_Protein_Mix	1186	AVU38_gp158	Ralstonia phage RSL2	GCA_001503055.1
BAU71412.1	000764	Structural_Protein_Mix	444	-	Ralstonia phage RSL2	GCA_001503055.1
AXQ70464.1	000764	Structural_Protein_Mix	383	HOU04_gp065	Synechococcus phage S-T4	GCA_003443335.1
AXQ70575.1	000764	Structural_Protein_Mix	293	HOU04_gp176	Synechococcus phage S-T4	GCA_003443335.1
AXQ70533.1	000764	Structural_Protein_Mix	191	HOU04_gp134	Synechococcus phage S-T4	GCA_003443335.1
AOV59893.1	000764	Structural_Protein_Mix	316	N231010_194	Synechococcus phage S-CAM4	GCA_002922155.1
AXG66614.1	000764	Structural_Protein_Mix	133	JA13_211	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66625.1	000764	Structural_Protein_Mix	395	JA13_222	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66679.1	000764	Structural_Protein_Mix	658	JA13_276	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66709.1	000764	Structural_Protein_Mix	537	JA13_306	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66717.1	000764	Structural_Protein_Mix	260	JA13_314	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66718.1	000764	Structural_Protein_Mix	172	JA13_315	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
BAQ02721.2	000764	Structural_Protein_Mix	316	-	Ralstonia phage RSL2	GCA_001503055.1
QIG62868.1	000764	Structural_Protein_Mix	195	SEPL_255	Salmonella phage SE_PL	GCA_011067555.1
BAQ02592.1	000764	Structural_Protein_Mix	690	AVU38_gp064	Ralstonia phage RSL2	GCA_001503055.1
AXG66825.1	000764	Structural_Protein_Mix	324	JA29_099	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AOV59871.1	000764	Structural_Protein_Mix	203	N231010_172	Synechococcus phage S-CAM4	GCA_002922155.1
AXG66868.1	000764	Structural_Protein_Mix	641	JA29_142	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AOV59828.1	000764	Structural_Protein_Mix	380	N231010_129	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59731.1	000764	Structural_Protein_Mix	582	N231010_032	Synechococcus phage S-CAM4	GCA_002922155.1
AXG66939.1	000764	Structural_Protein_Mix	133	JA29_213	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66949.1	000764	Structural_Protein_Mix	394	JA29_223	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66999.1	000764	Structural_Protein_Mix	721	JA29_273	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67027.1	000764	Structural_Protein_Mix	538	JA29_301	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67035.1	000764	Structural_Protein_Mix	266	JA29_309	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67036.1	000764	Structural_Protein_Mix	173	JA29_310	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
BAQ02739.1	000764	Structural_Protein_Mix	543	AVU38_gp211	Ralstonia phage RSL2	GCA_001503055.1
BAS04961.2	000764	Structural_Protein_Mix	1183	AVU11_gp169	Ralstonia phage RSF1	GCA_001500875.1
BAU71421.1	000764	Structural_Protein_Mix	353	AVU11_agp43	Ralstonia phage RSF1	GCA_001500875.1
BAS05009.1	000764	Structural_Protein_Mix	542	AVU11_gp217	Ralstonia phage RSF1	GCA_001500875.1
BAS04859.1	000764	Structural_Protein_Mix	373	AVU11_gp067	Ralstonia phage RSF1	GCA_001500875.1
AOV59418.1	000764	Structural_Protein_Mix	364	C440309_195	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59395.1	000764	Structural_Protein_Mix	203	C440309_172	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59352.1	000764	Structural_Protein_Mix	380	C440309_129	Synechococcus phage S-CAM4	GCA_002922145.1
AXG67586.1	000764	Structural_Protein_Mix	133	JA33_212	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67596.1	000764	Structural_Protein_Mix	401	JA33_222	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67648.1	000764	Structural_Protein_Mix	649	JA33_274	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67678.1	000764	Structural_Protein_Mix	537	JA33_304	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67686.1	000764	Structural_Protein_Mix	263	JA33_312	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67687.1	000764	Structural_Protein_Mix	172	JA33_313	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AOV59255.1	000764	Structural_Protein_Mix	582	C440309_032	Synechococcus phage S-CAM4	GCA_002922145.1
QBZ70663.1	000764	Structural_Protein_Mix	1232	pETSU_082	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70664.1	000764	Structural_Protein_Mix	1262	pETSU_083	Edwardsiella virus pEt-SU	GCA_004800915.1
BAS04992.2	000764	Structural_Protein_Mix	303	AVU11_gp200	Ralstonia phage RSF1	GCA_001500875.1
AMR59684.1	000764	Structural_Protein_Mix	455	SEGD1_035	Enterobacteria phage SEGD1	GCA_002601865.1
BAS04858.1	000764	Structural_Protein_Mix	690	AVU11_gp066	Ralstonia phage RSF1	GCA_001500875.1
QBP07586.1	000764	Structural_Protein_Mix	69	DERBICUS_160	Erwinia phage Derbicus	GCA_004521655.1
BAS04913.2	000764	Structural_Protein_Mix	656	AVU11_gp121	Ralstonia phage RSF1	GCA_001500875.1
QBP07460.1	000764	Structural_Protein_Mix	472	DERBICUS_34	Erwinia phage Derbicus	GCA_004521655.1
AHI60167.1	000764	Structural_Protein_Mix	324	Ea357_017	Erwinia phage Ea35-70	GCA_000914635.1
AHI60168.1	000764	Structural_Protein_Mix	420	Ea357_018	Erwinia phage Ea35-70	GCA_000914635.1
AHI60169.1	000764	Structural_Protein_Mix	1163	Ea357_019	Erwinia phage Ea35-70	GCA_000914635.1
AHI60170.1	000764	Structural_Protein_Mix	1150	Ea357_020	Erwinia phage Ea35-70	GCA_000914635.1
AHI60262.1	000764	Structural_Protein_Mix	260	Ea357_111	Erwinia phage Ea35-70	GCA_000914635.1
AHI60280.1	000764	Structural_Protein_Mix	279	Ea357_129	Erwinia phage Ea35-70	GCA_000914635.1
AHI60396.1	000764	Structural_Protein_Mix	514	Ea357_243	Erwinia phage Ea35-70	GCA_000914635.1
AHI60434.1	000764	Structural_Protein_Mix	325	Ea357_280	Erwinia phage Ea35-70	GCA_000914635.1
BAW19332.1	000764	Structural_Protein_Mix	425	-	Ralstonia phage RP31	GCA_002617365.1
ANZ49813.1	000764	Structural_Protein_Mix	69	MACHINA_175	Erwinia phage Machina	GCA_002758035.1
ANZ49814.1	000764	Structural_Protein_Mix	130	MACHINA_176	Erwinia phage Machina	GCA_002758035.1
ANZ49815.1	000764	Structural_Protein_Mix	129	MACHINA_177	Erwinia phage Machina	GCA_002758035.1
QIG62869.1	000764	Structural_Protein_Mix	897	SEPL_256	Salmonella phage SE_PL	GCA_011067555.1
ANZ49686.1	000764	Structural_Protein_Mix	456	MACHINA_48	Erwinia phage Machina	GCA_002758035.1
AGX01734.1	000764	Structural_Protein_Mix	452	CF95_gp012	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01802.1	000764	Structural_Protein_Mix	1292	CF95_gp080	Erwinia phage PhiEaH1	GCA_000914555.1
AOV59656.1	000764	Structural_Protein_Mix	364	S330809_195	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59633.1	000764	Structural_Protein_Mix	203	S330809_172	Synechococcus phage S-CAM4	GCA_002366065.1
AGX01912.1	000764	Structural_Protein_Mix	364	CF95_gp190	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01911.1	000764	Structural_Protein_Mix	606	yomR	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01915.1	000764	Structural_Protein_Mix	867	yomR	Erwinia phage PhiEaH1	GCA_000914555.1
AOV59590.1	000764	Structural_Protein_Mix	380	S330809_129	Synechococcus phage S-CAM4	GCA_002366065.1
QBP07220.1	000764	Structural_Protein_Mix	201	REBECCA_113	Erwinia phage Rebecca	GCA_004521635.1
QBP07238.1	000764	Structural_Protein_Mix	279	REBECCA_131	Erwinia phage Rebecca	GCA_004521635.1
QBP07125.1	000764	Structural_Protein_Mix	328	REBECCA_17	Erwinia phage Rebecca	GCA_004521635.1
QBP07126.1	000764	Structural_Protein_Mix	420	REBECCA_18	Erwinia phage Rebecca	GCA_004521635.1
QBP07127.1	000764	Structural_Protein_Mix	1163	REBECCA_19	Erwinia phage Rebecca	GCA_004521635.1
QBP07128.1	000764	Structural_Protein_Mix	1156	REBECCA_20	Erwinia phage Rebecca	GCA_004521635.1
QBP07352.1	000764	Structural_Protein_Mix	514	REBECCA_247	Erwinia phage Rebecca	GCA_004521635.1
QBP07391.1	000764	Structural_Protein_Mix	325	REBECCA_286	Erwinia phage Rebecca	GCA_004521635.1
BAW19396.1	000764	Structural_Protein_Mix	600	-	Ralstonia phage RP31	GCA_002617365.1
AXF51310.1	000764	Structural_Protein_Mix	69	WELLINGTON_181	Erwinia phage Wellington	GCA_003344985.1
AXF51424.1	000764	Structural_Protein_Mix	135	WELLINGTON_182	Erwinia phage Wellington	GCA_003344985.1
BAW19463.1	000764	Structural_Protein_Mix	575	-	Ralstonia phage RP31	GCA_002617365.1
AXF51175.1	000764	Structural_Protein_Mix	445	WELLINGTON_44	Erwinia phage Wellington	GCA_003344985.1
BAW19331.1	000764	Structural_Protein_Mix	534	-	Ralstonia phage RP31	GCA_002617365.1
AFQ96759.1	000764	Structural_Protein_Mix	454	G173_gp214	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96631.1	000764	Structural_Protein_Mix	68	G173_gp086	Erwinia phage phiEaH2	GCA_000902915.1
BAW19047.1	000764	Structural_Protein_Mix	425	FDH28_gp073	Ralstonia phage RP12	GCA_002617345.1
QIG63037.1	000764	Structural_Protein_Mix	267	SEPL_424	Salmonella phage SE_PL	GCA_011067555.1
AOV59493.1	000764	Structural_Protein_Mix	582	S330809_032	Synechococcus phage S-CAM4	GCA_002366065.1
BAW19110.1	000764	Structural_Protein_Mix	600	FDH28_gp285	Ralstonia phage RP12	GCA_002617345.1
AWY08417.1	000764	Structural_Protein_Mix	676	Alexandra_145	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08425.1	000764	Structural_Protein_Mix	625	Alexandra_153	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08627.1	000764	Structural_Protein_Mix	286	Alexandra_164	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BAW19177.1	000764	Structural_Protein_Mix	575	FDH28_gp218	Ralstonia phage RP12	GCA_002617345.1
AWY08498.1	000764	Structural_Protein_Mix	159	Alexandra_236	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08506.1	000764	Structural_Protein_Mix	424	Alexandra_247	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08580.1	000764	Structural_Protein_Mix	525	Alexandra_329	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QDH50715.1	000764	Structural_Protein_Mix	258	-	Synechococcus phage S-B43	GCA_006869725.1
AWY08588.1	000764	Structural_Protein_Mix	172	Alexandra_339	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08371.1	000764	Structural_Protein_Mix	193	Alexandra_96	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48196.1	000764	Structural_Protein_Mix	68	ASESINO_183	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
QDH50712.1	000764	Structural_Protein_Mix	210	-	Synechococcus phage S-B43	GCA_006869725.1
BAW19046.1	000764	Structural_Protein_Mix	534	FDH28_gp072	Ralstonia phage RP12	GCA_002617345.1
ANZ48062.1	000764	Structural_Protein_Mix	454	ASESINO_49	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85899.1	000764	Structural_Protein_Mix	260	BOSOLAPHORUS_112	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85900.1	000764	Structural_Protein_Mix	201	BOSOLAPHORUS_113	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85918.1	000764	Structural_Protein_Mix	279	BOSOLAPHORUS_131	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85805.1	000764	Structural_Protein_Mix	324	BOSOLAPHORUS_17	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85806.1	000764	Structural_Protein_Mix	420	BOSOLAPHORUS_18	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85807.1	000764	Structural_Protein_Mix	1163	BOSOLAPHORUS_19	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86034.1	000764	Structural_Protein_Mix	514	BOSOLAPHORUS_248	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86073.1	000764	Structural_Protein_Mix	325	BOSOLAPHORUS_287	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AWN09063.1	000764	Structural_Protein_Mix	455	MLDJOKPK_00133	Salmonella phage SPAsTU	GCA_003183805.1
ANZ48469.1	000764	Structural_Protein_Mix	68	CAITLIN_174	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
AAL83046.1	000764	Structural_Protein_Mix	789	PHIKZ145	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ48337.1	000764	Structural_Protein_Mix	455	CAITLIN_42	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48748.1	000764	Structural_Protein_Mix	72	CHRISDB_186	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48749.1	000764	Structural_Protein_Mix	131	CHRISDB_187	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AAL83032.1	000764	Structural_Protein_Mix	771	PHIKZ131	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ48610.1	000764	Structural_Protein_Mix	455	CHRISDB_48	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52214.1	000764	Structural_Protein_Mix	260	DM_116	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52215.1	000764	Structural_Protein_Mix	201	DM_117	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52233.1	000764	Structural_Protein_Mix	279	DM_135	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52115.2	000764	Structural_Protein_Mix	324	DM_17	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANH52116.1	000764	Structural_Protein_Mix	420	DM_18	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52117.1	000764	Structural_Protein_Mix	1163	DM_19	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52118.2	000764	Structural_Protein_Mix	1151	DM_20	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52351.1	000764	Structural_Protein_Mix	514	DM_251	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52389.2	000764	Structural_Protein_Mix	325	DM_290	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AAL83036.1	000764	Structural_Protein_Mix	463	PHIKZ135	Pseudomonas virus phiKZ	GCA_000842965.1
AUG86218.1	000764	Structural_Protein_Mix	260	DESERTFOX_111	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86219.1	000764	Structural_Protein_Mix	201	DESERTFOX_112	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86237.1	000764	Structural_Protein_Mix	279	DESERTFOX_130	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86125.1	000764	Structural_Protein_Mix	324	DESERTFOX_17	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86126.1	000764	Structural_Protein_Mix	420	DESERTFOX_18	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86127.1	000764	Structural_Protein_Mix	1163	DESERTFOX_19	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86128.1	000764	Structural_Protein_Mix	1149	DESERTFOX_20	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86353.1	000764	Structural_Protein_Mix	514	DESERTFOX_246	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86393.1	000764	Structural_Protein_Mix	325	DESERTFOX_286	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AAL83034.1	000764	Structural_Protein_Mix	462	PHIKZ133	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ49009.1	000764	Structural_Protein_Mix	69	EARLPHILLIPIV_160	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49011.1	000764	Structural_Protein_Mix	128	EARLPHILLIPIV_162	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
AAL83035.1	000764	Structural_Protein_Mix	457	PHIKZ134	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ48884.1	000764	Structural_Protein_Mix	472	EARLPHILLIPIV_34	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49257.1	000764	Structural_Protein_Mix	69	HUXLEY_175	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
AAL83102.1	000764	Structural_Protein_Mix	649	PHIKZ201	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ49131.1	000764	Structural_Protein_Mix	456	HUXLEY_49	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03815.1	000764	Structural_Protein_Mix	1172	JOAD_100	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03817.1	000764	Structural_Protein_Mix	245	JOAD_98	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03816.1	000764	Structural_Protein_Mix	1168	JOAD_99	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49534.1	000764	Structural_Protein_Mix	69	KWAN_182	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QEM41884.1	000764	Structural_Protein_Mix	760	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANZ49396.1	000764	Structural_Protein_Mix	445	KWAN_44	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86540.1	000764	Structural_Protein_Mix	260	MADMEL_112	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86541.1	000764	Structural_Protein_Mix	201	MADMEL_113	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86559.1	000764	Structural_Protein_Mix	279	MADMEL_131	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86445.1	000764	Structural_Protein_Mix	324	MADMEL_17	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86446.1	000764	Structural_Protein_Mix	420	MADMEL_18	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86447.1	000764	Structural_Protein_Mix	1163	MADMEL_19	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86448.1	000764	Structural_Protein_Mix	1151	MADMEL_20	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86676.1	000764	Structural_Protein_Mix	514	MADMEL_249	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86714.1	000764	Structural_Protein_Mix	325	MADMEL_287	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
QEM41899.1	000764	Structural_Protein_Mix	726	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AUG86865.1	000764	Structural_Protein_Mix	260	MORTIMER_116	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86883.1	000764	Structural_Protein_Mix	279	MORTIMER_134	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86766.1	000764	Structural_Protein_Mix	324	MORTIMER_17	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86767.1	000764	Structural_Protein_Mix	420	MORTIMER_18	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86768.1	000764	Structural_Protein_Mix	1163	MORTIMER_19	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86769.1	000764	Structural_Protein_Mix	1149	MORTIMER_20	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86999.1	000764	Structural_Protein_Mix	514	MORTIMER_251	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87039.1	000764	Structural_Protein_Mix	325	MORTIMER_291	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
QEM41958.1	000764	Structural_Protein_Mix	1016	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANZ50085.1	000764	Structural_Protein_Mix	69	PARSHIK_176	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50086.1	000764	Structural_Protein_Mix	130	PARSHIK_177	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QEM41887.1	000764	Structural_Protein_Mix	468	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANZ49959.1	000764	Structural_Protein_Mix	456	PARSHIK_50	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50356.1	000764	Structural_Protein_Mix	69	PHOBOS_166	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QEM41886.1	000764	Structural_Protein_Mix	455	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANZ50224.1	000764	Structural_Protein_Mix	472	PHOBOS_34	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51893.1	000764	Structural_Protein_Mix	260	RAY_112	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51911.1	000764	Structural_Protein_Mix	279	RAY_130	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51798.1	000764	Structural_Protein_Mix	324	RAY_17	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51799.1	000764	Structural_Protein_Mix	420	RAY_18	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51800.1	000764	Structural_Protein_Mix	1163	RAY_19	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51801.1	000764	Structural_Protein_Mix	1151	RAY_20	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52025.1	000764	Structural_Protein_Mix	514	RAY_245	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52064.1	000764	Structural_Protein_Mix	325	RAY_284	Erwinia phage vB_EamM_RAY	GCA_002624345.1
QEM41888.1	000764	Structural_Protein_Mix	454	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ASU03570.1	000764	Structural_Protein_Mix	1172	RISINGSUN_100	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03572.1	000764	Structural_Protein_Mix	245	RISINGSUN_98	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03571.1	000764	Structural_Protein_Mix	1168	RISINGSUN_99	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51577.1	000764	Structural_Protein_Mix	260	SIMMY50_115	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51595.1	000764	Structural_Protein_Mix	279	SIMMY50_133	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51480.1	000764	Structural_Protein_Mix	324	SIMMY50_18	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51481.1	000764	Structural_Protein_Mix	420	SIMMY50_19	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51482.1	000764	Structural_Protein_Mix	1163	SIMMY50_20	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51483.1	000764	Structural_Protein_Mix	1151	SIMMY50_21	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51709.1	000764	Structural_Protein_Mix	514	SIMMY50_250	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51747.1	000764	Structural_Protein_Mix	325	SIMMY50_289	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
QEM41796.1	000764	Structural_Protein_Mix	439	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANJ64924.1	000764	Structural_Protein_Mix	260	SPECIALG_114	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64942.1	000764	Structural_Protein_Mix	279	SPECIALG_132	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64827.2	000764	Structural_Protein_Mix	324	SPECIALG_17	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64828.1	000764	Structural_Protein_Mix	420	SPECIALG_18	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64829.1	000764	Structural_Protein_Mix	1163	SPECIALG_19	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64830.1	000764	Structural_Protein_Mix	1151	SPECIALG_20	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65060.1	000764	Structural_Protein_Mix	514	SPECIALG_249	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65099.2	000764	Structural_Protein_Mix	325	SPECIALG_288	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QCG76118.1	000764	Structural_Protein_Mix	395	EST35_0237	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ANZ50608.1	000764	Structural_Protein_Mix	68	STRATTON_183	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QDH50629.1	000764	Structural_Protein_Mix	209	-	Synechococcus phage S-B43	GCA_006869725.1
ANZ50610.1	000764	Structural_Protein_Mix	127	STRATTON_185	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AEP83865.1	000764	Structural_Protein_Mix	455	SPN3US_0032	Salmonella phage SPN3US	GCA_001042275.1
ANZ50472.1	000764	Structural_Protein_Mix	454	STRATTON_47	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARW58734.1	000764	Structural_Protein_Mix	193	Y3_094	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QKE54331.1	000764	Structural_Protein_Mix	323	ACSA002_0170	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QJB22878.1	000764	Structural_Protein_Mix	649	fnug_235	Pseudomonas phage fnug	GCA_012837215.1
QDH50470.1	000764	Structural_Protein_Mix	353	-	Synechococcus phage S-B43	GCA_006869725.1
QJB22817.1	000764	Structural_Protein_Mix	789	fnug_174	Pseudomonas phage fnug	GCA_012837215.1
QDH50644.1	000764	Structural_Protein_Mix	318	-	Synechococcus phage S-B43	GCA_006869725.1
ARW58789.1	000764	Structural_Protein_Mix	626	Y3_149	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58800.1	000764	Structural_Protein_Mix	282	Y3_160	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QDH50713.1	000764	Structural_Protein_Mix	483	-	Synechococcus phage S-B43	GCA_006869725.1
ARW58871.1	000764	Structural_Protein_Mix	168	Y3_231	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58882.1	000764	Structural_Protein_Mix	420	Y3_242	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58955.1	000764	Structural_Protein_Mix	512	Y3_315	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QDH50627.1	000764	Structural_Protein_Mix	462	-	Synechococcus phage S-B43	GCA_006869725.1
ARW58964.1	000764	Structural_Protein_Mix	187	Y3_324	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QJB22806.1	000764	Structural_Protein_Mix	463	fnug_163	Pseudomonas phage fnug	GCA_012837215.1
QJB22805.1	000764	Structural_Protein_Mix	457	fnug_162	Pseudomonas phage fnug	GCA_012837215.1
AQT28584.1	000764	Structural_Protein_Mix	477	YOLOSWAG_102	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28619.1	000764	Structural_Protein_Mix	680	YOLOSWAG_139	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28627.1	000764	Structural_Protein_Mix	648	YOLOSWAG_147	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28638.1	000764	Structural_Protein_Mix	279	YOLOSWAG_158	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDH50628.1	000764	Structural_Protein_Mix	443	-	Synechococcus phage S-B43	GCA_006869725.1
AQT28703.1	000764	Structural_Protein_Mix	163	YOLOSWAG_225	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28714.1	000764	Structural_Protein_Mix	420	YOLOSWAG_237	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28782.1	000764	Structural_Protein_Mix	539	YOLOSWAG_313	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDH50642.1	000764	Structural_Protein_Mix	410	-	Synechococcus phage S-B43	GCA_006869725.1
AQT28791.1	000764	Structural_Protein_Mix	173	YOLOSWAG_322	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28568.1	000764	Structural_Protein_Mix	193	YOLOSWAG_85	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QJB22804.1	000764	Structural_Protein_Mix	462	fnug_161	Pseudomonas phage fnug	GCA_012837215.1
AIT14133.1	000764	Structural_Protein_Mix	245	PBI_121Q_243	Escherichia phage 121Q	GCA_000926855.1
AIT13924.1	000764	Structural_Protein_Mix	210	PBI_121Q_27	Escherichia phage 121Q	GCA_000926855.1
AIT14389.1	000764	Structural_Protein_Mix	898	PBI_121Q_499	Escherichia phage 121Q	GCA_000926855.1
QDH50535.1	000764	Structural_Protein_Mix	172	-	Synechococcus phage S-B43	GCA_006869725.1
AIT14391.1	000764	Structural_Protein_Mix	886	PBI_121Q_501	Escherichia phage 121Q	GCA_000926855.1
QJB22802.1	000764	Structural_Protein_Mix	771	fnug_159	Pseudomonas phage fnug	GCA_012837215.1
QDH50495.1	000764	Structural_Protein_Mix	147	-	Synechococcus phage S-B43	GCA_006869725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIT14490.1	000764	Structural_Protein_Mix	282	PBI_121Q_600	Escherichia phage 121Q	GCA_000926855.1
QDH50553.1	000764	Structural_Protein_Mix	507	-	Synechococcus phage S-B43	GCA_006869725.1
AIT14497.1	000764	Structural_Protein_Mix	536	PBI_121Q_607	Escherichia phage 121Q	GCA_000926855.1
QAY00414.1	000764	Structural_Protein_Mix	210	Ecwhy1_133	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00452.1	000764	Structural_Protein_Mix	542	Ecwhy1_172	Escherichia phage Ecwhy_1	GCA_004146585.1
QCW23075.1	000764	Structural_Protein_Mix	210	-	Synechococcus phage S-B05	GCA_006083695.1
QAY00459.1	000764	Structural_Protein_Mix	277	Ecwhy1_179	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00486.1	000764	Structural_Protein_Mix	1644	Ecwhy1_207	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00487.1	000764	Structural_Protein_Mix	1899	Ecwhy1_208	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00498.1	000764	Structural_Protein_Mix	330	Ecwhy1_219	Escherichia phage Ecwhy_1	GCA_004146585.1
QCW22986.1	000764	Structural_Protein_Mix	204	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22887.1	000764	Structural_Protein_Mix	352	-	Synechococcus phage S-B05	GCA_006083695.1
QAY00559.1	000764	Structural_Protein_Mix	898	Ecwhy1_280	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34752.1	000764	Structural_Protein_Mix	195	ACQ29_gp072	Escherichia phage PBECO4	GCA_001041035.1
AGC35195.1	000764	Structural_Protein_Mix	536	ACQ29_gp515	Escherichia phage PBECO4	GCA_001041035.1
AGC35201.1	000764	Structural_Protein_Mix	286	ACQ29_gp521	Escherichia phage PBECO4	GCA_001041035.1
QKE54332.1	000764	Structural_Protein_Mix	415	ACSA002_0180	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AGC34681.1	000764	Structural_Protein_Mix	515	ACQ29_gp001	Escherichia phage PBECO4	GCA_001041035.1
AGC34751.1	000764	Structural_Protein_Mix	886	ACQ29_gp071	Escherichia phage PBECO4	GCA_001041035.1
AGC34753.1	000764	Structural_Protein_Mix	898	ACQ29_gp073	Escherichia phage PBECO4	GCA_001041035.1
QCW23078.1	000764	Structural_Protein_Mix	332	-	Synechococcus phage S-B05	GCA_006083695.1
AGC35157.1	000764	Structural_Protein_Mix	210	ACQ29_gp477	Escherichia phage PBECO4	GCA_001041035.1
BBM61616.1	000764	Structural_Protein_Mix	210	EO157G_0270	Escherichia phage SP27	GCA_008033345.1
BBM61808.1	000764	Structural_Protein_Mix	245	EO157G_2190	Escherichia phage SP27	GCA_008033345.1
BBM62060.1	000764	Structural_Protein_Mix	898	EO157G_4710	Escherichia phage SP27	GCA_008033345.1
BBM62061.1	000764	Structural_Protein_Mix	195	EO157G_4720	Escherichia phage SP27	GCA_008033345.1
BBM62062.1	000764	Structural_Protein_Mix	909	EO157G_4730	Escherichia phage SP27	GCA_008033345.1
ATN94790.1	000764	Structural_Protein_Mix	771	SL2_213	Pseudomonas phage SL2	GCA_002956015.1
QCW22993.1	000764	Structural_Protein_Mix	320	-	Synechococcus phage S-B05	GCA_006083695.1
BBM62162.1	000764	Structural_Protein_Mix	282	EO157G_5730	Escherichia phage SP27	GCA_008033345.1
QCW22906.1	000764	Structural_Protein_Mix	480	-	Synechococcus phage S-B05	GCA_006083695.1
BBM62169.1	000764	Structural_Protein_Mix	536	EO157G_5800	Escherichia phage SP27	GCA_008033345.1
QCW23076.1	000764	Structural_Protein_Mix	461	-	Synechococcus phage S-B05	GCA_006083695.1
AXC36867.1	000764	Structural_Protein_Mix	195	-	Escherichia phage UB	GCA_003341455.1
AXC36766.1	000764	Structural_Protein_Mix	536	-	Escherichia phage UB	GCA_003341455.1
AXC36773.1	000764	Structural_Protein_Mix	282	-	Escherichia phage UB	GCA_003341455.1
ATN94788.1	000764	Structural_Protein_Mix	462	SL2_211	Pseudomonas phage SL2	GCA_002956015.1
AXC36866.1	000764	Structural_Protein_Mix	886	-	Escherichia phage UB	GCA_003341455.1
AXC36868.1	000764	Structural_Protein_Mix	898	-	Escherichia phage UB	GCA_003341455.1
QCW22982.1	000764	Structural_Protein_Mix	444	-	Synechococcus phage S-B05	GCA_006083695.1
AXC36730.1	000764	Structural_Protein_Mix	210	-	Escherichia phage UB	GCA_003341455.1
AXC36547.1	000764	Structural_Protein_Mix	245	-	Escherichia phage UB	GCA_003341455.1
QCW22991.1	000764	Structural_Protein_Mix	433	-	Synechococcus phage S-B05	GCA_006083695.1
ATN94787.1	000764	Structural_Protein_Mix	457	SL2_210	Pseudomonas phage SL2	GCA_002956015.1
QCW22989.1	000764	Structural_Protein_Mix	406	-	Synechococcus phage S-B05	GCA_006083695.1
ARM70733.1	000764	Structural_Protein_Mix	270	phiC120_c26	Escherichia phage phiC120	GCA_002621185.1
QCW22983.1	000764	Structural_Protein_Mix	311	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22985.1	000764	Structural_Protein_Mix	101	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23073.1	000764	Structural_Protein_Mix	177	-	Synechococcus phage S-B05	GCA_006083695.1
ATN94786.1	000764	Structural_Protein_Mix	463	SL2_209	Pseudomonas phage SL2	GCA_002956015.1
QKN85873.1	000764	Structural_Protein_Mix	455	ACEC001_0350	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86005.1	000764	Structural_Protein_Mix	68	ACEC001_1650	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86006.1	000764	Structural_Protein_Mix	134	ACEC001_1655	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86007.1	000764	Structural_Protein_Mix	130	ACEC001_1660	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QCW22947.1	000764	Structural_Protein_Mix	175	-	Synechococcus phage S-B05	GCA_006083695.1
QBO61573.1	000764	Structural_Protein_Mix	245	G17_00077	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61768.1	000764	Structural_Protein_Mix	210	G17_00279	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61806.1	000764	Structural_Protein_Mix	536	G17_00317	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QCW23021.1	000764	Structural_Protein_Mix	500	-	Synechococcus phage S-B05	GCA_006083695.1
QBO61813.1	000764	Structural_Protein_Mix	282	G17_00324	Escherichia phage vB_EcoM_G17	GCA_004521135.1
ASR76099.1	000764	Structural_Protein_Mix	338	PBI_BELLAMY_54	Synechococcus phage Bellamy	GCA_002627525.1
ATN94775.1	000764	Structural_Protein_Mix	789	SL2_198	Pseudomonas phage SL2	GCA_002956015.1
QBO61911.1	000764	Structural_Protein_Mix	909	G17_00422	Escherichia phage vB_EcoM_G17	GCA_004521135.1
ASR76096.1	000764	Structural_Protein_Mix	727	PBI_BELLAMY_51	Synechococcus phage Bellamy	GCA_002627525.1
QBO61913.1	000764	Structural_Protein_Mix	898	G17_00424	Escherichia phage vB_EcoM_G17	GCA_004521135.1
ASR76087.1	000764	Structural_Protein_Mix	160	PBI_BELLAMY_42	Synechococcus phage Bellamy	GCA_002627525.1
QBO63821.1	000764	Structural_Protein_Mix	169	Goslar_00028	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63822.1	000764	Structural_Protein_Mix	717	Goslar_00029	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ATN94714.1	000764	Structural_Protein_Mix	649	SL2_137	Pseudomonas phage SL2	GCA_002956015.1
QBO63966.1	000764	Structural_Protein_Mix	426	Goslar_00173	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13812.1	000764	Structural_Protein_Mix	210	vBEcoMphAPEC6_gp183c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ASR76086.1	000764	Structural_Protein_Mix	711	PBI_BELLAMY_41	Synechococcus phage Bellamy	GCA_002627525.1
QDF13857.1	000764	Structural_Protein_Mix	282	vBEcoMphAPEC6_gp228c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ASR76083.1	000764	Structural_Protein_Mix	663	PBI_BELLAMY_38	Synechococcus phage Bellamy	GCA_002627525.1
QBJ02602.1	000764	Structural_Protein_Mix	451	PSA21_73	Pseudomonas phage Psa21	GCA_004340405.1
QDF13947.1	000764	Structural_Protein_Mix	898	vBEcoMphAPEC6_gp323c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80378.1	000764	Structural_Protein_Mix	898	PSLUR01_00401	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ASR76078.1	000764	Structural_Protein_Mix	635	PBI_BELLAMY_33	Synechococcus phage Bellamy	GCA_002627525.1
SCA80380.1	000764	Structural_Protein_Mix	909	PSLUR01_00403	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QBJ02796.1	000764	Structural_Protein_Mix	505	PSA21_270	Pseudomonas phage Psa21	GCA_004340405.1
ASR76076.1	000764	Structural_Protein_Mix	296	PBI_BELLAMY_31	Synechococcus phage Bellamy	GCA_002627525.1
SCA80474.1	000764	Structural_Protein_Mix	282	PSLUR01_00497	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ASR76074.1	000764	Structural_Protein_Mix	481	PBI_BELLAMY_29	Synechococcus phage Bellamy	GCA_002627525.1
SCA80481.1	000764	Structural_Protein_Mix	536	PSLUR01_00504	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80519.1	000764	Structural_Protein_Mix	210	PSLUR01_00542	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QBJ02794.1	000764	Structural_Protein_Mix	352	PSA21_268	Pseudomonas phage Psa21	GCA_004340405.1
ASR76073.1	000764	Structural_Protein_Mix	821	PBI_BELLAMY_28	Synechococcus phage Bellamy	GCA_002627525.1
AAX78748.1	000764	Structural_Protein_Mix	262	RB43ORF226w	Escherichia virus RB43	GCA_000863505.1
ASR76217.1	000764	Structural_Protein_Mix	267	PBI_BELLAMY_174	Synechococcus phage Bellamy	GCA_002627525.1
AAX78745.1	000764	Structural_Protein_Mix	82	RB43ORF223w	Escherichia virus RB43	GCA_000863505.1
QGH71978.1	000764	Structural_Protein_Mix	254	N1M2_115	Klebsiella phage N1M2	GCA_010092605.1
QGH71979.1	000764	Structural_Protein_Mix	1239	N1M2_116	Klebsiella phage N1M2	GCA_010092605.1
QGH71980.1	000764	Structural_Protein_Mix	1254	N1M2_117	Klebsiella phage N1M2	GCA_010092605.1
QGH71992.1	000764	Structural_Protein_Mix	599	N1M2_129	Klebsiella phage N1M2	GCA_010092605.1
AFA44323.1	000764	Structural_Protein_Mix	304	RaK2_00050	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44364.1	000764	Structural_Protein_Mix	257	RaK2_00091	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ASR76177.1	000764	Structural_Protein_Mix	362	PBI_BELLAMY_132	Synechococcus phage Bellamy	GCA_002627525.1
QKE54333.1	000764	Structural_Protein_Mix	1143	ACSA002_0190	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AFA44408.1	000764	Structural_Protein_Mix	207	RaK2_00135	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72543.1	000764	Structural_Protein_Mix	109	-	Myoviridae sp.	GCA_003657725.1
AXH72566.1	000764	Structural_Protein_Mix	163	-	Myoviridae sp.	GCA_003657725.1
AXH72776.1	000764	Structural_Protein_Mix	460	-	Myoviridae sp.	GCA_003657725.1
AXH72726.1	000764	Structural_Protein_Mix	329	-	Myoviridae sp.	GCA_003657725.1
ASR76166.1	000764	Structural_Protein_Mix	850	PBI_BELLAMY_121	Synechococcus phage Bellamy	GCA_002627525.1
QHJ79059.1	000764	Structural_Protein_Mix	280	-	Myoviridae sp.	GCA_012593985.1
QBJ02714.1	000764	Structural_Protein_Mix	450	PSA21_188	Pseudomonas phage Psa21	GCA_004340405.1
QGT54558.1	000764	Structural_Protein_Mix	276	b3_0317	Synechococcus phage B3	GCA_009745215.1
QGT54526.1	000764	Structural_Protein_Mix	390	b3_0285	Synechococcus phage B3	GCA_009745215.1
QBJ02713.1	000764	Structural_Protein_Mix	466	PSA21_187	Pseudomonas phage Psa21	GCA_004340405.1
QIG65697.1	000764	Structural_Protein_Mix	372	phiOC_p031	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QGT54923.1	000764	Structural_Protein_Mix	276	b23_0310	Synechococcus phage B23	GCA_009745195.1
QIG65711.1	000764	Structural_Protein_Mix	280	phiOC_p045	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QGT54891.1	000764	Structural_Protein_Mix	390	b23_0278	Synechococcus phage B23	GCA_009745195.1
QBJ02712.1	000764	Structural_Protein_Mix	449	PSA21_186	Pseudomonas phage Psa21	GCA_004340405.1
AMM43709.1	000764	Structural_Protein_Mix	254	CBB_144	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43712.1	000764	Structural_Protein_Mix	902	CBB_147	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43713.1	000764	Structural_Protein_Mix	916	CBB_148	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43714.1	000764	Structural_Protein_Mix	916	CBB_149	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43778.1	000764	Structural_Protein_Mix	309	CBB_213	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43791.1	000764	Structural_Protein_Mix	1553	CBB_226	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QBJ02710.1	000764	Structural_Protein_Mix	763	PSA21_184	Pseudomonas phage Psa21	GCA_004340405.1
AEH03658.1	000764	Structural_Protein_Mix	826	235	Pseudomonas phage PhiPA3	GCA_001502095.1
QKE54334.1	000764	Structural_Protein_Mix	1150	ACSA002_0200	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AMM43862.1	000764	Structural_Protein_Mix	214	CBB_298	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AIX30675.1	000764	Structural_Protein_Mix	268	Syn7803US37_198	Synechococcus phage ACG-2014f	GCA_002594065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SBV38189.1	000764	Structural_Protein_Mix	432	BN7874_020	Phage NCTB	GCA_900092385.1
SBV38242.1	000764	Structural_Protein_Mix	632	BN7874_073	Phage NCTB	GCA_900092385.1
AEH03589.1	000764	Structural_Protein_Mix	1093	166	Pseudomonas phage PhiPA3	GCA_001502095.1
AIX30616.1	000764	Structural_Protein_Mix	367	Syn7803US37_139	Synechococcus phage ACG-2014f	GCA_002594065.1
SBV38269.1	000764	Structural_Protein_Mix	151	BN7874_100	Phage NCTB	GCA_900092385.1
SBV38287.1	000764	Structural_Protein_Mix	192	BN7874_118	Phage NCTB	GCA_900092385.1
AEH03588.1	000764	Structural_Protein_Mix	911	165	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03577.1	000764	Structural_Protein_Mix	470	154	Pseudomonas phage PhiPA3	GCA_001502095.1
AFF28153.1	000764	Structural_Protein_Mix	248	PAU_155	Sphingomonas phage PAU	GCA_000902455.1
AEH03576.1	000764	Structural_Protein_Mix	477	153	Pseudomonas phage PhiPA3	GCA_001502095.1
SBV38370.1	000764	Structural_Protein_Mix	551	BN7874_200	Phage NCTB	GCA_900092385.1
SBV38406.1	000764	Structural_Protein_Mix	645	BN7874_222	Phage NCTB	GCA_900092385.1
AKF13330.1	000764	Structural_Protein_Mix	303	PHIN3_65	Sinorhizobium phage phiN3	GCA_001501175.1
AEH03575.1	000764	Structural_Protein_Mix	456	152	Pseudomonas phage PhiPA3	GCA_001502095.1
QGZ14450.1	000764	Structural_Protein_Mix	713	HWC77_gp087	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14452.1	000764	Structural_Protein_Mix	738	HWC77_gp089	Photobacterium phage PDCC-1	GCA_009800445.1
AGH26104.1	000764	Structural_Protein_Mix	350	CPMG_00003	Prochlorococcus phage MED4-213	GCA_000904535.1
AEH03573.1	000764	Structural_Protein_Mix	738	150	Pseudomonas phage PhiPA3	GCA_001502095.1
AGH26183.1	000764	Structural_Protein_Mix	300	CPMG_00082	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26274.1	000764	Structural_Protein_Mix	287	CPMG_00174	Prochlorococcus phage MED4-213	GCA_000904535.1
AKF12597.1	000764	Structural_Protein_Mix	303	PHIM7_49	Sinorhizobium phage phiM7	GCA_002622405.1
AAX44402.1	000764	Structural_Protein_Mix	455	PSSM2_024	Prochlorococcus phage P-SSM2	GCA_000859585.1
AEH03491.1	000764	Structural_Protein_Mix	441	064	Pseudomonas phage PhiPA3	GCA_001502095.1
AAX44405.1	000764	Structural_Protein_Mix	289	PSSM2_027	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44406.1	000764	Structural_Protein_Mix	559	PSSM2_028	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44504.1	000764	Structural_Protein_Mix	485	PSSM2_126	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44579.1	000764	Structural_Protein_Mix	97	PSSM2_202	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44673.1	000764	Structural_Protein_Mix	254	PSSM2_296	Prochlorococcus phage P-SSM2	GCA_000859585.1
AKF12957.1	000764	Structural_Protein_Mix	303	PHIM19_50	Sinorhizobium phage phiM19	GCA_002605865.1
AAX44512.1	000764	Structural_Protein_Mix	366	PSSM2_134	Prochlorococcus phage P-SSM2	GCA_000859585.1
ARV76925.1	000764	Structural_Protein_Mix	633	PHABIO_294	Pseudomonas phage Phabio	GCA_002624965.1
AGN12245.1	000764	Structural_Protein_Mix	559	PRTG_00087	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12246.1	000764	Structural_Protein_Mix	289	PRTG_00088	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGR47698.1	000764	Structural_Protein_Mix	303	SmphiM12_066	Sinorhizobium phage phiM12	GCA_001023565.1
AGN12249.1	000764	Structural_Protein_Mix	455	PRTG_00091	Prochlorococcus phage P-SSM5	GCA_002991095.1
QFP93049.1	000764	Structural_Protein_Mix	822	-	Serratia phage PCH45	GCA_009187865.1
QFP93098.1	000764	Structural_Protein_Mix	353	-	Serratia phage PCH45	GCA_009187865.1
AGN12304.1	000764	Structural_Protein_Mix	254	PRTG_00151	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12394.1	000764	Structural_Protein_Mix	97	PRTG_00241	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12454.1	000764	Structural_Protein_Mix	366	PRTG_00307	Prochlorococcus phage P-SSM5	GCA_002991095.1
QFP93079.1	000764	Structural_Protein_Mix	473	-	Serratia phage PCH45	GCA_009187865.1
AGN12462.1	000764	Structural_Protein_Mix	485	PRTG_00315	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93412.1	000764	Structural_Protein_Mix	671	AVU42_gp028	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93414.1	000764	Structural_Protein_Mix	559	AVU42_gp032	Prochlorococcus phage P-TIM68	GCA_001503075.1
QFP93193.1	000764	Structural_Protein_Mix	159	-	Serratia phage PCH45	GCA_009187865.1
AIR93413.1	000764	Structural_Protein_Mix	131	AVU42_gp031	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93446.1	000764	Structural_Protein_Mix	379	AVU42_gp108	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93407.1	000764	Structural_Protein_Mix	459	AVU42_gp022	Prochlorococcus phage P-TIM68	GCA_001503075.1
QFP93058.1	000764	Structural_Protein_Mix	687	-	Serratia phage PCH45	GCA_009187865.1
QDB71176.1	000764	Structural_Protein_Mix	450	CPT_Moabite_146	Serratia phage Moabite	GCA_006384735.1
AIR93436.1	000764	Structural_Protein_Mix	961	AVU42_gp096	Prochlorococcus phage P-TIM68	GCA_001503075.1
QDB71175.1	000764	Structural_Protein_Mix	742	CPT_Moabite_145	Serratia phage Moabite	GCA_006384735.1
AIR93409.1	000764	Structural_Protein_Mix	985	AVU42_gp024	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93497.1	000764	Structural_Protein_Mix	180	AVU42_gp162	Prochlorococcus phage P-TIM68	GCA_001503075.1
AQW89068.1	000764	Structural_Protein_Mix	265	BF_0543	Serratia phage BF	GCA_002619745.1
AQW89066.1	000764	Structural_Protein_Mix	280	BF_0541	Serratia phage BF	GCA_002619745.1
ADO99136.1	000764	Structural_Protein_Mix	616	Syn1_035	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99137.1	000764	Structural_Protein_Mix	884	Syn1_036	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99138.1	000764	Structural_Protein_Mix	589	Syn1_037	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99267.1	000764	Structural_Protein_Mix	285	Syn1_166	Prochlorococcus phage Syn1	GCA_000892495.1
AQW88970.1	000764	Structural_Protein_Mix	137	BF_0445	Serratia phage BF	GCA_002619745.1
ADO99224.1	000764	Structural_Protein_Mix	394	Syn1_123	Prochlorococcus phage Syn1	GCA_000892495.1
AQW88821.1	000764	Structural_Protein_Mix	218	BF_0296	Serratia phage BF	GCA_002619745.1
QKE54416.1	000764	Structural_Protein_Mix	281	ACSA002_1020	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QMP24010.1	000764	Structural_Protein_Mix	415	-	Proteus phage 10	GCA_014071245.1
QMP24163.1	000764	Structural_Protein_Mix	494	-	Proteus phage 10	GCA_014071245.1
QMP24012.1	000764	Structural_Protein_Mix	1003	-	Proteus phage 10	GCA_014071245.1
QMP24011.1	000764	Structural_Protein_Mix	1154	-	Proteus phage 10	GCA_014071245.1
ARV76837.1	000764	Structural_Protein_Mix	452	PHABIO_206	Pseudomonas phage Phabio	GCA_002624965.1
QMP24186.1	000764	Structural_Protein_Mix	266	-	Proteus phage 10	GCA_014071245.1
QMP24187.1	000764	Structural_Protein_Mix	270	-	Proteus phage 10	GCA_014071245.1
AQW88750.1	000764	Structural_Protein_Mix	1490	BF_0225	Serratia phage BF	GCA_002619745.1
ABY63045.1	000764	Structural_Protein_Mix	738	201phi2-1p216	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63047.1	000764	Structural_Protein_Mix	455	201phi2-1p218	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63048.1	000764	Structural_Protein_Mix	458	201phi2-1p219	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63049.1	000764	Structural_Protein_Mix	435	201phi2-1p220	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76836.1	000764	Structural_Protein_Mix	457	PHABIO_205	Pseudomonas phage Phabio	GCA_002624965.1
ABY63124.1	000764	Structural_Protein_Mix	641	201phi2-1p298	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27250.1	000764	Structural_Protein_Mix	1046	PPEV_gp156	Pseudomonas phage EL	GCA_000866825.1
CAG27208.1	000764	Structural_Protein_Mix	1184	PPEV_gp114	Pseudomonas phage EL	GCA_000866825.1
CAG27209.1	000764	Structural_Protein_Mix	1193	PPEV_gp115	Pseudomonas phage EL	GCA_000866825.1
CAG27207.1	000764	Structural_Protein_Mix	247	PPEV_gp113	Pseudomonas phage EL	GCA_000866825.1
AQW88734.1	000764	Structural_Protein_Mix	322	BF_0209	Serratia phage BF	GCA_002619745.1
ARV76834.1	000764	Structural_Protein_Mix	760	PHABIO_203	Pseudomonas phage Phabio	GCA_002624965.1
ANM44924.1	000764	Structural_Protein_Mix	771	KTN4_166	Pseudomonas phage KTN4	GCA_002607225.1
ANM44926.1	000764	Structural_Protein_Mix	462	KTN4_168	Pseudomonas phage KTN4	GCA_002607225.1
ANM44927.1	000764	Structural_Protein_Mix	457	KTN4_169	Pseudomonas phage KTN4	GCA_002607225.1
ANM44928.1	000764	Structural_Protein_Mix	463	KTN4_170	Pseudomonas phage KTN4	GCA_002607225.1
ANM44939.1	000764	Structural_Protein_Mix	789	KTN4_181	Pseudomonas phage KTN4	GCA_002607225.1
QKE54420.1	000764	Structural_Protein_Mix	200	ACSA002_1060	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ANM45000.1	000764	Structural_Protein_Mix	649	KTN4_242	Pseudomonas phage KTN4	GCA_002607225.1
AQW88668.1	000764	Structural_Protein_Mix	920	BF_0143	Serratia phage BF	GCA_002619745.1
AQW88667.1	000764	Structural_Protein_Mix	913	BF_0142	Serratia phage BF	GCA_002619745.1
AQW88666.1	000764	Structural_Protein_Mix	899	BF_0141	Serratia phage BF	GCA_002619745.1
AFH14673.1	000764	Structural_Protein_Mix	260	Lu11_0140	Pseudomonas phage Lu11	GCA_000897175.1
AFH14685.1	000764	Structural_Protein_Mix	180	Lu11_0152	Pseudomonas phage Lu11	GCA_000897175.1
AFH14688.1	000764	Structural_Protein_Mix	616	Lu11_0154	Pseudomonas phage Lu11	GCA_000897175.1
AFH14695.1	000764	Structural_Protein_Mix	159	Lu11_0161	Pseudomonas phage Lu11	GCA_000897175.1
AFH14696.1	000764	Structural_Protein_Mix	177	Lu11_0162	Pseudomonas phage Lu11	GCA_000897175.1
AFH14707.1	000764	Structural_Protein_Mix	427	Lu11_0172	Pseudomonas phage Lu11	GCA_000897175.1
ATA65496.1	000764	Structural_Protein_Mix	140	2050HW_00161	Serratia phage 2050HW	GCA_002628125.1
AFH14758.1	000764	Structural_Protein_Mix	142	Lu11_0221	Pseudomonas phage Lu11	GCA_000897175.1
AGS82134.1	000764	Structural_Protein_Mix	186	PaBG_00260	Pseudomonas phage PaBG	GCA_000912555.1
QKE11221.1	000764	Structural_Protein_Mix	268	PaBG_00250	Pseudomonas phage PaBG	GCA_000912555.1
ATA65395.1	000764	Structural_Protein_Mix	321	2050HW_00060	Serratia phage 2050HW	GCA_002628125.1
ATA65394.1	000764	Structural_Protein_Mix	514	2050HW_00059	Serratia phage 2050HW	GCA_002628125.1
ARV77307.1	000764	Structural_Protein_Mix	1013	NOXIFER_138	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77308.1	000764	Structural_Protein_Mix	575	NOXIFER_139	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77319.1	000764	Structural_Protein_Mix	447	NOXIFER_150	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77320.1	000764	Structural_Protein_Mix	629	NOXIFER_151	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77321.1	000764	Structural_Protein_Mix	459	NOXIFER_152	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77323.1	000764	Structural_Protein_Mix	709	NOXIFER_154	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77394.1	000764	Structural_Protein_Mix	593	NOXIFER_229	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77460.1	000764	Structural_Protein_Mix	290	NOXIFER_295	Pseudomonas phage Noxifer	GCA_002625005.1
ATA65393.1	000764	Structural_Protein_Mix	238	2050HW_00058	Serratia phage 2050HW	GCA_002628125.1
ARV77234.1	000764	Structural_Protein_Mix	454	NOXIFER_63	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89579.1	000764	Structural_Protein_Mix	254	OBP_142	Pseudomonas phage OBP	GCA_000896635.1
AEV89580.1	000764	Structural_Protein_Mix	1246	OBP_143	Pseudomonas phage OBP	GCA_000896635.1
AEV89581.1	000764	Structural_Protein_Mix	1274	OBP_144	Pseudomonas phage OBP	GCA_000896635.1
AEV89598.1	000764	Structural_Protein_Mix	810	OBP_161	Pseudomonas phage OBP	GCA_000896635.1
AEV89599.1	000764	Structural_Protein_Mix	423	OBP_162	Pseudomonas phage OBP	GCA_000896635.1
QBX32385.1	000764	Structural_Protein_Mix	502	-	Pseudomonas phage PA1C	GCA_004785505.1
QKE54649.1	000764	Structural_Protein_Mix	272	ACSA002_3320	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QBX32218.1	000764	Structural_Protein_Mix	438	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32315.1	000764	Structural_Protein_Mix	454	-	Pseudomonas phage PA1C	GCA_004785505.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX32313.1	000764	Structural_Protein_Mix	455	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32314.1	000764	Structural_Protein_Mix	468	-	Pseudomonas phage PA1C	GCA_004785505.1
AGS82092.1	000764	Structural_Protein_Mix	396	PaBG_00217	Pseudomonas phage PaBG	GCA_000912555.1
QBX32311.1	000764	Structural_Protein_Mix	760	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32326.1	000764	Structural_Protein_Mix	822	-	Pseudomonas phage PA1C	GCA_004785505.1
QKE54422.1	000764	Structural_Protein_Mix	369	ACSA002_1080	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AGS82033.1	000764	Structural_Protein_Mix	292	PaBG_00151	Pseudomonas phage PaBG	GCA_000912555.1
QKE54571.1	000764	Structural_Protein_Mix	492	ACSA002_2550	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AGS81978.1	000764	Structural_Protein_Mix	541	PaBG_00093	Pseudomonas phage PaBG	GCA_000912555.1
AGS82001.2	000764	Structural_Protein_Mix	403	PaBG_00117	Pseudomonas phage PaBG	GCA_000912555.1
AGS82008.1	000764	Structural_Protein_Mix	202	PaBG_00124	Pseudomonas phage PaBG	GCA_000912555.1
QKE54467.1	000764	Structural_Protein_Mix	284	ACSA002_1530	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AGS82015.1	000764	Structural_Protein_Mix	440	PaBG_00131	Pseudomonas phage PaBG	GCA_000912555.1
AGS82018.1	000764	Structural_Protein_Mix	141	PaBG_00136	Pseudomonas phage PaBG	GCA_000912555.1
AZU98196.1	000764	Structural_Protein_Mix	1560	CPT_Munch_252	Salmonella phage Munch	GCA_004015485.1
QBZ70678.1	000764	Structural_Protein_Mix	712	pETSU_097	Edwardsiella virus pEt-SU	GCA_004800915.1
AFA44371.1	000764	Structural_Protein_Mix	595	RaK2_00098	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
BAQ02593.1	000764	Structural_Protein_Mix	373	AVU38_gp065	Ralstonia phage RSL2	GCA_001503055.1
ANZ48200.1	000764	Structural_Protein_Mix	399	ASESINO_187	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50611.1	000764	Structural_Protein_Mix	399	STRATTON_186	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AFQ96634.1	000764	Structural_Protein_Mix	399	G173_gp089	Erwinia phage phiEaH2	GCA_000902915.1
AQT28062.1	000764	Structural_Protein_Mix	465	pVa21_121	Vibrio phage pVa-21	GCA_002619305.1
AXQ68314.1	000764	Structural_Protein_Mix	362	CcrBL10_gp110c	Caulobacter phage CcrBL10	GCA_003443255.1
QBJ02633.1	000764	Structural_Protein_Mix	212	PSA21_105	Pseudomonas phage Psa21	GCA_004340405.1
AMM43819.1	000764	Structural_Protein_Mix	274	CBB_254	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAG41537.1	000764	Structural_Protein_Mix	570	RSL1_ORF092	Ralstonia phage phiRSL1	GCA_000879455.1
AMM44834.1	000764	Structural_Protein_Mix	203	SP15_035	Bacillus phage SP-15	GCA_001754685.1
ASU00019.1	000764	Structural_Protein_Mix	651	PBI_PBS1_197	Bacillus virus PBS1	GCA_002601325.1
AEO93455.1	000764	Structural_Protein_Mix	186	G_195	Bacillus virus G	GCA_000917535.1
AXG67146.1	000764	Structural_Protein_Mix	273	AD1_102	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
ABY63059.1	000764	Structural_Protein_Mix	1480	201phi2-1p230	Pseudomonas phage 201phi2-1	GCA_000875305.1
AXG67151.1	000764	Structural_Protein_Mix	210	AD1_107	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
SBV38305.1	000764	Structural_Protein_Mix	506	BN7874_136	Phage NCTB	GCA_900092385.1
SBV38302.1	000764	Structural_Protein_Mix	164	BN7874_133	Phage NCTB	GCA_900092385.1
SBV38297.1	000764	Structural_Protein_Mix	280	BN7874_128	Phage NCTB	GCA_900092385.1
AUG86732.1	000764	Structural_Protein_Mix	1032	MADMEL_305	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AYD79895.1	000764	Structural_Protein_Mix	272	JA11_090	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79899.1	000764	Structural_Protein_Mix	164	JA11_094	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AWY08384.1	000764	Structural_Protein_Mix	163	Alexandra_111	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AFH14769.1	000764	Structural_Protein_Mix	228	Lu11_0232	Pseudomonas phage Lu11	GCA_000897175.1
AYD79900.1	000764	Structural_Protein_Mix	210	JA11_095	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79901.1	000764	Structural_Protein_Mix	324	JA11_096	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66494.1	000764	Structural_Protein_Mix	272	JA13_091	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AFH14771.1	000764	Structural_Protein_Mix	340	Lu11_0234	Pseudomonas phage Lu11	GCA_000897175.1
AXG66498.1	000764	Structural_Protein_Mix	164	JA13_095	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AGS82121.1	000764	Structural_Protein_Mix	173	PaBG_00247	Pseudomonas phage PaBG	GCA_000912555.1
AXG66500.1	000764	Structural_Protein_Mix	324	JA13_097	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AGS82120.2	000764	Structural_Protein_Mix	229	PaBG_00246	Pseudomonas phage PaBG	GCA_000912555.1
QEM41900.1	000764	Structural_Protein_Mix	1107	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AXG66819.1	000764	Structural_Protein_Mix	272	JA29_093	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66823.1	000764	Structural_Protein_Mix	164	JA29_097	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66824.1	000764	Structural_Protein_Mix	210	JA29_098	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67464.1	000764	Structural_Protein_Mix	272	JA33_090	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67468.1	000764	Structural_Protein_Mix	164	JA33_094	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67469.1	000764	Structural_Protein_Mix	210	JA33_095	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67470.1	000764	Structural_Protein_Mix	324	JA33_096	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGS82119.1	000764	Structural_Protein_Mix	459	PaBG_00245	Pseudomonas phage PaBG	GCA_000912555.1
AQT28577.1	000764	Structural_Protein_Mix	273	YOLOSWAG_95	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28583.1	000764	Structural_Protein_Mix	209	YOLOSWAG_101	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28582.1	000764	Structural_Protein_Mix	162	YOLOSWAG_100	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ARW58750.1	000764	Structural_Protein_Mix	478	Y3_110	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QJB22818.1	000764	Structural_Protein_Mix	1069	fnug_175	Pseudomonas phage fnug	GCA_012837215.1
ARW58748.1	000764	Structural_Protein_Mix	163	Y3_108	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58744.1	000764	Structural_Protein_Mix	272	Y3_104	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BAW19413.1	000764	Structural_Protein_Mix	1089	-	Ralstonia phage RP31	GCA_002617365.1
BAW19403.1	000764	Structural_Protein_Mix	170	-	Ralstonia phage RP31	GCA_002617365.1
QBX32327.1	000764	Structural_Protein_Mix	1107	-	Pseudomonas phage PA1C	GCA_004785505.1
AMS01097.1	000764	Structural_Protein_Mix	651	AR9_g012	Bacillus phage AR9	GCA_001743835.1
BAW19117.1	000764	Structural_Protein_Mix	170	FDH28_gp278	Ralstonia phage RP12	GCA_002617345.1
AWY08380.1	000764	Structural_Protein_Mix	273	Alexandra_107	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BAW19127.1	000764	Structural_Protein_Mix	1089	FDH28_gp268	Ralstonia phage RP12	GCA_002617345.1
AXG66499.1	000764	Structural_Protein_Mix	210	JA13_096	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
ATN94774.1	000764	Structural_Protein_Mix	1093	SL2_197	Pseudomonas phage SL2	GCA_002956015.1
AIX30492.1	000764	Structural_Protein_Mix	929	Syn7803US37_15	Synechococcus phage ACG-2014f	GCA_002594065.1
ANM44940.1	000764	Structural_Protein_Mix	1093	KTN4_182	Pseudomonas phage KTN4	GCA_002607225.1
ANH51765.1	000764	Structural_Protein_Mix	1032	SIMMY50_307	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH52082.1	000764	Structural_Protein_Mix	1032	RAY_302	Erwinia phage vB_EamM_RAY	GCA_002624345.1
AUG86091.1	000764	Structural_Protein_Mix	1032	BOSOLAPHORUS_305	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AAL83047.1	000764	Structural_Protein_Mix	1093	PHIKZ146	Pseudomonas virus phiKZ	GCA_000842965.1
AUG86411.1	000764	Structural_Protein_Mix	1032	DESERTFOX_304	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANH52407.1	000764	Structural_Protein_Mix	1035	DM_308	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ASV44734.1	000764	Structural_Protein_Mix	610	FDI40_gp288	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANJ65117.1	000764	Structural_Protein_Mix	1023	SPECIALG_306	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBP07409.1	000764	Structural_Protein_Mix	1035	REBECCA_304	Erwinia phage Rebecca	GCA_004521635.1
AHI60452.1	000764	Structural_Protein_Mix	1035	Ea357_298	Erwinia phage Ea35-70	GCA_000914635.1
AUG87057.1	000764	Structural_Protein_Mix	1035	MORTIMER_309	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
QMP24211.1	000764	Structural_Protein_Mix	840	-	Proteus phage 10	GCA_014071245.1
AUZ95231.1	000764	Structural_Protein_Mix	786	FDI40_gp472	Agrobacterium phage Atu_ph07	GCA_002628245.1
QKE54632.1	000764	Structural_Protein_Mix	1383	ACSA002_3150	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARV76849.1	000764	Structural_Protein_Mix	1113	PHABIO_218	Pseudomonas phage Phabio	GCA_002624965.1
AWY08386.1	000764	Structural_Protein_Mix	480	Alexandra_114	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AIX30751.1	000764	Structural_Protein_Mix	224	Syn7803US37_274	Synechococcus phage ACG-2014f	GCA_002594065.1
AXG67152.1	000764	Structural_Protein_Mix	479	AD1_108	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AUZ95086.1	000764	Structural_Protein_Mix	709	FDI40_gp327	Agrobacterium phage Atu_ph07	GCA_002628245.1
AON97216.1	000764	Structural_Protein_Mix	462	E_208	Cronobacter phage vB_CsaM_IeE	GCA_002611805.1
ANS05950.1	000764	Structural_Protein_Mix	463	ABCD_0202	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78734.1	000764	Structural_Protein_Mix	463	RB43ORF212w	Escherichia virus RB43	GCA_000863505.1
QHJ79044.1	000764	Structural_Protein_Mix	456	-	Myoviridae sp.	GCA_012593985.1
AIX30752.1	000764	Structural_Protein_Mix	215	Syn7803US37_275	Synechococcus phage ACG-2014f	GCA_002594065.1
AGR47756.1	000764	Structural_Protein_Mix	901	SmphiM12_124	Sinorhizobium phage phiM12	GCA_001023565.1
AKZ65595.1	000764	Structural_Protein_Mix	781	PHIN3_103	Sinorhizobium phage phiN3	GCA_001501175.1
AKF12635.1	000764	Structural_Protein_Mix	901	PHIM7_88	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12995.1	000764	Structural_Protein_Mix	901	PHIM19_89	Sinorhizobium phage phiM19	GCA_002605865.1
AQW88777.1	000764	Structural_Protein_Mix	291	BF_0252	Serratia phage BF	GCA_002619745.1
QCG76033.1	000764	Structural_Protein_Mix	270	EST35_0151	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAE47740.1	000764	Structural_Protein_Mix	183	CST042	Clostridium phage c-st	GCA_000865225.1
BBA65380.1	000764	Structural_Protein_Mix	528	-	Xanthomonas phage XacN1	GCA_003173815.1
BAW19501.1	000764	Structural_Protein_Mix	591	-	Ralstonia phage RP31	GCA_002617365.1
BAW19215.1	000764	Structural_Protein_Mix	591	FDH28_gp180	Ralstonia phage RP12	GCA_002617345.1
ANZ48751.1	000764	Structural_Protein_Mix	399	CHRISDB_189	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48472.1	000764	Structural_Protein_Mix	399	CAITLIN_177	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ50359.1	000764	Structural_Protein_Mix	399	PHOBOS_169	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QBX06677.1	000764	Structural_Protein_Mix	578	BcepSaruman_264	Burkholderia phage BcepSaruman	GCA_004771375.1
QHJ85928.1	000764	Structural_Protein_Mix	479	KKIINIFJ_00016	Pseudomonas phage PN05	GCA_009931935.1
QDH83681.1	000764	Structural_Protein_Mix	516	H1O15_gp130	Achromobacter phage Motura	GCA_006964305.1
QBQ74647.1	000764	Structural_Protein_Mix	581	BcepSauron_267	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41644.1	000764	Structural_Protein_Mix	498	RSL1_ORF195	Ralstonia phage phiRSL1	GCA_000879455.1
QBO63883.1	000764	Structural_Protein_Mix	1324	Goslar_00090	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QIW90824.1	000764	Structural_Protein_Mix	356	GCAPEGMB_00509	Vibrio phage V07	GCA_012361095.1
ANZ49537.1	000764	Structural_Protein_Mix	399	KWAN_185	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51312.1	000764	Structural_Protein_Mix	399	WELLINGTON_184	Erwinia phage Wellington	GCA_003344985.1
QGT54521.1	000764	Structural_Protein_Mix	876	b3_0279	Synechococcus phage B3	GCA_009745215.1
QGT54886.1	000764	Structural_Protein_Mix	876	b23_0272	Synechococcus phage B23	GCA_009745195.1
ANZ49260.1	000764	Structural_Protein_Mix	399	HUXLEY_178	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49816.1	000764	Structural_Protein_Mix	399	MACHINA_178	Erwinia phage Machina	GCA_002758035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ50088.1	000764	Structural_Protein_Mix	399	PARSHIK_179	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ARM70802.1	000764	Structural_Protein_Mix	259	phiC120_c96	Escherichia phage phiC120	GCA_002621185.1
AIA64805.1	000764	Structural_Protein_Mix	262	S13_006	Cronobacter phage S13	GCA_001503575.1
ANZ49012.1	000764	Structural_Protein_Mix	399	EARLPHILLIPIV_163	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
QBP07589.1	000764	Structural_Protein_Mix	399	DERBICUS_163	Erwinia phage Derbicus	GCA_004521655.1
ARM70730.1	000764	Structural_Protein_Mix	78	phiC120_c23	Escherichia phage phiC120	GCA_002621185.1
AND75267.1	000764	Structural_Protein_Mix	574	ME3_106	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AOV59492.1	000764	Structural_Protein_Mix	495	S330809_031	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59254.1	000764	Structural_Protein_Mix	495	C440309_031	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59730.1	000764	Structural_Protein_Mix	490	N231010_031	Synechococcus phage S-CAM4	GCA_002922155.1
ASV44157.1	000764	Structural_Protein_Mix	662	PBI_SCTP2_142	Salicola phage SCTP-2	GCA_002625545.1
ANM44850.1	000764	Structural_Protein_Mix	433	KTN4_092	Pseudomonas phage KTN4	GCA_002607225.1
ATN94863.1	000764	Structural_Protein_Mix	459	SL2_286	Pseudomonas phage SL2	GCA_002956015.1
QJB22728.1	000764	Structural_Protein_Mix	459	fnug_85	Pseudomonas phage fnug	GCA_012837215.1
AAL82971.1	000764	Structural_Protein_Mix	433	PHIKZ070	Pseudomonas virus phiKZ	GCA_000842965.1
AXC36813.1	000764	Structural_Protein_Mix	326	-	Escherichia phage UB	GCA_003341455.1
QDF13892.1	000764	Structural_Protein_Mix	326	vBEcoMphAPEC6_gp267c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
BBM62123.1	000764	Structural_Protein_Mix	326	EO157G_5340	Escherichia phage SP27	GCA_008033345.1
AIT14450.1	000764	Structural_Protein_Mix	326	PBI_121Q_560	Escherichia phage 121Q	GCA_000926855.1
QBO61852.1	000764	Structural_Protein_Mix	326	G17_00363	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AGC34693.1	000764	Structural_Protein_Mix	326	ACQ29_gp013	Escherichia phage PBECO4	GCA_001041035.1
SCA80435.1	000764	Structural_Protein_Mix	325	PSLUR01_00458	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMR59818.1	000764	Structural_Protein_Mix	400	SEGD1_171	Enterobacteria phage SEGD1	GCA_002601865.1
AEP84000.1	000764	Structural_Protein_Mix	400	SPN3US_0167	Salmonella phage SPN3US	GCA_001042275.1
QNI20865.1	000764	Structural_Protein_Mix	412	-	Salmonella phage JN03	GCA_014319805.1
QKN86008.1	000764	Structural_Protein_Mix	400	ACEC001_1670	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09167.1	000764	Structural_Protein_Mix	400	MLDJOKPK_00274	Salmonella phage SPAsTU	GCA_003183805.1
QDH50484.1	000764	Structural_Protein_Mix	589	-	Synechococcus phage S-B43	GCA_006869725.1
QCW22873.1	000764	Structural_Protein_Mix	630	-	Synechococcus phage S-B05	GCA_006083695.1
QIG62801.1	000764	Structural_Protein_Mix	350	SEPL_188	Salmonella phage SE_PL	GCA_011067555.1
QCW18926.1	000764	Structural_Protein_Mix	350	7t3_0405	Salmonella phage 7t3	GCA_006083215.1
AZU98183.1	000764	Structural_Protein_Mix	350	CPT_Munch_239	Salmonella phage Munch	GCA_004015485.1
ARV76737.1	000764	Structural_Protein_Mix	444	PHABIO_106	Pseudomonas phage Phabio	GCA_002624965.1
QBO61841.1	000764	Structural_Protein_Mix	1841	G17_00352	Escherichia phage vB_EcoM_G17	GCA_004521135.1
BBM62134.1	000764	Structural_Protein_Mix	1841	EO157G_5450	Escherichia phage SP27	GCA_008033345.1
SCA80446.1	000764	Structural_Protein_Mix	1841	PSLUR01_00469	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDF13883.1	000764	Structural_Protein_Mix	1841	vBEcoMphAPEC6_gp256	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AIT14461.1	000764	Structural_Protein_Mix	1841	PBI_121Q_571	Escherichia phage 121Q	GCA_000926855.1
AXC36801.1	000764	Structural_Protein_Mix	1959	-	Escherichia phage UB	GCA_003341455.1
BAW19537.1	000764	Structural_Protein_Mix	580	-	Ralstonia phage RP31	GCA_002617365.1
BAW19251.1	000764	Structural_Protein_Mix	580	FDH28_gp144	Ralstonia phage RP12	GCA_002617345.1
ASV44114.1	000764	Structural_Protein_Mix	1735	PBI_SCTP2_99	Salicola phage SCTP-2	GCA_002625545.1
AGN12247.1	000764	Structural_Protein_Mix	548	PRTG_00089	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44404.1	000764	Structural_Protein_Mix	548	PSSM2_026	Prochlorococcus phage P-SSM2	GCA_000859585.1
QCW22908.1	000764	Structural_Protein_Mix	780	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50551.1	000764	Structural_Protein_Mix	780	-	Synechococcus phage S-B43	GCA_006869725.1
AXG66543.1	000764	Structural_Protein_Mix	654	JA13_140	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AYD79944.1	000764	Structural_Protein_Mix	643	JA11_139	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG67513.1	000764	Structural_Protein_Mix	643	JA33_139	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QDJ96361.1	000764	Structural_Protein_Mix	756	Xoosp13_174	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGH07460.1	000764	Structural_Protein_Mix	354	CYVG_00016	Cyanophage S-SSM6a	GCA_002710385.1
AXG67364.1	000764	Structural_Protein_Mix	273	AD1_320	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67365.1	000764	Structural_Protein_Mix	178	AD1_321	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79934.1	000764	Structural_Protein_Mix	652	JA11_129	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG67228.1	000764	Structural_Protein_Mix	229	AD1_184	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67184.1	000764	Structural_Protein_Mix	664	AD1_140	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79978.1	000764	Structural_Protein_Mix	220	JA11_173	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66533.1	000764	Structural_Protein_Mix	652	JA13_130	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
QJT70048.1	000764	Structural_Protein_Mix	578	SynMITS9220M01_035	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG66576.1	000764	Structural_Protein_Mix	220	JA13_173	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66858.1	000764	Structural_Protein_Mix	662	JA29_132	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66901.1	000764	Structural_Protein_Mix	221	JA29_175	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67503.1	000764	Structural_Protein_Mix	652	JA33_129	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXQ70468.1	000764	Structural_Protein_Mix	544	HOU04_gp069	Synechococcus phage S-T4	GCA_003443335.1
QAU04452.1	000764	Structural_Protein_Mix	172	ValB1MD_033	Vibrio phage ValB1MD	GCA_004138815.1
QAU04511.1	000764	Structural_Protein_Mix	493	ValB1MD_172	Vibrio phage ValB1MD	GCA_004138815.1
QBZ70662.1	000764	Structural_Protein_Mix	253	pETSU_081	Edwardsiella virus pEt-SU	GCA_004800915.1
AGX01914.1	000764	Structural_Protein_Mix	184	CF95_gp192	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01921.1	000764	Structural_Protein_Mix	277	CF95_gp199	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07219.1	000764	Structural_Protein_Mix	269	REBECCA_112	Erwinia phage Rebecca	GCA_004521635.1
AWY08457.1	000764	Structural_Protein_Mix	221	Alexandra_189	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08586.1	000764	Structural_Protein_Mix	267	Alexandra_337	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48198.1	000764	Structural_Protein_Mix	151	ASESINO_185	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50609.1	000764	Structural_Protein_Mix	155	STRATTON_184	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARW58781.1	000764	Structural_Protein_Mix	691	Y3_141	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AGH56989.1	000764	Structural_Protein_Mix	266	CPXG_00186	Cyanophage P-RSM6	GCA_000906155.1
ARW58825.1	000764	Structural_Protein_Mix	225	Y3_185	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58963.1	000764	Structural_Protein_Mix	259	Y3_323	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28659.1	000764	Structural_Protein_Mix	228	YOLOSWAG_180	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDH50467.1	000764	Structural_Protein_Mix	427	-	Synechococcus phage S-B43	GCA_006869725.1
AQT28790.1	000764	Structural_Protein_Mix	263	YOLOSWAG_321	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14390.1	000764	Structural_Protein_Mix	195	PBI_121Q_500	Escherichia phage 121Q	GCA_000926855.1
QAY00557.1	000764	Structural_Protein_Mix	909	Ecwhy1_278	Escherichia phage Ecwhy_1	GCA_004146585.1
QCW23079.1	000764	Structural_Protein_Mix	202	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23087.1	000764	Structural_Protein_Mix	331	-	Synechococcus phage S-B05	GCA_006083695.1
QBO61912.1	000764	Structural_Protein_Mix	195	G17_00423	Escherichia phage vB_EcoM_G17	GCA_004521135.1
ASR76089.1	000764	Structural_Protein_Mix	351	PBI_BELLAMY_44	Synechococcus phage Bellamy	GCA_002627525.1
ASR76080.1	000764	Structural_Protein_Mix	234	PBI_BELLAMY_35	Synechococcus phage Bellamy	GCA_002627525.1
SCA80379.1	000764	Structural_Protein_Mix	195	PSLUR01_00402	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDJ97276.1	000764	Structural_Protein_Mix	251	D6_0116	Aeromonas phage D6	GCA_007051205.2
QIG65671.1	000764	Structural_Protein_Mix	315	phiOC_p005	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43824.1	000764	Structural_Protein_Mix	539	CBB_260	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38182.1	000764	Structural_Protein_Mix	147	BN7874_013	Phage NCTB	GCA_900092385.1
SBV38247.1	000764	Structural_Protein_Mix	294	BN7874_078	Phage NCTB	GCA_900092385.1
SBV38248.1	000764	Structural_Protein_Mix	194	BN7874_079	Phage NCTB	GCA_900092385.1
SBV38431.1	000764	Structural_Protein_Mix	495	BN7874_239	Phage NCTB	GCA_900092385.1
QDH47109.1	000764	Structural_Protein_Mix	251	LAh10_48	Aeromonas phage LAh10	GCA_006863975.1
SBV38500.1	000764	Structural_Protein_Mix	215	BN7874_281	Phage NCTB	GCA_900092385.1
QFP93047.1	000764	Structural_Protein_Mix	1156	-	Serratia phage PCH45	GCA_009187865.1
AIR93406.1	000764	Structural_Protein_Mix	564	AVU42_gp021	Prochlorococcus phage P-TIM68	GCA_001503075.1
AXQ68701.1	000764	Structural_Protein_Mix	336	CcrPW_gp162c	Caulobacter phage CcrPW	GCA_003443275.1
AIR93417.1	000764	Structural_Protein_Mix	741	AVU42_gp035	Prochlorococcus phage P-TIM68	GCA_001503075.1
AFU88024.1	000764	Structural_Protein_Mix	335	CcrColossus_gp154	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ69216.1	000764	Structural_Protein_Mix	284	CcrBL9_gp192	Caulobacter phage CcrBL9	GCA_003443295.1
QDB71083.1	000764	Structural_Protein_Mix	441	CPT_Moabite_051	Serratia phage Moabite	GCA_006384735.1
ABY62958.1	000764	Structural_Protein_Mix	441	201phi2-1p126	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44806.1	000764	Structural_Protein_Mix	271	KTN4_048	Pseudomonas phage KTN4	GCA_002607225.1
AFH14598.1	000764	Structural_Protein_Mix	634	Lu11_0067	Pseudomonas phage Lu11	GCA_000897175.1
QDH47033.1	000764	Structural_Protein_Mix	596	LAh10_62	Aeromonas phage LAh10	GCA_006863975.1
AFH14609.1	000764	Structural_Protein_Mix	425	Lu11_0077	Pseudomonas phage Lu11	GCA_000897175.1
AFH14642.1	000764	Structural_Protein_Mix	429	Lu11_0110	Pseudomonas phage Lu11	GCA_000897175.1
ATA65659.1	000764	Structural_Protein_Mix	441	2050HW_00324	Serratia phage 2050HW	GCA_002628125.1
QDH83469.1	000764	Structural_Protein_Mix	268	H1O15_gp337	Achromobacter phage Motura	GCA_006964305.1
QBQ74809.1	000764	Structural_Protein_Mix	152	BcepSauron_429	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74553.1	000764	Structural_Protein_Mix	215	BcepSauron_173	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74552.1	000764	Structural_Protein_Mix	275	BcepSauron_172	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74546.1	000764	Structural_Protein_Mix	156	BcepSauron_166	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06840.1	000764	Structural_Protein_Mix	151	BcepSaruman_427	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06588.1	000764	Structural_Protein_Mix	215	BcepSaruman_175	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06587.1	000764	Structural_Protein_Mix	275	BcepSaruman_174	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06580.1	000764	Structural_Protein_Mix	155	BcepSaruman_167	Burkholderia phage BcepSaruman	GCA_004771375.1
QDH83471.1	000764	Structural_Protein_Mix	295	H1O15_gp335	Achromobacter phage Motura	GCA_006964305.1
ARV77466.1	000764	Structural_Protein_Mix	291	NOXIFER_301	Pseudomonas phage Noxifer	GCA_002625005.1
QIW90778.1	000764	Structural_Protein_Mix	227	GCAPEGMB_00460	Vibrio phage V07	GCA_012361095.1
QDH83599.1	000764	Structural_Protein_Mix	190	H1O15_gp189	Achromobacter phage Motura	GCA_006964305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QHJ86098.1	000764	Structural_Protein_Mix	187	KKIINIFJ_00186	Pseudomonas phage PN05	GCA_009931935.1
AST99874.1	000764	Structural_Protein_Mix	198	PBI_PBS1_52	Bacillus virus PBS1	GCA_002601325.1
AGS81966.1	000764	Structural_Protein_Mix	643	PaBG_00082	Pseudomonas phage PaBG	GCA_000912555.1
AGS82009.1	000764	Structural_Protein_Mix	150	PaBG_00125	Pseudomonas phage PaBG	GCA_000912555.1
ALN97905.1	000764	Structural_Protein_Mix	182	Bp8pS_226	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AGS82067.1	000764	Structural_Protein_Mix	332	PaBG_00191	Pseudomonas phage PaBG	GCA_000912555.1
ARV76838.1	000764	Structural_Protein_Mix	444	PHABIO_207	Pseudomonas phage Phabio	GCA_002624965.1
AEH03591.1	000764	Structural_Protein_Mix	345	168	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02727.1	000764	Structural_Protein_Mix	1496	PSA21_201	Pseudomonas phage Psa21	GCA_004340405.1
ATN94905.1	000764	Structural_Protein_Mix	271	SL2_328	Pseudomonas phage SL2	GCA_002956015.1
ALN97710.1	000764	Structural_Protein_Mix	167	Bp8pS_031	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QJB22685.1	000764	Structural_Protein_Mix	271	fnug_42	Pseudomonas phage fnug	GCA_012837215.1
AAL82936.1	000764	Structural_Protein_Mix	271	PHIKZ035	Pseudomonas virus phiKZ	GCA_000842965.1
AMS01248.1	000764	Structural_Protein_Mix	199	AR9_g164	Bacillus phage AR9	GCA_001743835.1
BAQ02642.1	000764	Structural_Protein_Mix	696	AVU38_gp114	Ralstonia phage RSL2	GCA_001503055.1
BAG41773.2	000764	Structural_Protein_Mix	317	RSL1_ORF326	Ralstonia phage phiRSL1	GCA_000879455.1
ABS83605.1	000764	Structural_Protein_Mix	352	0305phi8-36p044	Bacillus phage 0305phi8-36	GCA_000871045.1
BAG41516.1	000764	Structural_Protein_Mix	361	RSL1_ORF070	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44023.1	000764	Structural_Protein_Mix	327	PBI_SCTP2_8	Salicola phage SCTP-2	GCA_002625545.1
AXG67547.1	000764	Structural_Protein_Mix	220	JA33_173	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QIG64466.1	000764	Structural_Protein_Mix	555	DAC23_191	Bacteroides phage DAC23	GCA_013387745.1
QIG64210.1	000764	Structural_Protein_Mix	549	DAC22_199	Bacteroides phage DAC22	GCA_013387735.1
QIG63946.1	000764	Structural_Protein_Mix	560	DAC20_196	Bacteroides phage DAC20	GCA_013387725.1
QIG63685.1	000764	Structural_Protein_Mix	560	DAC19_197	Bacteroides phage DAC19	GCA_013387715.1
QIG63421.1	000764	Structural_Protein_Mix	560	DAC16_191	Bacteroides phage DAC16	GCA_013387695.1
AFH14772.1	000764	Structural_Protein_Mix	173	Lu11_0236	Pseudomonas phage Lu11	GCA_000897175.1
ARW58749.1	000764	Structural_Protein_Mix	210	Y3_109	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AWY08385.1	000764	Structural_Protein_Mix	210	Alexandra_112	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
SBV38303.1	000764	Structural_Protein_Mix	212	BN7874_134	Phage NCTB	GCA_900092385.1
AFH14774.1	000764	Structural_Protein_Mix	675	Lu11_0238	Pseudomonas phage Lu11	GCA_000897175.1
AZU98368.1	000764	Structural_Protein_Mix	441	CPT_Munch_428	Salmonella phage Munch	GCA_004015485.1
QDH83602.1	000764	Structural_Protein_Mix	542	H1O15_gp186	Achromobacter phage Motura	GCA_006964305.1
AXG67523.1	000764	Structural_Protein_Mix	284	JA33_149	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG66878.1	000764	Structural_Protein_Mix	284	JA29_152	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AYD79954.1	000764	Structural_Protein_Mix	284	JA11_149	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66553.1	000764	Structural_Protein_Mix	284	JA13_150	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AGN12250.1	000764	Structural_Protein_Mix	597	PRTG_00092	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44401.1	000764	Structural_Protein_Mix	597	PSSM2_023	Prochlorococcus phage P-SSM2	GCA_000859585.1
BBA65539.1	000764	Structural_Protein_Mix	529	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96535.1	000764	Structural_Protein_Mix	502	Xoosp13_349	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AJK27528.1	000764	Structural_Protein_Mix	491	PTIM40_101	Cyanophage P-TIM40	GCA_001470935.1
AGH56929.1	000764	Structural_Protein_Mix	500	CPXG_00126	Cyanophage P-RSM6	GCA_000906155.1
SOK58718.1	000764	Structural_Protein_Mix	528	g441	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDH47018.1	000764	Structural_Protein_Mix	988	LAh10_85	Aeromonas phage LAh10	GCA_006863975.1
SOK59253.1	000764	Structural_Protein_Mix	537	g445	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QDJ97323.1	000764	Structural_Protein_Mix	956	D6_0164	Aeromonas phage D6	GCA_007051205.2
AFC21877.1	000764	Structural_Protein_Mix	577	GAP32_424	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ARB15587.1	000764	Structural_Protein_Mix	787	Ccr34_gp078	Caulobacter phage Ccr34	GCA_002619525.1
AFO71378.1	000764	Structural_Protein_Mix	399	CR5_158	Cronobacter phage CR5	GCA_000910235.1
QDH50496.1	000764	Structural_Protein_Mix	349	-	Synechococcus phage S-B43	GCA_006869725.1
AOO14936.1	000764	Structural_Protein_Mix	413	W1230910_090	Cyanophage S-RIM14	GCA_002599125.1
QCW22830.1	000764	Structural_Protein_Mix	458	-	Synechococcus phage S-B05	GCA_006083695.1
AOO14287.1	000764	Structural_Protein_Mix	413	Sn110110_093	Cyanophage S-RIM14	GCA_002599065.1
AGH07530.1	000764	Structural_Protein_Mix	714	CYVG_00086	Cyanophage S-SSM6a	GCA_002710385.1
AIR93428.1	000764	Structural_Protein_Mix	814	AVU42_gp087	Prochlorococcus phage P-TIM68	GCA_001503075.1
AGG54297.1	000764	Structural_Protein_Mix	392	CYWG_00013	Cyanophage S-SSM6b	GCA_002710425.1
BBA65338.1	000764	Structural_Protein_Mix	213	-	Xanthomonas phage XacN1	GCA_003173815.1
AMS01199.1	000764	Structural_Protein_Mix	152	AR9_g115	Bacillus phage AR9	GCA_001743835.1
QBX32386.1	000764	Structural_Protein_Mix	428	-	Pseudomonas phage PA1C	GCA_004785505.1
AFC21594.1	000764	Structural_Protein_Mix	912	GAP32_144	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QJT70041.1	000764	Structural_Protein_Mix	616	SynMITS9220M01_028	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QMP24009.1	000764	Structural_Protein_Mix	396	-	Proteus phage 10	GCA_014071245.1
AJK27471.1	000764	Structural_Protein_Mix	269	PTIM40_44	Cyanophage P-TIM40	GCA_001470935.1
AST99823.1	000764	Structural_Protein_Mix	152	PBI_PBS1_1	Bacillus virus PBS1	GCA_002601325.1
ALN97875.1	000764	Structural_Protein_Mix	310	Bp8pS_196	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QAY00558.1	000764	Structural_Protein_Mix	195	Ecwhy1_279	Escherichia phage Ecwhy_1	GCA_004146585.1
ARM70986.1	000764	Structural_Protein_Mix	516	phiC120_c281	Escherichia phage phiC120	GCA_002621185.1
ARM70720.1	000764	Structural_Protein_Mix	516	phiC120_c13	Escherichia phage phiC120	GCA_002621185.1
AFO71354.1	000765	virion_structural_protein	266	CR5_134	Cronobacter phage CR5	GCA_000910235.1
AFO71355.1	000765	virion_structural_protein	280	CR5_135	Cronobacter phage CR5	GCA_000910235.1
AFO71356.1	000765	virion_structural_protein	281	CR5_136	Cronobacter phage CR5	GCA_000910235.1
AFO71357.1	000765	virion_structural_protein	306	CR5_137	Cronobacter phage CR5	GCA_000910235.1
AFO71358.1	000765	virion_structural_protein	339	CR5_138	Cronobacter phage CR5	GCA_000910235.1
AFO71359.1	000765	virion_structural_protein	297	CR5_139	Cronobacter phage CR5	GCA_000910235.1
AFO71360.1	000765	virion_structural_protein	272	CR5_140	Cronobacter phage CR5	GCA_000910235.1
AFO71361.1	000765	virion_structural_protein	292	CR5_141	Cronobacter phage CR5	GCA_000910235.1
AFO71362.1	000765	virion_structural_protein	275	CR5_142	Cronobacter phage CR5	GCA_000910235.1
AFO71363.1	000765	virion_structural_protein	438	CR5_143	Cronobacter phage CR5	GCA_000910235.1
AFO71365.1	000765	virion_structural_protein	509	CR5_145	Cronobacter phage CR5	GCA_000910235.1
AFO71366.1	000765	virion_structural_protein	347	CR5_146	Cronobacter phage CR5	GCA_000910235.1
AFO71367.1	000765	virion_structural_protein	295	CR5_147	Cronobacter phage CR5	GCA_000910235.1
AMR59772.1	000765	virion_structural_protein	177	SEGD1_125	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59788.1	000765	virion_structural_protein	265	SEGD1_141	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59789.1	000765	virion_structural_protein	280	SEGD1_142	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59790.1	000765	virion_structural_protein	281	SEGD1_143	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59791.1	000765	virion_structural_protein	303	SEGD1_144	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59792.1	000765	virion_structural_protein	279	SEGD1_145	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59793.1	000765	virion_structural_protein	295	SEGD1_146	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59794.1	000765	virion_structural_protein	275	SEGD1_147	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59795.1	000765	virion_structural_protein	470	SEGD1_148	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59796.1	000765	virion_structural_protein	332	SEGD1_149	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59797.1	000765	virion_structural_protein	307	SEGD1_150	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59798.1	000765	virion_structural_protein	498	SEGD1_151	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59799.1	000765	virion_structural_protein	329	SEGD1_152	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59800.1	000765	virion_structural_protein	299	SEGD1_153	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59801.1	000765	virion_structural_protein	480	SEGD1_154	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59802.1	000765	virion_structural_protein	332	SEGD1_155	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59803.1	000765	virion_structural_protein	300	SEGD1_156	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59804.1	000765	virion_structural_protein	439	SEGD1_157	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59888.1	000765	virion_structural_protein	183	SEGD1_241	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07562.1	000765	virion_structural_protein	290	DERBICUS_136	Erwinia phage Derbicus	GCA_004521655.1
QBP07563.1	000765	virion_structural_protein	280	DERBICUS_137	Erwinia phage Derbicus	GCA_004521655.1
QBP07564.1	000765	virion_structural_protein	281	DERBICUS_138	Erwinia phage Derbicus	GCA_004521655.1
QBP07565.1	000765	virion_structural_protein	306	DERBICUS_139	Erwinia phage Derbicus	GCA_004521655.1
QBP07566.1	000765	virion_structural_protein	333	DERBICUS_140	Erwinia phage Derbicus	GCA_004521655.1
QBP07567.1	000765	virion_structural_protein	296	DERBICUS_141	Erwinia phage Derbicus	GCA_004521655.1
QBP07568.1	000765	virion_structural_protein	272	DERBICUS_142	Erwinia phage Derbicus	GCA_004521655.1
QBP07569.1	000765	virion_structural_protein	292	DERBICUS_143	Erwinia phage Derbicus	GCA_004521655.1
QBP07570.1	000765	virion_structural_protein	275	DERBICUS_144	Erwinia phage Derbicus	GCA_004521655.1
QBP07571.1	000765	virion_structural_protein	460	DERBICUS_145	Erwinia phage Derbicus	GCA_004521655.1
QBP07572.1	000765	virion_structural_protein	338	DERBICUS_146	Erwinia phage Derbicus	GCA_004521655.1
QBP07573.1	000765	virion_structural_protein	295	DERBICUS_147	Erwinia phage Derbicus	GCA_004521655.1
QBP07574.1	000765	virion_structural_protein	509	DERBICUS_148	Erwinia phage Derbicus	GCA_004521655.1
QBP07575.1	000765	virion_structural_protein	325	DERBICUS_149	Erwinia phage Derbicus	GCA_004521655.1
QBP07576.1	000765	virion_structural_protein	300	DERBICUS_150	Erwinia phage Derbicus	GCA_004521655.1
AHI60158.1	000765	virion_structural_protein	291	Ea357_008	Erwinia phage Ea35-70	GCA_000914635.1
AHI60159.1	000765	virion_structural_protein	272	Ea357_009	Erwinia phage Ea35-70	GCA_000914635.1
AHI60161.1	000765	virion_structural_protein	289	Ea357_011	Erwinia phage Ea35-70	GCA_000914635.1
AHI60432.1	000765	virion_structural_protein	167	Ea357_278	Erwinia phage Ea35-70	GCA_000914635.1
AHI60433.1	000765	virion_structural_protein	169	Ea357_279	Erwinia phage Ea35-70	GCA_000914635.1
AHI60450.1	000765	virion_structural_protein	115	Ea357_296	Erwinia phage Ea35-70	GCA_000914635.1
AHI60453.1	000765	virion_structural_protein	177	Ea357_299	Erwinia phage Ea35-70	GCA_000914635.1
AHI60468.1	000765	virion_structural_protein	210	Ea357_314	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49786.1	000765	virion_structural_protein	264	MACHINA_148	Erwinia phage Machina	GCA_002758035.1
ANZ49787.1	000765	virion_structural_protein	270	MACHINA_149	Erwinia phage Machina	GCA_002758035.1

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ANZ49788.1	000765	virion_structural_protein	281	MACHINA_150	Erwinia phage Machina	GCA_002758035.1
ANZ49789.1	000765	virion_structural_protein	303	MACHINA_151	Erwinia phage Machina	GCA_002758035.1
ANZ49790.1	000765	virion_structural_protein	279	MACHINA_152	Erwinia phage Machina	GCA_002758035.1
ANZ49791.1	000765	virion_structural_protein	295	MACHINA_153	Erwinia phage Machina	GCA_002758035.1
ANZ49792.1	000765	virion_structural_protein	275	MACHINA_154	Erwinia phage Machina	GCA_002758035.1
ANZ49793.1	000765	virion_structural_protein	457	MACHINA_155	Erwinia phage Machina	GCA_002758035.1
ANZ49794.1	000765	virion_structural_protein	331	MACHINA_156	Erwinia phage Machina	GCA_002758035.1
ANZ49795.1	000765	virion_structural_protein	309	MACHINA_157	Erwinia phage Machina	GCA_002758035.1
ANZ49796.1	000765	virion_structural_protein	464	MACHINA_158	Erwinia phage Machina	GCA_002758035.1
ANZ49797.1	000765	virion_structural_protein	338	MACHINA_159	Erwinia phage Machina	GCA_002758035.1
ANZ49798.1	000765	virion_structural_protein	294	MACHINA_160	Erwinia phage Machina	GCA_002758035.1
ANZ49799.1	000765	virion_structural_protein	510	MACHINA_161	Erwinia phage Machina	GCA_002758035.1
ANZ49800.1	000765	virion_structural_protein	331	MACHINA_162	Erwinia phage Machina	GCA_002758035.1
ANZ49801.1	000765	virion_structural_protein	300	MACHINA_163	Erwinia phage Machina	GCA_002758035.1
AGX01801.1	000765	virion_structural_protein	182	CF95_gp079	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01806.1	000765	virion_structural_protein	292	CF95_gp084	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01809.1	000765	virion_structural_protein	309	CF95_gp087	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01804.1	000765	virion_structural_protein	310	CF95_gp082	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01808.1	000765	virion_structural_protein	320	CF95_gp086	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01805.1	000765	virion_structural_protein	321	CF95_gp083	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01807.1	000765	virion_structural_protein	425	CF95_gp085	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01928.1	000765	virion_structural_protein	282	CF95_gp206	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01919.1	000765	virion_structural_protein	276	CF95_gp197	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07119.1	000765	virion_structural_protein	289	REBECCA_11	Erwinia phage Rebecca	GCA_004521635.1
QBP07269.1	000765	virion_structural_protein	238	REBECCA_162	Erwinia phage Rebecca	GCA_004521635.1
QBP07389.1	000765	virion_structural_protein	166	REBECCA_284	Erwinia phage Rebecca	GCA_004521635.1
QBP07390.1	000765	virion_structural_protein	180	REBECCA_285	Erwinia phage Rebecca	GCA_004521635.1
QBP07407.1	000765	virion_structural_protein	115	REBECCA_302	Erwinia phage Rebecca	GCA_004521635.1
QBP07410.1	000765	virion_structural_protein	177	REBECCA_305	Erwinia phage Rebecca	GCA_004521635.1
QBP07425.1	000765	virion_structural_protein	237	REBECCA_320	Erwinia phage Rebecca	GCA_004521635.1
QBP07178.1	000765	virion_structural_protein	233	REBECCA_70	Erwinia phage Rebecca	GCA_004521635.1
QBP07116.1	000765	virion_structural_protein	291	REBECCA_8	Erwinia phage Rebecca	GCA_004521635.1
QBP07117.1	000765	virion_structural_protein	272	REBECCA_9	Erwinia phage Rebecca	GCA_004521635.1
AXF51287.1	000765	virion_structural_protein	266	WELLINGTON_158	Erwinia phage Wellington	GCA_003344985.1
AXF51288.1	000765	virion_structural_protein	277	WELLINGTON_159	Erwinia phage Wellington	GCA_003344985.1
AXF51289.1	000765	virion_structural_protein	281	WELLINGTON_160	Erwinia phage Wellington	GCA_003344985.1
AXF51290.1	000765	virion_structural_protein	308	WELLINGTON_161	Erwinia phage Wellington	GCA_003344985.1
AXF51291.1	000765	virion_structural_protein	278	WELLINGTON_162	Erwinia phage Wellington	GCA_003344985.1
AXF51292.1	000765	virion_structural_protein	295	WELLINGTON_163	Erwinia phage Wellington	GCA_003344985.1
AXF51293.1	000765	virion_structural_protein	275	WELLINGTON_164	Erwinia phage Wellington	GCA_003344985.1
AXF51294.1	000765	virion_structural_protein	470	WELLINGTON_165	Erwinia phage Wellington	GCA_003344985.1
AXF51295.1	000765	virion_structural_protein	333	WELLINGTON_166	Erwinia phage Wellington	GCA_003344985.1
AXF51296.1	000765	virion_structural_protein	313	WELLINGTON_167	Erwinia phage Wellington	GCA_003344985.1
AXF51297.1	000765	virion_structural_protein	472	WELLINGTON_168	Erwinia phage Wellington	GCA_003344985.1
AXF51298.1	000765	virion_structural_protein	329	WELLINGTON_169	Erwinia phage Wellington	GCA_003344985.1
AXF51299.1	000765	virion_structural_protein	299	WELLINGTON_170	Erwinia phage Wellington	GCA_003344985.1
AFQ96702.1	000765	virion_structural_protein	180	G173_gp157	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96606.1	000765	virion_structural_protein	284	G173_gp061	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96604.1	000765	virion_structural_protein	284	G173_gp059	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96616.1	000765	virion_structural_protein	294	G173_gp071	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96609.1	000765	virion_structural_protein	295	G173_gp064	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96607.1	000765	virion_structural_protein	298	G173_gp062	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96619.1	000765	virion_structural_protein	298	G173_gp074	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96613.1	000765	virion_structural_protein	309	G173_gp068	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96618.1	000765	virion_structural_protein	327	G173_gp073	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96612.1	000765	virion_structural_protein	329	G173_gp067	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96615.1	000765	virion_structural_protein	345	G173_gp070	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96614.1	000765	virion_structural_protein	466	G173_gp069	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96611.1	000765	virion_structural_protein	472	G173_gp066	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96617.1	000765	virion_structural_protein	507	G173_gp072	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96605.1	000765	virion_structural_protein	277	G173_gp060	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96608.1	000765	virion_structural_protein	278	G173_gp063	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96610.1	000765	virion_structural_protein	281	G173_gp065	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48152.1	000765	virion_structural_protein	182	ASESINO_139	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48168.1	000765	virion_structural_protein	265	ASESINO_155	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48169.1	000765	virion_structural_protein	267	ASESINO_156	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48170.1	000765	virion_structural_protein	284	ASESINO_157	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48171.1	000765	virion_structural_protein	298	ASESINO_158	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48172.1	000765	virion_structural_protein	278	ASESINO_159	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48173.1	000765	virion_structural_protein	295	ASESINO_160	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48174.1	000765	virion_structural_protein	281	ASESINO_161	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48175.1	000765	virion_structural_protein	472	ASESINO_162	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48176.1	000765	virion_structural_protein	331	ASESINO_163	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48177.1	000765	virion_structural_protein	309	ASESINO_164	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48178.1	000765	virion_structural_protein	467	ASESINO_165	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48179.1	000765	virion_structural_protein	342	ASESINO_166	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48180.1	000765	virion_structural_protein	296	ASESINO_167	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48181.1	000765	virion_structural_protein	509	ASESINO_168	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48182.1	000765	virion_structural_protein	328	ASESINO_169	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48183.1	000765	virion_structural_protein	298	ASESINO_170	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48272.1	000765	virion_structural_protein	180	ASESINO_259	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85799.1	000765	virion_structural_protein	289	BOSOLAPHORUS_11	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85949.1	000765	virion_structural_protein	238	BOSOLAPHORUS_162	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86071.1	000765	virion_structural_protein	167	BOSOLAPHORUS_285	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86072.1	000765	virion_structural_protein	169	BOSOLAPHORUS_286	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86089.1	000765	virion_structural_protein	115	BOSOLAPHORUS_303	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86092.1	000765	virion_structural_protein	177	BOSOLAPHORUS_306	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86107.1	000765	virion_structural_protein	210	BOSOLAPHORUS_321	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85796.1	000765	virion_structural_protein	291	BOSOLAPHORUS_8	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85797.1	000765	virion_structural_protein	272	BOSOLAPHORUS_9	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48442.1	000765	virion_structural_protein	264	CAITLIN_147	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48443.1	000765	virion_structural_protein	270	CAITLIN_148	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48444.1	000765	virion_structural_protein	281	CAITLIN_149	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48445.1	000765	virion_structural_protein	303	CAITLIN_150	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48446.1	000765	virion_structural_protein	279	CAITLIN_151	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48447.1	000765	virion_structural_protein	295	CAITLIN_152	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48448.1	000765	virion_structural_protein	275	CAITLIN_153	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48449.1	000765	virion_structural_protein	456	CAITLIN_154	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48450.1	000765	virion_structural_protein	330	CAITLIN_155	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48451.1	000765	virion_structural_protein	308	CAITLIN_156	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48452.1	000765	virion_structural_protein	465	CAITLIN_157	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48453.1	000765	virion_structural_protein	346	CAITLIN_158	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48454.1	000765	virion_structural_protein	294	CAITLIN_159	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48455.1	000765	virion_structural_protein	510	CAITLIN_160	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48456.1	000765	virion_structural_protein	331	CAITLIN_161	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48457.1	000765	virion_structural_protein	299	CAITLIN_162	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48717.1	000765	virion_structural_protein	264	CHRISDB_155	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48718.1	000765	virion_structural_protein	270	CHRISDB_156	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48719.1	000765	virion_structural_protein	281	CHRISDB_157	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48720.1	000765	virion_structural_protein	303	CHRISDB_158	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48721.1	000765	virion_structural_protein	279	CHRISDB_159	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48722.1	000765	virion_structural_protein	295	CHRISDB_160	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48723.1	000765	virion_structural_protein	275	CHRISDB_161	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48724.1	000765	virion_structural_protein	472	CHRISDB_162	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48725.1	000765	virion_structural_protein	331	CHRISDB_163	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48726.1	000765	virion_structural_protein	309	CHRISDB_164	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48727.1	000765	virion_structural_protein	480	CHRISDB_165	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48728.1	000765	virion_structural_protein	329	CHRISDB_166	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48729.1	000765	virion_structural_protein	299	CHRISDB_167	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48730.1	000765	virion_structural_protein	463	CHRISDB_168	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48731.1	000765	virion_structural_protein	345	CHRISDB_169	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48732.1	000765	virion_structural_protein	294	CHRISDB_170	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48733.1	000765	virion_structural_protein	509	CHRISDB_171	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48734.1	000765	virion_structural_protein	326	CHRISDB_172	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48735.1	000765	virion_structural_protein	300	CHRISDB_173	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48822.1	000765	virion_structural_protein	186	CHRISDB_260	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52109.1	000765	virion_structural_protein	289	DM_11	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52264.1	000765	virion_structural_protein	238	DM_166	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52387.1	000765	virion_structural_protein	167	DM_288	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52388.2	000765	virion_structural_protein	169	DM_289	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52405.1	000765	virion_structural_protein	115	DM_306	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52408.1	000765	virion_structural_protein	177	DM_309	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52423.2	000765	virion_structural_protein	210	DM_324	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52106.1	000765	virion_structural_protein	291	DM_8	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52107.1	000765	virion_structural_protein	272	DM_9	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86119.1	000765	virion_structural_protein	289	DESERTFOX_11	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86268.1	000765	virion_structural_protein	238	DESERTFOX_161	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86391.1	000765	virion_structural_protein	167	DESERTFOX_284	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86392.1	000765	virion_structural_protein	169	DESERTFOX_285	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86409.1	000765	virion_structural_protein	115	DESERTFOX_302	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86412.1	000765	virion_structural_protein	177	DESERTFOX_305	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86427.1	000765	virion_structural_protein	210	DESERTFOX_320	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86116.1	000765	virion_structural_protein	291	DESERTFOX_8	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86117.1	000765	virion_structural_protein	272	DESERTFOX_9	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48985.1	000765	virion_structural_protein	266	EARLPHILLIPIV_136	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48986.1	000765	virion_structural_protein	270	EARLPHILLIPIV_137	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48987.1	000765	virion_structural_protein	281	EARLPHILLIPIV_138	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48988.1	000765	virion_structural_protein	306	EARLPHILLIPIV_139	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48989.1	000765	virion_structural_protein	333	EARLPHILLIPIV_140	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48990.1	000765	virion_structural_protein	296	EARLPHILLIPIV_141	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48991.1	000765	virion_structural_protein	272	EARLPHILLIPIV_142	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48992.1	000765	virion_structural_protein	292	EARLPHILLIPIV_143	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48993.1	000765	virion_structural_protein	275	EARLPHILLIPIV_144	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48994.1	000765	virion_structural_protein	464	EARLPHILLIPIV_145	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48995.1	000765	virion_structural_protein	338	EARLPHILLIPIV_146	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48996.1	000765	virion_structural_protein	295	EARLPHILLIPIV_147	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48997.1	000765	virion_structural_protein	509	EARLPHILLIPIV_148	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48998.1	000765	virion_structural_protein	325	EARLPHILLIPIV_149	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48999.1	000765	virion_structural_protein	300	EARLPHILLIPIV_150	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49230.1	000765	virion_structural_protein	264	HUXLEY_148	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49231.1	000765	virion_structural_protein	270	HUXLEY_149	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49232.1	000765	virion_structural_protein	281	HUXLEY_150	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49233.1	000765	virion_structural_protein	303	HUXLEY_151	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49234.1	000765	virion_structural_protein	279	HUXLEY_152	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49235.1	000765	virion_structural_protein	295	HUXLEY_153	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49236.1	000765	virion_structural_protein	275	HUXLEY_154	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49237.1	000765	virion_structural_protein	457	HUXLEY_155	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49238.1	000765	virion_structural_protein	331	HUXLEY_156	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49239.1	000765	virion_structural_protein	309	HUXLEY_157	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49240.1	000765	virion_structural_protein	464	HUXLEY_158	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49241.1	000765	virion_structural_protein	338	HUXLEY_159	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49242.1	000765	virion_structural_protein	294	HUXLEY_160	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49243.1	000765	virion_structural_protein	510	HUXLEY_161	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49244.1	000765	virion_structural_protein	331	HUXLEY_162	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49245.1	000765	virion_structural_protein	300	HUXLEY_163	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03717.1	000765	virion_structural_protein	289	JOAD_198	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03716.1	000765	virion_structural_protein	583	JOAD_199	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03715.1	000765	virion_structural_protein	298	JOAD_200	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03714.1	000765	virion_structural_protein	310	JOAD_201	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03713.1	000765	virion_structural_protein	286	JOAD_202	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03712.1	000765	virion_structural_protein	554	JOAD_203	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03711.1	000765	virion_structural_protein	296	JOAD_204	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03710.1	000765	virion_structural_protein	321	JOAD_205	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03709.1	000765	virion_structural_protein	284	JOAD_206	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03708.1	000765	virion_structural_protein	194	JOAD_207	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03707.1	000765	virion_structural_protein	211	JOAD_208	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03706.1	000765	virion_structural_protein	291	JOAD_209	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49511.1	000765	virion_structural_protein	266	KWAN_159	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49512.1	000765	virion_structural_protein	267	KWAN_160	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49513.1	000765	virion_structural_protein	281	KWAN_161	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49514.1	000765	virion_structural_protein	308	KWAN_162	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49515.1	000765	virion_structural_protein	278	KWAN_163	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49516.1	000765	virion_structural_protein	295	KWAN_164	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49517.1	000765	virion_structural_protein	275	KWAN_165	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49518.1	000765	virion_structural_protein	470	KWAN_166	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49519.1	000765	virion_structural_protein	333	KWAN_167	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49520.1	000765	virion_structural_protein	313	KWAN_168	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49521.1	000765	virion_structural_protein	470	KWAN_169	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49522.1	000765	virion_structural_protein	329	KWAN_170	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49523.1	000765	virion_structural_protein	299	KWAN_171	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86439.1	000765	virion_structural_protein	289	MADMEL_11	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86590.1	000765	virion_structural_protein	238	MADMEL_162	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86712.1	000765	virion_structural_protein	167	MADMEL_285	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86713.1	000765	virion_structural_protein	169	MADMEL_286	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86730.1	000765	virion_structural_protein	115	MADMEL_303	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86733.1	000765	virion_structural_protein	177	MADMEL_306	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86748.1	000765	virion_structural_protein	210	MADMEL_321	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86436.1	000765	virion_structural_protein	291	MADMEL_8	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86437.1	000765	virion_structural_protein	272	MADMEL_9	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86760.1	000765	virion_structural_protein	289	MORTIMER_11	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86914.1	000765	virion_structural_protein	238	MORTIMER_165	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87037.1	000765	virion_structural_protein	167	MORTIMER_289	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87038.1	000765	virion_structural_protein	169	MORTIMER_290	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87055.1	000765	virion_structural_protein	115	MORTIMER_307	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87058.1	000765	virion_structural_protein	177	MORTIMER_310	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87073.1	000765	virion_structural_protein	210	MORTIMER_325	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86757.1	000765	virion_structural_protein	291	MORTIMER_8	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86758.1	000765	virion_structural_protein	272	MORTIMER_9	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50058.1	000765	virion_structural_protein	264	PARSHIK_149	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50059.1	000765	virion_structural_protein	270	PARSHIK_150	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50060.1	000765	virion_structural_protein	281	PARSHIK_151	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50061.1	000765	virion_structural_protein	303	PARSHIK_152	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50062.1	000765	virion_structural_protein	279	PARSHIK_153	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50063.1	000765	virion_structural_protein	295	PARSHIK_154	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50064.1	000765	virion_structural_protein	275	PARSHIK_155	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50065.1	000765	virion_structural_protein	457	PARSHIK_156	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50066.1	000765	virion_structural_protein	331	PARSHIK_157	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50067.1	000765	virion_structural_protein	309	PARSHIK_158	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50068.1	000765	virion_structural_protein	464	PARSHIK_159	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50069.1	000765	virion_structural_protein	338	PARSHIK_160	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50070.1	000765	virion_structural_protein	294	PARSHIK_161	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50071.1	000765	virion_structural_protein	510	PARSHIK_162	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50072.1	000765	virion_structural_protein	331	PARSHIK_163	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50073.1	000765	virion_structural_protein	300	PARSHIK_164	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50327.1	000765	virion_structural_protein	266	PHOBOS_137	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50328.1	000765	virion_structural_protein	270	PHOBOS_138	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50329.1	000765	virion_structural_protein	281	PHOBOS_139	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50330.1	000765	virion_structural_protein	307	PHOBOS_140	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50331.1	000765	virion_structural_protein	279	PHOBOS_141	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50332.1	000765	virion_structural_protein	294	PHOBOS_142	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50333.1	000765	virion_structural_protein	280	PHOBOS_143	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50334.1	000765	virion_structural_protein	439	PHOBOS_144	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50336.1	000765	virion_structural_protein	467	PHOBOS_146	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50337.1	000765	virion_structural_protein	332	PHOBOS_147	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50338.1	000765	virion_structural_protein	307	PHOBOS_148	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50339.1	000765	virion_structural_protein	483	PHOBOS_149	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50340.1	000765	virion_structural_protein	329	PHOBOS_150	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50341.1	000765	virion_structural_protein	302	PHOBOS_151	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50342.1	000765	virion_structural_protein	509	PHOBOS_152	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50343.1	000765	virion_structural_protein	326	PHOBOS_153	Erwinia phage vB_EamM_Phobos	GCA_001743635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ50344.1	000765	virion_structural_protein	300	PHOBOS_154	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51792.1	000765	virion_structural_protein	289	RAY_11	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52062.1	000765	virion_structural_protein	167	RAY_282	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52063.1	000765	virion_structural_protein	169	RAY_283	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52080.1	000765	virion_structural_protein	115	RAY_300	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52083.1	000765	virion_structural_protein	177	RAY_303	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52098.1	000765	virion_structural_protein	210	RAY_318	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51789.1	000765	virion_structural_protein	291	RAY_8	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51790.1	000765	virion_structural_protein	272	RAY_9	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03474.1	000765	virion_structural_protein	289	RISINGSUN_196	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03473.1	000765	virion_structural_protein	583	RISINGSUN_197	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03472.1	000765	virion_structural_protein	298	RISINGSUN_198	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03471.1	000765	virion_structural_protein	310	RISINGSUN_199	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03470.1	000765	virion_structural_protein	286	RISINGSUN_200	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03469.1	000765	virion_structural_protein	554	RISINGSUN_201	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03468.1	000765	virion_structural_protein	296	RISINGSUN_202	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03467.1	000765	virion_structural_protein	321	RISINGSUN_203	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03466.1	000765	virion_structural_protein	284	RISINGSUN_204	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03465.1	000765	virion_structural_protein	194	RISINGSUN_205	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03464.1	000765	virion_structural_protein	211	RISINGSUN_206	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03463.1	000765	virion_structural_protein	291	RISINGSUN_207	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51472.1	000765	virion_structural_protein	272	SIMMY50_10	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51474.1	000765	virion_structural_protein	289	SIMMY50_12	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51745.1	000765	virion_structural_protein	167	SIMMY50_287	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51746.1	000765	virion_structural_protein	169	SIMMY50_288	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51763.1	000765	virion_structural_protein	115	SIMMY50_305	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51766.1	000765	virion_structural_protein	177	SIMMY50_308	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51781.1	000765	virion_structural_protein	210	SIMMY50_323	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51471.1	000765	virion_structural_protein	291	SIMMY50_9	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64821.1	000765	virion_structural_protein	289	SPECIALG_11	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65097.1	000765	virion_structural_protein	167	SPECIALG_286	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65098.1	000765	virion_structural_protein	169	SPECIALG_287	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65115.1	000765	virion_structural_protein	115	SPECIALG_304	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65118.1	000765	virion_structural_protein	177	SPECIALG_307	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65133.1	000765	virion_structural_protein	210	SPECIALG_322	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64818.1	000765	virion_structural_protein	291	SPECIALG_8	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64819.1	000765	virion_structural_protein	272	SPECIALG_9	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50581.1	000765	virion_structural_protein	265	STRATTON_156	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50582.1	000765	virion_structural_protein	267	STRATTON_157	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50583.1	000765	virion_structural_protein	284	STRATTON_158	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50584.1	000765	virion_structural_protein	298	STRATTON_159	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50585.1	000765	virion_structural_protein	278	STRATTON_160	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50586.1	000765	virion_structural_protein	295	STRATTON_161	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50587.1	000765	virion_structural_protein	281	STRATTON_162	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50588.1	000765	virion_structural_protein	472	STRATTON_163	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50589.1	000765	virion_structural_protein	329	STRATTON_164	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50590.1	000765	virion_structural_protein	309	STRATTON_165	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50591.1	000765	virion_structural_protein	466	STRATTON_166	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50592.1	000765	virion_structural_protein	338	STRATTON_167	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50593.1	000765	virion_structural_protein	296	STRATTON_168	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50594.1	000765	virion_structural_protein	507	STRATTON_169	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50595.1	000765	virion_structural_protein	327	STRATTON_170	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50596.1	000765	virion_structural_protein	298	STRATTON_171	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50684.1	000765	virion_structural_protein	180	STRATTON_259	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85962.1	000765	virion_structural_protein	179	ACEC001_1240	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85979.1	000765	virion_structural_protein	265	ACEC001_1400	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85980.1	000765	virion_structural_protein	280	ACEC001_1410	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85981.1	000765	virion_structural_protein	281	ACEC001_1420	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85982.1	000765	virion_structural_protein	303	ACEC001_1430	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85983.1	000765	virion_structural_protein	279	ACEC001_1440	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85984.1	000765	virion_structural_protein	295	ACEC001_1450	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85985.1	000765	virion_structural_protein	275	ACEC001_1460	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85986.1	000765	virion_structural_protein	470	ACEC001_1470	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85987.1	000765	virion_structural_protein	332	ACEC001_1480	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85988.1	000765	virion_structural_protein	307	ACEC001_1490	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85989.1	000765	virion_structural_protein	498	ACEC001_1500	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85990.1	000765	virion_structural_protein	329	ACEC001_1510	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85991.1	000765	virion_structural_protein	299	ACEC001_1520	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85992.1	000765	virion_structural_protein	439	ACEC001_1530	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86078.1	000765	virion_structural_protein	183	ACEC001_2350	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63816.1	000765	virion_structural_protein	180	Goslar_00023	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63824.1	000765	virion_structural_protein	301	Goslar_00031	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63826.1	000765	virion_structural_protein	283	Goslar_00033	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63827.1	000765	virion_structural_protein	311	Goslar_00034	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
AMM44113.1	000765	virion_structural_protein	285	CBB_550	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44115.1	000765	virion_structural_protein	280	CBB_552	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44117.1	000765	virion_structural_protein	265	CBB_554	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QMP24203.1	000765	virion_structural_protein	116	-	Proteus phage 10	GCA_014071245.1
QMP24091.1	000765	virion_structural_protein	170	-	Proteus phage 10	GCA_014071245.1
QMP24000.1	000765	virion_structural_protein	290	-	Proteus phage 10	GCA_014071245.1
QMP24003.1	000765	virion_structural_protein	277	-	Proteus phage 10	GCA_014071245.1
QMP24212.1	000765	virion_structural_protein	194	-	Proteus phage 10	GCA_014071245.1
QMP24001.1	000765	virion_structural_protein	273	-	Proteus phage 10	GCA_014071245.1
ABY63263.1	000765	virion_structural_protein	286	201phi2-1p440	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63264.1	000765	virion_structural_protein	652	201phi2-1p441	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63265.1	000765	virion_structural_protein	321	201phi2-1p442	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63275.1	000765	virion_structural_protein	250	201phi2-1p452	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63279.1	000765	virion_structural_protein	419	201phi2-1p456	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27247.1	000765	virion_structural_protein	308	PPEV_gp153	Pseudomonas phage EL	GCA_000866825.1
CAG27249.1	000765	virion_structural_protein	500	PPEV_gp155	Pseudomonas phage EL	GCA_000866825.1
CAG27241.1	000765	virion_structural_protein	209	PPEV_gp147	Pseudomonas phage EL	GCA_000866825.1
ANM44868.1	000765	virion_structural_protein	504	KTN4_110	Pseudomonas phage KTN4	GCA_002607225.1
ANM45117.1	000765	virion_structural_protein	335	KTN4_359	Pseudomonas phage KTN4	GCA_002607225.1
ARV77302.1	000765	virion_structural_protein	297	NOXIFER_133	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77303.1	000765	virion_structural_protein	302	NOXIFER_134	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77304.1	000765	virion_structural_protein	313	NOXIFER_135	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77305.1	000765	virion_structural_protein	338	NOXIFER_136	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77249.1	000765	virion_structural_protein	701	NOXIFER_78	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77250.1	000765	virion_structural_protein	445	NOXIFER_79	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32189.1	000765	virion_structural_protein	305	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32533.1	000765	virion_structural_protein	312	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32393.1	000765	virion_structural_protein	316	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32391.1	000765	virion_structural_protein	316	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32390.1	000765	virion_structural_protein	317	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32392.1	000765	virion_structural_protein	328	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32540.1	000765	virion_structural_protein	335	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32236.1	000765	virion_structural_protein	422	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32532.1	000765	virion_structural_protein	522	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32537.1	000765	virion_structural_protein	618	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32154.1	000765	virion_structural_protein	216	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76757.1	000765	virion_structural_protein	513	PHABIO_126	Pseudomonas phage Phabio	GCA_002624965.1
ARV76812.1	000765	virion_structural_protein	493	PHABIO_181	Pseudomonas phage Phabio	GCA_002624965.1
ARV77068.1	000765	virion_structural_protein	301	PHABIO_437	Pseudomonas phage Phabio	GCA_002624965.1
ARV77069.1	000765	virion_structural_protein	297	PHABIO_438	Pseudomonas phage Phabio	GCA_002624965.1
AEH03504.1	000765	virion_structural_protein	511	080	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03505.1	000765	virion_structural_protein	211	081	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03506.1	000765	virion_structural_protein	168	082	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03507.1	000765	virion_structural_protein	504	083	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03659.1	000765	virion_structural_protein	322	236	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03660.1	000765	virion_structural_protein	329	237	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03661.1	000765	virion_structural_protein	323	238	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03783.1	000765	virion_structural_protein	619	360	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03785.1	000765	virion_structural_protein	285	362	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02943.1	000765	virion_structural_protein	235	PSA21_425	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02618.1	000765	virion_structural_protein	201	PSA21_90	Pseudomonas phage Psa21	GCA_004340405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATN94590.1	000765	virion_structural_protein	335	SL2_013	Pseudomonas phage SL2	GCA_002956015.1
ATN94595.1	000765	virion_structural_protein	324	SL2_018	Pseudomonas phage SL2	GCA_002956015.1
ATN94596.1	000765	virion_structural_protein	649	SL2_019	Pseudomonas phage SL2	GCA_002956015.1
ATN94597.1	000765	virion_structural_protein	286	SL2_020	Pseudomonas phage SL2	GCA_002956015.1
ATN94845.1	000765	virion_structural_protein	504	SL2_268	Pseudomonas phage SL2	GCA_002956015.1
QJB22745.1	000765	virion_structural_protein	504	fnug_102	Pseudomonas phage fnug	GCA_012837215.1
QJB22994.1	000765	virion_structural_protein	335	fnug_351	Pseudomonas phage fnug	GCA_012837215.1
QCG76189.1	000765	virion_structural_protein	315	EST35_0308	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM41767.1	000765	virion_structural_protein	305	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41962.1	000765	virion_structural_protein	316	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41964.1	000765	virion_structural_protein	316	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41961.1	000765	virion_structural_protein	317	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41963.1	000765	virion_structural_protein	328	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41815.1	000765	virion_structural_protein	422	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM42106.1	000765	virion_structural_protein	312	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM42105.1	000765	virion_structural_protein	522	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM42111.1	000765	virion_structural_protein	631	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41735.1	000765	virion_structural_protein	216	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83199.1	000765	virion_structural_protein	335	PHIKZ298	Pseudomonas virus phiKZ	GCA_000842965.1
AAL82984.1	000765	virion_structural_protein	504	PHIKZ083	Pseudomonas virus phiKZ	GCA_000842965.1
BAQ02711.1	000765	virion_structural_protein	330	AVU38_gp183	Ralstonia phage RSL2	GCA_001503055.1
BAQ02712.1	000765	virion_structural_protein	337	AVU38_gp184	Ralstonia phage RSL2	GCA_001503055.1
BAQ02713.1	000765	virion_structural_protein	338	AVU38_gp185	Ralstonia phage RSL2	GCA_001503055.1
ASV44449.1	000765	virion_structural_protein	246	PBI_SCTP2_434	Salicola phage SCTP-2	GCA_002625545.1
ASV44501.1	000765	virion_structural_protein	246	PBI_SCTP2_486	Salicola phage SCTP-2	GCA_002625545.1
ASV44097.1	000765	virion_structural_protein	245	PBI_SCTP2_82	Salicola phage SCTP-2	GCA_002625545.1
QNI20838.1	000765	virion_structural_protein	127	-	Salmonella phage JN03	GCA_014319805.1
QNI20826.1	000765	virion_structural_protein	179	-	Salmonella phage JN03	GCA_014319805.1
QNI20843.1	000765	virion_structural_protein	295	-	Salmonella phage JN03	GCA_014319805.1
QNI20853.1	000765	virion_structural_protein	298	-	Salmonella phage JN03	GCA_014319805.1
QNI20850.1	000765	virion_structural_protein	299	-	Salmonella phage JN03	GCA_014319805.1
QNI20841.1	000765	virion_structural_protein	303	-	Salmonella phage JN03	GCA_014319805.1
QNI20847.1	000765	virion_structural_protein	307	-	Salmonella phage JN03	GCA_014319805.1
QNI20852.1	000765	virion_structural_protein	326	-	Salmonella phage JN03	GCA_014319805.1
QNI20849.1	000765	virion_structural_protein	329	-	Salmonella phage JN03	GCA_014319805.1
QNI20846.1	000765	virion_structural_protein	332	-	Salmonella phage JN03	GCA_014319805.1
QNI20845.1	000765	virion_structural_protein	496	-	Salmonella phage JN03	GCA_014319805.1
QNI20848.1	000765	virion_structural_protein	498	-	Salmonella phage JN03	GCA_014319805.1
QNI20851.1	000765	virion_structural_protein	504	-	Salmonella phage JN03	GCA_014319805.1
QNI20842.1	000765	virion_structural_protein	279	-	Salmonella phage JN03	GCA_014319805.1
QNI20840.1	000765	virion_structural_protein	281	-	Salmonella phage JN03	GCA_014319805.1
QNI20922.1	000765	virion_structural_protein	183	-	Salmonella phage JN03	GCA_014319805.1
QNI20839.1	000765	virion_structural_protein	270	-	Salmonella phage JN03	GCA_014319805.1
QNI20844.1	000765	virion_structural_protein	275	-	Salmonella phage JN03	GCA_014319805.1
AWN08972.1	000765	virion_structural_protein	480	MLDJOKPK_00001	Salmonella phage SPAsTU	GCA_003183805.1
AWN08973.1	000765	virion_structural_protein	307	MLDJOKPK_00002	Salmonella phage SPAsTU	GCA_003183805.1
AWN08974.1	000765	virion_structural_protein	332	MLDJOKPK_00003	Salmonella phage SPAsTU	GCA_003183805.1
AWN08975.1	000765	virion_structural_protein	470	MLDJOKPK_00004	Salmonella phage SPAsTU	GCA_003183805.1
AWN08976.1	000765	virion_structural_protein	275	MLDJOKPK_00005	Salmonella phage SPAsTU	GCA_003183805.1
AWN08977.1	000765	virion_structural_protein	295	MLDJOKPK_00006	Salmonella phage SPAsTU	GCA_003183805.1
AWN08978.1	000765	virion_structural_protein	279	MLDJOKPK_00007	Salmonella phage SPAsTU	GCA_003183805.1
AWN08979.1	000765	virion_structural_protein	303	MLDJOKPK_00008	Salmonella phage SPAsTU	GCA_003183805.1
AWN08980.1	000765	virion_structural_protein	281	MLDJOKPK_00009	Salmonella phage SPAsTU	GCA_003183805.1
AWN08981.2	000765	virion_structural_protein	280	MLDJOKPK_00010	Salmonella phage SPAsTU	GCA_003183805.1
AWN08982.1	000765	virion_structural_protein	265	MLDJOKPK_00011	Salmonella phage SPAsTU	GCA_003183805.1
AWN08992.1	000765	virion_structural_protein	180	MLDJOKPK_00031	Salmonella phage SPAsTU	GCA_003183805.1
AWN09115.1	000765	virion_structural_protein	180	MLDJOKPK_00203	Salmonella phage SPAsTU	GCA_003183805.1
AXF51138.1	000765	virion_structural_protein	295	MLDJOKPK_00290	Salmonella phage SPAsTU	GCA_003183805.1
AXF51139.1	000765	virion_structural_protein	347	MLDJOKPK_00291	Salmonella phage SPAsTU	GCA_003183805.1
AXF51140.1	000765	virion_structural_protein	505	MLDJOKPK_00292	Salmonella phage SPAsTU	GCA_003183805.1
AWN09176.1	000765	virion_structural_protein	305	MLDJOKPK_00293	Salmonella phage SPAsTU	GCA_003183805.1
AXF51141.1	000765	virion_structural_protein	223	MLDJOKPK_00294	Salmonella phage SPAsTU	GCA_003183805.1
AEP83955.1	000765	virion_structural_protein	177	SPN3US_0122	Salmonella phage SPN3US	GCA_001042275.1
AEP83971.1	000765	virion_structural_protein	265	SPN3US_0138	Salmonella phage SPN3US	GCA_001042275.1
AEP83972.1	000765	virion_structural_protein	270	SPN3US_0139	Salmonella phage SPN3US	GCA_001042275.1
AEP83973.1	000765	virion_structural_protein	281	SPN3US_0140	Salmonella phage SPN3US	GCA_001042275.1
AEP83974.1	000765	virion_structural_protein	303	SPN3US_0141	Salmonella phage SPN3US	GCA_001042275.1
AEP83975.1	000765	virion_structural_protein	279	SPN3US_0142	Salmonella phage SPN3US	GCA_001042275.1
AEP83976.1	000765	virion_structural_protein	295	SPN3US_0143	Salmonella phage SPN3US	GCA_001042275.1
AEP83977.1	000765	virion_structural_protein	275	SPN3US_0144	Salmonella phage SPN3US	GCA_001042275.1
AEP83978.1	000765	virion_structural_protein	470	SPN3US_0145	Salmonella phage SPN3US	GCA_001042275.1
AEP83979.1	000765	virion_structural_protein	332	SPN3US_0146	Salmonella phage SPN3US	GCA_001042275.1
AEP83980.1	000765	virion_structural_protein	307	SPN3US_0147	Salmonella phage SPN3US	GCA_001042275.1
AEP83981.1	000765	virion_structural_protein	498	SPN3US_0148	Salmonella phage SPN3US	GCA_001042275.1
AEP83982.1	000765	virion_structural_protein	329	SPN3US_0149	Salmonella phage SPN3US	GCA_001042275.1
AEP83983.1	000765	virion_structural_protein	299	SPN3US_0150	Salmonella phage SPN3US	GCA_001042275.1
AEP83984.1	000765	virion_structural_protein	480	SPN3US_0151	Salmonella phage SPN3US	GCA_001042275.1
AEP83985.1	000765	virion_structural_protein	332	SPN3US_0152	Salmonella phage SPN3US	GCA_001042275.1
AEP83986.1	000765	virion_structural_protein	300	SPN3US_0153	Salmonella phage SPN3US	GCA_001042275.1
AEP83987.1	000765	virion_structural_protein	439	SPN3US_0154	Salmonella phage SPN3US	GCA_001042275.1
AEP84070.1	000765	virion_structural_protein	183	SPN3US_0237	Salmonella phage SPN3US	GCA_001042275.1
QKE54322.1	000765	virion_structural_protein	294	ACSA002_0080	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54323.1	000765	virion_structural_protein	278	ACSA002_0090	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54325.1	000765	virion_structural_protein	278	ACSA002_0110	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54410.1	000765	virion_structural_protein	315	ACSA002_0960	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54411.1	000765	virion_structural_protein	278	ACSA002_0970	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54412.1	000765	virion_structural_protein	312	ACSA002_0980	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54413.1	000765	virion_structural_protein	323	ACSA002_0990	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54414.1	000765	virion_structural_protein	278	ACSA002_1000	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54415.1	000765	virion_structural_protein	319	ACSA002_1010	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54465.1	000765	virion_structural_protein	234	ACSA002_1510	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54601.1	000765	virion_structural_protein	239	ACSA002_2840	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54610.1	000765	virion_structural_protein	227	ACSA002_2930	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54627.1	000765	virion_structural_protein	105	ACSA002_3100	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54628.1	000765	virion_structural_protein	307	ACSA002_3110	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54629.1	000765	virion_structural_protein	333	ACSA002_3120	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54630.1	000765	virion_structural_protein	393	ACSA002_3130	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54633.1	000765	virion_structural_protein	173	ACSA002_3160	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65383.1	000765	virion_structural_protein	279	2050HW_00048	Serratia phage 2050HW	GCA_002628125.1
QDB71165.1	000765	virion_structural_protein	279	CPT_Moabite_135	Serratia phage Moabite	GCA_006384735.1
QFP93195.1	000765	virion_structural_protein	160	-	Serratia phage PCH45	GCA_009187865.1
QFP93113.1	000765	virion_structural_protein	289	-	Serratia phage PCH45	GCA_009187865.1
QFP93108.1	000765	virion_structural_protein	311	-	Serratia phage PCH45	GCA_009187865.1
QFP93138.1	000765	virion_structural_protein	229	-	Serratia phage PCH45	GCA_009187865.1
AQT27989.1	000765	virion_structural_protein	288	pVa21_047	Vibrio phage pVa-21	GCA_002619305.1
AFC21448.1	000766	RCC1	385	GAP32_001	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14124.1	000766	RCC1	298	PBI_121Q_234	Escherichia phage 121Q	GCA_000926855.1
AIT14126.1	000766	RCC1	369	PBI_121Q_236	Escherichia phage 121Q	GCA_000926855.1
AIT14128.1	000766	RCC1	269	PBI_121Q_238	Escherichia phage 121Q	GCA_000926855.1
AIT14129.1	000766	RCC1	333	PBI_121Q_239	Escherichia phage 121Q	GCA_000926855.1
AIT14131.1	000766	RCC1	383	PBI_121Q_241	Escherichia phage 121Q	GCA_000926855.1
AIT14132.1	000766	RCC1	382	PBI_121Q_242	Escherichia phage 121Q	GCA_000926855.1
AIT14134.1	000766	RCC1	396	PBI_121Q_244	Escherichia phage 121Q	GCA_000926855.1
AIT14135.1	000766	RCC1	379	PBI_121Q_245	Escherichia phage 121Q	GCA_000926855.1
AIT14136.1	000766	RCC1	369	PBI_121Q_246	Escherichia phage 121Q	GCA_000926855.1
AIT14137.1	000766	RCC1	380	PBI_121Q_247	Escherichia phage 121Q	GCA_000926855.1
AIT14138.1	000766	RCC1	382	PBI_121Q_248	Escherichia phage 121Q	GCA_000926855.1
QAY00789.1	000766	RCC1	382	Ecwhy1_516	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00790.1	000766	RCC1	369	Ecwhy1_517	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00791.1	000766	RCC1	393	Ecwhy1_518	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00792.1	000766	RCC1	397	Ecwhy1_519	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00793.1	000766	RCC1	376	Ecwhy1_520	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00795.1	000766	RCC1	343	Ecwhy1_522	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00796.1	000766	RCC1	381	Ecwhy1_523	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00797.1	000766	RCC1	396	Ecwhy1_524	Escherichia phage Ecwhy_1	GCA_004146585.1

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QAY00798.1	000766	RCC1	395	Ecwhy1_525	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00799.1	000766	RCC1	405	Ecwhy1_526	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00800.1	000766	RCC1	378	Ecwhy1_527	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34976.1	000766	RCC1	298	ACQ29_gp296	Escherichia phage PBECO4	GCA_001041035.1
AGC34971.1	000766	RCC1	351	ACQ29_gp291	Escherichia phage PBECO4	GCA_001041035.1
AGC34967.1	000766	RCC1	369	ACQ29_gp287	Escherichia phage PBECO4	GCA_001041035.1
AGC34969.1	000766	RCC1	382	ACQ29_gp289	Escherichia phage PBECO4	GCA_001041035.1
AGC34974.1	000766	RCC1	385	ACQ29_gp294	Escherichia phage PBECO4	GCA_001041035.1
AGC34975.1	000766	RCC1	388	ACQ29_gp295	Escherichia phage PBECO4	GCA_001041035.1
AGC34970.1	000766	RCC1	396	ACQ29_gp290	Escherichia phage PBECO4	GCA_001041035.1
AGC34968.1	000766	RCC1	401	ACQ29_gp288	Escherichia phage PBECO4	GCA_001041035.1
AGC34972.1	000766	RCC1	405	ACQ29_gp292	Escherichia phage PBECO4	GCA_001041035.1
AGC34966.1	000766	RCC1	406	ACQ29_gp286	Escherichia phage PBECO4	GCA_001041035.1
BBM61802.1	000766	RCC1	106	EO157G_2130	Escherichia phage SP27	GCA_008033345.1
BBM61803.1	000766	RCC1	389	EO157G_2140	Escherichia phage SP27	GCA_008033345.1
BBM61804.1	000766	RCC1	369	EO157G_2150	Escherichia phage SP27	GCA_008033345.1
BBM61805.1	000766	RCC1	269	EO157G_2160	Escherichia phage SP27	GCA_008033345.1
BBM61806.1	000766	RCC1	391	EO157G_2170	Escherichia phage SP27	GCA_008033345.1
BBM61807.1	000766	RCC1	383	EO157G_2180	Escherichia phage SP27	GCA_008033345.1
BBM61809.1	000766	RCC1	395	EO157G_2200	Escherichia phage SP27	GCA_008033345.1
BBM61810.1	000766	RCC1	382	EO157G_2210	Escherichia phage SP27	GCA_008033345.1
BBM61811.1	000766	RCC1	379	EO157G_2220	Escherichia phage SP27	GCA_008033345.1
BBM61812.1	000766	RCC1	369	EO157G_2230	Escherichia phage SP27	GCA_008033345.1
BBM61813.1	000766	RCC1	400	EO157G_2240	Escherichia phage SP27	GCA_008033345.1
BBM61814.1	000766	RCC1	392	EO157G_2250	Escherichia phage SP27	GCA_008033345.1
AXC36551.1	000766	RCC1	269	-	Escherichia phage UB	GCA_003341455.1
AXC36556.1	000766	RCC1	298	-	Escherichia phage UB	GCA_003341455.1
AXC36544.1	000766	RCC1	369	-	Escherichia phage UB	GCA_003341455.1
AXC36543.1	000766	RCC1	372	-	Escherichia phage UB	GCA_003341455.1
AXC36548.1	000766	RCC1	380	-	Escherichia phage UB	GCA_003341455.1
AXC36553.1	000766	RCC1	389	-	Escherichia phage UB	GCA_003341455.1
AXC36549.1	000766	RCC1	391	-	Escherichia phage UB	GCA_003341455.1
AXC36546.1	000766	RCC1	395	-	Escherichia phage UB	GCA_003341455.1
AXC36550.1	000766	RCC1	395	-	Escherichia phage UB	GCA_003341455.1
AXC36545.1	000766	RCC1	395	-	Escherichia phage UB	GCA_003341455.1
AXC36554.1	000766	RCC1	401	-	Escherichia phage UB	GCA_003341455.1
QBO61566.1	000766	RCC1	378	G17_00070	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61567.1	000766	RCC1	400	G17_00071	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61568.1	000766	RCC1	369	G17_00072	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61569.1	000766	RCC1	389	G17_00073	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61570.1	000766	RCC1	382	G17_00074	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61571.1	000766	RCC1	380	G17_00075	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61572.1	000766	RCC1	395	G17_00076	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61574.1	000766	RCC1	391	G17_00078	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61575.1	000766	RCC1	380	G17_00079	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61576.1	000766	RCC1	269	G17_00080	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61577.1	000766	RCC1	389	G17_00081	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13632.1	000766	RCC1	380	vBEcoMphAPEC6_gp001	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13633.1	000766	RCC1	434	vBEcoMphAPEC6_gp002	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13634.1	000766	RCC1	389	vBEcoMphAPEC6_gp003	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13636.1	000766	RCC1	383	vBEcoMphAPEC6_gp005	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13637.1	000766	RCC1	391	vBEcoMphAPEC6_gp006	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13638.1	000766	RCC1	269	vBEcoMphAPEC6_gp007	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13640.1	000766	RCC1	369	vBEcoMphAPEC6_gp009	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13641.1	000766	RCC1	389	vBEcoMphAPEC6_gp010	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14172.1	000766	RCC1	382	vBEcoMphAPEC6_gp549	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14173.1	000766	RCC1	380	vBEcoMphAPEC6_gp550	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14174.1	000766	RCC1	380	vBEcoMphAPEC6_gp551	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80114.1	000766	RCC1	298	PSLUR01_00137	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80116.1	000766	RCC1	389	PSLUR01_00139	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80117.1	000766	RCC1	380	PSLUR01_00140	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80118.1	000766	RCC1	380	PSLUR01_00141	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80119.1	000766	RCC1	343	PSLUR01_00142	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80121.1	000766	RCC1	396	PSLUR01_00144	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80122.1	000766	RCC1	382	PSLUR01_00145	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80123.1	000766	RCC1	379	PSLUR01_00146	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80124.1	000766	RCC1	369	PSLUR01_00147	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80125.1	000766	RCC1	400	PSLUR01_00148	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80126.1	000766	RCC1	392	PSLUR01_00149	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80127.1	000766	RCC1	369	PSLUR01_00150	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80128.1	000766	RCC1	378	PSLUR01_00151	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18642.1	000766	RCC1	376	7t3_0121	Salmonella phage 7t3	GCA_006083215.1
QCW18643.1	000766	RCC1	392	7t3_0122	Salmonella phage 7t3	GCA_006083215.1
QCW18644.1	000766	RCC1	398	7t3_0123	Salmonella phage 7t3	GCA_006083215.1
QCW18645.1	000766	RCC1	388	7t3_0124	Salmonella phage 7t3	GCA_006083215.1
QCW18646.1	000766	RCC1	385	7t3_0125	Salmonella phage 7t3	GCA_006083215.1
QCW18648.1	000766	RCC1	286	7t3_0127	Salmonella phage 7t3	GCA_006083215.1
QCW18650.1	000766	RCC1	389	7t3_0129	Salmonella phage 7t3	GCA_006083215.1
QCW18652.1	000766	RCC1	358	7t3_0131	Salmonella phage 7t3	GCA_006083215.1
QCW18654.1	000766	RCC1	383	7t3_0133	Salmonella phage 7t3	GCA_006083215.1
QCW18655.1	000766	RCC1	381	7t3_0134	Salmonella phage 7t3	GCA_006083215.1
QCW18656.1	000766	RCC1	398	7t3_0135	Salmonella phage 7t3	GCA_006083215.1
QCW18657.1	000766	RCC1	374	7t3_0136	Salmonella phage 7t3	GCA_006083215.1
QCW18658.1	000766	RCC1	399	7t3_0137	Salmonella phage 7t3	GCA_006083215.1
AZU98467.1	000766	RCC1	376	CPT_Munch_535	Salmonella phage Munch	GCA_004015485.1
AZU98468.1	000766	RCC1	392	CPT_Munch_536	Salmonella phage Munch	GCA_004015485.1
AZU98469.1	000766	RCC1	398	CPT_Munch_537	Salmonella phage Munch	GCA_004015485.1
AZU98470.1	000766	RCC1	388	CPT_Munch_538	Salmonella phage Munch	GCA_004015485.1
AZU98471.1	000766	RCC1	385	CPT_Munch_539	Salmonella phage Munch	GCA_004015485.1
AZU98473.1	000766	RCC1	373	CPT_Munch_541	Salmonella phage Munch	GCA_004015485.1
AZU98474.1	000766	RCC1	389	CPT_Munch_542	Salmonella phage Munch	GCA_004015485.1
AZU98475.1	000766	RCC1	394	CPT_Munch_543	Salmonella phage Munch	GCA_004015485.1
AZU98477.1	000766	RCC1	377	CPT_Munch_545	Salmonella phage Munch	GCA_004015485.1
AZU98478.1	000766	RCC1	381	CPT_Munch_546	Salmonella phage Munch	GCA_004015485.1
AZU98479.1	000766	RCC1	398	CPT_Munch_547	Salmonella phage Munch	GCA_004015485.1
AZU98480.1	000766	RCC1	380	CPT_Munch_548	Salmonella phage Munch	GCA_004015485.1
AZU98481.1	000766	RCC1	374	CPT_Munch_549	Salmonella phage Munch	GCA_004015485.1
AZU98482.1	000766	RCC1	399	CPT_Munch_550	Salmonella phage Munch	GCA_004015485.1
QIG63032.1	000766	RCC1	399	SEPL_419	Salmonella phage SE_PL	GCA_011067555.1
QIG63033.1	000766	RCC1	374	SEPL_420	Salmonella phage SE_PL	GCA_011067555.1
QIG63034.1	000766	RCC1	398	SEPL_421	Salmonella phage SE_PL	GCA_011067555.1
QIG63035.1	000766	RCC1	381	SEPL_422	Salmonella phage SE_PL	GCA_011067555.1
QIG63036.1	000766	RCC1	377	SEPL_423	Salmonella phage SE_PL	GCA_011067555.1
QIG63038.1	000766	RCC1	358	SEPL_425	Salmonella phage SE_PL	GCA_011067555.1
QIG63039.1	000766	RCC1	389	SEPL_426	Salmonella phage SE_PL	GCA_011067555.1
QIG63041.1	000766	RCC1	305	SEPL_428	Salmonella phage SE_PL	GCA_011067555.1
QIG63043.1	000766	RCC1	385	SEPL_430	Salmonella phage SE_PL	GCA_011067555.1
QIG63044.1	000766	RCC1	388	SEPL_431	Salmonella phage SE_PL	GCA_011067555.1
QIG63045.1	000766	RCC1	398	SEPL_432	Salmonella phage SE_PL	GCA_011067555.1
QIG63046.1	000766	RCC1	392	SEPL_433	Salmonella phage SE_PL	GCA_011067555.1
QIG63047.1	000766	RCC1	376	SEPL_434	Salmonella phage SE_PL	GCA_011067555.1
QKE54611.1	000766	RCC1	370	ACSA002_2940	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54645.1	000766	RCC1	397	ACSA002_3280	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AQW89065.1	000766	RCC1	378	BF_0540	Serratia phage BF	GCA_002619745.1
AQW89067.1	000766	RCC1	374	BF_0542	Serratia phage BF	GCA_002619745.1
AQW89070.1	000766	RCC1	384	BF_0545	Serratia phage BF	GCA_002619745.1
AQW89071.1	000766	RCC1	385	BF_0546	Serratia phage BF	GCA_002619745.1
AQW89074.1	000766	RCC1	360	BF_0549	Serratia phage BF	GCA_002619745.1
SOK59342.1	000766	RCC1	382	g534c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59343.1	000766	RCC1	376	g535c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59344.1	000766	RCC1	366	g536c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59345.1	000766	RCC1	388	g537c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59346.1	000766	RCC1	382	g538c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58804.1	000766	RCC1	382	g527c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58805.1	000766	RCC1	376	g528c	Yersinia phage fHe-Yen9-04	GCA_002990485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58806.1	000766	RCC1	366	g529c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58807.1	000766	RCC1	388	g530c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58808.1	000766	RCC1	382	g531c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01431.1	000767	Glutaredoxin	89	-	Aeromonas phage 65.2	GCA_002618145.1
APU01429.1	000767	Glutaredoxin	93	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28762.1	000767	Glutaredoxin	93	AP1_0044	Aeromonas phage AP1	GCA_014183365.1
QMV28764.1	000767	Glutaredoxin	89	AP1_0046	Aeromonas phage AP1	GCA_014183365.1
ATI17467.1	000767	Glutaredoxin	89	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17469.1	000767	Glutaredoxin	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00530.1	000767	Glutaredoxin	89	HWB28_gp022	Aeromonas phage AS-zj	GCA_002627665.1
ASU00528.1	000767	Glutaredoxin	93	HWB28_gp024	Aeromonas phage AS-zj	GCA_002627665.1
AUE22578.1	000767	Glutaredoxin	90	Ah1_00037	Aeromonas phage Ah1	GCA_002957415.1
AUE22577.1	000767	Glutaredoxin	94	Ah1_00036	Aeromonas phage Ah1	GCA_002957415.1
QAX98613.1	000767	Glutaredoxin	96	ASfcp2_280	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98614.1	000767	Glutaredoxin	90	ASfcp2_281	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97907.1	000767	Glutaredoxin	89	ASswx1_264	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97909.1	000767	Glutaredoxin	93	ASswx1_266	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01241.1	000767	Glutaredoxin	93	ASwh1_176	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01243.1	000767	Glutaredoxin	89	ASwh1_178	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39404.1	000767	Glutaredoxin	89	CC2_268	Aeromonas phage CC2	GCA_000903495.1
AFN39303.1	000767	Glutaredoxin	93	CC2_266	Aeromonas phage CC2	GCA_000903495.1
QDJ97434.1	000767	Glutaredoxin	87	D6_0007	Aeromonas phage D6	GCA_007051205.2
QDJ96773.1	000767	Glutaredoxin	86	PS1_0015	Aeromonas phage PS1	GCA_007051165.2
QFR59406.1	000767	Glutaredoxin	86	PS2_0015	Aeromonas phage PS2	GCA_009388305.2
ADQ52751.1	000767	Glutaredoxin	90	PX29p032	Aeromonas phage PX29	GCA_000920195.1
ADQ52750.1	000767	Glutaredoxin	96	PX29p031	Aeromonas phage PX29	GCA_000920195.1
ADM80006.1	000767	Glutaredoxin	95	phiAS5_ORF0163	Aeromonas phage phiAS5	GCA_000887715.1
ADM80007.1	000767	Glutaredoxin	90	phiAS5_ORF0164	Aeromonas phage phiAS5	GCA_000887715.1
AAR90898.1	000767	Glutaredoxin	89	65p040	Aeromonas virus 65	GCA_000893255.1
AAR90900.1	000767	Glutaredoxin	93	65p038	Aeromonas virus 65	GCA_000893255.1
AAQ17693.1	000767	Glutaredoxin	90	nrdC	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17692.1	000767	Glutaredoxin	94	nrdH	Aeromonas virus Aeh1	GCA_000843245.1
AUZ94918.1	000767	Glutaredoxin	78	FDI40_gp121	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANS06120.1	000767	Glutaredoxin	90	ABCD_0243	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS06116.1	000767	Glutaredoxin	92	ABCD_0257	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65033.1	000767	Glutaredoxin	96	S13_236	Cronobacter phage S13	GCA_001503575.1
AFC21638.1	000767	Glutaredoxin	78	GAP32_188	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97262.1	000767	Glutaredoxin	89	E_254	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97276.1	000767	Glutaredoxin	92	E_268	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56810.1	000767	Glutaredoxin	83	CPXG_00007	Cyanophage P-RSM6	GCA_000906155.1
AJK27649.1	000767	Glutaredoxin	83	PTIM40_230	Cyanophage P-TIM40	GCA_001470935.1
AJK27439.1	000767	Glutaredoxin	86	PTIM40_12	Cyanophage P-TIM40	GCA_001470935.1
AOO14337.1	000767	Glutaredoxin	80	Sn110110_143	Cyanophage S-RIM14	GCA_002599065.1
AOO14405.1	000767	Glutaredoxin	78	Sn110110_212	Cyanophage S-RIM14	GCA_002599065.1
AOO14986.1	000767	Glutaredoxin	80	W1230910_140	Cyanophage S-RIM14	GCA_002599125.1
AOO15054.1	000767	Glutaredoxin	78	W1230910_209	Cyanophage S-RIM14	GCA_002599125.1
AMO43033.1	000767	Glutaredoxin	63	R1080702_018	Cyanophage S-RIM32	GCA_001754165.1
AMO43227.1	000767	Glutaredoxin	82	R1080702_222	Cyanophage S-RIM32	GCA_001754165.1
AMO43274.1	000767	Glutaredoxin	81	W270710_029	Cyanophage S-RIM44	GCA_002599145.1
AMO43459.1	000767	Glutaredoxin	81	W270710_220	Cyanophage S-RIM44	GCA_002599145.1
AOO11508.1	000767	Glutaredoxin	81	ES420910_026	Cyanophage S-RIM44	GCA_002599165.1
AOO11699.1	000767	Glutaredoxin	81	ES420910_222	Cyanophage S-RIM44	GCA_002599165.1
AOO11746.1	000767	Glutaredoxin	81	Np050604_029	Cyanophage S-RIM44	GCA_002599185.1
AOO11931.1	000767	Glutaredoxin	81	Np050604_220	Cyanophage S-RIM44	GCA_002599185.1
AOO11973.1	000767	Glutaredoxin	81	Np200711_026	Cyanophage S-RIM44	GCA_002599205.1
AOO12165.1	000767	Glutaredoxin	81	Np200711_223	Cyanophage S-RIM44	GCA_002599205.1
AOO12209.1	000767	Glutaredoxin	81	Np420711_026	Cyanophage S-RIM44	GCA_002599225.1
AOO12400.1	000767	Glutaredoxin	81	Np420711_222	Cyanophage S-RIM44	GCA_002599225.1
AOO12447.1	000767	Glutaredoxin	81	Sn080709_029	Cyanophage S-RIM44	GCA_002599245.1
AOO12632.1	000767	Glutaredoxin	81	Sn080709_220	Cyanophage S-RIM44	GCA_002599245.1
AOO12674.1	000767	Glutaredoxin	81	Sn130910_026	Cyanophage S-RIM44	GCA_002599265.1
AOO12865.1	000767	Glutaredoxin	81	Sn130910_222	Cyanophage S-RIM44	GCA_002599265.1
AOO12912.1	000767	Glutaredoxin	81	W2100709_029	Cyanophage S-RIM44	GCA_002599285.1
AOO13098.1	000767	Glutaredoxin	81	W2100709_221	Cyanophage S-RIM44	GCA_002599285.1
AGH07591.1	000767	Glutaredoxin	80	CYVG_00147	Cyanophage S-SSM6a	GCA_002710385.1
AGH07614.1	000767	Glutaredoxin	82	CYVG_00171	Cyanophage S-SSM6a	GCA_002710385.1
AGG54383.1	000767	Glutaredoxin	80	CYWG_00099	Cyanophage S-SSM6b	GCA_002710425.1
AGG54473.1	000767	Glutaredoxin	79	CYWG_00189	Cyanophage S-SSM6b	GCA_002710425.1
QBZ70817.1	000767	Glutaredoxin	90	pETSU_236	Edwardsiella virus pEt-SU	GCA_004800915.1
AIT14431.1	000767	Glutaredoxin	82	PBI_121Q_541	Escherichia phage 121Q	GCA_000926855.1
QAY00517.1	000767	Glutaredoxin	82	Ecwhy1_238	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34711.1	000767	Glutaredoxin	82	ACQ29_gp031	Escherichia phage PBECO4	GCA_001041035.1
BBM62103.1	000767	Glutaredoxin	82	EO157G_5140	Escherichia phage SP27	GCA_008033345.1
AXC36830.1	000767	Glutaredoxin	82	-	Escherichia phage UB	GCA_003341455.1
ARM70895.1	000767	Glutaredoxin	107	phiC120_c190	Escherichia phage phiC120	GCA_002621185.1
ARM70907.1	000767	Glutaredoxin	87	phiC120_c202	Escherichia phage phiC120	GCA_002621185.1
QBO61870.1	000767	Glutaredoxin	82	G17_00381	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13910.1	000767	Glutaredoxin	82	vBEcoMphAPEC6_gp285c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80417.1	000767	Glutaredoxin	82	PSLUR01_00440	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78780.1	000767	Glutaredoxin	90	RB43ORF258w	Escherichia virus RB43	GCA_000863505.1
AAX78797.1	000767	Glutaredoxin	92	RB43ORF275w	Escherichia virus RB43	GCA_000863505.1
QGH72116.1	000767	Glutaredoxin	79	N1M2_254	Klebsiella phage N1M2	GCA_010092605.1
AFA44306.1	000767	Glutaredoxin	82	RaK2_00033	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78899.1	000767	Glutaredoxin	98	-	Myoviridae sp.	GCA_012593985.1
QIG66024.1	000767	Glutaredoxin	76	phiOC_p382	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43759.1	000767	Glutaredoxin	78	CBB_194	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26223.1	000767	Glutaredoxin	64	CPMG_00122	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44693.1	000767	Glutaredoxin	82	PSSM2_315.5	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12283.1	000767	Glutaredoxin	82	PRTG_00130	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93573.1	000767	Glutaredoxin	78	AVU42_gp235	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99320.1	000767	Glutaredoxin	81	Syn1_224	Prochlorococcus phage Syn1	GCA_000892495.1
AEV89449.1	000767	Glutaredoxin	88	OBP_012	Pseudomonas phage OBP	GCA_000896635.1
QCG76062.1	000767	Glutaredoxin	83	EST35_0181	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44444.1	000767	Glutaredoxin	74	PBI_SCTP2_429	Salicola phage SCTP-2	GCA_002625545.1
QCW18909.1	000767	Glutaredoxin	88	7t3_0388	Salmonella phage 7t3	GCA_006083215.1
AZU98166.1	000767	Glutaredoxin	88	CPT_Munch_222	Salmonella phage Munch	GCA_004015485.1
QIG62818.1	000767	Glutaredoxin	88	SEPL_205	Salmonella phage SE_PL	GCA_011067555.1
AQW88715.1	000767	Glutaredoxin	78	BF_0190	Serratia phage BF	GCA_002619745.1
AGR47886.1	000767	Glutaredoxin	79	SmphiM12_254	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13088.1	000767	Glutaredoxin	79	PHIM19_183	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12728.1	000767	Glutaredoxin	79	PHIM7_183	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13457.1	000767	Glutaredoxin	79	PHIN3_194	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30641.1	000767	Glutaredoxin	80	Syn7803US37_164	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30753.1	000767	Glutaredoxin	77	Syn7803US37_276	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54978.1	000767	Glutaredoxin	84	b23_0372	Synechococcus phage B23	GCA_009745195.1
QGT54613.1	000767	Glutaredoxin	84	b3_0378	Synechococcus phage B3	GCA_009745215.1
ASR76299.1	000767	Glutaredoxin	77	PBI_BELLAMY_263	Synechococcus phage Bellamy	GCA_002627525.1
ASR76309.1	000767	Glutaredoxin	79	PBI_BELLAMY_273	Synechococcus phage Bellamy	GCA_002627525.1
QCW22938.1	000767	Glutaredoxin	80	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23051.1	000767	Glutaredoxin	81	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50700.1	000767	Glutaredoxin	79	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50623.1	000767	Glutaredoxin	80	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59484.1	000767	Glutaredoxin	56	S330809_023	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59682.1	000767	Glutaredoxin	83	S330809_221	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59246.1	000767	Glutaredoxin	79	C440309_023	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59444.1	000767	Glutaredoxin	83	C440309_221	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59722.1	000767	Glutaredoxin	78	N231010_023	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59919.1	000767	Glutaredoxin	83	N231010_220	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70460.1	000767	Glutaredoxin	50	HOU04_gp061	Synechococcus phage S-T4	GCA_003443335.1
QJT70253.1	000767	Glutaredoxin	82	SynMITS9220M01_247	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70246.1	000767	Glutaredoxin	78	SynMITS9220M01_240	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64348.1	000767	Glutaredoxin	99	KVP40.0279	Vibrio phage KVP40	GCA_000843785.1
QIW90662.1	000767	Glutaredoxin	71	GCAPEGMB_00315	Vibrio phage V07	GCA_012361095.1
QIW91136.1	000767	Glutaredoxin	71	COHAPHLL_00300	Vibrio phage V09	GCA_012361135.1
QHJ74457.1	000767	Glutaredoxin	99	VH12019_00130	Vibrio phage VH1_2019	GCA_009931825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGB06951.1	000767	Glutaredoxin	99	CF80_gp164	Vibrio phage VH7D	GCA_000914495.1
QBX06194.1	000767	Glutaredoxin	99	ValB1HC_241	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61211.1	000767	Glutaredoxin	99	AVU32_gp370	Vibrio phage ValKK3	GCA_001501635.1
AGN30325.1	000767	Glutaredoxin	99	VPFG_00327	Vibrio phage nt-1	GCA_000910195.2
ALP47203.1	000767	Glutaredoxin	99	phiGrn1_0011	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47594.1	000767	Glutaredoxin	99	phiST2_0143	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54819.1	000767	Glutaredoxin	99	vBValMR10Z_279	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07114.1	000767	Glutaredoxin	87	VmeM32_00127	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07119.1	000767	Glutaredoxin	104	VmeM32_00132	Vibrio phage vB_VmeM-32	GCA_002608825.1
QAX96640.1	000767	Glutaredoxin	79	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96958.1	000767	Glutaredoxin	79	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96004.1	000767	Glutaredoxin	79	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96322.1	000767	Glutaredoxin	79	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFN37509.1	000767	Glutaredoxin	99	pp2_276	Vibriophage phi-pp2	GCA_002630725.1
BBA65314.1	000767	Glutaredoxin	75	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65313.1	000767	Glutaredoxin	79	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96348.1	000767	Glutaredoxin	79	Xoosp13_161	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96349.1	000767	Glutaredoxin	74	Xoosp13_162	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58997.1	000767	Glutaredoxin	78	g189	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58462.1	000767	Glutaredoxin	78	g185	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56823.1	000768	2OG-FeII_Oxy_5	200	CPXG_00020	Cyanophage P-RSM6	GCA_000906155.1
AGH56825.1	000768	2OG-FeII_Oxy_5	181	CPXG_00022	Cyanophage P-RSM6	GCA_000906155.1
AGH56871.1	000768	2OG-FeII_Oxy_5	205	CPXG_00068	Cyanophage P-RSM6	GCA_000906155.1
AGH56941.1	000768	2OG-FeII_Oxy_5	209	CPXG_00138	Cyanophage P-RSM6	GCA_000906155.1
AGH56968.1	000768	2OG-FeII_Oxy_5	189	CPXG_00165	Cyanophage P-RSM6	GCA_000906155.1
AGH56972.1	000768	2OG-FeII_Oxy_5	211	CPXG_00169	Cyanophage P-RSM6	GCA_000906155.1
AGH56977.1	000768	2OG-FeII_Oxy_5	201	CPXG_00174	Cyanophage P-RSM6	GCA_000906155.1
AGH56983.1	000768	2OG-FeII_Oxy_5	212	CPXG_00180	Cyanophage P-RSM6	GCA_000906155.1
AGH56984.1	000768	2OG-FeII_Oxy_5	238	CPXG_00181	Cyanophage P-RSM6	GCA_000906155.1
AGH56991.1	000768	2OG-FeII_Oxy_5	247	CPXG_00188	Cyanophage P-RSM6	GCA_000906155.1
AJK27583.1	000768	2OG-FeII_Oxy_5	211	PTIM40_156	Cyanophage P-TIM40	GCA_001470935.1
AJK27584.1	000768	2OG-FeII_Oxy_5	205	PTIM40_157	Cyanophage P-TIM40	GCA_001470935.1
AJK27663.1	000768	2OG-FeII_Oxy_5	208	PTIM40_2	Cyanophage P-TIM40	GCA_001470935.1
AJK27617.1	000768	2OG-FeII_Oxy_5	189	PTIM40_203	Cyanophage P-TIM40	GCA_001470935.1
AJK27477.1	000768	2OG-FeII_Oxy_5	226	PTIM40_50	Cyanophage P-TIM40	GCA_001470935.1
AJK27480.1	000768	2OG-FeII_Oxy_5	236	PTIM40_53	Cyanophage P-TIM40	GCA_001470935.1
AJK27513.1	000768	2OG-FeII_Oxy_5	210	PTIM40_86	Cyanophage P-TIM40	GCA_001470935.1
AOO14230.1	000768	2OG-FeII_Oxy_5	213	Sn110110_036	Cyanophage S-RIM14	GCA_002599065.1
AOO14231.1	000768	2OG-FeII_Oxy_5	226	Sn110110_037	Cyanophage S-RIM14	GCA_002599065.1
AOO14252.1	000768	2OG-FeII_Oxy_5	219	Sn110110_058	Cyanophage S-RIM14	GCA_002599065.1
AOO14390.1	000768	2OG-FeII_Oxy_5	215	Sn110110_197	Cyanophage S-RIM14	GCA_002599065.1
AOO14882.1	000768	2OG-FeII_Oxy_5	213	W1230910_036	Cyanophage S-RIM14	GCA_002599125.1
AOO14883.1	000768	2OG-FeII_Oxy_5	226	W1230910_037	Cyanophage S-RIM14	GCA_002599125.1
AOO14904.1	000768	2OG-FeII_Oxy_5	219	W1230910_058	Cyanophage S-RIM14	GCA_002599125.1
AOO15038.1	000768	2OG-FeII_Oxy_5	215	W1230910_193	Cyanophage S-RIM14	GCA_002599125.1
AMO43052.1	000768	2OG-FeII_Oxy_5	205	R1080702_043	Cyanophage S-RIM32	GCA_001754165.1
AMO43122.1	000768	2OG-FeII_Oxy_5	96	R1080702_113	Cyanophage S-RIM32	GCA_001754165.1
AMO43206.1	000768	2OG-FeII_Oxy_5	204	R1080702_199	Cyanophage S-RIM32	GCA_001754165.1
AMO43275.1	000768	2OG-FeII_Oxy_5	205	W270710_030	Cyanophage S-RIM44	GCA_002599145.1
AMO43347.1	000768	2OG-FeII_Oxy_5	199	W270710_103	Cyanophage S-RIM44	GCA_002599145.1
AMO43444.1	000768	2OG-FeII_Oxy_5	170	W270710_204	Cyanophage S-RIM44	GCA_002599145.1
AOO11509.1	000768	2OG-FeII_Oxy_5	205	ES420910_027	Cyanophage S-RIM44	GCA_002599165.1
AOO11553.1	000768	2OG-FeII_Oxy_5	207	ES420910_072	Cyanophage S-RIM44	GCA_002599165.1
AOO11585.1	000768	2OG-FeII_Oxy_5	209	ES420910_104	Cyanophage S-RIM44	GCA_002599165.1
AOO11587.1	000768	2OG-FeII_Oxy_5	190	ES420910_106	Cyanophage S-RIM44	GCA_002599165.1
AOO11747.1	000768	2OG-FeII_Oxy_5	205	Np050604_030	Cyanophage S-RIM44	GCA_002599185.1
AOO11819.1	000768	2OG-FeII_Oxy_5	199	Np050604_103	Cyanophage S-RIM44	GCA_002599185.1
AOO11916.1	000768	2OG-FeII_Oxy_5	170	Np050604_204	Cyanophage S-RIM44	GCA_002599185.1
AOO11974.1	000768	2OG-FeII_Oxy_5	205	Np200711_027	Cyanophage S-RIM44	GCA_002599205.1
AOO12018.1	000768	2OG-FeII_Oxy_5	207	Np200711_072	Cyanophage S-RIM44	GCA_002599205.1
AOO12050.1	000768	2OG-FeII_Oxy_5	209	Np200711_104	Cyanophage S-RIM44	GCA_002599205.1
AOO12052.1	000768	2OG-FeII_Oxy_5	190	Np200711_106	Cyanophage S-RIM44	GCA_002599205.1
AOO12210.1	000768	2OG-FeII_Oxy_5	205	Np420711_027	Cyanophage S-RIM44	GCA_002599225.1
AOO12254.1	000768	2OG-FeII_Oxy_5	207	Np420711_072	Cyanophage S-RIM44	GCA_002599225.1
AOO12286.1	000768	2OG-FeII_Oxy_5	209	Np420711_104	Cyanophage S-RIM44	GCA_002599225.1
AOO12288.1	000768	2OG-FeII_Oxy_5	190	Np420711_106	Cyanophage S-RIM44	GCA_002599225.1
AOO12448.1	000768	2OG-FeII_Oxy_5	205	Sn080709_030	Cyanophage S-RIM44	GCA_002599245.1
AOO12520.1	000768	2OG-FeII_Oxy_5	199	Sn080709_103	Cyanophage S-RIM44	GCA_002599245.1
AOO12617.1	000768	2OG-FeII_Oxy_5	170	Sn080709_204	Cyanophage S-RIM44	GCA_002599245.1
AOO12675.1	000768	2OG-FeII_Oxy_5	205	Sn130910_027	Cyanophage S-RIM44	GCA_002599265.1
AOO12719.1	000768	2OG-FeII_Oxy_5	207	Sn130910_072	Cyanophage S-RIM44	GCA_002599265.1
AOO12751.1	000768	2OG-FeII_Oxy_5	209	Sn130910_104	Cyanophage S-RIM44	GCA_002599265.1
AOO12753.1	000768	2OG-FeII_Oxy_5	190	Sn130910_106	Cyanophage S-RIM44	GCA_002599265.1
AOO12913.1	000768	2OG-FeII_Oxy_5	205	W2100709_030	Cyanophage S-RIM44	GCA_002599285.1
AOO12986.1	000768	2OG-FeII_Oxy_5	199	W2100709_104	Cyanophage S-RIM44	GCA_002599285.1
AOO13083.1	000768	2OG-FeII_Oxy_5	170	W2100709_205	Cyanophage S-RIM44	GCA_002599285.1
AGH07500.1	000768	2OG-FeII_Oxy_5	219	CYVG_00056	Cyanophage S-SSM6a	GCA_002710385.1
AGH07562.1	000768	2OG-FeII_Oxy_5	215	CYVG_00118	Cyanophage S-SSM6a	GCA_002710385.1
AGH07579.1	000768	2OG-FeII_Oxy_5	177	CYVG_00135	Cyanophage S-SSM6a	GCA_002710385.1
AGH07648.1	000768	2OG-FeII_Oxy_5	174	CYVG_00205	Cyanophage S-SSM6a	GCA_002710385.1
AGH07663.1	000768	2OG-FeII_Oxy_5	214	CYVG_00220	Cyanophage S-SSM6a	GCA_002710385.1
AGH07664.1	000768	2OG-FeII_Oxy_5	233	CYVG_00221	Cyanophage S-SSM6a	GCA_002710385.1
AGH07665.1	000768	2OG-FeII_Oxy_5	235	CYVG_00222	Cyanophage S-SSM6a	GCA_002710385.1
AGH07671.1	000768	2OG-FeII_Oxy_5	198	CYVG_00228	Cyanophage S-SSM6a	GCA_002710385.1
AGG54312.1	000768	2OG-FeII_Oxy_5	233	CYWG_00028	Cyanophage S-SSM6b	GCA_002710425.1
AGG54356.1	000768	2OG-FeII_Oxy_5	184	CYWG_00072	Cyanophage S-SSM6b	GCA_002710425.1
AGG54368.1	000768	2OG-FeII_Oxy_5	245	CYWG_00084	Cyanophage S-SSM6b	GCA_002710425.1
AGG54373.1	000768	2OG-FeII_Oxy_5	203	CYWG_00089	Cyanophage S-SSM6b	GCA_002710425.1
AGG54390.1	000768	2OG-FeII_Oxy_5	222	CYWG_00106	Cyanophage S-SSM6b	GCA_002710425.1
AGG54469.1	000768	2OG-FeII_Oxy_5	177	CYWG_00185	Cyanophage S-SSM6b	GCA_002710425.1
AGH26122.1	000768	2OG-FeII_Oxy_5	196	CPMG_00021	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26177.1	000768	2OG-FeII_Oxy_5	205	CPMG_00076	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26254.1	000768	2OG-FeII_Oxy_5	208	CPMG_00153	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26282.1	000768	2OG-FeII_Oxy_5	215	CPMG_00182	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44380.1	000768	2OG-FeII_Oxy_5	210	PSSM2_002	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44483.1	000768	2OG-FeII_Oxy_5	213	PSSM2_105	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44514.1	000768	2OG-FeII_Oxy_5	194	PSSM2_136	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44526.1	000768	2OG-FeII_Oxy_5	195	PSSM2_148	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44533.1	000768	2OG-FeII_Oxy_5	226	PSSM2_155	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44537.1	000768	2OG-FeII_Oxy_5	194	PSSM2_159	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44538.1	000768	2OG-FeII_Oxy_5	185	PSSM2_160	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44562.1	000768	2OG-FeII_Oxy_5	233	PSSM2_184	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44596.1	000768	2OG-FeII_Oxy_5	188	PSSM2_219	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44639.1	000768	2OG-FeII_Oxy_5	203	PSSM2_262	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44697.1	000768	2OG-FeII_Oxy_5	196	PSSM2_319	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12165.1	000768	2OG-FeII_Oxy_5	213	PRTG_00007	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12267.1	000768	2OG-FeII_Oxy_5	210	PRTG_00113	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12279.1	000768	2OG-FeII_Oxy_5	196	PRTG_00126	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12332.1	000768	2OG-FeII_Oxy_5	203	PRTG_00179	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12374.1	000768	2OG-FeII_Oxy_5	188	PRTG_00221	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12410.1	000768	2OG-FeII_Oxy_5	227	PRTG_00258	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12433.1	000768	2OG-FeII_Oxy_5	185	PRTG_00283	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12434.1	000768	2OG-FeII_Oxy_5	194	PRTG_00284	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12438.1	000768	2OG-FeII_Oxy_5	226	PRTG_00288	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12442.1	000768	2OG-FeII_Oxy_5	195	PRTG_00293	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12452.1	000768	2OG-FeII_Oxy_5	194	PRTG_00305	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99128.1	000768	2OG-FeII_Oxy_5	119	Syn1_026	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99205.1	000768	2OG-FeII_Oxy_5	199	Syn1_104	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99304.1	000768	2OG-FeII_Oxy_5	170	Syn1_207	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76090.1	000768	2OG-FeII_Oxy_5	157	PBI_BELLAMY_45	Synechococcus phage Bellamy	GCA_002627525.1
ASR76093.1	000768	2OG-FeII_Oxy_5	183	PBI_BELLAMY_48	Synechococcus phage Bellamy	GCA_002627525.1
QCW23028.1	000768	2OG-FeII_Oxy_5	202	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50613.1	000768	2OG-FeII_Oxy_5	103	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50517.1	000768	2OG-FeII_Oxy_5	202	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59502.1	000768	2OG-FeII_Oxy_5	192	S330809_041	Synechococcus phage S-CAM4	GCA_002366065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59523.1	000768	2OG-FeII_Oxy_5	199	S330809_062	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59530.1	000768	2OG-FeII_Oxy_5	180	S330809_069	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59559.1	000768	2OG-FeII_Oxy_5	228	S330809_098	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59567.1	000768	2OG-FeII_Oxy_5	214	S330809_106	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59264.1	000768	2OG-FeII_Oxy_5	192	C440309_041	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59285.1	000768	2OG-FeII_Oxy_5	199	C440309_062	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59292.1	000768	2OG-FeII_Oxy_5	180	C440309_069	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59321.1	000768	2OG-FeII_Oxy_5	228	C440309_098	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59329.1	000768	2OG-FeII_Oxy_5	214	C440309_106	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59740.1	000768	2OG-FeII_Oxy_5	192	N231010_041	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59761.1	000768	2OG-FeII_Oxy_5	199	N231010_062	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59768.1	000768	2OG-FeII_Oxy_5	182	N231010_069	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59797.1	000768	2OG-FeII_Oxy_5	228	N231010_098	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59805.1	000768	2OG-FeII_Oxy_5	214	N231010_106	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70555.1	000768	2OG-FeII_Oxy_5	190	HOU04_gp156	Synechococcus phage S-T4	GCA_003443335.1
AXQ70521.1	000768	2OG-FeII_Oxy_5	209	HOU04_gp122	Synechococcus phage S-T4	GCA_003443335.1
APU01502.1	000769	MobE-homing-endonuclease	219	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22559.1	000769	MobE-homing-endonuclease	251	Ah1_00018	Aeromonas phage Ah1	GCA_002957415.1
QAX98493.1	000769	MobE-homing-endonuclease	263	ASfcp2_156	Aeromonas phage AsFcp_2	GCA_004146885.1
ADM79979.1	000769	MobE-homing-endonuclease	247	phiAS5_ORF0136	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53123.1	000769	MobE-homing-endonuclease	219	65p115	Aeromonas virus 65	GCA_000893255.1
AAQ17703.1	000769	MobE-homing-endonuclease	237	mobE	Aeromonas virus Aeh1	GCA_000843245.1
AON97067.1	000769	MobE-homing-endonuclease	236	E_058	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97271.1	000769	MobE-homing-endonuclease	213	E_263	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70824.1	000769	MobE-homing-endonuclease	265	phiC120_c118	Escherichia phage phiC120	GCA_002621185.1
AAX78738.1	000769	MobE-homing-endonuclease	204	RB43ORF216w	Escherichia virus RB43	GCA_000863505.1
AXH72807.1	000769	MobE-homing-endonuclease	278	-	Myoviridae sp.	GCA_003657725.1
AGR47680.2	000769	MobE-homing-endonuclease	217	SmphiM12_048	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12942.1	000769	MobE-homing-endonuclease	217	PHIM19_35	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12582.1	000769	MobE-homing-endonuclease	217	PHIM7_34	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13580.1	000769	MobE-homing-endonuclease	218	PHIN3_317	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13320.1	000769	MobE-homing-endonuclease	221	PHIN3_55	Sinorhizobium phage phiN3	GCA_001501175.1
QCW23038.1	000769	MobE-homing-endonuclease	141	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50725.1	000769	MobE-homing-endonuclease	141	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50703.1	000769	MobE-homing-endonuclease	167	-	Synechococcus phage S-B43	GCA_006869725.1
QHJ74487.1	000769	MobE-homing-endonuclease	181	VH12019_00160	Vibrio phage VH1_2019	GCA_009931825.1
QAU04483.1	000769	MobE-homing-endonuclease	242	ValB1MD_103	Vibrio phage ValB1MD	GCA_004138815.1
ALP47430.1	000769	MobE-homing-endonuclease	233	phiST2_0369	Vibrio phage phi-ST2	GCA_002757135.1
ALY07087.1	000769	MobE-homing-endonuclease	274	VmeM32_00098	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37507.1	000769	MobE-homing-endonuclease	223	pp2_274	Vibriophage phi-pp2	GCA_002630725.1
AFN37312.1	000769	MobE-homing-endonuclease	208	pp2_079	Vibriophage phi-pp2	GCA_002630725.1
AFN37352.1	000769	MobE-homing-endonuclease	233	pp2_119	Vibriophage phi-pp2	GCA_002630725.1
AMM44945.1	000769	MobE-homing-endonuclease	230	SP15_147	Bacillus phage SP-15	GCA_001754685.1
QDH83676.1	000770	Uri-nuclease+HTH	293	H1O15_gp135	Achromobacter phage Motura	GCA_006964305.1
AUE22553.1	000770	Uri-nuclease+HTH	122	Ah1_00012	Aeromonas phage Ah1	GCA_002957415.1
QAX98465.1	000770	Uri-nuclease+HTH	213	ASfcp2_125	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52925.1	000770	Uri-nuclease+HTH	227	PX29p206	Aeromonas phage PX29	GCA_000920195.1
AUZ94960.1	000770	Uri-nuclease+HTH	237	FDI40_gp178	Agrobacterium phage Atu_ph07	GCA_002628245.1
QDJ96536.1	000770	Uri-nuclease+HTH	283	Xoosp13_350	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AMM44902.1	000770	Uri-nuclease+HTH	445	SP15_103	Bacillus phage SP-15	GCA_001754685.1
AMM44909.1	000770	Uri-nuclease+HTH	230	SP15_110	Bacillus phage SP-15	GCA_001754685.1
AEO93564.1	000770	Uri-nuclease+HTH	270	G_305	Bacillus virus G	GCA_000917535.1
AEO93589.1	000770	Uri-nuclease+HTH	265	G_330	Bacillus virus G	GCA_000917535.1
QDJ96468.1	000770	Uri-nuclease+HTH	260	Xoosp13_282	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AEO93840.1	000770	Uri-nuclease+HTH	210	G_595	Bacillus virus G	GCA_000917535.1
QNJ54633.1	000770	Uri-nuclease+HTH	194	vBValMR10Z_92	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QBX06577.1	000770	Uri-nuclease+HTH	298	BcepSaruman_164	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06642.1	000770	Uri-nuclease+HTH	317	BcepSaruman_229	Burkholderia phage BcepSaruman	GCA_004771375.1
ALP47453.1	000770	Uri-nuclease+HTH	194	phiST2_0326	Vibrio phage phi-ST2	GCA_002757135.1
QBQ74634.1	000770	Uri-nuclease+HTH	245	BcepSauron_254	Burkholderia phage BcepSauron	GCA_005394215.1
AON97232.1	000770	Uri-nuclease+HTH	212	E_224	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97266.1	000770	Uri-nuclease+HTH	283	E_258	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXG66752.1	000770	Uri-nuclease+HTH	266	JA29_026	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
ALP47050.1	000770	Uri-nuclease+HTH	238	phiGrn1_0098	Vibrio phage phi-Grn1	GCA_002757115.1
ASU03483.1	000770	Uri-nuclease+HTH	264	RISINGSUN_187	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AGN30131.1	000770	Uri-nuclease+HTH	167	VPFG_00129	Vibrio phage nt-1	GCA_000910195.2
AJT61075.1	000770	Uri-nuclease+HTH	216	AVU32_gp234	Vibrio phage ValKK3	GCA_001501635.1
QAU04576.1	000770	Uri-nuclease+HTH	221	ValB1MD_319	Vibrio phage ValB1MD	GCA_004138815.1
QHJ74482.1	000770	Uri-nuclease+HTH	200	VH12019_00155	Vibrio phage VH1_2019	GCA_009931825.1
AIX30769.1	000770	Uri-nuclease+HTH	165	Syn7803US37_292	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30623.1	000770	Uri-nuclease+HTH	168	Syn7803US37_146	Synechococcus phage ACG-2014f	GCA_002594065.1
AKF13312.1	000770	Uri-nuclease+HTH	215	PHIN3_47	Sinorhizobium phage phiN3	GCA_001501175.1
ASV44381.1	000770	Uri-nuclease+HTH	320	PBI_SCTP2_366	Salicola phage SCTP-2	GCA_002625545.1
AKF13578.1	000770	Uri-nuclease+HTH	286	PHIN3_315	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13513.1	000770	Uri-nuclease+HTH	208	PHIN3_250	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47772.2	000770	Uri-nuclease+HTH	269	SmphiM12_140	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47802.1	000770	Uri-nuclease+HTH	178	SmphiM12_170	Sinorhizobium phage phiM12	GCA_001023565.1
AGR48118.1	000770	Uri-nuclease+HTH	264	SmphiM12_486	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13018.1	000770	Uri-nuclease+HTH	178	PHIM19_112	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13099.1	000770	Uri-nuclease+HTH	241	PHIM19_194	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13001.1	000770	Uri-nuclease+HTH	269	PHIM19_95	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12658.1	000770	Uri-nuclease+HTH	178	PHIM7_111	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12739.1	000770	Uri-nuclease+HTH	241	PHIM7_194	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12641.1	000770	Uri-nuclease+HTH	269	PHIM7_94	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13390.1	000770	Uri-nuclease+HTH	178	PHIN3_125	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13469.1	000770	Uri-nuclease+HTH	241	PHIN3_206	Sinorhizobium phage phiN3	GCA_001501175.1
prev15ph1000000458	000770	Uri-nuclease+HTH	254	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93614.1	000770	Uri-nuclease+HTH	356	G_355	Bacillus virus G	GCA_000917535.1
QDJ96356.1	000770	Uri-nuclease+HTH	270	Xoosp13_169	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54893.1	000770	Uri-nuclease+HTH	253	b23_0280	Synechococcus phage B23	GCA_009745195.1
QGT54673.1	000770	Uri-nuclease+HTH	207	b23_0045	Synechococcus phage B23	GCA_009745195.1
QGT54303.1	000770	Uri-nuclease+HTH	207	b3_0045	Synechococcus phage B3	GCA_009745215.1
QGT54528.1	000770	Uri-nuclease+HTH	253	b3_0287	Synechococcus phage B3	GCA_009745215.1
QIG65987.1	000770	Uri-nuclease+HTH	199	phiOC_p345	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BAS04860.1	000770	Uri-nuclease+HTH	305	AVU11_gp068	Ralstonia phage RSF1	GCA_001500875.1
QGT54957.1	000770	Uri-nuclease+HTH	221	b23_0351	Synechococcus phage B23	GCA_009745195.1
QGT54592.1	000770	Uri-nuclease+HTH	221	b3_0357	Synechococcus phage B3	GCA_009745215.1
AEH03502.1	000770	Uri-nuclease+HTH	397	078	Pseudomonas phage PhiPA3	GCA_001502095.1
QDB71124.1	000770	Uri-nuclease+HTH	448	CPT_Moabite_094	Serratia phage Moabite	GCA_006384735.1
ASU03726.1	000770	Uri-nuclease+HTH	264	JOAD_189	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ATA65697.1	000770	Uri-nuclease+HTH	304	2050HW_00362	Serratia phage 2050HW	GCA_002628125.1
SOK58576.1	000770	Uri-nuclease+HTH	245	g299	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ATN94671.1	000770	Uri-nuclease+HTH	269	SL2_094	Pseudomonas phage SL2	GCA_002956015.1
QBJ02918.1	000770	Uri-nuclease+HTH	185	PSA21_392	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02567.1	000770	Uri-nuclease+HTH	216	PSA21_37	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02599.1	000770	Uri-nuclease+HTH	193	PSA21_70	Pseudomonas phage Psa21	GCA_004340405.1
AAQ64216.1	000770	Uri-nuclease+HTH	231	KVP40.0146	Vibrio phage KVP40	GCA_000843785.1
QHJ74327.1	000770	Uri-nuclease+HTH	231	VH12019_00408	Vibrio phage VH1_2019	GCA_009931825.1
ALP47432.1	000770	Uri-nuclease+HTH	231	phiST2_0012	Vibrio phage phi-ST2	GCA_002757135.1
APU01479.1	000771	T4-gp15_tss	274	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28719.1	000771	T4-gp15_tss	270	AP1_001	Aeromonas phage AP1	GCA_014183365.1
ATI17418.1	000771	T4-gp15_tss	270	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00178.1	000771	T4-gp15_tss	253	HWB28_gp374	Aeromonas phage AS-zj	GCA_002627665.1
AUE22751.1	000771	T4-gp15_tss	276	Ah1_00233	Aeromonas phage Ah1	GCA_002957415.1
QAX98468.1	000771	T4-gp15_tss	274	ASfcp2_128	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97858.1	000771	T4-gp15_tss	270	ASswx1_215	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01292.1	000771	T4-gp15_tss	272	ASwh1_229	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39545.1	000771	T4-gp15_tss	270	CC2_319	Aeromonas phage CC2	GCA_000903495.1
ADQ52928.1	000771	T4-gp15_tss	258	PX29p209	Aeromonas phage PX29	GCA_000920195.1
ADM79852.1	000771	T4-gp15_tss	273	phiAS5_ORF0009	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53102.1	000771	T4-gp15_tss	274	65p092	Aeromonas virus 65	GCA_000893255.1
AAQ17876.1	000771	T4-gp15_tss	275	15	Aeromonas virus Aeh1	GCA_000843245.1
ASV44717.1	000771	T4-gp15_tss	457	FDI40_gp140	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANS05985.1	000771	T4-gp15_tss	274	ABCD_0206	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64889.1	000771	T4-gp15_tss	281	S13_090	Cronobacter phage S13	GCA_001503575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21677.1	000771	T4-gp15_tss	445	GAP32_227	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97221.1	000771	T4-gp15_tss	273	E_213	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56920.1	000771	T4-gp15_tss	309	CPXG_00117	Cyanophage P-RSM6	GCA_000906155.1
AJK27537.1	000771	T4-gp15_tss	264	PTIM40_110	Cyanophage P-TIM40	GCA_001470935.1
AOO14296.1	000771	T4-gp15_tss	278	Sn110110_102	Cyanophage S-RIM14	GCA_002599065.1
AOO14945.1	000771	T4-gp15_tss	278	W1230910_099	Cyanophage S-RIM14	GCA_002599125.1
AMO43126.1	000771	T4-gp15_tss	266	R1080702_117	Cyanophage S-RIM32	GCA_001754165.1
AMO43351.1	000771	T4-gp15_tss	266	W270710_107	Cyanophage S-RIM44	GCA_002599145.1
AOO11595.1	000771	T4-gp15_tss	266	ES420910_114	Cyanophage S-RIM44	GCA_002599165.1
AOO11823.1	000771	T4-gp15_tss	266	Np050604_107	Cyanophage S-RIM44	GCA_002599185.1
AOO12060.1	000771	T4-gp15_tss	266	Np200711_114	Cyanophage S-RIM44	GCA_002599205.1
AOO12296.1	000771	T4-gp15_tss	266	Np420711_114	Cyanophage S-RIM44	GCA_002599225.1
AOO12524.1	000771	T4-gp15_tss	266	Sn080709_107	Cyanophage S-RIM44	GCA_002599245.1
AOO12761.1	000771	T4-gp15_tss	266	Sn130910_114	Cyanophage S-RIM44	GCA_002599265.1
AOO12990.1	000771	T4-gp15_tss	266	W2100709_108	Cyanophage S-RIM44	GCA_002599285.1
AGH07450.1	000771	T4-gp15_tss	360	CYVG_00006	Cyanophage S-SSM6a	GCA_002710385.1
AGG54288.1	000771	T4-gp15_tss	259	CYWG_00004	Cyanophage S-SSM6b	GCA_002710425.1
AIT14469.1	000771	T4-gp15_tss	447	PBI_121Q_579	Escherichia phage 121Q	GCA_000926855.1
QAY00478.1	000771	T4-gp15_tss	447	Ecwhy1_199	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35221.1	000771	T4-gp15_tss	447	ACQ29_gp541	Escherichia phage PBECO4	GCA_001041035.1
BBM62142.1	000771	T4-gp15_tss	447	EO157G_5530	Escherichia phage SP27	GCA_008033345.1
AXC36793.1	000771	T4-gp15_tss	447	-	Escherichia phage UB	GCA_003341455.1
ARM70724.1	000771	T4-gp15_tss	273	phiC120_c17	Escherichia phage phiC120	GCA_002621185.1
QBO61833.1	000771	T4-gp15_tss	447	G17_00344	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13877.1	000771	T4-gp15_tss	447	vBEcoMphAPEC6_gp248	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80454.1	000771	T4-gp15_tss	447	PSLUR01_00477	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78739.1	000771	T4-gp15_tss	246	RB43ORF217w	Escherichia virus RB43	GCA_000863505.1
AFA44340.1	000771	T4-gp15_tss	441	RaK2_00067	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72824.1	000771	T4-gp15_tss	474	-	Myoviridae sp.	GCA_003657725.1
QHJ79050.1	000771	T4-gp15_tss	281	-	Myoviridae sp.	GCA_012593985.1
QIG65704.1	000771	T4-gp15_tss	265	phiOC_p038	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43798.1	000771	T4-gp15_tss	445	CBB_233	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26116.1	000771	T4-gp15_tss	291	CPMG_00015	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44500.1	000771	T4-gp15_tss	280	PSSM2_122	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12466.1	000771	T4-gp15_tss	280	PRTG_00319	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93434.1	000771	T4-gp15_tss	332	AVU42_gp094	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99209.1	000771	T4-gp15_tss	266	Syn1_108	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76044.1	000771	T4-gp15_tss	456	EST35_0162	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44255.1	000771	T4-gp15_tss	453	PBI_SCTP2_240	Salicola phage SCTP-2	GCA_002625545.1
QCW18949.1	000771	T4-gp15_tss	445	7t3_0428	Salmonella phage 7t3	GCA_006083215.1
AZU98203.1	000771	T4-gp15_tss	445	CPT_Munch_259	Salmonella phage Munch	GCA_004015485.1
QIG62781.1	000771	T4-gp15_tss	445	SEPL_168	Salmonella phage SE_PL	GCA_011067555.1
AQW88757.1	000771	T4-gp15_tss	445	BF_0232	Serratia phage BF	GCA_002619745.1
AGR47749.1	000771	T4-gp15_tss	268	SmphiM12_117	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13267.1	000771	T4-gp15_tss	268	PHIM19_85	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12907.1	000771	T4-gp15_tss	268	PHIM7_84	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13363.1	000771	T4-gp15_tss	268	PHIN3_99	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30603.1	000771	T4-gp15_tss	266	Syn7803US37_126	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54878.1	000771	T4-gp15_tss	333	b23_0264	Synechococcus phage B23	GCA_009745195.1
QGT54513.1	000771	T4-gp15_tss	333	b3_0271	Synechococcus phage B3	GCA_009745215.1
ASR76164.1	000771	T4-gp15_tss	333	PBI_BELLAMY_119	Synechococcus phage Bellamy	GCA_002627525.1
QCW22869.1	000771	T4-gp15_tss	332	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50489.1	000771	T4-gp15_tss	332	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59571.1	000771	T4-gp15_tss	266	S330809_110	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59333.1	000771	T4-gp15_tss	266	C440309_110	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59809.1	000771	T4-gp15_tss	266	N231010_110	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70588.1	000771	T4-gp15_tss	193	HOU04_gp189	Synechococcus phage S-T4	GCA_003443335.1
QJT70104.1	000771	T4-gp15_tss	333	SynMITS9220M01_091	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64421.1	000771	T4-gp15_tss	450	KVP40.0352	Vibrio phage KVP40	GCA_000843785.1
QIW90366.1	000771	T4-gp15_tss	434	GCAPEGMB_00019	Vibrio phage V07	GCA_012361095.1
QIW91063.1	000771	T4-gp15_tss	434	COHAPHLL_00200	Vibrio phage V09	GCA_012361135.1
QHJ74535.1	000771	T4-gp15_tss	450	VH12019_00235	Vibrio phage VH1_2019	GCA_009931825.1
AGB06993.1	000771	T4-gp15_tss	319	CF80_gp206	Vibrio phage VH7D	GCA_000914495.1
QBX06121.1	000771	T4-gp15_tss	319	ValB1HC_167	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04512.1	000771	T4-gp15_tss	455	ValB1MD_173	Vibrio phage ValB1MD	GCA_004138815.1
AJT61133.1	000771	T4-gp15_tss	319	AVU32_gp292	Vibrio phage ValKK3	GCA_001501635.1
AGN30025.2	000771	T4-gp15_tss	378	VPFG_00017	Vibrio phage nt-1	GCA_000910195.2
ALP47013.1	000771	T4-gp15_tss	319	phiGrn1_0086	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47383.1	000771	T4-gp15_tss	353	phiST2_0218	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54746.1	000771	T4-gp15_tss	319	vBValMR10Z_206	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07099.1	000771	T4-gp15_tss	245	VmeM32_00110	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37584.1	000771	T4-gp15_tss	377	pp2_352	Vibriophage phi-pp2	GCA_002630725.1
BBA65516.1	000771	T4-gp15_tss	269	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96516.1	000771	T4-gp15_tss	269	Xoosp13_330	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59038.1	000771	T4-gp15_tss	445	g230c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58503.1	000771	T4-gp15_tss	445	g226c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01481.1	000772	neck-protein	306	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28721.1	000772	neck-protein	306	AP1_003	Aeromonas phage AP1	GCA_014183365.1
ATI17416.1	000772	neck-protein	306	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00180.1	000772	neck-protein	306	HWB28_gp372	Aeromonas phage AS-zj	GCA_002627665.1
AUE22748.1	000772	neck-protein	278	Ah1_00230	Aeromonas phage Ah1	GCA_002957415.1
QAX98464.1	000772	neck-protein	307	ASfcp2_124	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97856.1	000772	neck-protein	306	ASswx1_213	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01294.1	000772	neck-protein	305	ASwh1_231	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39547.1	000772	neck-protein	306	CC2_321	Aeromonas phage CC2	GCA_000903495.1
ADQ52924.1	000772	neck-protein	307	PX29p205	Aeromonas phage PX29	GCA_000920195.1
ADM79849.1	000772	neck-protein	306	phiAS5_ORF0006	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53103.1	000772	neck-protein	306	65p095	Aeromonas virus 65	GCA_000893255.1
AAP04362.2	000772	neck-protein	306	13	Aeromonas virus Aeh1	GCA_000843245.1
ASV44720.1	000772	neck-protein	256	FDI40_gp143	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63699.1	000772	neck-protein	235	CP21_239	Campylobacter virus CP21	GCA_000902535.1
ANS05973.1	000772	neck-protein	307	ABCD_0204	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64891.1	000772	neck-protein	312	S13_092	Cronobacter phage S13	GCA_001503575.1
AFC21645.1	000772	neck-protein	261	GAP32_195	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97218.1	000772	neck-protein	307	E_210	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56922.1	000772	neck-protein	266	CPXG_00119	Cyanophage P-RSM6	GCA_000906155.1
AJK27535.1	000772	neck-protein	266	PTIM40_108	Cyanophage P-TIM40	GCA_001470935.1
AOO14294.1	000772	neck-protein	268	Sn110110_100	Cyanophage S-RIM14	GCA_002599065.1
AOO14943.1	000772	neck-protein	268	W1230910_097	Cyanophage S-RIM14	GCA_002599125.1
AMO43124.1	000772	neck-protein	276	R1080702_115	Cyanophage S-RIM32	GCA_001754165.1
AMO43349.1	000772	neck-protein	276	W270710_105	Cyanophage S-RIM44	GCA_002599145.1
AOO11593.1	000772	neck-protein	276	ES420910_112	Cyanophage S-RIM44	GCA_002599165.1
AOO11821.1	000772	neck-protein	276	Np050604_105	Cyanophage S-RIM44	GCA_002599185.1
AOO12058.1	000772	neck-protein	276	Np200711_112	Cyanophage S-RIM44	GCA_002599205.1
AOO12294.1	000772	neck-protein	276	Np420711_112	Cyanophage S-RIM44	GCA_002599225.1
AOO12522.1	000772	neck-protein	276	Sn080709_105	Cyanophage S-RIM44	GCA_002599245.1
AOO12759.1	000772	neck-protein	276	Sn130910_112	Cyanophage S-RIM44	GCA_002599265.1
AOO12988.1	000772	neck-protein	276	W2100709_106	Cyanophage S-RIM44	GCA_002599285.1
AGH07448.1	000772	neck-protein	272	CYVG_00004	Cyanophage S-SSM6a	GCA_002710385.1
AGG54290.1	000772	neck-protein	268	CYWG_00006	Cyanophage S-SSM6b	GCA_002710425.1
AIT14438.1	000772	neck-protein	268	PBI_121Q_548	Escherichia phage 121Q	GCA_000926855.1
QAY00511.1	000772	neck-protein	263	Ecwhy1_232	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34705.1	000772	neck-protein	258	ACQ29_gp025	Escherichia phage PBECO4	GCA_001041035.1
BBM62109.1	000772	neck-protein	263	EO157G_5200	Escherichia phage SP27	GCA_008033345.1
AXC36824.1	000772	neck-protein	263	-	Escherichia phage UB	GCA_003341455.1
ARM70722.1	000772	neck-protein	308	phiC120_c15	Escherichia phage phiC120	GCA_002621185.1
ARM70988.1	000772	neck-protein	313	phiC120_c283	Escherichia phage phiC120	GCA_002621185.1
QBO61864.1	000772	neck-protein	263	G17_00375	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13905.1	000772	neck-protein	263	vBEcoMphAPEC6_gp280c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80423.1	000772	neck-protein	263	PSLUR01_00446	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78736.1	000772	neck-protein	307	RB43ORF214w	Escherichia virus RB43	GCA_000863505.1
AFA44311.1	000772	neck-protein	266	RaK2_00038	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72722.1	000772	neck-protein	269	-	Myoviridae sp.	GCA_003657725.1
QHJ79048.1	000772	neck-protein	311	-	Myoviridae sp.	GCA_012593985.1
QIG65709.1	000772	neck-protein	247	phiOC_p043	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMM43766.1	000772	neck-protein	261	CBB_201	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26118.1	000772	neck-protein	271	CPMG_00017	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44498.1	000772	neck-protein	281	PSSM2_120	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12468.1	000772	neck-protein	281	PRTG_00321	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93432.1	000772	neck-protein	284	AVU42_gp092	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99207.1	000772	neck-protein	276	Syn1_106	Prochlorococcus phage Syn1	GCA_000892495.1
QCG76074.1	000772	neck-protein	250	EST35_0193	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44281.1	000772	neck-protein	254	PBI_SCTP2_266	Salicola phage SCTP-2	GCA_002625545.1
QCW18915.1	000772	neck-protein	262	7t3_0394	Salmonella phage 7t3	GCA_006083215.1
AZU98172.1	000772	neck-protein	262	CPT_Munch_228	Salmonella phage Munch	GCA_004015485.1
QIG62812.1	000772	neck-protein	262	SEPL_199	Salmonella phage SE_PL	GCA_011067555.1
AQW88722.1	000772	neck-protein	260	BF_0197	Serratia phage BF	GCA_002619745.1
AGR47751.1	000772	neck-protein	246	SmphiM12_119	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12993.1	000772	neck-protein	246	PHIM19_87	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12633.1	000772	neck-protein	246	PHIM7_86	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13365.1	000772	neck-protein	246	PHIN3_101	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30601.1	000772	neck-protein	297	Syn7803US37_124	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54876.1	000772	neck-protein	272	b23_0262	Synechococcus phage B23	GCA_009745195.1
QGT54511.1	000772	neck-protein	272	b3_0269	Synechococcus phage B3	GCA_009745215.1
ASR76162.1	000772	neck-protein	280	PBI_BELLAMY_117	Synechococcus phage Bellamy	GCA_002627525.1
QCW22826.1	000772	neck-protein	290	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50491.1	000772	neck-protein	290	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59569.1	000772	neck-protein	266	S330809_108	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59331.1	000772	neck-protein	266	C440309_108	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59807.1	000772	neck-protein	266	N231010_108	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70590.1	000772	neck-protein	279	HOU04_gp191	Synechococcus phage S-T4	GCA_003443335.1
QJT70102.1	000772	neck-protein	282	SynMITS9220M01_089	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64419.1	000772	neck-protein	307	KVP40.0350	Vibrio phage KVP40	GCA_000843785.1
QIW90364.1	000772	neck-protein	307	GCAPEGMB_00017	Vibrio phage V07	GCA_012361095.1
QIW91065.1	000772	neck-protein	307	COHAPHLL_00202	Vibrio phage V09	GCA_012361135.1
QHJ74533.1	000772	neck-protein	307	VH12019_00233	Vibrio phage VH1_2019	GCA_009931825.1
AGB06991.1	000772	neck-protein	309	CF80_gp204	Vibrio phage VH7D	GCA_000914495.1
QBX06123.1	000772	neck-protein	309	ValB1HC_169	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04540.1	000772	neck-protein	242	ValB1MD_253	Vibrio phage ValB1MD	GCA_004138815.1
AJT61135.1	000772	neck-protein	309	AVU32_gp294	Vibrio phage ValKK3	GCA_001501635.1
AGN30023.1	000772	neck-protein	305	VPFG_00015	Vibrio phage nt-1	GCA_000910195.2
ALP47018.1	000772	neck-protein	309	phiGrn1_0084	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47398.1	000772	neck-protein	309	phiST2_0216	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54748.1	000772	neck-protein	309	vBValMR10Z_208	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07234.1	000772	neck-protein	304	VmeM32_00248	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37582.1	000772	neck-protein	307	pp2_350	Vibriophage phi-pp2	GCA_002630725.1
SOK59004.1	000772	neck-protein	260	g196	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58469.1	000772	neck-protein	260	g192	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70463.1	000773	HNH	343	CF8_0050	Aeromonas phage CF8	GCA_006384595.2
QDB70243.1	000773	HNH	346	CF8_0075	Aeromonas phage CF8	GCA_006384595.2
QDB70248.1	000773	HNH	345	CF8_0080	Aeromonas phage CF8	GCA_006384595.2
QDJ96768.1	000773	HNH	348	PS1_0010	Aeromonas phage PS1	GCA_007051165.2
QDJ96805.1	000773	HNH	343	PS1_0046	Aeromonas phage PS1	GCA_007051165.2
QDJ96810.1	000773	HNH	263	PS1_0051	Aeromonas phage PS1	GCA_007051165.2
QDJ96814.1	000773	HNH	347	PS1_0055	Aeromonas phage PS1	GCA_007051165.2
QDJ96822.1	000773	HNH	338	PS1_0063	Aeromonas phage PS1	GCA_007051165.2
QDJ96837.1	000773	HNH	441	PS1_0078	Aeromonas phage PS1	GCA_007051165.2
QDJ96849.1	000773	HNH	332	PS1_0090	Aeromonas phage PS1	GCA_007051165.2
QDJ96888.1	000773	HNH	276	PS1_0129	Aeromonas phage PS1	GCA_007051165.2
QDJ96658.1	000773	HNH	503	PS1_0147	Aeromonas phage PS1	GCA_007051165.2
QDJ96735.1	000773	HNH	455	PS1_0224	Aeromonas phage PS1	GCA_007051165.2
QFR59401.1	000773	HNH	348	PS2_0010	Aeromonas phage PS2	GCA_009388305.2
QFR59436.1	000773	HNH	343	PS2_0045	Aeromonas phage PS2	GCA_009388305.2
QFR59441.1	000773	HNH	263	PS2_0050	Aeromonas phage PS2	GCA_009388305.2
QFR59451.1	000773	HNH	117	PS2_0060	Aeromonas phage PS2	GCA_009388305.2
QFR59452.1	000773	HNH	210	PS2_0061	Aeromonas phage PS2	GCA_009388305.2
QFR59467.1	000773	HNH	441	PS2_0076	Aeromonas phage PS2	GCA_009388305.2
QFR59480.1	000773	HNH	251	PS2_0089	Aeromonas phage PS2	GCA_009388305.2
QFR59481.1	000773	HNH	332	PS2_0090	Aeromonas phage PS2	GCA_009388305.2
QFR59291.1	000773	HNH	494	PS2_0150	Aeromonas phage PS2	GCA_009388305.2
QFR59313.1	000773	HNH	348	PS2_0172	Aeromonas phage PS2	GCA_009388305.2
QFR59368.1	000773	HNH	455	PS2_0226	Aeromonas phage PS2	GCA_009388305.2
AMS01355.1	000773	HNH	184	AR9_g271	Bacillus phage AR9	GCA_001743835.1
AST99984.1	000773	HNH	184	PBI_PBS1_163	Bacillus virus PBS1	GCA_002601325.1
QBQ74604.1	000773	HNH	191	BcepSauron_224	Burkholderia phage BcepSauron	GCA_005394215.1
QBP07197.1	000773	HNH	278	REBECCA_90	Erwinia phage Rebecca	GCA_004521635.1
AUG85877.1	000773	HNH	277	BOSOLAPHORUS_90	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52191.1	000773	HNH	278	DM_93	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86195.1	000773	HNH	278	DESERTFOX_88	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03793.1	000773	HNH	310	JOAD_122	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03835.1	000773	HNH	172	JOAD_80	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86630.1	000773	HNH	170	MADMEL_202	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86518.1	000773	HNH	278	MADMEL_90	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86842.1	000773	HNH	277	MORTIMER_93	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51870.1	000773	HNH	277	RAY_89	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03590.1	000773	HNH	172	RISINGSUN_80	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51554.1	000773	HNH	277	SIMMY50_92	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65012.1	000773	HNH	171	SPECIALG_203	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64902.1	000773	HNH	277	SPECIALG_92	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AXC36645.1	000773	HNH	174	-	Escherichia phage UB	GCA_003341455.1
QBO63862.1	000773	HNH	396	Goslar_00069	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63979.1	000773	HNH	336	Goslar_00186	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64021.1	000773	HNH	490	Goslar_00230	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72028.1	000773	HNH	265	N1M2_165	Klebsiella phage N1M2	GCA_010092605.1
QGH71926.1	000773	HNH	354	N1M2_63	Klebsiella phage N1M2	GCA_010092605.1
QGZ14559.1	000773	HNH	260	HWC77_gp196	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14513.1	000773	HNH	416	HWC77_gp150	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27119.1	000773	HNH	326	PPEV_gp025	Pseudomonas phage EL	GCA_000866825.1
CAG27279.1	000773	HNH	423	PPEV_gp185	Pseudomonas phage EL	GCA_000866825.1
ANM44833.1	000773	HNH	273	KTN4_075	Pseudomonas phage KTN4	GCA_002607225.1
ANM44834.1	000773	HNH	334	KTN4_076	Pseudomonas phage KTN4	GCA_002607225.1
AEH03633.1	000773	HNH	330	210	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02928.1	000773	HNH	240	PSA21_403	Pseudomonas phage Psa21	GCA_004340405.1
ATN94879.1	000773	HNH	273	SL2_302	Pseudomonas phage SL2	GCA_002956015.1
QJB22711.1	000773	HNH	273	fnug_68	Pseudomonas phage fnug	GCA_012837215.1
QJB22712.1	000773	HNH	366	fnug_69	Pseudomonas phage fnug	GCA_012837215.1
AAL82973.1	000773	HNH	316	PHIKZ072	Pseudomonas virus phiKZ	GCA_000842965.1
AAL82957.1	000773	HNH	334	PHIKZ056	Pseudomonas virus phiKZ	GCA_000842965.1
AAL83080.1	000773	HNH	357	PHIKZ179	Pseudomonas virus phiKZ	GCA_000842965.1
ASV44395.1	000773	HNH	175	PBI_SCTP2_380	Salicola phage SCTP-2	GCA_002625545.1
AZU97983.1	000773	HNH	165	CPT_Munch_039	Salmonella phage Munch	GCA_004015485.1
ATA65436.1	000773	HNH	328	2050HW_00101	Serratia phage 2050HW	GCA_002628125.1
AKF13102.1	000773	HNH	161	PHIM19_197	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12742.1	000773	HNH	161	PHIM7_197	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13472.1	000773	HNH	161	PHIN3_209	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30771.1	000773	HNH	155	Syn7803US37_294	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54864.1	000773	HNH	178	b23_0250	Synechococcus phage B23	GCA_009745195.1
QGT54499.1	000773	HNH	178	b3_0257	Synechococcus phage B3	GCA_009745215.1
QCW23070.1	000773	HNH	166	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50682.1	000773	HNH	166	-	Synechococcus phage S-B43	GCA_006869725.1
QAU04174.1	000773	HNH	260	HWC03_gp019	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04221.1	000773	HNH	416	HWC03_gp066	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23208.1	000773	HNH	323	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AXH70976.1	000773	HNH	240	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47520.1	000773	HNH	323	HWC35_gp126	Vibrio phage USC-1	GCA_006864065.1
BAW98359.1	000773	HNH	156	FDH33_gp150	Vibrio phage pTD1	GCA_002618825.1
QAX96766.1	000773	HNH	315	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96694.1	000773	HNH	449	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97085.1	000773	HNH	315	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX97012.1	000773	HNH	449	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96131.1	000773	HNH	315	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96058.1	000773	HNH	449	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96449.1	000773	HNH	315	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96376.1	000773	HNH	449	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20975.1	000773	HNH	317	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26310.1	000773	HNH	225	g287	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000220	000773	HNH	179	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000172	000773	HNH	179	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70417.1	000774	virion_structural-Cluster50_1clades	1140	CF8_0004	Aeromonas phage CF8	GCA_006384595.2
QDJ97425.1	000774	virion_structural-Cluster50_1clades	1149	D6_0266	Aeromonas phage D6	GCA_007051205.2
QDH47013.1	000774	virion_structural-Cluster50_1clades	1149	LAh10_173	Aeromonas phage LAh10	GCA_006863975.1
QDJ96762.1	000774	virion_structural-Cluster50_1clades	938	PS1_0004	Aeromonas phage PS1	GCA_007051165.2
QFR59395.1	000774	virion_structural-Cluster50_1clades	938	PS2_0004	Aeromonas phage PS2	GCA_009388305.2
AFO71442.1	000774	virion_structural-Cluster50_1clades	836	CR5_222	Cronobacter phage CR5	GCA_000910235.1
QBZ70811.1	000774	virion_structural-Cluster50_1clades	933	pETSU_230	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59910.1	000774	virion_structural-Cluster50_1clades	538	SEGD1_263	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59911.1	000774	virion_structural-Cluster50_1clades	295	SEGD1_264	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07656.1	000774	virion_structural-Cluster50_1clades	836	DERBICUS_230	Erwinia phage Derbicus	GCA_004521655.1
AHI60331.1	000774	virion_structural-Cluster50_1clades	850	Ea357_179	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49908.1	000774	virion_structural-Cluster50_1clades	841	MACHINA_270	Erwinia phage Machina	GCA_002758035.1
AGX01795.1	000774	virion_structural-Cluster50_1clades	851	CF95_gp073	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07290.1	000774	virion_structural-Cluster50_1clades	850	REBECCA_183	Erwinia phage Rebecca	GCA_004521635.1
AXF51409.1	000774	virion_structural-Cluster50_1clades	838	WELLINGTON_283	Erwinia phage Wellington	GCA_003344985.1
AFQ96721.1	000774	virion_structural-Cluster50_1clades	839	G173_gp176	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48292.1	000774	virion_structural-Cluster50_1clades	839	ASESINO_279	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85970.1	000774	virion_structural-Cluster50_1clades	850	BOSOLAPHORUS_183	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48563.1	000774	virion_structural-Cluster50_1clades	836	CAITLIN_268	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48841.1	000774	virion_structural-Cluster50_1clades	836	CHRISDB_279	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52285.1	000774	virion_structural-Cluster50_1clades	850	DM_187	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86289.1	000774	virion_structural-Cluster50_1clades	850	DESERTFOX_182	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49080.1	000774	virion_structural-Cluster50_1clades	836	EARLPHILLIPIV_231	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49351.1	000774	virion_structural-Cluster50_1clades	841	HUXLEY_269	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03671.1	000774	virion_structural-Cluster50_1clades	862	JOAD_244	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49634.1	000774	virion_structural-Cluster50_1clades	838	KWAN_282	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86611.1	000774	virion_structural-Cluster50_1clades	850	MADMEL_183	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86935.1	000774	virion_structural-Cluster50_1clades	850	MORTIMER_186	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50179.1	000774	virion_structural-Cluster50_1clades	841	PARSHIK_270	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50427.1	000774	virion_structural-Cluster50_1clades	836	PHOBOS_237	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51962.1	000774	virion_structural-Cluster50_1clades	850	RAY_181	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03428.1	000774	virion_structural-Cluster50_1clades	862	RISINGSUN_242	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51646.1	000774	virion_structural-Cluster50_1clades	850	SIMMY50_184	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64993.1	000774	virion_structural-Cluster50_1clades	850	SPECIALG_183	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50703.1	000774	virion_structural-Cluster50_1clades	839	STRATTON_278	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86099.1	000774	virion_structural-Cluster50_1clades	837	ACEC001_2560	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64007.1	000774	virion_structural-Cluster50_1clades	864	Goslar_00215	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72109.1	000774	virion_structural-Cluster50_1clades	937	N1M2_246	Klebsiella phage N1M2	GCA_010092605.1
QGZ14548.1	000774	virion_structural-Cluster50_1clades	860	HWC77_gp185	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24113.1	000774	virion_structural-Cluster50_1clades	852	-	Proteus phage 10	GCA_014071245.1
ABY62862.1	000774	virion_structural-Cluster50_1clades	883	201phi2-1p028	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27102.1	000774	virion_structural-Cluster50_1clades	870	PPEV_gp008	Pseudomonas phage EL	GCA_000866825.1
ANM44795.1	000774	virion_structural-Cluster50_1clades	898	KTN4_037	Pseudomonas phage KTN4	GCA_002607225.1
ARV77190.1	000774	virion_structural-Cluster50_1clades	895	NOXIFER_19	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89441.1	000774	virion_structural-Cluster50_1clades	936	OBP_004	Pseudomonas phage OBP	GCA_000896635.1
QBX32156.1	000774	virion_structural-Cluster50_1clades	898	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76648.1	000774	virion_structural-Cluster50_1clades	884	PHABIO_17	Pseudomonas phage Phabio	GCA_002624965.1
AEH03435.1	000774	virion_structural-Cluster50_1clades	823	009	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02539.1	000774	virion_structural-Cluster50_1clades	904	PSA21_9	Pseudomonas phage Psa21	GCA_004340405.1
ATN94916.1	000774	virion_structural-Cluster50_1clades	898	SL2_339	Pseudomonas phage SL2	GCA_002956015.1
QJB22674.1	000774	virion_structural-Cluster50_1clades	898	fnug_31	Pseudomonas phage fnug	GCA_012837215.1
QEM41737.1	000774	virion_structural-Cluster50_1clades	898	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82928.1	000774	virion_structural-Cluster50_1clades	898	PHIKZ027	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19000.1	000774	virion_structural-Cluster50_1clades	862	FDH28_gp026	Ralstonia phage RP12	GCA_002617345.1
BAW19288.1	000774	virion_structural-Cluster50_1clades	862	-	Ralstonia phage RP31	GCA_002617365.1
BAS04820.2	000774	virion_structural-Cluster50_1clades	826	AVU11_gp028	Ralstonia phage RSF1	GCA_001500875.1
BAQ02553.1	000774	virion_structural-Cluster50_1clades	866	AVU38_gp025	Ralstonia phage RSL2	GCA_001503055.1
QNI20941.1	000774	virion_structural-Cluster50_1clades	837	-	Salmonella phage JN03	GCA_014319805.1
AWN09095.2	000774	virion_structural-Cluster50_1clades	837	MLDJOKPK_00182	Salmonella phage SPAsTU	GCA_003183805.1
AEP84091.1	000774	virion_structural-Cluster50_1clades	837	SPN3US_0258	Salmonella phage SPN3US	GCA_001042275.1
QKE54491.1	000774	virion_structural-Cluster50_1clades	856	ACSA002_1770	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65605.1	000774	virion_structural-Cluster50_1clades	852	2050HW_00270	Serratia phage 2050HW	GCA_002628125.1
QDB71369.1	000774	virion_structural-Cluster50_1clades	852	CPT_Moabite_339	Serratia phage Moabite	GCA_006384735.1
QFP93051.1	000774	virion_structural-Cluster50_1clades	844	-	Serratia phage PCH45	GCA_009187865.1
QAU04186.1	000774	virion_structural-Cluster50_1clades	860	HWC03_gp031	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23173.1	000774	virion_structural-Cluster50_1clades	860	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80918.1	000774	virion_structural-Cluster50_1clades	860	Aphrodite1_0169	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70780.1	000774	virion_structural-Cluster50_1clades	843	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47556.1	000774	virion_structural-Cluster50_1clades	860	HWC35_gp162	Vibrio phage USC-1	GCA_006864065.1
BAW98371.1	000774	virion_structural-Cluster50_1clades	860	FDH33_gp162	Vibrio phage pTD1	GCA_002618825.1
AQT28124.1	000774	virion_structural-Cluster50_1clades	804	pVa21_183	Vibrio phage pVa-21	GCA_002619305.1
QAX96738.1	000774	virion_structural-Cluster50_1clades	947	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97057.1	000774	virion_structural-Cluster50_1clades	947	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96103.1	000774	virion_structural-Cluster50_1clades	947	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96421.1	000774	virion_structural-Cluster50_1clades	947	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21000.1	000774	virion_structural-Cluster50_1clades	883	-	Vibrio phage vB_pir03	GCA_014319855.1
QGY75123.1	000775	virion_structural-Cluster51_1clades	513	CF8_0109	Aeromonas phage CF8	GCA_006384595.2
QDJ97255.1	000775	virion_structural-Cluster51_1clades	516	D6_0095	Aeromonas phage D6	GCA_007051205.2
QDH47044.1	000775	virion_structural-Cluster51_1clades	516	LAh10_27	Aeromonas phage LAh10	GCA_006863975.1
QDJ96868.1	000775	virion_structural-Cluster51_1clades	503	PS1_0109	Aeromonas phage PS1	GCA_007051165.2
QFR59500.1	000775	virion_structural-Cluster51_1clades	503	PS2_0109	Aeromonas phage PS2	GCA_009388305.2
AFO71279.1	000775	virion_structural-Cluster51_1clades	495	CR5_059	Cronobacter phage CR5	GCA_000910235.1
QBZ70637.1	000775	virion_structural-Cluster51_1clades	533	pETSU_056	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59711.1	000775	virion_structural-Cluster51_1clades	500	SEGD1_062	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07486.1	000775	virion_structural-Cluster51_1clades	495	DERBICUS_60	Erwinia phage Derbicus	GCA_004521655.1
AHI60454.1	000775	virion_structural-Cluster51_1clades	518	Ea357_300	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49712.1	000775	virion_structural-Cluster51_1clades	508	MACHINA_74	Erwinia phage Machina	GCA_002758035.1
AGX01944.1	000775	virion_structural-Cluster51_1clades	510	CF95_gp222	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07411.1	000775	virion_structural-Cluster51_1clades	518	REBECCA_306	Erwinia phage Rebecca	GCA_004521635.1
AXF51204.1	000775	virion_structural-Cluster51_1clades	500	WELLINGTON_74	Erwinia phage Wellington	GCA_003344985.1
AFQ96790.1	000775	virion_structural-Cluster51_1clades	503	G173_gp245	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48091.1	000775	virion_structural-Cluster51_1clades	503	ASESINO_78	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86093.1	000775	virion_structural-Cluster51_1clades	518	BOSOLAPHORUS_307	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48364.1	000775	virion_structural-Cluster51_1clades	505	CAITLIN_69	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48637.1	000775	virion_structural-Cluster51_1clades	506	CHRISDB_75	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52409.1	000775	virion_structural-Cluster51_1clades	518	DM_310	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86413.1	000775	virion_structural-Cluster51_1clades	518	DESERTFOX_306	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48910.1	000775	virion_structural-Cluster51_1clades	495	EARLPHILLIPIV_60	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49157.1	000775	virion_structural-Cluster51_1clades	508	HUXLEY_75	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03840.1	000775	virion_structural-Cluster51_1clades	496	JOAD_75	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49426.1	000775	virion_structural-Cluster51_1clades	500	KWAN_74	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86734.1	000775	virion_structural-Cluster51_1clades	518	MADMEL_307	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87059.1	000775	virion_structural-Cluster51_1clades	518	MORTIMER_311	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49985.1	000775	virion_structural-Cluster51_1clades	508	PARSHIK_76	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50252.1	000775	virion_structural-Cluster51_1clades	496	PHOBOS_62	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52084.1	000775	virion_structural-Cluster51_1clades	518	RAY_304	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03595.1	000775	virion_structural-Cluster51_1clades	496	RISINGSUN_75	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51767.1	000775	virion_structural-Cluster51_1clades	518	SIMMY50_309	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65119.1	000775	virion_structural-Cluster51_1clades	518	SPECIALG_308	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50502.1	000775	virion_structural-Cluster51_1clades	503	STRATTON_77	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85902.1	000775	virion_structural-Cluster51_1clades	500	ACEC001_0640	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63844.1	000775	virion_structural-Cluster51_1clades	521	Goslar_00051	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71954.1	000775	virion_structural-Cluster51_1clades	528	N1M2_91	Klebsiella phage N1M2	GCA_010092605.1
QGZ14415.1	000775	virion_structural-Cluster51_1clades	532	HWC77_gp052	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24213.1	000775	virion_structural-Cluster51_1clades	515	-	Proteus phage 10	GCA_014071245.1
ABY62991.1	000775	virion_structural-Cluster51_1clades	553	201phi2-1p161	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27162.1	000775	virion_structural-Cluster51_1clades	497	PPEV_gp068	Pseudomonas phage EL	GCA_000866825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANM44883.1	000775	virion_structural-Cluster51_1clades	542	KTN4_125	Pseudomonas phage KTN4	GCA_002607225.1
ARV77504.1	000775	virion_structural-Cluster51_1clades	559	NOXIFER_97	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89555.1	000775	virion_structural-Cluster51_1clades	529	OBP_118	Pseudomonas phage OBP	GCA_000896635.1
QBX32260.1	000775	virion_structural-Cluster51_1clades	548	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76775.1	000775	virion_structural-Cluster51_1clades	548	PHABIO_144	Pseudomonas phage Phabio	GCA_002624965.1
AEH03527.1	000775	virion_structural-Cluster51_1clades	560	103	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02638.1	000775	virion_structural-Cluster51_1clades	540	PSA21_110	Pseudomonas phage Psa21	GCA_004340405.1
ATN94830.1	000775	virion_structural-Cluster51_1clades	542	SL2_253	Pseudomonas phage SL2	GCA_002956015.1
QJB22760.1	000775	virion_structural-Cluster51_1clades	542	fnug_117	Pseudomonas phage fnug	GCA_012837215.1
QEM41834.1	000775	virion_structural-Cluster51_1clades	548	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82999.1	000775	virion_structural-Cluster51_1clades	542	PHIKZ098	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19208.1	000775	virion_structural-Cluster51_1clades	527	FDH28_gp187	Ralstonia phage RP12	GCA_002617345.1
BAW19494.1	000775	virion_structural-Cluster51_1clades	527	-	Ralstonia phage RP31	GCA_002617365.1
BAS04969.2	000775	virion_structural-Cluster51_1clades	508	AVU11_gp177	Ralstonia phage RSF1	GCA_001500875.1
BAQ02694.2	000775	virion_structural-Cluster51_1clades	513	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20777.1	000775	virion_structural-Cluster51_1clades	500	-	Salmonella phage JN03	GCA_014319805.1
AWN09039.1	000775	virion_structural-Cluster51_1clades	504	MLDJOKPK_00103	Salmonella phage SPAsTU	GCA_003183805.1
AEP83894.1	000775	virion_structural-Cluster51_1clades	500	SPN3US_0061	Salmonella phage SPN3US	GCA_001042275.1
QKE54634.1	000775	virion_structural-Cluster51_1clades	512	ACSA002_3170	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65362.1	000775	virion_structural-Cluster51_1clades	284	2050HW_00027	Serratia phage 2050HW	GCA_002628125.1
ATA65363.1	000775	virion_structural-Cluster51_1clades	239	2050HW_00028	Serratia phage 2050HW	GCA_002628125.1
QDB71148.1	000775	virion_structural-Cluster51_1clades	516	CPT_Moabite_118	Serratia phage Moabite	GCA_006384735.1
QFP93070.1	000775	virion_structural-Cluster51_1clades	517	-	Serratia phage PCH45	GCA_009187865.1
QAU04321.1	000775	virion_structural-Cluster51_1clades	532	HWC03_gp166	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23257.1	000775	virion_structural-Cluster51_1clades	534	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80939.1	000775	virion_structural-Cluster51_1clades	534	Aphrodite1_0088	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70848.1	000775	virion_structural-Cluster51_1clades	537	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47471.1	000775	virion_structural-Cluster51_1clades	534	HWC35_gp077	Vibrio phage USC-1	GCA_006864065.1
BAW98292.1	000775	virion_structural-Cluster51_1clades	531	FDH33_gp083	Vibrio phage pTD1	GCA_002618825.1
AQT27943.1	000775	virion_structural-Cluster51_1clades	515	pVa21_001	Vibrio phage pVa-21	GCA_002619305.1
QAX96644.1	000775	virion_structural-Cluster51_1clades	531	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96962.1	000775	virion_structural-Cluster51_1clades	531	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96008.1	000775	virion_structural-Cluster51_1clades	531	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96326.1	000775	virion_structural-Cluster51_1clades	531	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21096.1	000775	virion_structural-Cluster51_1clades	534	-	Vibrio phage vB_pir03	GCA_014319855.1
QMV29161.1	000776	virion_structural-Cluster52_1clades	190	AP1_0463	Aeromonas phage AP1	GCA_014183365.1
QDB70278.1	000776	virion_structural-Cluster52_1clades	430	CF8_0110	Aeromonas phage CF8	GCA_006384595.2
QDJ97256.1	000776	virion_structural-Cluster52_1clades	431	D6_0096	Aeromonas phage D6	GCA_007051205.2
QDH47060.1	000776	virion_structural-Cluster52_1clades	431	LAh10_28	Aeromonas phage LAh10	GCA_006863975.1
QDJ96869.1	000776	virion_structural-Cluster52_1clades	431	PS1_0110	Aeromonas phage PS1	GCA_007051165.2
QFR59501.1	000776	virion_structural-Cluster52_1clades	431	PS2_0110	Aeromonas phage PS2	GCA_009388305.2
AFO71280.1	000776	virion_structural-Cluster52_1clades	444	CR5_060	Cronobacter phage CR5	GCA_000910235.1
QBZ70638.1	000776	virion_structural-Cluster52_1clades	432	pETSU_057	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59712.1	000776	virion_structural-Cluster52_1clades	451	SEGD1_063	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07487.1	000776	virion_structural-Cluster52_1clades	443	DERBICUS_61	Erwinia phage Derbicus	GCA_004521655.1
AHI60455.1	000776	virion_structural-Cluster52_1clades	409	Ea357_301	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49713.1	000776	virion_structural-Cluster52_1clades	443	MACHINA_75	Erwinia phage Machina	GCA_002758035.1
AGX01943.1	000776	virion_structural-Cluster52_1clades	436	CF95_gp221	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07412.1	000776	virion_structural-Cluster52_1clades	423	REBECCA_307	Erwinia phage Rebecca	GCA_004521635.1
AXF51205.1	000776	virion_structural-Cluster52_1clades	441	WELLINGTON_75	Erwinia phage Wellington	GCA_003344985.1
AFQ96791.1	000776	virion_structural-Cluster52_1clades	450	G173_gp246	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48092.1	000776	virion_structural-Cluster52_1clades	450	ASESINO_79	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86094.1	000776	virion_structural-Cluster52_1clades	423	BOSOLAPHORUS_308	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48365.1	000776	virion_structural-Cluster52_1clades	441	CAITLIN_70	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48638.1	000776	virion_structural-Cluster52_1clades	441	CHRISDB_76	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52410.2	000776	virion_structural-Cluster52_1clades	409	DM_311	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86414.1	000776	virion_structural-Cluster52_1clades	409	DESERTFOX_307	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48911.1	000776	virion_structural-Cluster52_1clades	443	EARLPHILLIPIV_61	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49158.1	000776	virion_structural-Cluster52_1clades	443	HUXLEY_76	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03839.1	000776	virion_structural-Cluster52_1clades	428	JOAD_76	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49427.1	000776	virion_structural-Cluster52_1clades	441	KWAN_75	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86735.1	000776	virion_structural-Cluster52_1clades	409	MADMEL_308	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87060.1	000776	virion_structural-Cluster52_1clades	409	MORTIMER_312	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49986.1	000776	virion_structural-Cluster52_1clades	443	PARSHIK_77	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50253.1	000776	virion_structural-Cluster52_1clades	444	PHOBOS_63	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52085.1	000776	virion_structural-Cluster52_1clades	409	RAY_305	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03594.1	000776	virion_structural-Cluster52_1clades	428	RISINGSUN_76	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51768.1	000776	virion_structural-Cluster52_1clades	409	SIMMY50_310	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65120.2	000776	virion_structural-Cluster52_1clades	409	SPECIALG_309	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50503.1	000776	virion_structural-Cluster52_1clades	450	STRATTON_78	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85903.1	000776	virion_structural-Cluster52_1clades	451	ACEC001_0650	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63843.1	000776	virion_structural-Cluster52_1clades	438	Goslar_00050	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71955.1	000776	virion_structural-Cluster52_1clades	433	N1M2_92	Klebsiella phage N1M2	GCA_010092605.1
QGZ14416.1	000776	virion_structural-Cluster52_1clades	429	HWC77_gp053	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24214.1	000776	virion_structural-Cluster52_1clades	442	-	Proteus phage 10	GCA_014071245.1
ABY62992.1	000776	virion_structural-Cluster52_1clades	471	201phi2-1p162	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27163.1	000776	virion_structural-Cluster52_1clades	431	PPEV_gp069	Pseudomonas phage EL	GCA_000866825.1
ANM44884.1	000776	virion_structural-Cluster52_1clades	469	KTN4_126	Pseudomonas phage KTN4	GCA_002607225.1
ARV77267.1	000776	virion_structural-Cluster52_1clades	468	NOXIFER_98	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89556.1	000776	virion_structural-Cluster52_1clades	432	OBP_119	Pseudomonas phage OBP	GCA_000896635.1
QBX32261.1	000776	virion_structural-Cluster52_1clades	468	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76776.1	000776	virion_structural-Cluster52_1clades	469	PHABIO_145	Pseudomonas phage Phabio	GCA_002624965.1
AEH03528.1	000776	virion_structural-Cluster52_1clades	472	104	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02639.1	000776	virion_structural-Cluster52_1clades	475	PSA21_111	Pseudomonas phage Psa21	GCA_004340405.1
ATN94829.1	000776	virion_structural-Cluster52_1clades	469	SL2_252	Pseudomonas phage SL2	GCA_002956015.1
QJB22761.1	000776	virion_structural-Cluster52_1clades	469	fnug_118	Pseudomonas phage fnug	GCA_012837215.1
QEM41835.1	000776	virion_structural-Cluster52_1clades	468	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83000.1	000776	virion_structural-Cluster52_1clades	469	PHIKZ099	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19207.1	000776	virion_structural-Cluster52_1clades	453	FDH28_gp188	Ralstonia phage RP12	GCA_002617345.1
BAW19493.1	000776	virion_structural-Cluster52_1clades	453	-	Ralstonia phage RP31	GCA_002617365.1
BAS04968.1	000776	virion_structural-Cluster52_1clades	449	AVU11_gp176	Ralstonia phage RSF1	GCA_001500875.1
BAQ02693.1	000776	virion_structural-Cluster52_1clades	449	AVU38_gp165	Ralstonia phage RSL2	GCA_001503055.1
QNI20778.1	000776	virion_structural-Cluster52_1clades	451	-	Salmonella phage JN03	GCA_014319805.1
AWN09038.1	000776	virion_structural-Cluster52_1clades	451	MLDJOKPK_00102	Salmonella phage SPAsTU	GCA_003183805.1
AEP83895.1	000776	virion_structural-Cluster52_1clades	451	SPN3US_0062	Salmonella phage SPN3US	GCA_001042275.1
QKE54635.1	000776	virion_structural-Cluster52_1clades	431	ACSA002_3180	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65364.1	000776	virion_structural-Cluster52_1clades	450	2050HW_00029	Serratia phage 2050HW	GCA_002628125.1
QDB71149.1	000776	virion_structural-Cluster52_1clades	450	CPT_Moabite_119	Serratia phage Moabite	GCA_006384735.1
QFP93080.1	000776	virion_structural-Cluster52_1clades	462	-	Serratia phage PCH45	GCA_009187865.1
QAU04320.1	000776	virion_structural-Cluster52_1clades	429	HWC03_gp165	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23258.1	000776	virion_structural-Cluster52_1clades	429	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80960.1	000776	virion_structural-Cluster52_1clades	429	Aphrodite1_0087	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70849.1	000776	virion_structural-Cluster52_1clades	400	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47470.1	000776	virion_structural-Cluster52_1clades	429	HWC35_gp076	Vibrio phage USC-1	GCA_006864065.1
BAW98291.1	000776	virion_structural-Cluster52_1clades	428	FDH33_gp082	Vibrio phage pTD1	GCA_002618825.1
AQT27944.1	000776	virion_structural-Cluster52_1clades	467	pVa21_002	Vibrio phage pVa-21	GCA_002619305.1
QAX96643.1	000776	virion_structural-Cluster52_1clades	406	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96961.1	000776	virion_structural-Cluster52_1clades	406	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96007.1	000776	virion_structural-Cluster52_1clades	406	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96325.1	000776	virion_structural-Cluster52_1clades	406	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21097.1	000776	virion_structural-Cluster52_1clades	405	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70376.1	000777	virion_structural-Cluster53_1clades	444	CF8_0207	Aeromonas phage CF8	GCA_006384595.2
QDJ97375.1	000777	virion_structural-Cluster53_1clades	445	D6_0216	Aeromonas phage D6	GCA_007051205.2
QDH47058.1	000777	virion_structural-Cluster53_1clades	445	LAh10_130	Aeromonas phage LAh10	GCA_006863975.1
QDJ96718.1	000777	virion_structural-Cluster53_1clades	444	PS1_0207	Aeromonas phage PS1	GCA_007051165.2
QFR59351.1	000777	virion_structural-Cluster53_1clades	444	PS2_0209	Aeromonas phage PS2	GCA_009388305.2
AFO71402.1	000777	virion_structural-Cluster53_1clades	445	CR5_182	Cronobacter phage CR5	GCA_000910235.1
QBZ70760.1	000777	virion_structural-Cluster53_1clades	445	pETSU_179	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59855.1	000777	virion_structural-Cluster53_1clades	226	SEGD1_208	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59856.1	000777	virion_structural-Cluster53_1clades	203	SEGD1_209	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07614.1	000777	virion_structural-Cluster53_1clades	445	DERBICUS_188	Erwinia phage Derbicus	GCA_004521655.1
AHI60295.1	000777	virion_structural-Cluster53_1clades	437	Ea357_144	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49852.1	000777	virion_structural-Cluster53_1clades	452	MACHINA_214	Erwinia phage Machina	GCA_002758035.1
AGX01901.1	000777	virion_structural-Cluster53_1clades	433	CF95_gp179	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07253.1	000777	virion_structural-Cluster53_1clades	437	REBECCA_146	Erwinia phage Rebecca	GCA_004521635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXF51354.1	000777	virion_structural-Cluster53_1clades	460	WELLINGTON_228	Erwinia phage Wellington	GCA_003344985.1
AFQ96669.1	000777	virion_structural-Cluster53_1clades	455	G173_gp124	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48235.1	000777	virion_structural-Cluster53_1clades	454	ASESINO_222	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85933.1	000777	virion_structural-Cluster53_1clades	437	BOSOLAPHORUS_146	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48509.1	000777	virion_structural-Cluster53_1clades	453	CAITLIN_214	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48786.1	000777	virion_structural-Cluster53_1clades	453	CHRISDB_224	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52248.1	000777	virion_structural-Cluster53_1clades	437	DM_150	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86252.1	000777	virion_structural-Cluster53_1clades	437	DESERTFOX_145	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49038.1	000777	virion_structural-Cluster53_1clades	445	EARLPHILLIPIV_189	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49296.1	000777	virion_structural-Cluster53_1clades	452	HUXLEY_214	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03699.1	000777	virion_structural-Cluster53_1clades	445	JOAD_216	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49580.1	000777	virion_structural-Cluster53_1clades	460	KWAN_228	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86574.1	000777	virion_structural-Cluster53_1clades	437	MADMEL_146	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86898.1	000777	virion_structural-Cluster53_1clades	437	MORTIMER_149	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50124.1	000777	virion_structural-Cluster53_1clades	452	PARSHIK_215	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50386.1	000777	virion_structural-Cluster53_1clades	444	PHOBOS_196	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51926.1	000777	virion_structural-Cluster53_1clades	437	RAY_145	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03456.1	000777	virion_structural-Cluster53_1clades	445	RISINGSUN_214	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51610.1	000777	virion_structural-Cluster53_1clades	437	SIMMY50_148	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64957.1	000777	virion_structural-Cluster53_1clades	437	SPECIALG_147	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50649.1	000777	virion_structural-Cluster53_1clades	455	STRATTON_224	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86043.1	000777	virion_structural-Cluster53_1clades	459	ACEC001_2000	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64039.1	000777	virion_structural-Cluster53_1clades	446	Goslar_00248	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72067.1	000777	virion_structural-Cluster53_1clades	443	N1M2_204	Klebsiella phage N1M2	GCA_010092605.1
QGZ14496.1	000777	virion_structural-Cluster53_1clades	442	HWC77_gp133	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24076.1	000777	virion_structural-Cluster53_1clades	437	-	Proteus phage 10	GCA_014071245.1
ABY63071.1	000777	virion_structural-Cluster53_1clades	449	201phi2-1p243	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27263.1	000777	virion_structural-Cluster53_1clades	448	PPEV_gp169	Pseudomonas phage EL	GCA_000866825.1
ANM44952.1	000777	virion_structural-Cluster53_1clades	445	KTN4_194	Pseudomonas phage KTN4	GCA_002607225.1
ARV77341.1	000777	virion_structural-Cluster53_1clades	437	NOXIFER_172	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89696.1	000777	virion_structural-Cluster53_1clades	443	OBP_259	Pseudomonas phage OBP	GCA_000896635.1
QBX32339.1	000777	virion_structural-Cluster53_1clades	335	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76862.1	000777	virion_structural-Cluster53_1clades	435	PHABIO_231	Pseudomonas phage Phabio	GCA_002624965.1
AEH03604.1	000777	virion_structural-Cluster53_1clades	437	181	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02741.1	000777	virion_structural-Cluster53_1clades	437	PSA21_215	Pseudomonas phage Psa21	GCA_004340405.1
ATN94762.1	000777	virion_structural-Cluster53_1clades	445	SL2_185	Pseudomonas phage SL2	GCA_002956015.1
QJB22830.1	000777	virion_structural-Cluster53_1clades	445	fnug_187	Pseudomonas phage fnug	GCA_012837215.1
QEM41913.1	000777	virion_structural-Cluster53_1clades	435	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83058.1	000777	virion_structural-Cluster53_1clades	445	PHIKZ157	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19039.1	000777	virion_structural-Cluster53_1clades	432	FDH28_gp065	Ralstonia phage RP12	GCA_002617345.1
BAW19324.1	000777	virion_structural-Cluster53_1clades	432	-	Ralstonia phage RP31	GCA_002617365.1
BAS04851.1	000777	virion_structural-Cluster53_1clades	433	AVU11_gp059	Ralstonia phage RSF1	GCA_001500875.1
BAQ02585.1	000777	virion_structural-Cluster53_1clades	433	AVU38_gp057	Ralstonia phage RSL2	GCA_001503055.1
QNI20891.1	000777	virion_structural-Cluster53_1clades	459	-	Salmonella phage JN03	GCA_014319805.1
AWN09142.2	000777	virion_structural-Cluster53_1clades	459	MLDJOKPK_00237	Salmonella phage SPAsTU	GCA_003183805.1
AEP84036.1	000777	virion_structural-Cluster53_1clades	459	SPN3US_0203	Salmonella phage SPN3US	GCA_001042275.1
QKE54449.1	000777	virion_structural-Cluster53_1clades	441	ACSA002_1350	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65407.1	000777	virion_structural-Cluster53_1clades	433	2050HW_00072	Serratia phage 2050HW	GCA_002628125.1
QDB71186.1	000777	virion_structural-Cluster53_1clades	433	CPT_Moabite_156	Serratia phage Moabite	GCA_006384735.1
QFP93085.1	000777	virion_structural-Cluster53_1clades	437	-	Serratia phage PCH45	GCA_009187865.1
QAU04238.1	000777	virion_structural-Cluster53_1clades	442	HWC03_gp083	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23125.1	000777	virion_structural-Cluster53_1clades	442	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80957.1	000777	virion_structural-Cluster53_1clades	442	Aphrodite1_0006	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70748.1	000777	virion_structural-Cluster53_1clades	431	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47602.1	000777	virion_structural-Cluster53_1clades	442	HWC35_gp208	Vibrio phage USC-1	GCA_006864065.1
BAW98417.1	000777	virion_structural-Cluster53_1clades	443	FDH33_gp208	Vibrio phage pTD1	GCA_002618825.1
AQT28077.1	000777	virion_structural-Cluster53_1clades	440	pVa21_136	Vibrio phage pVa-21	GCA_002619305.1
QAX96790.1	000777	virion_structural-Cluster53_1clades	431	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97109.1	000777	virion_structural-Cluster53_1clades	431	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96155.1	000777	virion_structural-Cluster53_1clades	431	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96473.1	000777	virion_structural-Cluster53_1clades	431	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20958.1	000777	virion_structural-Cluster53_1clades	431	-	Vibrio phage vB_pir03	GCA_014319855.1
QMV29169.1	000778	virion_structural-Cluster54_1clades	122	AP1_0472	Aeromonas phage AP1	GCA_014183365.1
QDB70292.1	000778	virion_structural-Cluster54_1clades	306	CF8_0124	Aeromonas phage CF8	GCA_006384595.2
QDJ97269.1	000778	virion_structural-Cluster54_1clades	306	D6_0109	Aeromonas phage D6	GCA_007051205.2
QDH47089.1	000778	virion_structural-Cluster54_1clades	306	LAh10_41	Aeromonas phage LAh10	GCA_006863975.1
QDJ96883.1	000778	virion_structural-Cluster54_1clades	305	PS1_0124	Aeromonas phage PS1	GCA_007051165.2
QFR59515.1	000778	virion_structural-Cluster54_1clades	305	PS2_0124	Aeromonas phage PS2	GCA_009388305.2
AFO71298.1	000778	virion_structural-Cluster54_1clades	293	CR5_078	Cronobacter phage CR5	GCA_000910235.1
QBZ70655.1	000778	virion_structural-Cluster54_1clades	306	pETSU_074	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59735.1	000778	virion_structural-Cluster54_1clades	114	SEGD1_086	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07507.1	000778	virion_structural-Cluster54_1clades	293	DERBICUS_81	Erwinia phage Derbicus	GCA_004521655.1
AHI60160.1	000778	virion_structural-Cluster54_1clades	291	Ea357_010	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49734.1	000778	virion_structural-Cluster54_1clades	294	MACHINA_96	Erwinia phage Machina	GCA_002758035.1
AGX01927.1	000778	virion_structural-Cluster54_1clades	331	CF95_gp205	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07118.1	000778	virion_structural-Cluster54_1clades	291	REBECCA_10	Erwinia phage Rebecca	GCA_004521635.1
AXF51234.1	000778	virion_structural-Cluster54_1clades	295	WELLINGTON_104	Erwinia phage Wellington	GCA_003344985.1
AFQ96553.1	000778	virion_structural-Cluster54_1clades	295	G173_gp008	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48113.1	000778	virion_structural-Cluster54_1clades	295	ASESINO_100	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85798.1	000778	virion_structural-Cluster54_1clades	291	BOSOLAPHORUS_10	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48388.1	000778	virion_structural-Cluster54_1clades	295	CAITLIN_93	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48660.1	000778	virion_structural-Cluster54_1clades	295	CHRISDB_98	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52108.1	000778	virion_structural-Cluster54_1clades	291	DM_10	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86118.1	000778	virion_structural-Cluster54_1clades	291	DESERTFOX_10	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48931.1	000778	virion_structural-Cluster54_1clades	293	EARLPHILLIPIV_81	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49179.1	000778	virion_structural-Cluster54_1clades	294	HUXLEY_97	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03824.1	000778	virion_structural-Cluster54_1clades	315	JOAD_91	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49455.1	000778	virion_structural-Cluster54_1clades	295	KWAN_103	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86438.1	000778	virion_structural-Cluster54_1clades	291	MADMEL_10	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86759.1	000778	virion_structural-Cluster54_1clades	291	MORTIMER_10	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50007.1	000778	virion_structural-Cluster54_1clades	294	PARSHIK_98	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50271.1	000778	virion_structural-Cluster54_1clades	293	PHOBOS_81	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51791.1	000778	virion_structural-Cluster54_1clades	291	RAY_10	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03579.1	000778	virion_structural-Cluster54_1clades	315	RISINGSUN_91	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51473.1	000778	virion_structural-Cluster54_1clades	291	SIMMY50_11	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64820.1	000778	virion_structural-Cluster54_1clades	291	SPECIALG_10	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50527.1	000778	virion_structural-Cluster54_1clades	295	STRATTON_102	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85924.1	000778	virion_structural-Cluster54_1clades	295	ACEC001_0860	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63825.1	000778	virion_structural-Cluster54_1clades	294	Goslar_00032	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71971.1	000778	virion_structural-Cluster54_1clades	310	N1M2_108	Klebsiella phage N1M2	GCA_010092605.1
QGZ14444.1	000778	virion_structural-Cluster54_1clades	304	HWC77_gp081	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24002.1	000778	virion_structural-Cluster54_1clades	295	-	Proteus phage 10	GCA_014071245.1
ABY63053.1	000778	virion_structural-Cluster54_1clades	298	201phi2-1p224	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27200.1	000778	virion_structural-Cluster54_1clades	315	PPEV_gp106	Pseudomonas phage EL	GCA_000866825.1
ANM44932.1	000778	virion_structural-Cluster54_1clades	298	KTN4_174	Pseudomonas phage KTN4	GCA_002607225.1
ARV77315.1	000778	virion_structural-Cluster54_1clades	296	NOXIFER_146	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89572.1	000778	virion_structural-Cluster54_1clades	308	OBP_135	Pseudomonas phage OBP	GCA_000896635.1
QBX32319.1	000778	virion_structural-Cluster54_1clades	291	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76842.1	000778	virion_structural-Cluster54_1clades	301	PHABIO_211	Pseudomonas phage Phabio	GCA_002624965.1
AEH03581.1	000778	virion_structural-Cluster54_1clades	300	158	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02718.1	000778	virion_structural-Cluster54_1clades	299	PSA21_192	Pseudomonas phage Psa21	GCA_004340405.1
ATN94782.1	000778	virion_structural-Cluster54_1clades	298	SL2_205	Pseudomonas phage SL2	GCA_002956015.1
QJB22810.1	000778	virion_structural-Cluster54_1clades	298	fnug_167	Pseudomonas phage fnug	GCA_012837215.1
QEM41892.1	000778	virion_structural-Cluster54_1clades	298	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83040.1	000778	virion_structural-Cluster54_1clades	298	PHIKZ139	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19061.1	000778	virion_structural-Cluster54_1clades	294	FDH28_gp087	Ralstonia phage RP12	GCA_002617345.1
BAW19346.1	000778	virion_structural-Cluster54_1clades	294	-	Ralstonia phage RP31	GCA_002617365.1
BAS04891.1	000778	virion_structural-Cluster54_1clades	284	AVU11_gp099	Ralstonia phage RSF1	GCA_001500875.1
BAQ02618.1	000778	virion_structural-Cluster54_1clades	284	AVU38_gp090	Ralstonia phage RSL2	GCA_001503055.1
QNI20794.1	000778	virion_structural-Cluster54_1clades	295	-	Salmonella phage JN03	GCA_014319805.1
AWN09017.2	000778	virion_structural-Cluster54_1clades	295	MLDJOKPK_00075	Salmonella phage SPAsTU	GCA_003183805.1
AEP83917.1	000778	virion_structural-Cluster54_1clades	295	SPN3US_0084	Salmonella phage SPN3US	GCA_001042275.1
QKE54324.1	000778	virion_structural-Cluster54_1clades	295	ACSA002_0100	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65385.1	000778	virion_structural-Cluster54_1clades	201	2050HW_00050	Serratia phage 2050HW	GCA_002628125.1
QDB71167.1	000778	virion_structural-Cluster54_1clades	312	CPT_Moabite_137	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFP93104.1	000778	virion_structural-Cluster54_1clades	327	-	Serratia phage PCH45	GCA_009187865.1
QAU04290.1	000778	virion_structural-Cluster54_1clades	304	HWC03_gp135	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23287.1	000778	virion_structural-Cluster54_1clades	304	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80991.1	000778	virion_structural-Cluster54_1clades	304	Aphrodite1_0058	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70860.1	000778	virion_structural-Cluster54_1clades	278	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47441.1	000778	virion_structural-Cluster54_1clades	304	HWC35_gp047	Vibrio phage USC-1	GCA_006864065.1
BAW98262.1	000778	virion_structural-Cluster54_1clades	304	FDH33_gp053	Vibrio phage pTD1	GCA_002618825.1
AQT27961.1	000778	virion_structural-Cluster54_1clades	289	pVa21_019	Vibrio phage pVa-21	GCA_002619305.1
QAX96629.1	000778	virion_structural-Cluster54_1clades	278	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96947.1	000778	virion_structural-Cluster54_1clades	278	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95993.1	000778	virion_structural-Cluster54_1clades	278	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96311.1	000778	virion_structural-Cluster54_1clades	278	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21112.1	000778	virion_structural-Cluster54_1clades	276	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70418.1	000779	virion_structural-Cluster56_1clades	578	CF8_0005	Aeromonas phage CF8	GCA_006384595.2
QDJ97426.1	000779	virion_structural-Cluster56_1clades	580	D6_0267	Aeromonas phage D6	GCA_007051205.2
QDH47035.1	000779	virion_structural-Cluster56_1clades	580	LAh10_174	Aeromonas phage LAh10	GCA_006863975.1
QDJ96763.1	000779	virion_structural-Cluster56_1clades	579	PS1_0005	Aeromonas phage PS1	GCA_007051165.2
QFR59396.1	000779	virion_structural-Cluster56_1clades	579	PS2_0005	Aeromonas phage PS2	GCA_009388305.2
AFO71443.1	000779	virion_structural-Cluster56_1clades	548	CR5_223	Cronobacter phage CR5	GCA_000910235.1
QBZ70812.1	000779	virion_structural-Cluster56_1clades	578	pETSU_231	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59912.1	000779	virion_structural-Cluster56_1clades	547	SEGD1_265	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07657.1	000779	virion_structural-Cluster56_1clades	548	DERBICUS_231	Erwinia phage Derbicus	GCA_004521655.1
AHI60332.1	000779	virion_structural-Cluster56_1clades	572	Ea357_180	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49909.1	000779	virion_structural-Cluster56_1clades	546	MACHINA_271	Erwinia phage Machina	GCA_002758035.1
AGX01794.1	000779	virion_structural-Cluster56_1clades	569	CF95_gp072	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07291.1	000779	virion_structural-Cluster56_1clades	572	REBECCA_184	Erwinia phage Rebecca	GCA_004521635.1
AXF51410.1	000779	virion_structural-Cluster56_1clades	547	WELLINGTON_284	Erwinia phage Wellington	GCA_003344985.1
AFQ96722.1	000779	virion_structural-Cluster56_1clades	547	G173_gp177	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48293.1	000779	virion_structural-Cluster56_1clades	547	ASESINO_280	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85971.1	000779	virion_structural-Cluster56_1clades	572	BOSOLAPHORUS_184	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48564.1	000779	virion_structural-Cluster56_1clades	547	CAITLIN_269	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48842.1	000779	virion_structural-Cluster56_1clades	547	CHRISDB_280	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52286.1	000779	virion_structural-Cluster56_1clades	572	DM_188	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86290.1	000779	virion_structural-Cluster56_1clades	572	DESERTFOX_183	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49081.1	000779	virion_structural-Cluster56_1clades	548	EARLPHILLIPIV_232	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49352.1	000779	virion_structural-Cluster56_1clades	546	HUXLEY_270	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03672.1	000779	virion_structural-Cluster56_1clades	571	JOAD_243	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49635.1	000779	virion_structural-Cluster56_1clades	547	KWAN_283	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86612.1	000779	virion_structural-Cluster56_1clades	572	MADMEL_184	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86936.1	000779	virion_structural-Cluster56_1clades	572	MORTIMER_187	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50180.1	000779	virion_structural-Cluster56_1clades	546	PARSHIK_271	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50428.1	000779	virion_structural-Cluster56_1clades	548	PHOBOS_238	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51963.1	000779	virion_structural-Cluster56_1clades	572	RAY_182	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03429.1	000779	virion_structural-Cluster56_1clades	571	RISINGSUN_241	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51647.1	000779	virion_structural-Cluster56_1clades	572	SIMMY50_185	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64994.1	000779	virion_structural-Cluster56_1clades	572	SPECIALG_184	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50704.1	000779	virion_structural-Cluster56_1clades	547	STRATTON_279	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86100.1	000779	virion_structural-Cluster56_1clades	547	ACEC001_2570	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64006.1	000779	virion_structural-Cluster56_1clades	577	Goslar_00214	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72110.1	000779	virion_structural-Cluster56_1clades	580	N1M2_247	Klebsiella phage N1M2	GCA_010092605.1
QGZ14549.1	000779	virion_structural-Cluster56_1clades	1587	HWC77_gp186	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24114.1	000779	virion_structural-Cluster56_1clades	585	-	Proteus phage 10	GCA_014071245.1
ABY62861.1	000779	virion_structural-Cluster56_1clades	553	201phi2-1p027	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27103.1	000779	virion_structural-Cluster56_1clades	574	PPEV_gp009	Pseudomonas phage EL	GCA_000866825.1
ANM44794.1	000779	virion_structural-Cluster56_1clades	552	KTN4_036	Pseudomonas phage KTN4	GCA_002607225.1
ARV77189.1	000779	virion_structural-Cluster56_1clades	547	NOXIFER_18	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89442.1	000779	virion_structural-Cluster56_1clades	579	OBP_005	Pseudomonas phage OBP	GCA_000896635.1
QBX32155.1	000779	virion_structural-Cluster56_1clades	554	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76647.1	000779	virion_structural-Cluster56_1clades	551	PHABIO_16	Pseudomonas phage Phabio	GCA_002624965.1
AEH03434.1	000779	virion_structural-Cluster56_1clades	552	008	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02538.1	000779	virion_structural-Cluster56_1clades	561	PSA21_8	Pseudomonas phage Psa21	GCA_004340405.1
ATN94917.1	000779	virion_structural-Cluster56_1clades	552	SL2_340	Pseudomonas phage SL2	GCA_002956015.1
QJB22673.1	000779	virion_structural-Cluster56_1clades	552	fnug_30	Pseudomonas phage fnug	GCA_012837215.1
QEM41736.1	000779	virion_structural-Cluster56_1clades	554	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82927.1	000779	virion_structural-Cluster56_1clades	552	PHIKZ026	Pseudomonas virus phiKZ	GCA_000842965.1
BAW18999.1	000779	virion_structural-Cluster56_1clades	569	FDH28_gp025	Ralstonia phage RP12	GCA_002617345.1
BAW19287.1	000779	virion_structural-Cluster56_1clades	569	-	Ralstonia phage RP31	GCA_002617365.1
BAS04819.1	000779	virion_structural-Cluster56_1clades	572	AVU11_gp027	Ralstonia phage RSF1	GCA_001500875.1
BAQ02552.2	000779	virion_structural-Cluster56_1clades	551	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20942.1	000779	virion_structural-Cluster56_1clades	547	-	Salmonella phage JN03	GCA_014319805.1
AWN09094.1	000779	virion_structural-Cluster56_1clades	547	MLDJOKPK_00181	Salmonella phage SPAsTU	GCA_003183805.1
AEP84092.1	000779	virion_structural-Cluster56_1clades	547	SPN3US_0259	Salmonella phage SPN3US	GCA_001042275.1
QKE54492.1	000779	virion_structural-Cluster56_1clades	574	ACSA002_1780	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65606.1	000779	virion_structural-Cluster56_1clades	573	2050HW_00271	Serratia phage 2050HW	GCA_002628125.1
QDB71370.1	000779	virion_structural-Cluster56_1clades	573	CPT_Moabite_340	Serratia phage Moabite	GCA_006384735.1
QFP93064.1	000779	virion_structural-Cluster56_1clades	576	-	Serratia phage PCH45	GCA_009187865.1
QAU04185.1	000779	virion_structural-Cluster56_1clades	1587	HWC03_gp030	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23174.1	000779	virion_structural-Cluster56_1clades	1587	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80911.1	000779	virion_structural-Cluster56_1clades	1588	Aphrodite1_0168	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70781.1	000779	virion_structural-Cluster56_1clades	550	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47555.1	000779	virion_structural-Cluster56_1clades	1587	HWC35_gp161	Vibrio phage USC-1	GCA_006864065.1
BAW98370.1	000779	virion_structural-Cluster56_1clades	2486	FDH33_gp161	Vibrio phage pTD1	GCA_002618825.1
AQT28125.1	000779	virion_structural-Cluster56_1clades	557	pVa21_184	Vibrio phage pVa-21	GCA_002619305.1
QAX96737.1	000779	virion_structural-Cluster56_1clades	552	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97056.1	000779	virion_structural-Cluster56_1clades	552	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96102.1	000779	virion_structural-Cluster56_1clades	552	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96420.1	000779	virion_structural-Cluster56_1clades	552	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21001.1	000779	virion_structural-Cluster56_1clades	553	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70264.1	000780	virion_structural-Cluster57_1clades	972	CF8_0096	Aeromonas phage CF8	GCA_006384595.2
QDJ97242.1	000780	virion_structural-Cluster57_1clades	972	D6_0082	Aeromonas phage D6	GCA_007051205.2
QDH47019.1	000780	virion_structural-Cluster57_1clades	972	LAh10_14	Aeromonas phage LAh10	GCA_006863975.1
QDJ96855.1	000780	virion_structural-Cluster57_1clades	973	PS1_0096	Aeromonas phage PS1	GCA_007051165.2
QFR59487.1	000780	virion_structural-Cluster57_1clades	973	PS2_0096	Aeromonas phage PS2	GCA_009388305.2
AFO71269.1	000780	virion_structural-Cluster57_1clades	974	CR5_049	Cronobacter phage CR5	GCA_000910235.1
QBZ70625.1	000780	virion_structural-Cluster57_1clades	978	pETSU_044	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59699.1	000780	virion_structural-Cluster57_1clades	960	SEGD1_050	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07476.1	000780	virion_structural-Cluster57_1clades	974	DERBICUS_50	Erwinia phage Derbicus	GCA_004521655.1
AHI60440.1	000780	virion_structural-Cluster57_1clades	985	Ea357_286	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49702.1	000780	virion_structural-Cluster57_1clades	982	MACHINA_64	Erwinia phage Machina	GCA_002758035.1
AGX01953.1	000780	virion_structural-Cluster57_1clades	981	CF95_gp231	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07397.1	000780	virion_structural-Cluster57_1clades	985	REBECCA_292	Erwinia phage Rebecca	GCA_004521635.1
AXF51192.1	000780	virion_structural-Cluster57_1clades	984	WELLINGTON_62	Erwinia phage Wellington	GCA_003344985.1
AFQ96777.1	000780	virion_structural-Cluster57_1clades	977	G173_gp232	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48078.1	000780	virion_structural-Cluster57_1clades	985	ASESINO_65	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86079.1	000780	virion_structural-Cluster57_1clades	985	BOSOLAPHORUS_293	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48353.1	000780	virion_structural-Cluster57_1clades	982	CAITLIN_58	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48626.1	000780	virion_structural-Cluster57_1clades	982	CHRISDB_64	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52395.1	000780	virion_structural-Cluster57_1clades	985	DM_296	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86399.1	000780	virion_structural-Cluster57_1clades	985	DESERTFOX_292	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48900.1	000780	virion_structural-Cluster57_1clades	974	EARLPHILLIPIV_50	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49147.1	000780	virion_structural-Cluster57_1clades	982	HUXLEY_65	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03854.1	000780	virion_structural-Cluster57_1clades	974	JOAD_61	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49414.1	000780	virion_structural-Cluster57_1clades	984	KWAN_62	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86720.1	000780	virion_structural-Cluster57_1clades	985	MADMEL_293	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87045.1	000780	virion_structural-Cluster57_1clades	985	MORTIMER_297	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49975.1	000780	virion_structural-Cluster57_1clades	982	PARSHIK_66	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50241.1	000780	virion_structural-Cluster57_1clades	973	PHOBOS_51	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52070.1	000780	virion_structural-Cluster57_1clades	985	RAY_290	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03609.1	000780	virion_structural-Cluster57_1clades	974	RISINGSUN_61	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51753.1	000780	virion_structural-Cluster57_1clades	985	SIMMY50_295	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65105.1	000780	virion_structural-Cluster57_1clades	985	SPECIALG_294	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50489.1	000780	virion_structural-Cluster57_1clades	985	STRATTON_64	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85889.1	000780	virion_structural-Cluster57_1clades	986	ACEC001_0510	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63856.1	000780	virion_structural-Cluster57_1clades	997	Goslar_00063	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71941.1	000780	virion_structural-Cluster57_1clades	995	N1M2_78	Klebsiella phage N1M2	GCA_010092605.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGZ14402.1	000780	virion_structural-Cluster57_1clades	980	HWC77_gp039	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24193.1	000780	virion_structural-Cluster57_1clades	981	-	Proteus phage 10	GCA_014071245.1
ABY62979.1	000780	virion_structural-Cluster57_1clades	974	201phi2-1p149	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27150.1	000780	virion_structural-Cluster57_1clades	976	PPEV_gp056	Pseudomonas phage EL	GCA_000866825.1
ANM44872.1	000780	virion_structural-Cluster57_1clades	971	KTN4_114	Pseudomonas phage KTN4	GCA_002607225.1
ARV77258.1	000780	virion_structural-Cluster57_1clades	961	NOXIFER_88	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89541.1	000780	virion_structural-Cluster57_1clades	988	OBP_104	Pseudomonas phage OBP	GCA_000896635.1
QBX32244.1	000780	virion_structural-Cluster57_1clades	971	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76764.1	000780	virion_structural-Cluster57_1clades	976	PHABIO_133	Pseudomonas phage Phabio	GCA_002624965.1
AEH03514.1	000780	virion_structural-Cluster57_1clades	951	090	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02625.1	000780	virion_structural-Cluster57_1clades	965	PSA21_97	Pseudomonas phage Psa21	GCA_004340405.1
ATN94841.1	000780	virion_structural-Cluster57_1clades	971	SL2_264	Pseudomonas phage SL2	GCA_002956015.1
QJB22749.1	000780	virion_structural-Cluster57_1clades	971	fnug_106	Pseudomonas phage fnug	GCA_012837215.1
QEM41822.1	000780	virion_structural-Cluster57_1clades	971	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82988.1	000780	virion_structural-Cluster57_1clades	971	PHIKZ087	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19220.1	000780	virion_structural-Cluster57_1clades	975	FDH28_gp175	Ralstonia phage RP12	GCA_002617345.1
BAW19506.1	000780	virion_structural-Cluster57_1clades	975	-	Ralstonia phage RP31	GCA_002617365.1
BAS04977.1	000780	virion_structural-Cluster57_1clades	972	AVU11_gp185	Ralstonia phage RSF1	GCA_001500875.1
BAQ02703.1	000780	virion_structural-Cluster57_1clades	972	AVU38_gp175	Ralstonia phage RSL2	GCA_001503055.1
QNI20764.1	000780	virion_structural-Cluster57_1clades	986	-	Salmonella phage JN03	GCA_014319805.1
AWN09049.2	000780	virion_structural-Cluster57_1clades	986	MLDJOKPK_00117	Salmonella phage SPAsTU	GCA_003183805.1
AEP83881.1	000780	virion_structural-Cluster57_1clades	986	SPN3US_0048	Salmonella phage SPN3US	GCA_001042275.1
QKE54617.1	000780	virion_structural-Cluster57_1clades	984	ACSA002_3000	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65350.1	000780	virion_structural-Cluster57_1clades	965	2050HW_00015	Serratia phage 2050HW	GCA_002628125.1
QDB71137.1	000780	virion_structural-Cluster57_1clades	965	CPT_Moabite_107	Serratia phage Moabite	GCA_006384735.1
QFP93045.1	000780	virion_structural-Cluster57_1clades	980	-	Serratia phage PCH45	GCA_009187865.1
QAU04334.1	000780	virion_structural-Cluster57_1clades	974	HWC03_gp179	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23242.1	000780	virion_structural-Cluster57_1clades	979	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80916.1	000780	virion_structural-Cluster57_1clades	979	Aphrodite1_0103	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70840.1	000780	virion_structural-Cluster57_1clades	952	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47486.1	000780	virion_structural-Cluster57_1clades	979	HWC35_gp092	Vibrio phage USC-1	GCA_006864065.1
BAW98306.1	000780	virion_structural-Cluster57_1clades	973	FDH33_gp097	Vibrio phage pTD1	GCA_002618825.1
AQT28177.1	000780	virion_structural-Cluster57_1clades	977	pVa21_236	Vibrio phage pVa-21	GCA_002619305.1
QAX96652.1	000780	virion_structural-Cluster57_1clades	953	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96970.1	000780	virion_structural-Cluster57_1clades	953	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96016.1	000780	virion_structural-Cluster57_1clades	953	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96334.1	000780	virion_structural-Cluster57_1clades	953	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21088.1	000780	virion_structural-Cluster57_1clades	948	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70290.1	000781	virion_structural-Cluster59_1clades	706	CF8_0122	Aeromonas phage CF8	GCA_006384595.2
QDJ97267.1	000781	virion_structural-Cluster59_1clades	710	D6_0107	Aeromonas phage D6	GCA_007051205.2
QDH47026.1	000781	virion_structural-Cluster59_1clades	710	LAh10_39	Aeromonas phage LAh10	GCA_006863975.1
QDJ96881.1	000781	virion_structural-Cluster59_1clades	702	PS1_0122	Aeromonas phage PS1	GCA_007051165.2
QFR59513.1	000781	virion_structural-Cluster59_1clades	702	PS2_0122	Aeromonas phage PS2	GCA_009388305.2
AFO71296.1	000781	virion_structural-Cluster59_1clades	723	CR5_076	Cronobacter phage CR5	GCA_000910235.1
QBZ70653.1	000781	virion_structural-Cluster59_1clades	710	pETSU_072	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59733.1	000781	virion_structural-Cluster59_1clades	727	SEGD1_084	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07505.1	000781	virion_structural-Cluster59_1clades	690	DERBICUS_79	Erwinia phage Derbicus	GCA_004521655.1
AHI60157.1	000781	virion_structural-Cluster59_1clades	756	Ea357_007	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49732.1	000781	virion_structural-Cluster59_1clades	727	MACHINA_94	Erwinia phage Machina	GCA_002758035.1
AGX01929.1	000781	virion_structural-Cluster59_1clades	771	CF95_gp207	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07115.1	000781	virion_structural-Cluster59_1clades	791	REBECCA_7	Erwinia phage Rebecca	GCA_004521635.1
AXF51232.1	000781	virion_structural-Cluster59_1clades	726	WELLINGTON_102	Erwinia phage Wellington	GCA_003344985.1
AFQ96551.1	000781	virion_structural-Cluster59_1clades	729	G173_gp006	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48111.1	000781	virion_structural-Cluster59_1clades	729	ASESINO_98	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85795.1	000781	virion_structural-Cluster59_1clades	791	BOSOLAPHORUS_7	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48386.1	000781	virion_structural-Cluster59_1clades	730	CAITLIN_91	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48658.1	000781	virion_structural-Cluster59_1clades	728	CHRISDB_96	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52105.1	000781	virion_structural-Cluster59_1clades	791	DM_7	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86115.1	000781	virion_structural-Cluster59_1clades	791	DESERTFOX_7	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48929.1	000781	virion_structural-Cluster59_1clades	723	EARLPHILLIPIV_79	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49177.1	000781	virion_structural-Cluster59_1clades	727	HUXLEY_95	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03826.1	000781	virion_structural-Cluster59_1clades	764	JOAD_89	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49453.1	000781	virion_structural-Cluster59_1clades	726	KWAN_101	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86435.1	000781	virion_structural-Cluster59_1clades	791	MADMEL_7	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86756.1	000781	virion_structural-Cluster59_1clades	791	MORTIMER_7	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50005.1	000781	virion_structural-Cluster59_1clades	727	PARSHIK_96	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50269.1	000781	virion_structural-Cluster59_1clades	723	PHOBOS_79	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51788.1	000781	virion_structural-Cluster59_1clades	791	RAY_7	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03581.1	000781	virion_structural-Cluster59_1clades	764	RISINGSUN_89	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51469.1	000781	virion_structural-Cluster59_1clades	734	SIMMY50_7	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64817.1	000781	virion_structural-Cluster59_1clades	791	SPECIALG_7	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50525.1	000781	virion_structural-Cluster59_1clades	729	STRATTON_100	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85922.1	000781	virion_structural-Cluster59_1clades	727	ACEC001_0840	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63828.1	000781	virion_structural-Cluster59_1clades	803	Goslar_00035	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71969.1	000781	virion_structural-Cluster59_1clades	706	N1M2_106	Klebsiella phage N1M2	GCA_010092605.1
QGZ14443.1	000781	virion_structural-Cluster59_1clades	703	HWC77_gp080	Photobacterium phage PDCC-1	GCA_009800445.1
QMP23999.1	000781	virion_structural-Cluster59_1clades	781	-	Proteus phage 10	GCA_014071245.1
ABY63042.1	000781	virion_structural-Cluster59_1clades	723	201phi2-1p213	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27198.1	000781	virion_structural-Cluster59_1clades	773	PPEV_gp104	Pseudomonas phage EL	GCA_000866825.1
ANM44921.1	000781	virion_structural-Cluster59_1clades	724	KTN4_163	Pseudomonas phage KTN4	GCA_002607225.1
ARV77300.1	000781	virion_structural-Cluster59_1clades	711	NOXIFER_131	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89570.1	000781	virion_structural-Cluster59_1clades	708	OBP_133	Pseudomonas phage OBP	GCA_000896635.1
QBX32308.1	000781	virion_structural-Cluster59_1clades	722	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76831.1	000781	virion_structural-Cluster59_1clades	724	PHABIO_200	Pseudomonas phage Phabio	GCA_002624965.1
AEH03570.1	000781	virion_structural-Cluster59_1clades	723	147	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02707.1	000781	virion_structural-Cluster59_1clades	720	PSA21_181	Pseudomonas phage Psa21	GCA_004340405.1
ATN94793.1	000781	virion_structural-Cluster59_1clades	724	SL2_216	Pseudomonas phage SL2	GCA_002956015.1
QJB22799.1	000781	virion_structural-Cluster59_1clades	724	fnug_156	Pseudomonas phage fnug	GCA_012837215.1
QEM41881.1	000781	virion_structural-Cluster59_1clades	722	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83029.1	000781	virion_structural-Cluster59_1clades	724	PHIKZ128	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19062.1	000781	virion_structural-Cluster59_1clades	748	FDH28_gp088	Ralstonia phage RP12	GCA_002617345.1
BAW19347.1	000781	virion_structural-Cluster59_1clades	748	-	Ralstonia phage RP31	GCA_002617365.1
BAS04892.2	000781	virion_structural-Cluster59_1clades	715	AVU11_gp100	Ralstonia phage RSF1	GCA_001500875.1
BAQ02619.2	000781	virion_structural-Cluster59_1clades	727	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20792.1	000781	virion_structural-Cluster59_1clades	727	-	Salmonella phage JN03	GCA_014319805.1
AWN09019.1	000781	virion_structural-Cluster59_1clades	727	MLDJOKPK_00077	Salmonella phage SPAsTU	GCA_003183805.1
AEP83915.1	000781	virion_structural-Cluster59_1clades	727	SPN3US_0082	Salmonella phage SPN3US	GCA_001042275.1
QKE54321.1	000781	virion_structural-Cluster59_1clades	820	ACSA002_0070	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65382.1	000781	virion_structural-Cluster59_1clades	856	2050HW_00047	Serratia phage 2050HW	GCA_002628125.1
QDB71164.1	000781	virion_structural-Cluster59_1clades	856	CPT_Moabite_134	Serratia phage Moabite	GCA_006384735.1
QFP93053.1	000781	virion_structural-Cluster59_1clades	781	-	Serratia phage PCH45	GCA_009187865.1
QAU04291.1	000781	virion_structural-Cluster59_1clades	703	HWC03_gp136	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23286.1	000781	virion_structural-Cluster59_1clades	703	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80927.1	000781	virion_structural-Cluster59_1clades	703	Aphrodite1_0059	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70861.1	000781	virion_structural-Cluster59_1clades	689	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47442.1	000781	virion_structural-Cluster59_1clades	703	HWC35_gp048	Vibrio phage USC-1	GCA_006864065.1
BAW98263.1	000781	virion_structural-Cluster59_1clades	702	FDH33_gp054	Vibrio phage pTD1	GCA_002618825.1
AQT27959.1	000781	virion_structural-Cluster59_1clades	674	pVa21_017	Vibrio phage pVa-21	GCA_002619305.1
QAX96628.1	000781	virion_structural-Cluster59_1clades	696	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96946.1	000781	virion_structural-Cluster59_1clades	696	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95992.1	000781	virion_structural-Cluster59_1clades	696	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96310.1	000781	virion_structural-Cluster59_1clades	696	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21113.1	000781	virion_structural-Cluster59_1clades	685	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70425.1	000782	structural_head_proteinCluster63_1clades	492	CF8_0012	Aeromonas phage CF8	GCA_006384595.2
QDJ97430.1	000782	structural_head_proteinCluster63_1clades	498	D6_0003	Aeromonas phage D6	GCA_007051205.2
QDH47051.1	000782	structural_head_proteinCluster63_1clades	498	LAh10_177	Aeromonas phage LAh10	GCA_006863975.1
QDJ96771.1	000782	structural_head_proteinCluster63_1clades	491	PS1_0013	Aeromonas phage PS1	GCA_007051165.2
QFR59404.1	000782	structural_head_proteinCluster63_1clades	491	PS2_0013	Aeromonas phage PS2	GCA_009388305.2
AFO71449.1	000782	structural_head_proteinCluster63_1clades	440	CR5_229	Cronobacter phage CR5	GCA_000910235.1
QBZ70815.1	000782	structural_head_proteinCluster63_1clades	463	pETSU_234	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59914.1	000782	structural_head_proteinCluster63_1clades	458	SEGD1_267	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07662.1	000782	structural_head_proteinCluster63_1clades	440	DERBICUS_236	Erwinia phage Derbicus	GCA_004521655.1
AHI60337.1	000782	structural_head_proteinCluster63_1clades	449	Ea357_185	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49912.1	000782	structural_head_proteinCluster63_1clades	459	MACHINA_274	Erwinia phage Machina	GCA_002758035.1
AGX01790.1	000782	structural_head_proteinCluster63_1clades	406	CF95_gp068	Erwinia phage PhiEaH1	GCA_000914555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBP07296.1	000782	structural_head_proteinCluster63_1clades	449	REBECCA_189	Erwinia phage Rebecca	GCA_004521635.1
AXF51413.1	000782	structural_head_proteinCluster63_1clades	442	WELLINGTON_287	Erwinia phage Wellington	GCA_003344985.1
AFQ96724.1	000782	structural_head_proteinCluster63_1clades	407	G173_gp179	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48296.1	000782	structural_head_proteinCluster63_1clades	458	ASESINO_283	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85976.1	000782	structural_head_proteinCluster63_1clades	449	BOSOLAPHORUS_189	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48567.1	000782	structural_head_proteinCluster63_1clades	457	CAITLIN_272	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48845.1	000782	structural_head_proteinCluster63_1clades	457	CHRISDB_283	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52291.1	000782	structural_head_proteinCluster63_1clades	449	DM_193	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86295.1	000782	structural_head_proteinCluster63_1clades	449	DESERTFOX_188	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49086.1	000782	structural_head_proteinCluster63_1clades	440	EARLPHILLIPIV_237	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49355.1	000782	structural_head_proteinCluster63_1clades	459	HUXLEY_273	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03911.1	000782	structural_head_proteinCluster63_1clades	444	JOAD_4	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49638.1	000782	structural_head_proteinCluster63_1clades	442	KWAN_286	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86617.1	000782	structural_head_proteinCluster63_1clades	449	MADMEL_189	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86941.1	000782	structural_head_proteinCluster63_1clades	449	MORTIMER_192	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50183.1	000782	structural_head_proteinCluster63_1clades	459	PARSHIK_274	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50433.1	000782	structural_head_proteinCluster63_1clades	440	PHOBOS_243	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51968.1	000782	structural_head_proteinCluster63_1clades	449	RAY_187	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03666.1	000782	structural_head_proteinCluster63_1clades	444	RISINGSUN_4	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51652.1	000782	structural_head_proteinCluster63_1clades	449	SIMMY50_190	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64999.1	000782	structural_head_proteinCluster63_1clades	449	SPECIALG_190	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50707.1	000782	structural_head_proteinCluster63_1clades	458	STRATTON_282	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86103.1	000782	structural_head_proteinCluster63_1clades	458	ACEC001_2600	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64003.1	000782	structural_head_proteinCluster63_1clades	412	Goslar_00211	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72113.1	000782	structural_head_proteinCluster63_1clades	488	N1M2_250	Klebsiella phage N1M2	GCA_010092605.1
QGZ14554.1	000782	structural_head_proteinCluster63_1clades	456	HWC77_gp191	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24118.1	000782	structural_head_proteinCluster63_1clades	447	-	Proteus phage 10	GCA_014071245.1
ABY62869.1	000782	structural_head_proteinCluster63_1clades	414	201phi2-1p036	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27107.1	000782	structural_head_proteinCluster63_1clades	453	PPEV_gp013	Pseudomonas phage EL	GCA_000866825.1
ANM44802.1	000782	structural_head_proteinCluster63_1clades	412	KTN4_044	Pseudomonas phage KTN4	GCA_002607225.1
ARV77197.1	000782	structural_head_proteinCluster63_1clades	410	NOXIFER_26	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89446.1	000782	structural_head_proteinCluster63_1clades	493	OBP_009	Pseudomonas phage OBP	GCA_000896635.1
QBX32165.1	000782	structural_head_proteinCluster63_1clades	414	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76653.1	000782	structural_head_proteinCluster63_1clades	411	PHABIO_22	Pseudomonas phage Phabio	GCA_002624965.1
AEH03443.1	000782	structural_head_proteinCluster63_1clades	414	017	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02546.1	000782	structural_head_proteinCluster63_1clades	415	PSA21_16	Pseudomonas phage Psa21	GCA_004340405.1
ATN94909.1	000782	structural_head_proteinCluster63_1clades	412	SL2_332	Pseudomonas phage SL2	GCA_002956015.1
QJB22681.1	000782	structural_head_proteinCluster63_1clades	412	fnug_38	Pseudomonas phage fnug	GCA_012837215.1
QEM41746.1	000782	structural_head_proteinCluster63_1clades	414	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82933.2	000782	structural_head_proteinCluster63_1clades	412	PHIKZ032	Pseudomonas virus phiKZ	GCA_000842965.1
BAW18997.1	000782	structural_head_proteinCluster63_1clades	461	FDH28_gp023	Ralstonia phage RP12	GCA_002617345.1
BAW19285.1	000782	structural_head_proteinCluster63_1clades	421	-	Ralstonia phage RP31	GCA_002617365.1
BAS04814.1	000782	structural_head_proteinCluster63_1clades	415	AVU11_gp022	Ralstonia phage RSF1	GCA_001500875.1
BAQ02549.1	000782	structural_head_proteinCluster63_1clades	415	AVU38_gp021	Ralstonia phage RSL2	GCA_001503055.1
QNI20944.1	000782	structural_head_proteinCluster63_1clades	458	-	Salmonella phage JN03	GCA_014319805.1
AWN09092.1	000782	structural_head_proteinCluster63_1clades	458	MLDJOKPK_00178	Salmonella phage SPAsTU	GCA_003183805.1
AEP84095.1	000782	structural_head_proteinCluster63_1clades	458	SPN3US_0262	Salmonella phage SPN3US	GCA_001042275.1
QKE54499.1	000782	structural_head_proteinCluster63_1clades	454	ACSA002_1850	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65609.1	000782	structural_head_proteinCluster63_1clades	415	2050HW_00274	Serratia phage 2050HW	GCA_002628125.1
QDB71035.1	000782	structural_head_proteinCluster63_1clades	415	CPT_Moabite_003	Serratia phage Moabite	GCA_006384735.1
QFP93088.1	000782	structural_head_proteinCluster63_1clades	407	-	Serratia phage PCH45	GCA_009187865.1
QAU04180.1	000782	structural_head_proteinCluster63_1clades	456	HWC03_gp025	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23179.1	000782	structural_head_proteinCluster63_1clades	456	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80954.1	000782	structural_head_proteinCluster63_1clades	456	Aphrodite1_0163	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70784.1	000782	structural_head_proteinCluster63_1clades	409	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47550.1	000782	structural_head_proteinCluster63_1clades	456	HWC35_gp156	Vibrio phage USC-1	GCA_006864065.1
BAW98363.1	000782	structural_head_proteinCluster63_1clades	456	FDH33_gp154	Vibrio phage pTD1	GCA_002618825.1
AQT28131.1	000782	structural_head_proteinCluster63_1clades	435	pVa21_190	Vibrio phage pVa-21	GCA_002619305.1
QAX96735.1	000782	structural_head_proteinCluster63_1clades	401	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97054.1	000782	structural_head_proteinCluster63_1clades	401	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96100.1	000782	structural_head_proteinCluster63_1clades	401	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96418.1	000782	structural_head_proteinCluster63_1clades	401	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21003.1	000782	structural_head_proteinCluster63_1clades	404	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70266.1	000783	virion_structural-Cluster64_1clades	361	CF8_0098	Aeromonas phage CF8	GCA_006384595.2
QDJ97244.1	000783	virion_structural-Cluster64_1clades	370	D6_0084	Aeromonas phage D6	GCA_007051205.2
QDH47070.1	000783	virion_structural-Cluster64_1clades	370	LAh10_16	Aeromonas phage LAh10	GCA_006863975.1
QDJ96857.1	000783	virion_structural-Cluster64_1clades	360	PS1_0098	Aeromonas phage PS1	GCA_007051165.2
QFR59489.1	000783	virion_structural-Cluster64_1clades	360	PS2_0098	Aeromonas phage PS2	GCA_009388305.2
AFO71271.1	000783	virion_structural-Cluster64_1clades	382	CR5_051	Cronobacter phage CR5	GCA_000910235.1
QBZ70627.1	000783	virion_structural-Cluster64_1clades	360	pETSU_046	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59701.1	000783	virion_structural-Cluster64_1clades	372	SEGD1_052	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07478.1	000783	virion_structural-Cluster64_1clades	395	DERBICUS_52	Erwinia phage Derbicus	GCA_004521655.1
AHI60442.1	000783	virion_structural-Cluster64_1clades	388	Ea357_288	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49704.1	000783	virion_structural-Cluster64_1clades	413	MACHINA_66	Erwinia phage Machina	GCA_002758035.1
AGX01951.1	000783	virion_structural-Cluster64_1clades	368	CF95_gp229	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07399.1	000783	virion_structural-Cluster64_1clades	388	REBECCA_294	Erwinia phage Rebecca	GCA_004521635.1
AXF51194.1	000783	virion_structural-Cluster64_1clades	387	WELLINGTON_64	Erwinia phage Wellington	GCA_003344985.1
AFQ96779.1	000783	virion_structural-Cluster64_1clades	417	G173_gp234	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48080.1	000783	virion_structural-Cluster64_1clades	417	ASESINO_67	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86081.1	000783	virion_structural-Cluster64_1clades	388	BOSOLAPHORUS_295	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48355.1	000783	virion_structural-Cluster64_1clades	392	CAITLIN_60	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48628.1	000783	virion_structural-Cluster64_1clades	392	CHRISDB_66	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52397.1	000783	virion_structural-Cluster64_1clades	388	DM_298	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86401.1	000783	virion_structural-Cluster64_1clades	388	DESERTFOX_294	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48902.1	000783	virion_structural-Cluster64_1clades	382	EARLPHILLIPIV_52	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49149.1	000783	virion_structural-Cluster64_1clades	413	HUXLEY_67	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03852.1	000783	virion_structural-Cluster64_1clades	367	JOAD_63	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49416.1	000783	virion_structural-Cluster64_1clades	387	KWAN_64	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86722.1	000783	virion_structural-Cluster64_1clades	388	MADMEL_295	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87047.1	000783	virion_structural-Cluster64_1clades	388	MORTIMER_299	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49977.1	000783	virion_structural-Cluster64_1clades	413	PARSHIK_68	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50243.1	000783	virion_structural-Cluster64_1clades	382	PHOBOS_53	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52072.1	000783	virion_structural-Cluster64_1clades	388	RAY_292	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03607.1	000783	virion_structural-Cluster64_1clades	367	RISINGSUN_63	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51755.1	000783	virion_structural-Cluster64_1clades	388	SIMMY50_297	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65107.1	000783	virion_structural-Cluster64_1clades	388	SPECIALG_296	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50491.1	000783	virion_structural-Cluster64_1clades	417	STRATTON_66	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85891.1	000783	virion_structural-Cluster64_1clades	372	ACEC001_0530	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63854.1	000783	virion_structural-Cluster64_1clades	368	Goslar_00061	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71943.1	000783	virion_structural-Cluster64_1clades	362	N1M2_80	Klebsiella phage N1M2	GCA_010092605.1
QGZ14404.1	000783	virion_structural-Cluster64_1clades	369	HWC77_gp041	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24195.1	000783	virion_structural-Cluster64_1clades	381	-	Proteus phage 10	GCA_014071245.1
ABY62981.1	000783	virion_structural-Cluster64_1clades	400	201phi2-1p151	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27152.1	000783	virion_structural-Cluster64_1clades	364	PPEV_gp058	Pseudomonas phage EL	GCA_000866825.1
ANM44874.1	000783	virion_structural-Cluster64_1clades	387	KTN4_116	Pseudomonas phage KTN4	GCA_002607225.1
ARV77260.1	000783	virion_structural-Cluster64_1clades	384	NOXIFER_90	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89543.1	000783	virion_structural-Cluster64_1clades	363	OBP_106	Pseudomonas phage OBP	GCA_000896635.1
QBX32246.1	000783	virion_structural-Cluster64_1clades	310	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76766.1	000783	virion_structural-Cluster64_1clades	385	PHABIO_135	Pseudomonas phage Phabio	GCA_002624965.1
AEH03516.1	000783	virion_structural-Cluster64_1clades	386	092	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02627.1	000783	virion_structural-Cluster64_1clades	409	PSA21_99	Pseudomonas phage Psa21	GCA_004340405.1
ATN94839.1	000783	virion_structural-Cluster64_1clades	387	SL2_262	Pseudomonas phage SL2	GCA_002956015.1
QJB22751.1	000783	virion_structural-Cluster64_1clades	387	fnug_108	Pseudomonas phage fnug	GCA_012837215.1
QEM41824.1	000783	virion_structural-Cluster64_1clades	394	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82990.1	000783	virion_structural-Cluster64_1clades	387	PHIKZ089	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19218.1	000783	virion_structural-Cluster64_1clades	431	FDH28_gp177	Ralstonia phage RP12	GCA_002617345.1
BAW19504.1	000783	virion_structural-Cluster64_1clades	422	-	Ralstonia phage RP31	GCA_002617365.1
BAS04975.1	000783	virion_structural-Cluster64_1clades	364	AVU11_gp183	Ralstonia phage RSF1	GCA_001500875.1
BAQ02701.1	000783	virion_structural-Cluster64_1clades	366	AVU38_gp173	Ralstonia phage RSL2	GCA_001503055.1
QNI20766.1	000783	virion_structural-Cluster64_1clades	372	-	Salmonella phage JN03	GCA_014319805.1
AWN09047.1	000783	virion_structural-Cluster64_1clades	372	MLDJOKPK_00115	Salmonella phage SPAsTU	GCA_003183805.1
AEP83883.1	000783	virion_structural-Cluster64_1clades	372	SPN3US_0050	Salmonella phage SPN3US	GCA_001042275.1
QKE54619.1	000783	virion_structural-Cluster64_1clades	394	ACSA002_3020	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65352.1	000783	virion_structural-Cluster64_1clades	405	2050HW_00017	Serratia phage 2050HW	GCA_002628125.1
QDB71139.1	000783	virion_structural-Cluster64_1clades	405	CPT_Moabite_109	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFP93095.1	000783	virion_structural-Cluster64_1clades	379	-	Serratia phage PCH45	GCA_009187865.1
QAU04332.1	000783	virion_structural-Cluster64_1clades	369	HWC03_gp177	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23244.1	000783	virion_structural-Cluster64_1clades	373	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80976.1	000783	virion_structural-Cluster64_1clades	373	Aphrodite1_0101	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70842.1	000783	virion_structural-Cluster64_1clades	358	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47484.1	000783	virion_structural-Cluster64_1clades	373	HWC35_gp090	Vibrio phage USC-1	GCA_006864065.1
BAW98304.1	000783	virion_structural-Cluster64_1clades	283	FDH33_gp095	Vibrio phage pTD1	GCA_002618825.1
AQT28179.1	000783	virion_structural-Cluster64_1clades	494	pVa21_238	Vibrio phage pVa-21	GCA_002619305.1
QAX96650.1	000783	virion_structural-Cluster64_1clades	379	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96968.1	000783	virion_structural-Cluster64_1clades	379	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96014.1	000783	virion_structural-Cluster64_1clades	379	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96332.1	000783	virion_structural-Cluster64_1clades	379	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21090.1	000783	virion_structural-Cluster64_1clades	368	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70280.1	000784	virion_structural-Cluster66_1clades	449	CF8_0112	Aeromonas phage CF8	GCA_006384595.2
QDJ97258.1	000784	virion_structural-Cluster66_1clades	450	D6_0098	Aeromonas phage D6	GCA_007051205.2
QDH47056.1	000784	virion_structural-Cluster66_1clades	450	LAh10_30	Aeromonas phage LAh10	GCA_006863975.1
QDJ96871.1	000784	virion_structural-Cluster66_1clades	448	PS1_0112	Aeromonas phage PS1	GCA_007051165.2
QFR59503.1	000784	virion_structural-Cluster66_1clades	448	PS2_0112	Aeromonas phage PS2	GCA_009388305.2
AFO71282.1	000784	virion_structural-Cluster66_1clades	429	CR5_062	Cronobacter phage CR5	GCA_000910235.1
QBZ70640.1	000784	virion_structural-Cluster66_1clades	450	pETSU_059	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59714.1	000784	virion_structural-Cluster66_1clades	437	SEGD1_065	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07489.1	000784	virion_structural-Cluster66_1clades	429	DERBICUS_63	Erwinia phage Derbicus	GCA_004521655.1
AHI60457.1	000784	virion_structural-Cluster66_1clades	453	Ea357_303	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49715.1	000784	virion_structural-Cluster66_1clades	434	MACHINA_77	Erwinia phage Machina	GCA_002758035.1
AGX01940.1	000784	virion_structural-Cluster66_1clades	447	CF95_gp219	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07414.1	000784	virion_structural-Cluster66_1clades	453	REBECCA_309	Erwinia phage Rebecca	GCA_004521635.1
AXF51207.1	000784	virion_structural-Cluster66_1clades	434	WELLINGTON_77	Erwinia phage Wellington	GCA_003344985.1
AFQ96793.1	000784	virion_structural-Cluster66_1clades	436	G173_gp248	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48094.1	000784	virion_structural-Cluster66_1clades	436	ASESINO_81	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86096.1	000784	virion_structural-Cluster66_1clades	453	BOSOLAPHORUS_310	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48367.1	000784	virion_structural-Cluster66_1clades	435	CAITLIN_72	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48640.1	000784	virion_structural-Cluster66_1clades	434	CHRISDB_78	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52412.2	000784	virion_structural-Cluster66_1clades	453	DM_313	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86416.1	000784	virion_structural-Cluster66_1clades	453	DESERTFOX_309	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48913.1	000784	virion_structural-Cluster66_1clades	429	EARLPHILLIPIV_63	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49160.1	000784	virion_structural-Cluster66_1clades	434	HUXLEY_78	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03837.1	000784	virion_structural-Cluster66_1clades	444	JOAD_78	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49429.1	000784	virion_structural-Cluster66_1clades	434	KWAN_77	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86737.1	000784	virion_structural-Cluster66_1clades	453	MADMEL_310	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87062.1	000784	virion_structural-Cluster66_1clades	453	MORTIMER_314	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49988.1	000784	virion_structural-Cluster66_1clades	434	PARSHIK_79	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50255.1	000784	virion_structural-Cluster66_1clades	429	PHOBOS_65	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52087.1	000784	virion_structural-Cluster66_1clades	453	RAY_307	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03592.1	000784	virion_structural-Cluster66_1clades	444	RISINGSUN_78	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51770.1	000784	virion_structural-Cluster66_1clades	453	SIMMY50_312	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65122.1	000784	virion_structural-Cluster66_1clades	453	SPECIALG_311	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50505.1	000784	virion_structural-Cluster66_1clades	436	STRATTON_80	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85905.1	000784	virion_structural-Cluster66_1clades	437	ACEC001_0670	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63841.1	000784	virion_structural-Cluster66_1clades	455	Goslar_00048	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71957.1	000784	virion_structural-Cluster66_1clades	447	N1M2_94	Klebsiella phage N1M2	GCA_010092605.1
QGZ14418.1	000784	virion_structural-Cluster66_1clades	443	HWC77_gp055	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24216.1	000784	virion_structural-Cluster66_1clades	448	-	Proteus phage 10	GCA_014071245.1
ABY62994.1	000784	virion_structural-Cluster66_1clades	459	201phi2-1p164	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27165.1	000784	virion_structural-Cluster66_1clades	445	PPEV_gp071	Pseudomonas phage EL	GCA_000866825.1
ANM44886.1	000784	virion_structural-Cluster66_1clades	460	KTN4_128	Pseudomonas phage KTN4	GCA_002607225.1
ARV77269.1	000784	virion_structural-Cluster66_1clades	455	NOXIFER_100	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89558.1	000784	virion_structural-Cluster66_1clades	446	OBP_121	Pseudomonas phage OBP	GCA_000896635.1
QBX32263.1	000784	virion_structural-Cluster66_1clades	461	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76778.1	000784	virion_structural-Cluster66_1clades	457	PHABIO_147	Pseudomonas phage Phabio	GCA_002624965.1
AEH03530.1	000784	virion_structural-Cluster66_1clades	461	106	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02641.1	000784	virion_structural-Cluster66_1clades	465	PSA21_113	Pseudomonas phage Psa21	GCA_004340405.1
ATN94827.1	000784	virion_structural-Cluster66_1clades	460	SL2_250	Pseudomonas phage SL2	GCA_002956015.1
QJB22763.1	000784	virion_structural-Cluster66_1clades	460	fnug_120	Pseudomonas phage fnug	GCA_012837215.1
QEM41837.1	000784	virion_structural-Cluster66_1clades	461	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83002.1	000784	virion_structural-Cluster66_1clades	460	PHIKZ101	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19205.1	000784	virion_structural-Cluster66_1clades	453	FDH28_gp190	Ralstonia phage RP12	GCA_002617345.1
BAW19491.1	000784	virion_structural-Cluster66_1clades	453	-	Ralstonia phage RP31	GCA_002617365.1
BAS04966.1	000784	virion_structural-Cluster66_1clades	460	AVU11_gp174	Ralstonia phage RSF1	GCA_001500875.1
BAQ02691.2	000784	virion_structural-Cluster66_1clades	453	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20780.1	000784	virion_structural-Cluster66_1clades	437	-	Salmonella phage JN03	GCA_014319805.1
AWN09036.1	000784	virion_structural-Cluster66_1clades	436	MLDJOKPK_00100	Salmonella phage SPAsTU	GCA_003183805.1
AEP83897.1	000784	virion_structural-Cluster66_1clades	437	SPN3US_0064	Salmonella phage SPN3US	GCA_001042275.1
QKE54637.1	000784	virion_structural-Cluster66_1clades	448	ACSA002_3200	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65366.1	000784	virion_structural-Cluster66_1clades	403	2050HW_00031	Serratia phage 2050HW	GCA_002628125.1
QDB71151.1	000784	virion_structural-Cluster66_1clades	444	CPT_Moabite_121	Serratia phage Moabite	GCA_006384735.1
QFP93083.1	000784	virion_structural-Cluster66_1clades	449	-	Serratia phage PCH45	GCA_009187865.1
QAU04318.1	000784	virion_structural-Cluster66_1clades	443	HWC03_gp163	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23260.1	000784	virion_structural-Cluster66_1clades	443	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80956.1	000784	virion_structural-Cluster66_1clades	443	Aphrodite1_0085	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70851.1	000784	virion_structural-Cluster66_1clades	460	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47468.1	000784	virion_structural-Cluster66_1clades	443	HWC35_gp074	Vibrio phage USC-1	GCA_006864065.1
BAW98289.1	000784	virion_structural-Cluster66_1clades	443	FDH33_gp080	Vibrio phage pTD1	GCA_002618825.1
AQT27946.1	000784	virion_structural-Cluster66_1clades	401	pVa21_004	Vibrio phage pVa-21	GCA_002619305.1
QAX96641.1	000784	virion_structural-Cluster66_1clades	449	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96959.1	000784	virion_structural-Cluster66_1clades	449	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96005.1	000784	virion_structural-Cluster66_1clades	449	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96323.1	000784	virion_structural-Cluster66_1clades	449	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21099.1	000784	virion_structural-Cluster66_1clades	454	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70265.1	000785	virion_structural-Cluster67_1clades	359	CF8_0097	Aeromonas phage CF8	GCA_006384595.2
QDJ97243.1	000785	virion_structural-Cluster67_1clades	358	D6_0083	Aeromonas phage D6	GCA_007051205.2
QDH47075.1	000785	virion_structural-Cluster67_1clades	358	LAh10_15	Aeromonas phage LAh10	GCA_006863975.1
QDJ96856.1	000785	virion_structural-Cluster67_1clades	357	PS1_0097	Aeromonas phage PS1	GCA_007051165.2
QFR59488.1	000785	virion_structural-Cluster67_1clades	357	PS2_0097	Aeromonas phage PS2	GCA_009388305.2
AFO71270.1	000785	virion_structural-Cluster67_1clades	406	CR5_050	Cronobacter phage CR5	GCA_000910235.1
QBZ70626.1	000785	virion_structural-Cluster67_1clades	304	pETSU_045	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59700.1	000785	virion_structural-Cluster67_1clades	419	SEGD1_051	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07477.1	000785	virion_structural-Cluster67_1clades	406	DERBICUS_51	Erwinia phage Derbicus	GCA_004521655.1
AHI60441.1	000785	virion_structural-Cluster67_1clades	341	Ea357_287	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49703.1	000785	virion_structural-Cluster67_1clades	422	MACHINA_65	Erwinia phage Machina	GCA_002758035.1
AGX01952.1	000785	virion_structural-Cluster67_1clades	432	CF95_gp230	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07398.1	000785	virion_structural-Cluster67_1clades	341	REBECCA_293	Erwinia phage Rebecca	GCA_004521635.1
AXF51193.1	000785	virion_structural-Cluster67_1clades	417	WELLINGTON_63	Erwinia phage Wellington	GCA_003344985.1
AFQ96778.1	000785	virion_structural-Cluster67_1clades	432	G173_gp233	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48079.1	000785	virion_structural-Cluster67_1clades	432	ASESINO_66	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86080.1	000785	virion_structural-Cluster67_1clades	341	BOSOLAPHORUS_294	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48354.1	000785	virion_structural-Cluster67_1clades	420	CAITLIN_59	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48627.1	000785	virion_structural-Cluster67_1clades	420	CHRISDB_65	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52396.2	000785	virion_structural-Cluster67_1clades	341	DM_297	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86400.1	000785	virion_structural-Cluster67_1clades	341	DESERTFOX_293	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48901.1	000785	virion_structural-Cluster67_1clades	406	EARLPHILLIPIV_51	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49148.1	000785	virion_structural-Cluster67_1clades	422	HUXLEY_66	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03853.1	000785	virion_structural-Cluster67_1clades	358	JOAD_62	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49415.1	000785	virion_structural-Cluster67_1clades	417	KWAN_63	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86721.1	000785	virion_structural-Cluster67_1clades	341	MADMEL_294	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87046.1	000785	virion_structural-Cluster67_1clades	341	MORTIMER_298	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49976.1	000785	virion_structural-Cluster67_1clades	422	PARSHIK_67	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50242.1	000785	virion_structural-Cluster67_1clades	407	PHOBOS_52	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52071.1	000785	virion_structural-Cluster67_1clades	341	RAY_291	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03608.1	000785	virion_structural-Cluster67_1clades	358	RISINGSUN_62	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51754.1	000785	virion_structural-Cluster67_1clades	341	SIMMY50_296	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65106.2	000785	virion_structural-Cluster67_1clades	341	SPECIALG_295	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50490.1	000785	virion_structural-Cluster67_1clades	432	STRATTON_65	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85890.1	000785	virion_structural-Cluster67_1clades	419	ACEC001_0520	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63855.1	000785	virion_structural-Cluster67_1clades	401	Goslar_00062	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71942.1	000785	virion_structural-Cluster67_1clades	361	N1M2_79	Klebsiella phage N1M2	GCA_010092605.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGZ14403.1	000785	virion_structural-Cluster67_1clades	347	HWC77_gp040	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24194.1	000785	virion_structural-Cluster67_1clades	340	-	Proteus phage 10	GCA_014071245.1
ABY62980.1	000785	virion_structural-Cluster67_1clades	359	201phi2-1p150	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27151.1	000785	virion_structural-Cluster67_1clades	357	PPEV_gp057	Pseudomonas phage EL	GCA_000866825.1
ANM44873.1	000785	virion_structural-Cluster67_1clades	349	KTN4_115	Pseudomonas phage KTN4	GCA_002607225.1
ARV77259.1	000785	virion_structural-Cluster67_1clades	354	NOXIFER_89	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89542.1	000785	virion_structural-Cluster67_1clades	359	OBP_105	Pseudomonas phage OBP	GCA_000896635.1
QBX32245.1	000785	virion_structural-Cluster67_1clades	347	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76765.1	000785	virion_structural-Cluster67_1clades	348	PHABIO_134	Pseudomonas phage Phabio	GCA_002624965.1
AEH03515.1	000785	virion_structural-Cluster67_1clades	331	091	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02626.1	000785	virion_structural-Cluster67_1clades	361	PSA21_98	Pseudomonas phage Psa21	GCA_004340405.1
ATN94840.1	000785	virion_structural-Cluster67_1clades	349	SL2_263	Pseudomonas phage SL2	GCA_002956015.1
QJB22750.1	000785	virion_structural-Cluster67_1clades	349	fnug_107	Pseudomonas phage fnug	GCA_012837215.1
QEM41823.1	000785	virion_structural-Cluster67_1clades	347	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82989.1	000785	virion_structural-Cluster67_1clades	349	PHIKZ088	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19219.1	000785	virion_structural-Cluster67_1clades	385	FDH28_gp176	Ralstonia phage RP12	GCA_002617345.1
BAW19505.1	000785	virion_structural-Cluster67_1clades	385	-	Ralstonia phage RP31	GCA_002617365.1
BAS04976.2	000785	virion_structural-Cluster67_1clades	238	AVU11_agp37	Ralstonia phage RSF1	GCA_001500875.1
BAQ02702.2	000785	virion_structural-Cluster67_1clades	396	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20765.1	000785	virion_structural-Cluster67_1clades	420	-	Salmonella phage JN03	GCA_014319805.1
AWN09048.1	000785	virion_structural-Cluster67_1clades	420	MLDJOKPK_00116	Salmonella phage SPAsTU	GCA_003183805.1
AEP83882.1	000785	virion_structural-Cluster67_1clades	419	SPN3US_0049	Salmonella phage SPN3US	GCA_001042275.1
QKE54618.1	000785	virion_structural-Cluster67_1clades	380	ACSA002_3010	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65351.1	000785	virion_structural-Cluster67_1clades	386	2050HW_00016	Serratia phage 2050HW	GCA_002628125.1
QDB71138.1	000785	virion_structural-Cluster67_1clades	386	CPT_Moabite_108	Serratia phage Moabite	GCA_006384735.1
QFP93090.1	000785	virion_structural-Cluster67_1clades	396	-	Serratia phage PCH45	GCA_009187865.1
QAU04333.1	000785	virion_structural-Cluster67_1clades	347	HWC03_gp178	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23243.1	000785	virion_structural-Cluster67_1clades	347	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80982.1	000785	virion_structural-Cluster67_1clades	347	Aphrodite1_0102	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70841.1	000785	virion_structural-Cluster67_1clades	371	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47485.1	000785	virion_structural-Cluster67_1clades	347	HWC35_gp091	Vibrio phage USC-1	GCA_006864065.1
BAW98305.1	000785	virion_structural-Cluster67_1clades	349	FDH33_gp096	Vibrio phage pTD1	GCA_002618825.1
AQT28178.1	000785	virion_structural-Cluster67_1clades	384	pVa21_237	Vibrio phage pVa-21	GCA_002619305.1
QAX96651.1	000785	virion_structural-Cluster67_1clades	345	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96969.1	000785	virion_structural-Cluster67_1clades	345	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96015.1	000785	virion_structural-Cluster67_1clades	345	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96333.1	000785	virion_structural-Cluster67_1clades	345	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21089.1	000785	virion_structural-Cluster67_1clades	348	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70303.1	000786	virion_structural-Cluster68_1clades	319	CF8_0135	Aeromonas phage CF8	GCA_006384595.2
QDJ97280.1	000786	virion_structural-Cluster68_1clades	328	D6_0120	Aeromonas phage D6	GCA_007051205.2
QDH47084.1	000786	virion_structural-Cluster68_1clades	322	LAh10_52	Aeromonas phage LAh10	GCA_006863975.1
QDJ96897.1	000786	virion_structural-Cluster68_1clades	317	PS1_0138	Aeromonas phage PS1	GCA_007051165.2
QFR59527.1	000786	virion_structural-Cluster68_1clades	317	PS2_0136	Aeromonas phage PS2	GCA_009388305.2
AFO71384.1	000786	virion_structural-Cluster68_1clades	302	CR5_164	Cronobacter phage CR5	GCA_000910235.1
QBZ70666.1	000786	virion_structural-Cluster68_1clades	325	pETSU_085	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59825.1	000786	virion_structural-Cluster68_1clades	310	SEGD1_178	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07595.1	000786	virion_structural-Cluster68_1clades	302	DERBICUS_169	Erwinia phage Derbicus	GCA_004521655.1
AHI60171.1	000786	virion_structural-Cluster68_1clades	312	Ea357_021	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49822.1	000786	virion_structural-Cluster68_1clades	308	MACHINA_184	Erwinia phage Machina	GCA_002758035.1
AGX01910.1	000786	virion_structural-Cluster68_1clades	326	CF95_gp188	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07129.1	000786	virion_structural-Cluster68_1clades	312	REBECCA_21	Erwinia phage Rebecca	GCA_004521635.1
AXF51320.1	000786	virion_structural-Cluster68_1clades	308	WELLINGTON_192	Erwinia phage Wellington	GCA_003344985.1
AFQ96640.1	000786	virion_structural-Cluster68_1clades	308	G173_gp095	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48206.1	000786	virion_structural-Cluster68_1clades	308	ASESINO_193	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85809.1	000786	virion_structural-Cluster68_1clades	312	BOSOLAPHORUS_21	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48478.1	000786	virion_structural-Cluster68_1clades	317	CAITLIN_183	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48757.1	000786	virion_structural-Cluster68_1clades	308	CHRISDB_195	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52119.1	000786	virion_structural-Cluster68_1clades	312	DM_21	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86129.1	000786	virion_structural-Cluster68_1clades	312	DESERTFOX_21	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49018.1	000786	virion_structural-Cluster68_1clades	302	EARLPHILLIPIV_169	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49266.1	000786	virion_structural-Cluster68_1clades	308	HUXLEY_184	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03813.1	000786	virion_structural-Cluster68_1clades	327	JOAD_102	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49545.1	000786	virion_structural-Cluster68_1clades	308	KWAN_193	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86449.1	000786	virion_structural-Cluster68_1clades	312	MADMEL_21	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86770.1	000786	virion_structural-Cluster68_1clades	312	MORTIMER_21	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50094.1	000786	virion_structural-Cluster68_1clades	308	PARSHIK_185	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50365.1	000786	virion_structural-Cluster68_1clades	309	PHOBOS_175	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51802.1	000786	virion_structural-Cluster68_1clades	312	RAY_21	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03568.1	000786	virion_structural-Cluster68_1clades	327	RISINGSUN_102	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51484.1	000786	virion_structural-Cluster68_1clades	312	SIMMY50_22	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64831.1	000786	virion_structural-Cluster68_1clades	312	SPECIALG_21	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50617.1	000786	virion_structural-Cluster68_1clades	308	STRATTON_192	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86014.1	000786	virion_structural-Cluster68_1clades	310	ACEC001_1730	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63806.1	000786	virion_structural-Cluster68_1clades	362	Goslar_00013	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71982.1	000786	virion_structural-Cluster68_1clades	331	N1M2_119	Klebsiella phage N1M2	GCA_010092605.1
QGZ14454.1	000786	virion_structural-Cluster68_1clades	350	HWC77_gp091	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24013.1	000786	virion_structural-Cluster68_1clades	350	-	Proteus phage 10	GCA_014071245.1
ABY63077.1	000786	virion_structural-Cluster68_1clades	279	201phi2-1p249	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27211.1	000786	virion_structural-Cluster68_1clades	335	PPEV_gp117	Pseudomonas phage EL	GCA_000866825.1
ANM44960.1	000786	virion_structural-Cluster68_1clades	293	KTN4_202	Pseudomonas phage KTN4	GCA_002607225.1
ARV77335.1	000786	virion_structural-Cluster68_1clades	269	NOXIFER_166	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89583.1	000786	virion_structural-Cluster68_1clades	326	OBP_146	Pseudomonas phage OBP	GCA_000896635.1
QBX32347.1	000786	virion_structural-Cluster68_1clades	269	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76868.1	000786	virion_structural-Cluster68_1clades	277	PHABIO_237	Pseudomonas phage Phabio	GCA_002624965.1
AEH03612.1	000786	virion_structural-Cluster68_1clades	261	189	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02749.1	000786	virion_structural-Cluster68_1clades	289	PSA21_223	Pseudomonas phage Psa21	GCA_004340405.1
ATN94754.1	000786	virion_structural-Cluster68_1clades	293	SL2_177	Pseudomonas phage SL2	GCA_002956015.1
QJB22838.1	000786	virion_structural-Cluster68_1clades	293	fnug_195	Pseudomonas phage fnug	GCA_012837215.1
QEM41921.1	000786	virion_structural-Cluster68_1clades	269	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83065.2	000786	virion_structural-Cluster68_1clades	293	PHIKZ164	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19041.1	000786	virion_structural-Cluster68_1clades	312	FDH28_gp067	Ralstonia phage RP12	GCA_002617345.1
BAW19326.1	000786	virion_structural-Cluster68_1clades	312	-	Ralstonia phage RP31	GCA_002617365.1
BAS04856.1	000786	virion_structural-Cluster68_1clades	332	AVU11_gp064	Ralstonia phage RSF1	GCA_001500875.1
BAQ02590.2	000786	virion_structural-Cluster68_1clades	291	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20869.1	000786	virion_structural-Cluster68_1clades	310	-	Salmonella phage JN03	GCA_014319805.1
AWN09162.1	000786	virion_structural-Cluster68_1clades	318	MLDJOKPK_00268	Salmonella phage SPAsTU	GCA_003183805.1
AEP84006.1	000786	virion_structural-Cluster68_1clades	310	SPN3US_0173	Salmonella phage SPN3US	GCA_001042275.1
QKE54335.1	000786	virion_structural-Cluster68_1clades	320	ACSA002_0210	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65398.1	000786	virion_structural-Cluster68_1clades	327	2050HW_00063	Serratia phage 2050HW	GCA_002628125.1
QDB71178.1	000786	virion_structural-Cluster68_1clades	329	CPT_Moabite_148	Serratia phage Moabite	GCA_006384735.1
QFP93103.1	000786	virion_structural-Cluster68_1clades	330	-	Serratia phage PCH45	GCA_009187865.1
QAU04280.1	000786	virion_structural-Cluster68_1clades	350	HWC03_gp125	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23297.1	000786	virion_structural-Cluster68_1clades	350	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80981.1	000786	virion_structural-Cluster68_1clades	350	Aphrodite1_0048	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70744.1	000786	virion_structural-Cluster68_1clades	292	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47431.1	000786	virion_structural-Cluster68_1clades	350	HWC35_gp037	Vibrio phage USC-1	GCA_006864065.1
BAW98252.1	000786	virion_structural-Cluster68_1clades	374	FDH33_gp043	Vibrio phage pTD1	GCA_002618825.1
AQT28068.1	000786	virion_structural-Cluster68_1clades	356	pVa21_127	Vibrio phage pVa-21	GCA_002619305.1
QAX96786.1	000786	virion_structural-Cluster68_1clades	360	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97105.1	000786	virion_structural-Cluster68_1clades	360	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96151.1	000786	virion_structural-Cluster68_1clades	360	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96469.1	000786	virion_structural-Cluster68_1clades	360	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21281.1	000786	virion_structural-Cluster68_1clades	274	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70416.1	000787	structural_protein-Cluster69_1clades	291	CF8_0003	Aeromonas phage CF8	GCA_006384595.2
QDJ97424.1	000787	structural_protein-Cluster69_1clades	291	D6_0265	Aeromonas phage D6	GCA_007051205.2
QDH47096.1	000787	structural_protein-Cluster69_1clades	291	LAh10_172	Aeromonas phage LAh10	GCA_006863975.1
QDJ96761.1	000787	structural_protein-Cluster69_1clades	291	PS1_0003	Aeromonas phage PS1	GCA_007051165.2
QFR59394.1	000787	structural_protein-Cluster69_1clades	291	PS2_0003	Aeromonas phage PS2	GCA_009388305.2
AFO71441.1	000787	structural_protein-Cluster69_1clades	304	CR5_221	Cronobacter phage CR5	GCA_000910235.1
QBZ70810.1	000787	structural_protein-Cluster69_1clades	291	pETSU_229	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59909.1	000787	structural_protein-Cluster69_1clades	301	SEGD1_262	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07655.1	000787	structural_protein-Cluster69_1clades	304	DERBICUS_229	Erwinia phage Derbicus	GCA_004521655.1
AHI60330.1	000787	structural_protein-Cluster69_1clades	320	Ea357_178	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49907.1	000787	structural_protein-Cluster69_1clades	302	MACHINA_269	Erwinia phage Machina	GCA_002758035.1
AGX01796.1	000787	structural_protein-Cluster69_1clades	305	CF95_gp074	Erwinia phage PhiEaH1	GCA_000914555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBP07289.1	000787	structural_protein-Cluster69_1clades	334	REBECCA_182	Erwinia phage Rebecca	GCA_004521635.1
AXF51408.1	000787	structural_protein-Cluster69_1clades	301	WELLINGTON_282	Erwinia phage Wellington	GCA_003344985.1
AFQ96720.1	000787	structural_protein-Cluster69_1clades	302	G173_gp175	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48291.1	000787	structural_protein-Cluster69_1clades	302	ASESINO_278	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85969.1	000787	structural_protein-Cluster69_1clades	320	BOSOLAPHORUS_182	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48562.1	000787	structural_protein-Cluster69_1clades	302	CAITLIN_267	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48840.1	000787	structural_protein-Cluster69_1clades	302	CHRISDB_278	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52284.2	000787	structural_protein-Cluster69_1clades	320	DM_186	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86288.1	000787	structural_protein-Cluster69_1clades	320	DESERTFOX_181	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49079.1	000787	structural_protein-Cluster69_1clades	304	EARLPHILLIPIV_230	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49350.1	000787	structural_protein-Cluster69_1clades	302	HUXLEY_268	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03670.1	000787	structural_protein-Cluster69_1clades	293	JOAD_245	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49633.1	000787	structural_protein-Cluster69_1clades	301	KWAN_281	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86610.1	000787	structural_protein-Cluster69_1clades	320	MADMEL_182	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86934.1	000787	structural_protein-Cluster69_1clades	320	MORTIMER_185	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50178.1	000787	structural_protein-Cluster69_1clades	302	PARSHIK_269	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50426.1	000787	structural_protein-Cluster69_1clades	304	PHOBOS_236	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51961.1	000787	structural_protein-Cluster69_1clades	320	RAY_180	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03427.1	000787	structural_protein-Cluster69_1clades	293	RISINGSUN_243	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51645.1	000787	structural_protein-Cluster69_1clades	320	SIMMY50_183	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64992.2	000787	structural_protein-Cluster69_1clades	320	SPECIALG_182	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50702.1	000787	structural_protein-Cluster69_1clades	302	STRATTON_277	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86098.1	000787	structural_protein-Cluster69_1clades	301	ACEC001_2550	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64008.1	000787	structural_protein-Cluster69_1clades	315	Goslar_00216	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72108.1	000787	structural_protein-Cluster69_1clades	291	N1M2_245	Klebsiella phage N1M2	GCA_010092605.1
QGZ14547.1	000787	structural_protein-Cluster69_1clades	292	HWC77_gp184	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24112.1	000787	structural_protein-Cluster69_1clades	318	-	Proteus phage 10	GCA_014071245.1
ABY62863.1	000787	structural_protein-Cluster69_1clades	311	201phi2-1p029	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27101.1	000787	structural_protein-Cluster69_1clades	292	PPEV_gp007	Pseudomonas phage EL	GCA_000866825.1
ANM44796.1	000787	structural_protein-Cluster69_1clades	320	KTN4_038	Pseudomonas phage KTN4	GCA_002607225.1
ARV77191.1	000787	structural_protein-Cluster69_1clades	306	NOXIFER_20	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89440.1	000787	structural_protein-Cluster69_1clades	291	OBP_003	Pseudomonas phage OBP	GCA_000896635.1
QBX32157.1	000787	structural_protein-Cluster69_1clades	311	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76649.1	000787	structural_protein-Cluster69_1clades	310	PHABIO_18	Pseudomonas phage Phabio	GCA_002624965.1
AEH03436.1	000787	structural_protein-Cluster69_1clades	228	010	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02540.1	000787	structural_protein-Cluster69_1clades	311	PSA21_10	Pseudomonas phage Psa21	GCA_004340405.1
ATN94915.1	000787	structural_protein-Cluster69_1clades	320	SL2_338	Pseudomonas phage SL2	GCA_002956015.1
QJB22675.1	000787	structural_protein-Cluster69_1clades	320	fnug_32	Pseudomonas phage fnug	GCA_012837215.1
QEM41738.1	000787	structural_protein-Cluster69_1clades	311	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82929.1	000787	structural_protein-Cluster69_1clades	320	PHIKZ028	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19001.1	000787	structural_protein-Cluster69_1clades	307	FDH28_gp027	Ralstonia phage RP12	GCA_002617345.1
BAW19289.1	000787	structural_protein-Cluster69_1clades	307	-	Ralstonia phage RP31	GCA_002617365.1
BAS04821.1	000787	structural_protein-Cluster69_1clades	299	AVU11_gp029	Ralstonia phage RSF1	GCA_001500875.1
BAQ02554.1	000787	structural_protein-Cluster69_1clades	299	AVU38_gp026	Ralstonia phage RSL2	GCA_001503055.1
QNI20940.1	000787	structural_protein-Cluster69_1clades	355	-	Salmonella phage JN03	GCA_014319805.1
AWN09096.1	000787	structural_protein-Cluster69_1clades	301	MLDJOKPK_00183	Salmonella phage SPAsTU	GCA_003183805.1
AEP84090.1	000787	structural_protein-Cluster69_1clades	301	SPN3US_0257	Salmonella phage SPN3US	GCA_001042275.1
QKE54490.1	000787	structural_protein-Cluster69_1clades	316	ACSA002_1760	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65604.1	000787	structural_protein-Cluster69_1clades	306	2050HW_00269	Serratia phage 2050HW	GCA_002628125.1
QDB71368.1	000787	structural_protein-Cluster69_1clades	311	CPT_Moabite_338	Serratia phage Moabite	GCA_006384735.1
QFP93109.1	000787	structural_protein-Cluster69_1clades	309	-	Serratia phage PCH45	GCA_009187865.1
QAU04187.1	000787	structural_protein-Cluster69_1clades	292	HWC03_gp032	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23172.1	000787	structural_protein-Cluster69_1clades	292	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80997.1	000787	structural_protein-Cluster69_1clades	292	Aphrodite1_0170	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70779.1	000787	structural_protein-Cluster69_1clades	356	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47557.1	000787	structural_protein-Cluster69_1clades	292	HWC35_gp163	Vibrio phage USC-1	GCA_006864065.1
BAW98372.1	000787	structural_protein-Cluster69_1clades	292	FDH33_gp163	Vibrio phage pTD1	GCA_002618825.1
AQT28123.1	000787	structural_protein-Cluster69_1clades	333	pVa21_182	Vibrio phage pVa-21	GCA_002619305.1
QAX96739.1	000787	structural_protein-Cluster69_1clades	314	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97058.1	000787	structural_protein-Cluster69_1clades	314	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96104.1	000787	structural_protein-Cluster69_1clades	314	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96422.1	000787	structural_protein-Cluster69_1clades	314	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20999.1	000787	structural_protein-Cluster69_1clades	313	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70414.1	000788	virion_structural-Cluster70_1clades	300	CF8_0001	Aeromonas phage CF8	GCA_006384595.2
QDJ97422.1	000788	virion_structural-Cluster70_1clades	300	D6_0263	Aeromonas phage D6	GCA_007051205.2
QDH47092.1	000788	virion_structural-Cluster70_1clades	300	LAh10_170	Aeromonas phage LAh10	GCA_006863975.1
QDJ96759.1	000788	virion_structural-Cluster70_1clades	300	PS1_0001	Aeromonas phage PS1	GCA_007051165.2
QFR59392.1	000788	virion_structural-Cluster70_1clades	300	PS2_0001	Aeromonas phage PS2	GCA_009388305.2
AFO71439.1	000788	virion_structural-Cluster70_1clades	292	CR5_219	Cronobacter phage CR5	GCA_000910235.1
QBZ70808.1	000788	virion_structural-Cluster70_1clades	301	pETSU_227	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59907.1	000788	virion_structural-Cluster70_1clades	291	SEGD1_260	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07653.1	000788	virion_structural-Cluster70_1clades	292	DERBICUS_227	Erwinia phage Derbicus	GCA_004521655.1
AHI60328.1	000788	virion_structural-Cluster70_1clades	291	Ea357_176	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49905.1	000788	virion_structural-Cluster70_1clades	291	MACHINA_267	Erwinia phage Machina	GCA_002758035.1
AGX01798.1	000788	virion_structural-Cluster70_1clades	298	CF95_gp076	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07287.1	000788	virion_structural-Cluster70_1clades	291	REBECCA_180	Erwinia phage Rebecca	GCA_004521635.1
AXF51406.1	000788	virion_structural-Cluster70_1clades	292	WELLINGTON_280	Erwinia phage Wellington	GCA_003344985.1
AFQ96718.1	000788	virion_structural-Cluster70_1clades	292	G173_gp173	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48289.1	000788	virion_structural-Cluster70_1clades	292	ASESINO_276	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85967.1	000788	virion_structural-Cluster70_1clades	291	BOSOLAPHORUS_180	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48560.1	000788	virion_structural-Cluster70_1clades	292	CAITLIN_265	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48838.1	000788	virion_structural-Cluster70_1clades	291	CHRISDB_276	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52282.1	000788	virion_structural-Cluster70_1clades	291	DM_184	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86286.1	000788	virion_structural-Cluster70_1clades	291	DESERTFOX_179	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49077.1	000788	virion_structural-Cluster70_1clades	292	EARLPHILLIPIV_228	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49348.1	000788	virion_structural-Cluster70_1clades	291	HUXLEY_266	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03913.1	000788	virion_structural-Cluster70_1clades	298	JOAD_2	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49631.1	000788	virion_structural-Cluster70_1clades	292	KWAN_279	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86608.1	000788	virion_structural-Cluster70_1clades	291	MADMEL_180	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86932.1	000788	virion_structural-Cluster70_1clades	291	MORTIMER_183	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50176.1	000788	virion_structural-Cluster70_1clades	291	PARSHIK_267	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50424.1	000788	virion_structural-Cluster70_1clades	292	PHOBOS_234	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51959.1	000788	virion_structural-Cluster70_1clades	291	RAY_178	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03668.1	000788	virion_structural-Cluster70_1clades	298	RISINGSUN_2	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51643.1	000788	virion_structural-Cluster70_1clades	291	SIMMY50_181	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64990.1	000788	virion_structural-Cluster70_1clades	291	SPECIALG_180	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50700.1	000788	virion_structural-Cluster70_1clades	292	STRATTON_275	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86096.1	000788	virion_structural-Cluster70_1clades	291	ACEC001_2530	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64010.1	000788	virion_structural-Cluster70_1clades	296	Goslar_00218	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72106.1	000788	virion_structural-Cluster70_1clades	300	N1M2_243	Klebsiella phage N1M2	GCA_010092605.1
QGZ14545.1	000788	virion_structural-Cluster70_1clades	299	HWC77_gp182	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24110.1	000788	virion_structural-Cluster70_1clades	289	-	Proteus phage 10	GCA_014071245.1
ABY62865.1	000788	virion_structural-Cluster70_1clades	291	201phi2-1p032	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27099.1	000788	virion_structural-Cluster70_1clades	302	PPEV_gp005	Pseudomonas phage EL	GCA_000866825.1
ANM44798.1	000788	virion_structural-Cluster70_1clades	293	KTN4_040	Pseudomonas phage KTN4	GCA_002607225.1
ARV77193.1	000788	virion_structural-Cluster70_1clades	288	NOXIFER_22	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89438.1	000788	virion_structural-Cluster70_1clades	300	OBP_001	Pseudomonas phage OBP	GCA_000896635.1
QBX32159.1	000788	virion_structural-Cluster70_1clades	291	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76651.1	000788	virion_structural-Cluster70_1clades	291	PHABIO_20	Pseudomonas phage Phabio	GCA_002624965.1
AEH03438.1	000788	virion_structural-Cluster70_1clades	291	012	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02542.1	000788	virion_structural-Cluster70_1clades	289	PSA21_12	Pseudomonas phage Psa21	GCA_004340405.1
ATN94913.1	000788	virion_structural-Cluster70_1clades	293	SL2_336	Pseudomonas phage SL2	GCA_002956015.1
QJB22677.1	000788	virion_structural-Cluster70_1clades	293	fnug_34	Pseudomonas phage fnug	GCA_012837215.1
QEM41740.1	000788	virion_structural-Cluster70_1clades	291	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82931.1	000788	virion_structural-Cluster70_1clades	293	PHIKZ030	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19004.1	000788	virion_structural-Cluster70_1clades	306	FDH28_gp030	Ralstonia phage RP12	GCA_002617345.1
BAW19291.1	000788	virion_structural-Cluster70_1clades	306	-	Ralstonia phage RP31	GCA_002617365.1
BAS04823.1	000788	virion_structural-Cluster70_1clades	288	AVU11_gp031	Ralstonia phage RSF1	GCA_001500875.1
BAQ02556.1	000788	virion_structural-Cluster70_1clades	288	AVU38_gp028	Ralstonia phage RSL2	GCA_001503055.1
QNI20938.1	000788	virion_structural-Cluster70_1clades	291	-	Salmonella phage JN03	GCA_014319805.1
AWN09098.1	000788	virion_structural-Cluster70_1clades	291	MLDJOKPK_00185	Salmonella phage SPAsTU	GCA_003183805.1
AEP84088.1	000788	virion_structural-Cluster70_1clades	291	SPN3US_0255	Salmonella phage SPN3US	GCA_001042275.1
QKE54488.1	000788	virion_structural-Cluster70_1clades	288	ACSA002_1740	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65602.1	000788	virion_structural-Cluster70_1clades	289	2050HW_00267	Serratia phage 2050HW	GCA_002628125.1
QDB71366.1	000788	virion_structural-Cluster70_1clades	289	CPT_Moabite_336	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFP93114.1	000788	virion_structural-Cluster70_1clades	288	-	Serratia phage PCH45	GCA_009187865.1
QAU04189.1	000788	virion_structural-Cluster70_1clades	299	HWC03_gp034	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23170.1	000788	virion_structural-Cluster70_1clades	299	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80993.1	000788	virion_structural-Cluster70_1clades	299	Aphrodite1_0172	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70777.1	000788	virion_structural-Cluster70_1clades	290	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47559.1	000788	virion_structural-Cluster70_1clades	299	HWC35_gp165	Vibrio phage USC-1	GCA_006864065.1
BAW98374.1	000788	virion_structural-Cluster70_1clades	298	FDH33_gp165	Vibrio phage pTD1	GCA_002618825.1
AQT28121.1	000788	virion_structural-Cluster70_1clades	283	pVa21_180	Vibrio phage pVa-21	GCA_002619305.1
QAX96741.1	000788	virion_structural-Cluster70_1clades	286	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97060.1	000788	virion_structural-Cluster70_1clades	286	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96106.1	000788	virion_structural-Cluster70_1clades	286	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96424.1	000788	virion_structural-Cluster70_1clades	286	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20996.1	000788	virion_structural-Cluster70_1clades	288	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70426.1	000789	virion_structural-Cluster71_1clades	282	CF8_0013	Aeromonas phage CF8	GCA_006384595.2
QDJ97177.2	000789	virion_structural-Cluster71_1clades	288	D6_0004	Aeromonas phage D6	GCA_007051205.2
QDH47091.1	000789	virion_structural-Cluster71_1clades	301	LAh10_178	Aeromonas phage LAh10	GCA_006863975.1
QDJ96772.1	000789	virion_structural-Cluster71_1clades	283	PS1_0014	Aeromonas phage PS1	GCA_007051165.2
QFR59405.1	000789	virion_structural-Cluster71_1clades	283	PS2_0014	Aeromonas phage PS2	GCA_009388305.2
AFO71228.1	000789	virion_structural-Cluster71_1clades	270	CR5_008	Cronobacter phage CR5	GCA_000910235.1
QBZ70816.1	000789	virion_structural-Cluster71_1clades	281	pETSU_235	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59657.1	000789	virion_structural-Cluster71_1clades	270	SEGD1_006	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07435.1	000789	virion_structural-Cluster71_1clades	270	DERBICUS_8	Erwinia phage Derbicus	GCA_004521655.1
AHI60359.1	000789	virion_structural-Cluster71_1clades	283	Ea357_206	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49661.1	000789	virion_structural-Cluster71_1clades	270	MACHINA_23	Erwinia phage Machina	GCA_002758035.1
AGX01757.1	000789	virion_structural-Cluster71_1clades	276	CF95_gp035	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07316.1	000789	virion_structural-Cluster71_1clades	283	REBECCA_211	Erwinia phage Rebecca	GCA_004521635.1
AXF51149.1	000789	virion_structural-Cluster71_1clades	270	WELLINGTON_18	Erwinia phage Wellington	GCA_003344985.1
AFQ96737.1	000789	virion_structural-Cluster71_1clades	270	G173_gp192	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48038.1	000789	virion_structural-Cluster71_1clades	270	ASESINO_25	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85997.1	000789	virion_structural-Cluster71_1clades	283	BOSOLAPHORUS_211	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48312.1	000789	virion_structural-Cluster71_1clades	270	CAITLIN_17	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48585.1	000789	virion_structural-Cluster71_1clades	270	CHRISDB_23	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52314.1	000789	virion_structural-Cluster71_1clades	283	DM_214	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86316.1	000789	virion_structural-Cluster71_1clades	283	DESERTFOX_209	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48858.1	000789	virion_structural-Cluster71_1clades	270	EARLPHILLIPIV_8	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49106.1	000789	virion_structural-Cluster71_1clades	270	HUXLEY_24	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03912.1	000789	virion_structural-Cluster71_1clades	281	JOAD_3	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49371.1	000789	virion_structural-Cluster71_1clades	270	KWAN_18	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86639.1	000789	virion_structural-Cluster71_1clades	283	MADMEL_211	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86962.1	000789	virion_structural-Cluster71_1clades	283	MORTIMER_214	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49934.1	000789	virion_structural-Cluster71_1clades	270	PARSHIK_25	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50198.1	000789	virion_structural-Cluster71_1clades	270	PHOBOS_8	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51989.1	000789	virion_structural-Cluster71_1clades	283	RAY_209	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03667.1	000789	virion_structural-Cluster71_1clades	281	RISINGSUN_3	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51673.1	000789	virion_structural-Cluster71_1clades	283	SIMMY50_214	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65023.1	000789	virion_structural-Cluster71_1clades	283	SPECIALG_212	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50448.1	000789	virion_structural-Cluster71_1clades	270	STRATTON_23	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85846.1	000789	virion_structural-Cluster71_1clades	270	ACEC001_0090	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63994.1	000789	virion_structural-Cluster71_1clades	280	Goslar_00202	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72114.1	000789	virion_structural-Cluster71_1clades	225	N1M2_251	Klebsiella phage N1M2	GCA_010092605.1
QGZ14555.1	000789	virion_structural-Cluster71_1clades	281	HWC77_gp192	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24133.1	000789	virion_structural-Cluster71_1clades	283	-	Proteus phage 10	GCA_014071245.1
ABY62906.1	000789	virion_structural-Cluster71_1clades	274	201phi2-1p073	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27108.1	000789	virion_structural-Cluster71_1clades	282	PPEV_gp014	Pseudomonas phage EL	GCA_000866825.1
ANM44816.1	000789	virion_structural-Cluster71_1clades	266	KTN4_058	Pseudomonas phage KTN4	GCA_002607225.1
ARV77205.1	000789	virion_structural-Cluster71_1clades	268	NOXIFER_34	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89447.1	000789	virion_structural-Cluster71_1clades	282	OBP_010	Pseudomonas phage OBP	GCA_000896635.1
QBX32190.1	000789	virion_structural-Cluster71_1clades	270	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76688.1	000789	virion_structural-Cluster71_1clades	272	PHABIO_57	Pseudomonas phage Phabio	GCA_002624965.1
AEH03464.1	000789	virion_structural-Cluster71_1clades	266	037	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02566.1	000789	virion_structural-Cluster71_1clades	270	PSA21_36	Pseudomonas phage Psa21	GCA_004340405.1
ATN94895.1	000789	virion_structural-Cluster71_1clades	266	SL2_318	Pseudomonas phage SL2	GCA_002956015.1
QJB22695.1	000789	virion_structural-Cluster71_1clades	266	fnug_52	Pseudomonas phage fnug	GCA_012837215.1
QEM41768.1	000789	virion_structural-Cluster71_1clades	270	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82943.1	000789	virion_structural-Cluster71_1clades	266	PHIKZ042	Pseudomonas virus phiKZ	GCA_000842965.1
BAW18990.1	000789	virion_structural-Cluster71_1clades	267	FDH28_gp016	Ralstonia phage RP12	GCA_002617345.1
BAW19278.1	000789	virion_structural-Cluster71_1clades	267	-	Ralstonia phage RP31	GCA_002617365.1
BAS04804.1	000789	virion_structural-Cluster71_1clades	270	AVU11_gp012	Ralstonia phage RSF1	GCA_001500875.1
BAQ02540.1	000789	virion_structural-Cluster71_1clades	270	AVU38_gp012	Ralstonia phage RSL2	GCA_001503055.1
QNI20726.1	000789	virion_structural-Cluster71_1clades	270	-	Salmonella phage JN03	GCA_014319805.1
AWN09085.1	000789	virion_structural-Cluster71_1clades	270	MLDJOKPK_00159	Salmonella phage SPAsTU	GCA_003183805.1
AEP83841.1	000789	virion_structural-Cluster71_1clades	270	SPN3US_0008	Salmonella phage SPN3US	GCA_001042275.1
QKE54533.1	000789	virion_structural-Cluster71_1clades	282	ACSA002_2170	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65629.1	000789	virion_structural-Cluster71_1clades	277	2050HW_00294	Serratia phage 2050HW	GCA_002628125.1
QDB71056.1	000789	virion_structural-Cluster71_1clades	277	CPT_Moabite_024	Serratia phage Moabite	GCA_006384735.1
QFP93120.1	000789	virion_structural-Cluster71_1clades	278	-	Serratia phage PCH45	GCA_009187865.1
QAU04179.1	000789	virion_structural-Cluster71_1clades	281	HWC03_gp024	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23180.1	000789	virion_structural-Cluster71_1clades	281	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80999.1	000789	virion_structural-Cluster71_1clades	281	Aphrodite1_0162	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70799.1	000789	virion_structural-Cluster71_1clades	252	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47549.1	000789	virion_structural-Cluster71_1clades	281	HWC35_gp155	Vibrio phage USC-1	GCA_006864065.1
BAW98362.1	000789	virion_structural-Cluster71_1clades	281	FDH33_gp153	Vibrio phage pTD1	GCA_002618825.1
AQT28140.1	000789	virion_structural-Cluster71_1clades	271	pVa21_199	Vibrio phage pVa-21	GCA_002619305.1
QAX96710.1	000789	virion_structural-Cluster71_1clades	260	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97028.1	000789	virion_structural-Cluster71_1clades	260	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96074.1	000789	virion_structural-Cluster71_1clades	260	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96392.1	000789	virion_structural-Cluster71_1clades	260	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21035.1	000789	virion_structural-Cluster71_1clades	254	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70474.1	000790	virion_structural-Cluster72_1clades	271	CF8_0062	Aeromonas phage CF8	GCA_006384595.2
QDJ97214.1	000790	virion_structural-Cluster72_1clades	268	D6_0054	Aeromonas phage D6	GCA_007051205.2
QDH47103.1	000790	virion_structural-Cluster72_1clades	268	LAh10_220	Aeromonas phage LAh10	GCA_006863975.1
QDJ96821.1	000790	virion_structural-Cluster72_1clades	270	PS1_0062	Aeromonas phage PS1	GCA_007051165.2
QFR59450.1	000790	virion_structural-Cluster72_1clades	270	PS2_0059	Aeromonas phage PS2	GCA_009388305.2
AFO71249.1	000790	virion_structural-Cluster72_1clades	273	CR5_029	Cronobacter phage CR5	GCA_000910235.1
QBZ70592.1	000790	virion_structural-Cluster72_1clades	263	pETSU_011	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59679.1	000790	virion_structural-Cluster72_1clades	278	SEGD1_030	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07456.1	000790	virion_structural-Cluster72_1clades	273	DERBICUS_30	Erwinia phage Derbicus	GCA_004521655.1
AHI60390.1	000790	virion_structural-Cluster72_1clades	266	Ea357_237	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49682.1	000790	virion_structural-Cluster72_1clades	281	MACHINA_44	Erwinia phage Machina	GCA_002758035.1
AGX01738.1	000790	virion_structural-Cluster72_1clades	286	CF95_gp016	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07346.1	000790	virion_structural-Cluster72_1clades	266	REBECCA_241	Erwinia phage Rebecca	GCA_004521635.1
AXF51171.1	000790	virion_structural-Cluster72_1clades	272	WELLINGTON_40	Erwinia phage Wellington	GCA_003344985.1
AFQ96755.1	000790	virion_structural-Cluster72_1clades	278	G173_gp210	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48058.1	000790	virion_structural-Cluster72_1clades	278	ASESINO_45	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86028.1	000790	virion_structural-Cluster72_1clades	266	BOSOLAPHORUS_242	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48333.1	000790	virion_structural-Cluster72_1clades	274	CAITLIN_38	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48606.1	000790	virion_structural-Cluster72_1clades	273	CHRISDB_44	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52345.2	000790	virion_structural-Cluster72_1clades	266	DM_245	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86347.1	000790	virion_structural-Cluster72_1clades	266	DESERTFOX_240	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48880.1	000790	virion_structural-Cluster72_1clades	273	EARLPHILLIPIV_30	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49127.1	000790	virion_structural-Cluster72_1clades	281	HUXLEY_45	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03878.1	000790	virion_structural-Cluster72_1clades	260	JOAD_37	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49392.1	000790	virion_structural-Cluster72_1clades	272	KWAN_40	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86670.1	000790	virion_structural-Cluster72_1clades	266	MADMEL_243	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86993.1	000790	virion_structural-Cluster72_1clades	266	MORTIMER_245	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49955.1	000790	virion_structural-Cluster72_1clades	281	PARSHIK_46	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50220.1	000790	virion_structural-Cluster72_1clades	273	PHOBOS_30	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52019.1	000790	virion_structural-Cluster72_1clades	266	RAY_239	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03633.1	000790	virion_structural-Cluster72_1clades	260	RISINGSUN_37	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51703.1	000790	virion_structural-Cluster72_1clades	266	SIMMY50_244	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65054.1	000790	virion_structural-Cluster72_1clades	266	SPECIALG_243	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50468.1	000790	virion_structural-Cluster72_1clades	278	STRATTON_43	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85869.1	000790	virion_structural-Cluster72_1clades	278	ACEC001_0310	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63970.1	000790	virion_structural-Cluster72_1clades	265	Goslar_00177	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71908.1	000790	virion_structural-Cluster72_1clades	264	N1M2_45	Klebsiella phage N1M2	GCA_010092605.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGZ14376.1	000790	virion_structural-Cluster72_1clades	265	HWC77_gp013	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24159.1	000790	virion_structural-Cluster72_1clades	265	-	Proteus phage 10	GCA_014071245.1
ABY62954.1	000790	virion_structural-Cluster72_1clades	274	201phi2-1p122	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27125.1	000790	virion_structural-Cluster72_1clades	265	PPEV_gp031	Pseudomonas phage EL	GCA_000866825.1
ANM44846.1	000790	virion_structural-Cluster72_1clades	276	KTN4_088	Pseudomonas phage KTN4	GCA_002607225.1
ARV77230.1	000790	virion_structural-Cluster72_1clades	277	NOXIFER_59	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89503.1	000790	virion_structural-Cluster72_1clades	266	OBP_066	Pseudomonas phage OBP	GCA_000896635.1
QBX32214.1	000790	virion_structural-Cluster72_1clades	275	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76733.1	000790	virion_structural-Cluster72_1clades	275	PHABIO_102	Pseudomonas phage Phabio	GCA_002624965.1
AEH03487.1	000790	virion_structural-Cluster72_1clades	276	060	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02597.1	000790	virion_structural-Cluster72_1clades	277	PSA21_68	Pseudomonas phage Psa21	GCA_004340405.1
ATN94867.1	000790	virion_structural-Cluster72_1clades	276	SL2_290	Pseudomonas phage SL2	GCA_002956015.1
QJB22724.1	000790	virion_structural-Cluster72_1clades	276	fnug_81	Pseudomonas phage fnug	GCA_012837215.1
QEM41792.1	000790	virion_structural-Cluster72_1clades	275	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82967.1	000790	virion_structural-Cluster72_1clades	276	PHIKZ066	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19255.1	000790	virion_structural-Cluster72_1clades	276	FDH28_gp140	Ralstonia phage RP12	GCA_002617345.1
BAW19541.1	000790	virion_structural-Cluster72_1clades	276	-	Ralstonia phage RP31	GCA_002617365.1
BAS05013.2	000790	virion_structural-Cluster72_1clades	281	AVU11_gp221	Ralstonia phage RSF1	GCA_001500875.1
BAQ02743.1	000790	virion_structural-Cluster72_1clades	278	AVU38_gp215	Ralstonia phage RSL2	GCA_001503055.1
QNI20744.1	000790	virion_structural-Cluster72_1clades	278	-	Salmonella phage JN03	GCA_014319805.1
AWN09067.1	000790	virion_structural-Cluster72_1clades	278	MLDJOKPK_00137	Salmonella phage SPAsTU	GCA_003183805.1
AEP83861.1	000790	virion_structural-Cluster72_1clades	278	SPN3US_0028	Salmonella phage SPN3US	GCA_001042275.1
QKE54566.1	000790	virion_structural-Cluster72_1clades	266	ACSA002_2500	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65655.1	000790	virion_structural-Cluster72_1clades	274	2050HW_00320	Serratia phage 2050HW	GCA_002628125.1
QDB71079.1	000790	virion_structural-Cluster72_1clades	274	CPT_Moabite_047	Serratia phage Moabite	GCA_006384735.1
QFP93122.1	000790	virion_structural-Cluster72_1clades	276	-	Serratia phage PCH45	GCA_009187865.1
QAU04360.1	000790	virion_structural-Cluster72_1clades	265	HWC03_gp205	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23216.1	000790	virion_structural-Cluster72_1clades	265	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81002.1	000790	virion_structural-Cluster72_1clades	265	Aphrodite1_0129	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70818.1	000790	virion_structural-Cluster72_1clades	264	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47512.1	000790	virion_structural-Cluster72_1clades	256	HWC35_gp118	Vibrio phage USC-1	GCA_006864065.1
BAW98331.1	000790	virion_structural-Cluster72_1clades	262	FDH33_gp122	Vibrio phage pTD1	GCA_002618825.1
AQT28155.1	000790	virion_structural-Cluster72_1clades	275	pVa21_214	Vibrio phage pVa-21	GCA_002619305.1
QAX96679.1	000790	virion_structural-Cluster72_1clades	264	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96997.1	000790	virion_structural-Cluster72_1clades	264	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96043.1	000790	virion_structural-Cluster72_1clades	264	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96361.1	000790	virion_structural-Cluster72_1clades	264	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21063.1	000790	virion_structural-Cluster72_1clades	265	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70468.1	000791	Cluster74_1clades	224	CF8_0055	Aeromonas phage CF8	GCA_006384595.2
QDJ97207.1	000791	Cluster74_1clades	221	D6_0047	Aeromonas phage D6	GCA_007051205.2
QDH47134.1	000791	Cluster74_1clades	221	LAh10_214	Aeromonas phage LAh10	GCA_006863975.1
QDJ96812.1	000791	Cluster74_1clades	216	PS1_0053	Aeromonas phage PS1	GCA_007051165.2
QFR59443.1	000791	Cluster74_1clades	216	PS2_0052	Aeromonas phage PS2	GCA_009388305.2
AFO71245.1	000791	Cluster74_1clades	194	CR5_025	Cronobacter phage CR5	GCA_000910235.1
QBZ70586.1	000791	Cluster74_1clades	222	pETSU_005	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59675.1	000791	Cluster74_1clades	193	SEGD1_026	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07452.1	000791	Cluster74_1clades	194	DERBICUS_26	Erwinia phage Derbicus	GCA_004521655.1
AHI60379.1	000791	Cluster74_1clades	215	Ea357_226	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49678.1	000791	Cluster74_1clades	193	MACHINA_40	Erwinia phage Machina	GCA_002758035.1
AGX01742.1	000791	Cluster74_1clades	211	-	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07336.1	000791	Cluster74_1clades	215	REBECCA_231	Erwinia phage Rebecca	GCA_004521635.1
AXF51167.1	000791	Cluster74_1clades	196	WELLINGTON_36	Erwinia phage Wellington	GCA_003344985.1
AFQ96751.1	000791	Cluster74_1clades	176	G173_gp206	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48054.1	000791	Cluster74_1clades	193	ASESINO_41	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86017.1	000791	Cluster74_1clades	215	BOSOLAPHORUS_231	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48329.1	000791	Cluster74_1clades	193	CAITLIN_34	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48602.1	000791	Cluster74_1clades	193	CHRISDB_40	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52335.1	000791	Cluster74_1clades	215	DM_235	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86336.1	000791	Cluster74_1clades	215	DESERTFOX_229	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48876.1	000791	Cluster74_1clades	192	EARLPHILLIPIV_26	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49123.1	000791	Cluster74_1clades	193	HUXLEY_41	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03885.1	000791	Cluster74_1clades	214	JOAD_30	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49388.1	000791	Cluster74_1clades	196	KWAN_36	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86661.1	000791	Cluster74_1clades	215	MADMEL_233	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86982.1	000791	Cluster74_1clades	215	MORTIMER_234	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49951.1	000791	Cluster74_1clades	193	PARSHIK_42	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50216.1	000791	Cluster74_1clades	192	PHOBOS_26	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52009.1	000791	Cluster74_1clades	215	RAY_229	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03640.1	000791	Cluster74_1clades	214	RISINGSUN_30	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51693.1	000791	Cluster74_1clades	215	SIMMY50_234	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65044.1	000791	Cluster74_1clades	215	SPECIALG_233	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50464.1	000791	Cluster74_1clades	193	STRATTON_39	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85865.1	000791	Cluster74_1clades	193	ACEC001_0270	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63977.1	000791	Cluster74_1clades	212	Goslar_00184	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71901.1	000791	Cluster74_1clades	222	N1M2_38	Klebsiella phage N1M2	GCA_010092605.1
QGZ14370.1	000791	Cluster74_1clades	219	HWC77_gp007	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24149.1	000791	Cluster74_1clades	206	-	Proteus phage 10	GCA_014071245.1
ABY62946.1	000791	Cluster74_1clades	203	201phi2-1p114	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27121.1	000791	Cluster74_1clades	213	PPEV_gp027	Pseudomonas phage EL	GCA_000866825.1
ANM44839.1	000791	Cluster74_1clades	203	KTN4_081	Pseudomonas phage KTN4	GCA_002607225.1
ARV77223.1	000791	Cluster74_1clades	203	NOXIFER_52	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89496.1	000791	Cluster74_1clades	223	OBP_059	Pseudomonas phage OBP	GCA_000896635.1
QBX32208.1	000791	Cluster74_1clades	204	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76724.1	000791	Cluster74_1clades	204	PHABIO_93	Pseudomonas phage Phabio	GCA_002624965.1
AEH03482.1	000791	Cluster74_1clades	203	055	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02589.1	000791	Cluster74_1clades	202	PSA21_60	Pseudomonas phage Psa21	GCA_004340405.1
ATN94874.1	000791	Cluster74_1clades	203	SL2_297	Pseudomonas phage SL2	GCA_002956015.1
QJB22717.1	000791	Cluster74_1clades	203	fnug_74	Pseudomonas phage fnug	GCA_012837215.1
QEM41786.1	000791	Cluster74_1clades	204	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82960.1	000791	Cluster74_1clades	203	PHIKZ059	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19260.1	000791	Cluster74_1clades	207	FDH28_gp135	Ralstonia phage RP12	GCA_002617345.1
BAW19547.1	000791	Cluster74_1clades	207	-	Ralstonia phage RP31	GCA_002617365.1
BAS05018.1	000791	Cluster74_1clades	218	AVU11_gp226	Ralstonia phage RSF1	GCA_001500875.1
BAQ02748.2	000791	Cluster74_1clades	192	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20740.1	000791	Cluster74_1clades	193	-	Salmonella phage JN03	GCA_014319805.1
AWN09071.2	000791	Cluster74_1clades	197	MLDJOKPK_00142	Salmonella phage SPAsTU	GCA_003183805.1
AEP83857.1	000791	Cluster74_1clades	193	SPN3US_0024	Salmonella phage SPN3US	GCA_001042275.1
QKE54552.1	000791	Cluster74_1clades	209	ACSA002_2360	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65650.1	000791	Cluster74_1clades	206	2050HW_00315	Serratia phage 2050HW	GCA_002628125.1
QDB71074.1	000791	Cluster74_1clades	206	CPT_Moabite_042	Serratia phage Moabite	GCA_006384735.1
QFP93158.1	000791	Cluster74_1clades	205	-	Serratia phage PCH45	GCA_009187865.1
QAU04366.1	000791	Cluster74_1clades	219	HWC03_gp211	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23210.1	000791	Cluster74_1clades	218	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81021.1	000791	Cluster74_1clades	218	Aphrodite1_0135	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70814.1	000791	Cluster74_1clades	212	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47518.1	000791	Cluster74_1clades	218	HWC35_gp124	Vibrio phage USC-1	GCA_006864065.1
BAW98337.1	000791	Cluster74_1clades	197	FDH33_gp128	Vibrio phage pTD1	GCA_002618825.1
AQT28151.1	000791	Cluster74_1clades	205	pVa21_210	Vibrio phage pVa-21	GCA_002619305.1
QAX96683.1	000791	Cluster74_1clades	209	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97001.1	000791	Cluster74_1clades	209	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96047.1	000791	Cluster74_1clades	209	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96365.1	000791	Cluster74_1clades	209	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21059.1	000791	Cluster74_1clades	201	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70375.1	000792	virion-structural-Cluster76_1clades	210	CF8_0206	Aeromonas phage CF8	GCA_006384595.2
QDJ97374.1	000792	virion-structural-Cluster76_1clades	216	D6_0215	Aeromonas phage D6	GCA_007051205.2
QDH47135.1	000792	virion-structural-Cluster76_1clades	216	LAh10_129	Aeromonas phage LAh10	GCA_006863975.1
QDJ96717.1	000792	virion-structural-Cluster76_1clades	211	PS1_0206	Aeromonas phage PS1	GCA_007051165.2
QFR59350.1	000792	virion-structural-Cluster76_1clades	211	PS2_0208	Aeromonas phage PS2	GCA_009388305.2
AFO71401.1	000792	virion-structural-Cluster76_1clades	203	CR5_181	Cronobacter phage CR5	GCA_000910235.1
QBZ70759.1	000792	virion-structural-Cluster76_1clades	211	pETSU_178	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59854.1	000792	virion-structural-Cluster76_1clades	207	SEGD1_207	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07613.1	000792	virion-structural-Cluster76_1clades	203	DERBICUS_187	Erwinia phage Derbicus	GCA_004521655.1
AHI60294.1	000792	virion-structural-Cluster76_1clades	212	Ea357_143	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49851.1	000792	virion-structural-Cluster76_1clades	205	MACHINA_213	Erwinia phage Machina	GCA_002758035.1
AGX01902.1	000792	virion-structural-Cluster76_1clades	205	CF95_gp180	Erwinia phage PhiEaH1	GCA_000914555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBP07252.1	000792	virion-structural-Cluster76_1clades	212	REBECCA_145	Erwinia phage Rebecca	GCA_004521635.1
AXF51353.1	000792	virion-structural-Cluster76_1clades	211	WELLINGTON_227	Erwinia phage Wellington	GCA_003344985.1
AFQ96668.1	000792	virion-structural-Cluster76_1clades	207	G173_gp123	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48234.1	000792	virion-structural-Cluster76_1clades	207	ASESINO_221	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85932.1	000792	virion-structural-Cluster76_1clades	212	BOSOLAPHORUS_145	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48508.1	000792	virion-structural-Cluster76_1clades	205	CAITLIN_213	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48785.1	000792	virion-structural-Cluster76_1clades	205	CHRISDB_223	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52247.1	000792	virion-structural-Cluster76_1clades	212	DM_149	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86251.1	000792	virion-structural-Cluster76_1clades	212	DESERTFOX_144	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49037.1	000792	virion-structural-Cluster76_1clades	203	EARLPHILLIPIV_188	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49295.1	000792	virion-structural-Cluster76_1clades	205	HUXLEY_213	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03700.1	000792	virion-structural-Cluster76_1clades	211	JOAD_215	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49579.1	000792	virion-structural-Cluster76_1clades	211	KWAN_227	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86573.1	000792	virion-structural-Cluster76_1clades	212	MADMEL_145	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86897.1	000792	virion-structural-Cluster76_1clades	212	MORTIMER_148	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50123.1	000792	virion-structural-Cluster76_1clades	205	PARSHIK_214	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50385.1	000792	virion-structural-Cluster76_1clades	205	PHOBOS_195	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51925.1	000792	virion-structural-Cluster76_1clades	212	RAY_144	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03457.1	000792	virion-structural-Cluster76_1clades	211	RISINGSUN_213	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51609.1	000792	virion-structural-Cluster76_1clades	212	SIMMY50_147	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64956.1	000792	virion-structural-Cluster76_1clades	212	SPECIALG_146	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50648.1	000792	virion-structural-Cluster76_1clades	207	STRATTON_223	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86042.1	000792	virion-structural-Cluster76_1clades	207	ACEC001_1990	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64040.1	000792	virion-structural-Cluster76_1clades	208	Goslar_00249	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72066.1	000792	virion-structural-Cluster76_1clades	212	N1M2_203	Klebsiella phage N1M2	GCA_010092605.1
QGZ14495.1	000792	virion-structural-Cluster76_1clades	211	HWC77_gp132	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24075.1	000792	virion-structural-Cluster76_1clades	212	-	Proteus phage 10	GCA_014071245.1
ABY63073.1	000792	virion-structural-Cluster76_1clades	207	201phi2-1p245	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27262.1	000792	virion-structural-Cluster76_1clades	210	PPEV_gp168	Pseudomonas phage EL	GCA_000866825.1
ANM44956.1	000792	virion-structural-Cluster76_1clades	211	KTN4_198	Pseudomonas phage KTN4	GCA_002607225.1
ARV77343.1	000792	virion-structural-Cluster76_1clades	204	NOXIFER_174	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89695.1	000792	virion-structural-Cluster76_1clades	212	OBP_258	Pseudomonas phage OBP	GCA_000896635.1
QBX32343.1	000792	virion-structural-Cluster76_1clades	209	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76864.1	000792	virion-structural-Cluster76_1clades	207	PHABIO_233	Pseudomonas phage Phabio	GCA_002624965.1
AEH03608.1	000792	virion-structural-Cluster76_1clades	210	185	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02742.1	000792	virion-structural-Cluster76_1clades	207	PSA21_216	Pseudomonas phage Psa21	GCA_004340405.1
ATN94758.1	000792	virion-structural-Cluster76_1clades	211	SL2_181	Pseudomonas phage SL2	GCA_002956015.1
QJB22834.1	000792	virion-structural-Cluster76_1clades	211	fnug_191	Pseudomonas phage fnug	GCA_012837215.1
QEM41917.1	000792	virion-structural-Cluster76_1clades	209	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83062.2	000792	virion-structural-Cluster76_1clades	203	PHIKZ161	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19040.1	000792	virion-structural-Cluster76_1clades	210	FDH28_gp066	Ralstonia phage RP12	GCA_002617345.1
BAW19325.1	000792	virion-structural-Cluster76_1clades	210	-	Ralstonia phage RP31	GCA_002617365.1
BAS04852.1	000792	virion-structural-Cluster76_1clades	209	AVU11_gp060	Ralstonia phage RSF1	GCA_001500875.1
BAQ02586.1	000792	virion-structural-Cluster76_1clades	210	AVU38_gp058	Ralstonia phage RSL2	GCA_001503055.1
QNI20890.1	000792	virion-structural-Cluster76_1clades	207	-	Salmonella phage JN03	GCA_014319805.1
AWN09143.1	000792	virion-structural-Cluster76_1clades	207	MLDJOKPK_00238	Salmonella phage SPAsTU	GCA_003183805.1
AEP84035.1	000792	virion-structural-Cluster76_1clades	207	SPN3US_0202	Salmonella phage SPN3US	GCA_001042275.1
QKE54448.1	000792	virion-structural-Cluster76_1clades	204	ACSA002_1340	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65406.1	000792	virion-structural-Cluster76_1clades	202	2050HW_00071	Serratia phage 2050HW	GCA_002628125.1
QDB71185.1	000792	virion-structural-Cluster76_1clades	202	CPT_Moabite_155	Serratia phage Moabite	GCA_006384735.1
QFP93161.1	000792	virion-structural-Cluster76_1clades	203	-	Serratia phage PCH45	GCA_009187865.1
QAU04239.1	000792	virion-structural-Cluster76_1clades	211	HWC03_gp084	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23124.1	000792	virion-structural-Cluster76_1clades	211	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81023.1	000792	virion-structural-Cluster76_1clades	211	Aphrodite1_0007	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70747.1	000792	virion-structural-Cluster76_1clades	200	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47603.1	000792	virion-structural-Cluster76_1clades	211	HWC35_gp209	Vibrio phage USC-1	GCA_006864065.1
BAW98418.1	000792	virion-structural-Cluster76_1clades	210	FDH33_gp209	Vibrio phage pTD1	GCA_002618825.1
AQT28076.1	000792	virion-structural-Cluster76_1clades	217	pVa21_135	Vibrio phage pVa-21	GCA_002619305.1
QAX96791.1	000792	virion-structural-Cluster76_1clades	199	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97110.1	000792	virion-structural-Cluster76_1clades	199	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96156.1	000792	virion-structural-Cluster76_1clades	199	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96474.1	000792	virion-structural-Cluster76_1clades	199	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20957.1	000792	virion-structural-Cluster76_1clades	203	-	Vibrio phage vB_pir03	GCA_014319855.1
QDB70387.1	000793	virion-structural-Cluster78_1clades	243	CF8_0218	Aeromonas phage CF8	GCA_006384595.2
QDJ97386.1	000793	virion-structural-Cluster78_1clades	242	D6_0227	Aeromonas phage D6	GCA_007051205.2
QDH47117.1	000793	virion-structural-Cluster78_1clades	242	LAh10_141	Aeromonas phage LAh10	GCA_006863975.1
QDJ96729.1	000793	virion-structural-Cluster78_1clades	242	PS1_0218	Aeromonas phage PS1	GCA_007051165.2
QFR59362.1	000793	virion-structural-Cluster78_1clades	242	PS2_0220	Aeromonas phage PS2	GCA_009388305.2
AFO71414.1	000793	virion-structural-Cluster78_1clades	240	CR5_194	Cronobacter phage CR5	GCA_000910235.1
QBZ70772.1	000793	virion-structural-Cluster78_1clades	241	pETSU_191	Edwardsiella virus pEt-SU	GCA_004800915.1
QBP07627.1	000793	virion-structural-Cluster78_1clades	240	DERBICUS_201	Erwinia phage Derbicus	GCA_004521655.1
AHI60306.1	000793	virion-structural-Cluster78_1clades	242	Ea357_155	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49870.1	000793	virion-structural-Cluster78_1clades	242	MACHINA_232	Erwinia phage Machina	GCA_002758035.1
AGX01891.1	000793	virion-structural-Cluster78_1clades	236	CF95_gp169	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07264.1	000793	virion-structural-Cluster78_1clades	242	REBECCA_157	Erwinia phage Rebecca	GCA_004521635.1
AXF51373.1	000793	virion-structural-Cluster78_1clades	242	WELLINGTON_247	Erwinia phage Wellington	GCA_003344985.1
AFQ96686.1	000793	virion-structural-Cluster78_1clades	243	G173_gp141	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48254.1	000793	virion-structural-Cluster78_1clades	243	ASESINO_241	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85944.1	000793	virion-structural-Cluster78_1clades	242	BOSOLAPHORUS_157	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48527.1	000793	virion-structural-Cluster78_1clades	243	CAITLIN_232	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48804.1	000793	virion-structural-Cluster78_1clades	242	CHRISDB_242	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52259.1	000793	virion-structural-Cluster78_1clades	242	DM_161	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86263.1	000793	virion-structural-Cluster78_1clades	242	DESERTFOX_156	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49051.1	000793	virion-structural-Cluster78_1clades	240	EARLPHILLIPIV_202	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49314.1	000793	virion-structural-Cluster78_1clades	242	HUXLEY_232	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03691.1	000793	virion-structural-Cluster78_1clades	247	JOAD_224	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49599.1	000793	virion-structural-Cluster78_1clades	242	KWAN_247	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86585.1	000793	virion-structural-Cluster78_1clades	242	MADMEL_157	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86909.1	000793	virion-structural-Cluster78_1clades	242	MORTIMER_160	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50142.1	000793	virion-structural-Cluster78_1clades	242	PARSHIK_233	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50398.1	000793	virion-structural-Cluster78_1clades	240	PHOBOS_208	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51937.1	000793	virion-structural-Cluster78_1clades	242	RAY_156	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03448.1	000793	virion-structural-Cluster78_1clades	247	RISINGSUN_222	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51621.1	000793	virion-structural-Cluster78_1clades	242	SIMMY50_159	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64968.1	000793	virion-structural-Cluster78_1clades	242	SPECIALG_158	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50667.1	000793	virion-structural-Cluster78_1clades	243	STRATTON_242	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86060.1	000793	virion-structural-Cluster78_1clades	242	ACEC001_2170	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64029.1	000793	virion-structural-Cluster78_1clades	262	Goslar_00238	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72078.1	000793	virion-structural-Cluster78_1clades	242	N1M2_215	Klebsiella phage N1M2	GCA_010092605.1
QGZ14504.1	000793	virion-structural-Cluster78_1clades	241	HWC77_gp141	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24085.1	000793	virion-structural-Cluster78_1clades	254	-	Proteus phage 10	GCA_014071245.1
ABY63060.1	000793	virion-structural-Cluster78_1clades	241	201phi2-1p231	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27271.1	000793	virion-structural-Cluster78_1clades	260	PPEV_gp177	Pseudomonas phage EL	GCA_000866825.1
ANM44941.1	000793	virion-structural-Cluster78_1clades	238	KTN4_183	Pseudomonas phage KTN4	GCA_002607225.1
ARV77325.1	000793	virion-structural-Cluster78_1clades	233	NOXIFER_156	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89707.1	000793	virion-structural-Cluster78_1clades	244	OBP_270	Pseudomonas phage OBP	GCA_000896635.1
QBX32328.1	000793	virion-structural-Cluster78_1clades	253	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76850.1	000793	virion-structural-Cluster78_1clades	241	PHABIO_219	Pseudomonas phage Phabio	GCA_002624965.1
AEH03593.1	000793	virion-structural-Cluster78_1clades	237	170	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02729.1	000793	virion-structural-Cluster78_1clades	253	PSA21_203	Pseudomonas phage Psa21	GCA_004340405.1
ATN94773.1	000793	virion-structural-Cluster78_1clades	238	SL2_196	Pseudomonas phage SL2	GCA_002956015.1
QJB22819.1	000793	virion-structural-Cluster78_1clades	238	fnug_176	Pseudomonas phage fnug	GCA_012837215.1
QEM41901.1	000793	virion-structural-Cluster78_1clades	253	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83048.1	000793	virion-structural-Cluster78_1clades	238	PHIKZ147	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19026.1	000793	virion-structural-Cluster78_1clades	323	FDH28_gp052	Ralstonia phage RP12	GCA_002617345.1
BAW19312.1	000793	virion-structural-Cluster78_1clades	323	-	Ralstonia phage RP31	GCA_002617365.1
BAS04841.1	000793	virion-structural-Cluster78_1clades	264	AVU11_gp049	Ralstonia phage RSF1	GCA_001500875.1
BAQ02574.1	000793	virion-structural-Cluster78_1clades	264	AVU38_gp046	Ralstonia phage RSL2	GCA_001503055.1
QNI20906.1	000793	virion-structural-Cluster78_1clades	242	-	Salmonella phage JN03	GCA_014319805.1
AXF51114.1	000793	virion-structural-Cluster78_1clades	240	MLDJOKPK_00221	Salmonella phage SPAsTU	GCA_003183805.1
AEP84052.1	000793	virion-structural-Cluster78_1clades	242	SPN3US_0219	Salmonella phage SPN3US	GCA_001042275.1
QKE54460.1	000793	virion-structural-Cluster78_1clades	241	ACSA002_1460	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65418.1	000793	virion-structural-Cluster78_1clades	133	2050HW_00083	Serratia phage 2050HW	GCA_002628125.1
QDB71196.1	000793	virion-structural-Cluster78_1clades	233	CPT_Moabite_166	Serratia phage Moabite	GCA_006384735.1
QFP93123.1	000793	virion-structural-Cluster78_1clades	266	-	Serratia phage PCH45	GCA_009187865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAU04230.1	000793	virion-structural-Cluster78_1clades	241	HWC03_gp075	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23133.1	000793	virion-structural-Cluster78_1clades	244	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81010.1	000793	virion-structural-Cluster78_1clades	244	Aphrodite1_0207	Vibrio phage Aphrodite1	GCA_002958015.1
AXH70758.1	000793	virion-structural-Cluster78_1clades	232	-	Vibrio phage BONAISHI	GCA_003441475.1
QDH47594.1	000793	virion-structural-Cluster78_1clades	244	HWC35_gp200	Vibrio phage USC-1	GCA_006864065.1
BAW98409.1	000793	virion-structural-Cluster78_1clades	245	FDH33_gp200	Vibrio phage pTD1	GCA_002618825.1
AQT28094.1	000793	virion-structural-Cluster78_1clades	237	pVa21_153	Vibrio phage pVa-21	GCA_002619305.1
QAX96776.1	000793	virion-structural-Cluster78_1clades	227	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97095.1	000793	virion-structural-Cluster78_1clades	227	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96141.1	000793	virion-structural-Cluster78_1clades	227	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96459.1	000793	virion-structural-Cluster78_1clades	227	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20967.1	000793	virion-structural-Cluster78_1clades	227	-	Vibrio phage vB_pir03	GCA_014319855.1
AGH56843.1	000794	virion_structural-Cluster82_1clades	167	CPXG_00040	Cyanophage P-RSM6	GCA_000906155.1
AGH56844.1	000794	virion_structural-Cluster82_1clades	497	CPXG_00041	Cyanophage P-RSM6	GCA_000906155.1
AGH56917.1	000794	virion_structural-Cluster82_1clades	538	CPXG_00114	Cyanophage P-RSM6	GCA_000906155.1
AJK27540.1	000794	virion_structural-Cluster82_1clades	769	PTIM40_113	Cyanophage P-TIM40	GCA_001470935.1
AJK27541.1	000794	virion_structural-Cluster82_1clades	89	PTIM40_114	Cyanophage P-TIM40	GCA_001470935.1
AJK27605.1	000794	virion_structural-Cluster82_1clades	455	PTIM40_184	Cyanophage P-TIM40	GCA_001470935.1
AOO14299.1	000794	virion_structural-Cluster82_1clades	156	Sn110110_105	Cyanophage S-RIM14	GCA_002599065.1
AOO14371.1	000794	virion_structural-Cluster82_1clades	315	Sn110110_177	Cyanophage S-RIM14	GCA_002599065.1
AOO14372.1	000794	virion_structural-Cluster82_1clades	687	Sn110110_178	Cyanophage S-RIM14	GCA_002599065.1
AOO14948.1	000794	virion_structural-Cluster82_1clades	156	W1230910_102	Cyanophage S-RIM14	GCA_002599125.1
AOO15019.1	000794	virion_structural-Cluster82_1clades	297	W1230910_173	Cyanophage S-RIM14	GCA_002599125.1
AOO15020.1	000794	virion_structural-Cluster82_1clades	687	W1230910_174	Cyanophage S-RIM14	GCA_002599125.1
AMO43130.1	000794	virion_structural-Cluster82_1clades	104	R1080702_121	Cyanophage S-RIM32	GCA_001754165.1
AMO43180.1	000794	virion_structural-Cluster82_1clades	226	R1080702_171	Cyanophage S-RIM32	GCA_001754165.1
AMO43181.1	000794	virion_structural-Cluster82_1clades	87	R1080702_172	Cyanophage S-RIM32	GCA_001754165.1
AMO43355.1	000794	virion_structural-Cluster82_1clades	91	W270710_111	Cyanophage S-RIM44	GCA_002599145.1
AMO43405.1	000794	virion_structural-Cluster82_1clades	301	W270710_161	Cyanophage S-RIM44	GCA_002599145.1
AOO11599.1	000794	virion_structural-Cluster82_1clades	91	ES420910_118	Cyanophage S-RIM44	GCA_002599165.1
AOO11649.1	000794	virion_structural-Cluster82_1clades	301	ES420910_168	Cyanophage S-RIM44	GCA_002599165.1
AOO11827.1	000794	virion_structural-Cluster82_1clades	91	Np050604_111	Cyanophage S-RIM44	GCA_002599185.1
AOO11877.1	000794	virion_structural-Cluster82_1clades	301	Np050604_161	Cyanophage S-RIM44	GCA_002599185.1
AOO12064.1	000794	virion_structural-Cluster82_1clades	91	Np200711_118	Cyanophage S-RIM44	GCA_002599205.1
AOO12115.1	000794	virion_structural-Cluster82_1clades	301	Np200711_169	Cyanophage S-RIM44	GCA_002599205.1
AOO12300.1	000794	virion_structural-Cluster82_1clades	91	Np420711_118	Cyanophage S-RIM44	GCA_002599225.1
AOO12350.1	000794	virion_structural-Cluster82_1clades	301	Np420711_168	Cyanophage S-RIM44	GCA_002599225.1
AOO12528.1	000794	virion_structural-Cluster82_1clades	91	Sn080709_111	Cyanophage S-RIM44	GCA_002599245.1
AOO12578.1	000794	virion_structural-Cluster82_1clades	301	Sn080709_161	Cyanophage S-RIM44	GCA_002599245.1
AOO12765.1	000794	virion_structural-Cluster82_1clades	91	Sn130910_118	Cyanophage S-RIM44	GCA_002599265.1
AOO12815.1	000794	virion_structural-Cluster82_1clades	301	Sn130910_168	Cyanophage S-RIM44	GCA_002599265.1
AOO12994.1	000794	virion_structural-Cluster82_1clades	91	W2100709_112	Cyanophage S-RIM44	GCA_002599285.1
AOO13044.1	000794	virion_structural-Cluster82_1clades	301	W2100709_162	Cyanophage S-RIM44	GCA_002599285.1
AGH07507.1	000794	virion_structural-Cluster82_1clades	277	CYVG_00063	Cyanophage S-SSM6a	GCA_002710385.1
AGH07546.1	000794	virion_structural-Cluster82_1clades	493	CYVG_00102	Cyanophage S-SSM6a	GCA_002710385.1
AGH07547.1	000794	virion_structural-Cluster82_1clades	121	CYVG_00103	Cyanophage S-SSM6a	GCA_002710385.1
AGH07548.1	000794	virion_structural-Cluster82_1clades	994	CYVG_00104	Cyanophage S-SSM6a	GCA_002710385.1
AGG54285.1	000794	virion_structural-Cluster82_1clades	392	CYWG_00001	Cyanophage S-SSM6b	GCA_002710425.1
AGG54430.1	000794	virion_structural-Cluster82_1clades	375	CYWG_00146	Cyanophage S-SSM6b	GCA_002710425.1
AGG54431.1	000794	virion_structural-Cluster82_1clades	547	CYWG_00147	Cyanophage S-SSM6b	GCA_002710425.1
AGH26112.1	000794	virion_structural-Cluster82_1clades	167	CPMG_00011	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26278.1	000794	virion_structural-Cluster82_1clades	435	CPMG_00178	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44492.1	000794	virion_structural-Cluster82_1clades	169	PSSM2_114	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44501.1	000794	virion_structural-Cluster82_1clades	271	PSSM2_123	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44573.1	000794	virion_structural-Cluster82_1clades	451	PSSM2_195	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12400.1	000794	virion_structural-Cluster82_1clades	451	PRTG_00247	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12465.1	000794	virion_structural-Cluster82_1clades	271	PRTG_00318	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12474.1	000794	virion_structural-Cluster82_1clades	169	PRTG_00327	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93496.1	000794	virion_structural-Cluster82_1clades	1006	AVU42_gp159	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93461.1	000794	virion_structural-Cluster82_1clades	171	AVU42_gp123	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93492.1	000794	virion_structural-Cluster82_1clades	355	AVU42_gp155	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93449.1	000794	virion_structural-Cluster82_1clades	373	AVU42_gp111	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93437.1	000794	virion_structural-Cluster82_1clades	427	AVU42_gp097	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99213.1	000794	virion_structural-Cluster82_1clades	91	Syn1_112	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99264.1	000794	virion_structural-Cluster82_1clades	301	Syn1_163	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30607.1	000794	virion_structural-Cluster82_1clades	936	Syn7803US37_130	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30672.1	000794	virion_structural-Cluster82_1clades	498	Syn7803US37_195	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54922.1	000794	virion_structural-Cluster82_1clades	410	b23_0309	Synechococcus phage B23	GCA_009745195.1
QGT54557.1	000794	virion_structural-Cluster82_1clades	410	b3_0316	Synechococcus phage B3	GCA_009745215.1
ASR76214.1	000794	virion_structural-Cluster82_1clades	534	PBI_BELLAMY_171	Synechococcus phage Bellamy	GCA_002627525.1
ASR76215.1	000794	virion_structural-Cluster82_1clades	154	PBI_BELLAMY_172	Synechococcus phage Bellamy	GCA_002627525.1
QCW22945.1	000794	virion_structural-Cluster82_1clades	269	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22942.1	000794	virion_structural-Cluster82_1clades	401	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22876.1	000794	virion_structural-Cluster82_1clades	427	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50537.1	000794	virion_structural-Cluster82_1clades	269	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50481.1	000794	virion_structural-Cluster82_1clades	427	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59574.1	000794	virion_structural-Cluster82_1clades	141	S330809_113	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59630.1	000794	virion_structural-Cluster82_1clades	184	S330809_169	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59336.1	000794	virion_structural-Cluster82_1clades	141	C440309_113	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59392.1	000794	virion_structural-Cluster82_1clades	164	C440309_169	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59812.1	000794	virion_structural-Cluster82_1clades	141	N231010_113	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59868.1	000794	virion_structural-Cluster82_1clades	184	N231010_169	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70535.1	000794	virion_structural-Cluster82_1clades	539	HOU04_gp136	Synechococcus phage S-T4	GCA_003443335.1
QJT70168.1	000794	virion_structural-Cluster82_1clades	368	SynMITS9220M01_156	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56816.1	000795	TM+TM+TM+TM+TM+TM	361	CPXG_00013	Cyanophage P-RSM6	GCA_000906155.1
AJK27646.1	000795	TM+TM+TM+TM+TM+TM	361	PTIM40_221	Cyanophage P-TIM40	GCA_001470935.1
AOO14396.1	000795	TM+TM+TM+TM+TM+TM	358	Sn110110_203	Cyanophage S-RIM14	GCA_002599065.1
AOO14397.1	000795	TM+TM+TM+TM+TM+TM	351	Sn110110_204	Cyanophage S-RIM14	GCA_002599065.1
AOO15044.1	000795	TM+TM+TM+TM+TM+TM	358	W1230910_199	Cyanophage S-RIM14	GCA_002599125.1
AOO15046.1	000795	TM+TM+TM+TM+TM+TM	351	W1230910_201	Cyanophage S-RIM14	GCA_002599125.1
AMO43222.1	000795	TM+TM+TM+TM+TM+TM	359	R1080702_217	Cyanophage S-RIM32	GCA_001754165.1
AMO43226.1	000795	TM+TM+TM+TM+TM+TM	227	R1080702_221	Cyanophage S-RIM32	GCA_001754165.1
AMO43455.1	000795	TM+TM+TM+TM+TM+TM	359	W270710_216	Cyanophage S-RIM44	GCA_002599145.1
AMO43457.1	000795	TM+TM+TM+TM+TM+TM	351	W270710_218	Cyanophage S-RIM44	GCA_002599145.1
AOO11696.1	000795	TM+TM+TM+TM+TM+TM	359	ES420910_219	Cyanophage S-RIM44	GCA_002599165.1
AOO11697.1	000795	TM+TM+TM+TM+TM+TM	351	ES420910_220	Cyanophage S-RIM44	GCA_002599165.1
AOO11927.1	000795	TM+TM+TM+TM+TM+TM	359	Np050604_216	Cyanophage S-RIM44	GCA_002599185.1
AOO11929.1	000795	TM+TM+TM+TM+TM+TM	351	Np050604_218	Cyanophage S-RIM44	GCA_002599185.1
AOO12162.1	000795	TM+TM+TM+TM+TM+TM	359	Np200711_220	Cyanophage S-RIM44	GCA_002599205.1
AOO12163.1	000795	TM+TM+TM+TM+TM+TM	351	Np200711_221	Cyanophage S-RIM44	GCA_002599205.1
AOO12397.1	000795	TM+TM+TM+TM+TM+TM	359	Np420711_219	Cyanophage S-RIM44	GCA_002599225.1
AOO12398.1	000795	TM+TM+TM+TM+TM+TM	351	Np420711_220	Cyanophage S-RIM44	GCA_002599225.1
AOO12628.1	000795	TM+TM+TM+TM+TM+TM	359	Sn080709_216	Cyanophage S-RIM44	GCA_002599245.1
AOO12630.1	000795	TM+TM+TM+TM+TM+TM	351	Sn080709_218	Cyanophage S-RIM44	GCA_002599245.1
AOO12862.1	000795	TM+TM+TM+TM+TM+TM	359	Sn130910_219	Cyanophage S-RIM44	GCA_002599265.1
AOO12863.1	000795	TM+TM+TM+TM+TM+TM	351	Sn130910_220	Cyanophage S-RIM44	GCA_002599265.1
AOO13094.1	000795	TM+TM+TM+TM+TM+TM	359	W2100709_217	Cyanophage S-RIM44	GCA_002599285.1
AOO13096.1	000795	TM+TM+TM+TM+TM+TM	351	W2100709_219	Cyanophage S-RIM44	GCA_002599285.1
AGH07572.1	000795	TM+TM+TM+TM+TM+TM	286	CYVG_00128	Cyanophage S-SSM6a	GCA_002710385.1
AGH07573.1	000795	TM+TM+TM+TM+TM+TM	308	CYVG_00129	Cyanophage S-SSM6a	GCA_002710385.1
AGH07575.1	000795	TM+TM+TM+TM+TM+TM	285	CYVG_00131	Cyanophage S-SSM6a	GCA_002710385.1
AGH07588.1	000795	TM+TM+TM+TM+TM+TM	361	CYVG_00144	Cyanophage S-SSM6a	GCA_002710385.1
AGG54393.1	000795	TM+TM+TM+TM+TM+TM	362	CYWG_00109	Cyanophage S-SSM6b	GCA_002710425.1
AGH26237.1	000795	TM+TM+TM+TM+TM+TM	358	CPMG_00136	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26238.1	000795	TM+TM+TM+TM+TM+TM	363	CPMG_00137	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44642.1	000795	TM+TM+TM+TM+TM+TM	264	PSSM2_265	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44662.1	000795	TM+TM+TM+TM+TM+TM	360	PSSM2_285	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12313.1	000795	TM+TM+TM+TM+TM+TM	360	PRTG_00160	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12329.1	000795	TM+TM+TM+TM+TM+TM	264	PRTG_00176	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93568.1	000795	TM+TM+TM+TM+TM+TM	361	psbA	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93570.1	000795	TM+TM+TM+TM+TM+TM	359	psbD	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93521.1	000795	TM+TM+TM+TM+TM+TM	266	AVU42_gp184	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93518.1	000795	TM+TM+TM+TM+TM+TM	298	AVU42_gp181	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99316.1	000795	TM+TM+TM+TM+TM+TM	359	Syn1_220	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99318.1	000795	TM+TM+TM+TM+TM+TM	351	Syn1_222	Prochlorococcus phage Syn1	GCA_000892495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIX30703.1	000795	TM+TM+TM+TM+TM+TM	264	Syn7803US37_226	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30719.1	000795	TM+TM+TM+TM+TM+TM	359	Syn7803US37_242	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30723.1	000795	TM+TM+TM+TM+TM+TM	352	Syn7803US37_246	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54953.1	000795	TM+TM+TM+TM+TM+TM	263	b23_0347	Synechococcus phage B23	GCA_009745195.1
QGT54588.1	000795	TM+TM+TM+TM+TM+TM	263	b3_0353	Synechococcus phage B3	GCA_009745215.1
ASR76237.1	000795	TM+TM+TM+TM+TM+TM	268	PBI_BELLAMY_201	Synechococcus phage Bellamy	GCA_002627525.1
ASR76295.1	000795	TM+TM+TM+TM+TM+TM	358	PBI_BELLAMY_259	Synechococcus phage Bellamy	GCA_002627525.1
ASR76296.1	000795	TM+TM+TM+TM+TM+TM	351	PBI_BELLAMY_260	Synechococcus phage Bellamy	GCA_002627525.1
QCW22961.1	000795	TM+TM+TM+TM+TM+TM	264	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22967.1	000795	TM+TM+TM+TM+TM+TM	268	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23047.1	000795	TM+TM+TM+TM+TM+TM	323	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22973.1	000795	TM+TM+TM+TM+TM+TM	324	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23049.1	000795	TM+TM+TM+TM+TM+TM	353	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50569.1	000795	TM+TM+TM+TM+TM+TM	264	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50563.1	000795	TM+TM+TM+TM+TM+TM	268	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50557.1	000795	TM+TM+TM+TM+TM+TM	324	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50676.1	000795	TM+TM+TM+TM+TM+TM	465	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59673.1	000795	TM+TM+TM+TM+TM+TM	323	S330809_212	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59675.1	000795	TM+TM+TM+TM+TM+TM	323	S330809_214	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59435.1	000795	TM+TM+TM+TM+TM+TM	323	C440309_212	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59437.1	000795	TM+TM+TM+TM+TM+TM	351	C440309_214	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59910.1	000795	TM+TM+TM+TM+TM+TM	323	N231010_211	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59912.1	000795	TM+TM+TM+TM+TM+TM	351	N231010_213	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70504.1	000795	TM+TM+TM+TM+TM+TM	250	HOU04_gp105	Synechococcus phage S-T4	GCA_003443335.1
AXQ70506.1	000795	TM+TM+TM+TM+TM+TM	263	HOU04_gp107	Synechococcus phage S-T4	GCA_003443335.1
AXQ70485.1	000795	TM+TM+TM+TM+TM+TM	352	HOU04_gp086	Synechococcus phage S-T4	GCA_003443335.1
AXQ70487.1	000795	TM+TM+TM+TM+TM+TM	359	HOU04_gp088	Synechococcus phage S-T4	GCA_003443335.1
QJT70194.1	000795	TM+TM+TM+TM+TM+TM	288	SynMITS9220M01_188	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70239.1	000795	TM+TM+TM+TM+TM+TM	360	SynMITS9220M01_233	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70241.1	000795	TM+TM+TM+TM+TM+TM	268	SynMITS9220M01_235	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01491.1	000796	baseplate_wedge_subunit	651	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28800.1	000796	baseplate_wedge_subunit	651	AP1_0093	Aeromonas phage AP1	GCA_014183365.1
ATI17406.1	000796	baseplate_wedge_subunit	651	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00189.1	000796	baseplate_wedge_subunit	651	HWB28_gp363	Aeromonas phage AS-zj	GCA_002627665.1
AUE22734.1	000796	baseplate_wedge_subunit	647	Ah1_00216	Aeromonas phage Ah1	GCA_002957415.1
QAX98455.1	000796	baseplate_wedge_subunit	651	ASfcp2_113	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97846.1	000796	baseplate_wedge_subunit	651	ASswx1_203	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01306.1	000796	baseplate_wedge_subunit	652	ASwh1_243	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39554.1	000796	baseplate_wedge_subunit	651	CC2_332	Aeromonas phage CC2	GCA_000903495.1
ADQ52913.1	000796	baseplate_wedge_subunit	651	PX29p194	Aeromonas phage PX29	GCA_000920195.1
ADM80180.1	000796	baseplate_wedge_subunit	651	phiAS5_ORF0337	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53112.1	000796	baseplate_wedge_subunit	651	65p104	Aeromonas virus 65	GCA_000893255.1
AAQ17865.1	000796	baseplate_wedge_subunit	651	6	Aeromonas virus Aeh1	GCA_000843245.1
ANS05934.1	000796	baseplate_wedge_subunit	637	ABCD_0196	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64901.1	000796	baseplate_wedge_subunit	646	S13_102	Cronobacter phage S13	GCA_001503575.1
AON97210.1	000796	baseplate_wedge_subunit	637	E_202	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56932.1	000796	baseplate_wedge_subunit	698	CPXG_00129	Cyanophage P-RSM6	GCA_000906155.1
AJK27525.1	000796	baseplate_wedge_subunit	700	PTIM40_98	Cyanophage P-TIM40	GCA_001470935.1
AOO14284.1	000796	baseplate_wedge_subunit	701	Sn110110_090	Cyanophage S-RIM14	GCA_002599065.1
AOO14933.1	000796	baseplate_wedge_subunit	710	W1230910_087	Cyanophage S-RIM14	GCA_002599125.1
AMO43109.1	000796	baseplate_wedge_subunit	602	R1080702_100	Cyanophage S-RIM32	GCA_001754165.1
AMO43336.1	000796	baseplate_wedge_subunit	602	W270710_092	Cyanophage S-RIM44	GCA_002599145.1
AOO11569.1	000796	baseplate_wedge_subunit	602	ES420910_088	Cyanophage S-RIM44	GCA_002599165.1
AOO11808.1	000796	baseplate_wedge_subunit	602	Np050604_092	Cyanophage S-RIM44	GCA_002599185.1
AOO12034.1	000796	baseplate_wedge_subunit	602	Np200711_088	Cyanophage S-RIM44	GCA_002599205.1
AOO12270.1	000796	baseplate_wedge_subunit	602	Np420711_088	Cyanophage S-RIM44	GCA_002599225.1
AOO12509.1	000796	baseplate_wedge_subunit	602	Sn080709_092	Cyanophage S-RIM44	GCA_002599245.1
AOO12735.1	000796	baseplate_wedge_subunit	602	Sn130910_088	Cyanophage S-RIM44	GCA_002599265.1
AOO12975.1	000796	baseplate_wedge_subunit	602	W2100709_093	Cyanophage S-RIM44	GCA_002599285.1
AGH07717.1	000796	baseplate_wedge_subunit	624	CYVG_00274	Cyanophage S-SSM6a	GCA_002710385.1
AGG54300.1	000796	baseplate_wedge_subunit	664	CYWG_00016	Cyanophage S-SSM6b	GCA_002710425.1
ARM70980.1	000796	baseplate_wedge_subunit	656	phiC120_c275	Escherichia phage phiC120	GCA_002621185.1
ARM70714.1	000796	baseplate_wedge_subunit	656	phiC120_c7	Escherichia phage phiC120	GCA_002621185.1
AAX78728.1	000796	baseplate_wedge_subunit	617	RB43ORF206w	Escherichia virus RB43	GCA_000863505.1
QHJ79038.1	000796	baseplate_wedge_subunit	640	-	Myoviridae sp.	GCA_012593985.1
QIG65717.1	000796	baseplate_wedge_subunit	627	phiOC_p051	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26137.1	000796	baseplate_wedge_subunit	616	CPMG_00036	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44488.1	000796	baseplate_wedge_subunit	647	PSSM2_110	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12160.1	000796	baseplate_wedge_subunit	647	PRTG_00002	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93426.1	000796	baseplate_wedge_subunit	704	AVU42_gp085	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99194.1	000796	baseplate_wedge_subunit	602	Syn1_093	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47769.1	000796	baseplate_wedge_subunit	594	SmphiM12_137	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13000.1	000796	baseplate_wedge_subunit	594	PHIM19_94	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12640.1	000796	baseplate_wedge_subunit	594	PHIM7_93	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13373.1	000796	baseplate_wedge_subunit	594	PHIN3_108	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30594.1	000796	baseplate_wedge_subunit	641	Syn7803US37_117	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54870.1	000796	baseplate_wedge_subunit	632	b23_0256	Synechococcus phage B23	GCA_009745195.1
QGT54505.1	000796	baseplate_wedge_subunit	632	b3_0263	Synechococcus phage B3	GCA_009745215.1
ASR76155.1	000796	baseplate_wedge_subunit	692	PBI_BELLAMY_110	Synechococcus phage Bellamy	GCA_002627525.1
QCW22832.1	000796	baseplate_wedge_subunit	680	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50593.1	000796	baseplate_wedge_subunit	598	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50498.1	000796	baseplate_wedge_subunit	680	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59549.1	000796	baseplate_wedge_subunit	598	S330809_088	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59311.1	000796	baseplate_wedge_subunit	598	C440309_088	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59787.1	000796	baseplate_wedge_subunit	598	N231010_088	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70597.1	000796	baseplate_wedge_subunit	636	HOU04_gp198	Synechococcus phage S-T4	GCA_003443335.1
QJT70095.1	000796	baseplate_wedge_subunit	644	SynMITS9220M01_082	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64410.1	000796	baseplate_wedge_subunit	652	KVP40.0341	Vibrio phage KVP40	GCA_000843785.1
QIW90355.1	000796	baseplate_wedge_subunit	652	GCAPEGMB_00008	Vibrio phage V07	GCA_012361095.1
QIW91074.1	000796	baseplate_wedge_subunit	652	COHAPHLL_00211	Vibrio phage V09	GCA_012361135.1
QHJ74523.1	000796	baseplate_wedge_subunit	652	VH12019_00223	Vibrio phage VH1_2019	GCA_009931825.1
AGB06982.1	000796	baseplate_wedge_subunit	652	CF80_gp195	Vibrio phage VH7D	GCA_000914495.1
QBX06132.1	000796	baseplate_wedge_subunit	652	ValB1HC_178	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61144.1	000796	baseplate_wedge_subunit	652	AVU32_gp303	Vibrio phage ValKK3	GCA_001501635.1
AGN30014.1	000796	baseplate_wedge_subunit	652	VPFG_00006	Vibrio phage nt-1	GCA_000910195.2
ALP46969.1	000796	baseplate_wedge_subunit	652	phiGrn1_0075	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47349.1	000796	baseplate_wedge_subunit	652	phiST2_0207	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54757.1	000796	baseplate_wedge_subunit	652	vBValMR10Z_217	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07050.1	000796	baseplate_wedge_subunit	635	VmeM32_00059	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37573.1	000796	baseplate_wedge_subunit	652	pp2_341	Vibriophage phi-pp2	GCA_002630725.1
APU01489.1	000797	Phage-Gp8	327	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28798.1	000797	Phage-Gp8	327	AP1_0091	Aeromonas phage AP1	GCA_014183365.1
ATI17408.1	000797	Phage-Gp8	327	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00188.1	000797	Phage-Gp8	327	HWB28_gp364	Aeromonas phage AS-zj	GCA_002627665.1
AUE22736.1	000797	Phage-Gp8	175	Ah1_00218	Aeromonas phage Ah1	GCA_002957415.1
AUE22737.1	000797	Phage-Gp8	153	Ah1_00219	Aeromonas phage Ah1	GCA_002957415.1
QAX97848.1	000797	Phage-Gp8	327	ASswx1_205	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01304.1	000797	Phage-Gp8	327	ASwh1_241	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39552.1	000797	Phage-Gp8	327	CC2_329	Aeromonas phage CC2	GCA_000903495.1
ADQ52915.1	000797	Phage-Gp8	328	PX29p196	Aeromonas phage PX29	GCA_000920195.1
ADM80182.1	000797	Phage-Gp8	328	phiAS5_ORF0339	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53109.1	000797	Phage-Gp8	327	65p101	Aeromonas virus 65	GCA_000893255.1
AAQ17867.1	000797	Phage-Gp8	328	8	Aeromonas virus Aeh1	GCA_000843245.1
ANS05967.1	000797	Phage-Gp8	330	ABCD_0198	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64899.1	000797	Phage-Gp8	328	S13_100	Cronobacter phage S13	GCA_001503575.1
AON97212.1	000797	Phage-Gp8	330	E_204	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56927.1	000797	Phage-Gp8	511	CPXG_00124	Cyanophage P-RSM6	GCA_000906155.1
AJK27530.1	000797	Phage-Gp8	511	PTIM40_103	Cyanophage P-TIM40	GCA_001470935.1
AOO14289.1	000797	Phage-Gp8	510	Sn110110_095	Cyanophage S-RIM14	GCA_002599065.1
AOO14938.1	000797	Phage-Gp8	510	W1230910_092	Cyanophage S-RIM14	GCA_002599125.1
AMO43112.1	000797	Phage-Gp8	632	R1080702_103	Cyanophage S-RIM32	GCA_001754165.1
AMO43339.1	000797	Phage-Gp8	627	W270710_095	Cyanophage S-RIM44	GCA_002599145.1
AOO11572.1	000797	Phage-Gp8	627	ES420910_091	Cyanophage S-RIM44	GCA_002599165.1
AOO11811.1	000797	Phage-Gp8	627	Np050604_095	Cyanophage S-RIM44	GCA_002599185.1
AOO12037.1	000797	Phage-Gp8	627	Np200711_091	Cyanophage S-RIM44	GCA_002599205.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12273.1	000797	Phage-Gp8	627	Np420711_091	Cyanophage S-RIM44	GCA_002599225.1
AOO12512.1	000797	Phage-Gp8	627	Sn080709_095	Cyanophage S-RIM44	GCA_002599245.1
AOO12738.1	000797	Phage-Gp8	627	Sn130910_091	Cyanophage S-RIM44	GCA_002599265.1
AOO12978.1	000797	Phage-Gp8	627	W2100709_096	Cyanophage S-RIM44	GCA_002599285.1
AGH07721.1	000797	Phage-Gp8	531	CYVG_00278	Cyanophage S-SSM6a	GCA_002710385.1
AGG54295.1	000797	Phage-Gp8	510	CYWG_00011	Cyanophage S-SSM6b	GCA_002710425.1
ARM70982.1	000797	Phage-Gp8	334	phiC120_c277	Escherichia phage phiC120	GCA_002621185.1
ARM70716.1	000797	Phage-Gp8	334	phiC120_c9	Escherichia phage phiC120	GCA_002621185.1
AAX78730.1	000797	Phage-Gp8	330	RB43ORF208w	Escherichia virus RB43	GCA_000863505.1
QHJ79040.1	000797	Phage-Gp8	328	-	Myoviridae sp.	GCA_012593985.1
QIG65715.1	000797	Phage-Gp8	499	phiOC_p049	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26135.1	000797	Phage-Gp8	504	CPMG_00034	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44490.1	000797	Phage-Gp8	533	PSSM2_112	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12476.1	000797	Phage-Gp8	533	PRTG_00329	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93429.1	000797	Phage-Gp8	523	AVU42_gp088	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99197.1	000797	Phage-Gp8	627	Syn1_096	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47766.1	000797	Phage-Gp8	594	SmphiM12_134	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12998.1	000797	Phage-Gp8	594	PHIM19_92	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12638.1	000797	Phage-Gp8	594	PHIM7_91	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13371.1	000797	Phage-Gp8	594	PHIN3_106	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30596.1	000797	Phage-Gp8	514	Syn7803US37_119	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54873.1	000797	Phage-Gp8	526	b23_0259	Synechococcus phage B23	GCA_009745195.1
QGT54508.1	000797	Phage-Gp8	526	b3_0266	Synechococcus phage B3	GCA_009745215.1
ASR76157.1	000797	Phage-Gp8	517	PBI_BELLAMY_112	Synechococcus phage Bellamy	GCA_002627525.1
QCW22829.1	000797	Phage-Gp8	519	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50494.1	000797	Phage-Gp8	519	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50588.1	000797	Phage-Gp8	606	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59551.1	000797	Phage-Gp8	603	S330809_090	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59313.1	000797	Phage-Gp8	603	C440309_090	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59789.1	000797	Phage-Gp8	603	N231010_090	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70595.1	000797	Phage-Gp8	410	HOU04_gp196	Synechococcus phage S-T4	GCA_003443335.1
QJT70097.1	000797	Phage-Gp8	518	SynMITS9220M01_084	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64412.1	000797	Phage-Gp8	343	KVP40.0343	Vibrio phage KVP40	GCA_000843785.1
QIW90357.1	000797	Phage-Gp8	322	GCAPEGMB_00010	Vibrio phage V07	GCA_012361095.1
QIW91072.1	000797	Phage-Gp8	322	COHAPHLL_00209	Vibrio phage V09	GCA_012361135.1
QHJ74525.1	000797	Phage-Gp8	322	VH12019_00225	Vibrio phage VH1_2019	GCA_009931825.1
AGB06984.1	000797	Phage-Gp8	340	CF80_gp197	Vibrio phage VH7D	GCA_000914495.1
QBX06130.1	000797	Phage-Gp8	340	ValB1HC_176	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61142.1	000797	Phage-Gp8	340	AVU32_gp301	Vibrio phage ValKK3	GCA_001501635.1
AGN30016.2	000797	Phage-Gp8	343	VPFG_00008	Vibrio phage nt-1	GCA_000910195.2
ALP47008.1	000797	Phage-Gp8	340	phiGrn1_0077	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47388.1	000797	Phage-Gp8	340	phiST2_0209	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54755.1	000797	Phage-Gp8	340	vBValMR10Z_215	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07197.1	000797	Phage-Gp8	327	VmeM32_00211	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37575.1	000797	Phage-Gp8	340	pp2_343	Vibriophage phi-pp2	GCA_002630725.1
QDB70298.1	000798	virion_structural-Cluster89_1clades	410	CF8_0130	Aeromonas phage CF8	GCA_006384595.2
QDJ97275.1	000798	virion_structural-Cluster89_1clades	410	D6_0115	Aeromonas phage D6	GCA_007051205.2
QDH47063.1	000798	virion_structural-Cluster89_1clades	410	LAh10_47	Aeromonas phage LAh10	GCA_006863975.1
QDJ96892.1	000798	virion_structural-Cluster89_1clades	410	PS1_0133	Aeromonas phage PS1	GCA_007051165.2
QFR59522.1	000798	virion_structural-Cluster89_1clades	410	PS2_0131	Aeromonas phage PS2	GCA_009388305.2
AFO71382.1	000798	virion_structural-Cluster89_1clades	415	CR5_162	Cronobacter phage CR5	GCA_000910235.1
QBZ70661.1	000798	virion_structural-Cluster89_1clades	411	pETSU_080	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59823.1	000798	virion_structural-Cluster89_1clades	247	SEGD1_176	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07593.1	000798	virion_structural-Cluster89_1clades	446	DERBICUS_167	Erwinia phage Derbicus	GCA_004521655.1
AHI60166.1	000798	virion_structural-Cluster89_1clades	409	Ea357_016	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49820.1	000798	virion_structural-Cluster89_1clades	419	MACHINA_182	Erwinia phage Machina	GCA_002758035.1
AGX01916.1	000798	virion_structural-Cluster89_1clades	417	CF95_gp194	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07124.1	000798	virion_structural-Cluster89_1clades	409	REBECCA_16	Erwinia phage Rebecca	GCA_004521635.1
AXF51316.1	000798	virion_structural-Cluster89_1clades	418	WELLINGTON_188	Erwinia phage Wellington	GCA_003344985.1
AFQ96638.1	000798	virion_structural-Cluster89_1clades	420	G173_gp093	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48204.1	000798	virion_structural-Cluster89_1clades	420	ASESINO_191	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85804.1	000798	virion_structural-Cluster89_1clades	409	BOSOLAPHORUS_16	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48476.1	000798	virion_structural-Cluster89_1clades	419	CAITLIN_181	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48755.1	000798	virion_structural-Cluster89_1clades	418	CHRISDB_193	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52114.1	000798	virion_structural-Cluster89_1clades	409	DM_16	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86124.1	000798	virion_structural-Cluster89_1clades	409	DESERTFOX_16	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49016.1	000798	virion_structural-Cluster89_1clades	415	EARLPHILLIPIV_167	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49264.1	000798	virion_structural-Cluster89_1clades	419	HUXLEY_182	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03818.1	000798	virion_structural-Cluster89_1clades	413	JOAD_97	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49541.1	000798	virion_structural-Cluster89_1clades	418	KWAN_189	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86444.1	000798	virion_structural-Cluster89_1clades	409	MADMEL_16	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86765.1	000798	virion_structural-Cluster89_1clades	409	MORTIMER_16	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50092.1	000798	virion_structural-Cluster89_1clades	419	PARSHIK_183	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50363.1	000798	virion_structural-Cluster89_1clades	415	PHOBOS_173	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51797.1	000798	virion_structural-Cluster89_1clades	409	RAY_16	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03573.1	000798	virion_structural-Cluster89_1clades	413	RISINGSUN_97	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51479.1	000798	virion_structural-Cluster89_1clades	409	SIMMY50_17	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64826.1	000798	virion_structural-Cluster89_1clades	409	SPECIALG_16	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50615.1	000798	virion_structural-Cluster89_1clades	420	STRATTON_190	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86012.1	000798	virion_structural-Cluster89_1clades	420	ACEC001_1710	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63823.1	000798	virion_structural-Cluster89_1clades	426	Goslar_00030	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71977.1	000798	virion_structural-Cluster89_1clades	409	N1M2_114	Klebsiella phage N1M2	GCA_010092605.1
QGZ14449.1	000798	virion_structural-Cluster89_1clades	411	HWC77_gp086	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24008.1	000798	virion_structural-Cluster89_1clades	410	-	Proteus phage 10	GCA_014071245.1
ABY63044.1	000798	virion_structural-Cluster89_1clades	428	201phi2-1p215	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27206.1	000798	virion_structural-Cluster89_1clades	413	PPEV_gp112	Pseudomonas phage EL	GCA_000866825.1
ANM44923.1	000798	virion_structural-Cluster89_1clades	427	KTN4_165	Pseudomonas phage KTN4	GCA_002607225.1
ARV77324.1	000798	virion_structural-Cluster89_1clades	414	NOXIFER_155	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89578.1	000798	virion_structural-Cluster89_1clades	408	OBP_141	Pseudomonas phage OBP	GCA_000896635.1
QBX32310.1	000798	virion_structural-Cluster89_1clades	426	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76833.1	000798	virion_structural-Cluster89_1clades	425	PHABIO_202	Pseudomonas phage Phabio	GCA_002624965.1
AEH03572.1	000798	virion_structural-Cluster89_1clades	426	149	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02709.1	000798	virion_structural-Cluster89_1clades	415	PSA21_183	Pseudomonas phage Psa21	GCA_004340405.1
ATN94791.1	000798	virion_structural-Cluster89_1clades	427	SL2_214	Pseudomonas phage SL2	GCA_002956015.1
QJB22801.1	000798	virion_structural-Cluster89_1clades	427	fnug_158	Pseudomonas phage fnug	GCA_012837215.1
QEM41883.1	000798	virion_structural-Cluster89_1clades	426	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83031.1	000798	virion_structural-Cluster89_1clades	427	PHIKZ130	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19045.1	000798	virion_structural-Cluster89_1clades	418	FDH28_gp071	Ralstonia phage RP12	GCA_002617345.1
BAW19330.1	000798	virion_structural-Cluster89_1clades	418	-	Ralstonia phage RP31	GCA_002617365.1
BAS04857.1	000798	virion_structural-Cluster89_1clades	425	AVU11_gp065	Ralstonia phage RSF1	GCA_001500875.1
BAQ02591.1	000798	virion_structural-Cluster89_1clades	425	AVU38_gp063	Ralstonia phage RSL2	GCA_001503055.1
QNI20868.1	000798	virion_structural-Cluster89_1clades	234	-	Salmonella phage JN03	GCA_014319805.1
AWN09163.2	000798	virion_structural-Cluster89_1clades	420	MLDJOKPK_00270	Salmonella phage SPAsTU	GCA_003183805.1
AEP84004.1	000798	virion_structural-Cluster89_1clades	420	SPN3US_0171	Salmonella phage SPN3US	GCA_001042275.1
QKE54330.1	000798	virion_structural-Cluster89_1clades	409	ACSA002_0160	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65392.1	000798	virion_structural-Cluster89_1clades	416	2050HW_00057	Serratia phage 2050HW	GCA_002628125.1
QDB71174.1	000798	virion_structural-Cluster89_1clades	416	CPT_Moabite_144	Serratia phage Moabite	GCA_006384735.1
QFP93087.1	000798	virion_structural-Cluster89_1clades	421	-	Serratia phage PCH45	GCA_009187865.1
QAU04285.1	000798	virion_structural-Cluster89_1clades	411	HWC03_gp130	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23292.1	000798	virion_structural-Cluster89_1clades	411	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80967.1	000798	virion_structural-Cluster89_1clades	411	Aphrodite1_0053	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47436.1	000798	virion_structural-Cluster89_1clades	411	HWC35_gp042	Vibrio phage USC-1	GCA_006864065.1
BAW98257.1	000798	virion_structural-Cluster89_1clades	411	FDH33_gp048	Vibrio phage pTD1	GCA_002618825.1
AQT28067.1	000798	virion_structural-Cluster89_1clades	412	pVa21_126	Vibrio phage pVa-21	GCA_002619305.1
QDB70267.1	000799	virion_structural-Cluster90_1clades	291	CF8_0099	Aeromonas phage CF8	GCA_006384595.2
QDJ97245.1	000799	virion_structural-Cluster90_1clades	291	D6_0085	Aeromonas phage D6	GCA_007051205.2
QDH47095.1	000799	virion_structural-Cluster90_1clades	291	LAh10_17	Aeromonas phage LAh10	GCA_006863975.1
QDJ96858.1	000799	virion_structural-Cluster90_1clades	291	PS1_0099	Aeromonas phage PS1	GCA_007051165.2
QFR59490.1	000799	virion_structural-Cluster90_1clades	291	PS2_0099	Aeromonas phage PS2	GCA_009388305.2
AFO71272.1	000799	virion_structural-Cluster90_1clades	306	CR5_052	Cronobacter phage CR5	GCA_000910235.1
QBZ70628.1	000799	virion_structural-Cluster90_1clades	291	pETSU_047	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59702.1	000799	virion_structural-Cluster90_1clades	310	SEGD1_053	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07479.1	000799	virion_structural-Cluster90_1clades	306	DERBICUS_53	Erwinia phage Derbicus	GCA_004521655.1
AHI60443.1	000799	virion_structural-Cluster90_1clades	297	Ea357_289	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49705.1	000799	virion_structural-Cluster90_1clades	311	MACHINA_67	Erwinia phage Machina	GCA_002758035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGX01950.1	000799	virion_structural-Cluster90_1clades	302	CF95_gp228	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07400.1	000799	virion_structural-Cluster90_1clades	297	REBECCA_295	Erwinia phage Rebecca	GCA_004521635.1
AXF51195.1	000799	virion_structural-Cluster90_1clades	311	WELLINGTON_65	Erwinia phage Wellington	GCA_003344985.1
AFQ96780.1	000799	virion_structural-Cluster90_1clades	312	G173_gp235	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48081.1	000799	virion_structural-Cluster90_1clades	311	ASESINO_68	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86082.1	000799	virion_structural-Cluster90_1clades	297	BOSOLAPHORUS_296	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48356.1	000799	virion_structural-Cluster90_1clades	311	CAITLIN_61	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48629.1	000799	virion_structural-Cluster90_1clades	311	CHRISDB_67	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52398.1	000799	virion_structural-Cluster90_1clades	297	DM_299	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86402.1	000799	virion_structural-Cluster90_1clades	297	DESERTFOX_295	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48903.1	000799	virion_structural-Cluster90_1clades	306	EARLPHILLIPIV_53	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49150.1	000799	virion_structural-Cluster90_1clades	311	HUXLEY_68	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03851.1	000799	virion_structural-Cluster90_1clades	295	JOAD_64	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49417.1	000799	virion_structural-Cluster90_1clades	311	KWAN_65	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86723.1	000799	virion_structural-Cluster90_1clades	297	MADMEL_296	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87048.1	000799	virion_structural-Cluster90_1clades	297	MORTIMER_300	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49978.1	000799	virion_structural-Cluster90_1clades	311	PARSHIK_69	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50244.1	000799	virion_structural-Cluster90_1clades	307	PHOBOS_54	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52073.1	000799	virion_structural-Cluster90_1clades	297	RAY_293	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03606.1	000799	virion_structural-Cluster90_1clades	295	RISINGSUN_64	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51756.1	000799	virion_structural-Cluster90_1clades	297	SIMMY50_298	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65108.1	000799	virion_structural-Cluster90_1clades	297	SPECIALG_297	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50492.1	000799	virion_structural-Cluster90_1clades	312	STRATTON_67	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85892.1	000799	virion_structural-Cluster90_1clades	310	ACEC001_0540	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63853.1	000799	virion_structural-Cluster90_1clades	300	Goslar_00060	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71944.1	000799	virion_structural-Cluster90_1clades	294	N1M2_81	Klebsiella phage N1M2	GCA_010092605.1
QGZ14405.1	000799	virion_structural-Cluster90_1clades	293	HWC77_gp042	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24196.1	000799	virion_structural-Cluster90_1clades	303	-	Proteus phage 10	GCA_014071245.1
ABY62982.1	000799	virion_structural-Cluster90_1clades	297	201phi2-1p152	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27153.1	000799	virion_structural-Cluster90_1clades	294	PPEV_gp059	Pseudomonas phage EL	GCA_000866825.1
ANM44875.1	000799	virion_structural-Cluster90_1clades	309	KTN4_117	Pseudomonas phage KTN4	GCA_002607225.1
ARV77261.1	000799	virion_structural-Cluster90_1clades	304	NOXIFER_91	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89544.1	000799	virion_structural-Cluster90_1clades	293	OBP_107	Pseudomonas phage OBP	GCA_000896635.1
QBX32248.1	000799	virion_structural-Cluster90_1clades	297	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76767.1	000799	virion_structural-Cluster90_1clades	297	PHABIO_136	Pseudomonas phage Phabio	GCA_002624965.1
AEH03517.1	000799	virion_structural-Cluster90_1clades	297	093	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02628.1	000799	virion_structural-Cluster90_1clades	297	PSA21_100	Pseudomonas phage Psa21	GCA_004340405.1
ATN94838.1	000799	virion_structural-Cluster90_1clades	309	SL2_261	Pseudomonas phage SL2	GCA_002956015.1
QJB22752.1	000799	virion_structural-Cluster90_1clades	309	fnug_109	Pseudomonas phage fnug	GCA_012837215.1
QEM41825.1	000799	virion_structural-Cluster90_1clades	297	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82991.1	000799	virion_structural-Cluster90_1clades	309	PHIKZ090	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19217.1	000799	virion_structural-Cluster90_1clades	298	FDH28_gp178	Ralstonia phage RP12	GCA_002617345.1
BAW19503.1	000799	virion_structural-Cluster90_1clades	298	-	Ralstonia phage RP31	GCA_002617365.1
BAS04974.1	000799	virion_structural-Cluster90_1clades	296	AVU11_gp182	Ralstonia phage RSF1	GCA_001500875.1
BAQ02700.1	000799	virion_structural-Cluster90_1clades	296	AVU38_gp172	Ralstonia phage RSL2	GCA_001503055.1
QNI20767.1	000799	virion_structural-Cluster90_1clades	325	-	Salmonella phage JN03	GCA_014319805.1
AWN09046.1	000799	virion_structural-Cluster90_1clades	310	MLDJOKPK_00114	Salmonella phage SPAsTU	GCA_003183805.1
AEP83884.1	000799	virion_structural-Cluster90_1clades	310	SPN3US_0051	Salmonella phage SPN3US	GCA_001042275.1
QKE54620.1	000799	virion_structural-Cluster90_1clades	301	ACSA002_3030	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65353.1	000799	virion_structural-Cluster90_1clades	304	2050HW_00018	Serratia phage 2050HW	GCA_002628125.1
QDB71140.1	000799	virion_structural-Cluster90_1clades	304	CPT_Moabite_110	Serratia phage Moabite	GCA_006384735.1
QFP93110.1	000799	virion_structural-Cluster90_1clades	303	-	Serratia phage PCH45	GCA_009187865.1
QAU04331.1	000799	virion_structural-Cluster90_1clades	293	HWC03_gp176	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23245.1	000799	virion_structural-Cluster90_1clades	293	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80996.1	000799	virion_structural-Cluster90_1clades	293	Aphrodite1_0100	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47483.1	000799	virion_structural-Cluster90_1clades	293	HWC35_gp089	Vibrio phage USC-1	GCA_006864065.1
BAW98303.1	000799	virion_structural-Cluster90_1clades	293	FDH33_gp094	Vibrio phage pTD1	GCA_002618825.1
AQT28180.1	000799	virion_structural-Cluster90_1clades	305	pVa21_239	Vibrio phage pVa-21	GCA_002619305.1
QDB70475.1	000800	virion_structural-Cluster91_1clades	258	CF8_0063	Aeromonas phage CF8	GCA_006384595.2
QDJ97215.1	000800	virion_structural-Cluster91_1clades	252	D6_0055	Aeromonas phage D6	GCA_007051205.2
QDH47108.1	000800	virion_structural-Cluster91_1clades	252	LAh10_221	Aeromonas phage LAh10	GCA_006863975.1
QDJ96823.1	000800	virion_structural-Cluster91_1clades	245	PS1_0064	Aeromonas phage PS1	GCA_007051165.2
QFR59453.1	000800	virion_structural-Cluster91_1clades	245	PS2_0062	Aeromonas phage PS2	GCA_009388305.2
AFO71250.1	000800	virion_structural-Cluster91_1clades	231	CR5_030	Cronobacter phage CR5	GCA_000910235.1
QBZ70593.1	000800	virion_structural-Cluster91_1clades	266	pETSU_012	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59680.1	000800	virion_structural-Cluster91_1clades	217	SEGD1_031	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07457.1	000800	virion_structural-Cluster91_1clades	228	DERBICUS_31	Erwinia phage Derbicus	GCA_004521655.1
AHI60391.1	000800	virion_structural-Cluster91_1clades	256	Ea357_238	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49683.1	000800	virion_structural-Cluster91_1clades	218	MACHINA_45	Erwinia phage Machina	GCA_002758035.1
AGX01737.1	000800	virion_structural-Cluster91_1clades	259	CF95_gp015	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07347.1	000800	virion_structural-Cluster91_1clades	256	REBECCA_242	Erwinia phage Rebecca	GCA_004521635.1
AXF51172.1	000800	virion_structural-Cluster91_1clades	234	WELLINGTON_41	Erwinia phage Wellington	GCA_003344985.1
AFQ96756.1	000800	virion_structural-Cluster91_1clades	224	G173_gp211	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48059.1	000800	virion_structural-Cluster91_1clades	222	ASESINO_46	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86029.1	000800	virion_structural-Cluster91_1clades	256	BOSOLAPHORUS_243	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48334.1	000800	virion_structural-Cluster91_1clades	218	CAITLIN_39	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48607.1	000800	virion_structural-Cluster91_1clades	215	CHRISDB_45	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52346.1	000800	virion_structural-Cluster91_1clades	256	DM_246	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86348.1	000800	virion_structural-Cluster91_1clades	256	DESERTFOX_241	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48881.1	000800	virion_structural-Cluster91_1clades	227	EARLPHILLIPIV_31	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49128.1	000800	virion_structural-Cluster91_1clades	218	HUXLEY_46	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03877.1	000800	virion_structural-Cluster91_1clades	253	JOAD_38	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49393.1	000800	virion_structural-Cluster91_1clades	234	KWAN_41	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86671.1	000800	virion_structural-Cluster91_1clades	256	MADMEL_244	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86994.1	000800	virion_structural-Cluster91_1clades	256	MORTIMER_246	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49956.1	000800	virion_structural-Cluster91_1clades	218	PARSHIK_47	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50221.1	000800	virion_structural-Cluster91_1clades	228	PHOBOS_31	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52020.1	000800	virion_structural-Cluster91_1clades	256	RAY_240	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03632.1	000800	virion_structural-Cluster91_1clades	254	RISINGSUN_38	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51704.1	000800	virion_structural-Cluster91_1clades	256	SIMMY50_245	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65055.1	000800	virion_structural-Cluster91_1clades	256	SPECIALG_244	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50469.1	000800	virion_structural-Cluster91_1clades	224	STRATTON_44	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85870.1	000800	virion_structural-Cluster91_1clades	216	ACEC001_0320	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63969.1	000800	virion_structural-Cluster91_1clades	262	Goslar_00176	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH71909.1	000800	virion_structural-Cluster91_1clades	255	N1M2_46	Klebsiella phage N1M2	GCA_010092605.1
QGZ14377.1	000800	virion_structural-Cluster91_1clades	240	HWC77_gp014	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24160.1	000800	virion_structural-Cluster91_1clades	236	-	Proteus phage 10	GCA_014071245.1
ABY62955.1	000800	virion_structural-Cluster91_1clades	247	201phi2-1p123	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27126.1	000800	virion_structural-Cluster91_1clades	232	PPEV_gp032	Pseudomonas phage EL	GCA_000866825.1
ANM44847.1	000800	virion_structural-Cluster91_1clades	246	KTN4_089	Pseudomonas phage KTN4	GCA_002607225.1
ARV77231.1	000800	virion_structural-Cluster91_1clades	250	NOXIFER_60	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89504.1	000800	virion_structural-Cluster91_1clades	262	OBP_067	Pseudomonas phage OBP	GCA_000896635.1
QBX32215.1	000800	virion_structural-Cluster91_1clades	248	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76734.1	000800	virion_structural-Cluster91_1clades	249	PHABIO_103	Pseudomonas phage Phabio	GCA_002624965.1
AEH03488.1	000800	virion_structural-Cluster91_1clades	252	061	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02598.1	000800	virion_structural-Cluster91_1clades	249	PSA21_69	Pseudomonas phage Psa21	GCA_004340405.1
ATN94866.1	000800	virion_structural-Cluster91_1clades	246	SL2_289	Pseudomonas phage SL2	GCA_002956015.1
QJB22725.1	000800	virion_structural-Cluster91_1clades	246	fnug_82	Pseudomonas phage fnug	GCA_012837215.1
QEM41793.1	000800	virion_structural-Cluster91_1clades	248	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82968.1	000800	virion_structural-Cluster91_1clades	246	PHIKZ067	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19254.1	000800	virion_structural-Cluster91_1clades	240	FDH28_gp141	Ralstonia phage RP12	GCA_002617345.1
BAW19540.1	000800	virion_structural-Cluster91_1clades	238	-	Ralstonia phage RP31	GCA_002617365.1
BAS05012.1	000800	virion_structural-Cluster91_1clades	254	AVU11_gp220	Ralstonia phage RSF1	GCA_001500875.1
BAQ02742.1	000800	virion_structural-Cluster91_1clades	254	AVU38_gp214	Ralstonia phage RSL2	GCA_001503055.1
QNI20745.1	000800	virion_structural-Cluster91_1clades	232	-	Salmonella phage JN03	GCA_014319805.1
AWN09066.1	000800	virion_structural-Cluster91_1clades	217	MLDJOKPK_00136	Salmonella phage SPAsTU	GCA_003183805.1
AEP83862.1	000800	virion_structural-Cluster91_1clades	217	SPN3US_0029	Salmonella phage SPN3US	GCA_001042275.1
QKE54567.1	000800	virion_structural-Cluster91_1clades	245	ACSA002_2510	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65656.1	000800	virion_structural-Cluster91_1clades	263	2050HW_00321	Serratia phage 2050HW	GCA_002628125.1
QDB71080.1	000800	virion_structural-Cluster91_1clades	261	CPT_Moabite_048	Serratia phage Moabite	GCA_006384735.1
QFP93121.1	000800	virion_structural-Cluster91_1clades	267	-	Serratia phage PCH45	GCA_009187865.1
QAU04359.1	000800	virion_structural-Cluster91_1clades	241	HWC03_gp204	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23217.1	000800	virion_structural-Cluster91_1clades	238	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81014.1	000800	virion_structural-Cluster91_1clades	240	Aphrodite1_0128	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47511.1	000800	virion_structural-Cluster91_1clades	238	HWC35_gp117	Vibrio phage USC-1	GCA_006864065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAW98330.1	000800	virion_structural-Cluster91_1clades	245	FDH33_gp121	Vibrio phage pTD1	GCA_002618825.1
AQT28156.1	000800	virion_structural-Cluster91_1clades	213	pVa21_215	Vibrio phage pVa-21	GCA_002619305.1
APU01480.1	000801	T4_neck-protein	266	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28720.1	000801	T4_neck-protein	263	AP1_002	Aeromonas phage AP1	GCA_014183365.1
ATI17417.1	000801	T4_neck-protein	263	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00179.1	000801	T4_neck-protein	263	HWB28_gp373	Aeromonas phage AS-zj	GCA_002627665.1
AUE22749.1	000801	T4_neck-protein	262	Ah1_00231	Aeromonas phage Ah1	GCA_002957415.1
QAX98466.1	000801	T4_neck-protein	263	ASfcp2_126	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97857.1	000801	T4_neck-protein	263	ASswx1_214	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01293.1	000801	T4_neck-protein	268	ASwh1_230	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39546.1	000801	T4_neck-protein	263	CC2_320	Aeromonas phage CC2	GCA_000903495.1
ADQ52926.1	000801	T4_neck-protein	264	PX29p207	Aeromonas phage PX29	GCA_000920195.1
ADM79850.1	000801	T4_neck-protein	265	phiAS5_ORF0007	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17874.1	000801	T4_neck-protein	262	14	Aeromonas virus Aeh1	GCA_000843245.1
ANS05989.1	000801	T4_neck-protein	248	ABCD_0205	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64890.1	000801	T4_neck-protein	264	S13_091	Cronobacter phage S13	GCA_001503575.1
AON97219.1	000801	T4_neck-protein	248	E_211	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56921.1	000801	T4_neck-protein	291	CPXG_00118	Cyanophage P-RSM6	GCA_000906155.1
AJK27536.1	000801	T4_neck-protein	291	PTIM40_109	Cyanophage P-TIM40	GCA_001470935.1
AOO14295.1	000801	T4_neck-protein	387	Sn110110_101	Cyanophage S-RIM14	GCA_002599065.1
AOO14944.1	000801	T4_neck-protein	387	W1230910_098	Cyanophage S-RIM14	GCA_002599125.1
AMO43125.1	000801	T4_neck-protein	372	R1080702_116	Cyanophage S-RIM32	GCA_001754165.1
AMO43350.1	000801	T4_neck-protein	292	W270710_106	Cyanophage S-RIM44	GCA_002599145.1
AOO11594.1	000801	T4_neck-protein	292	ES420910_113	Cyanophage S-RIM44	GCA_002599165.1
AOO11822.1	000801	T4_neck-protein	292	Np050604_106	Cyanophage S-RIM44	GCA_002599185.1
AOO12059.1	000801	T4_neck-protein	292	Np200711_113	Cyanophage S-RIM44	GCA_002599205.1
AOO12295.1	000801	T4_neck-protein	292	Np420711_113	Cyanophage S-RIM44	GCA_002599225.1
AOO12523.1	000801	T4_neck-protein	292	Sn080709_106	Cyanophage S-RIM44	GCA_002599245.1
AOO12760.1	000801	T4_neck-protein	292	Sn130910_113	Cyanophage S-RIM44	GCA_002599265.1
AOO12989.1	000801	T4_neck-protein	292	W2100709_107	Cyanophage S-RIM44	GCA_002599285.1
AGG54289.1	000801	T4_neck-protein	308	CYWG_00005	Cyanophage S-SSM6b	GCA_002710425.1
ARM70723.1	000801	T4_neck-protein	254	phiC120_c16	Escherichia phage phiC120	GCA_002621185.1
AAX78737.1	000801	T4_neck-protein	248	RB43ORF215w	Escherichia virus RB43	GCA_000863505.1
QHJ79049.1	000801	T4_neck-protein	259	-	Myoviridae sp.	GCA_012593985.1
QIG65705.1	000801	T4_neck-protein	281	phiOC_p039	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26117.1	000801	T4_neck-protein	415	CPMG_00016	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44499.1	000801	T4_neck-protein	470	PSSM2_121	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12467.1	000801	T4_neck-protein	470	PRTG_00320	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93433.1	000801	T4_neck-protein	471	AVU42_gp093	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99208.1	000801	T4_neck-protein	292	Syn1_107	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47750.1	000801	T4_neck-protein	217	SmphiM12_118	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12992.1	000801	T4_neck-protein	217	PHIM19_86	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12632.1	000801	T4_neck-protein	217	PHIM7_85	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13364.1	000801	T4_neck-protein	217	PHIN3_100	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30602.1	000801	T4_neck-protein	492	Syn7803US37_125	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54877.1	000801	T4_neck-protein	468	b23_0263	Synechococcus phage B23	GCA_009745195.1
QGT54512.1	000801	T4_neck-protein	468	b3_0270	Synechococcus phage B3	GCA_009745215.1
ASR76163.1	000801	T4_neck-protein	483	PBI_BELLAMY_118	Synechococcus phage Bellamy	GCA_002627525.1
QDH50490.1	000801	T4_neck-protein	489	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59570.1	000801	T4_neck-protein	374	S330809_109	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59332.1	000801	T4_neck-protein	374	C440309_109	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59808.1	000801	T4_neck-protein	374	N231010_109	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70589.1	000801	T4_neck-protein	456	HOU04_gp190	Synechococcus phage S-T4	GCA_003443335.1
QJT70103.1	000801	T4_neck-protein	479	SynMITS9220M01_090	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64420.1	000801	T4_neck-protein	278	KVP40.0351	Vibrio phage KVP40	GCA_000843785.1
QIW90365.1	000801	T4_neck-protein	278	GCAPEGMB_00018	Vibrio phage V07	GCA_012361095.1
QIW91064.1	000801	T4_neck-protein	278	COHAPHLL_00201	Vibrio phage V09	GCA_012361135.1
QHJ74534.1	000801	T4_neck-protein	278	VH12019_00234	Vibrio phage VH1_2019	GCA_009931825.1
AGB06992.1	000801	T4_neck-protein	279	CF80_gp205	Vibrio phage VH7D	GCA_000914495.1
QBX06122.1	000801	T4_neck-protein	279	ValB1HC_168	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61134.1	000801	T4_neck-protein	279	AVU32_gp293	Vibrio phage ValKK3	GCA_001501635.1
AGN30024.2	000801	T4_neck-protein	278	VPFG_00016	Vibrio phage nt-1	GCA_000910195.2
ALP47034.1	000801	T4_neck-protein	279	phiGrn1_0085	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47413.1	000801	T4_neck-protein	279	phiST2_0217	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54747.1	000801	T4_neck-protein	279	vBValMR10Z_207	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07233.1	000801	T4_neck-protein	256	VmeM32_00247	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37583.1	000801	T4_neck-protein	278	pp2_351	Vibriophage phi-pp2	GCA_002630725.1
AFC21578.1	000802	IG+IG	673	GAP32_128	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21671.1	000802	IG+IG	287	GAP32_221	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21933.1	000802	IG+IG	377	GAP32_475	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14045.1	000802	IG+IG	384	PBI_121Q_155	Escherichia phage 121Q	GCA_000926855.1
AIT14361.1	000802	IG+IG	125	PBI_121Q_471	Escherichia phage 121Q	GCA_000926855.1
AIT14462.1	000802	IG+IG	298	PBI_121Q_572	Escherichia phage 121Q	GCA_000926855.1
AIT14463.1	000802	IG+IG	713	PBI_121Q_573	Escherichia phage 121Q	GCA_000926855.1
QAY00298.1	000802	IG+IG	385	Ecwhy1_16	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00484.1	000802	IG+IG	713	Ecwhy1_205	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00485.1	000802	IG+IG	299	Ecwhy1_206	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34778.1	000802	IG+IG	125	ACQ29_gp098	Escherichia phage PBECO4	GCA_001041035.1
AGC35228.1	000802	IG+IG	298	ACQ29_gp548	Escherichia phage PBECO4	GCA_001041035.1
AGC35048.1	000802	IG+IG	384	ACQ29_gp368	Escherichia phage PBECO4	GCA_001041035.1
AGC35227.1	000802	IG+IG	713	ACQ29_gp547	Escherichia phage PBECO4	GCA_001041035.1
BBM61728.1	000802	IG+IG	384	EO157G_1390	Escherichia phage SP27	GCA_008033345.1
BBM62032.1	000802	IG+IG	125	EO157G_4430	Escherichia phage SP27	GCA_008033345.1
BBM62135.1	000802	IG+IG	298	EO157G_5460	Escherichia phage SP27	GCA_008033345.1
BBM62136.1	000802	IG+IG	713	EO157G_5470	Escherichia phage SP27	GCA_008033345.1
AXC36899.1	000802	IG+IG	125	-	Escherichia phage UB	GCA_003341455.1
AXC36800.1	000802	IG+IG	298	-	Escherichia phage UB	GCA_003341455.1
AXC36625.1	000802	IG+IG	384	-	Escherichia phage UB	GCA_003341455.1
AXC36799.1	000802	IG+IG	713	-	Escherichia phage UB	GCA_003341455.1
QBO61654.1	000802	IG+IG	384	G17_00158	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61839.1	000802	IG+IG	713	G17_00350	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61840.1	000802	IG+IG	298	G17_00351	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61943.1	000802	IG+IG	125	G17_00454	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13707.1	000802	IG+IG	384	vBEcoMphAPEC6_gp077	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13971.1	000802	IG+IG	125	vBEcoMphAPEC6_gp347	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80040.1	000802	IG+IG	384	PSLUR01_00063	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80348.1	000802	IG+IG	125	PSLUR01_00371	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80447.1	000802	IG+IG	298	PSLUR01_00470	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80448.1	000802	IG+IG	713	PSLUR01_00471	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44334.1	000802	IG+IG	115	RaK2_00061	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44769.1	000802	IG+IG	212	RaK2_00496	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43677.1	000802	IG+IG	218	CBB_112	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43792.1	000802	IG+IG	286	CBB_227	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44059.1	000802	IG+IG	377	CBB_496	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ABY63207.1	000802	IG+IG	117	201phi2-1p382	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32477.1	000802	IG+IG	135	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77012.1	000802	IG+IG	120	PHABIO_381	Pseudomonas phage Phabio	GCA_002624965.1
AEH03738.1	000802	IG+IG	118	315	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02879.1	000802	IG+IG	186	PSA21_353	Pseudomonas phage Psa21	GCA_004340405.1
QCG76263.1	000802	IG+IG	326	EST35_0383	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM42049.1	000802	IG+IG	135	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW18812.1	000802	IG+IG	224	7t3_0291	Salmonella phage 7t3	GCA_006083215.1
QCW18943.1	000802	IG+IG	292	7t3_0422	Salmonella phage 7t3	GCA_006083215.1
QCW18578.1	000802	IG+IG	380	7t3_057	Salmonella phage 7t3	GCA_006083215.1
AZU98077.1	000802	IG+IG	224	CPT_Munch_133	Salmonella phage Munch	GCA_004015485.1
AZU98197.1	000802	IG+IG	293	CPT_Munch_253	Salmonella phage Munch	GCA_004015485.1
AZU98407.1	000802	IG+IG	375	CPT_Munch_475	Salmonella phage Munch	GCA_004015485.1
QIG62787.1	000802	IG+IG	292	SEPL_174	Salmonella phage SE_PL	GCA_011067555.1
QIG62905.1	000802	IG+IG	224	SEPL_292	Salmonella phage SE_PL	GCA_011067555.1
QIG63106.1	000802	IG+IG	380	SEPL_493	Salmonella phage SE_PL	GCA_011067555.1
AQW88630.1	000802	IG+IG	301	BF_0105	Serratia phage BF	GCA_002619745.1
AQW88751.1	000802	IG+IG	286	BF_0226	Serratia phage BF	GCA_002619745.1
AQW89013.1	000802	IG+IG	377	BF_0488	Serratia phage BF	GCA_002619745.1
SOK58906.1	000802	IG+IG	301	g098c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58907.1	000802	IG+IG	345	g099c	Yersinia phage fHe-Yen9-03	GCA_002990515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK59031.1	000802	IG+IG	286	g223c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59294.1	000802	IG+IG	377	g486c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58371.1	000802	IG+IG	301	g094c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58372.1	000802	IG+IG	345	g095c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58496.1	000802	IG+IG	286	g219c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58759.1	000802	IG+IG	377	g482c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01505.1	000803	T4_baseplate	259	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28929.1	000803	T4_baseplate	261	AP1_0222	Aeromonas phage AP1	GCA_014183665.1
ATI17392.1	000803	T4_baseplate	261	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00202.1	000803	T4_baseplate	261	HWB28_gp350	Aeromonas phage AS-zj	GCA_002627665.1
AUE22721.1	000803	T4_baseplate	258	Ah1_00203	Aeromonas phage Ah1	GCA_002957415.1
QAX98445.1	000803	T4_baseplate	258	ASfcp2_102	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97834.1	000803	T4_baseplate	261	ASswx1_190	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01318.1	000803	T4_baseplate	258	ASwh1_256	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39563.1	000803	T4_baseplate	261	CC2_345	Aeromonas phage CC2	GCA_000903495.1
ADQ52902.1	000803	T4_baseplate	258	PX29p183	Aeromonas phage PX29	GCA_000920195.1
ADM80169.1	000803	T4_baseplate	259	phiAS5_ORF0326	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53126.1	000803	T4_baseplate	228	65p118	Aeromonas virus 65	GCA_000893255.1
AAQ17854.1	000803	T4_baseplate	258	26	Aeromonas virus Aeh1	GCA_000843245.1
AIA64963.1	000803	T4_baseplate	248	S13_164	Cronobacter phage S13	GCA_001503575.1
AGH57010.1	000803	T4_baseplate	233	CPXG_00207	Cyanophage P-RSM6	GCA_000906155.1
AJK27445.1	000803	T4_baseplate	236	PTIM40_18	Cyanophage P-TIM40	GCA_001470935.1
AOO14203.1	000803	T4_baseplate	239	Sn110110_009	Cyanophage S-RIM14	GCA_002599065.1
AOO14855.1	000803	T4_baseplate	239	W1230910_009	Cyanophage S-RIM14	GCA_002599125.1
AMO43023.1	000803	T4_baseplate	238	R1080702_008	Cyanophage S-RIM32	GCA_001754165.1
AMO43254.1	000803	T4_baseplate	238	W270710_009	Cyanophage S-RIM44	GCA_002599145.1
AOO11491.1	000803	T4_baseplate	238	ES420910_009	Cyanophage S-RIM44	GCA_002599165.1
AOO11726.1	000803	T4_baseplate	238	Np050604_009	Cyanophage S-RIM44	GCA_002599185.1
AOO11956.1	000803	T4_baseplate	238	Np200711_009	Cyanophage S-RIM44	GCA_002599205.1
AOO12192.1	000803	T4_baseplate	238	Np420711_009	Cyanophage S-RIM44	GCA_002599225.1
AOO12427.1	000803	T4_baseplate	238	Sn080709_009	Cyanophage S-RIM44	GCA_002599245.1
AOO12657.1	000803	T4_baseplate	238	Sn130910_009	Cyanophage S-RIM44	GCA_002599265.1
AOO12892.1	000803	T4_baseplate	238	W2100709_009	Cyanophage S-RIM44	GCA_002599285.1
AGH07636.1	000803	T4_baseplate	238	CYVG_00193	Cyanophage S-SSM6a	GCA_002710385.1
AGG54361.1	000803	T4_baseplate	239	CYWG_00077	Cyanophage S-SSM6b	GCA_002710425.1
QHJ78971.1	000803	T4_baseplate	247	-	Myoviridae sp.	GCA_012593985.1
QIG65736.1	000803	T4_baseplate	239	phiOC_p071	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26197.1	000803	T4_baseplate	232	CPMG_00096	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44392.1	000803	T4_baseplate	239	PSSM2_014	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12257.1	000803	T4_baseplate	239	PRTG_00101	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93396.1	000803	T4_baseplate	239	AVU42_gp010	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99112.1	000803	T4_baseplate	238	Syn1_010	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47793.1	000803	T4_baseplate	234	SmphiM12_161	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13012.1	000803	T4_baseplate	234	PHIM19_106	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12652.1	000803	T4_baseplate	234	PHIM7_105	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13384.1	000803	T4_baseplate	234	PHIN3_119	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30485.1	000803	T4_baseplate	236	Syn7803US37_8	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54635.1	000803	T4_baseplate	240	b23_0007	Synechococcus phage B23	GCA_009745195.1
QGT54265.1	000803	T4_baseplate	240	b3_0007	Synechococcus phage B3	GCA_009745215.1
ASR76057.1	000803	T4_baseplate	239	PBI_BELLAMY_10	Synechococcus phage Bellamy	GCA_002627525.1
QCW22921.1	000803	T4_baseplate	238	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50636.1	000803	T4_baseplate	238	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59469.1	000803	T4_baseplate	237	S330809_008	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59231.1	000803	T4_baseplate	237	C440309_008	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59707.1	000803	T4_baseplate	237	N231010_008	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70443.1	000803	T4_baseplate	238	HOU04_gp044	Synechococcus phage S-T4	GCA_003443335.1
QJT70025.1	000803	T4_baseplate	239	SynMITS9220M01_009	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64398.1	000803	T4_baseplate	282	KVP40.0328	Vibrio phage KVP40	GCA_000843785.1
QIW90710.1	000803	T4_baseplate	282	GCAPEGMB_00391	Vibrio phage V07	GCA_012361095.1
QIW91087.1	000803	T4_baseplate	282	COHAPHLL_00224	Vibrio phage V09	GCA_012361135.1
QHJ74510.1	000803	T4_baseplate	282	VH12019_00210	Vibrio phage VH1_2019	GCA_009931825.1
AGB06974.1	000803	T4_baseplate	282	CF80_gp187	Vibrio phage VH7D	GCA_000914495.1
QBX06145.1	000803	T4_baseplate	282	ValB1HC_191	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61157.1	000803	T4_baseplate	282	AVU32_gp316	Vibrio phage ValKK3	GCA_001501635.1
AGN30379.1	000803	T4_baseplate	282	VPFG_00382	Vibrio phage nt-1	GCA_000910195.2
ALP47032.1	000803	T4_baseplate	282	phiGrn1_0062	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47411.1	000803	T4_baseplate	282	phiST2_0194	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54770.1	000803	T4_baseplate	282	vBValMR10Z_230	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07109.1	000803	T4_baseplate	252	VmeM32_00122	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37560.1	000803	T4_baseplate	282	pp2_328	Vibriophage phi-pp2	GCA_002630725.1
QDB70471.1	000804	virion_structural-Cluster113_1clades	135	CF8_0059	Aeromonas phage CF8	GCA_006384595.2
QDJ97211.1	000804	virion_structural-Cluster113_1clades	137	D6_0051	Aeromonas phage D6	GCA_007051205.2
QDH47178.1	000804	virion_structural-Cluster113_1clades	154	LAh10_217	Aeromonas phage LAh10	GCA_006863975.1
QDJ96818.1	000804	virion_structural-Cluster113_1clades	137	PS1_0059	Aeromonas phage PS1	GCA_007051165.2
QFR59447.1	000804	virion_structural-Cluster113_1clades	137	PS2_0056	Aeromonas phage PS2	GCA_009388305.2
AFO71246.1	000804	virion_structural-Cluster113_1clades	124	CR5_026	Cronobacter phage CR5	GCA_000910235.1
QBZ70589.1	000804	virion_structural-Cluster113_1clades	136	pETSU_008	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59676.1	000804	virion_structural-Cluster113_1clades	128	SEGD1_027	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07453.1	000804	virion_structural-Cluster113_1clades	124	DERBICUS_27	Erwinia phage Derbicus	GCA_004521655.1
AHI60387.1	000804	virion_structural-Cluster113_1clades	134	Ea357_234	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49679.1	000804	virion_structural-Cluster113_1clades	128	MACHINA_41	Erwinia phage Machina	GCA_002758035.1
QBP07343.1	000804	virion_structural-Cluster113_1clades	134	REBECCA_238	Erwinia phage Rebecca	GCA_004521635.1
AXF51168.1	000804	virion_structural-Cluster113_1clades	124	WELLINGTON_37	Erwinia phage Wellington	GCA_003344985.1
AFQ96752.1	000804	virion_structural-Cluster113_1clades	128	G173_gp207	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48055.1	000804	virion_structural-Cluster113_1clades	128	ASESINO_42	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86025.1	000804	virion_structural-Cluster113_1clades	134	BOSOLAPHORUS_239	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48330.1	000804	virion_structural-Cluster113_1clades	125	CAITLIN_35	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48603.1	000804	virion_structural-Cluster113_1clades	125	CHRISDB_41	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52342.1	000804	virion_structural-Cluster113_1clades	134	DM_242	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86344.1	000804	virion_structural-Cluster113_1clades	134	DESERTFOX_237	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48877.1	000804	virion_structural-Cluster113_1clades	124	EARLPHILLIPIV_27	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49124.1	000804	virion_structural-Cluster113_1clades	128	HUXLEY_42	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03881.1	000804	virion_structural-Cluster113_1clades	136	JOAD_34	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49389.1	000804	virion_structural-Cluster113_1clades	124	KWAN_37	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86749.1	000804	virion_structural-Cluster113_1clades	134	MADMEL_240	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86990.1	000804	virion_structural-Cluster113_1clades	134	MORTIMER_242	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49952.1	000804	virion_structural-Cluster113_1clades	128	PARSHIK_43	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50217.1	000804	virion_structural-Cluster113_1clades	124	PHOBOS_27	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52016.1	000804	virion_structural-Cluster113_1clades	134	RAY_236	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03636.1	000804	virion_structural-Cluster113_1clades	136	RISINGSUN_34	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51700.1	000804	virion_structural-Cluster113_1clades	134	SIMMY50_241	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65051.1	000804	virion_structural-Cluster113_1clades	134	SPECIALG_240	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50465.1	000804	virion_structural-Cluster113_1clades	128	STRATTON_40	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85866.1	000804	virion_structural-Cluster113_1clades	167	ACEC001_0280	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QGH71905.1	000804	virion_structural-Cluster113_1clades	135	N1M2_42	Klebsiella phage N1M2	GCA_010092605.1
QGZ14373.1	000804	virion_structural-Cluster113_1clades	140	HWC77_gp010	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24156.1	000804	virion_structural-Cluster113_1clades	135	-	Proteus phage 10	GCA_014071245.1
ABY62950.1	000804	virion_structural-Cluster113_1clades	89	201phi2-1p118	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27122.1	000804	virion_structural-Cluster113_1clades	135	PPEV_gp028	Pseudomonas phage EL	GCA_000866825.1
ANM44842.1	000804	virion_structural-Cluster113_1clades	136	KTN4_084	Pseudomonas phage KTN4	GCA_002607225.1
ARV77226.1	000804	virion_structural-Cluster113_1clades	134	NOXIFER_55	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89500.1	000804	virion_structural-Cluster113_1clades	136	OBP_063	Pseudomonas phage OBP	GCA_000896635.1
QBX32210.1	000804	virion_structural-Cluster113_1clades	134	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76729.1	000804	virion_structural-Cluster113_1clades	138	PHABIO_98	Pseudomonas phage Phabio	GCA_002624965.1
AEH03483.1	000804	virion_structural-Cluster113_1clades	89	056	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02593.1	000804	virion_structural-Cluster113_1clades	135	PSA21_64	Pseudomonas phage Psa21	GCA_004340405.1
ATN94871.1	000804	virion_structural-Cluster113_1clades	136	SL2_294	Pseudomonas phage SL2	GCA_002956015.1
QJB22720.1	000804	virion_structural-Cluster113_1clades	136	fnug_77	Pseudomonas phage fnug	GCA_012837215.1
QEM41788.1	000804	virion_structural-Cluster113_1clades	134	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82963.1	000804	virion_structural-Cluster113_1clades	136	PHIKZ062	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19259.1	000804	virion_structural-Cluster113_1clades	134	FDH28_gp136	Ralstonia phage RP12	GCA_002617345.1
BAW19545.1	000804	virion_structural-Cluster113_1clades	134	-	Ralstonia phage RP31	GCA_002617365.1
QNI20741.1	000804	virion_structural-Cluster113_1clades	168	-	Salmonella phage JN03	GCA_014319805.1
AWN09070.1	000804	virion_structural-Cluster113_1clades	128	MLDJOKPK_00140	Salmonella phage SPAsTU	GCA_003183805.1
AEP83858.1	000804	virion_structural-Cluster113_1clades	128	SPN3US_0025	Salmonella phage SPN3US	GCA_001042275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QKE54563.1	000804	virion_structural-Cluster113_1clades	135	ACSA002_2470	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QAU04363.1	000804	virion_structural-Cluster113_1clades	140	HWC03_gp208	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23213.1	000804	virion_structural-Cluster113_1clades	140	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81064.1	000804	virion_structural-Cluster113_1clades	140	Aphrodite1_0132	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47515.1	000804	virion_structural-Cluster113_1clades	140	HWC35_gp121	Vibrio phage USC-1	GCA_006864065.1
BAW98334.1	000804	virion_structural-Cluster113_1clades	141	FDH33_gp125	Vibrio phage pTD1	GCA_002618825.1
AQT28152.1	000804	virion_structural-Cluster113_1clades	138	pVa21_211	Vibrio phage pVa-21	GCA_002619305.1
AFO71379.1	000805	virion_structural-Cluster114_1clades	1900	CR5_159	Cronobacter phage CR5	GCA_000910235.1
AFO71380.1	000805	virion_structural-Cluster114_1clades	1340	CR5_160	Cronobacter phage CR5	GCA_000910235.1
AFO71381.1	000805	virion_structural-Cluster114_1clades	1208	CR5_161	Cronobacter phage CR5	GCA_000910235.1
AMR59819.1	000805	virion_structural-Cluster114_1clades	1088	SEGD1_172	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59820.1	000805	virion_structural-Cluster114_1clades	645	SEGD1_173	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59821.1	000805	virion_structural-Cluster114_1clades	1376	SEGD1_174	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59822.1	000805	virion_structural-Cluster114_1clades	1237	SEGD1_175	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07590.1	000805	virion_structural-Cluster114_1clades	1894	DERBICUS_164	Erwinia phage Derbicus	GCA_004521655.1
QBP07591.1	000805	virion_structural-Cluster114_1clades	1340	DERBICUS_165	Erwinia phage Derbicus	GCA_004521655.1
QBP07592.1	000805	virion_structural-Cluster114_1clades	1209	DERBICUS_166	Erwinia phage Derbicus	GCA_004521655.1
ANZ49817.1	000805	virion_structural-Cluster114_1clades	1663	MACHINA_179	Erwinia phage Machina	GCA_002758035.1
ANZ49818.1	000805	virion_structural-Cluster114_1clades	1359	MACHINA_180	Erwinia phage Machina	GCA_002758035.1
ANZ49819.1	000805	virion_structural-Cluster114_1clades	1011	MACHINA_181	Erwinia phage Machina	GCA_002758035.1
AXF51313.1	000805	virion_structural-Cluster114_1clades	1695	WELLINGTON_185	Erwinia phage Wellington	GCA_003344985.1
AXF51314.1	000805	virion_structural-Cluster114_1clades	1344	WELLINGTON_186	Erwinia phage Wellington	GCA_003344985.1
AXF51315.1	000805	virion_structural-Cluster114_1clades	1220	WELLINGTON_187	Erwinia phage Wellington	GCA_003344985.1
AFQ96637.1	000805	virion_structural-Cluster114_1clades	1236	G173_gp092	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96636.1	000805	virion_structural-Cluster114_1clades	1389	G173_gp091	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96635.1	000805	virion_structural-Cluster114_1clades	1676	G173_gp090	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48201.1	000805	virion_structural-Cluster114_1clades	1727	ASESINO_188	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48202.1	000805	virion_structural-Cluster114_1clades	1389	ASESINO_189	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48203.1	000805	virion_structural-Cluster114_1clades	1242	ASESINO_190	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48473.1	000805	virion_structural-Cluster114_1clades	1668	CAITLIN_178	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48474.1	000805	virion_structural-Cluster114_1clades	1362	CAITLIN_179	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48475.1	000805	virion_structural-Cluster114_1clades	1021	CAITLIN_180	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48752.1	000805	virion_structural-Cluster114_1clades	1672	CHRISDB_190	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48753.1	000805	virion_structural-Cluster114_1clades	1363	CHRISDB_191	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48754.1	000805	virion_structural-Cluster114_1clades	1230	CHRISDB_192	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49013.1	000805	virion_structural-Cluster114_1clades	1894	EARLPHILLIPIV_164	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49014.1	000805	virion_structural-Cluster114_1clades	1340	EARLPHILLIPIV_165	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49015.1	000805	virion_structural-Cluster114_1clades	1209	EARLPHILLIPIV_166	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49261.1	000805	virion_structural-Cluster114_1clades	1663	HUXLEY_179	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49262.1	000805	virion_structural-Cluster114_1clades	1359	HUXLEY_180	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49263.1	000805	virion_structural-Cluster114_1clades	1011	HUXLEY_181	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49538.1	000805	virion_structural-Cluster114_1clades	1695	KWAN_186	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49539.1	000805	virion_structural-Cluster114_1clades	1344	KWAN_187	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49540.1	000805	virion_structural-Cluster114_1clades	1220	KWAN_188	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50089.1	000805	virion_structural-Cluster114_1clades	1663	PARSHIK_180	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50090.1	000805	virion_structural-Cluster114_1clades	1359	PARSHIK_181	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50091.1	000805	virion_structural-Cluster114_1clades	1011	PARSHIK_182	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50360.1	000805	virion_structural-Cluster114_1clades	1899	PHOBOS_170	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50361.1	000805	virion_structural-Cluster114_1clades	1339	PHOBOS_171	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50362.1	000805	virion_structural-Cluster114_1clades	1207	PHOBOS_172	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50612.1	000805	virion_structural-Cluster114_1clades	1689	STRATTON_187	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50613.1	000805	virion_structural-Cluster114_1clades	1389	STRATTON_188	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50614.1	000805	virion_structural-Cluster114_1clades	1236	STRATTON_189	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86009.1	000805	virion_structural-Cluster114_1clades	1727	ACEC001_1680	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86010.1	000805	virion_structural-Cluster114_1clades	1376	ACEC001_1690	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86011.1	000805	virion_structural-Cluster114_1clades	1237	ACEC001_1700	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20867.1	000805	virion_structural-Cluster114_1clades	1237	-	Salmonella phage JN03	GCA_014319805.1
QNI20866.1	000805	virion_structural-Cluster114_1clades	1376	-	Salmonella phage JN03	GCA_014319805.1
QNI20947.1	000805	virion_structural-Cluster114_1clades	1727	-	Salmonella phage JN03	GCA_014319805.1
AWN09164.1	000805	virion_structural-Cluster114_1clades	1236	MLDJOKPK_00271	Salmonella phage SPAsTU	GCA_003183805.1
AWN09165.1	000805	virion_structural-Cluster114_1clades	1376	MLDJOKPK_00272	Salmonella phage SPAsTU	GCA_003183805.1
AWN09166.1	000805	virion_structural-Cluster114_1clades	1680	MLDJOKPK_00273	Salmonella phage SPAsTU	GCA_003183805.1
AEP84001.1	000805	virion_structural-Cluster114_1clades	1727	SPN3US_0168	Salmonella phage SPN3US	GCA_001042275.1
AEP84002.1	000805	virion_structural-Cluster114_1clades	1376	SPN3US_0169	Salmonella phage SPN3US	GCA_001042275.1
AEP84003.1	000805	virion_structural-Cluster114_1clades	1237	SPN3US_0170	Salmonella phage SPN3US	GCA_001042275.1
AQT28064.1	000805	virion_structural-Cluster114_1clades	1699	pVa21_123	Vibrio phage pVa-21	GCA_002619305.1
AQT28065.1	000805	virion_structural-Cluster114_1clades	1130	pVa21_124	Vibrio phage pVa-21	GCA_002619305.1
AQT28066.1	000805	virion_structural-Cluster114_1clades	1714	pVa21_125	Vibrio phage pVa-21	GCA_002619305.1
AFO71242.1	000806	virion_structural-Cluster118_1clades	353	CR5_022	Cronobacter phage CR5	GCA_000910235.1
AMR59671.1	000806	virion_structural-Cluster118_1clades	355	SEGD1_020	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07449.1	000806	virion_structural-Cluster118_1clades	353	DERBICUS_23	Erwinia phage Derbicus	GCA_004521655.1
AHI60371.1	000806	virion_structural-Cluster118_1clades	370	Ea357_218	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49675.1	000806	virion_structural-Cluster118_1clades	354	MACHINA_37	Erwinia phage Machina	GCA_002758035.1
AGX01745.1	000806	virion_structural-Cluster118_1clades	357	CF95_gp023	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07328.1	000806	virion_structural-Cluster118_1clades	370	REBECCA_223	Erwinia phage Rebecca	GCA_004521635.1
AXF51164.1	000806	virion_structural-Cluster118_1clades	353	WELLINGTON_33	Erwinia phage Wellington	GCA_003344985.1
AFQ96748.1	000806	virion_structural-Cluster118_1clades	353	G173_gp203	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48051.1	000806	virion_structural-Cluster118_1clades	353	ASESINO_38	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86009.1	000806	virion_structural-Cluster118_1clades	370	BOSOLAPHORUS_223	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48326.1	000806	virion_structural-Cluster118_1clades	362	CAITLIN_31	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48599.1	000806	virion_structural-Cluster118_1clades	363	CHRISDB_37	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52326.1	000806	virion_structural-Cluster118_1clades	370	DM_226	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86328.1	000806	virion_structural-Cluster118_1clades	370	DESERTFOX_221	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48873.1	000806	virion_structural-Cluster118_1clades	353	EARLPHILLIPIV_23	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49120.1	000806	virion_structural-Cluster118_1clades	354	HUXLEY_38	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49385.1	000806	virion_structural-Cluster118_1clades	353	KWAN_33	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86651.1	000806	virion_structural-Cluster118_1clades	370	MADMEL_223	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86974.1	000806	virion_structural-Cluster118_1clades	370	MORTIMER_226	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49948.1	000806	virion_structural-Cluster118_1clades	354	PARSHIK_39	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50213.1	000806	virion_structural-Cluster118_1clades	353	PHOBOS_23	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52001.1	000806	virion_structural-Cluster118_1clades	370	RAY_221	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51685.1	000806	virion_structural-Cluster118_1clades	370	SIMMY50_226	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65035.1	000806	virion_structural-Cluster118_1clades	370	SPECIALG_224	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50461.1	000806	virion_structural-Cluster118_1clades	353	STRATTON_36	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85861.1	000806	virion_structural-Cluster118_1clades	355	ACEC001_0230	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63982.1	000806	virion_structural-Cluster118_1clades	364	Goslar_00190	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24144.1	000806	virion_structural-Cluster118_1clades	376	-	Proteus phage 10	GCA_014071245.1
ABY62931.1	000806	virion_structural-Cluster118_1clades	363	201phi2-1p098	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44829.1	000806	virion_structural-Cluster118_1clades	363	KTN4_071	Pseudomonas phage KTN4	GCA_002607225.1
ARV77219.1	000806	virion_structural-Cluster118_1clades	358	NOXIFER_48	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32204.1	000806	virion_structural-Cluster118_1clades	361	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76709.1	000806	virion_structural-Cluster118_1clades	361	PHABIO_78	Pseudomonas phage Phabio	GCA_002624965.1
AEH03478.1	000806	virion_structural-Cluster118_1clades	310	051	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02584.1	000806	virion_structural-Cluster118_1clades	359	PSA21_54	Pseudomonas phage Psa21	GCA_004340405.1
ATN94883.1	000806	virion_structural-Cluster118_1clades	363	SL2_306	Pseudomonas phage SL2	GCA_002956015.1
QJB22707.1	000806	virion_structural-Cluster118_1clades	363	fnug_64	Pseudomonas phage fnug	GCA_012837215.1
QEM41781.1	000806	virion_structural-Cluster118_1clades	361	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82953.2	000806	virion_structural-Cluster118_1clades	348	PHIKZ052	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19263.1	000806	virion_structural-Cluster118_1clades	360	FDH28_gp132	Ralstonia phage RP12	GCA_002617345.1
BAW19550.1	000806	virion_structural-Cluster118_1clades	360	-	Ralstonia phage RP31	GCA_002617365.1
BAS05022.1	000806	virion_structural-Cluster118_1clades	348	AVU11_gp230	Ralstonia phage RSF1	GCA_001500875.1
BAQ02752.1	000806	virion_structural-Cluster118_1clades	359	AVU38_gp224	Ralstonia phage RSL2	GCA_001503055.1
QNI20737.1	000806	virion_structural-Cluster118_1clades	355	-	Salmonella phage JN03	GCA_014319805.1
AWN09074.1	000806	virion_structural-Cluster118_1clades	354	MLDJOKPK_00145	Salmonella phage SPAsTU	GCA_003183805.1
AEP83854.1	000806	virion_structural-Cluster118_1clades	355	SPN3US_0021	Salmonella phage SPN3US	GCA_001042275.1
QKE54545.1	000806	virion_structural-Cluster118_1clades	372	ACSA002_2290	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65643.1	000806	virion_structural-Cluster118_1clades	201	2050HW_00308	Serratia phage 2050HW	GCA_002628125.1
ATA65644.1	000806	virion_structural-Cluster118_1clades	175	2050HW_00309	Serratia phage 2050HW	GCA_002628125.1
QDB71071.1	000806	virion_structural-Cluster118_1clades	365	CPT_Moabite_039	Serratia phage Moabite	GCA_006384735.1
QFP93099.1	000806	virion_structural-Cluster118_1clades	361	-	Serratia phage PCH45	GCA_009187865.1
AXH70811.1	000806	virion_structural-Cluster118_1clades	353	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT28148.1	000806	virion_structural-Cluster118_1clades	354	pVa21_207	Vibrio phage pVa-21	GCA_002619305.1
QAX96698.1	000806	virion_structural-Cluster118_1clades	359	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97016.1	000806	virion_structural-Cluster118_1clades	359	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96062.1	000806	virion_structural-Cluster118_1clades	359	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96380.1	000806	virion_structural-Cluster118_1clades	359	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21047.1	000806	virion_structural-Cluster118_1clades	354	-	Vibrio phage vB_pir03	GCA_014319855.1
AGH56820.1	000807	SIG+Chloroa_b-bind+TM	71	CPXG_00017	Cyanophage P-RSM6	GCA_000906155.1
AJK27659.1	000807	SIG+Chloroa_b-bind+TM	35	PTIM40_214	Cyanophage P-TIM40	GCA_001470935.1
AJK27658.1	000807	SIG+Chloroa_b-bind+TM	66	PTIM40_213	Cyanophage P-TIM40	GCA_001470935.1
AOO14392.1	000807	SIG+Chloroa_b-bind+TM	69	Sn110110_199	Cyanophage S-RIM14	GCA_002599065.1
AOO15040.1	000807	SIG+Chloroa_b-bind+TM	69	W1230910_195	Cyanophage S-RIM14	GCA_002599125.1
AMO43216.1	000807	SIG+Chloroa_b-bind+TM	67	R1080702_211	Cyanophage S-RIM32	GCA_001754165.1
AMO43218.1	000807	SIG+Chloroa_b-bind+TM	39	R1080702_213	Cyanophage S-RIM32	GCA_001754165.1
AMO43447.1	000807	SIG+Chloroa_b-bind+TM	69	W270710_208	Cyanophage S-RIM44	GCA_002599145.1
AMO43450.1	000807	SIG+Chloroa_b-bind+TM	39	W270710_211	Cyanophage S-RIM44	GCA_002599145.1
AOO11688.1	000807	SIG+Chloroa_b-bind+TM	69	ES420910_211	Cyanophage S-RIM44	GCA_002599165.1
AOO11691.1	000807	SIG+Chloroa_b-bind+TM	39	ES420910_214	Cyanophage S-RIM44	GCA_002599165.1
AOO11919.1	000807	SIG+Chloroa_b-bind+TM	69	Np050604_208	Cyanophage S-RIM44	GCA_002599185.1
AOO11922.1	000807	SIG+Chloroa_b-bind+TM	39	Np050604_211	Cyanophage S-RIM44	GCA_002599185.1
AOO12154.1	000807	SIG+Chloroa_b-bind+TM	69	Np200711_212	Cyanophage S-RIM44	GCA_002599205.1
AOO12157.1	000807	SIG+Chloroa_b-bind+TM	39	Np200711_215	Cyanophage S-RIM44	GCA_002599205.1
AOO12389.1	000807	SIG+Chloroa_b-bind+TM	69	Np420711_211	Cyanophage S-RIM44	GCA_002599225.1
AOO12392.1	000807	SIG+Chloroa_b-bind+TM	39	Np420711_214	Cyanophage S-RIM44	GCA_002599225.1
AOO12620.1	000807	SIG+Chloroa_b-bind+TM	69	Sn080709_208	Cyanophage S-RIM44	GCA_002599245.1
AOO12623.1	000807	SIG+Chloroa_b-bind+TM	39	Sn080709_211	Cyanophage S-RIM44	GCA_002599245.1
AOO12854.1	000807	SIG+Chloroa_b-bind+TM	69	Sn130910_211	Cyanophage S-RIM44	GCA_002599265.1
AOO12857.1	000807	SIG+Chloroa_b-bind+TM	39	Sn130910_214	Cyanophage S-RIM44	GCA_002599265.1
AOO13086.1	000807	SIG+Chloroa_b-bind+TM	69	W2100709_209	Cyanophage S-RIM44	GCA_002599285.1
AOO13089.1	000807	SIG+Chloroa_b-bind+TM	39	W2100709_212	Cyanophage S-RIM44	GCA_002599285.1
AGH07581.1	000807	SIG+Chloroa_b-bind+TM	63	CYVG_00137	Cyanophage S-SSM6a	GCA_002710385.1
AGH07582.1	000807	SIG+Chloroa_b-bind+TM	51	CYVG_00138	Cyanophage S-SSM6a	GCA_002710385.1
AGG54397.1	000807	SIG+Chloroa_b-bind+TM	53	CYWG_00113	Cyanophage S-SSM6b	GCA_002710425.1
AGG54399.1	000807	SIG+Chloroa_b-bind+TM	63	CYWG_00115	Cyanophage S-SSM6b	GCA_002710425.1
AGH26245.1	000807	SIG+Chloroa_b-bind+TM	78	CPMG_00144	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44651.1	000807	SIG+Chloroa_b-bind+TM	35	PSSM2_274	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44650.1	000807	SIG+Chloroa_b-bind+TM	37	PSSM2_273	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44649.1	000807	SIG+Chloroa_b-bind+TM	72	PSSM2_272	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12321.1	000807	SIG+Chloroa_b-bind+TM	37	PRTG_00168	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12322.1	000807	SIG+Chloroa_b-bind+TM	72	PRTG_00169	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93539.1	000807	SIG+Chloroa_b-bind+TM	47	AVU42_gp202	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93540.1	000807	SIG+Chloroa_b-bind+TM	50	AVU42_gp203	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93538.1	000807	SIG+Chloroa_b-bind+TM	65	AVU42_gp201	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99310.1	000807	SIG+Chloroa_b-bind+TM	39	Syn1_214	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99307.1	000807	SIG+Chloroa_b-bind+TM	69	Syn1_211	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30713.1	000807	SIG+Chloroa_b-bind+TM	71	Syn7803US37_236	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30716.1	000807	SIG+Chloroa_b-bind+TM	69	Syn7803US37_239	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54967.1	000807	SIG+Chloroa_b-bind+TM	64	b23_0361	Synechococcus phage B23	GCA_009745195.1
QGT54968.1	000807	SIG+Chloroa_b-bind+TM	65	b23_0362	Synechococcus phage B23	GCA_009745195.1
QGT54602.1	000807	SIG+Chloroa_b-bind+TM	64	b3_0367	Synechococcus phage B3	GCA_009745215.1
QGT54603.1	000807	SIG+Chloroa_b-bind+TM	65	b3_0368	Synechococcus phage B3	GCA_009745215.1
ASR76268.1	000807	SIG+Chloroa_b-bind+TM	67	PBI_BELLAMY_232	Synechococcus phage Bellamy	GCA_002627525.1
ASR76270.1	000807	SIG+Chloroa_b-bind+TM	36	PBI_BELLAMY_234	Synechococcus phage Bellamy	GCA_002627525.1
QCW22956.1	000807	SIG+Chloroa_b-bind+TM	72	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50671.1	000807	SIG+Chloroa_b-bind+TM	72	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50666.1	000807	SIG+Chloroa_b-bind+TM	35	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59666.1	000807	SIG+Chloroa_b-bind+TM	69	S330809_205	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59670.1	000807	SIG+Chloroa_b-bind+TM	39	S330809_209	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59428.1	000807	SIG+Chloroa_b-bind+TM	69	C440309_205	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59432.1	000807	SIG+Chloroa_b-bind+TM	39	C440309_209	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59903.1	000807	SIG+Chloroa_b-bind+TM	69	N231010_204	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59907.1	000807	SIG+Chloroa_b-bind+TM	39	N231010_208	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70498.1	000807	SIG+Chloroa_b-bind+TM	39	HOU04_gp099	Synechococcus phage S-T4	GCA_003443335.1
AXQ70502.1	000807	SIG+Chloroa_b-bind+TM	57	HOU04_gp103	Synechococcus phage S-T4	GCA_003443335.1
QJT70236.1	000807	SIG+Chloroa_b-bind+TM	72	SynMITS9220M01_230	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70238.1	000807	SIG+Chloroa_b-bind+TM	35	SynMITS9220M01_232	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01560.1	000808	Cluster124_1clades	125	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28938.1	000808	Cluster124_1clades	125	AP1_0231	Aeromonas phage AP1	GCA_014183365.1
ATI17342.1	000808	Cluster124_1clades	125	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00251.1	000808	Cluster124_1clades	125	HWB28_gp301	Aeromonas phage AS-zj	GCA_002627665.1
AUE22596.1	000808	Cluster124_1clades	127	Ah1_00055	Aeromonas phage Ah1	GCA_002957415.1
QAX98634.1	000808	Cluster124_1clades	126	ASfcp2_301	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97787.1	000808	Cluster124_1clades	125	ASswx1_142	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01367.1	000808	Cluster124_1clades	125	ASwh1_307	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39449.1	000808	Cluster124_1clades	125	CC2_396	Aeromonas phage CC2	GCA_000903495.1
ADQ52774.1	000808	Cluster124_1clades	138	PX29p055	Aeromonas phage PX29	GCA_000920195.1
ADM80029.1	000808	Cluster124_1clades	126	phiAS5_ORF0186	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53183.1	000808	Cluster124_1clades	125	65p175	Aeromonas virus 65	GCA_000893255.1
AAQ17719.1	000808	Cluster124_1clades	127	Aeh1ORF059c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95007.1	000808	Cluster124_1clades	97	FDI40_gp225	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANS06081.1	000808	Cluster124_1clades	109	ABCD_0013	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65025.1	000808	Cluster124_1clades	114	S13_228	Cronobacter phage S13	GCA_001503575.1
AON97021.1	000808	Cluster124_1clades	110	E_012	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56946.1	000808	Cluster124_1clades	114	CPXG_00143	Cyanophage P-RSM6	GCA_000906155.1
AJK27507.1	000808	Cluster124_1clades	157	PTIM40_80	Cyanophage P-TIM40	GCA_001470935.1
AOO14251.1	000808	Cluster124_1clades	158	Sn110110_057	Cyanophage S-RIM14	GCA_002599065.1
AOO14903.1	000808	Cluster124_1clades	158	W1230910_057	Cyanophage S-RIM14	GCA_002599125.1
AMO43086.1	000808	Cluster124_1clades	148	R1080702_077	Cyanophage S-RIM32	GCA_001754165.1
AMO43315.1	000808	Cluster124_1clades	151	W270710_071	Cyanophage S-RIM44	GCA_002599145.1
AOO11548.1	000808	Cluster124_1clades	150	ES420910_067	Cyanophage S-RIM44	GCA_002599165.1
AOO11787.1	000808	Cluster124_1clades	151	Np050604_071	Cyanophage S-RIM44	GCA_002599185.1
AOO12013.1	000808	Cluster124_1clades	150	Np200711_067	Cyanophage S-RIM44	GCA_002599205.1
AOO12249.1	000808	Cluster124_1clades	150	Np420711_067	Cyanophage S-RIM44	GCA_002599225.1
AOO12488.1	000808	Cluster124_1clades	151	Sn080709_071	Cyanophage S-RIM44	GCA_002599245.1
AOO12714.1	000808	Cluster124_1clades	150	Sn130910_067	Cyanophage S-RIM44	GCA_002599265.1
AOO12953.1	000808	Cluster124_1clades	151	W2100709_071	Cyanophage S-RIM44	GCA_002599285.1
AGH07666.1	000808	Cluster124_1clades	167	CYVG_00223	Cyanophage S-SSM6a	GCA_002710385.1
AGG54333.1	000808	Cluster124_1clades	157	CYWG_00049	Cyanophage S-SSM6b	GCA_002710425.1
AAX78534.1	000808	Cluster124_1clades	109	RB43ORF012c	Escherichia virus RB43	GCA_000863505.1
AFA44610.1	000808	Cluster124_1clades	119	RaK2_00337	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72695.1	000808	Cluster124_1clades	103	-	Myoviridae sp.	GCA_003657725.1
AAX44450.1	000808	Cluster124_1clades	162	PSSM2_072	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12204.1	000808	Cluster124_1clades	162	PRTG_00046	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93609.1	000808	Cluster124_1clades	148	AVU42_gp064	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99169.1	000808	Cluster124_1clades	170	Syn1_068	Prochlorococcus phage Syn1	GCA_000892495.1
QCW18687.1	000808	Cluster124_1clades	123	7t3_0166	Salmonella phage 7t3	GCA_006083215.1
AZU97961.1	000808	Cluster124_1clades	123	CPT_Munch_017	Salmonella phage Munch	GCA_004015485.1
QIG63017.1	000808	Cluster124_1clades	123	SEPL_404	Salmonella phage SE_PL	GCA_011067555.1
AIX30577.1	000808	Cluster124_1clades	113	Syn7803US37_100	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54835.1	000808	Cluster124_1clades	143	b23_0220	Synechococcus phage B23	GCA_009745195.1
QGT54465.1	000808	Cluster124_1clades	143	b3_0222	Synechococcus phage B3	GCA_009745215.1
ASR76135.1	000808	Cluster124_1clades	123	PBI_BELLAMY_90	Synechococcus phage Bellamy	GCA_002627525.1
QCW22860.1	000808	Cluster124_1clades	108	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59519.1	000808	Cluster124_1clades	154	S330809_058	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59281.1	000808	Cluster124_1clades	153	C440309_058	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59757.1	000808	Cluster124_1clades	153	N231010_058	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70623.1	000808	Cluster124_1clades	136	HOU04_gp022	Synechococcus phage S-T4	GCA_003443335.1
AXQ70421.1	000808	Cluster124_1clades	136	HOU04_gp022	Synechococcus phage S-T4	GCA_003443335.1
QJT70073.1	000808	Cluster124_1clades	127	SynMITS9220M01_060	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBA65191.1	000808	Cluster124_1clades	110	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65650.1	000808	Cluster124_1clades	110	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96222.1	000808	Cluster124_1clades	109	Xoosp13_35	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AUE22827.1	000809	Cluster128_2clades	187	Ah1_00309	Aeromonas phage Ah1	GCA_002957415.1
QAX98541.1	000809	Cluster128_2clades	187	ASfcp2_205	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53004.1	000809	Cluster128_2clades	205	PX29p285	Aeromonas phage PX29	GCA_000920195.1
ADM79929.1	000809	Cluster128_2clades	187	phiAS5_ORF0086	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17956.1	000809	Cluster128_2clades	187	Aeh1ORF287c	Aeromonas virus Aeh1	GCA_000843245.1
ASV44749.1	000809	Cluster128_2clades	180	FDI40_gp668	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93404.1	000809	Cluster128_2clades	189	G_142	Bacillus virus G	GCA_000917535.1
AIA64825.1	000809	Cluster128_2clades	182	S13_026	Cronobacter phage S13	GCA_001503575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21789.1	000809	Cluster128_2clades	184	GAP32_339	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AHI60196.1	000809	Cluster128_2clades	196	Ea357_046	Erwinia phage Ea35-70	GCA_000914635.1
QBP07154.1	000809	Cluster128_2clades	196	REBECCA_46	Erwinia phage Rebecca	GCA_004521635.1
AUG85834.1	000809	Cluster128_2clades	196	BOSOLAPHORUS_46	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52145.1	000809	Cluster128_2clades	196	DM_47	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86154.1	000809	Cluster128_2clades	196	DESERTFOX_46	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86474.1	000809	Cluster128_2clades	196	MADMEL_46	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86795.1	000809	Cluster128_2clades	196	MORTIMER_46	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51827.1	000809	Cluster128_2clades	197	RAY_46	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51509.1	000809	Cluster128_2clades	196	SIMMY50_47	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64856.1	000809	Cluster128_2clades	196	SPECIALG_46	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT13966.1	000809	Cluster128_2clades	184	PBI_121Q_69	Escherichia phage 121Q	GCA_000926855.1
QAY00371.1	000809	Cluster128_2clades	184	Ecwhy1_90	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35116.1	000809	Cluster128_2clades	184	ACQ29_gp436	Escherichia phage PBECO4	GCA_001041035.1
BBM61658.1	000809	Cluster128_2clades	184	EO157G_0690	Escherichia phage SP27	GCA_008033345.1
AXC36690.1	000809	Cluster128_2clades	184	-	Escherichia phage UB	GCA_003341455.1
QBO61727.1	000809	Cluster128_2clades	184	G17_00238	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13772.1	000809	Cluster128_2clades	184	vBEcoMphAPEC6_gp143c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80560.1	000809	Cluster128_2clades	184	PSLUR01_00583	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44448.1	000809	Cluster128_2clades	184	RaK2_00175	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78837.1	000809	Cluster128_2clades	179	-	Myoviridae sp.	GCA_012593985.1
AMM43907.1	000809	Cluster128_2clades	184	CBB_344	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFH14880.1	000809	Cluster128_2clades	198	Lu11_0342	Pseudomonas phage Lu11	GCA_000897175.1
AGS81929.1	000809	Cluster128_2clades	189	PaBG_00045	Pseudomonas phage PaBG	GCA_000912555.1
QCW19065.1	000809	Cluster128_2clades	186	7t3_0545	Salmonella phage 7t3	GCA_006083215.1
AZU98311.1	000809	Cluster128_2clades	186	CPT_Munch_367	Salmonella phage Munch	GCA_004015485.1
QIG62673.1	000809	Cluster128_2clades	186	SEPL_060	Salmonella phage SE_PL	GCA_011067555.1
QKE54356.1	000809	Cluster128_2clades	203	ACSA002_0420	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65671.1	000809	Cluster128_2clades	109	2050HW_00336	Serratia phage 2050HW	GCA_002628125.1
ATA65672.1	000809	Cluster128_2clades	79	2050HW_00337	Serratia phage 2050HW	GCA_002628125.1
AQW88867.1	000809	Cluster128_2clades	185	BF_0342	Serratia phage BF	GCA_002619745.1
QDB71093.1	000809	Cluster128_2clades	193	CPT_Moabite_061	Serratia phage Moabite	GCA_006384735.1
AGR48094.1	000809	Cluster128_2clades	183	SmphiM12_462	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13263.1	000809	Cluster128_2clades	183	PHIM19_358	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12903.1	000809	Cluster128_2clades	183	PHIM7_358	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13626.1	000809	Cluster128_2clades	182	PHIN3_363	Sinorhizobium phage phiN3	GCA_001501175.1
BBI90547.1	000809	Cluster128_2clades	177	HYO65_gp155	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90855.1	000809	Cluster128_2clades	177	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25551.1	000809	Cluster128_2clades	178	BPT24_052	Tenacibaculum phage pT24	GCA_002611925.1
ALY07188.1	000809	Cluster128_2clades	191	VmeM32_00202	Vibrio phage vB_VmeM-32	GCA_002608825.1
BBA65406.1	000809	Cluster128_2clades	186	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96431.1	000809	Cluster128_2clades	188	Xoosp13_245	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59151.1	000809	Cluster128_2clades	185	g343	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58617.1	000809	Cluster128_2clades	185	g340	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000112	000809	Cluster128_2clades	180	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000079	000809	Cluster128_2clades	180	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUE22828.1	000810	SIG+TM	351	Ah1_00310	Aeromonas phage Ah1	GCA_002957415.1
QAX98542.1	000810	SIG+TM	351	ASfcp2_206	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53005.1	000810	SIG+TM	351	PX29p286	Aeromonas phage PX29	GCA_000920195.1
ADM79930.1	000810	SIG+TM	353	phiAS5_ORF0087	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17957.1	000810	SIG+TM	351	Aeh1ORF288c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95425.1	000810	SIG+TM	380	FDI40_gp669	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93406.1	000810	SIG+TM	385	G_144	Bacillus virus G	GCA_000917535.1
AIA64824.1	000810	SIG+TM	358	S13_025	Cronobacter phage S13	GCA_001503575.1
AFC21788.1	000810	SIG+TM	365	GAP32_338	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AHI60195.1	000810	SIG+TM	369	Ea357_045	Erwinia phage Ea35-70	GCA_000914635.1
QBP07153.1	000810	SIG+TM	369	REBECCA_45	Erwinia phage Rebecca	GCA_004521635.1
AUG85833.1	000810	SIG+TM	369	BOSOLAPHORUS_45	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52144.1	000810	SIG+TM	369	DM_46	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86153.1	000810	SIG+TM	369	DESERTFOX_45	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86473.1	000810	SIG+TM	369	MADMEL_45	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86794.1	000810	SIG+TM	369	MORTIMER_45	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51826.1	000810	SIG+TM	369	RAY_45	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51508.1	000810	SIG+TM	369	SIMMY50_46	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64855.1	000810	SIG+TM	369	SPECIALG_45	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT13965.1	000810	SIG+TM	364	PBI_121Q_68	Escherichia phage 121Q	GCA_000926855.1
QAY00372.1	000810	SIG+TM	364	Ecwhy1_91	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35117.1	000810	SIG+TM	348	ACQ29_gp437	Escherichia phage PBECO4	GCA_001041035.1
BBM61657.1	000810	SIG+TM	364	EO157G_0680	Escherichia phage SP27	GCA_008033345.1
AXC36691.1	000810	SIG+TM	364	-	Escherichia phage UB	GCA_003341455.1
QBO61728.1	000810	SIG+TM	364	G17_00239	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13773.1	000810	SIG+TM	364	vBEcoMphAPEC6_gp144c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80559.1	000810	SIG+TM	364	PSLUR01_00582	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44447.1	000810	SIG+TM	365	RaK2_00174	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78838.1	000810	SIG+TM	357	-	Myoviridae sp.	GCA_012593985.1
AMM43906.1	000810	SIG+TM	365	CBB_343	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFH14882.1	000810	SIG+TM	351	Lu11_0344	Pseudomonas phage Lu11	GCA_000897175.1
AGS81930.1	000810	SIG+TM	342	PaBG_00046	Pseudomonas phage PaBG	GCA_000912555.1
QCW19064.1	000810	SIG+TM	365	7t3_0544	Salmonella phage 7t3	GCA_006083215.1
AZU98310.1	000810	SIG+TM	365	CPT_Munch_366	Salmonella phage Munch	GCA_004015485.1
QIG62674.1	000810	SIG+TM	365	SEPL_061	Salmonella phage SE_PL	GCA_011067555.1
QKE54355.1	000810	SIG+TM	367	ACSA002_0410	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65670.1	000810	SIG+TM	352	2050HW_00335	Serratia phage 2050HW	GCA_002628125.1
AQW88866.1	000810	SIG+TM	364	BF_0341	Serratia phage BF	GCA_002619745.1
QDB71092.1	000810	SIG+TM	352	CPT_Moabite_060	Serratia phage Moabite	GCA_006384735.1
AGR48095.2	000810	SIG+TM	381	SmphiM12_463	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13264.1	000810	SIG+TM	381	PHIM19_359	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12904.1	000810	SIG+TM	381	PHIM7_359	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13627.1	000810	SIG+TM	381	PHIN3_364	Sinorhizobium phage phiN3	GCA_001501175.1
BBI90549.1	000810	SIG+TM	326	HYO65_gp157	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90857.1	000810	SIG+TM	326	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25550.1	000810	SIG+TM	358	BPT24_051	Tenacibaculum phage pT24	GCA_002611925.1
ALY07189.1	000810	SIG+TM	389	VmeM32_00203	Vibrio phage vB_VmeM-32	GCA_002608825.1
BBA65407.1	000810	SIG+TM	396	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96432.1	000810	SIG+TM	385	Xoosp13_246	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59150.1	000810	SIG+TM	364	g342	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58616.1	000810	SIG+TM	364	g339	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000776	000810	SIG+TM	387	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000529	000810	SIG+TM	387	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QCG76230.1	000811	virion_structural_Cluster132_1clades	141	EST35_0349	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAQ64129.1	000811	virion_structural_Cluster132_1clades	293	KVP40.0058	Vibrio phage KVP40	GCA_000843785.1
AAQ64186.1	000811	virion_structural_Cluster132_1clades	306	KVP40.0115	Vibrio phage KVP40	GCA_000843785.1
AAQ64187.1	000811	virion_structural_Cluster132_1clades	294	KVP40.0116	Vibrio phage KVP40	GCA_000843785.1
AAQ64439.1	000811	virion_structural_Cluster132_1clades	320	KVP40.0371	Vibrio phage KVP40	GCA_000843785.1
QIW90384.1	000811	virion_structural_Cluster132_1clades	320	GCAPEGMB_00037	Vibrio phage V07	GCA_012361095.1
QIW90452.1	000811	virion_structural_Cluster132_1clades	293	GCAPEGMB_00105	Vibrio phage V07	GCA_012361095.1
QIW90509.1	000811	virion_structural_Cluster132_1clades	217	GCAPEGMB_00162	Vibrio phage V07	GCA_012361095.1
QIW90829.1	000811	virion_structural_Cluster132_1clades	137	GCAPEGMB_00514	Vibrio phage V07	GCA_012361095.1
QIW90830.1	000811	virion_structural_Cluster132_1clades	283	GCAPEGMB_00515	Vibrio phage V07	GCA_012361095.1
QIW90919.1	000811	virion_structural_Cluster132_1clades	283	COHAPHLL_00056	Vibrio phage V09	GCA_012361135.1
QIW90920.1	000811	virion_structural_Cluster132_1clades	306	COHAPHLL_00057	Vibrio phage V09	GCA_012361135.1
QIW90977.1	000811	virion_structural_Cluster132_1clades	293	COHAPHLL_00114	Vibrio phage V09	GCA_012361135.1
QIW91045.1	000811	virion_structural_Cluster132_1clades	320	COHAPHLL_00182	Vibrio phage V09	GCA_012361135.1
QHJ74551.1	000811	virion_structural_Cluster132_1clades	320	VH12019_00251	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74241.1	000811	virion_structural_Cluster132_1clades	293	VH12019_00322	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74298.1	000811	virion_structural_Cluster132_1clades	306	VH12019_00379	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74299.1	000811	virion_structural_Cluster132_1clades	283	VH12019_00380	Vibrio phage VH1_2019	GCA_009931825.1
AGB06792.1	000811	virion_structural_Cluster132_1clades	291	CF80_gp005	Vibrio phage VH7D	GCA_000914495.1
AGB07066.1	000811	virion_structural_Cluster132_1clades	293	CF80_gp279	Vibrio phage VH7D	GCA_000914495.1
AGB06791.1	000811	virion_structural_Cluster132_1clades	306	CF80_gp004	Vibrio phage VH7D	GCA_000914495.1
QBX05974.1	000811	virion_structural_Cluster132_1clades	283	ValB1HC_020	Vibrio phage ValB1 HC	GCA_004771355.1
QBX05975.1	000811	virion_structural_Cluster132_1clades	306	ValB1HC_021	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06030.1	000811	virion_structural_Cluster132_1clades	293	ValB1HC_076	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06103.1	000811	virion_structural_Cluster132_1clades	306	ValB1HC_149	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60988.1	000811	virion_structural_Cluster132_1clades	149	AVU32_gp147	Vibrio phage ValKK3	GCA_001501635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AJT60986.1	000811	virion_structural_Cluster132_1clades	291	AVU32_gp145	Vibrio phage ValKK3	GCA_001501635.1
AJT61044.1	000811	virion_structural_Cluster132_1clades	295	AVU32_gp203	Vibrio phage ValKK3	GCA_001501635.1
AJT60987.1	000811	virion_structural_Cluster132_1clades	306	AVU32_gp146	Vibrio phage ValKK3	GCA_001501635.1
AJT61117.1	000811	virion_structural_Cluster132_1clades	306	AVU32_gp276	Vibrio phage ValKK3	GCA_001501635.1
AGN30040.1	000811	virion_structural_Cluster132_1clades	306	VPFG_00035	Vibrio phage nt-1	GCA_000910195.2
AGN30107.1	000811	virion_structural_Cluster132_1clades	295	VPFG_00105	Vibrio phage nt-1	GCA_000910195.2
AGN30166.1	000811	virion_structural_Cluster132_1clades	278	VPFG_00164	Vibrio phage nt-1	GCA_000910195.2
ALP47020.1	000811	virion_structural_Cluster132_1clades	306	phiGrn1_0103	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47027.1	000811	virion_structural_Cluster132_1clades	295	phiGrn1_0173	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47133.1	000811	virion_structural_Cluster132_1clades	149	phiGrn1_0225	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47021.1	000811	virion_structural_Cluster132_1clades	306	phiGrn1_0226	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47030.1	000811	virion_structural_Cluster132_1clades	291	phiGrn1_0227	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47401.1	000811	virion_structural_Cluster132_1clades	306	phiST2_0234	Vibrio phage phi-ST2	GCA_002757135.1
ALP47406.1	000811	virion_structural_Cluster132_1clades	295	phiST2_0304	Vibrio phage phi-ST2	GCA_002757135.1
ALP47517.1	000811	virion_structural_Cluster132_1clades	149	phiST2_0360	Vibrio phage phi-ST2	GCA_002757135.1
ALP47400.1	000811	virion_structural_Cluster132_1clades	306	phiST2_0361	Vibrio phage phi-ST2	GCA_002757135.1
ALP47408.1	000811	virion_structural_Cluster132_1clades	291	phiST2_0362	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54655.1	000811	virion_structural_Cluster132_1clades	293	vBValMR10Z_114	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54728.1	000811	virion_structural_Cluster132_1clades	306	vBValMR10Z_188	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54599.1	000811	virion_structural_Cluster132_1clades	291	vBValMR10Z_58	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54600.1	000811	virion_structural_Cluster132_1clades	306	vBValMR10Z_59	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37289.1	000811	virion_structural_Cluster132_1clades	293	pp2_056	Vibriophage phi-pp2	GCA_002630725.1
AFN37344.1	000811	virion_structural_Cluster132_1clades	88	pp2_111	Vibriophage phi-pp2	GCA_002630725.1
AFN37345.1	000811	virion_structural_Cluster132_1clades	179	pp2_112	Vibriophage phi-pp2	GCA_002630725.1
AFN37346.1	000811	virion_structural_Cluster132_1clades	283	pp2_113	Vibriophage phi-pp2	GCA_002630725.1
AFN37602.1	000811	virion_structural_Cluster132_1clades	320	pp2_370	Vibriophage phi-pp2	GCA_002630725.1
AFO71349.1	000812	Cluster133_1clades	128	CR5_129	Cronobacter phage CR5	GCA_000910235.1
AMR59770.1	000812	Cluster133_1clades	83	SEGD1_123	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07557.1	000812	Cluster133_1clades	127	DERBICUS_131	Erwinia phage Derbicus	GCA_004521655.1
AHI60325.1	000812	Cluster133_1clades	131	Ea357_173A	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49773.1	000812	Cluster133_1clades	120	MACHINA_135	Erwinia phage Machina	GCA_002758035.1
AGX01854.1	000812	Cluster133_1clades	132	CF95_gp132	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07284.1	000812	Cluster133_1clades	131	REBECCA_177	Erwinia phage Rebecca	GCA_004521635.1
AXF51279.1	000812	Cluster133_1clades	116	WELLINGTON_150	Erwinia phage Wellington	GCA_003344985.1
AFQ96588.1	000812	Cluster133_1clades	82	G173_gp043	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48149.1	000812	Cluster133_1clades	98	ASESINO_136	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85964.1	000812	Cluster133_1clades	131	BOSOLAPHORUS_177	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48427.1	000812	Cluster133_1clades	120	CAITLIN_132	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48700.1	000812	Cluster133_1clades	118	CHRISDB_138	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52279.1	000812	Cluster133_1clades	131	DM_181	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86283.1	000812	Cluster133_1clades	131	DESERTFOX_176	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48980.1	000812	Cluster133_1clades	127	EARLPHILLIPIV_131	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49217.1	000812	Cluster133_1clades	120	HUXLEY_135	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49502.1	000812	Cluster133_1clades	116	KWAN_150	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86605.1	000812	Cluster133_1clades	131	MADMEL_177	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86929.1	000812	Cluster133_1clades	131	MORTIMER_180	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50045.1	000812	Cluster133_1clades	120	PARSHIK_136	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50322.1	000812	Cluster133_1clades	129	PHOBOS_132	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51956.1	000812	Cluster133_1clades	131	RAY_175	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51640.1	000812	Cluster133_1clades	131	SIMMY50_178	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64987.1	000812	Cluster133_1clades	131	SPECIALG_177	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50565.1	000812	Cluster133_1clades	123	STRATTON_140	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85960.1	000812	Cluster133_1clades	127	ACEC001_1220	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64012.1	000812	Cluster133_1clades	137	Goslar_00220	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24109.1	000812	Cluster133_1clades	119	-	Proteus phage 10	GCA_014071245.1
ABY63064.1	000812	Cluster133_1clades	115	201phi2-1p235	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44945.1	000812	Cluster133_1clades	116	KTN4_187	Pseudomonas phage KTN4	GCA_002607225.1
ARV77329.1	000812	Cluster133_1clades	118	NOXIFER_160	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32332.1	000812	Cluster133_1clades	115	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76854.1	000812	Cluster133_1clades	115	PHABIO_223	Pseudomonas phage Phabio	GCA_002624965.1
AEH03597.1	000812	Cluster133_1clades	151	174	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02733.1	000812	Cluster133_1clades	114	PSA21_207	Pseudomonas phage Psa21	GCA_004340405.1
ATN94769.1	000812	Cluster133_1clades	116	SL2_192	Pseudomonas phage SL2	GCA_002956015.1
QJB22823.1	000812	Cluster133_1clades	116	fnug_180	Pseudomonas phage fnug	GCA_012837215.1
QEM41905.1	000812	Cluster133_1clades	115	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83052.1	000812	Cluster133_1clades	116	PHIKZ151	Pseudomonas virus phiKZ	GCA_000842965.1
QNI20824.1	000812	Cluster133_1clades	144	-	Salmonella phage JN03	GCA_014319805.1
AXF51065.1	000812	Cluster133_1clades	134	MLDJOKPK_00035	Salmonella phage SPAsTU	GCA_003183805.1
AEP83953.1	000812	Cluster133_1clades	127	SPN3US_0120	Salmonella phage SPN3US	GCA_001042275.1
QKE54485.1	000812	Cluster133_1clades	129	ACSA002_1710	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QDB71218.1	000812	Cluster133_1clades	141	CPT_Moabite_188	Serratia phage Moabite	GCA_006384735.1
QFP93225.1	000812	Cluster133_1clades	125	-	Serratia phage PCH45	GCA_009187865.1
AXH70754.1	000812	Cluster133_1clades	120	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT28100.1	000812	Cluster133_1clades	309	pVa21_159	Vibrio phage pVa-21	GCA_002619305.1
QAX96780.1	000812	Cluster133_1clades	122	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97099.1	000812	Cluster133_1clades	122	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96145.1	000812	Cluster133_1clades	122	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96463.1	000812	Cluster133_1clades	122	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AND75394.1	000813	YqeY	137	ME3_233	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01557.1	000813	YqeY	155	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28936.1	000813	YqeY	57	AP1_0229	Aeromonas phage AP1	GCA_014183365.1
QMV29088.1	000813	YqeY	56	AP1_0381	Aeromonas phage AP1	GCA_014183365.1
ATI17344.1	000813	YqeY	159	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00249.1	000813	YqeY	138	HWB28_gp303	Aeromonas phage AS-zj	GCA_002627665.1
AUE22781.1	000813	YqeY	160	Ah1_00263	Aeromonas phage Ah1	GCA_002957415.1
QAX98496.1	000813	YqeY	160	ASfcp2_160	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97789.1	000813	YqeY	159	ASswx1_144	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01365.1	000813	YqeY	159	ASwh1_305	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39491.1	000813	YqeY	138	CC2_394	Aeromonas phage CC2	GCA_000903495.1
ADQ52959.1	000813	YqeY	160	PX29p240	Aeromonas phage PX29	GCA_000920195.1
ADM79885.1	000813	YqeY	156	phiAS5_ORF0042	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53180.1	000813	YqeY	155	65p172	Aeromonas virus 65	GCA_000893255.1
AAQ17907.1	000813	YqeY	160	Aeh1ORF245c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95415.1	000813	YqeY	152	FDI40_gp656	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93767.1	000813	YqeY	146	G_509	Bacillus virus G	GCA_000917535.1
QBX06543.1	000813	YqeY	156	BcepSaruman_130	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74509.1	000813	YqeY	156	BcepSauron_129	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ69104.1	000813	YqeY	261	CcrBL9_gp080c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69659.1	000813	YqeY	261	CcrSC_gp077c	Caulobacter phage CcrSC	GCA_003443315.1
AIA64850.1	000813	YqeY	133	S13_051	Cronobacter phage S13	GCA_001503575.1
AFC21639.1	000813	YqeY	137	GAP32_189	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXH72856.1	000813	YqeY	145	-	Myoviridae sp.	GCA_003657725.1
QIG65895.1	000813	YqeY	129	phiOC_p234	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43760.1	000813	YqeY	137	CBB_195	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76055.1	000813	YqeY	143	EST35_0174	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44290.1	000813	YqeY	143	PBI_SCTP2_275	Salicola phage SCTP-2	GCA_002625545.1
AQW88716.1	000813	YqeY	135	BF_0191	Serratia phage BF	GCA_002619745.1
AGR47903.1	000813	YqeY	95	SmphiM12_271	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47904.1	000813	YqeY	46	SmphiM12_272	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13109.1	000813	YqeY	141	PHIM19_204	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12749.1	000813	YqeY	141	PHIM7_204	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13479.1	000813	YqeY	141	PHIN3_216	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64449.1	000813	YqeY	137	KVP40.0381	Vibrio phage KVP40	GCA_000843785.1
QIW90394.1	000813	YqeY	137	GCAPEGMB_00047	Vibrio phage V07	GCA_012361095.1
QIW91035.1	000813	YqeY	137	COHAPHLL_00172	Vibrio phage V09	GCA_012361135.1
QHJ74561.1	000813	YqeY	137	VH12019_00261	Vibrio phage VH1_2019	GCA_009931825.1
QBX06092.1	000813	YqeY	137	ValB1HC_138	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61106.1	000813	YqeY	137	AVU32_gp265	Vibrio phage ValKK3	GCA_001501635.1
AGN30049.1	000813	YqeY	137	VPFG_00044	Vibrio phage nt-1	GCA_000910195.2
ALP47143.1	000813	YqeY	137	phiGrn1_0112	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47530.1	000813	YqeY	137	phiST2_0243	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54718.1	000813	YqeY	137	vBValMR10Z_177	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07014.1	000813	YqeY	137	VmeM32_00020	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37612.1	000813	YqeY	137	pp2_380	Vibriophage phi-pp2	GCA_002630725.1
BBA65508.1	000813	YqeY	147	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ96510.1	000813	YqeY	148	Xoosp13_324	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58998.1	000813	YqeY	135	g190	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58463.1	000813	YqeY	135	g186	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000386	000813	YqeY	162	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000312	000813	YqeY	162	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFO71260.1	000814	virion_structural-Cluster135_1clades	720	CR5_040	Cronobacter phage CR5	GCA_000910235.1
AMR59691.1	000814	virion_structural-Cluster135_1clades	795	SEGD1_042	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07467.1	000814	virion_structural-Cluster135_1clades	721	DERBICUS_41	Erwinia phage Derbicus	GCA_004521655.1
AHI60417.1	000814	virion_structural-Cluster135_1clades	539	Ea357_263	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49693.1	000814	virion_structural-Cluster135_1clades	676	MACHINA_55	Erwinia phage Machina	GCA_002758035.1
QBP07374.1	000814	virion_structural-Cluster135_1clades	539	REBECCA_269	Erwinia phage Rebecca	GCA_004521635.1
AXF51182.1	000814	virion_structural-Cluster135_1clades	672	WELLINGTON_51	Erwinia phage Wellington	GCA_003344985.1
AFQ96767.1	000814	virion_structural-Cluster135_1clades	686	G173_gp222	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48069.1	000814	virion_structural-Cluster135_1clades	705	ASESINO_56	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG86056.1	000814	virion_structural-Cluster135_1clades	539	BOSOLAPHORUS_270	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48344.1	000814	virion_structural-Cluster135_1clades	651	CAITLIN_49	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48617.1	000814	virion_structural-Cluster135_1clades	659	CHRISDB_55	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52372.1	000814	virion_structural-Cluster135_1clades	539	DM_273	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86376.1	000814	virion_structural-Cluster135_1clades	539	DESERTFOX_269	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48891.1	000814	virion_structural-Cluster135_1clades	721	EARLPHILLIPIV_41	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49138.1	000814	virion_structural-Cluster135_1clades	674	HUXLEY_56	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49403.1	000814	virion_structural-Cluster135_1clades	672	KWAN_51	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86697.1	000814	virion_structural-Cluster135_1clades	539	MADMEL_270	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87022.1	000814	virion_structural-Cluster135_1clades	539	MORTIMER_274	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49966.1	000814	virion_structural-Cluster135_1clades	674	PARSHIK_57	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50231.1	000814	virion_structural-Cluster135_1clades	705	PHOBOS_41	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH52047.1	000814	virion_structural-Cluster135_1clades	539	RAY_267	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51730.1	000814	virion_structural-Cluster135_1clades	542	SIMMY50_272	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65082.1	000814	virion_structural-Cluster135_1clades	539	SPECIALG_271	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50479.1	000814	virion_structural-Cluster135_1clades	697	STRATTON_54	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85880.1	000814	virion_structural-Cluster135_1clades	656	ACEC001_0420	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63874.1	000814	virion_structural-Cluster135_1clades	554	Goslar_00081	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24177.1	000814	virion_structural-Cluster135_1clades	504	-	Proteus phage 10	GCA_014071245.1
ABY62967.1	000814	virion_structural-Cluster135_1clades	527	201phi2-1p136	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44861.1	000814	virion_structural-Cluster135_1clades	533	KTN4_103	Pseudomonas phage KTN4	GCA_002607225.1
ARV77244.1	000814	virion_structural-Cluster135_1clades	560	NOXIFER_73	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32231.1	000814	virion_structural-Cluster135_1clades	533	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76752.1	000814	virion_structural-Cluster135_1clades	530	PHABIO_121	Pseudomonas phage Phabio	GCA_002624965.1
AEH03498.1	000814	virion_structural-Cluster135_1clades	544	074	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02612.1	000814	virion_structural-Cluster135_1clades	543	PSA21_84	Pseudomonas phage Psa21	GCA_004340405.1
ATN94852.1	000814	virion_structural-Cluster135_1clades	533	SL2_275	Pseudomonas phage SL2	GCA_002956015.1
QJB22739.1	000814	virion_structural-Cluster135_1clades	533	fnug_96	Pseudomonas phage fnug	GCA_012837215.1
QEM41809.1	000814	virion_structural-Cluster135_1clades	533	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82978.1	000814	virion_structural-Cluster135_1clades	533	PHIKZ077	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19229.1	000814	virion_structural-Cluster135_1clades	548	FDH28_gp166	Ralstonia phage RP12	GCA_002617345.1
BAW19515.1	000814	virion_structural-Cluster135_1clades	548	-	Ralstonia phage RP31	GCA_002617365.1
BAS04988.1	000814	virion_structural-Cluster135_1clades	507	AVU11_gp196	Ralstonia phage RSF1	GCA_001500875.1
BAQ02717.1	000814	virion_structural-Cluster135_1clades	508	AVU38_gp189	Ralstonia phage RSL2	GCA_001503055.1
QNI20755.1	000814	virion_structural-Cluster135_1clades	656	-	Salmonella phage JN03	GCA_014319805.1
AWN09057.1	000814	virion_structural-Cluster135_1clades	687	MLDJOKPK_00127	Salmonella phage SPAsTU	GCA_003183805.1
AEP83872.1	000814	virion_structural-Cluster135_1clades	656	SPN3US_0039	Salmonella phage SPN3US	GCA_001042275.1
QKE54597.1	000814	virion_structural-Cluster135_1clades	549	ACSA002_2800	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65340.1	000814	virion_structural-Cluster135_1clades	581	2050HW_00005	Serratia phage 2050HW	GCA_002628125.1
QDB71128.1	000814	virion_structural-Cluster135_1clades	581	CPT_Moabite_098	Serratia phage Moabite	GCA_006384735.1
QFP93063.1	000814	virion_structural-Cluster135_1clades	604	-	Serratia phage PCH45	GCA_009187865.1
AQT28166.1	000814	virion_structural-Cluster135_1clades	476	pVa21_225	Vibrio phage pVa-21	GCA_002619305.1
ALN97724.1	000815	virion_structural-Cluster143_1clades	205	Bp8pS_045	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97732.1	000815	virion_structural-Cluster143_1clades	124	Bp8pS_053	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97733.1	000815	virion_structural-Cluster143_1clades	112	Bp8pS_054	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97734.1	000815	virion_structural-Cluster143_1clades	232	Bp8pS_055	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97735.1	000815	virion_structural-Cluster143_1clades	279	Bp8pS_056	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97736.1	000815	virion_structural-Cluster143_1clades	132	Bp8pS_057	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97737.1	000815	virion_structural-Cluster143_1clades	173	Bp8pS_058	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97749.1	000815	virion_structural-Cluster143_1clades	245	Bp8pS_070	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97750.1	000815	virion_structural-Cluster143_1clades	317	Bp8pS_071	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97778.1	000815	virion_structural-Cluster143_1clades	245	Bp8pS_099	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97779.1	000815	virion_structural-Cluster143_1clades	294	Bp8pS_100	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97780.1	000815	virion_structural-Cluster143_1clades	287	Bp8pS_101	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97781.1	000815	virion_structural-Cluster143_1clades	282	Bp8pS_102	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97782.1	000815	virion_structural-Cluster143_1clades	308	Bp8pS_103	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97783.1	000815	virion_structural-Cluster143_1clades	307	Bp8pS_104	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97802.1	000815	virion_structural-Cluster143_1clades	142	Bp8pS_123	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97803.1	000815	virion_structural-Cluster143_1clades	185	Bp8pS_124	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97804.1	000815	virion_structural-Cluster143_1clades	186	Bp8pS_125	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97805.1	000815	virion_structural-Cluster143_1clades	167	Bp8pS_126	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97806.1	000815	virion_structural-Cluster143_1clades	204	Bp8pS_127	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97871.1	000815	virion_structural-Cluster143_1clades	153	Bp8pS_192	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97872.1	000815	virion_structural-Cluster143_1clades	241	Bp8pS_193	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97873.1	000815	virion_structural-Cluster143_1clades	234	Bp8pS_194	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97913.1	000815	virion_structural-Cluster143_1clades	278	Bp8pS_234	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97914.1	000815	virion_structural-Cluster143_1clades	217	Bp8pS_235	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97915.1	000815	virion_structural-Cluster143_1clades	243	Bp8pS_236	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97916.1	000815	virion_structural-Cluster143_1clades	244	Bp8pS_237	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97917.1	000815	virion_structural-Cluster143_1clades	221	Bp8pS_238	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97918.1	000815	virion_structural-Cluster143_1clades	200	Bp8pS_239	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97919.1	000815	virion_structural-Cluster143_1clades	230	Bp8pS_240	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97920.1	000815	virion_structural-Cluster143_1clades	229	Bp8pS_241	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97921.1	000815	virion_structural-Cluster143_1clades	242	Bp8pS_242	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97984.1	000815	virion_structural-Cluster143_1clades	116	Bp8pS_305	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97986.1	000815	virion_structural-Cluster143_1clades	90	Bp8pS_307	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93639.1	000815	virion_structural-Cluster143_1clades	256	G_380	Bacillus virus G	GCA_000917535.1
AEO93795.1	000815	virion_structural-Cluster143_1clades	181	G_538	Bacillus virus G	GCA_000917535.1
AEO93803.1	000815	virion_structural-Cluster143_1clades	135	G_556	Bacillus virus G	GCA_000917535.1
AEO93804.1	000815	virion_structural-Cluster143_1clades	135	G_558	Bacillus virus G	GCA_000917535.1
AEO93805.1	000815	virion_structural-Cluster143_1clades	273	G_559	Bacillus virus G	GCA_000917535.1
AEO93806.1	000815	virion_structural-Cluster143_1clades	191	G_560	Bacillus virus G	GCA_000917535.1
AEO93808.1	000815	virion_structural-Cluster143_1clades	170	G_562	Bacillus virus G	GCA_000917535.1
AEO93809.1	000815	virion_structural-Cluster143_1clades	251	G_563	Bacillus virus G	GCA_000917535.1
BAE47703.1	000815	virion_structural-Cluster143_1clades	138	CST005	Clostridium phage c-st	GCA_000865225.1
BAE47704.1	000815	virion_structural-Cluster143_1clades	90	CST006	Clostridium phage c-st	GCA_000865225.1
QAY00408.1	000815	virion_structural-Cluster143_1clades	257	Ecwhy1_127	Escherichia phage Ecwhy_1	GCA_004146585.1
AMM43867.1	000815	virion_structural-Cluster143_1clades	257	CBB_304	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK59110.1	000815	virion_structural-Cluster143_1clades	257	g302	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58574.1	000815	virion_structural-Cluster143_1clades	257	g297	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCH63547.1	000816	Epimerase	302	CP21_085	Campylobacter virus CP21	GCA_000902535.1
AGH07446.1	000816	Epimerase	269	CYVG_00002	Cyanophage S-SSM6a	GCA_002710385.1
AGH07565.1	000816	Epimerase	351	CYVG_00121	Cyanophage S-SSM6a	GCA_002710385.1
AGH07567.1	000816	Epimerase	301	CYVG_00123	Cyanophage S-SSM6a	GCA_002710385.1
AAX44634.1	000816	Epimerase	333	PSSM2_257	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44635.1	000816	Epimerase	311	PSSM2_258	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44636.1	000816	Epimerase	292	PSSM2_259	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44647.1	000816	Epimerase	301	PSSM2_270	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44690.1	000816	Epimerase	272	PSSM2_313	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12286.1	000816	Epimerase	272	PRTG_00133	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12324.1	000816	Epimerase	301	PRTG_00171	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12335.1	000816	Epimerase	292	PRTG_00182	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12336.1	000816	Epimerase	311	PRTG_00183	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12337.1	000816	Epimerase	333	PRTG_00184	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93529.1	000816	Epimerase	269	AVU42_gp192	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93514.1	000816	Epimerase	349	AVU42_gp177	Prochlorococcus phage P-TIM68	GCA_001503075.1
QHJ86113.1	000816	Epimerase	134	KKIINIFJ_00202	Pseudomonas phage PN05	GCA_009931935.1
QHJ86044.1	000816	Epimerase	353	KKIINIFJ_00132	Pseudomonas phage PN05	GCA_009931935.1
QHJ86035.1	000816	Epimerase	348	KKIINIFJ_00123	Pseudomonas phage PN05	GCA_009931935.1
QHJ86153.1	000816	Epimerase	143	KKIINIFJ_00242	Pseudomonas phage PN05	GCA_009931935.1
QHJ86177.1	000816	Epimerase	207	KKIINIFJ_00267	Pseudomonas phage PN05	GCA_009931935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFF28183.1	000816	Epimerase	340	PAU_185	Sphingomonas phage PAU	GCA_000902455.1
AYD81321.1	000816	Epimerase	316	SEA_JUSTBECAUSE_156	Streptomyces phage JustBecause	GCA_003613775.1
QJD53724.1	000816	Epimerase	316	SEA_KELA_154	Streptomyces phage Kela	GCA_012934305.1
QBZ72053.1	000816	Epimerase	316	SEA_KRADAL_157	Streptomyces phage Kradal	GCA_004799925.1
AXH66316.1	000816	Epimerase	316	SEA_SATIS_157	Streptomyces phage Satis	GCA_003366315.1
AIX30700.1	000816	Epimerase	332	Syn7803US37_223	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30701.1	000816	Epimerase	308	Syn7803US37_224	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30710.1	000816	Epimerase	301	Syn7803US37_233	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30758.1	000816	Epimerase	330	Syn7803US37_281	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76236.1	000816	Epimerase	361	PBI_BELLAMY_200	Synechococcus phage Bellamy	GCA_002627525.1
ASR76255.1	000816	Epimerase	339	PBI_BELLAMY_219	Synechococcus phage Bellamy	GCA_002627525.1
QCW22977.1	000816	Epimerase	273	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22962.1	000816	Epimerase	282	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22965.1	000816	Epimerase	298	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22979.1	000816	Epimerase	305	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22976.1	000816	Epimerase	358	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50512.1	000816	Epimerase	130	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50554.1	000816	Epimerase	227	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50513.1	000816	Epimerase	273	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50568.1	000816	Epimerase	282	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50565.1	000816	Epimerase	298	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50515.1	000816	Epimerase	305	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70518.1	000816	Epimerase	366	HOU04_gp119	Synechococcus phage S-T4	GCA_003443335.1
QJT70193.1	000816	Epimerase	350	SynMITS9220M01_187	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70206.1	000816	Epimerase	345	SynMITS9220M01_200	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70213.1	000816	Epimerase	295	SynMITS9220M01_207	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASV44746.1	000817	virion_structural-Cluster147_1clades	310	FDI40_gp324	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95059.1	000817	virion_structural-Cluster147_1clades	347	FDI40_gp287	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95085.1	000817	virion_structural-Cluster147_1clades	694	FDI40_gp326	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95084.1	000817	virion_structural-Cluster147_1clades	712	FDI40_gp325	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARB13601.1	000817	virion_structural-Cluster147_1clades	647	Ccr10_gp073	Caulobacter phage Ccr10	GCA_002619445.1
ARB13602.1	000817	virion_structural-Cluster147_1clades	232	Ccr10_gp074	Caulobacter phage Ccr10	GCA_002619445.1
ARB13947.1	000817	virion_structural-Cluster147_1clades	647	Ccr2_gp072	Caulobacter phage Ccr2	GCA_002619465.1
ARB13948.1	000817	virion_structural-Cluster147_1clades	232	Ccr2_gp073	Caulobacter phage Ccr2	GCA_002619465.1
ARB14637.1	000817	virion_structural-Cluster147_1clades	647	Ccr29_gp080	Caulobacter phage Ccr29	GCA_002619485.1
ARB14638.1	000817	virion_structural-Cluster147_1clades	232	Ccr29_gp081	Caulobacter phage Ccr29	GCA_002619485.1
ARB14993.1	000817	virion_structural-Cluster147_1clades	647	Ccr32_gp074	Caulobacter phage Ccr32	GCA_002619505.1
ARB14994.1	000817	virion_structural-Cluster147_1clades	232	Ccr32_gp075	Caulobacter phage Ccr32	GCA_002619505.1
ARB15323.1	000817	virion_structural-Cluster147_1clades	647	Ccr34_gp074	Caulobacter phage Ccr34	GCA_002619525.1
ARB15324.1	000817	virion_structural-Cluster147_1clades	232	Ccr34_gp075	Caulobacter phage Ccr34	GCA_002619525.1
ARB14290.1	000817	virion_structural-Cluster147_1clades	647	Ccr5_gp072	Caulobacter phage Ccr5	GCA_002619545.1
ARB14291.1	000817	virion_structural-Cluster147_1clades	232	Ccr5_gp073	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68274.1	000817	virion_structural-Cluster147_1clades	628	CcrBL10_gp070	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68275.1	000817	virion_structural-Cluster147_1clades	232	CcrBL10_gp071	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69157.1	000817	virion_structural-Cluster147_1clades	626	CcrBL9_gp133	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69158.1	000817	virion_structural-Cluster147_1clades	726	CcrBL9_gp134	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69159.1	000817	virion_structural-Cluster147_1clades	230	CcrBL9_gp135	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87957.1	000817	virion_structural-Cluster147_1clades	591	CcrColossus_gp087	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87958.1	000817	virion_structural-Cluster147_1clades	770	CcrColossus_gp088	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87959.1	000817	virion_structural-Cluster147_1clades	231	CcrColossus_gp089	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68633.1	000817	virion_structural-Cluster147_1clades	627	CcrPW_gp094	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68634.1	000817	virion_structural-Cluster147_1clades	771	CcrPW_gp095	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68635.1	000817	virion_structural-Cluster147_1clades	231	CcrPW_gp096	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69712.1	000817	virion_structural-Cluster147_1clades	626	CcrSC_gp130	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69713.1	000817	virion_structural-Cluster147_1clades	726	CcrSC_gp131	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69714.1	000817	virion_structural-Cluster147_1clades	230	CcrSC_gp132	Caulobacter phage CcrSC	GCA_003443315.1
AFU87591.1	000817	virion_structural-Cluster147_1clades	636	CcrKarma_gp074	Caulobacter virus Karma	GCA_000901575.1
AFU87592.1	000817	virion_structural-Cluster147_1clades	232	CcrKarma_gp075	Caulobacter virus Karma	GCA_000901575.1
AFU87241.1	000817	virion_structural-Cluster147_1clades	647	CcrMagneto_gp071	Caulobacter virus Magneto	GCA_000903095.1
AFU87242.1	000817	virion_structural-Cluster147_1clades	232	CcrMagneto_gp072	Caulobacter virus Magneto	GCA_000903095.1
AFU86557.1	000817	virion_structural-Cluster147_1clades	647	CcrRogue_gp075	Caulobacter virus Rogue	GCA_000900555.1
AFU86558.1	000817	virion_structural-Cluster147_1clades	232	CcrRogue_gp076	Caulobacter virus Rogue	GCA_000900555.1
AFU88389.1	000817	virion_structural-Cluster147_1clades	647	CcrSwift_gp071	Caulobacter virus Swift	GCA_000899655.1
AFU88390.1	000817	virion_structural-Cluster147_1clades	232	CcrSwift_gp072	Caulobacter virus Swift	GCA_000899655.1
AFU86905.1	000817	virion_structural-Cluster147_1clades	647	CbK_gp073	Caulobacter virus phiCbK	GCA_000900535.1
AFU86906.1	000817	virion_structural-Cluster147_1clades	232	CbK_gp074	Caulobacter virus phiCbK	GCA_000900535.1
AXH72645.1	000817	virion_structural-Cluster147_1clades	467	-	Myoviridae sp.	GCA_003657725.1
AFH14776.1	000817	virion_structural-Cluster147_1clades	139	Lu11_0240	Pseudomonas phage Lu11	GCA_000897175.1
QCG76184.1	000817	virion_structural-Cluster147_1clades	657	EST35_0303	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44031.1	000817	virion_structural-Cluster147_1clades	656	PBI_SCTP2_16	Salicola phage SCTP-2	GCA_002625545.1
ASV44245.1	000817	virion_structural-Cluster147_1clades	618	PBI_SCTP2_230	Salicola phage SCTP-2	GCA_002625545.1
ASV44246.1	000817	virion_structural-Cluster147_1clades	354	PBI_SCTP2_231	Salicola phage SCTP-2	GCA_002625545.1
AMS01265.1	000818	SIG+Band_7	268	AR9_g181	Bacillus phage AR9	GCA_001743835.1
AST99892.1	000818	SIG+Band_7	268	PBI_PBS1_70	Bacillus virus PBS1	GCA_002601325.1
ARB13706.1	000818	SIG+Band_7	276	Ccr10_gp176c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14051.1	000818	SIG+Band_7	276	Ccr2_gp175c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14738.1	000818	SIG+Band_7	276	Ccr29_gp182	Caulobacter phage Ccr29	GCA_002619485.1
ARB15093.1	000818	SIG+Band_7	276	Ccr32_gp175	Caulobacter phage Ccr32	GCA_002619505.1
ARB15427.1	000818	SIG+Band_7	276	Ccr34_gp185	Caulobacter phage Ccr34	GCA_002619525.1
ARB14394.1	000818	SIG+Band_7	276	Ccr5_gp174c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68376.1	000818	SIG+Band_7	276	CcrBL10_gp172c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87699.1	000818	SIG+Band_7	277	CcrKarma_gp182	Caulobacter virus Karma	GCA_000901575.1
AFU87348.1	000818	SIG+Band_7	277	CcrMagneto_gp178	Caulobacter virus Magneto	GCA_000903095.1
AFU86659.1	000818	SIG+Band_7	276	CcrRogue_gp177	Caulobacter virus Rogue	GCA_000900555.1
AFU88495.1	000818	SIG+Band_7	265	CcrSwift_gp177	Caulobacter virus Swift	GCA_000899655.1
AFU87012.1	000818	SIG+Band_7	276	CbK_gp180	Caulobacter virus phiCbK	GCA_000900535.1
AFC21473.1	000818	SIG+Band_7	285	GAP32_025	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ASU03783.1	000818	SIG+Band_7	289	JOAD_132	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03539.1	000818	SIG+Band_7	289	RISINGSUN_131	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QIG57877.1	000818	SIG+Band_7	340	SEA_PAULODIABOLI_189	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72887.1	000818	SIG+Band_7	321	-	Myoviridae sp.	GCA_003657725.1
QIG65853.1	000818	SIG+Band_7	283	phiOC_p188	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43594.1	000818	SIG+Band_7	291	CBB_29	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44145.1	000818	SIG+Band_7	291	CBB_582	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QBX32474.1	000818	SIG+Band_7	288	-	Pseudomonas phage PA1C	GCA_004785505.1
QBJ02871.1	000818	SIG+Band_7	287	PSA21_345	Pseudomonas phage Psa21	GCA_004340405.1
QEM42046.1	000818	SIG+Band_7	288	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW19088.1	000818	SIG+Band_7	279	7t3_0570	Salmonella phage 7t3	GCA_006083215.1
AZU98327.1	000818	SIG+Band_7	279	CPT_Munch_385	Salmonella phage Munch	GCA_004015485.1
QIG62656.1	000818	SIG+Band_7	279	SEPL_043	Salmonella phage SE_PL	GCA_011067555.1
AQW88547.1	000818	SIG+Band_7	285	BF_0022	Serratia phage BF	GCA_002619745.1
AAQ64408.1	000818	SIG+Band_7	291	KVP40.0339	Vibrio phage KVP40	GCA_000843785.1
QIW90353.1	000818	SIG+Band_7	291	GCAPEGMB_00006	Vibrio phage V07	GCA_012361095.1
QIW91076.1	000818	SIG+Band_7	291	COHAPHLL_00213	Vibrio phage V09	GCA_012361135.1
QHJ74521.1	000818	SIG+Band_7	291	VH12019_00221	Vibrio phage VH1_2019	GCA_009931825.1
QBX06134.1	000818	SIG+Band_7	291	ValB1HC_180	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61146.1	000818	SIG+Band_7	291	AVU32_gp305	Vibrio phage ValKK3	GCA_001501635.1
AGN30012.1	000818	SIG+Band_7	291	VPFG_00004	Vibrio phage nt-1	GCA_000910195.2
ALP47029.1	000818	SIG+Band_7	291	phiGrn1_0073	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47409.1	000818	SIG+Band_7	291	phiST2_0205	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54759.1	000818	SIG+Band_7	291	vBValMR10Z_219	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37571.1	000818	SIG+Band_7	291	pp2_339	Vibriophage phi-pp2	GCA_002630725.1
BBA65228.1	000818	SIG+Band_7	303	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65687.1	000818	SIG+Band_7	303	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK58822.1	000818	SIG+Band_7	285	g014	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58289.1	000818	SIG+Band_7	285	g012	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000230	000818	SIG+Band_7	265	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000180	000818	SIG+Band_7	265	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70255.1	000819	virion_structural-Cluster149_1clades	334	CF8_0087	Aeromonas phage CF8	GCA_006384595.2
QDB70258.1	000819	virion_structural-Cluster149_1clades	335	CF8_0090	Aeromonas phage CF8	GCA_006384595.2
QGY75122.1	000819	virion_structural-Cluster149_1clades	300	CF8_0107	Aeromonas phage CF8	GCA_006384595.2
QDB70379.1	000819	virion_structural-Cluster149_1clades	323	CF8_0210	Aeromonas phage CF8	GCA_006384595.2
QDJ97235.1	000819	virion_structural-Cluster149_1clades	336	D6_0075	Aeromonas phage D6	GCA_007051205.2
QDJ97253.1	000819	virion_structural-Cluster149_1clades	313	D6_0093	Aeromonas phage D6	GCA_007051205.2
QDJ97378.1	000819	virion_structural-Cluster149_1clades	315	D6_0219	Aeromonas phage D6	GCA_007051205.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDH47082.1	000819	virion_structural-Cluster149_1clades	334	LAh10_133	Aeromonas phage LAh10	GCA_006863975.1
QDH47087.1	000819	virion_structural-Cluster149_1clades	313	LAh10_25	Aeromonas phage LAh10	GCA_006863975.1
QDH47080.1	000819	virion_structural-Cluster149_1clades	336	LAh10_8	Aeromonas phage LAh10	GCA_006863975.1
QDJ96844.1	000819	virion_structural-Cluster149_1clades	307	PS1_0085	Aeromonas phage PS1	GCA_007051165.2
QDJ96866.1	000819	virion_structural-Cluster149_1clades	297	PS1_0107	Aeromonas phage PS1	GCA_007051165.2
QDJ96721.1	000819	virion_structural-Cluster149_1clades	310	PS1_0210	Aeromonas phage PS1	GCA_007051165.2
QFR59474.1	000819	virion_structural-Cluster149_1clades	307	PS2_0083	Aeromonas phage PS2	GCA_009388305.2
QFR59498.1	000819	virion_structural-Cluster149_1clades	297	PS2_0107	Aeromonas phage PS2	GCA_009388305.2
QFR59354.1	000819	virion_structural-Cluster149_1clades	310	PS2_0212	Aeromonas phage PS2	GCA_009388305.2
QBZ70608.1	000819	virion_structural-Cluster149_1clades	263	pETSU_027	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70609.1	000819	virion_structural-Cluster149_1clades	248	pETSU_028	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70617.1	000819	virion_structural-Cluster149_1clades	255	pETSU_036	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70618.1	000819	virion_structural-Cluster149_1clades	337	pETSU_037	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70619.1	000819	virion_structural-Cluster149_1clades	348	pETSU_038	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70635.1	000819	virion_structural-Cluster149_1clades	310	pETSU_054	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70763.1	000819	virion_structural-Cluster149_1clades	347	pETSU_182	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03777.1	000819	virion_structural-Cluster149_1clades	304	JOAD_138	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03724.1	000819	virion_structural-Cluster149_1clades	308	JOAD_191	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03910.1	000819	virion_structural-Cluster149_1clades	354	JOAD_5	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03844.1	000819	virion_structural-Cluster149_1clades	301	JOAD_71	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03843.1	000819	virion_structural-Cluster149_1clades	368	JOAD_72	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03842.1	000819	virion_structural-Cluster149_1clades	475	JOAD_73	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03907.1	000819	virion_structural-Cluster149_1clades	304	JOAD_8	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03533.1	000819	virion_structural-Cluster149_1clades	304	RISINGSUN_137	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03481.1	000819	virion_structural-Cluster149_1clades	308	RISINGSUN_189	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03665.1	000819	virion_structural-Cluster149_1clades	354	RISINGSUN_5	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03599.1	000819	virion_structural-Cluster149_1clades	305	RISINGSUN_71	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03598.1	000819	virion_structural-Cluster149_1clades	368	RISINGSUN_72	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03597.1	000819	virion_structural-Cluster149_1clades	475	RISINGSUN_73	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03662.1	000819	virion_structural-Cluster149_1clades	304	RISINGSUN_8	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72070.1	000819	virion_structural-Cluster149_1clades	362	N1M2_207	Klebsiella phage N1M2	GCA_010092605.1
QGH71952.1	000819	virion_structural-Cluster149_1clades	279	N1M2_89	Klebsiella phage N1M2	GCA_010092605.1
CAG27259.1	000819	virion_structural-Cluster149_1clades	351	PPEV_gp165	Pseudomonas phage EL	GCA_000866825.1
CAG27160.1	000819	virion_structural-Cluster149_1clades	468	PPEV_gp066	Pseudomonas phage EL	GCA_000866825.1
CAG27144.1	000819	virion_structural-Cluster149_1clades	358	PPEV_gp050	Pseudomonas phage EL	GCA_000866825.1
AEV89526.1	000819	virion_structural-Cluster149_1clades	238	OBP_089	Pseudomonas phage OBP	GCA_000896635.1
AEV89553.1	000819	virion_structural-Cluster149_1clades	279	OBP_116	Pseudomonas phage OBP	GCA_000896635.1
AEV89699.1	000819	virion_structural-Cluster149_1clades	362	OBP_262	Pseudomonas phage OBP	GCA_000896635.1
QDB70271.1	000820	phiKZ_IP	387	CF8_0103	Aeromonas phage CF8	GCA_006384595.2
QDJ97249.1	000820	phiKZ_IP	388	D6_0089	Aeromonas phage D6	GCA_007051205.2
QDH47065.1	000820	phiKZ_IP	388	LAh10_21	Aeromonas phage LAh10	GCA_006863975.1
QDJ96862.1	000820	phiKZ_IP	394	PS1_0103	Aeromonas phage PS1	GCA_007051165.2
QFR59494.1	000820	phiKZ_IP	394	PS2_0103	Aeromonas phage PS2	GCA_009388305.2
QBZ70610.1	000820	phiKZ_IP	345	pETSU_029	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70631.1	000820	phiKZ_IP	425	pETSU_050	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03847.1	000820	phiKZ_IP	415	JOAD_68	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03602.1	000820	phiKZ_IP	415	RISINGSUN_68	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71948.1	000820	phiKZ_IP	407	N1M2_85	Klebsiella phage N1M2	GCA_010092605.1
QGZ14410.1	000820	phiKZ_IP	389	HWC77_gp047	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14412.1	000820	phiKZ_IP	412	HWC77_gp049	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14409.1	000820	phiKZ_IP	419	HWC77_gp046	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14411.1	000820	phiKZ_IP	422	HWC77_gp048	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27157.1	000820	phiKZ_IP	418	PPEV_gp063	Pseudomonas phage EL	GCA_000866825.1
AEV89547.1	000820	phiKZ_IP	346	OBP_110	Pseudomonas phage OBP	GCA_000896635.1
AEV89548.1	000820	phiKZ_IP	358	OBP_111	Pseudomonas phage OBP	GCA_000896635.1
AEV89549.1	000820	phiKZ_IP	403	OBP_112	Pseudomonas phage OBP	GCA_000896635.1
QAU04326.1	000820	phiKZ_IP	389	HWC03_gp171	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04324.1	000820	phiKZ_IP	412	HWC03_gp169	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04327.1	000820	phiKZ_IP	421	HWC03_gp172	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04325.1	000820	phiKZ_IP	422	HWC03_gp170	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23250.1	000820	phiKZ_IP	384	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23251.1	000820	phiKZ_IP	399	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23254.1	000820	phiKZ_IP	412	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23252.1	000820	phiKZ_IP	416	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23253.1	000820	phiKZ_IP	419	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23249.1	000820	phiKZ_IP	427	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80966.1	000820	phiKZ_IP	412	Aphrodite1_0091	Vibrio phage Aphrodite1	GCA_002958015.1
AUR80962.1	000820	phiKZ_IP	424	Aphrodite1_0092	Vibrio phage Aphrodite1	GCA_002958015.1
AUR80964.1	000820	phiKZ_IP	416	Aphrodite1_0093	Vibrio phage Aphrodite1	GCA_002958015.1
AUR80968.1	000820	phiKZ_IP	399	Aphrodite1_0094	Vibrio phage Aphrodite1	GCA_002958015.1
AUR80969.1	000820	phiKZ_IP	396	Aphrodite1_0095	Vibrio phage Aphrodite1	GCA_002958015.1
AUR80961.1	000820	phiKZ_IP	427	Aphrodite1_0096	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47478.1	000820	phiKZ_IP	384	HWC35_gp084	Vibrio phage USC-1	GCA_006864065.1
QDH47477.1	000820	phiKZ_IP	399	HWC35_gp083	Vibrio phage USC-1	GCA_006864065.1
QDH47474.1	000820	phiKZ_IP	412	HWC35_gp080	Vibrio phage USC-1	GCA_006864065.1
QDH47476.1	000820	phiKZ_IP	416	HWC35_gp082	Vibrio phage USC-1	GCA_006864065.1
QDH47475.1	000820	phiKZ_IP	419	HWC35_gp081	Vibrio phage USC-1	GCA_006864065.1
QDH47479.1	000820	phiKZ_IP	427	HWC35_gp085	Vibrio phage USC-1	GCA_006864065.1
BAW98298.1	000820	phiKZ_IP	390	FDH33_gp089	Vibrio phage pTD1	GCA_002618825.1
BAW98295.1	000820	phiKZ_IP	408	FDH33_gp086	Vibrio phage pTD1	GCA_002618825.1
BAW98296.1	000820	phiKZ_IP	409	FDH33_gp087	Vibrio phage pTD1	GCA_002618825.1
BAW98297.1	000820	phiKZ_IP	415	FDH33_gp088	Vibrio phage pTD1	GCA_002618825.1
BAW98299.1	000820	phiKZ_IP	430	FDH33_gp090	Vibrio phage pTD1	GCA_002618825.1
AUZ95313.1	000821	virion_structural-Cluster152_1clades	127	FDI40_gp554	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95001.1	000821	virion_structural-Cluster152_1clades	216	FDI40_gp219	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95153.1	000821	virion_structural-Cluster152_1clades	484	FDI40_gp394	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95146.1	000821	virion_structural-Cluster152_1clades	98	FDI40_gp387	Agrobacterium phage Atu_ph07	GCA_002628245.1
AYD79981.1	000821	virion_structural-Cluster152_1clades	654	JA11_176	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79982.1	000821	virion_structural-Cluster152_1clades	595	JA11_177	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66579.1	000821	virion_structural-Cluster152_1clades	654	JA13_176	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66580.1	000821	virion_structural-Cluster152_1clades	595	JA13_177	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66904.1	000821	virion_structural-Cluster152_1clades	653	JA29_178	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66905.1	000821	virion_structural-Cluster152_1clades	595	JA29_179	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67550.1	000821	virion_structural-Cluster152_1clades	654	JA33_176	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67551.1	000821	virion_structural-Cluster152_1clades	595	JA33_177	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08605.1	000821	virion_structural-Cluster152_1clades	629	Alexandra_191	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28661.1	000821	virion_structural-Cluster152_1clades	717	YOLOSWAG_182	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFH14744.1	000821	virion_structural-Cluster152_1clades	627	Lu11_0207	Pseudomonas phage Lu11	GCA_000897175.1
AFH14745.1	000821	virion_structural-Cluster152_1clades	887	Lu11_0208	Pseudomonas phage Lu11	GCA_000897175.1
AFH14746.1	000821	virion_structural-Cluster152_1clades	899	Lu11_0209	Pseudomonas phage Lu11	GCA_000897175.1
ASV44126.1	000821	virion_structural-Cluster152_1clades	175	PBI_SCTP2_111	Salicola phage SCTP-2	GCA_002625545.1
ASV44128.1	000821	virion_structural-Cluster152_1clades	177	PBI_SCTP2_113	Salicola phage SCTP-2	GCA_002625545.1
ASV44220.1	000821	virion_structural-Cluster152_1clades	178	PBI_SCTP2_205	Salicola phage SCTP-2	GCA_002625545.1
ASV44221.1	000821	virion_structural-Cluster152_1clades	115	PBI_SCTP2_206	Salicola phage SCTP-2	GCA_002625545.1
ASV44241.1	000821	virion_structural-Cluster152_1clades	352	PBI_SCTP2_226	Salicola phage SCTP-2	GCA_002625545.1
ASV44242.1	000821	virion_structural-Cluster152_1clades	365	PBI_SCTP2_227	Salicola phage SCTP-2	GCA_002625545.1
ASV44243.1	000821	virion_structural-Cluster152_1clades	370	PBI_SCTP2_228	Salicola phage SCTP-2	GCA_002625545.1
ASV44244.1	000821	virion_structural-Cluster152_1clades	167	PBI_SCTP2_229	Salicola phage SCTP-2	GCA_002625545.1
ASV44044.1	000821	virion_structural-Cluster152_1clades	134	PBI_SCTP2_29	Salicola phage SCTP-2	GCA_002625545.1
ASV44045.1	000821	virion_structural-Cluster152_1clades	173	PBI_SCTP2_30	Salicola phage SCTP-2	GCA_002625545.1
ASV44049.1	000821	virion_structural-Cluster152_1clades	468	PBI_SCTP2_34	Salicola phage SCTP-2	GCA_002625545.1
ASV44052.1	000821	virion_structural-Cluster152_1clades	301	PBI_SCTP2_37	Salicola phage SCTP-2	GCA_002625545.1
ASV44450.1	000821	virion_structural-Cluster152_1clades	648	PBI_SCTP2_435	Salicola phage SCTP-2	GCA_002625545.1
ASV44060.1	000821	virion_structural-Cluster152_1clades	444	PBI_SCTP2_45	Salicola phage SCTP-2	GCA_002625545.1
ASV44061.1	000821	virion_structural-Cluster152_1clades	547	PBI_SCTP2_46	Salicola phage SCTP-2	GCA_002625545.1
ASV44063.1	000821	virion_structural-Cluster152_1clades	243	PBI_SCTP2_48	Salicola phage SCTP-2	GCA_002625545.1
ASV44495.1	000821	virion_structural-Cluster152_1clades	205	PBI_SCTP2_480	Salicola phage SCTP-2	GCA_002625545.1
ASV44496.1	000821	virion_structural-Cluster152_1clades	204	PBI_SCTP2_481	Salicola phage SCTP-2	GCA_002625545.1
ASV44497.1	000821	virion_structural-Cluster152_1clades	168	PBI_SCTP2_482	Salicola phage SCTP-2	GCA_002625545.1
ASV44498.1	000821	virion_structural-Cluster152_1clades	136	PBI_SCTP2_483	Salicola phage SCTP-2	GCA_002625545.1
ASV44533.1	000821	virion_structural-Cluster152_1clades	262	PBI_SCTP2_518	Salicola phage SCTP-2	GCA_002625545.1
ASV44536.1	000821	virion_structural-Cluster152_1clades	124	PBI_SCTP2_521	Salicola phage SCTP-2	GCA_002625545.1
ASV44537.1	000821	virion_structural-Cluster152_1clades	236	PBI_SCTP2_522	Salicola phage SCTP-2	GCA_002625545.1
ASV44540.1	000821	virion_structural-Cluster152_1clades	239	PBI_SCTP2_525	Salicola phage SCTP-2	GCA_002625545.1
ASV44072.1	000821	virion_structural-Cluster152_1clades	171	PBI_SCTP2_57	Salicola phage SCTP-2	GCA_002625545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASV44073.1	000821	virion_structural-Cluster152_1clades	143	PBI_SCTP2_58	Salicola phage SCTP-2	GCA_002625545.1
ASV44076.1	000821	virion_structural-Cluster152_1clades	190	PBI_SCTP2_61	Salicola phage SCTP-2	GCA_002625545.1
QMV29091.1	000822	virion_structural-Cluster154_1clades	185	AP1_0384	Aeromonas phage AP1	GCA_014183365.1
ATI17247.1	000822	virion_structural-Cluster154_1clades	185	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00340.1	000822	virion_structural-Cluster154_1clades	185	HWB28_gp212	Aeromonas phage AS-zj	GCA_002627665.1
QAX97690.1	000822	virion_structural-Cluster154_1clades	185	ASswx1_44	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01459.1	000822	virion_structural-Cluster154_1clades	188	ASwh1_400	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39203.1	000822	virion_structural-Cluster154_1clades	184	CC2_067	Aeromonas phage CC2	GCA_000903495.1
ASV44757.1	000822	virion_structural-Cluster154_1clades	97	FDI40_gp684	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21577.1	000822	virion_structural-Cluster154_1clades	270	GAP32_127	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14374.1	000822	virion_structural-Cluster154_1clades	215	PBI_121Q_484	Escherichia phage 121Q	GCA_000926855.1
QAY00574.1	000822	virion_structural-Cluster154_1clades	215	Ecwhy1_295	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34767.1	000822	virion_structural-Cluster154_1clades	215	ACQ29_gp087	Escherichia phage PBECO4	GCA_001041035.1
BBM62045.1	000822	virion_structural-Cluster154_1clades	216	EO157G_4560	Escherichia phage SP27	GCA_008033345.1
AXC36882.1	000822	virion_structural-Cluster154_1clades	218	-	Escherichia phage UB	GCA_003341455.1
QBO61930.1	000822	virion_structural-Cluster154_1clades	216	G17_00441	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13961.1	000822	virion_structural-Cluster154_1clades	216	vBEcoMphAPEC6_gp337c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80361.1	000822	virion_structural-Cluster154_1clades	216	PSLUR01_00384	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44783.1	000822	virion_structural-Cluster154_1clades	286	RaK2_00510	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43694.1	000822	virion_structural-Cluster154_1clades	280	CBB_129	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18834.1	000822	virion_structural-Cluster154_1clades	282	7t3_0313	Salmonella phage 7t3	GCA_006083215.1
AZU98097.1	000822	virion_structural-Cluster154_1clades	282	CPT_Munch_153	Salmonella phage Munch	GCA_004015485.1
QIG62885.1	000822	virion_structural-Cluster154_1clades	282	SEPL_272	Salmonella phage SE_PL	GCA_011067555.1
AQW88647.1	000822	virion_structural-Cluster154_1clades	282	BF_0122	Serratia phage BF	GCA_002619745.1
AGR48038.1	000822	virion_structural-Cluster154_1clades	68	SmphiM12_406	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13221.1	000822	virion_structural-Cluster154_1clades	68	PHIM19_316	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12862.1	000822	virion_structural-Cluster154_1clades	68	PHIM7_316	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13584.1	000822	virion_structural-Cluster154_1clades	93	PHIN3_321	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28292.1	000822	virion_structural-Cluster154_1clades	276	PAU_295	Sphingomonas phage PAU	GCA_000902455.1
BBI90507.1	000822	virion_structural-Cluster154_1clades	106	HYO65_gp115	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90815.1	000822	virion_structural-Cluster154_1clades	106	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39202.1	000822	virion_structural-Cluster154_1clades	100	BPT24_077	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64106.1	000822	virion_structural-Cluster154_1clades	106	KVP40.0035	Vibrio phage KVP40	GCA_000843785.1
QIW90429.1	000822	virion_structural-Cluster154_1clades	106	GCAPEGMB_00082	Vibrio phage V07	GCA_012361095.1
QIW91000.1	000822	virion_structural-Cluster154_1clades	106	COHAPHLL_00137	Vibrio phage V09	GCA_012361135.1
QHJ74218.1	000822	virion_structural-Cluster154_1clades	106	VH12019_00299	Vibrio phage VH1_2019	GCA_009931825.1
AGB07042.1	000822	virion_structural-Cluster154_1clades	108	CF80_gp255	Vibrio phage VH7D	GCA_000914495.1
QBX06054.1	000822	virion_structural-Cluster154_1clades	105	ValB1HC_100	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61067.1	000822	virion_structural-Cluster154_1clades	106	AVU32_gp226	Vibrio phage ValKK3	GCA_001501635.1
AGN30084.1	000822	virion_structural-Cluster154_1clades	107	VPFG_00082	Vibrio phage nt-1	GCA_000910195.2
ALP47189.1	000822	virion_structural-Cluster154_1clades	106	phiGrn1_0150	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47580.1	000822	virion_structural-Cluster154_1clades	105	phiST2_0280	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54680.1	000822	virion_structural-Cluster154_1clades	108	vBValMR10Z_139	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37268.1	000822	virion_structural-Cluster154_1clades	106	pp2_034	Vibriophage phi-pp2	GCA_002630725.1
SOK58927.1	000822	virion_structural-Cluster154_1clades	274	g119	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58392.1	000822	virion_structural-Cluster154_1clades	274	g115	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH57009.1	000823	baseplate_hub_assembly	63	CPXG_00206	Cyanophage P-RSM6	GCA_000906155.1
AJK27446.1	000823	baseplate_hub_assembly	48	PTIM40_19	Cyanophage P-TIM40	GCA_001470935.1
AOO14204.1	000823	baseplate_hub_assembly	60	Sn110110_010	Cyanophage S-RIM14	GCA_002599065.1
AOO14856.1	000823	baseplate_hub_assembly	60	W1230910_010	Cyanophage S-RIM14	GCA_002599125.1
AMO43024.1	000823	baseplate_hub_assembly	59	R1080702_009	Cyanophage S-RIM32	GCA_001754165.1
AMO43255.1	000823	baseplate_hub_assembly	59	W270710_010	Cyanophage S-RIM44	GCA_002599145.1
AOO11492.1	000823	baseplate_hub_assembly	59	ES420910_010	Cyanophage S-RIM44	GCA_002599165.1
AOO11727.1	000823	baseplate_hub_assembly	59	Np050604_010	Cyanophage S-RIM44	GCA_002599185.1
AOO11957.1	000823	baseplate_hub_assembly	59	Np200711_010	Cyanophage S-RIM44	GCA_002599205.1
AOO12193.1	000823	baseplate_hub_assembly	59	Np420711_010	Cyanophage S-RIM44	GCA_002599225.1
AOO12428.1	000823	baseplate_hub_assembly	59	Sn080709_010	Cyanophage S-RIM44	GCA_002599245.1
AOO12658.1	000823	baseplate_hub_assembly	59	Sn130910_010	Cyanophage S-RIM44	GCA_002599265.1
AOO12893.1	000823	baseplate_hub_assembly	59	W2100709_010	Cyanophage S-RIM44	GCA_002599285.1
AGH07637.1	000823	baseplate_hub_assembly	63	CYVG_00194	Cyanophage S-SSM6a	GCA_002710385.1
AGH26196.1	000823	baseplate_hub_assembly	53	CPMG_00095	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44393.1	000823	baseplate_hub_assembly	57	PSSM2_015	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12256.1	000823	baseplate_hub_assembly	57	PRTG_00100	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93397.1	000823	baseplate_hub_assembly	57	AVU42_gp011	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99113.1	000823	baseplate_hub_assembly	43	Syn1_011	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47796.2	000823	baseplate_hub_assembly	53	SmphiM12_164	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13013.1	000823	baseplate_hub_assembly	53	PHIM19_107	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12653.1	000823	baseplate_hub_assembly	53	PHIM7_106	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13385.1	000823	baseplate_hub_assembly	53	PHIN3_120	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30486.1	000823	baseplate_hub_assembly	59	Syn7803US37_9	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54636.1	000823	baseplate_hub_assembly	54	b23_0008	Synechococcus phage B23	GCA_009745195.1
QGT54266.1	000823	baseplate_hub_assembly	54	b3_0008	Synechococcus phage B3	GCA_009745215.1
ASR76058.1	000823	baseplate_hub_assembly	56	PBI_BELLAMY_11	Synechococcus phage Bellamy	GCA_002627525.1
QCW22920.1	000823	baseplate_hub_assembly	55	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50635.1	000823	baseplate_hub_assembly	55	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70442.1	000823	baseplate_hub_assembly	44	HOU04_gp043	Synechococcus phage S-T4	GCA_003443335.1
QJT70026.1	000823	baseplate_hub_assembly	57	SynMITS9220M01_010	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64397.1	000823	baseplate_hub_assembly	55	KVP40.0327	Vibrio phage KVP40	GCA_000843785.1
QIW90709.1	000823	baseplate_hub_assembly	55	GCAPEGMB_00390	Vibrio phage V07	GCA_012361095.1
QIW91088.1	000823	baseplate_hub_assembly	55	COHAPHLL_00225	Vibrio phage V09	GCA_012361135.1
QHJ74509.1	000823	baseplate_hub_assembly	55	VH12019_00209	Vibrio phage VH1_2019	GCA_009931825.1
QBX06146.1	000823	baseplate_hub_assembly	55	ValB1HC_192	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61158.1	000823	baseplate_hub_assembly	55	AVU32_gp317	Vibrio phage ValKK3	GCA_001501635.1
AGN30378.1	000823	baseplate_hub_assembly	55	VPFG_00381	Vibrio phage nt-1	GCA_000910195.2
ALP47336.1	000823	baseplate_hub_assembly	39	phiGrn1_0061	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47703.1	000823	baseplate_hub_assembly	55	phiST2_0193	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54771.1	000823	baseplate_hub_assembly	55	vBValMR10Z_231	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37559.1	000823	baseplate_hub_assembly	39	pp2_327	Vibriophage phi-pp2	GCA_002630725.1
AEO93417.1	000824	HNH	138	G_157	Bacillus virus G	GCA_000917535.1
QBX06541.1	000824	HNH	142	BcepSaruman_128	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74507.1	000824	HNH	142	BcepSauron_127	Burkholderia phage BcepSauron	GCA_005394215.1
AFU88147.1	000824	HNH	230	CcrColossus_gp277	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68823.1	000824	HNH	230	CcrPW_gp284	Caulobacter phage CcrPW	GCA_003443275.1
AFC21968.1	000824	HNH	165	GAP32_508	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21980.1	000824	HNH	304	GAP32_520	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14060.1	000824	HNH	262	PBI_121Q_170	Escherichia phage 121Q	GCA_000926855.1
AIT14403.1	000824	HNH	203	PBI_121Q_513	Escherichia phage 121Q	GCA_000926855.1
QAY00548.1	000824	HNH	203	Ecwhy1_269	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34739.1	000824	HNH	203	ACQ29_gp059	Escherichia phage PBECO4	GCA_001041035.1
AGC35033.1	000824	HNH	262	ACQ29_gp353	Escherichia phage PBECO4	GCA_001041035.1
BBM61743.1	000824	HNH	262	EO157G_1540	Escherichia phage SP27	GCA_008033345.1
BBM62074.1	000824	HNH	203	EO157G_4850	Escherichia phage SP27	GCA_008033345.1
AXC36854.1	000824	HNH	203	-	Escherichia phage UB	GCA_003341455.1
AXC36610.1	000824	HNH	262	-	Escherichia phage UB	GCA_003341455.1
QBO61639.1	000824	HNH	262	G17_00143	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61899.1	000824	HNH	203	G17_00410	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13693.1	000824	HNH	262	vBEcoMphAPEC6_gp063c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13935.1	000824	HNH	203	vBEcoMphAPEC6_gp310c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80055.1	000824	HNH	262	PSLUR01_00078	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80389.1	000824	HNH	203	PSLUR01_00412	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44285.1	000824	HNH	194	RaK2_00012	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44091.1	000824	HNH	188	CBB_528	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44098.1	000824	HNH	306	CBB_535	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18867.1	000824	HNH	212	7t3_0346	Salmonella phage 7t3	GCA_006083215.1
QCW18606.1	000824	HNH	319	7t3_085	Salmonella phage 7t3	GCA_006083215.1
AZU98128.1	000824	HNH	212	CPT_Munch_184	Salmonella phage Munch	GCA_004015485.1
AZU98431.1	000824	HNH	319	CPT_Munch_499	Salmonella phage Munch	GCA_004015485.1
QIG62854.1	000824	HNH	212	SEPL_241	Salmonella phage SE_PL	GCA_011067555.1
QIG63082.1	000824	HNH	319	SEPL_469	Salmonella phage SE_PL	GCA_011067555.1
AQW89048.1	000824	HNH	170	BF_0523	Serratia phage BF	GCA_002619745.1
AQW89054.1	000824	HNH	289	BF_0529	Serratia phage BF	GCA_002619745.1
QGT54812.1	000824	HNH	193	b23_0197	Synechococcus phage B23	GCA_009745195.1
QGT54442.1	000824	HNH	193	b3_0199	Synechococcus phage B3	GCA_009745215.1
SOK58967.1	000824	HNH	177	g159	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59323.1	000824	HNH	166	g515	Yersinia phage fHe-Yen9-03	GCA_002990515.1

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SOK59332.1	000824	HNH	286	g524	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58433.1	000824	HNH	177	g156	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58785.1	000824	HNH	166	g508	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58794.1	000824	HNH	282	g517	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14260.1	000825	virion_structural-Cluster158_1clades	164	PBI_121Q_370	Escherichia phage 121Q	GCA_000926855.1
AIT14261.1	000825	virion_structural-Cluster158_1clades	156	PBI_121Q_371	Escherichia phage 121Q	GCA_000926855.1
AIT14262.1	000825	virion_structural-Cluster158_1clades	146	PBI_121Q_372	Escherichia phage 121Q	GCA_000926855.1
AIT14263.1	000825	virion_structural-Cluster158_1clades	162	PBI_121Q_373	Escherichia phage 121Q	GCA_000926855.1
AIT14264.1	000825	virion_structural-Cluster158_1clades	150	PBI_121Q_374	Escherichia phage 121Q	GCA_000926855.1
QAY00673.1	000825	virion_structural-Cluster158_1clades	147	Ecwhy1_398	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00674.1	000825	virion_structural-Cluster158_1clades	163	Ecwhy1_399	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00675.1	000825	virion_structural-Cluster158_1clades	146	Ecwhy1_400	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00676.1	000825	virion_structural-Cluster158_1clades	156	Ecwhy1_401	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00677.1	000825	virion_structural-Cluster158_1clades	163	Ecwhy1_402	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34870.1	000825	virion_structural-Cluster158_1clades	147	ACQ29_gp190	Escherichia phage PBECO4	GCA_001041035.1
AGC34868.1	000825	virion_structural-Cluster158_1clades	150	ACQ29_gp188	Escherichia phage PBECO4	GCA_001041035.1
AGC34871.1	000825	virion_structural-Cluster158_1clades	156	ACQ29_gp191	Escherichia phage PBECO4	GCA_001041035.1
AGC34869.1	000825	virion_structural-Cluster158_1clades	162	ACQ29_gp189	Escherichia phage PBECO4	GCA_001041035.1
AGC34872.1	000825	virion_structural-Cluster158_1clades	163	ACQ29_gp192	Escherichia phage PBECO4	GCA_001041035.1
BBM61935.1	000825	virion_structural-Cluster158_1clades	163	EO157G_3460	Escherichia phage SP27	GCA_008033345.1
BBM61936.1	000825	virion_structural-Cluster158_1clades	156	EO157G_3470	Escherichia phage SP27	GCA_008033345.1
BBM61937.1	000825	virion_structural-Cluster158_1clades	147	EO157G_3480	Escherichia phage SP27	GCA_008033345.1
BBM61938.1	000825	virion_structural-Cluster158_1clades	163	EO157G_3490	Escherichia phage SP27	GCA_008033345.1
BBM61939.1	000825	virion_structural-Cluster158_1clades	147	EO157G_3500	Escherichia phage SP27	GCA_008033345.1
AXC36978.1	000825	virion_structural-Cluster158_1clades	147	-	Escherichia phage UB	GCA_003341455.1
AXC36976.1	000825	virion_structural-Cluster158_1clades	150	-	Escherichia phage UB	GCA_003341455.1
AXC36979.1	000825	virion_structural-Cluster158_1clades	156	-	Escherichia phage UB	GCA_003341455.1
AXC36977.1	000825	virion_structural-Cluster158_1clades	162	-	Escherichia phage UB	GCA_003341455.1
AXC36980.1	000825	virion_structural-Cluster158_1clades	163	-	Escherichia phage UB	GCA_003341455.1
QBO62040.1	000825	virion_structural-Cluster158_1clades	150	G17_00551	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62041.1	000825	virion_structural-Cluster158_1clades	162	G17_00552	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62042.1	000825	virion_structural-Cluster158_1clades	147	G17_00553	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62043.1	000825	virion_structural-Cluster158_1clades	156	G17_00554	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62044.1	000825	virion_structural-Cluster158_1clades	163	G17_00555	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14061.1	000825	virion_structural-Cluster158_1clades	150	vBEcoMphAPEC6_gp438c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14062.1	000825	virion_structural-Cluster158_1clades	162	vBEcoMphAPEC6_gp439c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14063.1	000825	virion_structural-Cluster158_1clades	147	vBEcoMphAPEC6_gp440c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14064.1	000825	virion_structural-Cluster158_1clades	156	vBEcoMphAPEC6_gp441c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14065.1	000825	virion_structural-Cluster158_1clades	163	vBEcoMphAPEC6_gp442c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80249.1	000825	virion_structural-Cluster158_1clades	164	PSLUR01_00272	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80250.1	000825	virion_structural-Cluster158_1clades	156	PSLUR01_00273	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80251.1	000825	virion_structural-Cluster158_1clades	146	PSLUR01_00274	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80252.1	000825	virion_structural-Cluster158_1clades	162	PSLUR01_00275	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80253.1	000825	virion_structural-Cluster158_1clades	150	PSLUR01_00276	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44693.1	000825	virion_structural-Cluster158_1clades	176	RaK2_00420	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AAQ64246.1	000826	Cluster159_1clades	129	KVP40.0177	Vibrio phage KVP40	GCA_000843785.1
AAQ64248.1	000826	Cluster159_1clades	137	KVP40.0179	Vibrio phage KVP40	GCA_000843785.1
QIW90562.1	000826	Cluster159_1clades	129	GCAPEGMB_00215	Vibrio phage V07	GCA_012361095.1
QIW90564.1	000826	Cluster159_1clades	137	GCAPEGMB_00217	Vibrio phage V07	GCA_012361095.1
QIW91235.1	000826	Cluster159_1clades	137	COHAPHLL_00399	Vibrio phage V09	GCA_012361135.1
QIW91237.1	000826	Cluster159_1clades	129	COHAPHLL_00401	Vibrio phage V09	GCA_012361135.1
QHJ74360.1	000826	Cluster159_1clades	129	VH12019_00033	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74362.1	000826	Cluster159_1clades	137	VH12019_00035	Vibrio phage VH1_2019	GCA_009931825.1
AGB06856.1	000826	Cluster159_1clades	125	CF80_gp069	Vibrio phage VH7D	GCA_000914495.1
AGB06852.1	000826	Cluster159_1clades	135	CF80_gp065	Vibrio phage VH7D	GCA_000914495.1
AGB06855.1	000826	Cluster159_1clades	144	CF80_gp068	Vibrio phage VH7D	GCA_000914495.1
AGB06857.1	000826	Cluster159_1clades	150	CF80_gp070	Vibrio phage VH7D	GCA_000914495.1
QBX06288.1	000826	Cluster159_1clades	140	ValB1HC_335	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06289.1	000826	Cluster159_1clades	125	ValB1HC_336	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06290.1	000826	Cluster159_1clades	144	ValB1HC_337	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06293.1	000826	Cluster159_1clades	135	ValB1HC_340	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60919.1	000826	Cluster159_1clades	125	AVU32_gp078	Vibrio phage ValKK3	GCA_001501635.1
AJT60923.1	000826	Cluster159_1clades	135	AVU32_gp082	Vibrio phage ValKK3	GCA_001501635.1
AJT60918.1	000826	Cluster159_1clades	140	AVU32_gp077	Vibrio phage ValKK3	GCA_001501635.1
AJT60920.1	000826	Cluster159_1clades	144	AVU32_gp079	Vibrio phage ValKK3	GCA_001501635.1
AGN30227.1	000826	Cluster159_1clades	120	VPFG_00228	Vibrio phage nt-1	GCA_000910195.2
AGN30232.1	000826	Cluster159_1clades	118	VPFG_00233	Vibrio phage nt-1	GCA_000910195.2
AGN30233.1	000826	Cluster159_1clades	124	VPFG_00234	Vibrio phage nt-1	GCA_000910195.2
AGN30234.1	000826	Cluster159_1clades	173	VPFG_00235	Vibrio phage nt-1	GCA_000910195.2
AGN30235.1	000826	Cluster159_1clades	131	VPFG_00236	Vibrio phage nt-1	GCA_000910195.2
AGN30236.1	000826	Cluster159_1clades	122	VPFG_00237	Vibrio phage nt-1	GCA_000910195.2
AGN30237.1	000826	Cluster159_1clades	118	VPFG_00238	Vibrio phage nt-1	GCA_000910195.2
ALP47147.1	000826	Cluster159_1clades	135	phiGrn1_0291	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47136.1	000826	Cluster159_1clades	144	phiGrn1_0294	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47158.1	000826	Cluster159_1clades	125	phiGrn1_0295	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47139.1	000826	Cluster159_1clades	140	phiGrn1_0296	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47534.1	000826	Cluster159_1clades	135	phiST2_0048	Vibrio phage phi-ST2	GCA_002757135.1
ALP47522.1	000826	Cluster159_1clades	144	phiST2_0051	Vibrio phage phi-ST2	GCA_002757135.1
ALP47545.1	000826	Cluster159_1clades	125	phiST2_0052	Vibrio phage phi-ST2	GCA_002757135.1
ALP47526.1	000826	Cluster159_1clades	140	phiST2_0053	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54915.1	000826	Cluster159_1clades	140	vBValMR10Z_375	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54916.1	000826	Cluster159_1clades	125	vBValMR10Z_376	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54917.1	000826	Cluster159_1clades	144	vBValMR10Z_377	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54920.1	000826	Cluster159_1clades	135	vBValMR10Z_380	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37407.1	000826	Cluster159_1clades	129	pp2_174	Vibriophage phi-pp2	GCA_002630725.1
AFN37409.1	000826	Cluster159_1clades	137	pp2_176	Vibriophage phi-pp2	GCA_002630725.1
AFO71274.1	000827	SIG+phiKZ_IP	431	CR5_054	Cronobacter phage CR5	GCA_000910235.1
AFO71275.1	000827	SIG+phiKZ_IP	424	CR5_055	Cronobacter phage CR5	GCA_000910235.1
AMR59704.1	000827	SIG+phiKZ_IP	425	SEGD1_055	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59705.1	000827	SIG+phiKZ_IP	419	SEGD1_056	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07481.1	000827	SIG+phiKZ_IP	440	DERBICUS_55	Erwinia phage Derbicus	GCA_004521655.1
QBP07482.1	000827	SIG+phiKZ_IP	422	DERBICUS_56	Erwinia phage Derbicus	GCA_004521655.1
ANZ49707.1	000827	SIG+phiKZ_IP	442	MACHINA_69	Erwinia phage Machina	GCA_002758035.1
ANZ49708.1	000827	SIG+phiKZ_IP	426	MACHINA_70	Erwinia phage Machina	GCA_002758035.1
AXF51197.1	000827	SIG+phiKZ_IP	422	WELLINGTON_67	Erwinia phage Wellington	GCA_003344985.1
AXF51198.1	000827	SIG+phiKZ_IP	423	WELLINGTON_68	Erwinia phage Wellington	GCA_003344985.1
AFQ96783.1	000827	SIG+phiKZ_IP	417	G173_gp238	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96782.1	000827	SIG+phiKZ_IP	426	G173_gp237	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48083.1	000827	SIG+phiKZ_IP	426	ASESINO_70	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48084.1	000827	SIG+phiKZ_IP	419	ASESINO_71	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48358.1	000827	SIG+phiKZ_IP	424	CAITLIN_63	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48359.1	000827	SIG+phiKZ_IP	431	CAITLIN_64	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48631.1	000827	SIG+phiKZ_IP	425	CHRISDB_69	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48632.1	000827	SIG+phiKZ_IP	422	CHRISDB_70	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48905.1	000827	SIG+phiKZ_IP	431	EARLPHILLIPIV_55	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ48906.1	000827	SIG+phiKZ_IP	422	EARLPHILLIPIV_56	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49152.1	000827	SIG+phiKZ_IP	442	HUXLEY_70	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49153.1	000827	SIG+phiKZ_IP	426	HUXLEY_71	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49419.1	000827	SIG+phiKZ_IP	422	KWAN_67	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49420.1	000827	SIG+phiKZ_IP	423	KWAN_68	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49980.1	000827	SIG+phiKZ_IP	442	PARSHIK_71	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ49981.1	000827	SIG+phiKZ_IP	426	PARSHIK_72	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50246.1	000827	SIG+phiKZ_IP	430	PHOBOS_56	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50247.1	000827	SIG+phiKZ_IP	421	PHOBOS_57	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50494.1	000827	SIG+phiKZ_IP	426	STRATTON_69	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50495.1	000827	SIG+phiKZ_IP	417	STRATTON_70	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85894.1	000827	SIG+phiKZ_IP	425	ACEC001_0560	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85895.1	000827	SIG+phiKZ_IP	419	ACEC001_0570	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20770.1	000827	SIG+phiKZ_IP	419	-	Salmonella phage JN03	GCA_014319805.1
QNI20769.1	000827	SIG+phiKZ_IP	425	-	Salmonella phage JN03	GCA_014319805.1
AWN09043.1	000827	SIG+phiKZ_IP	421	MLDJOKPK_00111	Salmonella phage SPAsTU	GCA_003183805.1
AWN09044.1	000827	SIG+phiKZ_IP	425	MLDJOKPK_00112	Salmonella phage SPAsTU	GCA_003183805.1
AEP83886.1	000827	SIG+phiKZ_IP	425	SPN3US_0053	Salmonella phage SPN3US	GCA_001042275.1
AEP83887.1	000827	SIG+phiKZ_IP	419	SPN3US_0054	Salmonella phage SPN3US	GCA_001042275.1
AQT28182.1	000827	SIG+phiKZ_IP	410	pVa21_241	Vibrio phage pVa-21	GCA_002619305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFO71434.1	000828	Cluster163_1clades	205	CR5_214	Cronobacter phage CR5	GCA_000910235.1
AMR59898.1	000828	Cluster163_1clades	209	SEGD1_251	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07647.1	000828	Cluster163_1clades	204	DERBICUS_221	Erwinia phage Derbicus	GCA_004521655.1
AHI60319.1	000828	Cluster163_1clades	233	Ea357_168	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49897.1	000828	Cluster163_1clades	204	MACHINA_259	Erwinia phage Machina	GCA_002758035.1
AGX01862.1	000828	Cluster163_1clades	246	CF95_gp140	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07278.1	000828	Cluster163_1clades	233	REBECCA_171	Erwinia phage Rebecca	GCA_004521635.1
AXF51398.1	000828	Cluster163_1clades	208	WELLINGTON_272	Erwinia phage Wellington	GCA_003344985.1
AFQ96711.1	000828	Cluster163_1clades	209	G173_gp166	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48281.1	000828	Cluster163_1clades	209	ASESINO_268	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85958.1	000828	Cluster163_1clades	233	BOSOLAPHORUS_171	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48553.1	000828	Cluster163_1clades	204	CAITLIN_258	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48831.1	000828	Cluster163_1clades	206	CHRISDB_269	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52273.1	000828	Cluster163_1clades	233	DM_175	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86277.1	000828	Cluster163_1clades	233	DESERTFOX_170	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49071.1	000828	Cluster163_1clades	204	EARLPHILLIPIV_222	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49340.1	000828	Cluster163_1clades	204	HUXLEY_258	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49624.1	000828	Cluster163_1clades	208	KWAN_272	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86599.1	000828	Cluster163_1clades	233	MADMEL_171	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86923.1	000828	Cluster163_1clades	233	MORTIMER_174	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50168.1	000828	Cluster163_1clades	204	PARSHIK_259	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50418.1	000828	Cluster163_1clades	204	PHOBOS_228	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51950.1	000828	Cluster163_1clades	233	RAY_169	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51634.1	000828	Cluster163_1clades	233	SIMMY50_172	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64981.1	000828	Cluster163_1clades	233	SPECIALG_171	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50693.1	000828	Cluster163_1clades	209	STRATTON_268	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86087.1	000828	Cluster163_1clades	209	ACEC001_2440	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO64016.1	000828	Cluster163_1clades	243	Goslar_00224	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24100.1	000828	Cluster163_1clades	239	-	Proteus phage 10	GCA_014071245.1
ARV77297.1	000828	Cluster163_1clades	236	NOXIFER_128	Pseudomonas phage Noxifer	GCA_002625005.1
QNI20930.1	000828	Cluster163_1clades	209	-	Salmonella phage JN03	GCA_014319805.1
AWN09107.1	000828	Cluster163_1clades	209	MLDJOKPK_00194	Salmonella phage SPAsTU	GCA_003183805.1
AEP84079.1	000828	Cluster163_1clades	209	SPN3US_0246	Salmonella phage SPN3US	GCA_001042275.1
QKE54476.1	000828	Cluster163_1clades	237	ACSA002_1620	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65441.1	000828	Cluster163_1clades	105	2050HW_00106	Serratia phage 2050HW	GCA_002628125.1
ATA65442.1	000828	Cluster163_1clades	110	2050HW_00107	Serratia phage 2050HW	GCA_002628125.1
QDB71212.1	000828	Cluster163_1clades	237	CPT_Moabite_182	Serratia phage Moabite	GCA_006384735.1
QFP93133.1	000828	Cluster163_1clades	238	-	Serratia phage PCH45	GCA_009187865.1
AQT28113.1	000828	Cluster163_1clades	230	pVa21_172	Vibrio phage pVa-21	GCA_002619305.1
CCH63577.1	000829	IIGP1	241	CP21_115	Campylobacter virus CP21	GCA_000902535.1
AGH57014.1	000829	IIGP1	372	CPXG_00211	Cyanophage P-RSM6	GCA_000906155.1
AJK27441.1	000829	IIGP1	338	PTIM40_14	Cyanophage P-TIM40	GCA_001470935.1
AOO14200.1	000829	IIGP1	319	Sn110110_006	Cyanophage S-RIM14	GCA_002599065.1
AOO14852.1	000829	IIGP1	319	W1230910_006	Cyanophage S-RIM14	GCA_002599125.1
AMO43019.1	000829	IIGP1	372	R1080702_004	Cyanophage S-RIM32	GCA_001754165.1
AMO43250.1	000829	IIGP1	379	W270710_005	Cyanophage S-RIM44	GCA_002599145.1
AOO11487.1	000829	IIGP1	379	ES420910_005	Cyanophage S-RIM44	GCA_002599165.1
AOO11722.1	000829	IIGP1	379	Np050604_005	Cyanophage S-RIM44	GCA_002599185.1
AOO11952.1	000829	IIGP1	380	Np200711_005	Cyanophage S-RIM44	GCA_002599205.1
AOO12188.1	000829	IIGP1	379	Np420711_005	Cyanophage S-RIM44	GCA_002599225.1
AOO12423.1	000829	IIGP1	379	Sn080709_005	Cyanophage S-RIM44	GCA_002599245.1
AOO12653.1	000829	IIGP1	379	Sn130910_005	Cyanophage S-RIM44	GCA_002599265.1
AOO12888.1	000829	IIGP1	379	W2100709_005	Cyanophage S-RIM44	GCA_002599285.1
AGH07632.1	000829	IIGP1	670	CYVG_00189	Cyanophage S-SSM6a	GCA_002710385.1
AGG54364.1	000829	IIGP1	341	CYWG_00080	Cyanophage S-SSM6b	GCA_002710425.1
QIG65732.1	000829	IIGP1	274	phiOC_p067	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26201.1	000829	IIGP1	435	CPMG_00100	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44388.1	000829	IIGP1	386	PSSM2_010	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12260.1	000829	IIGP1	386	PRTG_00105	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93392.1	000829	IIGP1	460	AVU42_gp006	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99108.1	000829	IIGP1	379	Syn1_006	Prochlorococcus phage Syn1	GCA_000892495.1
AGR47785.1	000829	IIGP1	275	SmphiM12_153	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13008.1	000829	IIGP1	275	PHIM19_102	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12648.1	000829	IIGP1	275	PHIM7_101	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13380.1	000829	IIGP1	275	PHIN3_115	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30483.1	000829	IIGP1	319	Syn7803US37_6	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54631.1	000829	IIGP1	454	b23_0003	Synechococcus phage B23	GCA_009745195.1
QGT54261.1	000829	IIGP1	454	b3_0003	Synechococcus phage B3	GCA_009745215.1
ASR76053.1	000829	IIGP1	471	PBI_BELLAMY_6	Synechococcus phage Bellamy	GCA_002627525.1
QCW22926.1	000829	IIGP1	485	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50641.1	000829	IIGP1	303	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59465.1	000829	IIGP1	360	S330809_004	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59227.1	000829	IIGP1	360	C440309_004	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59703.1	000829	IIGP1	386	N231010_004	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70447.1	000829	IIGP1	267	HOU04_gp048	Synechococcus phage S-T4	GCA_003443335.1
QJT70021.1	000829	IIGP1	480	SynMITS9220M01_005	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QAU04562.1	000829	IIGP1	281	ValB1MD_279	Vibrio phage ValB1MD	GCA_004138815.1
AND75247.1	000830	Calcineurin	235	ME3_86	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83580.1	000830	Calcineurin	245	0305phi8-36p015	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44799.1	000830	Calcineurin	250	SP15_001	Bacillus phage SP-15	GCA_001754685.1
ARB13798.1	000830	Calcineurin	231	Ccr10_gp268	Caulobacter phage Ccr10	GCA_002619445.1
ARB14143.1	000830	Calcineurin	231	Ccr2_gp267	Caulobacter phage Ccr2	GCA_002619465.1
ARB14837.1	000830	Calcineurin	231	Ccr29_gp281	Caulobacter phage Ccr29	GCA_002619485.1
ARB15177.1	000830	Calcineurin	231	Ccr32_gp259	Caulobacter phage Ccr32	GCA_002619505.1
ARB15511.1	000830	Calcineurin	231	Ccr34_gp269	Caulobacter phage Ccr34	GCA_002619525.1
ARB14485.1	000830	Calcineurin	231	Ccr5_gp265	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68463.1	000830	Calcineurin	229	CcrBL10_gp259	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87795.1	000830	Calcineurin	231	CcrKarma_gp278	Caulobacter virus Karma	GCA_000901575.1
AFU87442.1	000830	Calcineurin	231	CcrMagneto_gp272	Caulobacter virus Magneto	GCA_000903095.1
AFU86749.1	000830	Calcineurin	230	CcrRogue_gp267	Caulobacter virus Rogue	GCA_000900555.1
AFU88588.1	000830	Calcineurin	231	CcrSwift_gp270	Caulobacter virus Swift	GCA_000899655.1
AFU87096.1	000830	Calcineurin	231	CbK_gp264	Caulobacter virus phiCbK	GCA_000900535.1
AFC21543.1	000830	Calcineurin	259	GAP32_095	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14345.1	000830	Calcineurin	247	PBI_121Q_455	Escherichia phage 121Q	GCA_000926855.1
QAY00599.1	000830	Calcineurin	247	Ecwhy1_322	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34794.1	000830	Calcineurin	247	ACQ29_gp114	Escherichia phage PBECO4	GCA_001041035.1
BBM62016.1	000830	Calcineurin	247	EO157G_4270	Escherichia phage SP27	GCA_008033345.1
AXC36910.1	000830	Calcineurin	247	-	Escherichia phage UB	GCA_003341455.1
QBO61959.1	000830	Calcineurin	247	G17_00470	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13986.1	000830	Calcineurin	252	vBEcoMphAPEC6_gp362c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80332.1	000830	Calcineurin	247	PSLUR01_00355	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44755.1	000830	Calcineurin	248	RaK2_00482	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG65801.1	000830	Calcineurin	237	phiOC_p136	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43662.1	000830	Calcineurin	259	CBB_97	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18797.1	000830	Calcineurin	247	7t3_0276	Salmonella phage 7t3	GCA_006083215.1
AZU98062.1	000830	Calcineurin	247	CPT_Munch_118	Salmonella phage Munch	GCA_004015485.1
QIG62920.1	000830	Calcineurin	247	SEPL_307	Salmonella phage SE_PL	GCA_011067555.1
AQW88615.1	000830	Calcineurin	259	BF_0090	Serratia phage BF	GCA_002619745.1
AGR47824.1	000830	Calcineurin	223	SmphiM12_192	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13036.1	000830	Calcineurin	223	PHIM19_131	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12676.1	000830	Calcineurin	224	PHIM7_130	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13408.1	000830	Calcineurin	224	PHIN3_145	Sinorhizobium phage phiN3	GCA_001501175.1
ALY07243.1	000830	Calcineurin	229	VmeM32_00257	Vibrio phage vB_VmeM-32	GCA_002608825.1
SOK58891.1	000830	Calcineurin	259	g083	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58354.1	000830	Calcineurin	259	g077	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AHI60395.1	000831	Cluster167_1clades	505	Ea357_242	Erwinia phage Ea35-70	GCA_000914635.1
AGX01735.1	000831	Cluster167_1clades	510	CF95_gp013	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07351.1	000831	Cluster167_1clades	505	REBECCA_246	Erwinia phage Rebecca	GCA_004521635.1
AUG86033.1	000831	Cluster167_1clades	505	BOSOLAPHORUS_247	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52350.1	000831	Cluster167_1clades	505	DM_250	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86352.1	000831	Cluster167_1clades	505	DESERTFOX_245	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86675.1	000831	Cluster167_1clades	505	MADMEL_248	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86998.1	000831	Cluster167_1clades	505	MORTIMER_250	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52024.1	000831	Cluster167_1clades	505	RAY_244	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51708.1	000831	Cluster167_1clades	505	SIMMY50_249	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANJ65059.1	000831	Cluster167_1clades	505	SPECIALG_248	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBO63967.1	000831	Cluster167_1clades	528	Goslar_00174	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24162.1	000831	Cluster167_1clades	498	-	Proteus phage 10	GCA_014071245.1
ABY62957.1	000831	Cluster167_1clades	557	201phi2-1p125	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44849.1	000831	Cluster167_1clades	557	KTN4_091	Pseudomonas phage KTN4	GCA_002607225.1
ARV77233.1	000831	Cluster167_1clades	530	NOXIFER_62	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32217.1	000831	Cluster167_1clades	544	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76736.1	000831	Cluster167_1clades	561	PHABIO_105	Pseudomonas phage Phabio	GCA_002624965.1
AEH03490.1	000831	Cluster167_1clades	548	063	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02601.1	000831	Cluster167_1clades	562	PSA21_72	Pseudomonas phage Psa21	GCA_004340405.1
ATN94864.1	000831	Cluster167_1clades	557	SL2_287	Pseudomonas phage SL2	GCA_002956015.1
QJB22727.1	000831	Cluster167_1clades	557	fnug_84	Pseudomonas phage fnug	GCA_012837215.1
QEM41795.1	000831	Cluster167_1clades	544	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82970.1	000831	Cluster167_1clades	557	PHIKZ069	Pseudomonas virus phiKZ	GCA_000842965.1
BAS05010.1	000831	Cluster167_1clades	482	AVU11_gp218	Ralstonia phage RSF1	GCA_001500875.1
BAQ02740.1	000831	Cluster167_1clades	485	AVU38_gp212	Ralstonia phage RSL2	GCA_001503055.1
QKE54570.1	000831	Cluster167_1clades	500	ACSA002_2540	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65658.1	000831	Cluster167_1clades	497	2050HW_00323	Serratia phage 2050HW	GCA_002628125.1
QDB71082.1	000831	Cluster167_1clades	497	CPT_Moabite_050	Serratia phage Moabite	GCA_006384735.1
QFP93075.1	000831	Cluster167_1clades	489	-	Serratia phage PCH45	GCA_009187865.1
AXH70821.1	000831	Cluster167_1clades	506	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT28158.1	000831	Cluster167_1clades	522	pVa21_217	Vibrio phage pVa-21	GCA_002619305.1
QAX96676.1	000831	Cluster167_1clades	502	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96994.1	000831	Cluster167_1clades	502	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96040.1	000831	Cluster167_1clades	502	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96358.1	000831	Cluster167_1clades	502	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21066.1	000831	Cluster167_1clades	485	-	Vibrio phage vB_pir03	GCA_014319855.1
APU01515.1	000832	Cluster168_1clades	316	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28780.1	000832	Cluster168_1clades	329	AP1_0073	Aeromonas phage AP1	GCA_014183365.1
ATI17383.1	000832	Cluster168_1clades	329	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00210.1	000832	Cluster168_1clades	329	HWB28_gp342	Aeromonas phage AS-zj	GCA_002627665.1
AUE22713.1	000832	Cluster168_1clades	369	Ah1_00193	Aeromonas phage Ah1	GCA_002957415.1
QAX97825.1	000832	Cluster168_1clades	329	ASswx1_181	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01327.1	000832	Cluster168_1clades	375	ASwh1_265	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39428.1	000832	Cluster168_1clades	329	CC2_354	Aeromonas phage CC2	GCA_000903495.1
ADQ52893.1	000832	Cluster168_1clades	367	PX29p174	Aeromonas phage PX29	GCA_000920195.1
ADM80160.1	000832	Cluster168_1clades	342	phiAS5_ORF0317	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53138.1	000832	Cluster168_1clades	341	65p130	Aeromonas virus 65	GCA_000893255.1
AAQ17846.1	000832	Cluster168_1clades	367	Aeh1ORF180c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21564.1	000832	Cluster168_1clades	312	GAP32_116	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21816.1	000832	Cluster168_1clades	420	GAP32_366	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43682.1	000832	Cluster168_1clades	315	CBB_117	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43939.1	000832	Cluster168_1clades	421	CBB_376	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19082.1	000832	Cluster168_1clades	423	7t3_0563	Salmonella phage 7t3	GCA_006083215.1
AZU98323.1	000832	Cluster168_1clades	423	CPT_Munch_380	Salmonella phage Munch	GCA_004015485.1
QIG62660.1	000832	Cluster168_1clades	423	SEPL_047	Salmonella phage SE_PL	GCA_011067555.1
AQW88899.1	000832	Cluster168_1clades	425	BF_0374	Serratia phage BF	GCA_002619745.1
QGT54829.1	000832	Cluster168_1clades	309	b23_0214	Synechococcus phage B23	GCA_009745195.1
QGT54459.1	000832	Cluster168_1clades	309	b3_0216	Synechococcus phage B3	GCA_009745215.1
AAQ64337.1	000832	Cluster168_1clades	422	KVP40.0268	Vibrio phage KVP40	GCA_000843785.1
QIW90652.1	000832	Cluster168_1clades	422	GCAPEGMB_00305	Vibrio phage V07	GCA_012361095.1
QIW91147.1	000832	Cluster168_1clades	422	COHAPHLL_00311	Vibrio phage V09	GCA_012361135.1
QHJ74447.1	000832	Cluster168_1clades	422	VH12019_00120	Vibrio phage VH1_2019	GCA_009931825.1
AGB06943.1	000832	Cluster168_1clades	409	CF80_gp156	Vibrio phage VH7D	GCA_000914495.1
QBX06203.1	000832	Cluster168_1clades	409	ValB1HC_250	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61220.1	000832	Cluster168_1clades	409	AVU32_gp379	Vibrio phage ValKK3	GCA_001501635.1
AGN30312.1	000832	Cluster168_1clades	424	VPFG_00314	Vibrio phage nt-1	GCA_000910195.2
ALP46993.1	000832	Cluster168_1clades	409	phiGrn1_0002	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47374.1	000832	Cluster168_1clades	409	phiST2_0134	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54828.1	000832	Cluster168_1clades	409	vBValMR10Z_288	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37497.1	000832	Cluster168_1clades	422	pp2_264	Vibriophage phi-pp2	GCA_002630725.1
QDJ96359.1	000832	Cluster168_1clades	346	Xoosp13_172	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58377.1	000832	Cluster168_1clades	310	g100	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58651.1	000832	Cluster168_1clades	425	g374	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56811.1	000833	SIG+OmpA-beta-barrel	124	CPXG_00008	Cyanophage P-RSM6	GCA_000906155.1
AJK27634.1	000833	SIG+OmpA-beta-barrel	122	PTIM40_229	Cyanophage P-TIM40	GCA_001470935.1
AOO14404.1	000833	SIG+OmpA-beta-barrel	123	Sn110110_211	Cyanophage S-RIM14	GCA_002599065.1
AOO15053.1	000833	SIG+OmpA-beta-barrel	123	W1230910_208	Cyanophage S-RIM14	GCA_002599125.1
AMO43215.1	000833	SIG+OmpA-beta-barrel	123	R1080702_210	Cyanophage S-RIM32	GCA_001754165.1
AMO43445.1	000833	SIG+OmpA-beta-barrel	123	W270710_206	Cyanophage S-RIM44	GCA_002599145.1
AOO11687.1	000833	SIG+OmpA-beta-barrel	123	ES420910_210	Cyanophage S-RIM44	GCA_002599165.1
AOO11917.1	000833	SIG+OmpA-beta-barrel	123	Np050604_206	Cyanophage S-RIM44	GCA_002599185.1
AOO12153.1	000833	SIG+OmpA-beta-barrel	123	Np200711_211	Cyanophage S-RIM44	GCA_002599205.1
AOO12388.1	000833	SIG+OmpA-beta-barrel	123	Np420711_210	Cyanophage S-RIM44	GCA_002599225.1
AOO12618.1	000833	SIG+OmpA-beta-barrel	123	Sn080709_206	Cyanophage S-RIM44	GCA_002599245.1
AOO12853.1	000833	SIG+OmpA-beta-barrel	123	Sn130910_210	Cyanophage S-RIM44	GCA_002599265.1
AOO13084.1	000833	SIG+OmpA-beta-barrel	123	W2100709_207	Cyanophage S-RIM44	GCA_002599285.1
AGH07578.1	000833	SIG+OmpA-beta-barrel	115	CYVG_00134	Cyanophage S-SSM6a	GCA_002710385.1
AGH07598.1	000833	SIG+OmpA-beta-barrel	118	CYVG_00154	Cyanophage S-SSM6a	GCA_002710385.1
AGG54436.1	000833	SIG+OmpA-beta-barrel	122	CYWG_00152	Cyanophage S-SSM6b	GCA_002710425.1
AGG54453.1	000833	SIG+OmpA-beta-barrel	121	CYWG_00169	Cyanophage S-SSM6b	GCA_002710425.1
AGH26224.1	000833	SIG+OmpA-beta-barrel	118	CPMG_00123	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44623.1	000833	SIG+OmpA-beta-barrel	129	PSSM2_246	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44624.1	000833	SIG+OmpA-beta-barrel	118	PSSM2_247	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12347.1	000833	SIG+OmpA-beta-barrel	118	PRTG_00194	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12348.1	000833	SIG+OmpA-beta-barrel	129	PRTG_00195	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93535.1	000833	SIG+OmpA-beta-barrel	124	AVU42_gp198	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99305.1	000833	SIG+OmpA-beta-barrel	184	Syn1_209	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30619.1	000833	SIG+OmpA-beta-barrel	135	Syn7803US37_142	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76265.1	000833	SIG+OmpA-beta-barrel	121	PBI_BELLAMY_229	Synechococcus phage Bellamy	GCA_002627525.1
ASR76266.1	000833	SIG+OmpA-beta-barrel	133	PBI_BELLAMY_230	Synechococcus phage Bellamy	GCA_002627525.1
QCW22959.1	000833	SIG+OmpA-beta-barrel	124	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22958.1	000833	SIG+OmpA-beta-barrel	165	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50674.1	000833	SIG+OmpA-beta-barrel	124	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50673.1	000833	SIG+OmpA-beta-barrel	165	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59475.1	000833	SIG+OmpA-beta-barrel	123	S330809_014	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59237.1	000833	SIG+OmpA-beta-barrel	123	C440309_014	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59713.1	000833	SIG+OmpA-beta-barrel	123	N231010_014	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70497.1	000833	SIG+OmpA-beta-barrel	123	HOU04_gp098	Synechococcus phage S-T4	GCA_003443335.1
QJT70219.1	000833	SIG+OmpA-beta-barrel	124	SynMITS9220M01_213	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70220.1	000833	SIG+OmpA-beta-barrel	122	SynMITS9220M01_214	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ABY62985.1	000834	phiKZ_IP	608	201phi2-1p155	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62986.1	000834	phiKZ_IP	387	201phi2-1p156	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62987.1	000834	phiKZ_IP	489	201phi2-1p157	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44878.1	000834	phiKZ_IP	435	KTN4_120	Pseudomonas phage KTN4	GCA_002607225.1
ANM44879.1	000834	phiKZ_IP	505	KTN4_121	Pseudomonas phage KTN4	GCA_002607225.1
ANM44880.1	000834	phiKZ_IP	547	KTN4_122	Pseudomonas phage KTN4	GCA_002607225.1
ARV77492.1	000834	phiKZ_IP	294	NOXIFER_327	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77263.1	000834	phiKZ_IP	416	NOXIFER_93	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77264.1	000834	phiKZ_IP	433	NOXIFER_94	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32251.1	000834	phiKZ_IP	331	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32255.1	000834	phiKZ_IP	386	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32254.1	000834	phiKZ_IP	420	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32252.1	000834	phiKZ_IP	423	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32256.1	000834	phiKZ_IP	477	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76770.1	000834	phiKZ_IP	483	PHABIO_139	Pseudomonas phage Phabio	GCA_002624965.1
ARV76771.1	000834	phiKZ_IP	401	PHABIO_140	Pseudomonas phage Phabio	GCA_002624965.1
ARV76772.1	000834	phiKZ_IP	487	PHABIO_141	Pseudomonas phage Phabio	GCA_002624965.1
AEH03521.1	000834	phiKZ_IP	371	097	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03522.1	000834	phiKZ_IP	426	098	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03523.1	000834	phiKZ_IP	384	099	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03524.1	000834	phiKZ_IP	502	100	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02632.1	000834	phiKZ_IP	384	PSA21_104	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02635.1	000834	phiKZ_IP	495	PSA21_107	Pseudomonas phage Psa21	GCA_004340405.1
ATN94833.1	000834	phiKZ_IP	547	SL2_256	Pseudomonas phage SL2	GCA_002956015.1

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ATN94834.1	000834	phiKZ_IP	505	SL2_257	Pseudomonas phage SL2	GCA_002956015.1
ATN94835.1	000834	phiKZ_IP	432	SL2_258	Pseudomonas phage SL2	GCA_002956015.1
QJB22755.1	000834	phiKZ_IP	432	fnug_112	Pseudomonas phage fnug	GCA_012837215.1
QJB22756.1	000834	phiKZ_IP	505	fnug_113	Pseudomonas phage fnug	GCA_012837215.1
QJB22757.1	000834	phiKZ_IP	547	fnug_114	Pseudomonas phage fnug	GCA_012837215.1
QEM41830.1	000834	phiKZ_IP	386	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41829.1	000834	phiKZ_IP	420	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41831.1	000834	phiKZ_IP	477	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41828.1	000834	phiKZ_IP	881	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82994.1	000834	phiKZ_IP	435	PHIKZ093	Pseudomonas virus phiKZ	GCA_000842965.1
AAL82995.1	000834	phiKZ_IP	505	PHIKZ094	Pseudomonas virus phiKZ	GCA_000842965.1
AAL82996.1	000834	phiKZ_IP	547	PHIKZ095	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71292.1	000835	Cluster173_1clades	335	CR5_072	Cronobacter phage CR5	GCA_000910235.1
AMR59726.1	000835	Cluster173_1clades	334	SEGD1_077	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07500.1	000835	Cluster173_1clades	335	DERBICUS_74	Erwinia phage Derbicus	GCA_004521655.1
AHI60151.1	000835	Cluster173_1clades	331	Ea357_001	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49726.1	000835	Cluster173_1clades	363	MACHINA_88	Erwinia phage Machina	GCA_002758035.1
QBP07109.1	000835	Cluster173_1clades	331	REBECCA_1	Erwinia phage Rebecca	GCA_004521635.1
AXF51223.1	000835	Cluster173_1clades	334	WELLINGTON_93	Erwinia phage Wellington	GCA_003344985.1
AFQ96808.1	000835	Cluster173_1clades	334	G173_gp001	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48106.1	000835	Cluster173_1clades	334	ASESINO_93	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85789.1	000835	Cluster173_1clades	331	BOSOLAPHORUS_1	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48379.1	000835	Cluster173_1clades	365	CAITLIN_84	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48652.1	000835	Cluster173_1clades	365	CHRISDB_90	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52099.1	000835	Cluster173_1clades	331	DM_1	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86109.1	000835	Cluster173_1clades	331	DESERTFOX_1	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48924.1	000835	Cluster173_1clades	335	EARLPHILLIPIV_74	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49171.1	000835	Cluster173_1clades	363	HUXLEY_89	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49444.1	000835	Cluster173_1clades	334	KWAN_92	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86429.1	000835	Cluster173_1clades	331	MADMEL_1	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86750.1	000835	Cluster173_1clades	331	MORTIMER_1	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49999.1	000835	Cluster173_1clades	363	PARSHIK_90	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50265.1	000835	Cluster173_1clades	335	PHOBOS_75	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51782.1	000835	Cluster173_1clades	331	RAY_1	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51463.1	000835	Cluster173_1clades	331	SIMMY50_1	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64811.1	000835	Cluster173_1clades	331	SPECIALG_1	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50520.1	000835	Cluster173_1clades	334	STRATTON_95	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85916.1	000835	Cluster173_1clades	334	ACEC001_0780	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QMP23995.1	000835	Cluster173_1clades	349	-	Proteus phage 10	GCA_014071245.1
BAW19067.1	000835	Cluster173_1clades	384	FDH28_gp093	Ralstonia phage RP12	GCA_002617345.1
BAW19352.1	000835	Cluster173_1clades	384	-	Ralstonia phage RP31	GCA_002617365.1
BAS04915.1	000835	Cluster173_1clades	382	AVU11_gp123	Ralstonia phage RSF1	GCA_001500875.1
BAQ02644.2	000835	Cluster173_1clades	209	-	Ralstonia phage RSL2	GCA_001503055.1
QNI20787.1	000835	Cluster173_1clades	334	-	Salmonella phage JN03	GCA_014319805.1
AWN09024.1	000835	Cluster173_1clades	334	MLDJOKPK_00083	Salmonella phage SPAsTU	GCA_003183805.1
AEP83909.1	000835	Cluster173_1clades	334	SPN3US_0076	Salmonella phage SPN3US	GCA_001042275.1
QKE54315.1	000835	Cluster173_1clades	334	ACSA002_0010	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFP93106.1	000835	Cluster173_1clades	311	-	Serratia phage PCH45	GCA_009187865.1
AFO71368.1	000836	Cluster176_1clades	180	CR5_148	Cronobacter phage CR5	GCA_000910235.1
AMR59810.1	000836	Cluster176_1clades	175	SEGD1_163	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07577.1	000836	Cluster176_1clades	171	DERBICUS_151	Erwinia phage Derbicus	GCA_004521655.1
QBP07578.1	000836	Cluster176_1clades	175	DERBICUS_152	Erwinia phage Derbicus	GCA_004521655.1
ANZ49803.1	000836	Cluster176_1clades	178	MACHINA_165	Erwinia phage Machina	GCA_002758035.1
ANZ49804.1	000836	Cluster176_1clades	166	MACHINA_166	Erwinia phage Machina	GCA_002758035.1
AXF51300.1	000836	Cluster176_1clades	169	WELLINGTON_171	Erwinia phage Wellington	GCA_003344985.1
AFQ96625.1	000836	Cluster176_1clades	168	G173_gp080	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96624.1	000836	Cluster176_1clades	174	G173_gp079	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48189.1	000836	Cluster176_1clades	178	ASESINO_176	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48190.1	000836	Cluster176_1clades	168	ASESINO_177	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48459.1	000836	Cluster176_1clades	176	CAITLIN_164	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48460.1	000836	Cluster176_1clades	166	CAITLIN_165	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48737.1	000836	Cluster176_1clades	177	CHRISDB_175	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48738.1	000836	Cluster176_1clades	184	CHRISDB_176	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48739.1	000836	Cluster176_1clades	170	CHRISDB_177	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49000.1	000836	Cluster176_1clades	171	EARLPHILLIPIV_151	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49001.1	000836	Cluster176_1clades	175	EARLPHILLIPIV_152	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49247.1	000836	Cluster176_1clades	178	HUXLEY_165	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49248.1	000836	Cluster176_1clades	166	HUXLEY_166	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49524.1	000836	Cluster176_1clades	169	KWAN_172	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50075.1	000836	Cluster176_1clades	178	PARSHIK_166	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50076.1	000836	Cluster176_1clades	166	PARSHIK_167	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50345.1	000836	Cluster176_1clades	166	PHOBOS_155	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50346.1	000836	Cluster176_1clades	167	PHOBOS_156	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50348.1	000836	Cluster176_1clades	187	PHOBOS_158	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50601.1	000836	Cluster176_1clades	174	STRATTON_176	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50602.1	000836	Cluster176_1clades	168	STRATTON_177	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85999.1	000836	Cluster176_1clades	182	ACEC001_1590	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20858.1	000836	Cluster176_1clades	180	-	Salmonella phage JN03	GCA_014319805.1
AXF51132.1	000836	Cluster176_1clades	169	MLDJOKPK_00280	Salmonella phage SPAsTU	GCA_003183805.1
AXF51133.1	000836	Cluster176_1clades	171	MLDJOKPK_00281	Salmonella phage SPAsTU	GCA_003183805.1
AXF51134.1	000836	Cluster176_1clades	179	MLDJOKPK_00282	Salmonella phage SPAsTU	GCA_003183805.1
AWN09172.1	000836	Cluster176_1clades	177	MLDJOKPK_00283	Salmonella phage SPAsTU	GCA_003183805.1
AEP83993.1	000836	Cluster176_1clades	175	SPN3US_0160	Salmonella phage SPN3US	GCA_001042275.1
QFP93173.1	000836	Cluster176_1clades	184	-	Serratia phage PCH45	GCA_009187865.1
AFO71415.1	000837	Cluster177_1clades	155	CR5_195	Cronobacter phage CR5	GCA_000910235.1
AMR59871.1	000837	Cluster177_1clades	156	SEGD1_224	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07628.1	000837	Cluster177_1clades	155	DERBICUS_202	Erwinia phage Derbicus	GCA_004521655.1
ANZ49871.1	000837	Cluster177_1clades	154	MACHINA_233	Erwinia phage Machina	GCA_002758035.1
AGX01890.1	000837	Cluster177_1clades	182	CF95_gp168	Erwinia phage PhiEaH1	GCA_000914555.1
AXF51374.1	000837	Cluster177_1clades	157	WELLINGTON_248	Erwinia phage Wellington	GCA_003344985.1
ANZ48255.1	000837	Cluster177_1clades	156	ASESINO_242	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48528.1	000837	Cluster177_1clades	163	CAITLIN_233	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48805.1	000837	Cluster177_1clades	158	CHRISDB_243	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49052.1	000837	Cluster177_1clades	155	EARLPHILLIPIV_203	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49315.1	000837	Cluster177_1clades	154	HUXLEY_233	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49600.1	000837	Cluster177_1clades	157	KWAN_248	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50143.1	000837	Cluster177_1clades	154	PARSHIK_234	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50399.1	000837	Cluster177_1clades	155	PHOBOS_209	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50668.1	000837	Cluster177_1clades	156	STRATTON_243	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86061.1	000837	Cluster177_1clades	156	ACEC001_2180	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
ABY63083.1	000837	Cluster177_1clades	175	201phi2-1p255	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44967.1	000837	Cluster177_1clades	171	KTN4_209	Pseudomonas phage KTN4	GCA_002607225.1
ARV77354.1	000837	Cluster177_1clades	170	NOXIFER_185	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32357.1	000837	Cluster177_1clades	170	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76875.1	000837	Cluster177_1clades	170	PHABIO_244	Pseudomonas phage Phabio	GCA_002624965.1
AEH03621.1	000837	Cluster177_1clades	172	198	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02757.1	000837	Cluster177_1clades	152	PSA21_231	Pseudomonas phage Psa21	GCA_004340405.1
ATN94747.1	000837	Cluster177_1clades	171	SL2_170	Pseudomonas phage SL2	GCA_002956015.1
QJB22845.1	000837	Cluster177_1clades	171	fnug_202	Pseudomonas phage fnug	GCA_012837215.1
QEM41931.1	000837	Cluster177_1clades	170	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83070.1	000837	Cluster177_1clades	171	PHIKZ169	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19025.1	000837	Cluster177_1clades	154	FDH28_gp051	Ralstonia phage RP12	GCA_002617345.1
BAW19311.1	000837	Cluster177_1clades	172	-	Ralstonia phage RP31	GCA_002617365.1
QNI20907.1	000837	Cluster177_1clades	156	-	Salmonella phage JN03	GCA_014319805.1
AWN09129.1	000837	Cluster177_1clades	158	MLDJOKPK_00220	Salmonella phage SPAsTU	GCA_003183805.1
AEP84053.1	000837	Cluster177_1clades	156	SPN3US_0220	Salmonella phage SPN3US	GCA_001042275.1
ATA65419.1	000837	Cluster177_1clades	170	2050HW_00084	Serratia phage 2050HW	GCA_002628125.1
QDB71197.1	000837	Cluster177_1clades	170	CPT_Moabite_167	Serratia phage Moabite	GCA_006384735.1
QFP93181.1	000837	Cluster177_1clades	174	-	Serratia phage PCH45	GCA_009187865.1
AQT28095.1	000837	Cluster177_1clades	146	pVa21_154	Vibrio phage pVa-21	GCA_002619305.1
APU01526.1	000838	Neutrophil_activating_protein	133	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28770.1	000838	Neutrophil_activating_protein	133	AP1_0052	Aeromonas phage AP1	GCA_014183365.1
ATI17374.1	000838	Neutrophil_activating_protein	133	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00220.1	000838	Neutrophil_activating_protein	133	HWB28_gp332	Aeromonas phage AS-zj	GCA_002627665.1
AUE22704.1	000838	Neutrophil_activating_protein	128	Ah1_00164	Aeromonas phage Ah1	GCA_002957415.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX98429.1	000838	Neutrophil_activating_protein	130	ASfcp2_85	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97815.1	000838	Neutrophil_activating_protein	133	ASswx1_171	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01337.1	000838	Neutrophil_activating_protein	133	ASwh1_276	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39432.1	000838	Neutrophil_activating_protein	133	CC2_365	Aeromonas phage CC2	GCA_000903495.1
ADQ52884.1	000838	Neutrophil_activating_protein	130	PX29p165	Aeromonas phage PX29	GCA_000920195.1
ADM80147.1	000838	Neutrophil_activating_protein	130	phiAS5_ORF0304	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53148.1	000838	Neutrophil_activating_protein	133	65p140	Aeromonas virus 65	GCA_000893255.1
AAQ17835.1	000838	Neutrophil_activating_protein	128	rI.-1	Aeromonas virus Aeh1	GCA_000843245.1
ANS06069.1	000838	Neutrophil_activating_protein	127	ABCD_0139	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64999.1	000838	Neutrophil_activating_protein	129	S13_202	Cronobacter phage S13	GCA_001503575.1
AFC21615.1	000838	Neutrophil_activating_protein	146	GAP32_165	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97147.1	000838	Neutrophil_activating_protein	127	E_139	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AIT14408.1	000838	Neutrophil_activating_protein	136	PBI_121Q_518	Escherichia phage 121Q	GCA_000926855.1
QAY00544.1	000838	Neutrophil_activating_protein	146	Ecwhy1_265	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34735.1	000838	Neutrophil_activating_protein	146	ACQ29_gp055	Escherichia phage PBECO4	GCA_001041035.1
BBM62079.1	000838	Neutrophil_activating_protein	146	EO157G_4900	Escherichia phage SP27	GCA_008033345.1
AXC36851.1	000838	Neutrophil_activating_protein	146	-	Escherichia phage UB	GCA_003341455.1
QBO61894.1	000838	Neutrophil_activating_protein	146	G17_00405	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13931.1	000838	Neutrophil_activating_protein	146	vBEcoMphAPEC6_gp306c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80393.1	000838	Neutrophil_activating_protein	146	PSLUR01_00416	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78662.1	000838	Neutrophil_activating_protein	77	RB43ORF140c	Escherichia virus RB43	GCA_000863505.1
AFA44288.1	000838	Neutrophil_activating_protein	149	RaK2_00015	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78932.1	000838	Neutrophil_activating_protein	123	-	Myoviridae sp.	GCA_012593985.1
AMM43734.1	000838	Neutrophil_activating_protein	146	CBB_169	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ASV44291.1	000838	Neutrophil_activating_protein	176	PBI_SCTP2_276	Salicola phage SCTP-2	GCA_002625545.1
QCW18875.1	000838	Neutrophil_activating_protein	146	7t3_0354	Salmonella phage 7t3	GCA_006083215.1
AZU98133.1	000838	Neutrophil_activating_protein	146	CPT_Munch_189	Salmonella phage Munch	GCA_004015485.1
QIG62849.1	000838	Neutrophil_activating_protein	146	SEPL_236	Salmonella phage SE_PL	GCA_011067555.1
AQW88689.1	000838	Neutrophil_activating_protein	147	BF_0164	Serratia phage BF	GCA_002619745.1
SOK58973.1	000838	Neutrophil_activating_protein	147	g165	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58439.1	000838	Neutrophil_activating_protein	147	g162	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01793.1	000839	Nterm+ZnR	84	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28995.1	000839	Nterm+ZnR	84	AP1_0288	Aeromonas phage AP1	GCA_014183365.1
ATI17512.1	000839	Nterm+ZnR	84	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00484.1	000839	Nterm+ZnR	84	HWB28_gp068	Aeromonas phage AS-zj	GCA_002627665.1
QAX97952.1	000839	Nterm+ZnR	84	ASswx1_310	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39386.1	000839	Nterm+ZnR	84	CC2_222	Aeromonas phage CC2	GCA_000903495.1
ADQ53436.1	000839	Nterm+ZnR	84	65p430	Aeromonas virus 65	GCA_000893255.1
QBX06770.1	000839	Nterm+ZnR	73	BcepSaruman_357	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74740.1	000839	Nterm+ZnR	73	BcepSauron_360	Burkholderia phage BcepSauron	GCA_005394215.1
AFC21540.1	000839	Nterm+ZnR	118	GAP32_092	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43659.1	000839	Nterm+ZnR	118	CBB_94	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAG41694.1	000839	Nterm+ZnR	134	RSL1_ORF246	Ralstonia phage phiRSL1	GCA_000879455.1
QCW18795.1	000839	Nterm+ZnR	109	7t3_0274	Salmonella phage 7t3	GCA_006083215.1
AZU98060.1	000839	Nterm+ZnR	109	CPT_Munch_116	Salmonella phage Munch	GCA_004015485.1
QIG62922.1	000839	Nterm+ZnR	109	SEPL_309	Salmonella phage SE_PL	GCA_011067555.1
AQW88610.1	000839	Nterm+ZnR	118	BF_0085	Serratia phage BF	GCA_002619745.1
AAQ64260.1	000839	Nterm+ZnR	102	KVP40.0191	Vibrio phage KVP40	GCA_000843785.1
QIW90576.1	000839	Nterm+ZnR	100	GCAPEGMB_00229	Vibrio phage V07	GCA_012361095.1
QIW91222.1	000839	Nterm+ZnR	100	COHAPHLL_00386	Vibrio phage V09	GCA_012361135.1
QHJ74374.1	000839	Nterm+ZnR	100	VH12019_00047	Vibrio phage VH1_2019	GCA_009931825.1
AGB06871.1	000839	Nterm+ZnR	100	CF80_gp084	Vibrio phage VH7D	GCA_000914495.1
AGB06869.1	000839	Nterm+ZnR	109	CF80_gp082	Vibrio phage VH7D	GCA_000914495.1
QBX06275.1	000839	Nterm+ZnR	100	ValB1HC_322	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06277.1	000839	Nterm+ZnR	109	ValB1HC_324	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60901.1	000839	Nterm+ZnR	100	AVU32_gp060	Vibrio phage ValKK3	GCA_001501635.1
AJT60903.1	000839	Nterm+ZnR	109	AVU32_gp062	Vibrio phage ValKK3	GCA_001501635.1
AGN30249.1	000839	Nterm+ZnR	100	VPFG_00250	Vibrio phage nt-1	GCA_000910195.2
ALP47228.1	000839	Nterm+ZnR	92	phiGrn1_0308	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47201.1	000839	Nterm+ZnR	100	phiGrn1_0310	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47572.1	000839	Nterm+ZnR	109	phiST2_0064	Vibrio phage phi-ST2	GCA_002757135.1
ALP47592.1	000839	Nterm+ZnR	100	phiST2_0066	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54902.1	000839	Nterm+ZnR	100	vBValMR10Z_362	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54904.1	000839	Nterm+ZnR	109	vBValMR10Z_364	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37422.1	000839	Nterm+ZnR	100	pp2_189	Vibriophage phi-pp2	GCA_002630725.1
SOK58887.1	000839	Nterm+ZnR	119	g079	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58350.1	000839	Nterm+ZnR	119	g073	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13684.1	000840	ATP-dependent-protease-subunit-HslV	169	Ccr10_gp154c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14029.1	000840	ATP-dependent-protease-subunit-HslV	169	Ccr2_gp153c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14716.1	000840	ATP-dependent-protease-subunit-HslV	169	Ccr29_gp160	Caulobacter phage Ccr29	GCA_002619485.1
ARB15071.1	000840	ATP-dependent-protease-subunit-HslV	169	Ccr32_gp153	Caulobacter phage Ccr32	GCA_002619505.1
ARB15405.1	000840	ATP-dependent-protease-subunit-HslV	169	Ccr34_gp163	Caulobacter phage Ccr34	GCA_002619525.1
ARB14372.1	000840	ATP-dependent-protease-subunit-HslV	169	Ccr5_gp152c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68353.1	000840	ATP-dependent-protease-subunit-HslV	170	CcrBL10_gp149c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69132.1	000840	ATP-dependent-protease-subunit-HslV	146	CcrBL9_gp108	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69376.1	000840	ATP-dependent-protease-subunit-HslV	157	CcrBL9_gp352	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87927.1	000840	ATP-dependent-protease-subunit-HslV	131	CcrColossus_gp057	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68599.1	000840	ATP-dependent-protease-subunit-HslV	142	CcrPW_gp060	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69584.1	000840	ATP-dependent-protease-subunit-HslV	146	CcrSC_gp002	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69686.1	000840	ATP-dependent-protease-subunit-HslV	143	CcrSC_gp104	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69936.1	000840	ATP-dependent-protease-subunit-HslV	157	CcrSC_gp354	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70084.1	000840	ATP-dependent-protease-subunit-HslV	146	CcrSC_gp502	Caulobacter phage CcrSC	GCA_003443315.1
AFU87677.1	000840	ATP-dependent-protease-subunit-HslV	169	CcrKarma_gp160	Caulobacter virus Karma	GCA_000901575.1
AFU87326.1	000840	ATP-dependent-protease-subunit-HslV	169	CcrMagneto_gp156	Caulobacter virus Magneto	GCA_000903095.1
AFU86637.1	000840	ATP-dependent-protease-subunit-HslV	170	CcrRogue_gp155	Caulobacter virus Rogue	GCA_000900555.1
AFU88473.1	000840	ATP-dependent-protease-subunit-HslV	169	CcrSwift_gp155	Caulobacter virus Swift	GCA_000899655.1
AFU86990.1	000840	ATP-dependent-protease-subunit-HslV	169	CbK_gp158	Caulobacter virus phiCbK	GCA_000900535.1
AMR59652.1	000840	ATP-dependent-protease-subunit-HslV	163	SEGD1_001	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49648.1	000840	ATP-dependent-protease-subunit-HslV	157	MACHINA_1	Erwinia phage Machina	GCA_002758035.1
AFQ96730.1	000840	ATP-dependent-protease-subunit-HslV	169	G173_gp185	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48026.1	000840	ATP-dependent-protease-subunit-HslV	167	ASESINO_1	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48303.1	000840	ATP-dependent-protease-subunit-HslV	165	CAITLIN_1	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48574.1	000840	ATP-dependent-protease-subunit-HslV	161	CHRISDB_1	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49092.1	000840	ATP-dependent-protease-subunit-HslV	157	HUXLEY_1	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49920.1	000840	ATP-dependent-protease-subunit-HslV	157	PARSHIK_1	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50438.1	000840	ATP-dependent-protease-subunit-HslV	169	STRATTON_1	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85838.1	000840	ATP-dependent-protease-subunit-HslV	163	ACEC001_0020	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
CAG27109.1	000840	ATP-dependent-protease-subunit-HslV	182	PPEV_gp015	Pseudomonas phage EL	GCA_000866825.1
QNI20721.1	000840	ATP-dependent-protease-subunit-HslV	163	-	Salmonella phage JN03	GCA_014319805.1
AXF51106.1	000840	ATP-dependent-protease-subunit-HslV	166	MLDJOKPK_00173	Salmonella phage SPAsTU	GCA_003183805.1
AEP83834.1	000840	ATP-dependent-protease-subunit-HslV	163	SPN3US_0001	Salmonella phage SPN3US	GCA_001042275.1
QIW90789.1	000840	ATP-dependent-protease-subunit-HslV	191	GCAPEGMB_00471	Vibrio phage V07	GCA_012361095.1
APU01404.1	000841	Gp23	146	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28894.1	000841	Gp23	143	AP1_0187	Aeromonas phage AP1	GCA_014183365.1
ATI17492.1	000841	Gp23	149	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00505.1	000841	Gp23	149	HWB28_gp047	Aeromonas phage AS-zj	GCA_002627665.1
AUE22555.1	000841	Gp23	155	Ah1_00014	Aeromonas phage Ah1	GCA_002957415.1
QAX98594.1	000841	Gp23	157	ASfcp2_261	Aeromonas phage AsFcp_2	GCA_004146885.1
QAY01217.1	000841	Gp23	149	ASwh1_152	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39394.1	000841	Gp23	135	CC2_242	Aeromonas phage CC2	GCA_000903495.1
ADQ52730.1	000841	Gp23	151	PX29p011	Aeromonas phage PX29	GCA_000920195.1
ADM79983.1	000841	Gp23	156	phiAS5_ORF0140	Aeromonas phage phiAS5	GCA_000887715.1
AAR90926.1	000841	Gp23	121	65p012	Aeromonas virus 65	GCA_000893255.1
AAQ17667.1	000841	Gp23	155	61.1	Aeromonas virus Aeh1	GCA_000843245.1
ANS06036.1	000841	Gp23	166	ABCD_0029	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65051.1	000841	Gp23	187	S13_254	Cronobacter phage S13	GCA_001503575.1
AON97039.1	000841	Gp23	163	E_030	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70850.1	000841	Gp23	155	phiC120_c144	Escherichia phage phiC120	GCA_002621185.1
AAX78551.1	000841	Gp23	166	RB43ORF029c	Escherichia virus RB43	GCA_000863505.1
QHJ78881.1	000841	Gp23	190	-	Myoviridae sp.	GCA_012593985.1
AGR48088.1	000841	Gp23	141	SmphiM12_456	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13258.1	000841	Gp23	141	PHIM19_353	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12898.1	000841	Gp23	141	PHIM7_353	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13621.1	000841	Gp23	141	PHIN3_358	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64090.1	000841	Gp23	158	KVP40.0019	Vibrio phage KVP40	GCA_000843785.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW90413.1	000841	Gp23	158	GCAPEGMB_00066	Vibrio phage V07	GCA_012361095.1
QIW91016.1	000841	Gp23	158	COHAPHLL_00153	Vibrio phage V09	GCA_012361135.1
QHJ74202.1	000841	Gp23	158	VH12019_00283	Vibrio phage VH1_2019	GCA_009931825.1
AGB07026.1	000841	Gp23	159	CF80_gp239	Vibrio phage VH7D	GCA_000914495.1
QBX06070.1	000841	Gp23	159	ValB1HC_116	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61084.1	000841	Gp23	159	AVU32_gp243	Vibrio phage ValKK3	GCA_001501635.1
AGN30070.1	000841	Gp23	159	VPFG_00068	Vibrio phage nt-1	GCA_000910195.2
ALP47115.1	000841	Gp23	159	phiGrn1_0134	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47497.1	000841	Gp23	159	phiST2_0264	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54696.1	000841	Gp23	159	vBValMR10Z_155	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07077.1	000841	Gp23	162	VmeM32_00086	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37253.1	000841	Gp23	158	pp2_019	Vibriophage phi-pp2	GCA_002630725.1
APU01490.1	000842	SIG+TM-baseplate_wedge_subunit	1171	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28799.1	000842	SIG+TM-baseplate_wedge_subunit	1167	AP1_0092	Aeromonas phage AP1	GCA_014183365.1
ATI17407.1	000842	SIG+TM-baseplate_wedge_subunit	1167	-	Aeromonas phage AS-szw	GCA_002743635.1
AUE22735.1	000842	SIG+TM-baseplate_wedge_subunit	1163	Ah1_00217	Aeromonas phage Ah1	GCA_002957415.1
QAX98456.1	000842	SIG+TM-baseplate_wedge_subunit	1163	ASfcp2_114	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97847.1	000842	SIG+TM-baseplate_wedge_subunit	1167	ASswx1_204	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01305.1	000842	SIG+TM-baseplate_wedge_subunit	1165	ASwh1_242	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39481.1	000842	SIG+TM-baseplate_wedge_subunit	895	CC2_330	Aeromonas phage CC2	GCA_000903495.1
AFN39553.1	000842	SIG+TM-baseplate_wedge_subunit	253	CC2_331	Aeromonas phage CC2	GCA_000903495.1
ADQ52914.1	000842	SIG+TM-baseplate_wedge_subunit	1163	PX29p195	Aeromonas phage PX29	GCA_000920195.1
ADM80181.1	000842	SIG+TM-baseplate_wedge_subunit	1163	phiAS5_ORF0338	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53111.1	000842	SIG+TM-baseplate_wedge_subunit	759	65p103	Aeromonas virus 65	GCA_000893255.1
ADQ53110.1	000842	SIG+TM-baseplate_wedge_subunit	379	65p102	Aeromonas virus 65	GCA_000893255.1
AAQ17866.1	000842	SIG+TM-baseplate_wedge_subunit	1163	7	Aeromonas virus Aeh1	GCA_000843245.1
ANS05922.1	000842	SIG+TM-baseplate_wedge_subunit	1027	ABCD_0197	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64900.1	000842	SIG+TM-baseplate_wedge_subunit	1026	S13_101	Cronobacter phage S13	GCA_001503575.1
AON97211.1	000842	SIG+TM-baseplate_wedge_subunit	1026	E_203	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70981.1	000842	SIG+TM-baseplate_wedge_subunit	1032	phiC120_c276	Escherichia phage phiC120	GCA_002621185.1
ARM70715.1	000842	SIG+TM-baseplate_wedge_subunit	1032	phiC120_c8	Escherichia phage phiC120	GCA_002621185.1
AAX78729.1	000842	SIG+TM-baseplate_wedge_subunit	1027	RB43ORF207w	Escherichia virus RB43	GCA_000863505.1
QHJ79039.1	000842	SIG+TM-baseplate_wedge_subunit	1024	-	Myoviridae sp.	GCA_012593985.1
AAQ64411.1	000842	SIG+TM-baseplate_wedge_subunit	1165	KVP40.0342	Vibrio phage KVP40	GCA_000843785.1
QIW90356.1	000842	SIG+TM-baseplate_wedge_subunit	1165	GCAPEGMB_00009	Vibrio phage V07	GCA_012361095.1
QIW91073.1	000842	SIG+TM-baseplate_wedge_subunit	1165	COHAPHLL_00210	Vibrio phage V09	GCA_012361135.1
QHJ74524.1	000842	SIG+TM-baseplate_wedge_subunit	1165	VH12019_00224	Vibrio phage VH1_2019	GCA_009931825.1
AGB06983.1	000842	SIG+TM-baseplate_wedge_subunit	1136	CF80_gp196	Vibrio phage VH7D	GCA_000914495.1
QBX06131.1	000842	SIG+TM-baseplate_wedge_subunit	1165	ValB1HC_177	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61143.1	000842	SIG+TM-baseplate_wedge_subunit	1165	AVU32_gp302	Vibrio phage ValKK3	GCA_001501635.1
AGN30015.1	000842	SIG+TM-baseplate_wedge_subunit	1155	VPFG_00007	Vibrio phage nt-1	GCA_000910195.2
ALP46959.1	000842	SIG+TM-baseplate_wedge_subunit	1165	phiGrn1_0076	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47339.1	000842	SIG+TM-baseplate_wedge_subunit	1165	phiST2_0208	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54756.1	000842	SIG+TM-baseplate_wedge_subunit	1165	vBValMR10Z_216	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07244.1	000842	SIG+TM-baseplate_wedge_subunit	1109	VmeM32_00258	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37574.1	000842	SIG+TM-baseplate_wedge_subunit	1165	pp2_342	Vibriophage phi-pp2	GCA_002630725.1
AGH56837.1	000843	TM	124	CPXG_00034	Cyanophage P-RSM6	GCA_000906155.1
AJK27608.1	000843	TM	124	PTIM40_190	Cyanophage P-TIM40	GCA_001470935.1
AOO14375.1	000843	TM	120	Sn110110_181	Cyanophage S-RIM14	GCA_002599065.1
AOO15023.1	000843	TM	120	W1230910_177	Cyanophage S-RIM14	GCA_002599125.1
AMO43409.1	000843	TM	118	W270710_165	Cyanophage S-RIM44	GCA_002599145.1
AOO11653.1	000843	TM	118	ES420910_172	Cyanophage S-RIM44	GCA_002599165.1
AOO11881.1	000843	TM	118	Np050604_165	Cyanophage S-RIM44	GCA_002599185.1
AOO12119.1	000843	TM	118	Np200711_173	Cyanophage S-RIM44	GCA_002599205.1
AOO12354.1	000843	TM	118	Np420711_172	Cyanophage S-RIM44	GCA_002599225.1
AOO12582.1	000843	TM	118	Sn080709_165	Cyanophage S-RIM44	GCA_002599245.1
AOO12819.1	000843	TM	118	Sn130910_172	Cyanophage S-RIM44	GCA_002599265.1
AOO13048.1	000843	TM	118	W2100709_166	Cyanophage S-RIM44	GCA_002599285.1
AGH07524.1	000843	TM	123	CYVG_00080	Cyanophage S-SSM6a	GCA_002710385.1
AGG54427.1	000843	TM	120	CYWG_00143	Cyanophage S-SSM6b	GCA_002710425.1
QIG66043.1	000843	TM	126	phiOC_p401	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26273.1	000843	TM	123	CPMG_00173	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44580.1	000843	TM	123	PSSM2_203	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12393.1	000843	TM	123	PRTG_00240	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93501.1	000843	TM	130	AVU42_gp163	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99268.1	000843	TM	118	Syn1_167	Prochlorococcus phage Syn1	GCA_000892495.1
AGR48089.1	000843	TM	124	SmphiM12_457	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13259.1	000843	TM	124	PHIM19_354	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12899.1	000843	TM	124	PHIM7_354	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13622.1	000843	TM	124	PHIN3_359	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30676.1	000843	TM	127	Syn7803US37_199	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54924.1	000843	TM	128	b23_0311	Synechococcus phage B23	GCA_009745195.1
QGT54559.1	000843	TM	128	b3_0318	Synechococcus phage B3	GCA_009745215.1
ASR76218.1	000843	TM	130	PBI_BELLAMY_175	Synechococcus phage Bellamy	GCA_002627525.1
QCW22948.1	000843	TM	126	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50534.1	000843	TM	126	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59634.1	000843	TM	117	S330809_173	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59396.1	000843	TM	117	C440309_173	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59872.1	000843	TM	117	N231010_173	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70172.1	000843	TM	130	SynMITS9220M01_160	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01484.1	000844	Fibritin_C	1041	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28724.1	000844	Fibritin_C	1041	AP1_006	Aeromonas phage AP1	GCA_014183365.1
ATI17413.1	000844	Fibritin_C	1041	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00183.1	000844	Fibritin_C	1041	HWB28_gp369	Aeromonas phage AS-zj	GCA_002627665.1
AUE22742.1	000844	Fibritin_C	882	Ah1_00224	Aeromonas phage Ah1	GCA_002957415.1
QAX98460.1	000844	Fibritin_C	1035	ASfcp2_120	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97853.1	000844	Fibritin_C	1041	ASswx1_210	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01297.1	000844	Fibritin_C	1040	ASwh1_234	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39548.1	000844	Fibritin_C	1041	CC2_324	Aeromonas phage CC2	GCA_000903495.1
ADQ52920.1	000844	Fibritin_C	1035	PX29p201	Aeromonas phage PX29	GCA_000920195.1
ADM79844.1	000844	Fibritin_C	923	phiAS5_ORF0001	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53105.1	000844	Fibritin_C	1041	65p097	Aeromonas virus 65	GCA_000893255.1
AAP04359.2	000844	Fibritin_C	1035	wac	Aeromonas virus Aeh1	GCA_000843245.1
ANS05925.1	000844	Fibritin_C	762	ABCD_0203	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64894.1	000844	Fibritin_C	1013	S13_095	Cronobacter phage S13	GCA_001503575.1
AON97217.1	000844	Fibritin_C	762	E_209	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70721.1	000844	Fibritin_C	480	phiC120_c14	Escherichia phage phiC120	GCA_002621185.1
ARM70987.1	000844	Fibritin_C	480	phiC120_c282	Escherichia phage phiC120	GCA_002621185.1
AAX78735.1	000844	Fibritin_C	762	RB43ORF213w	Escherichia virus RB43	GCA_000863505.1
QHJ79045.1	000844	Fibritin_C	976	-	Myoviridae sp.	GCA_012593985.1
AAQ64418.1	000844	Fibritin_C	559	KVP40.0349	Vibrio phage KVP40	GCA_000843785.1
QIW90363.1	000844	Fibritin_C	559	GCAPEGMB_00016	Vibrio phage V07	GCA_012361095.1
QIW91066.1	000844	Fibritin_C	559	COHAPHLL_00203	Vibrio phage V09	GCA_012361135.1
QHJ74532.1	000844	Fibritin_C	559	VH12019_00232	Vibrio phage VH1_2019	GCA_009931825.1
AGB06990.1	000844	Fibritin_C	560	CF80_gp203	Vibrio phage VH7D	GCA_000914495.1
QBX06124.1	000844	Fibritin_C	560	ValB1HC_170	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61136.1	000844	Fibritin_C	560	AVU32_gp295	Vibrio phage ValKK3	GCA_001501635.1
AGN30022.2	000844	Fibritin_C	570	VPFG_00014	Vibrio phage nt-1	GCA_000910195.2
ALP46974.1	000844	Fibritin_C	560	phiGrn1_0083	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47355.1	000844	Fibritin_C	560	phiST2_0215	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54749.1	000844	Fibritin_C	560	vBValMR10Z_209	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07237.1	000844	Fibritin_C	1123	VmeM32_00251	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37581.1	000844	Fibritin_C	559	pp2_349	Vibriophage phi-pp2	GCA_002630725.1
APU01487.1	000845	T4_gp9_10	714	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28727.1	000845	T4_gp9_10	712	AP1_009	Aeromonas phage AP1	GCA_014183365.1
ATI17410.1	000845	T4_gp9_10	712	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00186.1	000845	T4_gp9_10	712	HWB28_gp366	Aeromonas phage AS-zj	GCA_002627665.1
AUE22739.1	000845	T4_gp9_10	718	Ah1_00221	Aeromonas phage Ah1	GCA_002957415.1
QAX98458.1	000845	T4_gp9_10	717	ASfcp2_117	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97850.1	000845	T4_gp9_10	712	ASswx1_207	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01300.1	000845	T4_gp9_10	713	ASwh1_237	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39550.1	000845	T4_gp9_10	712	CC2_327	Aeromonas phage CC2	GCA_000903495.1
ADQ52917.1	000845	T4_gp9_10	717	PX29p198	Aeromonas phage PX29	GCA_000920195.1
ADM80184.1	000845	T4_gp9_10	717	phiAS5_ORF0341	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53108.1	000845	T4_gp9_10	1030	65p100	Aeromonas virus 65	GCA_000893255.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAQ17869.1	000845	T4_gp9_10	718	10	Aeromonas virus Aeh1	GCA_000843245.1
ANS05937.1	000845	T4_gp9_10	605	ABCD_0200	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64897.1	000845	T4_gp9_10	599	S13_098	Cronobacter phage S13	GCA_001503575.1
AON97214.1	000845	T4_gp9_10	605	E_206	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70718.1	000845	T4_gp9_10	604	phiC120_c11	Escherichia phage phiC120	GCA_002621185.1
ARM70984.1	000845	T4_gp9_10	604	phiC120_c279	Escherichia phage phiC120	GCA_002621185.1
AAX78732.1	000845	T4_gp9_10	605	RB43ORF210w	Escherichia virus RB43	GCA_000863505.1
QHJ79042.1	000845	T4_gp9_10	597	-	Myoviridae sp.	GCA_012593985.1
AAQ64414.1	000845	T4_gp9_10	748	KVP40.0345	Vibrio phage KVP40	GCA_000843785.1
QIW90359.1	000845	T4_gp9_10	748	GCAPEGMB_00012	Vibrio phage V07	GCA_012361095.1
QIW91070.1	000845	T4_gp9_10	748	COHAPHLI_00207	Vibrio phage V09	GCA_012361135.1
QHJ74527.1	000845	T4_gp9_10	748	VH12019_00227	Vibrio phage VH1_2019	GCA_009931825.1
AGB06986.1	000845	T4_gp9_10	748	CF80_gp199	Vibrio phage VH7D	GCA_000914495.1
QBX06128.1	000845	T4_gp9_10	748	ValB1HC_174	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61140.1	000845	T4_gp9_10	748	AVU32_gp299	Vibrio phage ValKK3	GCA_001501635.1
AGN30018.1	000845	T4_gp9_10	748	VPFG_00010	Vibrio phage nt-1	GCA_000910195.2
ALP46963.1	000845	T4_gp9_10	748	phiGrn1_0079	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47343.1	000845	T4_gp9_10	748	phiST2_0211	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54753.1	000845	T4_gp9_10	748	vBValMR10Z_213	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07240.1	000845	T4_gp9_10	713	VmeM32_00254	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37577.1	000845	T4_gp9_10	748	pp2_345	Vibriophage phi-pp2	GCA_002630725.1
AFO71336.1	000846	N-term+Nucleotide_pyrophosphohydrolase	293	CR5_116	Cronobacter phage CR5	GCA_000910235.1
AMR59886.1	000846	N-term+Nucleotide_pyrophosphohydrolase	313	SEGD1_239	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07544.1	000846	N-term+Nucleotide_pyrophosphohydrolase	299	DERBICUS_118	Erwinia phage Derbicus	GCA_004521655.1
AHI60253.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	Ea357_102	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49885.1	000846	N-term+Nucleotide_pyrophosphohydrolase	277	MACHINA_247	Erwinia phage Machina	GCA_002758035.1
QBP07211.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	REBECCA_104	Erwinia phage Rebecca	GCA_004521635.1
AXF51387.1	000846	N-term+Nucleotide_pyrophosphohydrolase	460	WELLINGTON_261	Erwinia phage Wellington	GCA_003344985.1
AFQ96699.1	000846	N-term+Nucleotide_pyrophosphohydrolase	301	G173_gp154	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48269.1	000846	N-term+Nucleotide_pyrophosphohydrolase	283	ASESINO_256	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85890.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	BOSOLAPHORUS_103	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48542.1	000846	N-term+Nucleotide_pyrophosphohydrolase	303	CAITLIN_247	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48819.1	000846	N-term+Nucleotide_pyrophosphohydrolase	307	CHRISDB_257	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52205.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	DM_107	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86209.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	DESERTFOX_102	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ48967.1	000846	N-term+Nucleotide_pyrophosphohydrolase	294	EARLPHILLIPIV_118	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49328.1	000846	N-term+Nucleotide_pyrophosphohydrolase	277	HUXLEY_246	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03754.1	000846	N-term+Nucleotide_pyrophosphohydrolase	204	JOAD_161	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49613.1	000846	N-term+Nucleotide_pyrophosphohydrolase	460	KWAN_261	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86532.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	MADMEL_104	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86855.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	MORTIMER_106	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50156.1	000846	N-term+Nucleotide_pyrophosphohydrolase	277	PARSHIK_247	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50308.1	000846	N-term+Nucleotide_pyrophosphohydrolase	307	PHOBOS_118	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANH51883.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	RAY_102	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03510.1	000846	N-term+Nucleotide_pyrophosphohydrolase	204	RISINGSUN_160	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51567.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	SIMMY50_105	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64915.1	000846	N-term+Nucleotide_pyrophosphohydrolase	215	SPECIALG_105	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50681.1	000846	N-term+Nucleotide_pyrophosphohydrolase	301	STRATTON_256	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86076.1	000846	N-term+Nucleotide_pyrophosphohydrolase	313	ACEC001_2330	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QIG65804.1	000846	N-term+Nucleotide_pyrophosphohydrolase	176	phiOC_p139	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QNI20920.1	000846	N-term+Nucleotide_pyrophosphohydrolase	313	-	Salmonella phage JN03	GCA_014319805.1
AWN09117.1	000846	N-term+Nucleotide_pyrophosphohydrolase	291	MLDJOKPK_00205	Salmonella phage SPAsTU	GCA_003183805.1
AEP84068.1	000846	N-term+Nucleotide_pyrophosphohydrolase	313	SPN3US_0235	Salmonella phage SPN3US	GCA_001042275.1
QKE54391.1	000846	N-term+Nucleotide_pyrophosphohydrolase	613	ACSA002_0770	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QDB70391.1	000847	virion_structural-Cluster191_1clades	370	CF8_0222	Aeromonas phage CF8	GCA_006384595.2
QDJ97391.1	000847	virion_structural-Cluster191_1clades	372	D6_0232	Aeromonas phage D6	GCA_007051205.2
QDH47069.1	000847	virion_structural-Cluster191_1clades	372	LAh10_146	Aeromonas phage LAh10	GCA_006863975.1
QDJ96734.1	000847	virion_structural-Cluster191_1clades	371	PS1_0223	Aeromonas phage PS1	GCA_007051165.2
QFR59367.1	000847	virion_structural-Cluster191_1clades	371	PS2_0225	Aeromonas phage PS2	GCA_009388305.2
QBZ70776.1	000847	virion_structural-Cluster191_1clades	371	pETSU_195	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60310.1	000847	virion_structural-Cluster191_1clades	356	Ea357_159	Erwinia phage Ea35-70	GCA_000914635.1
AGX01888.1	000847	virion_structural-Cluster191_1clades	355	CF95_gp165	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07268.1	000847	virion_structural-Cluster191_1clades	356	REBECCA_161	Erwinia phage Rebecca	GCA_004521635.1
AUG85948.1	000847	virion_structural-Cluster191_1clades	356	BOSOLAPHORUS_161	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52263.1	000847	virion_structural-Cluster191_1clades	356	DM_165	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86267.1	000847	virion_structural-Cluster191_1clades	356	DESERTFOX_160	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03687.1	000847	virion_structural-Cluster191_1clades	369	JOAD_228	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86589.1	000847	virion_structural-Cluster191_1clades	356	MADMEL_161	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86913.1	000847	virion_structural-Cluster191_1clades	356	MORTIMER_164	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51941.1	000847	virion_structural-Cluster191_1clades	356	RAY_160	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03444.1	000847	virion_structural-Cluster191_1clades	369	RISINGSUN_226	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51625.1	000847	virion_structural-Cluster191_1clades	356	SIMMY50_163	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64972.1	000847	virion_structural-Cluster191_1clades	356	SPECIALG_162	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGH72082.1	000847	virion_structural-Cluster191_1clades	371	N1M2_219	Klebsiella phage N1M2	GCA_010092605.1
QGZ14509.1	000847	virion_structural-Cluster191_1clades	376	HWC77_gp146	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24090.1	000847	virion_structural-Cluster191_1clades	357	-	Proteus phage 10	GCA_014071245.1
CAG27275.1	000847	virion_structural-Cluster191_1clades	369	PPEV_gp181	Pseudomonas phage EL	GCA_000866825.1
AEV89711.1	000847	virion_structural-Cluster191_1clades	375	OBP_274	Pseudomonas phage OBP	GCA_000896635.1
QKE54464.1	000847	virion_structural-Cluster191_1clades	355	ACSA002_1500	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65425.1	000847	virion_structural-Cluster191_1clades	319	2050HW_00090	Serratia phage 2050HW	GCA_002628125.1
QDB71201.1	000847	virion_structural-Cluster191_1clades	356	CPT_Moabite_171	Serratia phage Moabite	GCA_006384735.1
QFP93097.1	000847	virion_structural-Cluster191_1clades	364	-	Serratia phage PCH45	GCA_009187865.1
QAU04225.1	000847	virion_structural-Cluster191_1clades	376	HWC03_gp070	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23137.1	000847	virion_structural-Cluster191_1clades	376	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80974.1	000847	virion_structural-Cluster191_1clades	376	Aphrodite1_0203	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47590.1	000847	virion_structural-Cluster191_1clades	376	HWC35_gp196	Vibrio phage USC-1	GCA_006864065.1
BAW98405.1	000847	virion_structural-Cluster191_1clades	377	FDH33_gp196	Vibrio phage pTD1	GCA_002618825.1
APU01486.1	000848	GP11	294	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28726.1	000848	GP11	323	AP1_008	Aeromonas phage AP1	GCA_014183365.1
ATI17411.1	000848	GP11	323	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00185.1	000848	GP11	323	HWB28_gp367	Aeromonas phage AS-zj	GCA_002627665.1
AUE22740.1	000848	GP11	324	Ah1_00222	Aeromonas phage Ah1	GCA_002957415.1
QAX98459.1	000848	GP11	324	ASfcp2_118	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97851.1	000848	GP11	323	ASswx1_208	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01299.1	000848	GP11	323	ASwh1_236	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39549.1	000848	GP11	323	CC2_326	Aeromonas phage CC2	GCA_000903495.1
ADQ52918.1	000848	GP11	324	PX29p199	Aeromonas phage PX29	GCA_000920195.1
ADM80185.1	000848	GP11	324	phiAS5_ORF0342	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53107.1	000848	GP11	289	65p099	Aeromonas virus 65	GCA_000893255.1
AAQ17870.1	000848	GP11	324	11	Aeromonas virus Aeh1	GCA_000843245.1
ANS06000.1	000848	GP11	220	ABCD_0201	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64896.1	000848	GP11	212	S13_097	Cronobacter phage S13	GCA_001503575.1
AON97215.1	000848	GP11	220	E_207	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70719.1	000848	GP11	219	phiC120_c12	Escherichia phage phiC120	GCA_002621185.1
ARM70985.1	000848	GP11	219	phiC120_c280	Escherichia phage phiC120	GCA_002621185.1
AAX78733.1	000848	GP11	220	RB43ORF211w	Escherichia virus RB43	GCA_000863505.1
QHJ79043.1	000848	GP11	211	-	Myoviridae sp.	GCA_012593985.1
AAQ64415.1	000848	GP11	234	KVP40.0346	Vibrio phage KVP40	GCA_000843785.1
QIW90360.1	000848	GP11	228	GCAPEGMB_00013	Vibrio phage V07	GCA_012361095.1
QIW91069.1	000848	GP11	228	COHAPHLI_00206	Vibrio phage V09	GCA_012361135.1
QHJ74528.1	000848	GP11	228	VH12019_00228	Vibrio phage VH1_2019	GCA_009931825.1
AGB06987.1	000848	GP11	228	CF80_gp200	Vibrio phage VH7D	GCA_000914495.1
QBX06127.1	000848	GP11	228	ValB1HC_173	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61139.1	000848	GP11	228	AVU32_gp298	Vibrio phage ValKK3	GCA_001501635.1
AGN30019.2	000848	GP11	228	VPFG_00011	Vibrio phage nt-1	GCA_000910195.2
ALP47054.1	000848	GP11	228	phiGrn1_0080	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47435.1	000848	GP11	228	phiST2_0212	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54752.1	000848	GP11	228	vBValMR10Z_212	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07239.1	000848	GP11	317	VmeM32_00253	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37578.1	000848	GP11	228	pp2_346	Vibriophage phi-pp2	GCA_002630725.1
QDJ97316.1	000849	Tox-PLA2	117	D6_0156	Aeromonas phage D6	GCA_007051205.2
AFO71370.1	000849	Tox-PLA2	230	CR5_150	Cronobacter phage CR5	GCA_000910235.1
AMR59807.1	000849	Tox-PLA2	213	SEGD1_160	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07580.1	000849	Tox-PLA2	230	DERBICUS_154	Erwinia phage Derbicus	GCA_004521655.1
ANZ49805.1	000849	Tox-PLA2	236	MACHINA_167	Erwinia phage Machina	GCA_002758035.1

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AGX01822.1	000849	Tox-PLA2	124	CF95_gp100	Erwinia phage PhiEaH1	GCA_000914555.1
AXF51302.1	000849	Tox-PLA2	228	WELLINGTON_173	Erwinia phage Wellington	GCA_003344985.1
AFQ96622.1	000849	Tox-PLA2	213	G173_gp077	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48186.1	000849	Tox-PLA2	213	ASESINO_173	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48461.1	000849	Tox-PLA2	236	CAITLIN_166	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48740.1	000849	Tox-PLA2	237	CHRISDB_178	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49003.1	000849	Tox-PLA2	230	EARLPHILLIPIV_154	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49249.1	000849	Tox-PLA2	236	HUXLEY_167	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49526.1	000849	Tox-PLA2	225	KWAN_174	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50077.1	000849	Tox-PLA2	236	PARSHIK_168	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50350.1	000849	Tox-PLA2	230	PHOBOS_160	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50599.1	000849	Tox-PLA2	213	STRATTON_174	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85996.1	000849	Tox-PLA2	213	ACEC001_1560	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
ABY62838.1	000849	Tox-PLA2	153	201phi2-1p004	Pseudomonas phage 201phi2-1	GCA_000875305.1
AFH14571.1	000849	Tox-PLA2	150	Lu11_0040	Pseudomonas phage Lu11	GCA_000897175.1
ARV77173.1	000849	Tox-PLA2	163	NOXIFER_2	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32152.1	000849	Tox-PLA2	164	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03431.1	000849	Tox-PLA2	164	005	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02942.1	000849	Tox-PLA2	178	PSA21_424	Pseudomonas phage Psa21	GCA_004340405.1
QEM41733.1	000849	Tox-PLA2	164	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAS04959.2	000849	Tox-PLA2	135	AVU11_gp167	Ralstonia phage RSF1	GCA_001500875.1
BAQ02684.1	000849	Tox-PLA2	137	AVU38_gp156	Ralstonia phage RSL2	GCA_001503055.1
QNI20855.1	000849	Tox-PLA2	213	-	Salmonella phage JN03	GCA_014319805.1
AWN09174.1	000849	Tox-PLA2	213	MLDJOKPK_00286	Salmonella phage SPAsTU	GCA_003183805.1
AEP83990.1	000849	Tox-PLA2	213	SPN3US_0157	Salmonella phage SPN3US	GCA_001042275.1
QKE54400.1	000849	Tox-PLA2	131	ACSA002_0860	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFP93220.1	000849	Tox-PLA2	132	-	Serratia phage PCH45	GCA_009187865.1
AQT28051.1	000849	Tox-PLA2	226	pVa21_110	Vibrio phage pVa-21	GCA_002619305.1
AGX01731.1	000850	Cluster196_1clades	115	CF95_gp009	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07353.1	000850	Cluster196_1clades	111	REBECCA_248	Erwinia phage Rebecca	GCA_004521635.1
AUG86035.1	000850	Cluster196_1clades	111	BOSOLAPHORUS_249	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52352.1	000850	Cluster196_1clades	111	DM_252	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86354.1	000850	Cluster196_1clades	111	DESERTFOX_247	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86677.1	000850	Cluster196_1clades	111	MADMEL_250	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87000.1	000850	Cluster196_1clades	111	MORTIMER_252	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52026.1	000850	Cluster196_1clades	111	RAY_246	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51710.1	000850	Cluster196_1clades	111	SIMMY50_251	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65061.1	000850	Cluster196_1clades	111	SPECIALG_250	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QBO63965.1	000850	Cluster196_1clades	117	Goslar_00172	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QMP24164.1	000850	Cluster196_1clades	117	-	Proteus phage 10	GCA_014071245.1
ABY62959.1	000850	Cluster196_1clades	121	201phi2-1p127	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44851.1	000850	Cluster196_1clades	120	KTN4_093	Pseudomonas phage KTN4	GCA_002607225.1
ARV77235.1	000850	Cluster196_1clades	122	NOXIFER_64	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32219.1	000850	Cluster196_1clades	120	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76738.1	000850	Cluster196_1clades	121	PHABIO_107	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02603.1	000850	Cluster196_1clades	121	PSA21_74	Pseudomonas phage Psa21	GCA_004340405.1
ATN94862.1	000850	Cluster196_1clades	120	SL2_285	Pseudomonas phage SL2	GCA_002956015.1
QJB22729.1	000850	Cluster196_1clades	120	fnug_86	Pseudomonas phage fnug	GCA_012837215.1
QEM41797.1	000850	Cluster196_1clades	120	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAS05008.1	000850	Cluster196_1clades	113	AVU11_gp216	Ralstonia phage RSF1	GCA_001500875.1
BAQ02738.1	000850	Cluster196_1clades	113	AVU38_gp210	Ralstonia phage RSL2	GCA_001503055.1
QKE54572.1	000850	Cluster196_1clades	116	ACSA002_2560	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65661.1	000850	Cluster196_1clades	115	2050HW_00326	Serratia phage 2050HW	GCA_002628125.1
QDB71085.1	000850	Cluster196_1clades	115	CPT_Moabite_053	Serratia phage Moabite	GCA_006384735.1
QFP93236.1	000850	Cluster196_1clades	114	-	Serratia phage PCH45	GCA_009187865.1
AXH70823.1	000850	Cluster196_1clades	115	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT28160.1	000850	Cluster196_1clades	106	pVa21_219	Vibrio phage pVa-21	GCA_002619305.1
QAX96674.1	000850	Cluster196_1clades	115	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96992.1	000850	Cluster196_1clades	115	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96038.1	000850	Cluster196_1clades	115	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96356.1	000850	Cluster196_1clades	115	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
APU01488.1	000851	T4_gp9_10	308	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28728.1	000851	T4_gp9_10	308	AP1_0010	Aeromonas phage AP1	GCA_014183365.1
ATI17409.1	000851	T4_gp9_10	308	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00187.1	000851	T4_gp9_10	308	HWB28_gp365	Aeromonas phage AS-zj	GCA_002627665.1
AUE22738.1	000851	T4_gp9_10	308	Ah1_00220	Aeromonas phage Ah1	GCA_002957415.1
QAX98457.1	000851	T4_gp9_10	308	ASfcp2_116	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97849.1	000851	T4_gp9_10	308	ASswx1_206	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01301.1	000851	T4_gp9_10	308	ASwh1_238	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39551.1	000851	T4_gp9_10	308	CC2_328	Aeromonas phage CC2	GCA_000903495.1
ADQ52916.1	000851	T4_gp9_10	308	PX29p197	Aeromonas phage PX29	GCA_000920195.1
ADM80183.1	000851	T4_gp9_10	308	phiAS5_ORF0340	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17868.1	000851	T4_gp9_10	308	9	Aeromonas virus Aeh1	GCA_000843245.1
ANS05980.1	000851	T4_gp9_10	287	ABCD_0199	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64898.1	000851	T4_gp9_10	256	S13_099	Cronobacter phage S13	GCA_001503575.1
AON97213.1	000851	T4_gp9_10	287	E_205	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70717.1	000851	T4_gp9_10	287	phiC120_c10	Escherichia phage phiC120	GCA_002621185.1
ARM70983.1	000851	T4_gp9_10	287	phiC120_c278	Escherichia phage phiC120	GCA_002621185.1
AAX78731.1	000851	T4_gp9_10	287	RB43ORF209w	Escherichia virus RB43	GCA_000863505.1
QHJ79041.1	000851	T4_gp9_10	289	-	Myoviridae sp.	GCA_012593985.1
AAQ64413.1	000851	T4_gp9_10	327	KVP40.0344	Vibrio phage KVP40	GCA_000843785.1
QIW90358.1	000851	T4_gp9_10	318	GCAPEGMB_00011	Vibrio phage V07	GCA_012361095.1
QIW91071.1	000851	T4_gp9_10	318	COHAPHLL_00208	Vibrio phage V09	GCA_012361135.1
QHJ74526.1	000851	T4_gp9_10	318	VH12019_00226	Vibrio phage VH1_2019	GCA_009931825.1
AGB06985.1	000851	T4_gp9_10	322	CF80_gp198	Vibrio phage VH7D	GCA_000914495.1
QBX06129.1	000851	T4_gp9_10	318	ValB1HC_175	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61141.1	000851	T4_gp9_10	318	AVU32_gp300	Vibrio phage ValKK3	GCA_001501635.1
AGN30017.1	000851	T4_gp9_10	318	VPFG_00009	Vibrio phage nt-1	GCA_000910195.2
ALP47014.1	000851	T4_gp9_10	318	phiGrn1_0078	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47394.1	000851	T4_gp9_10	318	phiST2_0210	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54754.1	000851	T4_gp9_10	318	vBValMR10Z_214	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07241.1	000851	T4_gp9_10	307	VmeM32_00255	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37576.1	000851	T4_gp9_10	318	pp2_344	Vibriophage phi-pp2	GCA_002630725.1
AFU87953.1	000852	Cluster200_1clades	143	CcrColossus_gp083	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68628.1	000852	Cluster200_1clades	142	CcrPW_gp089c	Caulobacter phage CcrPW	GCA_003443275.1
AFC21457.1	000852	Cluster200_1clades	148	GAP32_010	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21798.1	000852	Cluster200_1clades	239	GAP32_348	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AGH07678.1	000852	Cluster200_1clades	159	CYVG_00235	Cyanophage S-SSM6a	GCA_002710385.1
AGG54325.1	000852	Cluster200_1clades	139	CYWG_00041	Cyanophage S-SSM6b	GCA_002710425.1
AMM43575.1	000852	Cluster200_1clades	148	CBB_10	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43919.1	000852	Cluster200_1clades	239	CBB_356	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44126.1	000852	Cluster200_1clades	148	CBB_563	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH26158.1	000852	Cluster200_1clades	149	CPMG_00057	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44448.1	000852	Cluster200_1clades	149	PSSM2_070	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12205.1	000852	Cluster200_1clades	149	PRTG_00047	Prochlorococcus phage P-SSM5	GCA_002991095.1
AQW88879.1	000852	Cluster200_1clades	242	BF_0354	Serratia phage BF	GCA_002619745.1
AIX30566.1	000852	Cluster200_1clades	128	Syn7803US37_89	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76118.1	000852	Cluster200_1clades	128	PBI_BELLAMY_73	Synechococcus phage Bellamy	GCA_002627525.1
AXQ70611.1	000852	Cluster200_1clades	143	HOU04_gp010	Synechococcus phage S-T4	GCA_003443335.1
AXQ70409.1	000852	Cluster200_1clades	143	HOU04_gp010	Synechococcus phage S-T4	GCA_003443335.1
QJT70059.1	000852	Cluster200_1clades	133	SynMITS9220M01_046	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64298.1	000852	Cluster200_1clades	129	KVP40.0229	Vibrio phage KVP40	GCA_000843785.1
QIW90614.1	000852	Cluster200_1clades	124	GCAPEGMB_00267	Vibrio phage V07	GCA_012361095.1
QIW91185.1	000852	Cluster200_1clades	124	COHAPHLL_00349	Vibrio phage V09	GCA_012361135.1
QHJ74409.1	000852	Cluster200_1clades	124	VH12019_00082	Vibrio phage VH1_2019	GCA_009931825.1
AGB06916.1	000852	Cluster200_1clades	124	CF80_gp129	Vibrio phage VH7D	GCA_000914495.1
QBX06230.1	000852	Cluster200_1clades	124	ValB1HC_277	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60856.1	000852	Cluster200_1clades	124	AVU32_gp015	Vibrio phage ValKK3	GCA_001501635.1
AGN30289.2	000852	Cluster200_1clades	124	VPFG_00290	Vibrio phage nt-1	GCA_000910195.2
ALP47159.1	000852	Cluster200_1clades	124	phiGrn1_0352	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47546.1	000852	Cluster200_1clades	124	phiST2_0107	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54855.1	000852	Cluster200_1clades	124	vBValMR10Z_315	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37459.1	000852	Cluster200_1clades	124	pp2_226	Vibriophage phi-pp2	GCA_002630725.1
SOK59165.1	000852	Cluster200_1clades	239	g357	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58633.1	000852	Cluster200_1clades	239	g356	Yersinia phage fHe-Yen9-04	GCA_002990485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH56876.1	000853	DUF3310	102	CPXG_00073	Cyanophage P-RSM6	GCA_000906155.1
AJK27579.1	000853	DUF3310	102	PTIM40_152	Cyanophage P-TIM40	GCA_001470935.1
AOO14339.1	000853	DUF3310	96	Sn110110_145	Cyanophage S-RIM14	GCA_002599065.1
AOO14988.1	000853	DUF3310	96	W1230910_142	Cyanophage S-RIM14	GCA_002599125.1
AMO43158.1	000853	DUF3310	95	R1080702_149	Cyanophage S-RIM32	GCA_001754165.1
AMO43382.1	000853	DUF3310	95	W270710_138	Cyanophage S-RIM44	GCA_002599145.1
AOO11627.1	000853	DUF3310	95	ES420910_146	Cyanophage S-RIM44	GCA_002599165.1
AOO11854.1	000853	DUF3310	95	Np050604_138	Cyanophage S-RIM44	GCA_002599185.1
AOO12092.1	000853	DUF3310	95	Np200711_146	Cyanophage S-RIM44	GCA_002599205.1
AOO12328.1	000853	DUF3310	95	Np420711_146	Cyanophage S-RIM44	GCA_002599225.1
AOO12555.1	000853	DUF3310	95	Sn080709_138	Cyanophage S-RIM44	GCA_002599245.1
AOO12793.1	000853	DUF3310	95	Sn130910_146	Cyanophage S-RIM44	GCA_002599265.1
AOO13021.1	000853	DUF3310	95	W2100709_139	Cyanophage S-RIM44	GCA_002599285.1
AGH07479.1	000853	DUF3310	222	CYVG_00035	Cyanophage S-SSM6a	GCA_002710385.1
AGG54471.1	000853	DUF3310	92	CYWG_00187	Cyanophage S-SSM6b	GCA_002710425.1
QIG65677.1	000853	DUF3310	164	phiOC_p011	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26304.1	000853	DUF3310	135	CPMG_00205	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44534.1	000853	DUF3310	220	PSSM2_156	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12437.1	000853	DUF3310	220	PRTG_00287	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93466.1	000853	DUF3310	189	AVU42_gp128	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99240.1	000853	DUF3310	95	Syn1_139	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30636.1	000853	DUF3310	141	Syn7803US37_159	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54909.1	000853	DUF3310	107	b23_0296	Synechococcus phage B23	GCA_009745195.1
QGT54544.1	000853	DUF3310	107	b3_0303	Synechococcus phage B3	GCA_009745215.1
ASR76194.1	000853	DUF3310	159	PBI_BELLAMY_149	Synechococcus phage Bellamy	GCA_002627525.1
QCW22904.1	000853	DUF3310	137	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50583.1	000853	DUF3310	106	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59606.1	000853	DUF3310	95	S330809_145	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59368.1	000853	DUF3310	95	C440309_145	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59844.1	000853	DUF3310	95	N231010_145	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70559.1	000853	DUF3310	170	HOU04_gp160	Synechococcus phage S-T4	GCA_003443335.1
QJT70139.1	000853	DUF3310	150	SynMITS9220M01_126	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01471.1	000854	prohead-core-protein	156	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28785.1	000854	prohead-core-protein	158	AP1_0078	Aeromonas phage AP1	GCA_014183365.1
ATI17426.1	000854	prohead-core-protein	158	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00169.1	000854	prohead-core-protein	158	HWB28_gp383	Aeromonas phage AS-zj	GCA_002627665.1
AUE22758.1	000854	prohead-core-protein	157	Ah1_00240	Aeromonas phage Ah1	GCA_002957415.1
QAX98474.1	000854	prohead-core-protein	158	ASfcp2_136	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97866.1	000854	prohead-core-protein	158	ASswx1_223	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01284.1	000854	prohead-core-protein	156	ASwh1_221	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39423.1	000854	prohead-core-protein	158	CC2_311	Aeromonas phage CC2	GCA_000903495.1
ADQ52936.1	000854	prohead-core-protein	158	PX29p217	Aeromonas phage PX29	GCA_000920195.1
ADM79859.1	000854	prohead-core-protein	158	phiAS5_ORF0016	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53094.1	000854	prohead-core-protein	156	65p084	Aeromonas virus 65	GCA_000893255.1
AAQ17883.1	000854	prohead-core-protein	157	68	Aeromonas virus Aeh1	GCA_000843245.1
ANS06059.1	000854	prohead-core-protein	135	ABCD_0213	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64882.1	000854	prohead-core-protein	127	S13_083	Cronobacter phage S13	GCA_001503575.1
AON97228.1	000854	prohead-core-protein	135	E_220	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70731.1	000854	prohead-core-protein	141	phiC120_c24	Escherichia phage phiC120	GCA_002621185.1
AAX78746.1	000854	prohead-core-protein	135	RB43ORF224w	Escherichia virus RB43	GCA_000863505.1
QHJ79057.1	000854	prohead-core-protein	126	-	Myoviridae sp.	GCA_012593985.1
AAQ64429.1	000854	prohead-core-protein	163	KVP40.0360	Vibrio phage KVP40	GCA_000843785.1
QIW90374.1	000854	prohead-core-protein	163	GCAPEGMB_00027	Vibrio phage V07	GCA_012361095.1
QIW91055.1	000854	prohead-core-protein	163	COHAPHLL_00192	Vibrio phage V09	GCA_012361135.1
QHJ74543.1	000854	prohead-core-protein	163	VH12019_00243	Vibrio phage VH1_2019	GCA_009931825.1
AGB07001.1	000854	prohead-core-protein	163	CF80_gp214	Vibrio phage VH7D	GCA_000914495.1
QBX06113.1	000854	prohead-core-protein	163	ValB1HC_159	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61125.1	000854	prohead-core-protein	163	AVU32_gp284	Vibrio phage ValKK3	GCA_001501635.1
AGN30033.1	000854	prohead-core-protein	161	VPFG_00025	Vibrio phage nt-1	GCA_000910195.2
ALP47109.1	000854	prohead-core-protein	163	phiGrn1_0094	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47491.1	000854	prohead-core-protein	163	phiST2_0226	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54738.1	000854	prohead-core-protein	163	vBValMR10Z_198	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07003.1	000854	prohead-core-protein	134	VmeM32_00007	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37592.1	000854	prohead-core-protein	163	pp2_360	Vibriophage phi-pp2	GCA_002630725.1
AGH56835.1	000855	TM	108	CPXG_00032	Cyanophage P-RSM6	GCA_000906155.1
AJK27610.1	000855	TM	129	PTIM40_192	Cyanophage P-TIM40	GCA_001470935.1
AOO14377.1	000855	TM	137	Sn110110_183	Cyanophage S-RIM14	GCA_002599065.1
AOO15025.1	000855	TM	137	W1230910_179	Cyanophage S-RIM14	GCA_002599125.1
AMO43185.1	000855	TM	144	R1080702_176	Cyanophage S-RIM32	GCA_001754165.1
AMO43411.1	000855	TM	144	W270710_167	Cyanophage S-RIM44	GCA_002599145.1
AOO11655.1	000855	TM	144	ES420910_174	Cyanophage S-RIM44	GCA_002599165.1
AOO11883.1	000855	TM	144	Np050604_167	Cyanophage S-RIM44	GCA_002599185.1
AOO12121.1	000855	TM	144	Np200711_175	Cyanophage S-RIM44	GCA_002599205.1
AOO12356.1	000855	TM	144	Np420711_174	Cyanophage S-RIM44	GCA_002599225.1
AOO12584.1	000855	TM	144	Sn080709_167	Cyanophage S-RIM44	GCA_002599245.1
AOO12821.1	000855	TM	144	Sn130910_174	Cyanophage S-RIM44	GCA_002599265.1
AOO13050.1	000855	TM	144	W2100709_168	Cyanophage S-RIM44	GCA_002599285.1
AGH07526.1	000855	TM	141	CYVG_00082	Cyanophage S-SSM6a	GCA_002710385.1
AGG54425.1	000855	TM	143	CYWG_00141	Cyanophage S-SSM6b	GCA_002710425.1
AGH26270.1	000855	TM	112	CPMG_00170	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44583.1	000855	TM	97	PSSM2_206	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12388.1	000855	TM	124	PRTG_00235	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93502.1	000855	TM	132	AVU42_gp165	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99270.1	000855	TM	144	Syn1_169	Prochlorococcus phage Syn1	GCA_000892495.1
AGR48086.1	000855	TM	157	SmphiM12_454	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13257.1	000855	TM	157	PHIM19_352	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12897.1	000855	TM	157	PHIM7_352	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13620.1	000855	TM	157	PHIN3_357	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30678.1	000855	TM	128	Syn7803US37_201	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76220.1	000855	TM	133	PBI_BELLAMY_177	Synechococcus phage Bellamy	GCA_002627525.1
QCW22950.1	000855	TM	127	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50532.1	000855	TM	127	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59636.1	000855	TM	138	S330809_175	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59398.1	000855	TM	138	C440309_175	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59874.1	000855	TM	138	N231010_175	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70174.1	000855	TM	128	SynMITS9220M01_162	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01423.1	000856	DUF2654	124	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28756.1	000856	DUF2654	129	AP1_0038	Aeromonas phage AP1	GCA_014183365.1
ATI17475.1	000856	DUF2654	129	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00522.1	000856	DUF2654	129	HWB28_gp030	Aeromonas phage AS-zj	GCA_002627665.1
AUE22571.1	000856	DUF2654	131	Ah1_00030	Aeromonas phage Ah1	GCA_002957415.1
QAX98607.1	000856	DUF2654	130	ASfcp2_274	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97915.1	000856	DUF2654	132	ASswx1_272	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01235.1	000856	DUF2654	118	ASwh1_170	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39521.1	000856	DUF2654	129	CC2_260	Aeromonas phage CC2	GCA_000903495.1
ADQ52744.1	000856	DUF2654	134	PX29p025	Aeromonas phage PX29	GCA_000920195.1
ADM80000.1	000856	DUF2654	129	phiAS5_ORF0157	Aeromonas phage phiAS5	GCA_000887715.1
AAR90906.1	000856	DUF2654	124	65p032	Aeromonas virus 65	GCA_000893255.1
AAQ17686.1	000856	DUF2654	130	a-gt.4	Aeromonas virus Aeh1	GCA_000843245.1
ANS06075.1	000856	DUF2654	115	ABCD_0052	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65039.1	000856	DUF2654	114	S13_242	Cronobacter phage S13	GCA_001503575.1
AON97063.1	000856	DUF2654	114	E_054	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70884.1	000856	DUF2654	107	phiC120_c179	Escherichia phage phiC120	GCA_002621185.1
AAX78574.1	000856	DUF2654	115	RB43ORF052w	Escherichia virus RB43	GCA_000863505.1
QHJ78893.1	000856	DUF2654	112	-	Myoviridae sp.	GCA_012593985.1
AAQ64140.1	000856	DUF2654	116	KVP40.0069	Vibrio phage KVP40	GCA_000843785.1
QIW90463.1	000856	DUF2654	116	GCAPEGMB_00116	Vibrio phage V07	GCA_012361095.1
QIW90966.1	000856	DUF2654	116	COHAPHLL_00103	Vibrio phage V09	GCA_012361135.1
QHJ74252.1	000856	DUF2654	116	VH12019_00333	Vibrio phage VH1_2019	GCA_009931825.1
AGB07076.1	000856	DUF2654	116	CF80_gp289	Vibrio phage VH7D	GCA_000914495.1
QBX06019.1	000856	DUF2654	116	ValB1HC_065	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61033.1	000856	DUF2654	116	AVU32_gp192	Vibrio phage ValKK3	GCA_001501635.1
AGN30118.1	000856	DUF2654	119	VPFG_00116	Vibrio phage nt-1	GCA_000910195.2
ALP47169.1	000856	DUF2654	116	phiGrn1_0184	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47555.1	000856	DUF2654	116	phiST2_0315	Vibrio phage phi-ST2	GCA_002757135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNJ54644.1	000856	DUF2654	116	vBValMR10Z_103	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07124.1	000856	DUF2654	112	VmeM32_00137	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37300.1	000856	DUF2654	116	pp2_067	Vibriophage phi-pp2	GCA_002630725.1
AGH57022.1	000857	BRK	76	CPXG_00219	Cyanophage P-RSM6	GCA_000906155.1
AJK27639.1	000857	BRK	76	PTIM40_236	Cyanophage P-TIM40	GCA_001470935.1
AOO14411.1	000857	BRK	76	Sn110110_218	Cyanophage S-RIM14	GCA_002599065.1
AOO15060.1	000857	BRK	76	W1230910_215	Cyanophage S-RIM14	GCA_002599125.1
AMO43241.1	000857	BRK	80	R1080702_236	Cyanophage S-RIM32	GCA_001754165.1
AMO43472.1	000857	BRK	79	W270710_233	Cyanophage S-RIM44	GCA_002599145.1
AOO11714.1	000857	BRK	79	ES420910_237	Cyanophage S-RIM44	GCA_002599165.1
AOO11944.1	000857	BRK	79	Np050604_233	Cyanophage S-RIM44	GCA_002599185.1
AOO12180.1	000857	BRK	79	Np200711_238	Cyanophage S-RIM44	GCA_002599205.1
AOO12415.1	000857	BRK	79	Np420711_237	Cyanophage S-RIM44	GCA_002599225.1
AOO12645.1	000857	BRK	79	Sn080709_233	Cyanophage S-RIM44	GCA_002599245.1
AOO12880.1	000857	BRK	79	Sn130910_237	Cyanophage S-RIM44	GCA_002599265.1
AOO13111.1	000857	BRK	79	W2100709_234	Cyanophage S-RIM44	GCA_002599285.1
AGH07624.1	000857	BRK	89	CYVG_00181	Cyanophage S-SSM6a	GCA_002710385.1
AGG54376.1	000857	BRK	76	CYWG_00092	Cyanophage S-SSM6b	GCA_002710425.1
AGH26217.1	000857	BRK	80	CPMG_00116	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44701.1	000857	BRK	93	PSSM2_323	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44703.1	000857	BRK	108	PSSM2_325	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12272.1	000857	BRK	99	PRTG_00119	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12274.1	000857	BRK	93	PRTG_00121	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93580.1	000857	BRK	80	AVU42_gp243	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99333.1	000857	BRK	82	Syn1_237	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30764.1	000857	BRK	75	Syn7803US37_287	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54988.1	000857	BRK	82	b23_0382	Synechococcus phage B23	GCA_009745195.1
QGT54623.1	000857	BRK	82	b3_0388	Synechococcus phage B3	GCA_009745215.1
ASR76313.1	000857	BRK	80	PBI_BELLAMY_277	Synechococcus phage Bellamy	GCA_002627525.1
QCW23062.1	000857	BRK	83	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59695.1	000857	BRK	87	S330809_234	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59457.1	000857	BRK	87	C440309_234	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59932.1	000857	BRK	87	N231010_233	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70454.1	000857	BRK	82	HOU04_gp055	Synechococcus phage S-T4	GCA_003443335.1
QJT70258.1	000857	BRK	67	SynMITS9220M01_252	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01439.1	000858	long-tail-fiber-proximal-subunit	1231	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28796.1	000858	long-tail-fiber-proximal-subunit	1230	AP1_0089	Aeromonas phage AP1	GCA_014183365.1
ATI17460.1	000858	long-tail-fiber-proximal-subunit	1230	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00136.1	000858	long-tail-fiber-proximal-subunit	1230	HWB28_gp014	Aeromonas phage AS-zj	GCA_002627665.1
AUE22854.1	000858	long-tail-fiber-proximal-subunit	1235	Ah1_00336	Aeromonas phage Ah1	GCA_002957415.1
QAX98565.1	000858	long-tail-fiber-proximal-subunit	1235	ASfcp2_231	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97900.1	000858	long-tail-fiber-proximal-subunit	1230	ASswx1_257	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01253.1	000858	long-tail-fiber-proximal-subunit	1229	ASwh1_188	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39527.1	000858	long-tail-fiber-proximal-subunit	1230	CC2_276	Aeromonas phage CC2	GCA_000903495.1
ADQ53030.1	000858	long-tail-fiber-proximal-subunit	1235	PX29p311	Aeromonas phage PX29	GCA_000920195.1
ADM79954.1	000858	long-tail-fiber-proximal-subunit	1237	phiAS5_ORF0111	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53059.1	000858	long-tail-fiber-proximal-subunit	1231	65p049	Aeromonas virus 65	GCA_000893255.1
AAQ17983.1	000858	long-tail-fiber-proximal-subunit	1236	34	Aeromonas virus Aeh1	GCA_000843245.1
ANS05921.1	000858	long-tail-fiber-proximal-subunit	1219	ABCD_0260	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64809.1	000858	long-tail-fiber-proximal-subunit	1230	S13_010	Cronobacter phage S13	GCA_001503575.1
AON97279.1	000858	long-tail-fiber-proximal-subunit	1219	E_271	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70798.1	000858	long-tail-fiber-proximal-subunit	1277	phiC120_c92	Escherichia phage phiC120	GCA_002621185.1
AAX78800.1	000858	long-tail-fiber-proximal-subunit	1219	RB43ORF278w	Escherichia virus RB43	GCA_000863505.1
QHJ78855.1	000858	long-tail-fiber-proximal-subunit	1227	-	Myoviridae sp.	GCA_012593985.1
AAQ64452.1	000858	long-tail-fiber-proximal-subunit	1256	KVP40.0384	Vibrio phage KVP40	GCA_000843785.1
QIW90397.1	000858	long-tail-fiber-proximal-subunit	1256	GCAPEGMB_00050	Vibrio phage V07	GCA_012361095.1
QIW91032.1	000858	long-tail-fiber-proximal-subunit	1256	COHAPHLL_00169	Vibrio phage V09	GCA_012361135.1
QHJ74564.1	000858	long-tail-fiber-proximal-subunit	1256	VH12019_00264	Vibrio phage VH1_2019	GCA_009931825.1
QBX06089.1	000858	long-tail-fiber-proximal-subunit	1235	ValB1HC_135	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61103.1	000858	long-tail-fiber-proximal-subunit	1227	AVU32_gp262	Vibrio phage ValKK3	GCA_001501635.1
AGN30052.1	000858	long-tail-fiber-proximal-subunit	1246	VPFG_00047	Vibrio phage nt-1	GCA_000910195.2
ALP46958.1	000858	long-tail-fiber-proximal-subunit	1227	phiGrn1_0115	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47338.1	000858	long-tail-fiber-proximal-subunit	1235	phiST2_0246	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54715.1	000858	long-tail-fiber-proximal-subunit	1235	vBValMR10Z_174	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07047.1	000858	long-tail-fiber-proximal-subunit	1260	VmeM32_00056	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37615.1	000858	long-tail-fiber-proximal-subunit	1256	pp2_383	Vibriophage phi-pp2	GCA_002630725.1
CCH63477.1	000859	RADICAL-SAM	319	CP21_015	Campylobacter virus CP21	GCA_000902535.1
AFO71373.1	000859	RADICAL-SAM	452	CR5_153	Cronobacter phage CR5	GCA_000910235.1
AMR59813.1	000859	RADICAL-SAM	442	SEGD1_166	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07583.1	000859	RADICAL-SAM	448	DERBICUS_157	Erwinia phage Derbicus	GCA_004521655.1
ANZ49810.1	000859	RADICAL-SAM	448	MACHINA_172	Erwinia phage Machina	GCA_002758035.1
AXF51307.1	000859	RADICAL-SAM	465	WELLINGTON_178	Erwinia phage Wellington	GCA_003344985.1
AFQ96628.1	000859	RADICAL-SAM	447	G173_gp083	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48193.1	000859	RADICAL-SAM	446	ASESINO_180	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48466.1	000859	RADICAL-SAM	447	CAITLIN_171	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48745.1	000859	RADICAL-SAM	446	CHRISDB_183	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49006.1	000859	RADICAL-SAM	448	EARLPHILLIPIV_157	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49254.1	000859	RADICAL-SAM	448	HUXLEY_172	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49531.1	000859	RADICAL-SAM	465	KWAN_179	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50082.1	000859	RADICAL-SAM	448	PARSHIK_173	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50353.1	000859	RADICAL-SAM	453	PHOBOS_163	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50605.1	000859	RADICAL-SAM	447	STRATTON_180	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86002.1	000859	RADICAL-SAM	442	ACEC001_1620	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20861.1	000859	RADICAL-SAM	442	-	Salmonella phage JN03	GCA_014319805.1
AWN09170.1	000859	RADICAL-SAM	442	MLDJOKPK_00277	Salmonella phage SPAsTU	GCA_003183805.1
AEP83996.1	000859	RADICAL-SAM	442	SPN3US_0163	Salmonella phage SPN3US	GCA_001042275.1
AAQ64329.1	000859	RADICAL-SAM	329	KVP40.0260	Vibrio phage KVP40	GCA_000843785.1
AAQ64341.1	000859	RADICAL-SAM	350	KVP40.0272	Vibrio phage KVP40	GCA_000843785.1
QIW90644.1	000859	RADICAL-SAM	329	GCAPEGMB_00297	Vibrio phage V07	GCA_012361095.1
QIW90655.1	000859	RADICAL-SAM	350	GCAPEGMB_00308	Vibrio phage V07	GCA_012361095.1
QIW91143.1	000859	RADICAL-SAM	350	COHAPHLL_00307	Vibrio phage V09	GCA_012361135.1
QIW91155.1	000859	RADICAL-SAM	329	COHAPHLL_00319	Vibrio phage V09	GCA_012361135.1
QHJ74439.1	000859	RADICAL-SAM	329	VH12019_00112	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74450.1	000859	RADICAL-SAM	350	VH12019_00123	Vibrio phage VH1_2019	GCA_009931825.1
AGN30318.1	000859	RADICAL-SAM	351	VPFG_00320	Vibrio phage nt-1	GCA_000910195.2
AFN37488.1	000859	RADICAL-SAM	329	pp2_255	Vibriophage phi-pp2	GCA_002630725.1
AFN37501.1	000859	RADICAL-SAM	350	pp2_268	Vibriophage phi-pp2	GCA_002630725.1
AFO71418.1	000860	Cluster211_1clades	416	CR5_198	Cronobacter phage CR5	GCA_000910235.1
AMR59874.1	000860	Cluster211_1clades	424	SEGD1_227	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07631.1	000860	Cluster211_1clades	400	DERBICUS_205	Erwinia phage Derbicus	GCA_004521655.1
ANZ49875.1	000860	Cluster211_1clades	442	MACHINA_237	Erwinia phage Machina	GCA_002758035.1
AXF51377.1	000860	Cluster211_1clades	446	WELLINGTON_251	Erwinia phage Wellington	GCA_003344985.1
AFQ96689.1	000860	Cluster211_1clades	437	G173_gp144	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48258.1	000860	Cluster211_1clades	436	ASESINO_245	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48532.1	000860	Cluster211_1clades	427	CAITLIN_237	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48808.1	000860	Cluster211_1clades	427	CHRISDB_246	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49055.1	000860	Cluster211_1clades	400	EARLPHILLIPIV_206	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49318.1	000860	Cluster211_1clades	442	HUXLEY_236	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49603.1	000860	Cluster211_1clades	446	KWAN_251	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50146.1	000860	Cluster211_1clades	442	PARSHIK_237	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50402.1	000860	Cluster211_1clades	398	PHOBOS_212	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50671.1	000860	Cluster211_1clades	437	STRATTON_246	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86064.1	000860	Cluster211_1clades	424	ACEC001_2210	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
ABY63089.1	000860	Cluster211_1clades	384	201phi2-1p261	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44972.1	000860	Cluster211_1clades	354	KTN4_214	Pseudomonas phage KTN4	GCA_002607225.1
ARV77359.1	000860	Cluster211_1clades	348	NOXIFER_190	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32361.1	000860	Cluster211_1clades	374	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76880.1	000860	Cluster211_1clades	378	PHABIO_249	Pseudomonas phage Phabio	GCA_002624965.1
AEH03625.1	000860	Cluster211_1clades	390	202	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02761.1	000860	Cluster211_1clades	346	PSA21_235	Pseudomonas phage Psa21	GCA_004340405.1
ATN94742.1	000860	Cluster211_1clades	354	SL2_165	Pseudomonas phage SL2	GCA_002956015.1
QJB22850.1	000860	Cluster211_1clades	354	fnug_207	Pseudomonas phage fnug	GCA_012837215.1
QEM41935.1	000860	Cluster211_1clades	374	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83075.1	000860	Cluster211_1clades	354	PHIKZ174	Pseudomonas virus phiKZ	GCA_000842965.1
QNI20910.1	000860	Cluster211_1clades	424	-	Salmonella phage JN03	GCA_014319805.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AWN09127.1	000860	Cluster211_1clades	419	MLDJOKPK_00217	Salmonella phage SPAsTU	GCA_003183805.1
AEP84056.1	000860	Cluster211_1clades	424	SPN3US_0223	Salmonella phage SPN3US	GCA_001042275.1
AQT28098.1	000860	Cluster211_1clades	337	pVa21_157	Vibrio phage pVa-21	GCA_002619305.1
AGH56873.1	000861	Cluster213_1clades	166	CPXG_00070	Cyanophage P-RSM6	GCA_000906155.1
AJK27577.1	000861	Cluster213_1clades	182	PTIM40_150	Cyanophage P-TIM40	GCA_001470935.1
AMO43389.1	000861	Cluster213_1clades	170	W270710_145	Cyanophage S-RIM44	GCA_002599145.1
AOO11634.1	000861	Cluster213_1clades	170	ES420910_153	Cyanophage S-RIM44	GCA_002599165.1
AOO11861.1	000861	Cluster213_1clades	170	Np050604_145	Cyanophage S-RIM44	GCA_002599185.1
AOO12099.1	000861	Cluster213_1clades	170	Np200711_153	Cyanophage S-RIM44	GCA_002599205.1
AOO12335.1	000861	Cluster213_1clades	170	Np420711_153	Cyanophage S-RIM44	GCA_002599225.1
AOO12562.1	000861	Cluster213_1clades	170	Sn080709_145	Cyanophage S-RIM44	GCA_002599245.1
AOO12800.1	000861	Cluster213_1clades	170	Sn130910_153	Cyanophage S-RIM44	GCA_002599265.1
AOO13028.1	000861	Cluster213_1clades	170	W2100709_146	Cyanophage S-RIM44	GCA_002599285.1
AGH07483.1	000861	Cluster213_1clades	177	CYVG_00039	Cyanophage S-SSM6a	GCA_002710385.1
AGG54443.1	000861	Cluster213_1clades	171	CYWG_00159	Cyanophage S-SSM6b	GCA_002710425.1
AGH26303.1	000861	Cluster213_1clades	170	CPMG_00203	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44529.1	000861	Cluster213_1clades	176	PSSM2_151	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12440.1	000861	Cluster213_1clades	176	PRTG_00291	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93471.1	000861	Cluster213_1clades	169	AVU42_gp133	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99247.1	000861	Cluster213_1clades	170	Syn1_146	Prochlorococcus phage Syn1	GCA_000892495.1
QHJ86067.1	000861	Cluster213_1clades	170	KKIINIFJ_00155	Pseudomonas phage PN05	GCA_009931935.1
QCG75981.1	000861	Cluster213_1clades	162	EST35_0099	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44288.1	000861	Cluster213_1clades	200	PBI_SCTP2_273	Salicola phage SCTP-2	GCA_002625545.1
AFF28192.1	000861	Cluster213_1clades	186	PAU_194	Sphingomonas phage PAU	GCA_000902455.1
AIX30638.1	000861	Cluster213_1clades	175	Syn7803US37_161	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54977.1	000861	Cluster213_1clades	169	b23_0371	Synechococcus phage B23	GCA_009745195.1
QGT54612.1	000861	Cluster213_1clades	169	b3_0377	Synechococcus phage B3	GCA_009745215.1
QCW23091.1	000861	Cluster213_1clades	174	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50580.1	000861	Cluster213_1clades	174	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59614.1	000861	Cluster213_1clades	170	S330809_153	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59376.1	000861	Cluster213_1clades	170	C440309_153	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59852.1	000861	Cluster213_1clades	170	N231010_153	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70556.1	000861	Cluster213_1clades	175	HOU04_gp157	Synechococcus phage S-T4	GCA_003443335.1
QAU04505.1	000861	Cluster213_1clades	197	ValB1MD_155	Vibrio phage ValB1MD	GCA_004138815.1
QAX98482.1	000862	QSregVF_b	378	ASfcp2_144	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52944.1	000862	QSregVF_b	389	PX29p225	Aeromonas phage PX29	GCA_000920195.1
ADM79867.1	000862	QSregVF_b	376	phiAS5_ORF0024	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17890.1	000862	QSregVF_b	378	Aeh1ORF229c	Aeromonas virus Aeh1	GCA_000843245.1
QBX06454.1	000862	QSregVF_b	268	BcepSaruman_041	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74422.1	000862	QSregVF_b	268	BcepSauron_042	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ69269.1	000862	QSregVF_b	278	CcrBL9_gp245c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69825.1	000862	QSregVF_b	280	CcrSC_gp243c	Caulobacter phage CcrSC	GCA_003443315.1
ANS05988.1	000862	QSregVF_b	262	ABCD_0268	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64876.1	000862	QSregVF_b	372	S13_077	Cronobacter phage S13	GCA_001503575.1
AON97287.1	000862	QSregVF_b	265	E_279	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78808.1	000862	QSregVF_b	262	RB43ORF286c	Escherichia virus RB43	GCA_000863505.1
QHJ79063.1	000862	QSregVF_b	373	-	Myoviridae sp.	GCA_012593985.1
QIG66012.1	000862	QSregVF_b	257	phiOC_p370	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ASV44056.1	000862	QSregVF_b	393	PBI_SCTP2_41	Salicola phage SCTP-2	GCA_002625545.1
AGR48013.1	000862	QSregVF_b	262	SmphiM12_381	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13198.1	000862	QSregVF_b	262	PHIM19_293	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12839.1	000862	QSregVF_b	262	PHIM7_293	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13559.1	000862	QSregVF_b	262	PHIN3_296	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64437.1	000862	QSregVF_b	394	KVP40.0369	Vibrio phage KVP40	GCA_000843785.1
QIW90383.1	000862	QSregVF_b	394	GCAPEGMB_00036	Vibrio phage V07	GCA_012361095.1
QIW91046.1	000862	QSregVF_b	394	COHAPHLL_00183	Vibrio phage V09	GCA_012361135.1
QHJ74550.1	000862	QSregVF_b	394	VH12019_00250	Vibrio phage VH1_2019	GCA_009931825.1
QBX06104.1	000862	QSregVF_b	394	ValB1HC_150	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61118.1	000862	QSregVF_b	394	AVU32_gp277	Vibrio phage ValKK3	GCA_001501635.1
AGN30039.1	000862	QSregVF_b	392	VPFG_00034	Vibrio phage nt-1	GCA_000910195.2
ALP46995.1	000862	QSregVF_b	394	phiGrn1_0102	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47376.1	000862	QSregVF_b	390	phiST2_0233	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54729.1	000862	QSregVF_b	394	vBValMR10Z_189	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37601.1	000862	QSregVF_b	394	pp2_369	Vibriophage phi-pp2	GCA_002630725.1
AXG67144.1	000863	Cluster220_1clades	274	AD1_100	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67198.1	000863	Cluster220_1clades	210	AD1_154	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67199.1	000863	Cluster220_1clades	212	AD1_155	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79893.1	000863	Cluster220_1clades	265	JA11_088	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79950.1	000863	Cluster220_1clades	214	JA11_145	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79951.1	000863	Cluster220_1clades	208	JA11_146	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66492.1	000863	Cluster220_1clades	265	JA13_089	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66549.1	000863	Cluster220_1clades	214	JA13_146	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66550.1	000863	Cluster220_1clades	208	JA13_147	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66817.1	000863	Cluster220_1clades	265	JA29_091	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66874.1	000863	Cluster220_1clades	214	JA29_148	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66875.1	000863	Cluster220_1clades	208	JA29_149	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67462.1	000863	Cluster220_1clades	265	JA33_088	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67519.1	000863	Cluster220_1clades	214	JA33_145	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67520.1	000863	Cluster220_1clades	208	JA33_146	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08378.1	000863	Cluster220_1clades	275	Alexandra_105	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08431.1	000863	Cluster220_1clades	210	Alexandra_159	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08432.1	000863	Cluster220_1clades	212	Alexandra_160	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58742.1	000863	Cluster220_1clades	275	Y3_102	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58795.1	000863	Cluster220_1clades	210	Y3_155	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58796.1	000863	Cluster220_1clades	212	Y3_156	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28633.1	000863	Cluster220_1clades	211	YOLOSWAG_153	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28634.1	000863	Cluster220_1clades	210	YOLOSWAG_154	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28575.1	000863	Cluster220_1clades	273	YOLOSWAG_93	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38295.1	000863	Cluster220_1clades	280	BN7874_126	Phage NCTB	GCA_900092385.1
SBV38450.1	000863	Cluster220_1clades	338	BN7874_249	Phage NCTB	GCA_900092385.1
SBV38452.1	000863	Cluster220_1clades	214	BN7874_250	Phage NCTB	GCA_900092385.1
AFH14612.1	000863	Cluster220_1clades	213	Lu11_0080	Pseudomonas phage Lu11	GCA_000897175.1
AGS82089.2	000863	Cluster220_1clades	214	PaBG_00214	Pseudomonas phage PaBG	GCA_000912555.1
AGS82127.1	000863	Cluster220_1clades	273	PaBG_00252	Pseudomonas phage PaBG	GCA_000912555.1
AUZ95345.1	000864	NMN_transporter	225	FDI40_gp586	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69367.1	000864	NMN_transporter	211	CcrBL9_gp343	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69927.1	000864	NMN_transporter	211	CcrSC_gp345	Caulobacter phage CcrSC	GCA_003443315.1
AFC21804.1	000864	NMN_transporter	267	GAP32_354	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QIG57946.1	000864	NMN_transporter	316	SEA_PAULODIABOLI_262	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG65785.1	000864	NMN_transporter	218	phiOC_p120	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43925.1	000864	NMN_transporter	267	CBB_362	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QKE54375.1	000864	NMN_transporter	214	ACSA002_0610	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AQW88885.1	000864	NMN_transporter	267	BF_0360	Serratia phage BF	GCA_002619745.1
AGR48039.1	000864	NMN_transporter	249	SmphiM12_407	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13222.1	000864	NMN_transporter	249	PHIM19_317	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12863.1	000864	NMN_transporter	249	PHIM7_317	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13585.1	000864	NMN_transporter	249	PHIN3_322	Sinorhizobium phage phiN3	GCA_001501175.1
AXH70922.1	000864	NMN_transporter	238	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64284.1	000864	NMN_transporter	221	KVP40.0215	Vibrio phage KVP40	GCA_000843785.1
QIW90600.1	000864	NMN_transporter	221	GCAPEGMB_00253	Vibrio phage V07	GCA_012361095.1
QIW91199.1	000864	NMN_transporter	221	COHAPHLL_00363	Vibrio phage V09	GCA_012361135.1
QHJ74396.1	000864	NMN_transporter	221	VH12019_00069	Vibrio phage VH1_2019	GCA_009931825.1
AGB06902.1	000864	NMN_transporter	224	CF80_gp115	Vibrio phage VH7D	GCA_000914495.1
QBX06244.1	000864	NMN_transporter	224	ValB1HC_291	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60870.1	000864	NMN_transporter	224	AVU32_gp029	Vibrio phage ValKK3	GCA_001501635.1
AGN30277.1	000864	NMN_transporter	227	VPFG_00278	Vibrio phage nt-1	GCA_000910195.2
ALP47056.1	000864	NMN_transporter	224	phiGrn1_0339	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47436.1	000864	NMN_transporter	224	phiST2_0094	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54870.1	000864	NMN_transporter	224	vBValMR10Z_330	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37445.1	000864	NMN_transporter	221	pp2_212	Vibriophage phi-pp2	GCA_002630725.1
SOK59171.1	000864	NMN_transporter	267	g363	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58638.1	000864	NMN_transporter	267	g361	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000042	000864	NMN_transporter	221	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000033	000864	NMN_transporter	221	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGH56911.1	000865	Cluster223_1clades	99	CPXG_00108	Cyanophage P-RSM6	GCA_000906155.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AJK27453.1	000865	Cluster223_1clades	99	PTIM40_26	Cyanophage P-TIM40	GCA_001470935.1
AOO14325.1	000865	Cluster223_1clades	104	Sn110110_131	Cyanophage S-RIM14	GCA_002599065.1
AOO14974.1	000865	Cluster223_1clades	104	W1230910_128	Cyanophage S-RIM14	GCA_002599125.1
AMO43031.1	000865	Cluster223_1clades	105	R1080702_016	Cyanophage S-RIM32	GCA_001754165.1
AMO43262.1	000865	Cluster223_1clades	77	W270710_017	Cyanophage S-RIM44	GCA_002599145.1
AOO11499.1	000865	Cluster223_1clades	77	ES420910_017	Cyanophage S-RIM44	GCA_002599165.1
AOO11734.1	000865	Cluster223_1clades	77	Np050604_017	Cyanophage S-RIM44	GCA_002599185.1
AOO11964.1	000865	Cluster223_1clades	77	Np200711_017	Cyanophage S-RIM44	GCA_002599205.1
AOO12200.1	000865	Cluster223_1clades	77	Np420711_017	Cyanophage S-RIM44	GCA_002599225.1
AOO12435.1	000865	Cluster223_1clades	77	Sn080709_017	Cyanophage S-RIM44	GCA_002599245.1
AOO12665.1	000865	Cluster223_1clades	77	Sn130910_017	Cyanophage S-RIM44	GCA_002599265.1
AOO12900.1	000865	Cluster223_1clades	77	W2100709_017	Cyanophage S-RIM44	GCA_002599285.1
AGH07515.1	000865	Cluster223_1clades	99	CYVG_00071	Cyanophage S-SSM6a	GCA_002710385.1
AGG54476.1	000865	Cluster223_1clades	104	CYWG_00192	Cyanophage S-SSM6b	GCA_002710425.1
AGH26230.1	000865	Cluster223_1clades	99	CPMG_00129	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44430.1	000865	Cluster223_1clades	99	PSSM2_052	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12221.1	000865	Cluster223_1clades	99	PRTG_00063	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99120.1	000865	Cluster223_1clades	104	Syn1_018	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30662.1	000865	Cluster223_1clades	104	Syn7803US37_185	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54971.1	000865	Cluster223_1clades	103	b23_0365	Synechococcus phage B23	GCA_009745195.1
QGT54606.1	000865	Cluster223_1clades	103	b3_0371	Synechococcus phage B3	GCA_009745215.1
ASR76307.1	000865	Cluster223_1clades	76	PBI_BELLAMY_271	Synechococcus phage Bellamy	GCA_002627525.1
QCW22937.1	000865	Cluster223_1clades	104	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50622.1	000865	Cluster223_1clades	104	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59476.1	000865	Cluster223_1clades	77	S330809_015	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59238.1	000865	Cluster223_1clades	80	C440309_015	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59714.1	000865	Cluster223_1clades	80	N231010_015	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70564.1	000865	Cluster223_1clades	87	HOU04_gp165	Synechococcus phage S-T4	GCA_003443335.1
QJT70134.1	000865	Cluster223_1clades	103	SynMITS9220M01_121	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56882.1	000866	DUF3110	87	CPXG_00079	Cyanophage P-RSM6	GCA_000906155.1
AJK27574.1	000866	DUF3110	88	PTIM40_147	Cyanophage P-TIM40	GCA_001470935.1
AOO14322.1	000866	DUF3110	83	Sn110110_128	Cyanophage S-RIM14	GCA_002599065.1
AOO14971.1	000866	DUF3110	83	W1230910_125	Cyanophage S-RIM14	GCA_002599125.1
AMO43153.1	000866	DUF3110	90	R1080702_144	Cyanophage S-RIM32	GCA_001754165.1
AMO43377.1	000866	DUF3110	90	W270710_133	Cyanophage S-RIM44	GCA_002599145.1
AOO11621.1	000866	DUF3110	90	ES420910_140	Cyanophage S-RIM44	GCA_002599165.1
AOO11849.1	000866	DUF3110	90	Np050604_133	Cyanophage S-RIM44	GCA_002599185.1
AOO12086.1	000866	DUF3110	90	Np200711_140	Cyanophage S-RIM44	GCA_002599205.1
AOO12322.1	000866	DUF3110	90	Np420711_140	Cyanophage S-RIM44	GCA_002599225.1
AOO12550.1	000866	DUF3110	90	Sn080709_133	Cyanophage S-RIM44	GCA_002599245.1
AOO12787.1	000866	DUF3110	90	Sn130910_140	Cyanophage S-RIM44	GCA_002599265.1
AOO13016.1	000866	DUF3110	90	W2100709_134	Cyanophage S-RIM44	GCA_002599285.1
AGH07472.1	000866	DUF3110	95	CYVG_00028	Cyanophage S-SSM6a	GCA_002710385.1
AGG54481.1	000866	DUF3110	85	CYWG_00197	Cyanophage S-SSM6b	GCA_002710425.1
AGH26308.1	000866	DUF3110	84	CPMG_00209	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44524.1	000866	DUF3110	92	PSSM2_146	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12443.1	000866	DUF3110	92	PRTG_00295	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93456.1	000866	DUF3110	92	AVU42_gp118	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99235.1	000866	DUF3110	90	Syn1_134	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30630.1	000866	DUF3110	97	Syn7803US37_153	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54905.1	000866	DUF3110	93	b23_0292	Synechococcus phage B23	GCA_009745195.1
QGT54540.1	000866	DUF3110	93	b3_0299	Synechococcus phage B3	GCA_009745215.1
ASR76188.1	000866	DUF3110	90	PBI_BELLAMY_143	Synechococcus phage Bellamy	GCA_002627525.1
QCW22899.1	000866	DUF3110	93	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59601.1	000866	DUF3110	88	S330809_140	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59363.1	000866	DUF3110	88	C440309_140	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59839.1	000866	DUF3110	88	N231010_140	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70566.1	000866	DUF3110	86	HOU04_gp167	Synechococcus phage S-T4	GCA_003443335.1
QJT70131.1	000866	DUF3110	92	SynMITS9220M01_118	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFC21480.1	000867	Cluster225_1clades	173	GAP32_032	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14089.1	000867	Cluster225_1clades	127	PBI_121Q_199	Escherichia phage 121Q	GCA_000926855.1
AIT14091.1	000867	Cluster225_1clades	495	PBI_121Q_201	Escherichia phage 121Q	GCA_000926855.1
QAY00829.1	000867	Cluster225_1clades	503	Ecwhy1_557	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00833.1	000867	Cluster225_1clades	127	Ecwhy1_561	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35005.1	000867	Cluster225_1clades	127	ACQ29_gp325	Escherichia phage PBECO4	GCA_001041035.1
AGC35003.1	000867	Cluster225_1clades	495	ACQ29_gp323	Escherichia phage PBECO4	GCA_001041035.1
BBM61772.1	000867	Cluster225_1clades	127	EO157G_1830	Escherichia phage SP27	GCA_008033345.1
BBM61773.1	000867	Cluster225_1clades	417	EO157G_1840	Escherichia phage SP27	GCA_008033345.1
AXC36584.1	000867	Cluster225_1clades	127	-	Escherichia phage UB	GCA_003341455.1
AXC36581.1	000867	Cluster225_1clades	515	-	Escherichia phage UB	GCA_003341455.1
QBO61608.1	000867	Cluster225_1clades	506	G17_00112	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61610.1	000867	Cluster225_1clades	127	G17_00114	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13666.1	000867	Cluster225_1clades	417	vBEcoMphAPEC6_gp035c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13668.1	000867	Cluster225_1clades	127	vBEcoMphAPEC6_gp037c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80083.1	000867	Cluster225_1clades	127	PSLUR01_00106	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80085.1	000867	Cluster225_1clades	509	PSLUR01_00108	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44548.1	000867	Cluster225_1clades	565	RaK2_00275	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44154.1	000867	Cluster225_1clades	172	CBB_38	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43603.1	000867	Cluster225_1clades	172	CBB_591	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18711.1	000867	Cluster225_1clades	177	7t3_0190	Salmonella phage 7t3	GCA_006083215.1
QCW18605.1	000867	Cluster225_1clades	126	7t3_084	Salmonella phage 7t3	GCA_006083215.1
AZU97984.1	000867	Cluster225_1clades	177	CPT_Munch_040	Salmonella phage Munch	GCA_004015485.1
AZU98430.1	000867	Cluster225_1clades	126	CPT_Munch_498	Salmonella phage Munch	GCA_004015485.1
QIG62995.1	000867	Cluster225_1clades	177	SEPL_382	Salmonella phage SE_PL	GCA_011067555.1
QIG63083.1	000867	Cluster225_1clades	126	SEPL_470	Salmonella phage SE_PL	GCA_011067555.1
AQW88552.1	000867	Cluster225_1clades	155	BF_0027	Serratia phage BF	GCA_002619745.1
SOK58825.1	000867	Cluster225_1clades	245	g017	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58292.1	000867	Cluster225_1clades	153	g015	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56846.1	000868	Cluster228_1clades	392	CPXG_00043	Cyanophage P-RSM6	GCA_000906155.1
AJK27604.1	000868	Cluster228_1clades	396	PTIM40_182	Cyanophage P-TIM40	GCA_001470935.1
AOO14369.1	000868	Cluster228_1clades	293	Sn110110_175	Cyanophage S-RIM14	GCA_002599065.1
AOO15017.1	000868	Cluster228_1clades	293	W1230910_171	Cyanophage S-RIM14	GCA_002599125.1
AMO43177.1	000868	Cluster228_1clades	399	R1080702_168	Cyanophage S-RIM32	GCA_001754165.1
AMO43402.1	000868	Cluster228_1clades	398	W270710_158	Cyanophage S-RIM44	GCA_002599145.1
AOO11646.1	000868	Cluster228_1clades	399	ES420910_165	Cyanophage S-RIM44	GCA_002599165.1
AOO11874.1	000868	Cluster228_1clades	398	Np050604_158	Cyanophage S-RIM44	GCA_002599185.1
AOO12112.1	000868	Cluster228_1clades	399	Np200711_166	Cyanophage S-RIM44	GCA_002599205.1
AOO12347.1	000868	Cluster228_1clades	399	Np420711_165	Cyanophage S-RIM44	GCA_002599225.1
AOO12575.1	000868	Cluster228_1clades	398	Sn080709_158	Cyanophage S-RIM44	GCA_002599245.1
AOO12812.1	000868	Cluster228_1clades	399	Sn130910_165	Cyanophage S-RIM44	GCA_002599265.1
AOO13041.1	000868	Cluster228_1clades	398	W2100709_159	Cyanophage S-RIM44	GCA_002599285.1
AGH07673.1	000868	Cluster228_1clades	321	CYVG_00230	Cyanophage S-SSM6a	GCA_002710385.1
AGG54433.1	000868	Cluster228_1clades	307	CYWG_00149	Cyanophage S-SSM6b	GCA_002710425.1
AGH26280.1	000868	Cluster228_1clades	401	CPMG_00180	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44453.1	000868	Cluster228_1clades	270	PSSM2_075	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12201.1	000868	Cluster228_1clades	296	PRTG_00043	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93422.1	000868	Cluster228_1clades	262	AVU42_gp052	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99261.1	000868	Cluster228_1clades	398	Syn1_160	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30549.1	000868	Cluster228_1clades	301	Syn7803US37_72	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76134.1	000868	Cluster228_1clades	303	PBI_BELLAMY_89	Synechococcus phage Bellamy	GCA_002627525.1
QCW23011.1	000868	Cluster228_1clades	293	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59627.1	000868	Cluster228_1clades	401	S330809_166	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59389.1	000868	Cluster228_1clades	385	C440309_166	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59865.1	000868	Cluster228_1clades	385	N231010_166	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70415.1	000868	Cluster228_1clades	293	HOU04_gp016	Synechococcus phage S-T4	GCA_003443335.1
AXQ70617.1	000868	Cluster228_1clades	293	HOU04_gp016	Synechococcus phage S-T4	GCA_003443335.1
QJT70072.1	000868	Cluster228_1clades	298	SynMITS9220M01_059	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QGY75124.1	000869	TM+TM	213	CF8_0127	Aeromonas phage CF8	GCA_006384595.2
QNH80843.1	000869	TM+TM	196	D6_0112	Aeromonas phage D6	GCA_007051205.2
QDH47122.1	000869	TM+TM	236	LAh10_44	Aeromonas phage LAh10	GCA_006863975.1
QDJ96887.1	000869	TM+TM	219	PS1_0128	Aeromonas phage PS1	GCA_007051165.2
QFR59519.1	000869	TM+TM	218	PS2_0128	Aeromonas phage PS2	GCA_009388305.2
QBZ70658.1	000869	TM+TM	216	pETSU_077	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60163.1	000869	TM+TM	169	Ea357_013	Erwinia phage Ea35-70	GCA_000914635.1
QBP07121.1	000869	TM+TM	169	REBECCA_13	Erwinia phage Rebecca	GCA_004521635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG85801.1	000869	TM+TM	169	BOSOLAPHORUS_13	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52111.2	000869	TM+TM	169	DM_13	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86121.1	000869	TM+TM	169	DESERTFOX_13	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03821.1	000869	TM+TM	131	JOAD_94	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86441.1	000869	TM+TM	169	MADMEL_13	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86762.1	000869	TM+TM	169	MORTIMER_13	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51794.1	000869	TM+TM	169	RAY_13	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03576.1	000869	TM+TM	131	RISINGSUN_94	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51476.1	000869	TM+TM	169	SIMMY50_14	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64823.1	000869	TM+TM	169	SPECIALG_13	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGH71974.1	000869	TM+TM	216	N1M2_111	Klebsiella phage N1M2	GCA_010092605.1
QGZ14446.1	000869	TM+TM	118	HWC77_gp083	Photobacterium phage PDCC-1	GCA_009800445.1
QMP24005.1	000869	TM+TM	119	-	Proteus phage 10	GCA_014071245.1
CAG27203.1	000869	TM+TM	123	PPEV_gp109	Pseudomonas phage EL	GCA_000866825.1
AEV89575.1	000869	TM+TM	216	OBP_138	Pseudomonas phage OBP	GCA_000896635.1
QKE54327.1	000869	TM+TM	133	ACSA002_0130	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QAU04288.1	000869	TM+TM	117	HWC03_gp133	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23289.1	000869	TM+TM	117	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81080.1	000869	TM+TM	117	Aphrodite1_0056	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47439.1	000869	TM+TM	117	HWC35_gp045	Vibrio phage USC-1	GCA_006864065.1
BAW98260.1	000869	TM+TM	122	FDH33_gp051	Vibrio phage pTD1	GCA_002618825.1
AGH56828.1	000870	Transaldolase	219	CPXG_00025	Cyanophage P-RSM6	GCA_000906155.1
AJK27645.1	000870	Transaldolase	219	PTIM40_199	Cyanophage P-TIM40	GCA_001470935.1
AOO14218.1	000870	Transaldolase	220	Sn110110_024	Cyanophage S-RIM14	GCA_002599065.1
AOO14870.1	000870	Transaldolase	220	W1230910_024	Cyanophage S-RIM14	GCA_002599125.1
AMO43209.1	000870	Transaldolase	215	R1080702_203	Cyanophage S-RIM32	GCA_001754165.1
AMO43438.1	000870	Transaldolase	215	W270710_198	Cyanophage S-RIM44	GCA_002599145.1
AOO11681.1	000870	Transaldolase	215	ES420910_203	Cyanophage S-RIM44	GCA_002599165.1
AOO11910.1	000870	Transaldolase	215	Np050604_198	Cyanophage S-RIM44	GCA_002599185.1
AOO12147.1	000870	Transaldolase	215	Np200711_204	Cyanophage S-RIM44	GCA_002599205.1
AOO12382.1	000870	Transaldolase	215	Np420711_203	Cyanophage S-RIM44	GCA_002599225.1
AOO12611.1	000870	Transaldolase	215	Sn080709_198	Cyanophage S-RIM44	GCA_002599245.1
AOO12847.1	000870	Transaldolase	215	Sn130910_203	Cyanophage S-RIM44	GCA_002599265.1
AOO13077.1	000870	Transaldolase	215	W2100709_199	Cyanophage S-RIM44	GCA_002599285.1
AGH07611.1	000870	Transaldolase	217	CYVG_00168	Cyanophage S-SSM6a	GCA_002710385.1
AGG54416.1	000870	Transaldolase	215	CYWG_00132	Cyanophage S-SSM6b	GCA_002710425.1
AGH26225.1	000870	Transaldolase	224	CPMG_00124	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44621.1	000870	Transaldolase	215	PSSM2_244	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12350.1	000870	Transaldolase	215	PRTG_00197	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93508.1	000870	Transaldolase	227	AVU42_gp172	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99297.1	000870	Transaldolase	215	Syn1_200	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30735.1	000870	Transaldolase	216	Syn7803US37_258	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76298.1	000870	Transaldolase	214	PBI_BELLAMY_262	Synechococcus phage Bellamy	GCA_002627525.1
QCW22963.1	000870	Transaldolase	216	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50567.1	000870	Transaldolase	216	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59644.1	000870	Transaldolase	215	S330809_183	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59406.1	000870	Transaldolase	215	C440309_183	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59882.1	000870	Transaldolase	215	N231010_183	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70478.1	000870	Transaldolase	216	HOU04_gp079	Synechococcus phage S-T4	GCA_003443335.1
QJT70245.1	000870	Transaldolase	214	SynMITS9220M01_239	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13544.1	000871	Cluster233_1clades	60	Ccr10_gp016	Caulobacter phage Ccr10	GCA_002619445.1
ARB13869.1	000871	Cluster233_1clades	60	Ccr10_gp339	Caulobacter phage Ccr10	GCA_002619445.1
ARB13890.1	000871	Cluster233_1clades	60	Ccr2_gp015	Caulobacter phage Ccr2	GCA_002619465.1
ARB14213.1	000871	Cluster233_1clades	60	Ccr2_gp337	Caulobacter phage Ccr2	GCA_002619465.1
ARB14573.1	000871	Cluster233_1clades	60	Ccr29_gp016	Caulobacter phage Ccr29	GCA_002619485.1
ARB14579.1	000871	Cluster233_1clades	60	Ccr29_gp022	Caulobacter phage Ccr29	GCA_002619485.1
ARB14908.1	000871	Cluster233_1clades	60	Ccr29_gp352	Caulobacter phage Ccr29	GCA_002619485.1
ARB14914.1	000871	Cluster233_1clades	60	Ccr29_gp358	Caulobacter phage Ccr29	GCA_002619485.1
ARB14934.1	000871	Cluster233_1clades	60	Ccr32_gp015	Caulobacter phage Ccr32	GCA_002619505.1
ARB15245.1	000871	Cluster233_1clades	60	Ccr32_gp327	Caulobacter phage Ccr32	GCA_002619505.1
ARB15265.1	000871	Cluster233_1clades	60	Ccr34_gp016	Caulobacter phage Ccr34	GCA_002619525.1
ARB15579.1	000871	Cluster233_1clades	60	Ccr34_gp337	Caulobacter phage Ccr34	GCA_002619525.1
ARB14233.1	000871	Cluster233_1clades	58	Ccr5_gp015	Caulobacter phage Ccr5	GCA_002619545.1
ARB14553.1	000871	Cluster233_1clades	58	Ccr5_gp333	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68216.1	000871	Cluster233_1clades	107	CcrBL10_gp012	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68534.1	000871	Cluster233_1clades	107	CcrBL10_gp330	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87887.1	000871	Cluster233_1clades	189	CcrColossus_gp017	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68558.1	000871	Cluster233_1clades	190	CcrPW_gp019	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69007.1	000871	Cluster233_1clades	190	CcrPW_gp468	Caulobacter phage CcrPW	GCA_003443275.1
AFU87531.1	000871	Cluster233_1clades	60	CcrKarma_gp014	Caulobacter virus Karma	GCA_000901575.1
AFU87864.1	000871	Cluster233_1clades	60	CcrKarma_gp347	Caulobacter virus Karma	GCA_000901575.1
AFU87184.1	000871	Cluster233_1clades	60	CcrMagneto_gp014	Caulobacter virus Magneto	GCA_000903095.1
AFU87512.1	000871	Cluster233_1clades	60	CcrMagneto_gp342	Caulobacter virus Magneto	GCA_000903095.1
AFU86496.1	000871	Cluster233_1clades	107	CcrRogue_gp014	Caulobacter virus Rogue	GCA_000900555.1
AFU86827.1	000871	Cluster233_1clades	107	CcrRogue_gp345	Caulobacter virus Rogue	GCA_000900555.1
AFU88331.1	000871	Cluster233_1clades	104	CcrSwift_gp013	Caulobacter virus Swift	GCA_000899655.1
AFU88656.1	000871	Cluster233_1clades	104	CcrSwift_gp338	Caulobacter virus Swift	GCA_000899655.1
AFU86847.1	000871	Cluster233_1clades	60	CbK_gp015	Caulobacter virus phiCbK	GCA_000900535.1
AFU87165.1	000871	Cluster233_1clades	60	CbK_gp333	Caulobacter virus phiCbK	GCA_000900535.1
APU01494.1	000872	Cluster234_1clades	170	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28803.1	000872	Cluster234_1clades	170	AP1_0096	Aeromonas phage AP1	GCA_014183365.1
ATI17403.1	000872	Cluster234_1clades	170	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00192.1	000872	Cluster234_1clades	170	HWB28_gp360	Aeromonas phage AS-zj	GCA_002627665.1
AUE22731.1	000872	Cluster234_1clades	184	Ah1_00213	Aeromonas phage Ah1	GCA_002957415.1
QAX98452.1	000872	Cluster234_1clades	183	ASfcp2_110	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97843.1	000872	Cluster234_1clades	170	ASswx1_200	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01309.1	000872	Cluster234_1clades	170	ASwh1_246	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39556.1	000872	Cluster234_1clades	170	CC2_335	Aeromonas phage CC2	GCA_000903495.1
ADQ52910.1	000872	Cluster234_1clades	183	PX29p191	Aeromonas phage PX29	GCA_000920195.1
ADM80177.1	000872	Cluster234_1clades	182	phiAS5_ORF0334	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53115.1	000872	Cluster234_1clades	170	65p107	Aeromonas virus 65	GCA_000893255.1
AAQ17862.1	000872	Cluster234_1clades	183	5.1	Aeromonas virus Aeh1	GCA_000843245.1
ARM70978.1	000872	Cluster234_1clades	157	phiC120_c273	Escherichia phage phiC120	GCA_002621185.1
ARM70712.1	000872	Cluster234_1clades	157	phiC120_c5	Escherichia phage phiC120	GCA_002621185.1
AAQ64405.1	000872	Cluster234_1clades	161	KVP40.0336	Vibrio phage KVP40	GCA_000843785.1
QIW90350.1	000872	Cluster234_1clades	161	GCAPEGMB_00003	Vibrio phage V07	GCA_012361095.1
QIW91079.1	000872	Cluster234_1clades	161	COHAPHLL_00216	Vibrio phage V09	GCA_012361135.1
QHJ74518.1	000872	Cluster234_1clades	161	VH12019_00218	Vibrio phage VH1_2019	GCA_009931825.1
AGB06979.1	000872	Cluster234_1clades	161	CF80_gp192	Vibrio phage VH7D	GCA_000914495.1
QBX06137.1	000872	Cluster234_1clades	136	ValB1HC_183	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61149.1	000872	Cluster234_1clades	161	AVU32_gp308	Vibrio phage ValKK3	GCA_001501635.1
AGN30009.2	000872	Cluster234_1clades	161	VPFG_00001	Vibrio phage nt-1	GCA_000910195.2
AGN30387.1	000872	Cluster234_1clades	161	VPFG_00390	Vibrio phage nt-1	GCA_000910195.2
ALP47146.1	000872	Cluster234_1clades	136	phiGrn1_0070	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47533.1	000872	Cluster234_1clades	136	phiST2_0202	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54762.1	000872	Cluster234_1clades	161	vBValMR10Z_222	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07246.1	000872	Cluster234_1clades	184	VmeM32_00260	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37568.1	000872	Cluster234_1clades	161	pp2_336	Vibriophage phi-pp2	GCA_002630725.1
AGH56855.1	000873	Sm_like domain	126	CPXG_00052	Cyanophage P-RSM6	GCA_000906155.1
AJK27600.1	000873	Sm_like domain	131	PTIM40_173	Cyanophage P-TIM40	GCA_001470935.1
AOO14356.1	000873	Sm_like domain	125	Sn110110_162	Cyanophage S-RIM14	GCA_002599065.1
AOO15005.1	000873	Sm_like domain	125	W1230910_159	Cyanophage S-RIM14	GCA_002599125.1
AMO43168.1	000873	Sm_like domain	152	R1080702_159	Cyanophage S-RIM32	GCA_001754165.1
AMO43394.1	000873	Sm_like domain	168	W270710_150	Cyanophage S-RIM44	GCA_002599145.1
AOO11638.1	000873	Sm_like domain	152	ES420910_157	Cyanophage S-RIM44	GCA_002599165.1
AOO11866.1	000873	Sm_like domain	168	Np050604_150	Cyanophage S-RIM44	GCA_002599185.1
AOO12104.1	000873	Sm_like domain	152	Np200711_158	Cyanophage S-RIM44	GCA_002599205.1
AOO12339.1	000873	Sm_like domain	152	Np420711_157	Cyanophage S-RIM44	GCA_002599225.1
AOO12567.1	000873	Sm_like domain	168	Sn080709_150	Cyanophage S-RIM44	GCA_002599245.1
AOO12804.1	000873	Sm_like domain	152	Sn130910_157	Cyanophage S-RIM44	GCA_002599265.1
AOO13033.1	000873	Sm_like domain	168	W2100709_151	Cyanophage S-RIM44	GCA_002599285.1
AGH07495.1	000873	Sm_like domain	111	CYVG_00051	Cyanophage S-SSM6a	GCA_002710385.1
AGG54452.1	000873	Sm_like domain	133	CYWG_00168	Cyanophage S-SSM6b	GCA_002710425.1
AGH26291.1	000873	Sm_like domain	141	CPMG_00191	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26292.1	000873	Sm_like domain	130	CPMG_00192	Prochlorococcus phage MED4-213	GCA_000904535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAX44558.1	000873	Sm_like domain	113	PSSM2_180	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12414.1	000873	Sm_like domain	113	PRTG_00262	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93481.1	000873	Sm_like domain	128	AVU42_gp145	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99253.1	000873	Sm_like domain	168	Syn1_152	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30645.1	000873	Sm_like domain	128	Syn7803US37_168	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76204.1	000873	Sm_like domain	124	PBI_BELLAMY_159	Synechococcus phage Bellamy	GCA_002627525.1
QCW23081.1	000873	Sm_like domain	109	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59618.1	000873	Sm_like domain	123	S330809_157	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59380.1	000873	Sm_like domain	123	C440309_157	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59856.1	000873	Sm_like domain	123	N231010_157	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70547.1	000873	Sm_like domain	122	HOU04_gp148	Synechococcus phage S-T4	GCA_003443335.1
QJT170154.1	000873	Sm_like domain	123	SynMITS9220M01_141	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56886.1	000874	Sm_like	152	CPXG_00083	Cyanophage P-RSM6	GCA_000906155.1
AJK27571.1	000874	Sm_like	140	PTIM40_144	Cyanophage P-TIM40	GCA_001470935.1
AOO14319.1	000874	Sm_like	132	Sn110110_125	Cyanophage S-RIM14	GCA_002599065.1
AOO14968.1	000874	Sm_like	132	W1230910_122	Cyanophage S-RIM14	GCA_002599125.1
AMO43149.1	000874	Sm_like	131	R1080702_140	Cyanophage S-RIM32	GCA_001754165.1
AMO43373.1	000874	Sm_like	131	W270710_129	Cyanophage S-RIM44	GCA_002599145.1
AOO11617.1	000874	Sm_like	131	ES420910_136	Cyanophage S-RIM44	GCA_002599165.1
AOO11845.1	000874	Sm_like	131	Np050604_129	Cyanophage S-RIM44	GCA_002599185.1
AOO12082.1	000874	Sm_like	131	Np200711_136	Cyanophage S-RIM44	GCA_002599205.1
AOO12318.1	000874	Sm_like	131	Np420711_136	Cyanophage S-RIM44	GCA_002599225.1
AOO12546.1	000874	Sm_like	131	Sn080709_129	Cyanophage S-RIM44	GCA_002599245.1
AOO12783.1	000874	Sm_like	131	Sn130910_136	Cyanophage S-RIM44	GCA_002599265.1
AOO13012.1	000874	Sm_like	131	W2100709_130	Cyanophage S-RIM44	GCA_002599285.1
AGH07467.1	000874	Sm_like	135	CYVG_00023	Cyanophage S-SSM6a	GCA_002710385.1
AGG54484.1	000874	Sm_like	147	CYWG_00200	Cyanophage S-SSM6b	GCA_002710425.1
AGH26312.1	000874	Sm_like	125	CPMG_00213	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44521.1	000874	Sm_like	137	PSSM2_143	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12446.1	000874	Sm_like	137	PRTG_00298	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93453.1	000874	Sm_like	130	AVU42_gp115	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99231.1	000874	Sm_like	131	Syn1_130	Prochlorococcus phage Syn1	GCA_000892495.1
QGT54901.1	000874	Sm_like	139	b23_0288	Synechococcus phage B23	GCA_009745195.1
QGT54536.1	000874	Sm_like	139	b3_0295	Synechococcus phage B3	GCA_009745215.1
ASR76185.1	000874	Sm_like	130	PBI_BELLAMY_140	Synechococcus phage Bellamy	GCA_002627525.1
QCW22895.1	000874	Sm_like	128	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50661.1	000874	Sm_like	128	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59598.1	000874	Sm_like	132	S330809_137	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59360.1	000874	Sm_like	132	C440309_137	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59836.1	000874	Sm_like	132	N231010_137	Synechococcus phage S-CAM4	GCA_002922155.1
QJT170126.1	000874	Sm_like	131	SynMITS9220M01_113	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH57018.1	000875	DUF1825	124	CPXG_00215	Cyanophage P-RSM6	GCA_000906155.1
AJK27431.1	000875	DUF1825	117	PTIM40_4	Cyanophage P-TIM40	GCA_001470935.1
AOO14196.1	000875	DUF1825	111	Sn110110_002	Cyanophage S-RIM14	GCA_002599065.1
AOO14848.1	000875	DUF1825	111	W1230910_002	Cyanophage S-RIM14	GCA_002599125.1
AMO43245.1	000875	DUF1825	114	R1080702_240	Cyanophage S-RIM32	GCA_001754165.1
AMO43246.1	000875	DUF1825	106	W270710_001	Cyanophage S-RIM44	GCA_002599145.1
AOO11483.1	000875	DUF1825	106	ES420910_001	Cyanophage S-RIM44	GCA_002599165.1
AOO11718.1	000875	DUF1825	106	Np050604_001	Cyanophage S-RIM44	GCA_002599185.1
AOO11948.1	000875	DUF1825	106	Np200711_001	Cyanophage S-RIM44	GCA_002599205.1
AOO12184.1	000875	DUF1825	106	Np420711_001	Cyanophage S-RIM44	GCA_002599225.1
AOO12419.1	000875	DUF1825	106	Sn080709_001	Cyanophage S-RIM44	GCA_002599245.1
AOO12649.1	000875	DUF1825	106	Sn130910_001	Cyanophage S-RIM44	GCA_002599265.1
AOO12884.1	000875	DUF1825	106	W2100709_001	Cyanophage S-RIM44	GCA_002599285.1
AGH07629.1	000875	DUF1825	113	CYVG_00186	Cyanophage S-SSM6a	GCA_002710385.1
AGG54369.1	000875	DUF1825	107	CYWG_00085	Cyanophage S-SSM6b	GCA_002710425.1
AGH26212.1	000875	DUF1825	106	CPMG_00111	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44385.1	000875	DUF1825	110	PSSM2_007	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12263.1	000875	DUF1825	110	PRTG_00108	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93389.1	000875	DUF1825	110	AVU42_gp003	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99103.1	000875	DUF1825	106	Syn1_001	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30770.1	000875	DUF1825	122	Syn7803US37_293	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76050.1	000875	DUF1825	114	PBI_BELLAMY_3	Synechococcus phage Bellamy	GCA_002627525.1
QCW23068.1	000875	DUF1825	99	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50684.1	000875	DUF1825	111	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59699.1	000875	DUF1825	100	S330809_238	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59461.1	000875	DUF1825	100	C440309_238	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59936.1	000875	DUF1825	100	N231010_237	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70450.1	000875	DUF1825	106	HOU04_gp051	Synechococcus phage S-T4	GCA_003443335.1
QJT170018.1	000875	DUF1825	112	SynMITS9220M01_002	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01500.1	000876	T4_tail_cap	356	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28990.1	000876	T4_tail_cap	352	AP1_0283	Aeromonas phage AP1	GCA_014183365.1
ATI17397.1	000876	T4_tail_cap	352	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00198.1	000876	T4_tail_cap	352	HWB28_gp354	Aeromonas phage AS-zj	GCA_002627665.1
AUE22726.1	000876	T4_tail_cap	262	Ah1_00208	Aeromonas phage Ah1	GCA_002957415.1
QAX98449.1	000876	T4_tail_cap	357	ASfcp2_106	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97838.1	000876	T4_tail_cap	352	ASswx1_194	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01314.1	000876	T4_tail_cap	355	ASwh1_252	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39559.1	000876	T4_tail_cap	352	CC2_341	Aeromonas phage CC2	GCA_000903495.1
ADQ52906.1	000876	T4_tail_cap	357	PX29p187	Aeromonas phage PX29	GCA_000920195.1
ADM80173.1	000876	T4_tail_cap	355	phiAS5_ORF0330	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53121.1	000876	T4_tail_cap	356	65p113	Aeromonas virus 65	GCA_000893255.1
AAQ17858.1	000876	T4_tail_cap	358	48	Aeromonas virus Aeh1	GCA_000843245.1
AIA64959.1	000876	T4_tail_cap	343	S13_160	Cronobacter phage S13	GCA_001503575.1
QHJ78975.1	000876	T4_tail_cap	334	-	Myoviridae sp.	GCA_012593985.1
AAQ64401.1	000876	T4_tail_cap	379	KVP40.0332	Vibrio phage KVP40	GCA_000843785.1
QIW90714.1	000876	T4_tail_cap	379	GCAPEGMB_00395	Vibrio phage V07	GCA_012361095.1
QIW91083.1	000876	T4_tail_cap	379	COHAPHLL_00220	Vibrio phage V09	GCA_012361135.1
QHJ74514.1	000876	T4_tail_cap	379	VH12019_00214	Vibrio phage VH1_2019	GCA_009931825.1
AGB06975.1	000876	T4_tail_cap	378	CF80_gp188	Vibrio phage VH7D	GCA_000914495.1
QBX06141.1	000876	T4_tail_cap	378	ValB1HC_187	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61153.1	000876	T4_tail_cap	378	AVU32_gp312	Vibrio phage ValKK3	GCA_001501635.1
AGN30383.1	000876	T4_tail_cap	385	VPFG_00386	Vibrio phage nt-1	GCA_000910195.2
ALP46997.1	000876	T4_tail_cap	378	phiGrn1_0067	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47378.1	000876	T4_tail_cap	378	phiST2_0198	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54766.1	000876	T4_tail_cap	378	vBValMR10Z_226	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07103.1	000876	T4_tail_cap	332	VmeM32_00116	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37564.1	000876	T4_tail_cap	379	pp2_332	Vibriophage phi-pp2	GCA_002630725.1
AGH56860.1	000877	Cluster242_1clades	161	CPXG_00057	Cyanophage P-RSM6	GCA_000906155.1
AJK27596.1	000877	Cluster242_1clades	167	PTIM40_169	Cyanophage P-TIM40	GCA_001470935.1
AOO14352.1	000877	Cluster242_1clades	164	Sn110110_158	Cyanophage S-RIM14	GCA_002599065.1
AOO15001.1	000877	Cluster242_1clades	164	W1230910_155	Cyanophage S-RIM14	GCA_002599125.1
AMO43196.1	000877	Cluster242_1clades	140	R1080702_187	Cyanophage S-RIM32	GCA_001754165.1
AMO43423.1	000877	Cluster242_1clades	164	W270710_179	Cyanophage S-RIM44	GCA_002599145.1
AOO11667.1	000877	Cluster242_1clades	164	ES420910_186	Cyanophage S-RIM44	GCA_002599165.1
AOO11895.1	000877	Cluster242_1clades	164	Np050604_179	Cyanophage S-RIM44	GCA_002599185.1
AOO12133.1	000877	Cluster242_1clades	164	Np200711_187	Cyanophage S-RIM44	GCA_002599205.1
AOO12368.1	000877	Cluster242_1clades	164	Np420711_186	Cyanophage S-RIM44	GCA_002599225.1
AOO12596.1	000877	Cluster242_1clades	164	Sn080709_179	Cyanophage S-RIM44	GCA_002599245.1
AOO12833.1	000877	Cluster242_1clades	164	Sn130910_186	Cyanophage S-RIM44	GCA_002599265.1
AOO13062.1	000877	Cluster242_1clades	164	W2100709_180	Cyanophage S-RIM44	GCA_002599285.1
AGH07541.1	000877	Cluster242_1clades	161	CYVG_00097	Cyanophage S-SSM6a	GCA_002710385.1
AGG54456.1	000877	Cluster242_1clades	171	CYWG_00172	Cyanophage S-SSM6b	GCA_002710425.1
AGH26246.1	000877	Cluster242_1clades	193	CPMG_00145	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44619.1	000877	Cluster242_1clades	155	PSSM2_242	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12352.1	000877	Cluster242_1clades	155	PRTG_00199	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93555.1	000877	Cluster242_1clades	166	AVU42_gp218	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99282.1	000877	Cluster242_1clades	164	Syn1_181	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76294.1	000877	Cluster242_1clades	164	PBI_BELLAMY_258	Synechococcus phage Bellamy	GCA_002627525.1
QCW23045.1	000877	Cluster242_1clades	165	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50679.1	000877	Cluster242_1clades	165	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59665.1	000877	Cluster242_1clades	164	S330809_204	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59427.1	000877	Cluster242_1clades	164	C440309_204	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59902.1	000877	Cluster242_1clades	164	N231010_203	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70488.1	000877	Cluster242_1clades	150	HOU04_gp089	Synechococcus phage S-T4	GCA_003443335.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QJT70235.1	000877	Cluster242_1clades	167	SynMITS9220M01_229	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27623.1	000878	Cluster243_1clades	93	PTIM40_211	Cyanophage P-TIM40	GCA_001470935.1
AOO14388.1	000878	Cluster243_1clades	80	Sn110110_195	Cyanophage S-RIM14	GCA_002599065.1
AOO15036.1	000878	Cluster243_1clades	80	W1230910_191	Cyanophage S-RIM14	GCA_002599125.1
AMO43212.1	000878	Cluster243_1clades	78	R1080702_206	Cyanophage S-RIM32	GCA_001754165.1
AMO43441.1	000878	Cluster243_1clades	85	W270710_201	Cyanophage S-RIM44	GCA_002599145.1
AOO11684.1	000878	Cluster243_1clades	85	ES420910_206	Cyanophage S-RIM44	GCA_002599165.1
AOO11913.1	000878	Cluster243_1clades	85	Np050604_201	Cyanophage S-RIM44	GCA_002599185.1
AOO12150.1	000878	Cluster243_1clades	85	Np200711_207	Cyanophage S-RIM44	GCA_002599205.1
AOO12385.1	000878	Cluster243_1clades	85	Np420711_206	Cyanophage S-RIM44	GCA_002599225.1
AOO12614.1	000878	Cluster243_1clades	85	Sn080709_201	Cyanophage S-RIM44	GCA_002599245.1
AOO12850.1	000878	Cluster243_1clades	85	Sn130910_206	Cyanophage S-RIM44	GCA_002599265.1
AOO13080.1	000878	Cluster243_1clades	85	W2100709_202	Cyanophage S-RIM44	GCA_002599285.1
AGH07559.1	000878	Cluster243_1clades	81	CYVG_00115	Cyanophage S-SSM6a	GCA_002710385.1
AGG54402.1	000878	Cluster243_1clades	78	CYWG_00118	Cyanophage S-SSM6b	GCA_002710425.1
AGH26255.1	000878	Cluster243_1clades	69	CPMG_00154	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44632.1	000878	Cluster243_1clades	79	PSSM2_255	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12339.1	000878	Cluster243_1clades	79	PRTG_00186	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93510.1	000878	Cluster243_1clades	76	AVU42_gp173	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99300.1	000878	Cluster243_1clades	100	Syn1_203	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30698.1	000878	Cluster243_1clades	78	Syn7803US37_221	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76234.1	000878	Cluster243_1clades	77	PBI_BELLAMY_198	Synechococcus phage Bellamy	GCA_002627525.1
QCW23025.1	000878	Cluster243_1clades	78	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50520.1	000878	Cluster243_1clades	78	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59647.1	000878	Cluster243_1clades	86	S330809_186	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59409.1	000878	Cluster243_1clades	86	C440309_186	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59885.1	000878	Cluster243_1clades	86	N231010_186	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70520.1	000878	Cluster243_1clades	79	HOU04_gp121	Synechococcus phage S-T4	GCA_003443335.1
QJT70191.1	000878	Cluster243_1clades	62	SynMITS9220M01_185	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56863.1	000879	Cluster244_1clades	79	CPXG_00060	Cyanophage P-RSM6	GCA_000906155.1
AJK27590.1	000879	Cluster244_1clades	78	PTIM40_163	Cyanophage P-TIM40	GCA_001470935.1
AOO14302.1	000879	Cluster244_1clades	85	Sn110110_108	Cyanophage S-RIM14	GCA_002599065.1
AOO14951.1	000879	Cluster244_1clades	85	W1230910_105	Cyanophage S-RIM14	GCA_002599125.1
AMO43192.1	000879	Cluster244_1clades	85	R1080702_183	Cyanophage S-RIM32	GCA_001754165.1
AMO43418.1	000879	Cluster244_1clades	79	W270710_174	Cyanophage S-RIM44	GCA_002599145.1
AOO11662.1	000879	Cluster244_1clades	79	ES420910_181	Cyanophage S-RIM44	GCA_002599165.1
AOO11890.1	000879	Cluster244_1clades	79	Np050604_174	Cyanophage S-RIM44	GCA_002599185.1
AOO12128.1	000879	Cluster244_1clades	79	Np200711_182	Cyanophage S-RIM44	GCA_002599205.1
AOO12363.1	000879	Cluster244_1clades	79	Np420711_181	Cyanophage S-RIM44	GCA_002599225.1
AOO12591.1	000879	Cluster244_1clades	79	Sn080709_174	Cyanophage S-RIM44	GCA_002599245.1
AOO12828.1	000879	Cluster244_1clades	79	Sn130910_181	Cyanophage S-RIM44	GCA_002599265.1
AOO13057.1	000879	Cluster244_1clades	79	W2100709_175	Cyanophage S-RIM44	GCA_002599285.1
AGH07533.1	000879	Cluster244_1clades	88	CYVG_00089	Cyanophage S-SSM6a	GCA_002710385.1
AGG54460.1	000879	Cluster244_1clades	75	CYWG_00176	Cyanophage S-SSM6b	GCA_002710425.1
AGH26251.1	000879	Cluster244_1clades	76	CPMG_00150	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44598.1	000879	Cluster244_1clades	88	PSSM2_221	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12372.1	000879	Cluster244_1clades	88	PRTG_00219	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93552.1	000879	Cluster244_1clades	85	AVU42_gp214	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99277.1	000879	Cluster244_1clades	99	Syn1_176	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76275.1	000879	Cluster244_1clades	80	PBI_BELLAMY_239	Synechococcus phage Bellamy	GCA_002627525.1
QCW23040.1	000879	Cluster244_1clades	85	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50727.1	000879	Cluster244_1clades	85	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59659.1	000879	Cluster244_1clades	79	S330809_198	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59421.1	000879	Cluster244_1clades	79	C440309_198	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59896.1	000879	Cluster244_1clades	79	N231010_197	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70492.1	000879	Cluster244_1clades	90	HOU04_gp093	Synechococcus phage S-T4	GCA_003443335.1
QJT70232.1	000879	Cluster244_1clades	79	SynMITS9220M01_226	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AHI60267.1	000880	Cluster247_1clades	179	Ea357_116	Erwinia phage Ea35-70	GCA_000914635.1
QBP07214.1	000880	Cluster247_1clades	242	REBECCA_107	Erwinia phage Rebecca	GCA_004521635.1
QBP07225.1	000880	Cluster247_1clades	179	REBECCA_118	Erwinia phage Rebecca	GCA_004521635.1
AUG85905.1	000880	Cluster247_1clades	179	BOSOLAPHORUS_118	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52220.1	000880	Cluster247_1clades	179	DM_122	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86213.1	000880	Cluster247_1clades	241	DESERTFOX_106	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86224.1	000880	Cluster247_1clades	179	DESERTFOX_117	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86535.1	000880	Cluster247_1clades	241	MADMEL_107	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86546.1	000880	Cluster247_1clades	179	MADMEL_118	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86859.1	000880	Cluster247_1clades	241	MORTIMER_110	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86870.1	000880	Cluster247_1clades	179	MORTIMER_121	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51887.1	000880	Cluster247_1clades	241	RAY_106	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51898.1	000880	Cluster247_1clades	179	RAY_117	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51571.1	000880	Cluster247_1clades	241	SIMMY50_109	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51582.1	000880	Cluster247_1clades	179	SIMMY50_120	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64919.2	000880	Cluster247_1clades	241	SPECIALG_109	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64929.1	000880	Cluster247_1clades	179	SPECIALG_119	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGZ14539.1	000880	Cluster247_1clades	420	HWC77_gp176	Photobacterium phage PDCC-1	GCA_009800445.1
AEV89515.1	000880	Cluster247_1clades	166	OBP_078	Pseudomonas phage OBP	GCA_000896635.1
QKE54427.1	000880	Cluster247_1clades	169	ACSA002_1130	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65569.1	000880	Cluster247_1clades	173	2050HW_00234	Serratia phage 2050HW	GCA_002628125.1
QDB71332.1	000880	Cluster247_1clades	173	CPT_Moabite_302	Serratia phage Moabite	GCA_006384735.1
QAU04195.1	000880	Cluster247_1clades	420	HWC03_gp040	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23165.1	000880	Cluster247_1clades	381	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80972.1	000880	Cluster247_1clades	385	Aphrodite1_0176	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47563.1	000880	Cluster247_1clades	381	HWC35_gp169	Vibrio phage USC-1	GCA_006864065.1
BAW98379.1	000880	Cluster247_1clades	378	FDH33_gp170	Vibrio phage pTD1	GCA_002618825.1
AGH56862.1	000881	Cluster248_1clades	267	CPXG_00059	Cyanophage P-RSM6	GCA_000906155.1
AJK27592.1	000881	Cluster248_1clades	266	PTIM40_165	Cyanophage P-TIM40	GCA_001470935.1
AOO14349.1	000881	Cluster248_1clades	256	Sn110110_155	Cyanophage S-RIM14	GCA_002599065.1
AOO14998.1	000881	Cluster248_1clades	256	W1230910_152	Cyanophage S-RIM14	GCA_002599125.1
AMO43194.1	000881	Cluster248_1clades	262	R1080702_185	Cyanophage S-RIM32	GCA_001754165.1
AMO43420.1	000881	Cluster248_1clades	268	W270710_176	Cyanophage S-RIM44	GCA_002599145.1
AOO11664.1	000881	Cluster248_1clades	270	ES420910_183	Cyanophage S-RIM44	GCA_002599165.1
AOO11892.1	000881	Cluster248_1clades	268	Np050604_176	Cyanophage S-RIM44	GCA_002599185.1
AOO12130.1	000881	Cluster248_1clades	268	Np200711_184	Cyanophage S-RIM44	GCA_002599205.1
AOO12365.1	000881	Cluster248_1clades	268	Np420711_183	Cyanophage S-RIM44	GCA_002599225.1
AOO12593.1	000881	Cluster248_1clades	268	Sn080709_176	Cyanophage S-RIM44	GCA_002599245.1
AOO12830.1	000881	Cluster248_1clades	268	Sn130910_183	Cyanophage S-RIM44	GCA_002599265.1
AOO13059.1	000881	Cluster248_1clades	268	W2100709_177	Cyanophage S-RIM44	GCA_002599285.1
AGH07537.1	000881	Cluster248_1clades	292	CYVG_00093	Cyanophage S-SSM6a	GCA_002710385.1
AGG54459.1	000881	Cluster248_1clades	259	CYWG_00175	Cyanophage S-SSM6b	GCA_002710425.1
AGH26249.1	000881	Cluster248_1clades	246	CPMG_00148	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44616.1	000881	Cluster248_1clades	335	PSSM2_239	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12355.1	000881	Cluster248_1clades	335	PRTG_00202	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93551.1	000881	Cluster248_1clades	257	AVU42_gp215	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99279.1	000881	Cluster248_1clades	268	Syn1_178	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76291.1	000881	Cluster248_1clades	264	PBI_BELLAMY_255	Synechococcus phage Bellamy	GCA_002627525.1
QDH50728.1	000881	Cluster248_1clades	175	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59662.1	000881	Cluster248_1clades	270	S330809_201	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59424.1	000881	Cluster248_1clades	270	C440309_201	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59899.1	000881	Cluster248_1clades	270	N231010_200	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70490.1	000881	Cluster248_1clades	255	HOU04_gp091	Synechococcus phage S-T4	GCA_003443335.1
QJT70233.1	000881	Cluster248_1clades	255	SynMITS9220M01_227	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AND75416.1	000882	Ccr29_gp230	285	ME3_255	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ARB13752.1	000882	Ccr29_gp230	328	Ccr10_gp222c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14097.1	000882	Ccr29_gp230	328	Ccr2_gp221c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14786.1	000882	Ccr29_gp230	328	Ccr29_gp230	Caulobacter phage Ccr29	GCA_002619485.1
ARB15130.1	000882	Ccr29_gp230	328	Ccr32_gp212	Caulobacter phage Ccr32	GCA_002619505.1
ARB15464.1	000882	Ccr29_gp230	328	Ccr34_gp222	Caulobacter phage Ccr34	GCA_002619525.1
ARB14439.1	000882	Ccr29_gp230	328	Ccr5_gp219c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68419.1	000882	Ccr29_gp230	327	CcrBL10_gp215c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87746.1	000882	Ccr29_gp230	328	CcrKarma_gp229	Caulobacter virus Karma	GCA_000901575.1
AFU87394.1	000882	Ccr29_gp230	328	CcrMagneto_gp224	Caulobacter virus Magneto	GCA_000903095.1
AFU86705.1	000882	Ccr29_gp230	327	CcrRogue_gp223	Caulobacter virus Rogue	GCA_000900555.1
AFU88542.1	000882	Ccr29_gp230	328	CcrSwift_gp224	Caulobacter virus Swift	GCA_000899655.1
AFU87049.1	000882	Ccr29_gp230	328	CbK_gp217	Caulobacter virus phiCbK	GCA_000900535.1
AIT14075.1	000882	Ccr29_gp230	220	PBI_121Q_185	Escherichia phage 121Q	GCA_000926855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY00848.1	000882	Ccr29_gp230	220	Ecwhy1_576	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35018.1	000882	Ccr29_gp230	220	ACQ29_gp338	Escherichia phage PBECO4	GCA_001041035.1
BBM61758.1	000882	Ccr29_gp230	220	EO157G_1690	Escherichia phage SP27	GCA_008033345.1
AXC36595.1	000882	Ccr29_gp230	220	-	Escherichia phage UB	GCA_003341455.1
QBO61624.1	000882	Ccr29_gp230	220	G17_00128	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13681.1	000882	Ccr29_gp230	220	vBEcoMphAPEC6_gp051c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80069.1	000882	Ccr29_gp230	220	PSLUR01_00092	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44535.1	000882	Ccr29_gp230	222	RaK2_00262	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44560.1	000882	Ccr29_gp230	210	RaK2_00287	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72646.1	000882	Ccr29_gp230	197	-	Myoviridae sp.	GCA_003657725.1
QCW18615.1	000882	Ccr29_gp230	215	7t3_094	Salmonella phage 7t3	GCA_006083215.1
AZU98440.1	000882	Ccr29_gp230	215	CPT_Munch_508	Salmonella phage Munch	GCA_004015485.1
QIG63073.1	000882	Ccr29_gp230	215	SEPL_460	Salmonella phage SE_PL	GCA_011067555.1
AGH56866.1	000883	TM+TM	132	CPXG_00063	Cyanophage P-RSM6	GCA_000906155.1
AJK27589.1	000883	TM+TM	100	PTIM40_162	Cyanophage P-TIM40	GCA_001470935.1
AOO14348.1	000883	TM+TM	99	Sn110110_154	Cyanophage S-RIM14	GCA_002599065.1
AOO14997.1	000883	TM+TM	99	W1230910_151	Cyanophage S-RIM14	GCA_002599125.1
AMO43191.1	000883	TM+TM	107	R1080702_182	Cyanophage S-RIM32	GCA_001754165.1
AMO43417.1	000883	TM+TM	95	W270710_173	Cyanophage S-RIM44	GCA_002599145.1
AOO11661.1	000883	TM+TM	95	ES420910_180	Cyanophage S-RIM44	GCA_002599165.1
AOO11889.1	000883	TM+TM	95	Np050604_173	Cyanophage S-RIM44	GCA_002599185.1
AOO12127.1	000883	TM+TM	95	Np200711_181	Cyanophage S-RIM44	GCA_002599205.1
AOO12362.1	000883	TM+TM	95	Np420711_180	Cyanophage S-RIM44	GCA_002599225.1
AOO12590.1	000883	TM+TM	95	Sn080709_173	Cyanophage S-RIM44	GCA_002599245.1
AOO12827.1	000883	TM+TM	95	Sn130910_180	Cyanophage S-RIM44	GCA_002599265.1
AOO13056.1	000883	TM+TM	95	W2100709_174	Cyanophage S-RIM44	GCA_002599285.1
AGH07532.1	000883	TM+TM	139	CYVG_00088	Cyanophage S-SSM6a	GCA_002710385.1
AGG54461.1	000883	TM+TM	96	CYWG_00177	Cyanophage S-SSM6b	GCA_002710425.1
AGH26252.1	000883	TM+TM	133	CPMG_00151	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44600.1	000883	TM+TM	163	PSSM2_223	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12370.1	000883	TM+TM	143	PRTG_00217	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93543.1	000883	TM+TM	138	AVU42_gp206	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99276.1	000883	TM+TM	95	Syn1_175	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76277.1	000883	TM+TM	151	PBI_BELLAMY_241	Synechococcus phage Bellamy	GCA_002627525.1
QCW23030.1	000883	TM+TM	99	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59658.1	000883	TM+TM	94	S330809_197	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59420.1	000883	TM+TM	94	C440309_197	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59895.1	000883	TM+TM	94	N231010_196	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70493.1	000883	TM+TM	97	HOU04_gp094	Synechococcus phage S-T4	GCA_003443335.1
QJT70227.1	000883	TM+TM	145	SynMITS9220M01_221	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14255.1	000884	Cluster252_1clades	112	PBI_121Q_365	Escherichia phage 121Q	GCA_000926855.1
AIT14256.1	000884	Cluster252_1clades	74	PBI_121Q_366	Escherichia phage 121Q	GCA_000926855.1
AIT14258.1	000884	Cluster252_1clades	118	PBI_121Q_368	Escherichia phage 121Q	GCA_000926855.1
AIT14259.1	000884	Cluster252_1clades	119	PBI_121Q_369	Escherichia phage 121Q	GCA_000926855.1
QAY00678.1	000884	Cluster252_1clades	119	Ecwhy1_403	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00679.1	000884	Cluster252_1clades	118	Ecwhy1_404	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00680.1	000884	Cluster252_1clades	125	Ecwhy1_405	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34873.1	000884	Cluster252_1clades	117	ACQ29_gp193	Escherichia phage PBECO4	GCA_001041035.1
AGC34874.1	000884	Cluster252_1clades	118	ACQ29_gp194	Escherichia phage PBECO4	GCA_001041035.1
AGC34875.1	000884	Cluster252_1clades	125	ACQ29_gp195	Escherichia phage PBECO4	GCA_001041035.1
BBM61932.1	000884	Cluster252_1clades	112	EO157G_3430	Escherichia phage SP27	GCA_008033345.1
BBM61933.1	000884	Cluster252_1clades	118	EO157G_3440	Escherichia phage SP27	GCA_008033345.1
BBM61934.1	000884	Cluster252_1clades	119	EO157G_3450	Escherichia phage SP27	GCA_008033345.1
AXC36982.1	000884	Cluster252_1clades	112	-	Escherichia phage UB	GCA_003341455.1
AXC36981.1	000884	Cluster252_1clades	91	-	Escherichia phage UB	GCA_003341455.1
QBO62045.1	000884	Cluster252_1clades	119	G17_00556	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62046.1	000884	Cluster252_1clades	118	G17_00557	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62048.1	000884	Cluster252_1clades	53	G17_00559	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62049.1	000884	Cluster252_1clades	125	G17_00560	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14066.1	000884	Cluster252_1clades	119	vBEcoMphAPEC6_gp443c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14067.1	000884	Cluster252_1clades	118	vBEcoMphAPEC6_gp444c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14069.1	000884	Cluster252_1clades	53	vBEcoMphAPEC6_gp446c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14070.1	000884	Cluster252_1clades	125	vBEcoMphAPEC6_gp447c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80244.1	000884	Cluster252_1clades	112	PSLUR01_00267	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80245.1	000884	Cluster252_1clades	53	PSLUR01_00268	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80247.1	000884	Cluster252_1clades	118	PSLUR01_00270	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80248.1	000884	Cluster252_1clades	119	PSLUR01_00271	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGH56957.1	000885	Cluster253_1clades	105	CPXG_00154	Cyanophage P-RSM6	GCA_000906155.1
AJK27512.1	000885	Cluster253_1clades	106	PTIM40_85	Cyanophage P-TIM40	GCA_001470935.1
AOO14274.1	000885	Cluster253_1clades	113	Sn110110_080	Cyanophage S-RIM14	GCA_002599065.1
AOO14923.1	000885	Cluster253_1clades	113	W1230910_077	Cyanophage S-RIM14	GCA_002599125.1
AMO43099.1	000885	Cluster253_1clades	112	R1080702_090	Cyanophage S-RIM32	GCA_001754165.1
AMO43325.1	000885	Cluster253_1clades	108	W270710_081	Cyanophage S-RIM44	GCA_002599145.1
AOO11559.1	000885	Cluster253_1clades	108	ES420910_078	Cyanophage S-RIM44	GCA_002599165.1
AOO11797.1	000885	Cluster253_1clades	108	Np050604_081	Cyanophage S-RIM44	GCA_002599185.1
AOO12024.1	000885	Cluster253_1clades	108	Np200711_078	Cyanophage S-RIM44	GCA_002599205.1
AOO12260.1	000885	Cluster253_1clades	108	Np420711_078	Cyanophage S-RIM44	GCA_002599225.1
AOO12498.1	000885	Cluster253_1clades	108	Sn080709_081	Cyanophage S-RIM44	GCA_002599245.1
AOO12725.1	000885	Cluster253_1clades	108	Sn130910_078	Cyanophage S-RIM44	GCA_002599265.1
AOO12963.1	000885	Cluster253_1clades	108	W2100709_081	Cyanophage S-RIM44	GCA_002599285.1
AGH07703.1	000885	Cluster253_1clades	111	CYVG_00260	Cyanophage S-SSM6a	GCA_002710385.1
AGG54308.1	000885	Cluster253_1clades	110	CYWG_00024	Cyanophage S-SSM6b	GCA_002710425.1
AIR93620.1	000885	Cluster253_1clades	106	AVU42_gp075	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99181.1	000885	Cluster253_1clades	108	Syn1_080	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76146.1	000885	Cluster253_1clades	115	PBI_BELLAMY_101	Synechococcus phage Bellamy	GCA_002627525.1
QCW22851.1	000885	Cluster253_1clades	114	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50710.1	000885	Cluster253_1clades	114	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50603.1	000885	Cluster253_1clades	117	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59536.1	000885	Cluster253_1clades	101	S330809_075	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59298.1	000885	Cluster253_1clades	108	C440309_075	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59774.1	000885	Cluster253_1clades	101	N231010_075	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70603.1	000885	Cluster253_1clades	110	HOU04_gp002	Synechococcus phage S-T4	GCA_003443335.1
AXQ70401.1	000885	Cluster253_1clades	110	HOU04_gp002	Synechococcus phage S-T4	GCA_003443335.1
QJT70085.1	000885	Cluster253_1clades	115	SynMITS9220M01_072	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01509.1	000886	Cluster254_1clades	74	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29114.1	000886	Cluster254_1clades	74	AP1_0411	Aeromonas phage AP1	GCA_014183365.1
ATI17388.1	000886	Cluster254_1clades	74	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00205.1	000886	Cluster254_1clades	74	HWB28_gp347	Aeromonas phage AS-zj	GCA_002627665.1
AUE22717.1	000886	Cluster254_1clades	77	Ah1_00199	Aeromonas phage Ah1	GCA_002957415.1
QAX98441.1	000886	Cluster254_1clades	77	ASfcp2_98	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97830.1	000886	Cluster254_1clades	74	ASswx1_186	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01322.1	000886	Cluster254_1clades	76	ASwh1_260	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39276.1	000886	Cluster254_1clades	74	CC2_349	Aeromonas phage CC2	GCA_000903495.1
ADQ52897.1	000886	Cluster254_1clades	77	PX29p178	Aeromonas phage PX29	GCA_000920195.1
ADM80164.1	000886	Cluster254_1clades	77	phiAS5_ORF0321	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53131.1	000886	Cluster254_1clades	74	65p123	Aeromonas virus 65	GCA_000893255.1
AAQ17850.1	000886	Cluster254_1clades	77	Aeh1ORF184c	Aeromonas virus Aeh1	GCA_000843245.1
AIA64967.1	000886	Cluster254_1clades	75	S13_168	Cronobacter phage S13	GCA_001503575.1
QHJ78967.1	000886	Cluster254_1clades	76	-	Myoviridae sp.	GCA_012593985.1
AAQ64393.1	000886	Cluster254_1clades	88	KVP40.0323	Vibrio phage KVP40	GCA_000843785.1
QIW90705.1	000886	Cluster254_1clades	88	GCAPEGMB_00386	Vibrio phage V07	GCA_012361095.1
QIW91092.1	000886	Cluster254_1clades	88	COHAPHLL_00229	Vibrio phage V09	GCA_012361135.1
QHJ74505.1	000886	Cluster254_1clades	88	VH12019_00205	Vibrio phage VH1_2019	GCA_009931825.1
QBX06150.1	000886	Cluster254_1clades	88	ValB1HC_196	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61162.1	000886	Cluster254_1clades	88	AVU32_gp321	Vibrio phage ValKK3	GCA_001501635.1
AGN30374.1	000886	Cluster254_1clades	91	VPFG_00377	Vibrio phage nt-1	GCA_000910195.2
ALP47241.1	000886	Cluster254_1clades	88	phiGrn1_0057	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47627.1	000886	Cluster254_1clades	88	phiST2_0189	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54775.1	000886	Cluster254_1clades	88	vBValMR10Z_235	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07105.1	000886	Cluster254_1clades	82	VmeM32_00118	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37555.1	000886	Cluster254_1clades	88	pp2_323	Vibriophage phi-pp2	GCA_002630725.1
ASV44745.1	000887	Cluster256_1clades	329	FDI40_gp321	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95083.1	000887	Cluster256_1clades	392	FDI40_gp323	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXG67194.1	000887	Cluster256_1clades	393	AD1_150	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67195.1	000887	Cluster256_1clades	328	AD1_151	Dickeya phage vB_DsoM_AD1	GCA_003568515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AYD79946.1	000887	Cluster256_1clades	384	JA11_141	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79947.1	000887	Cluster256_1clades	324	JA11_142	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66545.1	000887	Cluster256_1clades	384	JA13_142	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66546.1	000887	Cluster256_1clades	324	JA13_143	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66870.1	000887	Cluster256_1clades	384	JA29_144	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66871.1	000887	Cluster256_1clades	324	JA29_145	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67515.1	000887	Cluster256_1clades	384	JA33_141	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67516.1	000887	Cluster256_1clades	324	JA33_142	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08427.1	000887	Cluster256_1clades	393	Alexandra_155	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08428.1	000887	Cluster256_1clades	328	Alexandra_156	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58791.1	000887	Cluster256_1clades	389	Y3_151	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58792.1	000887	Cluster256_1clades	325	Y3_152	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28629.1	000887	Cluster256_1clades	392	YOLOSWAG_149	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28630.1	000887	Cluster256_1clades	323	YOLOSWAG_150	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38435.1	000887	Cluster256_1clades	346	BN7874_241	Phage NCTB	GCA_900092385.1
SBV38436.1	000887	Cluster256_1clades	398	BN7874_242	Phage NCTB	GCA_900092385.1
SBV38438.1	000887	Cluster256_1clades	348	BN7874_243	Phage NCTB	GCA_900092385.1
SBV38440.1	000887	Cluster256_1clades	344	BN7874_244	Phage NCTB	GCA_900092385.1
SBV38444.1	000887	Cluster256_1clades	342	BN7874_246	Phage NCTB	GCA_900092385.1
AFH14777.1	000887	Cluster256_1clades	396	Lu11_0241	Pseudomonas phage Lu11	GCA_000897175.1
AFH14778.1	000887	Cluster256_1clades	358	Lu11_0242	Pseudomonas phage Lu11	GCA_000897175.1
AGS82135.2	000887	Cluster256_1clades	330	PaBG_00261	Pseudomonas phage PaBG	GCA_000912555.1
ARB13620.1	000888	Cluster257_1clades	298	Ccr10_gp091	Caulobacter phage Ccr10	GCA_002619445.1
ARB13965.1	000888	Cluster257_1clades	298	Ccr2_gp090	Caulobacter phage Ccr2	GCA_002619465.1
ARB14654.1	000888	Cluster257_1clades	298	Ccr29_gp097	Caulobacter phage Ccr29	GCA_002619485.1
ARB15009.1	000888	Cluster257_1clades	298	Ccr32_gp090	Caulobacter phage Ccr32	GCA_002619505.1
ARB15340.1	000888	Cluster257_1clades	298	Ccr34_gp097	Caulobacter phage Ccr34	GCA_002619525.1
ARB14309.1	000888	Cluster257_1clades	298	Ccr5_gp091	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68291.1	000888	Cluster257_1clades	142	CcrBL10_gp087	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68292.1	000888	Cluster257_1clades	87	CcrBL10_gp088	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69188.1	000888	Cluster257_1clades	140	CcrBL9_gp164	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69189.1	000888	Cluster257_1clades	126	CcrBL9_gp165	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87986.1	000888	Cluster257_1clades	137	CcrColossus_gp116	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87987.1	000888	Cluster257_1clades	268	CcrColossus_gp117	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68662.1	000888	Cluster257_1clades	137	CcrPW_gp123	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68663.1	000888	Cluster257_1clades	69	CcrPW_gp124	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69741.1	000888	Cluster257_1clades	137	CcrSC_gp159	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69742.1	000888	Cluster257_1clades	126	CcrSC_gp160	Caulobacter phage CcrSC	GCA_003443315.1
AFU87611.1	000888	Cluster257_1clades	142	CcrKarma_gp094	Caulobacter virus Karma	GCA_000901575.1
AFU87612.1	000888	Cluster257_1clades	298	CcrKarma_gp095	Caulobacter virus Karma	GCA_000901575.1
AFU87260.1	000888	Cluster257_1clades	142	CcrMagneto_gp090	Caulobacter virus Magneto	GCA_000903095.1
AFU87261.1	000888	Cluster257_1clades	298	CcrMagneto_gp091	Caulobacter virus Magneto	GCA_000903095.1
AFU86574.1	000888	Cluster257_1clades	142	CcrRogue_gp092	Caulobacter virus Rogue	GCA_000900555.1
AFU86575.1	000888	Cluster257_1clades	293	CcrRogue_gp093	Caulobacter virus Rogue	GCA_000900555.1
AFU88407.1	000888	Cluster257_1clades	142	CcrSwift_gp089	Caulobacter virus Swift	GCA_000899655.1
AFU88408.1	000888	Cluster257_1clades	298	CcrSwift_gp090	Caulobacter virus Swift	GCA_000899655.1
AFU86925.1	000888	Cluster257_1clades	142	CbK_gp093	Caulobacter virus phiCbK	GCA_000900535.1
AFU86926.1	000888	Cluster257_1clades	298	CbK_gp094	Caulobacter virus phiCbK	GCA_000900535.1
QDB70429.1	000889	Cluster258_1clades	173	CF8_0017	Aeromonas phage CF8	GCA_006384595.2
QDB70351.1	000889	Cluster258_1clades	137	CF8_0182	Aeromonas phage CF8	GCA_006384595.2
QDJ97348.1	000889	Cluster258_1clades	157	D6_0189	Aeromonas phage D6	GCA_007051205.2
QDJ97350.1	000889	Cluster258_1clades	129	D6_0191	Aeromonas phage D6	GCA_007051205.2
QDH47175.1	000889	Cluster258_1clades	157	LAh10_107	Aeromonas phage LAh10	GCA_006863975.1
QDH47204.1	000889	Cluster258_1clades	129	LAh10_109	Aeromonas phage LAh10	GCA_006863975.1
QDJ96776.1	000889	Cluster258_1clades	137	PS1_0017	Aeromonas phage PS1	GCA_007051165.2
QDJ96777.1	000889	Cluster258_1clades	133	PS1_0018	Aeromonas phage PS1	GCA_007051165.2
QDJ96787.1	000889	Cluster258_1clades	119	PS1_0028	Aeromonas phage PS1	GCA_007051165.2
QDJ96788.1	000889	Cluster258_1clades	121	PS1_0029	Aeromonas phage PS1	GCA_007051165.2
QFR59408.1	000889	Cluster258_1clades	137	PS2_0017	Aeromonas phage PS2	GCA_009388305.2
QFR59409.1	000889	Cluster258_1clades	133	PS2_0018	Aeromonas phage PS2	GCA_009388305.2
QFR59418.1	000889	Cluster258_1clades	119	PS2_0027	Aeromonas phage PS2	GCA_009388305.2
QFR59419.1	000889	Cluster258_1clades	121	PS2_0028	Aeromonas phage PS2	GCA_009388305.2
QBZ70707.1	000889	Cluster258_1clades	295	pETSU_126	Edwardsiella virus pEt-SU	GCA_004800915.1
ARW58901.1	000889	Cluster258_1clades	124	Y3_261	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AIT14105.1	000889	Cluster258_1clades	123	PBI_121Q_215	Escherichia phage 121Q	GCA_000926855.1
QAY00817.1	000889	Cluster258_1clades	123	Ecwhy1_544	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34991.1	000889	Cluster258_1clades	123	ACQ29_gp311	Escherichia phage PBECO4	GCA_001041035.1
BBM61787.1	000889	Cluster258_1clades	123	EO157G_1980	Escherichia phage SP27	GCA_008033345.1
AXC36571.1	000889	Cluster258_1clades	79	-	Escherichia phage UB	GCA_003341455.1
QBO61594.1	000889	Cluster258_1clades	123	G17_00098	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80099.1	000889	Cluster258_1clades	123	PSLUR01_00122	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AEV89634.1	000889	Cluster258_1clades	273	OBP_197	Pseudomonas phage OBP	GCA_000896635.1
BAW19160.1	000889	Cluster258_1clades	209	FDH28_gp235	Ralstonia phage RP12	GCA_002617345.1
BAW19446.1	000889	Cluster258_1clades	209	-	Ralstonia phage RP31	GCA_002617365.1
ARB13831.1	000890	Cluster259_1clades	159	Ccr10_gp301	Caulobacter phage Ccr10	GCA_002619445.1
ARB13832.1	000890	Cluster259_1clades	202	Ccr10_gp302	Caulobacter phage Ccr10	GCA_002619445.1
ARB14176.1	000890	Cluster259_1clades	159	Ccr2_gp300	Caulobacter phage Ccr2	GCA_002619465.1
ARB14177.1	000890	Cluster259_1clades	202	Ccr2_gp301	Caulobacter phage Ccr2	GCA_002619465.1
ARB14870.1	000890	Cluster259_1clades	159	Ccr29_gp314	Caulobacter phage Ccr29	GCA_002619485.1
ARB14871.1	000890	Cluster259_1clades	202	Ccr29_gp315	Caulobacter phage Ccr29	GCA_002619485.1
ARB15208.1	000890	Cluster259_1clades	159	Ccr32_gp290	Caulobacter phage Ccr32	GCA_002619505.1
ARB15209.1	000890	Cluster259_1clades	202	Ccr32_gp291	Caulobacter phage Ccr32	GCA_002619505.1
ARB15542.1	000890	Cluster259_1clades	159	Ccr34_gp300	Caulobacter phage Ccr34	GCA_002619525.1
ARB15543.1	000890	Cluster259_1clades	202	Ccr34_gp301	Caulobacter phage Ccr34	GCA_002619525.1
ARB14517.1	000890	Cluster259_1clades	157	Ccr5_gp297	Caulobacter phage Ccr5	GCA_002619545.1
ARB14518.1	000890	Cluster259_1clades	202	Ccr5_gp298	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68497.1	000890	Cluster259_1clades	216	CcrBL10_gp293	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68499.1	000890	Cluster259_1clades	202	CcrBL10_gp295	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88136.1	000890	Cluster259_1clades	95	CcrColossus_gp266	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68812.1	000890	Cluster259_1clades	96	CcrPW_gp273	Caulobacter phage CcrPW	GCA_003443275.1
AFU87828.1	000890	Cluster259_1clades	159	CcrKarma_gp311	Caulobacter virus Karma	GCA_000901575.1
AFU87829.1	000890	Cluster259_1clades	253	CcrKarma_gp312	Caulobacter virus Karma	GCA_000901575.1
AFU87475.1	000890	Cluster259_1clades	159	CcrMagneto_gp305	Caulobacter virus Magneto	GCA_000903095.1
AFU87476.1	000890	Cluster259_1clades	253	CcrMagneto_gp306	Caulobacter virus Magneto	GCA_000903095.1
AFU86785.1	000890	Cluster259_1clades	218	CcrRogue_gp303	Caulobacter virus Rogue	GCA_000900555.1
AFU86787.1	000890	Cluster259_1clades	201	CcrRogue_gp305	Caulobacter virus Rogue	GCA_000900555.1
AFU88620.1	000890	Cluster259_1clades	159	CcrSwift_gp302	Caulobacter virus Swift	GCA_000899655.1
AFU88621.1	000890	Cluster259_1clades	202	CcrSwift_gp303	Caulobacter virus Swift	GCA_000899655.1
AFU87127.1	000890	Cluster259_1clades	159	CbK_gp295	Caulobacter virus phiCbK	GCA_000900535.1
AFU87128.1	000890	Cluster259_1clades	202	CbK_gp296	Caulobacter virus phiCbK	GCA_000900535.1
AJK27595.1	000891	Cluster264_1clades	146	PTIM40_168	Cyanophage P-TIM40	GCA_001470935.1
AOO14351.1	000891	Cluster264_1clades	145	Sn110110_157	Cyanophage S-RIM14	GCA_002599065.1
AOO15000.1	000891	Cluster264_1clades	144	W1230910_154	Cyanophage S-RIM14	GCA_002599125.1
AMO43195.1	000891	Cluster264_1clades	144	R1080702_186	Cyanophage S-RIM32	GCA_001754165.1
AMO43422.1	000891	Cluster264_1clades	93	W270710_178	Cyanophage S-RIM44	GCA_002599145.1
AOO11666.1	000891	Cluster264_1clades	93	ES420910_185	Cyanophage S-RIM44	GCA_002599165.1
AOO11894.1	000891	Cluster264_1clades	93	Np050604_178	Cyanophage S-RIM44	GCA_002599185.1
AOO12132.1	000891	Cluster264_1clades	93	Np200711_186	Cyanophage S-RIM44	GCA_002599205.1
AOO12367.1	000891	Cluster264_1clades	93	Np420711_185	Cyanophage S-RIM44	GCA_002599225.1
AOO12595.1	000891	Cluster264_1clades	93	Sn080709_178	Cyanophage S-RIM44	GCA_002599245.1
AOO12832.1	000891	Cluster264_1clades	93	Sn130910_185	Cyanophage S-RIM44	GCA_002599265.1
AOO13061.1	000891	Cluster264_1clades	93	W2100709_179	Cyanophage S-RIM44	GCA_002599285.1
AGH07540.1	000891	Cluster264_1clades	161	CYVG_00096	Cyanophage S-SSM6a	GCA_002710385.1
AGG54457.1	000891	Cluster264_1clades	149	CYWG_00173	Cyanophage S-SSM6b	GCA_002710425.1
AGH26247.1	000891	Cluster264_1clades	151	CPMG_00146	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44618.1	000891	Cluster264_1clades	156	PSSM2_241	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12353.1	000891	Cluster264_1clades	156	PRTG_00200	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93554.1	000891	Cluster264_1clades	158	AVU42_gp217	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99281.1	000891	Cluster264_1clades	151	Syn1_180	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76293.1	000891	Cluster264_1clades	156	PBI_BELLAMY_257	Synechococcus phage Bellamy	GCA_002627525.1
QCW23044.1	000891	Cluster264_1clades	147	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50680.1	000891	Cluster264_1clades	138	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59664.1	000891	Cluster264_1clades	145	S330809_203	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59426.1	000891	Cluster264_1clades	145	C440309_203	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59901.1	000891	Cluster264_1clades	145	N231010_202	Synechococcus phage S-CAM4	GCA_002922155.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ70489.1	000891	Cluster264_1clades	147	HOU04_gp090	Synechococcus phage S-T4	GCA_003443335.1
ARB13547.1	000892	Cluster265_1clades	148	Ccr10_gp019	Caulobacter phage Ccr10	GCA_002619445.1
ARB13872.1	000892	Cluster265_1clades	148	Ccr10_gp342	Caulobacter phage Ccr10	GCA_002619445.1
ARB13893.1	000892	Cluster265_1clades	148	Ccr2_gp018	Caulobacter phage Ccr2	GCA_002619465.1
ARB14216.1	000892	Cluster265_1clades	148	Ccr2_gp340	Caulobacter phage Ccr2	GCA_002619465.1
ARB14576.1	000892	Cluster265_1clades	148	Ccr29_gp019	Caulobacter phage Ccr29	GCA_002619485.1
ARB14582.1	000892	Cluster265_1clades	148	Ccr29_gp025	Caulobacter phage Ccr29	GCA_002619485.1
ARB14911.1	000892	Cluster265_1clades	148	Ccr29_gp355	Caulobacter phage Ccr29	GCA_002619485.1
ARB14917.1	000892	Cluster265_1clades	148	Ccr29_gp361	Caulobacter phage Ccr29	GCA_002619485.1
ARB14937.1	000892	Cluster265_1clades	148	Ccr32_gp018	Caulobacter phage Ccr32	GCA_002619505.1
ARB15248.1	000892	Cluster265_1clades	148	Ccr32_gp330	Caulobacter phage Ccr32	GCA_002619505.1
ARB15268.1	000892	Cluster265_1clades	148	Ccr34_gp019	Caulobacter phage Ccr34	GCA_002619525.1
ARB15582.1	000892	Cluster265_1clades	148	Ccr34_gp340	Caulobacter phage Ccr34	GCA_002619525.1
ARB14236.1	000892	Cluster265_1clades	148	Ccr5_gp018	Caulobacter phage Ccr5	GCA_002619545.1
ARB14556.1	000892	Cluster265_1clades	148	Ccr5_gp336	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68219.1	000892	Cluster265_1clades	146	CcrBL10_gp015	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68537.1	000892	Cluster265_1clades	146	CcrBL10_gp333	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87535.1	000892	Cluster265_1clades	148	CcrKarma_gp018	Caulobacter virus Karma	GCA_000901575.1
AFU87868.1	000892	Cluster265_1clades	148	CcrKarma_gp351	Caulobacter virus Karma	GCA_000901575.1
AFU87187.1	000892	Cluster265_1clades	148	CcrMagneto_gp017	Caulobacter virus Magneto	GCA_000903095.1
AFU87515.1	000892	Cluster265_1clades	148	CcrMagneto_gp345	Caulobacter virus Magneto	GCA_000903095.1
AFU86499.1	000892	Cluster265_1clades	146	CcrRogue_gp017	Caulobacter virus Rogue	GCA_000900555.1
AFU86830.1	000892	Cluster265_1clades	146	CcrRogue_gp348	Caulobacter virus Rogue	GCA_000900555.1
AFU88334.1	000892	Cluster265_1clades	148	CcrSwift_gp016	Caulobacter virus Swift	GCA_000899655.1
AFU88659.1	000892	Cluster265_1clades	148	CcrSwift_gp341	Caulobacter virus Swift	GCA_000899655.1
AFU86850.1	000892	Cluster265_1clades	148	CbK_gp018	Caulobacter virus phiCbK	GCA_000900535.1
AFU87168.1	000892	Cluster265_1clades	148	CbK_gp336	Caulobacter virus phiCbK	GCA_000900535.1
AGH56806.1	000893	Cluster266_1clades	92	CPXG_00003	Cyanophage P-RSM6	GCA_000906155.1
AOO14408.1	000893	Cluster266_1clades	90	Sn110110_215	Cyanophage S-RIM14	GCA_002599065.1
AOO15057.1	000893	Cluster266_1clades	85	W1230910_212	Cyanophage S-RIM14	GCA_002599125.1
AMO43232.1	000893	Cluster266_1clades	83	R1080702_227	Cyanophage S-RIM32	GCA_001754165.1
AMO43464.1	000893	Cluster266_1clades	81	W270710_225	Cyanophage S-RIM44	GCA_002599145.1
AOO11704.1	000893	Cluster266_1clades	81	ES420910_227	Cyanophage S-RIM44	GCA_002599165.1
AOO11936.1	000893	Cluster266_1clades	81	Np050604_225	Cyanophage S-RIM44	GCA_002599185.1
AOO12170.1	000893	Cluster266_1clades	81	Np200711_228	Cyanophage S-RIM44	GCA_002599205.1
AOO12405.1	000893	Cluster266_1clades	81	Np420711_227	Cyanophage S-RIM44	GCA_002599225.1
AOO12637.1	000893	Cluster266_1clades	81	Sn080709_225	Cyanophage S-RIM44	GCA_002599245.1
AOO12870.1	000893	Cluster266_1clades	81	Sn130910_227	Cyanophage S-RIM44	GCA_002599265.1
AOO13103.1	000893	Cluster266_1clades	81	W2100709_226	Cyanophage S-RIM44	GCA_002599285.1
AGH07618.1	000893	Cluster266_1clades	94	CYVG_00175	Cyanophage S-SSM6a	GCA_002710385.1
AGG54380.1	000893	Cluster266_1clades	90	CYWG_00096	Cyanophage S-SSM6b	GCA_002710425.1
AAX44696.1	000893	Cluster266_1clades	123	PSSM2_318	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12280.1	000893	Cluster266_1clades	123	PRTG_00127	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99325.1	000893	Cluster266_1clades	87	Syn1_229	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30525.1	000893	Cluster266_1clades	102	Syn7803US37_48	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76304.1	000893	Cluster266_1clades	114	PBI_BELLAMY_268	Synechococcus phage Bellamy	GCA_002627525.1
QCW23055.1	000893	Cluster266_1clades	88	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50696.1	000893	Cluster266_1clades	88	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59686.1	000893	Cluster266_1clades	80	S330809_225	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59448.1	000893	Cluster266_1clades	69	C440309_225	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59923.1	000893	Cluster266_1clades	69	N231010_224	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70457.1	000893	Cluster266_1clades	100	HOU04_gp058	Synechococcus phage S-T4	GCA_003443335.1
QJT70251.1	000893	Cluster266_1clades	111	SynMITS9220M01_245	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27621.1	000894	Cluster267_1clades	60	PTIM40_209	Cyanophage P-TIM40	GCA_001470935.1
AOO14246.1	000894	Cluster267_1clades	57	Sn110110_052	Cyanophage S-RIM14	GCA_002599065.1
AOO14898.1	000894	Cluster267_1clades	57	W1230910_052	Cyanophage S-RIM14	GCA_002599125.1
AMO43054.1	000894	Cluster267_1clades	62	R1080702_045	Cyanophage S-RIM32	GCA_001754165.1
AMO43293.1	000894	Cluster267_1clades	60	W270710_049	Cyanophage S-RIM44	GCA_002599145.1
AOO11527.1	000894	Cluster267_1clades	60	ES420910_046	Cyanophage S-RIM44	GCA_002599165.1
AOO11765.1	000894	Cluster267_1clades	60	Np050604_049	Cyanophage S-RIM44	GCA_002599185.1
AOO11992.1	000894	Cluster267_1clades	60	Np200711_046	Cyanophage S-RIM44	GCA_002599205.1
AOO12228.1	000894	Cluster267_1clades	60	Np420711_046	Cyanophage S-RIM44	GCA_002599225.1
AOO12466.1	000894	Cluster267_1clades	60	Sn080709_049	Cyanophage S-RIM44	GCA_002599245.1
AOO12693.1	000894	Cluster267_1clades	60	Sn130910_046	Cyanophage S-RIM44	GCA_002599265.1
AOO12931.1	000894	Cluster267_1clades	60	W2100709_049	Cyanophage S-RIM44	GCA_002599285.1
AGH07609.1	000894	Cluster267_1clades	64	CYVG_00166	Cyanophage S-SSM6a	GCA_002710385.1
AGH26250.1	000894	Cluster267_1clades	91	CPMG_00149	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44424.1	000894	Cluster267_1clades	100	PSSM2_046	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12226.1	000894	Cluster267_1clades	112	PRTG_00068	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93486.1	000894	Cluster267_1clades	73	AVU42_gp148	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99147.1	000894	Cluster267_1clades	60	Syn1_046	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30651.1	000894	Cluster267_1clades	52	Syn7803US37_174	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76105.1	000894	Cluster267_1clades	65	PBI_BELLAMY_60	Synechococcus phage Bellamy	GCA_002627525.1
QDH50652.1	000894	Cluster267_1clades	64	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59503.1	000894	Cluster267_1clades	65	S330809_042	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59265.1	000894	Cluster267_1clades	65	C440309_042	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59741.1	000894	Cluster267_1clades	65	N231010_042	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70544.1	000894	Cluster267_1clades	65	HOU04_gp145	Synechococcus phage S-T4	GCA_003443335.1
QJT70052.1	000894	Cluster267_1clades	60	SynMITS9220M01_039	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13542.1	000895	Cluster268_1clades	94	Ccr10_gp014	Caulobacter phage Ccr10	GCA_002619445.1
ARB13867.1	000895	Cluster268_1clades	94	Ccr10_gp337	Caulobacter phage Ccr10	GCA_002619445.1
ARB13889.1	000895	Cluster268_1clades	97	Ccr2_gp014	Caulobacter phage Ccr2	GCA_002619465.1
ARB14212.1	000895	Cluster268_1clades	97	Ccr2_gp336	Caulobacter phage Ccr2	GCA_002619465.1
ARB14571.1	000895	Cluster268_1clades	94	Ccr29_gp014	Caulobacter phage Ccr29	GCA_002619485.1
ARB14577.1	000895	Cluster268_1clades	94	Ccr29_gp020	Caulobacter phage Ccr29	GCA_002619485.1
ARB14906.1	000895	Cluster268_1clades	94	Ccr29_gp350	Caulobacter phage Ccr29	GCA_002619485.1
ARB14912.1	000895	Cluster268_1clades	94	Ccr29_gp356	Caulobacter phage Ccr29	GCA_002619485.1
ARB14932.1	000895	Cluster268_1clades	94	Ccr32_gp013	Caulobacter phage Ccr32	GCA_002619505.1
ARB15243.1	000895	Cluster268_1clades	94	Ccr32_gp325	Caulobacter phage Ccr32	GCA_002619505.1
ARB15263.1	000895	Cluster268_1clades	94	Ccr34_gp014	Caulobacter phage Ccr34	GCA_002619525.1
ARB15577.1	000895	Cluster268_1clades	94	Ccr34_gp335	Caulobacter phage Ccr34	GCA_002619525.1
ARB14231.1	000895	Cluster268_1clades	94	Ccr5_gp013	Caulobacter phage Ccr5	GCA_002619545.1
ARB14551.1	000895	Cluster268_1clades	94	Ccr5_gp331	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68215.1	000895	Cluster268_1clades	92	CcrBL10_gp011	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68533.1	000895	Cluster268_1clades	92	CcrBL10_gp329	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87530.1	000895	Cluster268_1clades	94	CcrKarma_gp013	Caulobacter virus Karma	GCA_000901575.1
AFU87863.1	000895	Cluster268_1clades	94	CcrKarma_gp346	Caulobacter virus Karma	GCA_000901575.1
AFU87183.1	000895	Cluster268_1clades	94	CcrMagneto_gp013	Caulobacter virus Magneto	GCA_000903095.1
AFU87511.1	000895	Cluster268_1clades	94	CcrMagneto_gp341	Caulobacter virus Magneto	GCA_000903095.1
AFU86495.1	000895	Cluster268_1clades	92	CcrRogue_gp013	Caulobacter virus Rogue	GCA_000900555.1
AFU86826.1	000895	Cluster268_1clades	92	CcrRogue_gp344	Caulobacter virus Rogue	GCA_000900555.1
AFU88330.1	000895	Cluster268_1clades	92	CcrSwift_gp012	Caulobacter virus Swift	GCA_000899655.1
AFU88655.1	000895	Cluster268_1clades	92	CcrSwift_gp337	Caulobacter virus Swift	GCA_000899655.1
AFU86845.1	000895	Cluster268_1clades	94	CbK_gp013	Caulobacter virus phiCbK	GCA_000900535.1
AFU87163.1	000895	Cluster268_1clades	94	CbK_gp331	Caulobacter virus phiCbK	GCA_000900535.1
AGH56861.1	000896	Cluster270_1clades	382	CPXG_00058	Cyanophage P-RSM6	GCA_000906155.1
AJK27593.1	000896	Cluster270_1clades	234	PTIM40_166	Cyanophage P-TIM40	GCA_001470935.1
AOO14350.1	000896	Cluster270_1clades	329	Sn110110_156	Cyanophage S-RIM14	GCA_002599065.1
AOO14999.1	000896	Cluster270_1clades	329	W1230910_153	Cyanophage S-RIM14	GCA_002599125.1
AMO43421.1	000896	Cluster270_1clades	233	W270710_177	Cyanophage S-RIM44	GCA_002599145.1
AOO11665.1	000896	Cluster270_1clades	233	ES420910_184	Cyanophage S-RIM44	GCA_002599165.1
AOO11893.1	000896	Cluster270_1clades	233	Np050604_177	Cyanophage S-RIM44	GCA_002599185.1
AOO12131.1	000896	Cluster270_1clades	233	Np200711_185	Cyanophage S-RIM44	GCA_002599205.1
AOO12366.1	000896	Cluster270_1clades	233	Np420711_184	Cyanophage S-RIM44	GCA_002599225.1
AOO12594.1	000896	Cluster270_1clades	233	Sn080709_177	Cyanophage S-RIM44	GCA_002599245.1
AOO12831.1	000896	Cluster270_1clades	233	Sn130910_184	Cyanophage S-RIM44	GCA_002599265.1
AOO13060.1	000896	Cluster270_1clades	233	W2100709_178	Cyanophage S-RIM44	GCA_002599285.1
AGH07539.1	000896	Cluster270_1clades	194	CYVG_00095	Cyanophage S-SSM6a	GCA_002710385.1
AGG54458.1	000896	Cluster270_1clades	297	CYWG_00174	Cyanophage S-SSM6b	GCA_002710425.1
AGH26248.1	000896	Cluster270_1clades	298	CPMG_00147	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44617.1	000896	Cluster270_1clades	341	PSSM2_240	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12354.1	000896	Cluster270_1clades	341	PRTG_00201	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93553.1	000896	Cluster270_1clades	295	AVU42_gp216	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99280.1	000896	Cluster270_1clades	233	Syn1_179	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76292.1	000896	Cluster270_1clades	326	PBI_BELLAMY_256	Synechococcus phage Bellamy	GCA_002627525.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW23043.1	000896	Cluster270_1clades	222	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59663.1	000896	Cluster270_1clades	303	S330809_202	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59425.1	000896	Cluster270_1clades	303	C440309_202	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59900.1	000896	Cluster270_1clades	303	N231010_201	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70234.1	000896	Cluster270_1clades	294	SynMITS9220M01_228	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AHI60261.1	000897	Cluster271_1clades	321	Ea357_110	Erwinia phage Ea35-70	GCA_000914635.1
AHI60336.1	000897	Cluster271_1clades	321	Ea357_184	Erwinia phage Ea35-70	GCA_000914635.1
QBP07218.1	000897	Cluster271_1clades	321	REBECCA_111	Erwinia phage Rebecca	GCA_004521635.1
QBP07295.1	000897	Cluster271_1clades	321	REBECCA_188	Erwinia phage Rebecca	GCA_004521635.1
AUG85898.1	000897	Cluster271_1clades	321	BOSOLAPHORUS_111	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG85975.1	000897	Cluster271_1clades	321	BOSOLAPHORUS_188	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52213.1	000897	Cluster271_1clades	321	DM_115	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52290.1	000897	Cluster271_1clades	321	DM_192	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86217.1	000897	Cluster271_1clades	321	DESERTFOX_110	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86294.1	000897	Cluster271_1clades	321	DESERTFOX_187	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86539.1	000897	Cluster271_1clades	321	MADMEL_111	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86616.1	000897	Cluster271_1clades	321	MADMEL_188	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86864.1	000897	Cluster271_1clades	321	MORTIMER_115	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG86940.1	000897	Cluster271_1clades	321	MORTIMER_191	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51892.1	000897	Cluster271_1clades	321	RAY_111	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51967.1	000897	Cluster271_1clades	321	RAY_186	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51576.1	000897	Cluster271_1clades	321	SIMMY50_114	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51651.1	000897	Cluster271_1clades	321	SIMMY50_189	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64923.1	000897	Cluster271_1clades	321	SPECIALG_113	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ64998.1	000897	Cluster271_1clades	321	SPECIALG_189	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24117.1	000897	Cluster271_1clades	322	-	Proteus phage 10	GCA_014071245.1
QKE54495.1	000897	Cluster271_1clades	325	ACSA002_1810	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54496.1	000897	Cluster271_1clades	322	ACSA002_1820	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54497.1	000897	Cluster271_1clades	336	ACSA002_1830	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54498.1	000897	Cluster271_1clades	324	ACSA002_1840	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13891.1	000898	Cluster272_1clades	196	Ccr2_gp016	Caulobacter phage Ccr2	GCA_002619465.1
ARB14214.1	000898	Cluster272_1clades	196	Ccr2_gp338	Caulobacter phage Ccr2	GCA_002619465.1
ARB14580.1	000898	Cluster272_1clades	196	Ccr29_gp023	Caulobacter phage Ccr29	GCA_002619485.1
ARB14915.1	000898	Cluster272_1clades	196	Ccr29_gp359	Caulobacter phage Ccr29	GCA_002619485.1
ARB14935.1	000898	Cluster272_1clades	196	Ccr32_gp016	Caulobacter phage Ccr32	GCA_002619505.1
ARB15246.1	000898	Cluster272_1clades	196	Ccr32_gp328	Caulobacter phage Ccr32	GCA_002619505.1
ARB15266.1	000898	Cluster272_1clades	196	Ccr34_gp017	Caulobacter phage Ccr34	GCA_002619525.1
ARB15580.1	000898	Cluster272_1clades	196	Ccr34_gp338	Caulobacter phage Ccr34	GCA_002619525.1
ARB14234.1	000898	Cluster272_1clades	194	Ccr5_gp016	Caulobacter phage Ccr5	GCA_002619545.1
ARB14554.1	000898	Cluster272_1clades	194	Ccr5_gp334	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68217.1	000898	Cluster272_1clades	222	CcrBL10_gp013	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68535.1	000898	Cluster272_1clades	222	CcrBL10_gp331	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87882.1	000898	Cluster272_1clades	121	CcrColossus_gp012	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68550.1	000898	Cluster272_1clades	189	CcrPW_gp011	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69000.1	000898	Cluster272_1clades	189	CcrPW_gp461	Caulobacter phage CcrPW	GCA_003443275.1
AFU87532.1	000898	Cluster272_1clades	196	CcrKarma_gp015	Caulobacter virus Karma	GCA_000901575.1
AFU87865.1	000898	Cluster272_1clades	196	CcrKarma_gp348	Caulobacter virus Karma	GCA_000901575.1
AFU87185.1	000898	Cluster272_1clades	196	CcrMagneto_gp015	Caulobacter virus Magneto	GCA_000903095.1
AFU87513.1	000898	Cluster272_1clades	196	CcrMagneto_gp343	Caulobacter virus Magneto	GCA_000903095.1
AFU86497.1	000898	Cluster272_1clades	190	CcrRogue_gp015	Caulobacter virus Rogue	GCA_000900555.1
AFU86828.1	000898	Cluster272_1clades	190	CcrRogue_gp346	Caulobacter virus Rogue	GCA_000900555.1
AFU88332.1	000898	Cluster272_1clades	222	CcrSwift_gp014	Caulobacter virus Swift	GCA_000899655.1
AFU88657.1	000898	Cluster272_1clades	222	CcrSwift_gp339	Caulobacter virus Swift	GCA_000899655.1
AFU86848.1	000898	Cluster272_1clades	196	CbK_gp016	Caulobacter virus phiCbK	GCA_000900535.1
AFU87166.1	000898	Cluster272_1clades	196	CbK_gp334	Caulobacter virus phiCbK	GCA_000900535.1
AXQ69056.1	000899	Cluster273_1clades	218	CcrBL9_gp032	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69572.1	000899	Cluster273_1clades	218	CcrBL9_gp548	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87885.1	000899	Cluster273_1clades	215	CcrColossus_gp015	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68556.1	000899	Cluster273_1clades	216	CcrPW_gp017	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69005.1	000899	Cluster273_1clades	216	CcrPW_gp466	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69615.1	000899	Cluster273_1clades	218	CcrSC_gp033	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70115.1	000899	Cluster273_1clades	218	CcrSC_gp533	Caulobacter phage CcrSC	GCA_003443315.1
AFC21483.1	000899	Cluster273_1clades	191	GAP32_035	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14161.1	000899	Cluster273_1clades	203	PBI_121Q_271	Escherichia phage 121Q	GCA_000926855.1
QAY00775.1	000899	Cluster273_1clades	203	Ecwhy1_502	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34954.1	000899	Cluster273_1clades	203	ACQ29_gp274	Escherichia phage PBECO4	GCA_001041035.1
BBM61834.1	000899	Cluster273_1clades	203	EO157G_2450	Escherichia phage SP27	GCA_008033345.1
AXC37055.1	000899	Cluster273_1clades	203	-	Escherichia phage UB	GCA_003341455.1
QBO61545.1	000899	Cluster273_1clades	203	G17_00049	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62151.1	000899	Cluster273_1clades	203	G17_00662	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14158.1	000899	Cluster273_1clades	203	vBEcoMphAPEC6_gp535c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80149.1	000899	Cluster273_1clades	203	PSLUR01_00172	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44600.1	000899	Cluster273_1clades	216	RaK2_00327	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43607.1	000899	Cluster273_1clades	200	CBB_42	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44158.1	000899	Cluster273_1clades	200	CBB_595	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18670.1	000899	Cluster273_1clades	205	7t3_0149	Salmonella phage 7t3	GCA_006083215.1
AZU97947.1	000899	Cluster273_1clades	205	CPT_Munch_003	Salmonella phage Munch	GCA_004015485.1
QIG63028.1	000899	Cluster273_1clades	205	SEPL_415	Salmonella phage SE_PL	GCA_011067555.1
AQW88556.1	000899	Cluster273_1clades	193	BF_0031	Serratia phage BF	GCA_002619745.1
SOK58832.1	000899	Cluster273_1clades	191	g024	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AGH56913.1	000900	Cupredoxin	115	CPXG_00110	Cyanophage P-RSM6	GCA_000906155.1
AOO14234.1	000900	Cupredoxin	107	Sn110110_040	Cyanophage S-RIM14	GCA_002599065.1
AOO14886.1	000900	Cupredoxin	107	W1230910_040	Cyanophage S-RIM14	GCA_002599125.1
AMO43202.1	000900	Cupredoxin	84	R1080702_193	Cyanophage S-RIM32	GCA_001754165.1
AMO43432.1	000900	Cupredoxin	107	W270710_188	Cyanophage S-RIM44	GCA_002599145.1
AOO11676.1	000900	Cupredoxin	107	ES420910_195	Cyanophage S-RIM44	GCA_002599165.1
AOO11904.1	000900	Cupredoxin	107	Np050604_188	Cyanophage S-RIM44	GCA_002599185.1
AOO12142.1	000900	Cupredoxin	107	Np200711_196	Cyanophage S-RIM44	GCA_002599205.1
AOO12377.1	000900	Cupredoxin	107	Np420711_195	Cyanophage S-RIM44	GCA_002599225.1
AOO12605.1	000900	Cupredoxin	107	Sn080709_188	Cyanophage S-RIM44	GCA_002599245.1
AOO12842.1	000900	Cupredoxin	107	Sn130910_195	Cyanophage S-RIM44	GCA_002599265.1
AOO13071.1	000900	Cupredoxin	107	W2100709_189	Cyanophage S-RIM44	GCA_002599285.1
AGH07513.1	000900	Cupredoxin	107	CYVG_00069	Cyanophage S-SSM6a	GCA_002710385.1
AGG54475.1	000900	Cupredoxin	107	CYWG_00191	Cyanophage S-SSM6b	GCA_002710425.1
AAX44607.1	000900	Cupredoxin	114	PSSM2_230	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12363.1	000900	Cupredoxin	114	PRTG_00210	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99291.1	000900	Cupredoxin	107	Syn1_190	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30479.1	000900	Cupredoxin	107	Syn7803US37_2	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76279.1	000900	Cupredoxin	107	PBI_BELLAMY_243	Synechococcus phage Bellamy	GCA_002627525.1
QCW23032.1	000900	Cupredoxin	107	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59576.1	000900	Cupredoxin	84	S330809_115	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59338.1	000900	Cupredoxin	84	C440309_115	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59814.1	000900	Cupredoxin	84	N231010_115	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70482.1	000900	Cupredoxin	107	HOU04_gp083	Synechococcus phage S-T4	GCA_003443335.1
QJT70231.1	000900	Cupredoxin	107	SynMITS9220M01_225	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMR59653.1	000901	Cluster277_1clades	80	SEGD1_002	Enterobacteria phage SEGD1	GCA_002601865.1
AHI60350.1	000901	Cluster277_1clades	98	Ea357_198	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49650.1	000901	Cluster277_1clades	75	MACHINA_4	Erwinia phage Machina	GCA_002758035.1
QBP07308.1	000901	Cluster277_1clades	98	REBECCA_203	Erwinia phage Rebecca	GCA_004521635.1
AXF51142.1	000901	Cluster277_1clades	82	WELLINGTON_1	Erwinia phage Wellington	GCA_003344985.1
ANZ48028.1	000901	Cluster277_1clades	74	ASESINO_4	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85989.1	000901	Cluster277_1clades	98	BOSOLAPHORUS_203	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48304.1	000901	Cluster277_1clades	73	CAITLIN_3	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48576.1	000901	Cluster277_1clades	73	CHRISDB_4	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52304.1	000901	Cluster277_1clades	98	DM_206	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86308.1	000901	Cluster277_1clades	98	DESERTFOX_201	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49094.1	000901	Cluster277_1clades	75	HUXLEY_4	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49363.1	000901	Cluster277_1clades	82	KWAN_1	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86631.1	000901	Cluster277_1clades	98	MADMEL_203	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86954.1	000901	Cluster277_1clades	98	MORTIMER_206	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ49923.1	000901	Cluster277_1clades	73	PARSHIK_5	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANH51981.1	000901	Cluster277_1clades	98	RAY_201	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51665.1	000901	Cluster277_1clades	98	SIMMY50_204	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65013.1	000901	Cluster277_1clades	98	SPECIALG_204	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50440.1	000901	Cluster277_1clades	74	STRATTON_4	Erwinia phage vB_EamM_Stratton	GCA_002600675.1

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ANZ50441.1	000901	Cluster277_1clades	80	STRATTON_5	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85839.1	000901	Cluster277_1clades	80	ACEC001_0030	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09089.1	000901	Cluster277_1clades	83	MLDJOKPK_00171	Salmonella phage SPAsTU	GCA_003183805.1
AEP83835.1	000901	Cluster277_1clades	80	SPN3US_0002	Salmonella phage SPN3US	GCA_001042275.1
QKE54523.1	000901	Cluster277_1clades	99	ACSA002_2070	Salmonella phage vB_SalM_SA002	GCA_014131285.1
APU01524.1	000902	Cluster278_1clades	66	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28772.1	000902	Cluster278_1clades	69	AP1_0054	Aeromonas phage AP1	GCA_014183365.1
ATI17376.1	000902	Cluster278_1clades	69	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00218.1	000902	Cluster278_1clades	69	HWB28_gp334	Aeromonas phage AS-zj	GCA_002627665.1
AUE22705.1	000902	Cluster278_1clades	79	Ah1_00176	Aeromonas phage Ah1	GCA_002957415.1
QAX98431.1	000902	Cluster278_1clades	79	ASfcp2_87	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97817.1	000902	Cluster278_1clades	69	ASswx1_173	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01335.1	000902	Cluster278_1clades	69	ASwh1_274	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39430.1	000902	Cluster278_1clades	68	CC2_363	Aeromonas phage CC2	GCA_000903495.1
ADQ52886.1	000902	Cluster278_1clades	79	PX29p167	Aeromonas phage PX29	GCA_000920195.1
ADM80155.1	000902	Cluster278_1clades	82	phiAS5_ORF0312	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53146.1	000902	Cluster278_1clades	68	65p138	Aeromonas virus 65	GCA_000893255.1
AAQ17839.1	000902	Cluster278_1clades	79	Aeh1ORF173c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64377.1	000902	Cluster278_1clades	76	KVP40.0307	Vibrio phage KVP40	GCA_000843785.1
QIW90693.1	000902	Cluster278_1clades	76	GCAPEGMB_00346	Vibrio phage V07	GCA_012361095.1
QIW91105.1	000902	Cluster278_1clades	76	COHAPHLL_00269	Vibrio phage V09	GCA_012361135.1
QHJ74490.1	000902	Cluster278_1clades	74	VH12019_00163	Vibrio phage VH1_2019	GCA_009931825.1
QBX06161.1	000902	Cluster278_1clades	75	ValB1HC_208	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61178.1	000902	Cluster278_1clades	77	AVU32_gp337	Vibrio phage ValKK3	GCA_001501635.1
AGN30355.1	000902	Cluster278_1clades	74	VPFG_00358	Vibrio phage nt-1	GCA_000910195.2
ALP47281.1	000902	Cluster278_1clades	75	phiGrn1_0044	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47655.1	000902	Cluster278_1clades	77	phiST2_0176	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54787.1	000902	Cluster278_1clades	75	vBValMR10Z_247	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07057.1	000902	Cluster278_1clades	67	VmeM32_00066	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37539.1	000902	Cluster278_1clades	74	pp2_306	Vibriophage phi-pp2	GCA_002630725.1
AGH56839.1	000903	Cluster279_1clades	64	CPXG_00036	Cyanophage P-RSM6	GCA_000906155.1
AJK27607.1	000903	Cluster279_1clades	60	PTIM40_186	Cyanophage P-TIM40	GCA_001470935.1
AOO14373.1	000903	Cluster279_1clades	64	Sn110110_179	Cyanophage S-RIM14	GCA_002599065.1
AOO15021.1	000903	Cluster279_1clades	64	W1230910_175	Cyanophage S-RIM14	GCA_002599125.1
AMO43182.1	000903	Cluster279_1clades	70	R1080702_173	Cyanophage S-RIM32	GCA_001754165.1
AMO43407.1	000903	Cluster279_1clades	66	W270710_163	Cyanophage S-RIM44	GCA_002599145.1
AOO11651.1	000903	Cluster279_1clades	66	ES420910_170	Cyanophage S-RIM44	GCA_002599165.1
AOO11879.1	000903	Cluster279_1clades	66	Np050604_163	Cyanophage S-RIM44	GCA_002599185.1
AOO12117.1	000903	Cluster279_1clades	66	Np200711_171	Cyanophage S-RIM44	GCA_002599205.1
AOO12352.1	000903	Cluster279_1clades	66	Np420711_170	Cyanophage S-RIM44	GCA_002599225.1
AOO12580.1	000903	Cluster279_1clades	66	Sn080709_163	Cyanophage S-RIM44	GCA_002599245.1
AOO12817.1	000903	Cluster279_1clades	66	Sn130910_170	Cyanophage S-RIM44	GCA_002599265.1
AOO13046.1	000903	Cluster279_1clades	66	W2100709_164	Cyanophage S-RIM44	GCA_002599285.1
AGH07522.1	000903	Cluster279_1clades	64	CYVG_00078	Cyanophage S-SSM6a	GCA_002710385.1
AGG54429.1	000903	Cluster279_1clades	65	CYWG_00145	Cyanophage S-SSM6b	GCA_002710425.1
AIR93498.1	000903	Cluster279_1clades	65	AVU42_gp161	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99266.1	000903	Cluster279_1clades	66	Syn1_165	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76216.1	000903	Cluster279_1clades	67	PBI_BELLAMY_173	Synechococcus phage Bellamy	GCA_002627525.1
QCW22946.1	000903	Cluster279_1clades	66	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50536.1	000903	Cluster279_1clades	66	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59632.1	000903	Cluster279_1clades	67	S330809_171	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59394.1	000903	Cluster279_1clades	67	C440309_171	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59870.1	000903	Cluster279_1clades	67	N231010_171	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70534.1	000903	Cluster279_1clades	65	HOU04_gp135	Synechococcus phage S-T4	GCA_003443335.1
QJT70170.1	000903	Cluster279_1clades	67	SynMITS9220M01_158	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13534.1	000904	Cluster280_1clades	69	Ccr10_gp006	Caulobacter phage Ccr10	GCA_002619445.1
ARB13859.1	000904	Cluster280_1clades	69	Ccr10_gp329	Caulobacter phage Ccr10	GCA_002619445.1
ARB13880.1	000904	Cluster280_1clades	63	Ccr2_gp005	Caulobacter phage Ccr2	GCA_002619465.1
ARB14203.1	000904	Cluster280_1clades	63	Ccr2_gp327	Caulobacter phage Ccr2	GCA_002619465.1
ARB14563.1	000904	Cluster280_1clades	45	Ccr29_gp006	Caulobacter phage Ccr29	GCA_002619485.1
ARB14898.1	000904	Cluster280_1clades	45	Ccr29_gp342	Caulobacter phage Ccr29	GCA_002619485.1
ARB14925.1	000904	Cluster280_1clades	69	Ccr32_gp006	Caulobacter phage Ccr32	GCA_002619505.1
ARB15236.1	000904	Cluster280_1clades	69	Ccr32_gp318	Caulobacter phage Ccr32	GCA_002619505.1
ARB15256.1	000904	Cluster280_1clades	69	Ccr34_gp007	Caulobacter phage Ccr34	GCA_002619525.1
ARB15570.1	000904	Cluster280_1clades	69	Ccr34_gp328	Caulobacter phage Ccr34	GCA_002619525.1
ARB14223.1	000904	Cluster280_1clades	45	Ccr5_gp005	Caulobacter phage Ccr5	GCA_002619545.1
ARB14543.1	000904	Cluster280_1clades	45	Ccr5_gp323	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68210.1	000904	Cluster280_1clades	55	CcrBL10_gp006	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68528.1	000904	Cluster280_1clades	55	CcrBL10_gp324	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87873.1	000904	Cluster280_1clades	68	CcrColossus_gp003	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87523.1	000904	Cluster280_1clades	69	CcrKarma_gp006	Caulobacter virus Karma	GCA_000901575.1
AFU87856.1	000904	Cluster280_1clades	69	CcrKarma_gp339	Caulobacter virus Karma	GCA_000901575.1
AFU87176.1	000904	Cluster280_1clades	69	CcrMagneto_gp006	Caulobacter virus Magneto	GCA_000903095.1
AFU87504.1	000904	Cluster280_1clades	69	CcrMagneto_gp334	Caulobacter virus Magneto	GCA_000903095.1
AFU86490.1	000904	Cluster280_1clades	64	CcrRogue_gp008	Caulobacter virus Rogue	GCA_000900555.1
AFU86821.1	000904	Cluster280_1clades	64	CcrRogue_gp339	Caulobacter virus Rogue	GCA_000900555.1
AFU88325.1	000904	Cluster280_1clades	64	CcrSwift_gp007	Caulobacter virus Swift	GCA_000899655.1
AFU88650.1	000904	Cluster280_1clades	64	CcrSwift_gp332	Caulobacter virus Swift	GCA_000899655.1
AFU86838.1	000904	Cluster280_1clades	69	CbK_gp006	Caulobacter virus phiCbK	GCA_000900535.1
AFU87156.1	000904	Cluster280_1clades	69	CbK_gp324	Caulobacter virus phiCbK	GCA_000900535.1
AFC21766.1	000905	Cluster281_1clades	535	GAP32_316	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21767.1	000905	Cluster281_1clades	844	GAP32_317	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13947.1	000905	Cluster281_1clades	523	PBI_121Q_50	Escherichia phage 121Q	GCA_000926855.1
QAY00390.1	000905	Cluster281_1clades	523	Ecwhy1_109	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35135.1	000905	Cluster281_1clades	523	ACQ29_gp455	Escherichia phage PBECO4	GCA_001041035.1
BBM61639.1	000905	Cluster281_1clades	523	EO157G_0500	Escherichia phage SP27	GCA_008033345.1
AXC36709.1	000905	Cluster281_1clades	480	-	Escherichia phage UB	GCA_003341455.1
QBO61746.1	000905	Cluster281_1clades	523	G17_00257	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13791.1	000905	Cluster281_1clades	523	vBEcoMphAPEC6_gp162c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80541.1	000905	Cluster281_1clades	523	PSLUR01_00564	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43884.1	000905	Cluster281_1clades	536	CBB_321	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43885.1	000905	Cluster281_1clades	847	CBB_322	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19044.1	000905	Cluster281_1clades	526	7t3_0524	Salmonella phage 7t3	GCA_006083215.1
QCW19045.1	000905	Cluster281_1clades	878	7t3_0525	Salmonella phage 7t3	GCA_006083215.1
AZU98291.1	000905	Cluster281_1clades	526	CPT_Munch_347	Salmonella phage Munch	GCA_004015485.1
AZU98292.1	000905	Cluster281_1clades	878	CPT_Munch_348	Salmonella phage Munch	GCA_004015485.1
QIG62692.1	000905	Cluster281_1clades	878	SEPL_079	Salmonella phage SE_PL	GCA_011067555.1
QIG62693.1	000905	Cluster281_1clades	526	SEPL_080	Salmonella phage SE_PL	GCA_011067555.1
AQW88844.1	000905	Cluster281_1clades	528	BF_0319	Serratia phage BF	GCA_002619745.1
AQW88845.1	000905	Cluster281_1clades	810	BF_0320	Serratia phage BF	GCA_002619745.1
SOK59128.1	000905	Cluster281_1clades	528	g320	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59129.1	000905	Cluster281_1clades	816	g321	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58594.1	000905	Cluster281_1clades	528	g317	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58595.1	000905	Cluster281_1clades	816	g318	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ94824.1	000906	Cluster282_2clades	336	FDI40_gp012	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21546.1	000906	Cluster282_2clades	406	GAP32_098	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14349.1	000906	Cluster282_2clades	399	PBI_121Q_459	Escherichia phage 121Q	GCA_000926855.1
QAY00595.1	000906	Cluster282_2clades	399	Ecwhy1_318	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34790.1	000906	Cluster282_2clades	399	ACQ29_gp110	Escherichia phage PBECO4	GCA_001041035.1
BBM62020.1	000906	Cluster282_2clades	399	EO157G_4310	Escherichia phage SP27	GCA_008033345.1
AXC36906.1	000906	Cluster282_2clades	399	-	Escherichia phage UB	GCA_003341455.1
QBO61955.1	000906	Cluster282_2clades	399	G17_00466	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13982.1	000906	Cluster282_2clades	399	vBEcoMphAPEC6_gp358c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80336.1	000906	Cluster282_2clades	399	PSLUR01_00359	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44758.1	000906	Cluster282_2clades	404	RaK2_00485	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43664.1	000906	Cluster282_2clades	412	CBB_99	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76157.1	000906	Cluster282_2clades	344	EST35_0276	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18800.1	000906	Cluster282_2clades	401	7t3_0279	Salmonella phage 7t3	GCA_006083215.1
AZU98065.1	000906	Cluster282_2clades	402	CPT_Munch_121	Salmonella phage Munch	GCA_004015485.1
QIG62917.1	000906	Cluster282_2clades	401	SEPL_304	Salmonella phage SE_PL	GCA_011067555.1
AQW88617.1	000906	Cluster282_2clades	410	BF_0092	Serratia phage BF	GCA_002619745.1
QAU04461.1	000906	Cluster282_2clades	385	ValB1MD_053	Vibrio phage ValB1MD	GCA_004138815.1
BBA65726.1	000906	Cluster282_2clades	282	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65267.1	000906	Cluster282_2clades	282	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK58893.1	000906	Cluster282_2clades	411	g085	Yersinia phage fHe-Yen9-03	GCA_002990515.1

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SOK58356.1	000906	Cluster282_2clades	409	g079	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000190	000906	Cluster282_2clades	493	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000153	000906	Cluster282_2clades	493	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QMV28819.1	000907	Cluster285_1clades	330	AP1_0112	Aeromonas phage AP1	GCA_014183365.1
ATI17607.1	000907	Cluster285_1clades	302	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00389.1	000907	Cluster285_1clades	302	HWB28_gp163	Aeromonas phage AS-zj	GCA_002627665.1
QAX98048.1	000907	Cluster285_1clades	302	ASswx1_408	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01097.1	000907	Cluster285_1clades	305	ASwh1_29	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39472.1	000907	Cluster285_1clades	302	CC2_122	Aeromonas phage CC2	GCA_000903495.1
AEO93464.1	000907	Cluster285_1clades	334	G_205	Bacillus virus G	GCA_000917535.1
ARM70951.1	000907	Cluster285_1clades	318	phiC120_c246	Escherichia phage phiC120	GCA_002621185.1
QIG65861.1	000907	Cluster285_1clades	297	phiOC_p196	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QCW18794.1	000907	Cluster285_1clades	296	7t3_0273	Salmonella phage 7t3	GCA_006083215.1
AZU98059.1	000907	Cluster285_1clades	296	CPT_Munch_115	Salmonella phage Munch	GCA_004015485.1
QIG62923.1	000907	Cluster285_1clades	296	SEPL_310	Salmonella phage SE_PL	GCA_011067555.1
AAQ64108.1	000907	Cluster285_1clades	253	KVP40.0037	Vibrio phage KVP40	GCA_000843785.1
QIW90431.1	000907	Cluster285_1clades	253	GCAPEGMB_00084	Vibrio phage V07	GCA_012361095.1
QIW90998.1	000907	Cluster285_1clades	253	COHAPHLL_00135	Vibrio phage V09	GCA_012361135.1
QHJ74220.1	000907	Cluster285_1clades	253	VH12019_00301	Vibrio phage VH1_2019	GCA_009931825.1
AGB07044.1	000907	Cluster285_1clades	253	CF80_gp257	Vibrio phage VH7D	GCA_000914495.1
QBX06052.1	000907	Cluster285_1clades	253	ValB1HC_098	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61065.1	000907	Cluster285_1clades	253	AVU32_gp224	Vibrio phage ValKK3	GCA_001501635.1
AGN30086.1	000907	Cluster285_1clades	253	VPFG_00084	Vibrio phage nt-1	GCA_000910195.2
ALP47041.1	000907	Cluster285_1clades	253	phiGrn1_0152	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47446.1	000907	Cluster285_1clades	204	phiST2_0282	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54678.1	000907	Cluster285_1clades	253	vBValMR10Z_137	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37270.1	000907	Cluster285_1clades	253	pp2_036	Vibriophage phi-pp2	GCA_002630725.1
APU01731.1	000908	Cluster289_1clades	107	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01412.1	000908	Cluster289_1clades	113	ASwh1_353	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53373.1	000908	Cluster289_1clades	107	65p365	Aeromonas virus 65	GCA_000893255.1
AIA64981.1	000908	Cluster289_1clades	173	S13_184	Cronobacter phage S13	GCA_001503575.1
AFC21623.1	000908	Cluster289_1clades	119	GAP32_173	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14418.1	000908	Cluster289_1clades	116	PBI_121Q_528	Escherichia phage 121Q	GCA_000926855.1
QAY00532.1	000908	Cluster289_1clades	114	Ecwhy1_253	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34724.1	000908	Cluster289_1clades	116	ACQ29_gp044	Escherichia phage PBECO4	GCA_001041035.1
BBM62090.1	000908	Cluster289_1clades	114	EO157G_5010	Escherichia phage SP27	GCA_008033345.1
AXC37014.1	000908	Cluster289_1clades	114	-	Escherichia phage UB	GCA_003341455.1
QBO61883.1	000908	Cluster289_1clades	114	G17_00394	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13921.1	000908	Cluster289_1clades	114	vBEcoMphAPEC6_gp296c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80404.1	000908	Cluster289_1clades	114	PSLUR01_00427	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44298.1	000908	Cluster289_1clades	113	RaK2_00025	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78954.1	000908	Cluster289_1clades	154	-	Myoviridae sp.	GCA_012593985.1
AMM43741.1	000908	Cluster289_1clades	119	CBB_176	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18888.1	000908	Cluster289_1clades	114	7t3_0367	Salmonella phage 7t3	GCA_006083215.1
AZU98146.1	000908	Cluster289_1clades	114	CPT_Munch_202	Salmonella phage Munch	GCA_004015485.1
QIG62837.1	000908	Cluster289_1clades	114	SEPL_224	Salmonella phage SE_PL	GCA_011067555.1
AQW88699.1	000908	Cluster289_1clades	177	BF_0174	Serratia phage BF	GCA_002619745.1
BBI90504.1	000908	Cluster289_1clades	125	HYO65_gp112	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90812.1	000908	Cluster289_1clades	125	-	Tenacibaculum phage PTm5	GCA_009730715.1
SOK58980.1	000908	Cluster289_1clades	176	g172	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58446.1	000908	Cluster289_1clades	176	g169	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13573.1	000909	Cluster290_1clades	79	Ccr10_gp045	Caulobacter phage Ccr10	GCA_002619445.1
ARB13574.1	000909	Cluster290_1clades	57	Ccr10_gp046	Caulobacter phage Ccr10	GCA_002619445.1
ARB13919.1	000909	Cluster290_1clades	79	Ccr2_gp044	Caulobacter phage Ccr2	GCA_002619465.1
ARB13920.1	000909	Cluster290_1clades	57	Ccr2_gp045	Caulobacter phage Ccr2	GCA_002619465.1
ARB14608.1	000909	Cluster290_1clades	79	Ccr29_gp051	Caulobacter phage Ccr29	GCA_002619485.1
ARB14609.1	000909	Cluster290_1clades	57	Ccr29_gp052	Caulobacter phage Ccr29	GCA_002619485.1
ARB14964.1	000909	Cluster290_1clades	79	Ccr32_gp045	Caulobacter phage Ccr32	GCA_002619505.1
ARB14965.1	000909	Cluster290_1clades	57	Ccr32_gp046	Caulobacter phage Ccr32	GCA_002619505.1
ARB15295.1	000909	Cluster290_1clades	79	Ccr34_gp046	Caulobacter phage Ccr34	GCA_002619525.1
ARB15296.1	000909	Cluster290_1clades	57	Ccr34_gp047	Caulobacter phage Ccr34	GCA_002619525.1
ARB14262.1	000909	Cluster290_1clades	79	Ccr5_gp044	Caulobacter phage Ccr5	GCA_002619545.1
ARB14263.1	000909	Cluster290_1clades	57	Ccr5_gp045	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68248.1	000909	Cluster290_1clades	134	CcrBL10_gp044	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69117.1	000909	Cluster290_1clades	56	CcrBL9_gp093	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69671.1	000909	Cluster290_1clades	56	CcrSC_gp089	Caulobacter phage CcrSC	GCA_003443315.1
AFU87563.1	000909	Cluster290_1clades	79	CcrKarma_gp046	Caulobacter virus Karma	GCA_000901575.1
AFU87564.1	000909	Cluster290_1clades	57	CcrKarma_gp047	Caulobacter virus Karma	GCA_000901575.1
AFU87213.1	000909	Cluster290_1clades	79	CcrMagneto_gp043	Caulobacter virus Magneto	GCA_000903095.1
AFU87214.1	000909	Cluster290_1clades	57	CcrMagneto_gp044	Caulobacter virus Magneto	GCA_000903095.1
AFU86530.1	000909	Cluster290_1clades	141	CcrRogue_gp048	Caulobacter virus Rogue	GCA_000900555.1
AFU88361.1	000909	Cluster290_1clades	79	CcrSwift_gp043	Caulobacter virus Swift	GCA_000899655.1
AFU88362.1	000909	Cluster290_1clades	62	CcrSwift_gp044	Caulobacter virus Swift	GCA_000899655.1
AFU86877.1	000909	Cluster290_1clades	79	CbK_gp045	Caulobacter virus phiCbK	GCA_000900535.1
AFU86878.1	000909	Cluster290_1clades	57	CbK_gp046	Caulobacter virus phiCbK	GCA_000900535.1
AMO43229.1	000910	SIG+DUF2973	76	R1080702_224	Cyanophage S-RIM32	GCA_001754165.1
AMO43461.1	000910	SIG+DUF2973	75	W270710_222	Cyanophage S-RIM44	GCA_002599145.1
AOO11701.1	000910	SIG+DUF2973	75	ES420910_224	Cyanophage S-RIM44	GCA_002599165.1
AOO11933.1	000910	SIG+DUF2973	75	Np050604_222	Cyanophage S-RIM44	GCA_002599185.1
AOO12167.1	000910	SIG+DUF2973	75	Np200711_225	Cyanophage S-RIM44	GCA_002599205.1
AOO12402.1	000910	SIG+DUF2973	75	Np420711_224	Cyanophage S-RIM44	GCA_002599225.1
AOO12634.1	000910	SIG+DUF2973	75	Sn080709_222	Cyanophage S-RIM44	GCA_002599245.1
AOO12867.1	000910	SIG+DUF2973	75	Sn130910_224	Cyanophage S-RIM44	GCA_002599265.1
AOO13100.1	000910	SIG+DUF2973	75	W2100709_223	Cyanophage S-RIM44	GCA_002599285.1
AGH07616.1	000910	SIG+DUF2973	75	CYVG_00173	Cyanophage S-SSM6a	GCA_002710385.1
AGH26221.1	000910	SIG+DUF2973	78	CPMG_00120	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44694.1	000910	SIG+DUF2973	136	PSSM2_316	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12282.1	000910	SIG+DUF2973	136	PRTG_00129	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93575.1	000910	SIG+DUF2973	79	AVU42_gp237	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99322.1	000910	SIG+DUF2973	75	Syn1_226	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30759.1	000910	SIG+DUF2973	76	Syn7803US37_282	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76302.1	000910	SIG+DUF2973	73	PBI_BELLAMY_266	Synechococcus phage Bellamy	GCA_002627525.1
QCW23053.1	000910	SIG+DUF2973	73	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50698.1	000910	SIG+DUF2973	73	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59684.1	000910	SIG+DUF2973	74	S330809_223	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59446.1	000910	SIG+DUF2973	74	C440309_223	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59921.1	000910	SIG+DUF2973	74	N231010_222	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70459.1	000910	SIG+DUF2973	72	HOU04_gp060	Synechococcus phage S-T4	GCA_003443335.1
QJT70249.1	000910	SIG+DUF2973	73	SynMITS9220M01_243	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13548.1	000911	Cluster292_1clades	130	Ccr10_gp020	Caulobacter phage Ccr10	GCA_002619445.1
ARB13873.1	000911	Cluster292_1clades	130	Ccr10_gp343	Caulobacter phage Ccr10	GCA_002619445.1
ARB13894.1	000911	Cluster292_1clades	130	Ccr2_gp019	Caulobacter phage Ccr2	GCA_002619465.1
ARB14217.1	000911	Cluster292_1clades	130	Ccr2_gp341	Caulobacter phage Ccr2	GCA_002619465.1
ARB14583.1	000911	Cluster292_1clades	130	Ccr29_gp026	Caulobacter phage Ccr29	GCA_002619485.1
ARB14918.1	000911	Cluster292_1clades	130	Ccr29_gp362	Caulobacter phage Ccr29	GCA_002619485.1
ARB14938.1	000911	Cluster292_1clades	130	Ccr32_gp019	Caulobacter phage Ccr32	GCA_002619505.1
ARB15249.1	000911	Cluster292_1clades	130	Ccr32_gp331	Caulobacter phage Ccr32	GCA_002619505.1
ARB15269.1	000911	Cluster292_1clades	130	Ccr34_gp020	Caulobacter phage Ccr34	GCA_002619525.1
ARB15583.1	000911	Cluster292_1clades	130	Ccr34_gp341	Caulobacter phage Ccr34	GCA_002619525.1
ARB14237.1	000911	Cluster292_1clades	130	Ccr5_gp019	Caulobacter phage Ccr5	GCA_002619545.1
ARB14557.1	000911	Cluster292_1clades	130	Ccr5_gp337	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68220.1	000911	Cluster292_1clades	130	CcrBL10_gp016	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68538.1	000911	Cluster292_1clades	130	CcrBL10_gp334	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87536.1	000911	Cluster292_1clades	130	CcrKarma_gp019	Caulobacter virus Karma	GCA_000901575.1
AFU87869.1	000911	Cluster292_1clades	130	CcrKarma_gp352	Caulobacter virus Karma	GCA_000901575.1
AFU87188.1	000911	Cluster292_1clades	130	CcrMagneto_gp018	Caulobacter virus Magneto	GCA_000903095.1
AFU87516.1	000911	Cluster292_1clades	130	CcrMagneto_gp346	Caulobacter virus Magneto	GCA_000903095.1
AFU86500.1	000911	Cluster292_1clades	130	CcrRogue_gp018	Caulobacter virus Rogue	GCA_000900555.1
AFU86831.1	000911	Cluster292_1clades	130	CcrRogue_gp349	Caulobacter virus Rogue	GCA_000900555.1
AFU88335.1	000911	Cluster292_1clades	130	CcrSwift_gp017	Caulobacter virus Swift	GCA_000899655.1
AFU88660.1	000911	Cluster292_1clades	130	CcrSwift_gp342	Caulobacter virus Swift	GCA_000899655.1
AFU86851.1	000911	Cluster292_1clades	130	CbK_gp019	Caulobacter virus phiCbK	GCA_000900535.1
AFU87169.1	000911	Cluster292_1clades	130	CbK_gp337	Caulobacter virus phiCbK	GCA_000900535.1
ARB13541.1	000912	Cluster293_1clades	90	Ccr10_gp013	Caulobacter phage Ccr10	GCA_002619445.1
ARB13866.1	000912	Cluster293_1clades	90	Ccr10_gp336	Caulobacter phage Ccr10	GCA_002619445.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB13888.1	000912	Cluster293_1clades	90	Ccr2_gp013	Caulobacter phage Ccr2	GCA_002619465.1
ARB14211.1	000912	Cluster293_1clades	90	Ccr2_gp335	Caulobacter phage Ccr2	GCA_002619465.1
ARB14570.1	000912	Cluster293_1clades	90	Ccr29_gp013	Caulobacter phage Ccr29	GCA_002619485.1
ARB14905.1	000912	Cluster293_1clades	90	Ccr29_gp349	Caulobacter phage Ccr29	GCA_002619485.1
ARB14931.1	000912	Cluster293_1clades	90	Ccr32_gp012	Caulobacter phage Ccr32	GCA_002619505.1
ARB15242.1	000912	Cluster293_1clades	90	Ccr32_gp324	Caulobacter phage Ccr32	GCA_002619505.1
ARB15262.1	000912	Cluster293_1clades	90	Ccr34_gp013	Caulobacter phage Ccr34	GCA_002619525.1
ARB15576.1	000912	Cluster293_1clades	90	Ccr34_gp334	Caulobacter phage Ccr34	GCA_002619525.1
ARB14230.1	000912	Cluster293_1clades	90	Ccr5_gp012	Caulobacter phage Ccr5	GCA_002619545.1
ARB14550.1	000912	Cluster293_1clades	90	Ccr5_gp330	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68214.1	000912	Cluster293_1clades	90	CcrBL10_gp010	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68532.1	000912	Cluster293_1clades	90	CcrBL10_gp328	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87529.1	000912	Cluster293_1clades	90	CcrKarma_gp012	Caulobacter virus Karma	GCA_000901575.1
AFU87862.1	000912	Cluster293_1clades	90	CcrKarma_gp345	Caulobacter virus Karma	GCA_000901575.1
AFU87182.1	000912	Cluster293_1clades	90	CcrMagneto_gp012	Caulobacter virus Magneto	GCA_000903095.1
AFU87510.1	000912	Cluster293_1clades	90	CcrMagneto_gp340	Caulobacter virus Magneto	GCA_000903095.1
AFU86494.1	000912	Cluster293_1clades	90	CcrRogue_gp012	Caulobacter virus Rogue	GCA_000900555.1
AFU86825.1	000912	Cluster293_1clades	90	CcrRogue_gp343	Caulobacter virus Rogue	GCA_000900555.1
AFU88329.1	000912	Cluster293_1clades	90	CcrSwift_gp011	Caulobacter virus Swift	GCA_000899655.1
AFU88654.1	000912	Cluster293_1clades	90	CcrSwift_gp336	Caulobacter virus Swift	GCA_000899655.1
AFU86844.1	000912	Cluster293_1clades	90	CbK_gp012	Caulobacter virus phiCbK	GCA_000900535.1
AFU87162.1	000912	Cluster293_1clades	90	CbK_gp330	Caulobacter virus phiCbK	GCA_000900535.1
ARB13529.1	000913	Cluster294_1clades	67	Ccr10_gp002	Caulobacter phage Ccr10	GCA_002619445.1
ARB13855.1	000913	Cluster294_1clades	67	Ccr10_gp325	Caulobacter phage Ccr10	GCA_002619445.1
ARB13876.1	000913	Cluster294_1clades	63	Ccr2_gp002	Caulobacter phage Ccr2	GCA_002619465.1
ARB14200.1	000913	Cluster294_1clades	63	Ccr2_gp324	Caulobacter phage Ccr2	GCA_002619465.1
ARB14559.1	000913	Cluster294_1clades	63	Ccr29_gp002	Caulobacter phage Ccr29	GCA_002619485.1
ARB14894.1	000913	Cluster294_1clades	63	Ccr29_gp338	Caulobacter phage Ccr29	GCA_002619485.1
ARB14921.1	000913	Cluster294_1clades	63	Ccr32_gp002	Caulobacter phage Ccr32	GCA_002619505.1
ARB15232.1	000913	Cluster294_1clades	63	Ccr32_gp314	Caulobacter phage Ccr32	GCA_002619505.1
ARB15252.1	000913	Cluster294_1clades	63	Ccr34_gp002	Caulobacter phage Ccr34	GCA_002619525.1
ARB15566.1	000913	Cluster294_1clades	63	Ccr34_gp324	Caulobacter phage Ccr34	GCA_002619525.1
ARB14220.1	000913	Cluster294_1clades	63	Ccr5_gp002	Caulobacter phage Ccr5	GCA_002619545.1
ARB14540.1	000913	Cluster294_1clades	63	Ccr5_gp320	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68206.1	000913	Cluster294_1clades	77	CcrBL10_gp002	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68524.1	000913	Cluster294_1clades	77	CcrBL10_gp320	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87518.1	000913	Cluster294_1clades	63	CcrKarma_gp001	Caulobacter virus Karma	GCA_000901575.1
AFU87851.1	000913	Cluster294_1clades	63	CcrKarma_gp334	Caulobacter virus Karma	GCA_000901575.1
AFU87171.1	000913	Cluster294_1clades	67	CcrMagneto_gp001	Caulobacter virus Magneto	GCA_000903095.1
AFU87499.1	000913	Cluster294_1clades	67	CcrMagneto_gp329	Caulobacter virus Magneto	GCA_000903095.1
AFU86483.1	000913	Cluster294_1clades	77	CcrRogue_gp001	Caulobacter virus Rogue	GCA_000900555.1
AFU86814.1	000913	Cluster294_1clades	77	CcrRogue_gp332	Caulobacter virus Rogue	GCA_000900555.1
AFU88319.1	000913	Cluster294_1clades	63	CcrSwift_gp001	Caulobacter virus Swift	GCA_000899655.1
AFU88644.1	000913	Cluster294_1clades	63	CcrSwift_gp326	Caulobacter virus Swift	GCA_000899655.1
AFU86833.1	000913	Cluster294_1clades	63	CbK_gp001	Caulobacter virus phiCbK	GCA_000900535.1
AFU87151.1	000913	Cluster294_1clades	63	CbK_gp319	Caulobacter virus phiCbK	GCA_000900535.1
ARB13549.1	000914	SIG+TM	64	Ccr10_gp021	Caulobacter phage Ccr10	GCA_002619445.1
ARB13874.1	000914	SIG+TM	64	Ccr10_gp344	Caulobacter phage Ccr10	GCA_002619445.1
ARB13895.1	000914	SIG+TM	64	Ccr2_gp020	Caulobacter phage Ccr2	GCA_002619465.1
ARB14218.1	000914	SIG+TM	64	Ccr2_gp342	Caulobacter phage Ccr2	GCA_002619465.1
ARB14584.1	000914	SIG+TM	64	Ccr29_gp027	Caulobacter phage Ccr29	GCA_002619485.1
ARB14919.1	000914	SIG+TM	64	Ccr29_gp363	Caulobacter phage Ccr29	GCA_002619485.1
ARB14939.1	000914	SIG+TM	64	Ccr32_gp020	Caulobacter phage Ccr32	GCA_002619505.1
ARB15250.1	000914	SIG+TM	64	Ccr32_gp332	Caulobacter phage Ccr32	GCA_002619505.1
ARB15270.1	000914	SIG+TM	64	Ccr34_gp021	Caulobacter phage Ccr34	GCA_002619525.1
ARB15584.1	000914	SIG+TM	64	Ccr34_gp342	Caulobacter phage Ccr34	GCA_002619525.1
ARB14238.1	000914	SIG+TM	64	Ccr5_gp020	Caulobacter phage Ccr5	GCA_002619545.1
ARB14558.1	000914	SIG+TM	64	Ccr5_gp338	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68221.1	000914	SIG+TM	63	CcrBL10_gp017	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68539.1	000914	SIG+TM	63	CcrBL10_gp335	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87537.1	000914	SIG+TM	64	CcrKarma_gp020	Caulobacter virus Karma	GCA_000901575.1
AFU87870.1	000914	SIG+TM	64	CcrKarma_gp353	Caulobacter virus Karma	GCA_000901575.1
AFU87189.1	000914	SIG+TM	64	CcrMagneto_gp019	Caulobacter virus Magneto	GCA_000903095.1
AFU87517.1	000914	SIG+TM	64	CcrMagneto_gp347	Caulobacter virus Magneto	GCA_000903095.1
AFU86501.1	000914	SIG+TM	63	CcrRogue_gp019	Caulobacter virus Rogue	GCA_000900555.1
AFU86832.1	000914	SIG+TM	63	CcrRogue_gp350	Caulobacter virus Rogue	GCA_000900555.1
AFU88336.1	000914	SIG+TM	64	CcrSwift_gp018	Caulobacter virus Swift	GCA_000899655.1
AFU88661.1	000914	SIG+TM	64	CcrSwift_gp343	Caulobacter virus Swift	GCA_000899655.1
AFU86852.1	000914	SIG+TM	64	CbK_gp020	Caulobacter virus phiCbK	GCA_000900535.1
AFU87170.1	000914	SIG+TM	64	CbK_gp338	Caulobacter virus phiCbK	GCA_000900535.1
AUZ94963.1	000915	Cluster296_1clades	1198	FDI40_gp181	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21681.1	000915	Cluster296_1clades	1154	GAP32_231	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14473.1	000915	Cluster296_1clades	1153	PBI_121Q_583	Escherichia phage 121Q	GCA_000926855.1
QAY00474.1	000915	Cluster296_1clades	1153	Ecwhy1_195	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35217.1	000915	Cluster296_1clades	1153	ACQ29_gp537	Escherichia phage PBECO4	GCA_001041035.1
BBM62146.1	000915	Cluster296_1clades	1153	EO157G_5570	Escherichia phage SP27	GCA_008033345.1
AXC36789.1	000915	Cluster296_1clades	1153	-	Escherichia phage UB	GCA_003341455.1
QBO61829.1	000915	Cluster296_1clades	1153	G17_00340	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13873.1	000915	Cluster296_1clades	1153	vBEcoMphAPEC6_gp244	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80458.1	000915	Cluster296_1clades	1153	PSLUR01_00481	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44344.1	000915	Cluster296_1clades	1154	RaK2_00071	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72696.1	000915	Cluster296_1clades	1088	-	Myoviridae sp.	GCA_003657725.1
AMM43802.1	000915	Cluster296_1clades	1154	CBB_237	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76011.1	000915	Cluster296_1clades	1319	EST35_0129	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44254.1	000915	Cluster296_1clades	1241	PBI_SCTP2_239	Salicola phage SCTP-2	GCA_002625545.1
QCW18954.1	000915	Cluster296_1clades	1154	7t3_0433	Salmonella phage 7t3	GCA_006083215.1
AZU98207.1	000915	Cluster296_1clades	1154	CPT_Munch_263	Salmonella phage Munch	GCA_004015485.1
QIG62777.1	000915	Cluster296_1clades	1154	SEPL_164	Salmonella phage SE_PL	GCA_011067555.1
AQW88761.1	000915	Cluster296_1clades	1153	BF_0236	Serratia phage BF	GCA_002619745.1
BBA65472.1	000915	Cluster296_1clades	971	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96481.1	000915	Cluster296_1clades	971	Xoosp13_295	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59042.1	000915	Cluster296_1clades	1153	g234c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58507.1	000915	Cluster296_1clades	1153	g230c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44719.1	000916	Cluster298_1clades	364	FDI40_gp142	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21678.1	000916	Cluster298_1clades	498	GAP32_228	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14470.1	000916	Cluster298_1clades	497	PBI_121Q_580	Escherichia phage 121Q	GCA_000926855.1
QAY00477.1	000916	Cluster298_1clades	498	Ecwhy1_198	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35220.1	000916	Cluster298_1clades	497	ACQ29_gp540	Escherichia phage PBECO4	GCA_001041035.1
BBM62143.1	000916	Cluster298_1clades	497	EO157G_5540	Escherichia phage SP27	GCA_008033345.1
AXC36791.1	000916	Cluster298_1clades	497	-	Escherichia phage UB	GCA_003341455.1
QBO61832.1	000916	Cluster298_1clades	497	G17_00343	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13876.1	000916	Cluster298_1clades	497	vBEcoMphAPEC6_gp247	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80455.1	000916	Cluster298_1clades	497	PSLUR01_00478	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44341.1	000916	Cluster298_1clades	486	RaK2_00068	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72757.1	000916	Cluster298_1clades	395	-	Myoviridae sp.	GCA_003657725.1
AMM43799.1	000916	Cluster298_1clades	498	CBB_234	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76045.1	000916	Cluster298_1clades	363	EST35_0163	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44276.1	000916	Cluster298_1clades	336	PBI_SCTP2_261	Salicola phage SCTP-2	GCA_002625545.1
QCW18950.1	000916	Cluster298_1clades	497	7t3_0429	Salmonella phage 7t3	GCA_006083215.1
AZU98204.1	000916	Cluster298_1clades	497	CPT_Munch_260	Salmonella phage Munch	GCA_004015485.1
QIG62780.1	000916	Cluster298_1clades	497	SEPL_167	Salmonella phage SE_PL	GCA_011067555.1
AQW88758.1	000916	Cluster298_1clades	495	BF_0233	Serratia phage BF	GCA_002619745.1
BBA65415.1	000916	Cluster298_1clades	551	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96438.1	000916	Cluster298_1clades	550	Xoosp13_252	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59039.1	000916	Cluster298_1clades	496	g231c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58504.1	000916	Cluster298_1clades	496	g227c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44765.1	000917	Cluster299_1clades	468	FDI40_gp696	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21687.1	000917	Cluster299_1clades	245	GAP32_237	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14480.1	000917	Cluster299_1clades	243	PBI_121Q_590	Escherichia phage 121Q	GCA_000926855.1
QAY00468.1	000917	Cluster299_1clades	243	Ecwhy1_189	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35211.1	000917	Cluster299_1clades	243	ACQ29_gp531	Escherichia phage PBECO4	GCA_001041035.1
BBM62152.1	000917	Cluster299_1clades	243	EO157G_5630	Escherichia phage SP27	GCA_008033345.1
AXC36783.1	000917	Cluster299_1clades	243	-	Escherichia phage UB	GCA_003341455.1
QBO61823.1	000917	Cluster299_1clades	243	G17_00334	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13867.1	000917	Cluster299_1clades	243	vBEcoMphAPEC6_gp238	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SCA80464.1	000917	Cluster299_1clades	243	PSLUR01_00487	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44354.1	000917	Cluster299_1clades	243	RaK2_00081	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72725.1	000917	Cluster299_1clades	324	-	Myoviridae sp.	GCA_003657725.1
AMM43808.1	000917	Cluster299_1clades	245	CBB_243	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76018.1	000917	Cluster299_1clades	211	EST35_0136	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44201.1	000917	Cluster299_1clades	226	PBI_SCTP2_186	Salicola phage SCTP-2	GCA_002625545.1
QCW18960.1	000917	Cluster299_1clades	243	7t3_0439	Salmonella phage 7t3	GCA_006083215.1
AZU98213.1	000917	Cluster299_1clades	243	CPT_Munch_269	Salmonella phage Munch	GCA_004015485.1
QIG62771.1	000917	Cluster299_1clades	243	SEPL_158	Salmonella phage SE_PL	GCA_011067555.1
AQW88767.1	000917	Cluster299_1clades	245	BF_0242	Serratia phage BF	GCA_002619745.1
BBA65466.1	000917	Cluster299_1clades	262	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96475.1	000917	Cluster299_1clades	253	Xoosp13_289	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59048.1	000917	Cluster299_1clades	245	g240c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58513.1	000917	Cluster299_1clades	245	g236c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ94959.1	000918	Cluster301_1clades	198	FDI40_gp177	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21674.1	000918	Cluster301_1clades	202	GAP32_224	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14466.1	000918	Cluster301_1clades	202	PBI_121Q_576	Escherichia phage 121Q	GCA_000926855.1
QAY00481.1	000918	Cluster301_1clades	202	Ecwhy1_202	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35224.1	000918	Cluster301_1clades	202	ACQ29_gp544	Escherichia phage PBECO4	GCA_001041035.1
BBM62139.1	000918	Cluster301_1clades	202	EO157G_5500	Escherichia phage SP27	GCA_008033345.1
AXC36796.1	000918	Cluster301_1clades	202	-	Escherichia phage UB	GCA_003341455.1
QBO61836.1	000918	Cluster301_1clades	202	G17_00347	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13880.1	000918	Cluster301_1clades	202	vBEcoMphAPEC6_gp251c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80451.1	000918	Cluster301_1clades	202	PSLUR01_00474	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44337.1	000918	Cluster301_1clades	201	RaK2_00064	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72704.1	000918	Cluster301_1clades	223	-	Myoviridae sp.	GCA_003657725.1
AMM43795.1	000918	Cluster301_1clades	202	CBB_230	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76008.1	000918	Cluster301_1clades	201	EST35_0126	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44154.1	000918	Cluster301_1clades	198	PBI_SCTP2_139	Salicola phage SCTP-2	GCA_002625545.1
QCW18946.1	000918	Cluster301_1clades	202	7t3_0425	Salmonella phage 7t3	GCA_006083215.1
AZU98200.1	000918	Cluster301_1clades	202	CPT_Munch_256	Salmonella phage Munch	GCA_004015485.1
QIG62784.1	000918	Cluster301_1clades	202	SEPL_171	Salmonella phage SE_PL	GCA_011067555.1
AQW88754.1	000918	Cluster301_1clades	202	BF_0229	Serratia phage BF	GCA_002619745.1
BBA65477.1	000918	Cluster301_1clades	402	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96485.1	000918	Cluster301_1clades	344	Xoosp13_299	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59034.1	000918	Cluster301_1clades	202	g226	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58499.1	000918	Cluster301_1clades	202	g222	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71313.1	000919	Cluster302_1clades	350	CR5_093	Cronobacter phage CR5	GCA_000910235.1
AMR59747.1	000919	Cluster302_1clades	377	SEGD1_098	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07522.1	000919	Cluster302_1clades	350	DERBICUS_96	Erwinia phage Derbicus	GCA_004521655.1
ANZ49744.1	000919	Cluster302_1clades	388	MACHINA_106	Erwinia phage Machina	GCA_002758035.1
AXF51244.1	000919	Cluster302_1clades	332	WELLINGTON_114	Erwinia phage Wellington	GCA_003344985.1
AXF51245.1	000919	Cluster302_1clades	380	WELLINGTON_115	Erwinia phage Wellington	GCA_003344985.1
AFQ96563.1	000919	Cluster302_1clades	329	G173_gp018	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96564.1	000919	Cluster302_1clades	383	G173_gp019	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48123.1	000919	Cluster302_1clades	383	ASESINO_110	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48397.1	000919	Cluster302_1clades	384	CAITLIN_102	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48670.1	000919	Cluster302_1clades	388	CHRISDB_108	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48945.1	000919	Cluster302_1clades	350	EARLPHILLIPIV_96	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49189.1	000919	Cluster302_1clades	388	HUXLEY_107	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49465.1	000919	Cluster302_1clades	332	KWAN_113	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49466.1	000919	Cluster302_1clades	380	KWAN_114	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50017.1	000919	Cluster302_1clades	388	PARSHIK_108	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50286.1	000919	Cluster302_1clades	350	PHOBOS_96	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50537.1	000919	Cluster302_1clades	329	STRATTON_112	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50538.1	000919	Cluster302_1clades	383	STRATTON_113	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85934.1	000919	Cluster302_1clades	377	ACEC001_0960	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20803.1	000919	Cluster302_1clades	377	-	Salmonella phage JN03	GCA_014319805.1
AWN09010.1	000919	Cluster302_1clades	376	MLDJOKPK_00064	Salmonella phage SPAsTU	GCA_003183805.1
AEP83927.1	000919	Cluster302_1clades	377	SPN3US_0094	Salmonella phage SPN3US	GCA_001042275.1
ASV44759.1	000920	Cluster305_1clades	280	FDI40_gp686	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21693.1	000920	Cluster305_1clades	285	GAP32_243	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14486.1	000920	Cluster305_1clades	278	PBI_121Q_596	Escherichia phage 121Q	GCA_000926855.1
QAY00463.1	000920	Cluster305_1clades	278	Ecwhy1_183	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35205.1	000920	Cluster305_1clades	278	ACQ29_gp525	Escherichia phage PBECO4	GCA_001041035.1
BBM62158.1	000920	Cluster305_1clades	278	EO157G_5690	Escherichia phage SP27	GCA_008033345.1
AXC36777.1	000920	Cluster305_1clades	278	-	Escherichia phage UB	GCA_003341455.1
QBO61817.1	000920	Cluster305_1clades	278	G17_00328	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13861.1	000920	Cluster305_1clades	278	vBEcoMphAPEC6_gp232	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80470.1	000920	Cluster305_1clades	278	PSLUR01_00493	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44360.1	000920	Cluster305_1clades	286	RaK2_00087	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72723.1	000920	Cluster305_1clades	285	-	Myoviridae sp.	GCA_003657725.1
AMM43815.1	000920	Cluster305_1clades	285	CBB_250	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76029.1	000920	Cluster305_1clades	284	EST35_0147	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44103.1	000920	Cluster305_1clades	308	PBI_SCTP2_88	Salicola phage SCTP-2	GCA_002625545.1
QCW18970.1	000920	Cluster305_1clades	291	7t3_0449	Salmonella phage 7t3	GCA_006083215.1
AZU98220.1	000920	Cluster305_1clades	291	CPT_Munch_276	Salmonella phage Munch	GCA_004015485.1
QIG62765.1	000920	Cluster305_1clades	291	SEPL_152	Salmonella phage SE_PL	GCA_011067555.1
AQW88773.1	000920	Cluster305_1clades	291	BF_0248	Serratia phage BF	GCA_002619745.1
BBA65465.1	000920	Cluster305_1clades	279	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96474.1	000920	Cluster305_1clades	294	Xoosp13_288	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59054.1	000920	Cluster305_1clades	291	g246c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58520.1	000920	Cluster305_1clades	291	g243c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AAQ64321.1	000921	Cluster309_1clades	231	KVP40.0252	Vibrio phage KVP40	GCA_000843785.1
AAQ64339.1	000921	Cluster309_1clades	224	KVP40.0270	Vibrio phage KVP40	GCA_000843785.1
QIW90636.1	000921	Cluster309_1clades	231	GCAPEGMB_00289	Vibrio phage V07	GCA_012361095.1
QIW90654.1	000921	Cluster309_1clades	239	GCAPEGMB_00307	Vibrio phage V07	GCA_012361095.1
QIW91145.1	000921	Cluster309_1clades	239	COHAPHLL_00309	Vibrio phage V09	GCA_012361135.1
QIW91163.1	000921	Cluster309_1clades	231	COHAPHLL_00327	Vibrio phage V09	GCA_012361135.1
QHJ74431.1	000921	Cluster309_1clades	231	VH12019_00104	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74449.1	000921	Cluster309_1clades	239	VH12019_00122	Vibrio phage VH1_2019	GCA_009931825.1
AGB06937.1	000921	Cluster309_1clades	233	CF80_gp150	Vibrio phage VH7D	GCA_000914495.1
AGB06945.1	000921	Cluster309_1clades	239	CF80_gp158	Vibrio phage VH7D	GCA_000914495.1
QBX06201.1	000921	Cluster309_1clades	239	ValB1HC_248	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06209.1	000921	Cluster309_1clades	233	ValB1HC_256	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61226.1	000921	Cluster309_1clades	227	AVU32_gp385	Vibrio phage ValKK3	GCA_001501635.1
AJT61218.1	000921	Cluster309_1clades	239	AVU32_gp377	Vibrio phage ValKK3	GCA_001501635.1
AGN30314.1	000921	Cluster309_1clades	242	VPFG_00316	Vibrio phage nt-1	GCA_000910195.2
ALP47047.1	000921	Cluster309_1clades	239	phiGrn1_0004	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47055.1	000921	Cluster309_1clades	227	phiGrn1_0373	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47431.1	000921	Cluster309_1clades	233	phiST2_0128	Vibrio phage phi-ST2	GCA_002757135.1
ALP47425.1	000921	Cluster309_1clades	239	phiST2_0136	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54826.1	000921	Cluster309_1clades	239	vBValMR10Z_286	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54834.1	000921	Cluster309_1clades	227	vBValMR10Z_294	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37480.1	000921	Cluster309_1clades	231	pp2_247	Vibriophage phi-pp2	GCA_002630725.1
AFN37499.1	000921	Cluster309_1clades	239	pp2_266	Vibriophage phi-pp2	GCA_002630725.1
AAQ64444.1	000922	Monomethylamine-methyltransferase	182	KVP40.0376	Vibrio phage KVP40	GCA_000843785.1
AAQ64435.1	000922	Monomethylamine-methyltransferase	163	KVP40.0367	Vibrio phage KVP40	GCA_000843785.1
QIW90381.1	000922	Monomethylamine-methyltransferase	163	GCAPEGMB_00034	Vibrio phage V07	GCA_012361095.1
QIW90389.1	000922	Monomethylamine-methyltransferase	168	GCAPEGMB_00042	Vibrio phage V07	GCA_012361095.1
QIW91040.1	000922	Monomethylamine-methyltransferase	169	COHAPHLL_00177	Vibrio phage V09	GCA_012361135.1
QIW91048.1	000922	Monomethylamine-methyltransferase	163	COHAPHLL_00185	Vibrio phage V09	GCA_012361135.1
QHJ74548.1	000922	Monomethylamine-methyltransferase	163	VH12019_00248	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74556.1	000922	Monomethylamine-methyltransferase	168	VH12019_00256	Vibrio phage VH1_2019	GCA_009931825.1
AGB07005.1	000922	Monomethylamine-methyltransferase	165	CF80_gp218	Vibrio phage VH7D	GCA_000914495.1
QBX06098.1	000922	Monomethylamine-methyltransferase	170	ValB1HC_144	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06106.1	000922	Monomethylamine-methyltransferase	165	ValB1HC_152	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61120.1	000922	Monomethylamine-methyltransferase	165	AVU32_gp279	Vibrio phage ValKK3	GCA_001501635.1
AJT61112.1	000922	Monomethylamine-methyltransferase	170	AVU32_gp271	Vibrio phage ValKK3	GCA_001501635.1
AGN30037.1	000922	Monomethylamine-methyltransferase	162	VPFG_00032	Vibrio phage nt-1	GCA_000910195.2
AGN30044.1	000922	Monomethylamine-methyltransferase	158	VPFG_00039	Vibrio phage nt-1	GCA_000910195.2
ALP47105.1	000922	Monomethylamine-methyltransferase	165	phiGrn1_0100	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47097.1	000922	Monomethylamine-methyltransferase	170	phiGrn1_0108	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47488.1	000922	Monomethylamine-methyltransferase	165	phiST2_0231	Vibrio phage phi-ST2	GCA_002757135.1
ALP47480.1	000922	Monomethylamine-methyltransferase	170	phiST2_0239	Vibrio phage phi-ST2	GCA_002757135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNJ54723.1	000922	Monomethylamine-methyltransferase	170	vBValMR10Z_183	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54731.1	000922	Monomethylamine-methyltransferase	164	vBValMR10Z_191	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37599.1	000922	Monomethylamine-methyltransferase	163	pp2_367	Vibriophage phi-pp2	GCA_002630725.1
AFN37607.1	000922	Monomethylamine-methyltransferase	168	pp2_375	Vibriophage phi-pp2	GCA_002630725.1
AXG67067.1	000923	Cluster313_1clades	97	AD1_023	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
QBZ70685.1	000923	Cluster313_1clades	84	pETSU_104	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60246.1	000923	Cluster313_1clades	73	Ea357_095	Erwinia phage Ea35-70	GCA_000914635.1
QBP07204.1	000923	Cluster313_1clades	73	REBECCA_97	Erwinia phage Rebecca	GCA_004521635.1
AUG85883.1	000923	Cluster313_1clades	73	BOSOLAPHORUS_96	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52198.1	000923	Cluster313_1clades	73	DM_100	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86202.1	000923	Cluster313_1clades	73	DESERTFOX_95	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03744.1	000923	Cluster313_1clades	77	JOAD_171	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86525.1	000923	Cluster313_1clades	73	MADMEL_97	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86848.1	000923	Cluster313_1clades	73	MORTIMER_99	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51876.1	000923	Cluster313_1clades	73	RAY_95	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03500.1	000923	Cluster313_1clades	77	RISINGSUN_170	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51560.1	000923	Cluster313_1clades	73	SIMMY50_98	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64908.1	000923	Cluster313_1clades	73	SPECIALG_98	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARV77437.1	000923	Cluster313_1clades	68	NOXIFER_272	Pseudomonas phage Noxifer	GCA_002625005.1
QBJ02935.1	000923	Cluster313_1clades	74	PSA21_413	Pseudomonas phage Psa21	GCA_004340405.1
QKE54417.1	000923	Cluster313_1clades	106	ACSA002_1030	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFP93262.1	000923	Cluster313_1clades	70	-	Serratia phage PCH45	GCA_009187865.1
AQT27997.1	000923	Cluster313_1clades	125	pVa21_055	Vibrio phage pVa-21	GCA_002619305.1
QAX96877.1	000923	Cluster313_1clades	162	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97182.1	000923	Cluster313_1clades	162	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96241.1	000923	Cluster313_1clades	162	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96559.1	000923	Cluster313_1clades	162	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ARB13827.1	000924	Cluster314_1clades	119	Ccr10_gp297	Caulobacter phage Ccr10	GCA_002619445.1
ARB13828.1	000924	Cluster314_1clades	125	Ccr10_gp298	Caulobacter phage Ccr10	GCA_002619445.1
ARB14172.1	000924	Cluster314_1clades	119	Ccr2_gp296	Caulobacter phage Ccr2	GCA_002619465.1
ARB14173.1	000924	Cluster314_1clades	125	Ccr2_gp297	Caulobacter phage Ccr2	GCA_002619465.1
ARB14866.1	000924	Cluster314_1clades	119	Ccr29_gp310	Caulobacter phage Ccr29	GCA_002619485.1
ARB14867.1	000924	Cluster314_1clades	125	Ccr29_gp311	Caulobacter phage Ccr29	GCA_002619485.1
ARB15204.1	000924	Cluster314_1clades	119	Ccr32_gp286	Caulobacter phage Ccr32	GCA_002619505.1
ARB15205.1	000924	Cluster314_1clades	126	Ccr32_gp287	Caulobacter phage Ccr32	GCA_002619505.1
ARB15538.1	000924	Cluster314_1clades	119	Ccr34_gp296	Caulobacter phage Ccr34	GCA_002619525.1
ARB15539.1	000924	Cluster314_1clades	126	Ccr34_gp297	Caulobacter phage Ccr34	GCA_002619525.1
ARB14513.1	000924	Cluster314_1clades	119	Ccr5_gp293	Caulobacter phage Ccr5	GCA_002619545.1
ARB14514.1	000924	Cluster314_1clades	126	Ccr5_gp294	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68494.1	000924	Cluster314_1clades	129	CcrBL10_gp290	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68892.1	000924	Cluster314_1clades	108	CcrPW_gp353	Caulobacter phage CcrPW	GCA_003443275.1
AFU87823.1	000924	Cluster314_1clades	119	CcrKarma_gp306	Caulobacter virus Karma	GCA_000901575.1
AFU87824.1	000924	Cluster314_1clades	126	CcrKarma_gp307	Caulobacter virus Karma	GCA_000901575.1
AFU87470.1	000924	Cluster314_1clades	119	CcrMagneto_gp300	Caulobacter virus Magneto	GCA_000903095.1
AFU87471.1	000924	Cluster314_1clades	124	CcrMagneto_gp301	Caulobacter virus Magneto	GCA_000903095.1
AFU86782.1	000924	Cluster314_1clades	128	CcrRogue_gp300	Caulobacter virus Rogue	GCA_000900555.1
AFU88615.1	000924	Cluster314_1clades	119	CcrSwift_gp297	Caulobacter virus Swift	GCA_000899655.1
AFU88616.1	000924	Cluster314_1clades	124	CcrSwift_gp298	Caulobacter virus Swift	GCA_000899655.1
AFU87123.1	000924	Cluster314_1clades	119	CbK_gp291	Caulobacter virus phiCbK	GCA_000900535.1
AFU87124.1	000924	Cluster314_1clades	126	CbK_gp292	Caulobacter virus phiCbK	GCA_000900535.1
AGH56916.1	000925	Cluster315_1clades	83	CPXG_00113	Cyanophage P-RSM6	GCA_000906155.1
AJK27542.1	000925	Cluster315_1clades	89	PTIM40_115	Cyanophage P-TIM40	GCA_001470935.1
AOO14301.1	000925	Cluster315_1clades	80	Sn110110_107	Cyanophage S-RIM14	GCA_002599065.1
AOO14950.1	000925	Cluster315_1clades	80	W1230910_104	Cyanophage S-RIM14	GCA_002599125.1
AMO43133.1	000925	Cluster315_1clades	73	R1080702_124	Cyanophage S-RIM32	GCA_001754165.1
AMO43358.1	000925	Cluster315_1clades	99	W270710_114	Cyanophage S-RIM44	GCA_002599145.1
AOO11602.1	000925	Cluster315_1clades	99	ES420910_121	Cyanophage S-RIM44	GCA_002599165.1
AOO11830.1	000925	Cluster315_1clades	99	Np050604_114	Cyanophage S-RIM44	GCA_002599185.1
AOO12067.1	000925	Cluster315_1clades	99	Np200711_121	Cyanophage S-RIM44	GCA_002599205.1
AOO12303.1	000925	Cluster315_1clades	99	Np420711_121	Cyanophage S-RIM44	GCA_002599225.1
AOO12531.1	000925	Cluster315_1clades	99	Sn080709_114	Cyanophage S-RIM44	GCA_002599245.1
AOO12768.1	000925	Cluster315_1clades	99	Sn130910_121	Cyanophage S-RIM44	GCA_002599265.1
AOO12997.1	000925	Cluster315_1clades	99	W2100709_115	Cyanophage S-RIM44	GCA_002599285.1
AGH07535.1	000925	Cluster315_1clades	77	CYVG_00091	Cyanophage S-SSM6a	GCA_002710385.1
AGG54502.1	000925	Cluster315_1clades	90	CYWG_00218	Cyanophage S-SSM6b	GCA_002710425.1
ADO99216.1	000925	Cluster315_1clades	99	Syn1_115	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30696.1	000925	Cluster315_1clades	103	Syn7803US37_219	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23046.1	000925	Cluster315_1clades	96	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50678.1	000925	Cluster315_1clades	96	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59583.1	000925	Cluster315_1clades	87	S330809_122	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59345.1	000925	Cluster315_1clades	87	C440309_122	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59821.1	000925	Cluster315_1clades	87	N231010_122	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70523.1	000925	Cluster315_1clades	86	HOU04_gp124	Synechococcus phage S-T4	GCA_003443335.1
ABY63074.1	000926	phiKZ_IP	613	201phi2-1p246	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63075.1	000926	phiKZ_IP	397	201phi2-1p247	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44957.1	000926	phiKZ_IP	522	KTN4_199	Pseudomonas phage KTN4	GCA_002607225.1
ANM44958.1	000926	phiKZ_IP	395	KTN4_200	Pseudomonas phage KTN4	GCA_002607225.1
ARV77345.1	000926	phiKZ_IP	397	NOXIFER_176	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32345.1	000926	phiKZ_IP	394	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32344.1	000926	phiKZ_IP	586	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76865.1	000926	phiKZ_IP	593	PHABIO_234	Pseudomonas phage Phabio	GCA_002624965.1
ARV76866.1	000926	phiKZ_IP	396	PHABIO_235	Pseudomonas phage Phabio	GCA_002624965.1
AEH03609.1	000926	phiKZ_IP	580	186	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03610.1	000926	phiKZ_IP	392	187	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02743.1	000926	phiKZ_IP	187	PSA21_217	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02744.1	000926	phiKZ_IP	180	PSA21_218	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02746.1	000926	phiKZ_IP	584	PSA21_220	Pseudomonas phage Psa21	GCA_004340405.1
ATN94756.1	000926	phiKZ_IP	395	SL2_179	Pseudomonas phage SL2	GCA_002956015.1
ATN94757.1	000926	phiKZ_IP	522	SL2_180	Pseudomonas phage SL2	GCA_002956015.1
QJB22835.1	000926	phiKZ_IP	522	fnug_192	Pseudomonas phage fnug	GCA_012837215.1
QJB22836.1	000926	phiKZ_IP	268	fnug_193	Pseudomonas phage fnug	GCA_012837215.1
QEM41919.1	000926	phiKZ_IP	394	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41918.1	000926	phiKZ_IP	586	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83064.1	000926	phiKZ_IP	395	PHIKZ163	Pseudomonas virus phiKZ	GCA_000842965.1
AAL83063.1	000926	phiKZ_IP	522	PHIKZ162	Pseudomonas virus phiKZ	GCA_000842965.1
AUZ94887.1	000927	Cluster320_1clades	169	FDI40_gp078	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21729.1	000927	Cluster320_1clades	281	GAP32_279	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13910.1	000927	Cluster320_1clades	281	PBI_121Q_13	Escherichia phage 121Q	GCA_000926855.1
AGC35171.1	000927	Cluster320_1clades	281	ACQ29_gp491	Escherichia phage PBECO4	GCA_001041035.1
BBM61602.1	000927	Cluster320_1clades	281	EO157G_0130	Escherichia phage SP27	GCA_008033345.1
AXC36743.1	000927	Cluster320_1clades	281	-	Escherichia phage UB	GCA_003341455.1
QBO61782.1	000927	Cluster320_1clades	281	G17_00293	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13826.1	000927	Cluster320_1clades	281	vBEcoMphAPEC6_gp197c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80505.1	000927	Cluster320_1clades	281	PSLUR01_00528	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44394.1	000927	Cluster320_1clades	265	RaK2_00121	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72801.1	000927	Cluster320_1clades	163	-	Myoviridae sp.	GCA_003657725.1
AMM43848.1	000927	Cluster320_1clades	281	CBB_284	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76099.1	000927	Cluster320_1clades	155	EST35_0218	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44161.1	000927	Cluster320_1clades	170	PBI_SCTP2_146	Salicola phage SCTP-2	GCA_002625545.1
QCW19007.1	000927	Cluster320_1clades	281	7t3_0487	Salmonella phage 7t3	GCA_006083215.1
AZU98254.1	000927	Cluster320_1clades	281	CPT_Munch_310	Salmonella phage Munch	GCA_004015485.1
QIG62730.1	000927	Cluster320_1clades	281	SEPL_117	Salmonella phage SE_PL	GCA_011067555.1
AQW88807.1	000927	Cluster320_1clades	282	BF_0282	Serratia phage BF	GCA_002619745.1
BBA65387.1	000927	Cluster320_1clades	150	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96415.1	000927	Cluster320_1clades	80	Xoosp13_229	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59090.1	000927	Cluster320_1clades	282	g282	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58554.1	000927	Cluster320_1clades	282	g277	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21755.1	000928	Cluster321_1clades	214	GAP32_305	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13935.1	000928	Cluster321_1clades	112	PBI_121Q_38	Escherichia phage 121Q	GCA_000926855.1
AIT13936.1	000928	Cluster321_1clades	105	PBI_121Q_39	Escherichia phage 121Q	GCA_000926855.1
QAY00401.1	000928	Cluster321_1clades	99	Ecwhy1_120	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00402.1	000928	Cluster321_1clades	135	Ecwhy1_121	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35146.1	000928	Cluster321_1clades	112	ACQ29_gp466	Escherichia phage PBECO4	GCA_001041035.1
BBM61627.1	000928	Cluster321_1clades	112	EO157G_0380	Escherichia phage SP27	GCA_008033345.1
BBM61628.1	000928	Cluster321_1clades	105	EO157G_0390	Escherichia phage SP27	GCA_008033345.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXC36719.1	000928	Cluster321_1clades	112	-	Escherichia phage UB	GCA_003341455.1
QBO61757.1	000928	Cluster321_1clades	105	G17_00268	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61758.1	000928	Cluster321_1clades	112	G17_00269	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13802.1	000928	Cluster321_1clades	112	vBEcoMphAPEC6_gp173	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80529.1	000928	Cluster321_1clades	112	PSLUR01_00552	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80530.1	000928	Cluster321_1clades	105	PSLUR01_00553	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44418.1	000928	Cluster321_1clades	214	RaK2_00145	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43873.1	000928	Cluster321_1clades	217	CBB_310	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19032.1	000928	Cluster321_1clades	219	7t3_0512	Salmonella phage 7t3	GCA_006083215.1
AZU98279.1	000928	Cluster321_1clades	219	CPT_Munch_335	Salmonella phage Munch	GCA_004015485.1
QIG62705.1	000928	Cluster321_1clades	219	SEPL_092	Salmonella phage SE_PL	GCA_011067555.1
AQW88832.1	000928	Cluster321_1clades	218	BF_0307	Serratia phage BF	GCA_002619745.1
SOK59116.1	000928	Cluster321_1clades	218	g308c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58582.1	000928	Cluster321_1clades	218	g305c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXQ69029.1	000929	PRC	218	CcrBL9_gp005	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69545.1	000929	PRC	218	CcrBL9_gp521	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ68542.1	000929	PRC	135	CcrPW_gp003	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68992.1	000929	PRC	135	CcrPW_gp453	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69588.1	000929	PRC	208	CcrSC_gp006	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70088.1	000929	PRC	208	CcrSC_gp506	Caulobacter phage CcrSC	GCA_003443315.1
AIT14178.1	000929	PRC	112	PBI_121Q_288	Escherichia phage 121Q	GCA_000926855.1
QAY00759.1	000929	PRC	113	Ecwhy1_485	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34937.1	000929	PRC	113	ACQ29_gp257	Escherichia phage PBECO4	GCA_001041035.1
BBM61853.1	000929	PRC	113	EO157G_2640	Escherichia phage SP27	GCA_008033345.1
AXC37041.1	000929	PRC	113	-	Escherichia phage UB	GCA_003341455.1
QBO61527.1	000929	PRC	113	G17_00031	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62133.1	000929	PRC	113	G17_00644	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14141.1	000929	PRC	113	vBEcoMphAPEC6_gp518c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80163.1	000929	PRC	113	PSLUR01_00186	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44615.1	000929	PRC	122	RaK2_00342	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18699.1	000929	PRC	102	7t3_0178	Salmonella phage 7t3	GCA_006083215.1
AZU97972.1	000929	PRC	102	CPT_Munch_028	Salmonella phage Munch	GCA_004015485.1
QIG63006.1	000929	PRC	102	SEPL_393	Salmonella phage SE_PL	GCA_011067555.1
AQW88535.1	000929	PRC	142	BF_0010	Serratia phage BF	GCA_002619745.1
SOK58816.1	000929	PRC	140	g008	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58284.1	000929	PRC	140	g007	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14409.1	000930	Cluster323_1clades	210	PBI_121Q_519	Escherichia phage 121Q	GCA_000926855.1
AIT14411.1	000930	Cluster323_1clades	194	PBI_121Q_521	Escherichia phage 121Q	GCA_000926855.1
QAY00540.1	000930	Cluster323_1clades	185	Ecwhy1_261	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00543.1	000930	Cluster323_1clades	205	Ecwhy1_264	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34731.1	000930	Cluster323_1clades	194	ACQ29_gp051	Escherichia phage PBECO4	GCA_001041035.1
AGC34734.1	000930	Cluster323_1clades	205	ACQ29_gp054	Escherichia phage PBECO4	GCA_001041035.1
BBM62080.1	000930	Cluster323_1clades	205	EO157G_4910	Escherichia phage SP27	GCA_008033345.1
BBM62083.1	000930	Cluster323_1clades	194	EO157G_4940	Escherichia phage SP27	GCA_008033345.1
AXC36847.1	000930	Cluster323_1clades	194	-	Escherichia phage UB	GCA_003341455.1
AXC36850.1	000930	Cluster323_1clades	205	-	Escherichia phage UB	GCA_003341455.1
QBO61890.1	000930	Cluster323_1clades	194	G17_00401	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61893.1	000930	Cluster323_1clades	215	G17_00404	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13927.1	000930	Cluster323_1clades	194	vBEcoMphAPEC6_gp302c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80394.1	000930	Cluster323_1clades	215	PSLUR01_00417	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80397.1	000930	Cluster323_1clades	194	PSLUR01_00420	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44290.1	000930	Cluster323_1clades	197	RaK2_00017	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18873.1	000930	Cluster323_1clades	195	7t3_0352	Salmonella phage 7t3	GCA_006083215.1
QCW18879.1	000930	Cluster323_1clades	178	7t3_0358	Salmonella phage 7t3	GCA_006083215.1
AZU98131.1	000930	Cluster323_1clades	195	CPT_Munch_187	Salmonella phage Munch	GCA_004015485.1
AZU98137.1	000930	Cluster323_1clades	178	CPT_Munch_193	Salmonella phage Munch	GCA_004015485.1
QIG62845.1	000930	Cluster323_1clades	178	SEPL_232	Salmonella phage SE_PL	GCA_011067555.1
QIG62851.1	000930	Cluster323_1clades	195	SEPL_238	Salmonella phage SE_PL	GCA_011067555.1
AGH56865.1	000931	SIG+TM	203	CPXG_00062	Cyanophage P-RSM6	GCA_000906155.1
AJK27591.1	000931	SIG+TM	204	PTIM40_164	Cyanophage P-TIM40	GCA_001470935.1
AMO43193.1	000931	SIG+TM	199	R1080702_184	Cyanophage S-RIM32	GCA_001754165.1
AMO43419.1	000931	SIG+TM	190	W270710_175	Cyanophage S-RIM44	GCA_002599145.1
AOO11663.1	000931	SIG+TM	190	ES420910_182	Cyanophage S-RIM44	GCA_002599165.1
AOO11891.1	000931	SIG+TM	190	Np050604_175	Cyanophage S-RIM44	GCA_002599185.1
AOO12129.1	000931	SIG+TM	190	Np200711_183	Cyanophage S-RIM44	GCA_002599205.1
AOO12364.1	000931	SIG+TM	190	Np420711_182	Cyanophage S-RIM44	GCA_002599225.1
AOO12592.1	000931	SIG+TM	190	Sn080709_175	Cyanophage S-RIM44	GCA_002599245.1
AOO12829.1	000931	SIG+TM	190	Sn130910_182	Cyanophage S-RIM44	GCA_002599265.1
AOO13058.1	000931	SIG+TM	190	W2100709_176	Cyanophage S-RIM44	GCA_002599285.1
AGH07462.1	000931	SIG+TM	207	CYVG_00018	Cyanophage S-SSM6a	GCA_002710385.1
AGH26316.1	000931	SIG+TM	196	CPMG_00217	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44601.1	000931	SIG+TM	204	PSSM2_224	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12369.1	000931	SIG+TM	203	PRTG_00216	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93544.1	000931	SIG+TM	199	AVU42_gp207	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99278.1	000931	SIG+TM	190	Syn1_177	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76278.1	000931	SIG+TM	192	PBI_BELLAMY_242	Synechococcus phage Bellamy	GCA_002627525.1
AOV59660.1	000931	SIG+TM	157	S330809_199	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59422.1	000931	SIG+TM	157	C440309_199	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59897.1	000931	SIG+TM	157	N231010_198	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70228.1	000931	SIG+TM	194	SynMITS9220M01_222	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13785.1	000932	Cluster326_1clades	137	Ccr10_gp255	Caulobacter phage Ccr10	GCA_002619445.1
ARB13786.1	000932	Cluster326_1clades	113	Ccr10_gp256	Caulobacter phage Ccr10	GCA_002619445.1
ARB14130.1	000932	Cluster326_1clades	137	Ccr2_gp254	Caulobacter phage Ccr2	GCA_002619465.1
ARB14131.1	000932	Cluster326_1clades	113	Ccr2_gp255	Caulobacter phage Ccr2	GCA_002619465.1
ARB14824.1	000932	Cluster326_1clades	137	Ccr29_gp268	Caulobacter phage Ccr29	GCA_002619485.1
ARB14825.1	000932	Cluster326_1clades	136	Ccr29_gp269	Caulobacter phage Ccr29	GCA_002619485.1
ARB15164.1	000932	Cluster326_1clades	137	Ccr32_gp246	Caulobacter phage Ccr32	GCA_002619505.1
ARB15165.1	000932	Cluster326_1clades	136	Ccr32_gp247	Caulobacter phage Ccr32	GCA_002619505.1
ARB15498.1	000932	Cluster326_1clades	137	Ccr34_gp256	Caulobacter phage Ccr34	GCA_002619525.1
ARB15499.1	000932	Cluster326_1clades	136	Ccr34_gp257	Caulobacter phage Ccr34	GCA_002619525.1
ARB14472.1	000932	Cluster326_1clades	137	Ccr5_gp252	Caulobacter phage Ccr5	GCA_002619545.1
ARB14473.1	000932	Cluster326_1clades	136	Ccr5_gp253	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68451.1	000932	Cluster326_1clades	180	CcrBL10_gp247	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87781.1	000932	Cluster326_1clades	137	CcrKarma_gp264	Caulobacter virus Karma	GCA_000901575.1
AFU87782.1	000932	Cluster326_1clades	136	CcrKarma_gp265	Caulobacter virus Karma	GCA_000901575.1
AFU87428.1	000932	Cluster326_1clades	137	CcrMagneto_gp258	Caulobacter virus Magneto	GCA_000903095.1
AFU87429.1	000932	Cluster326_1clades	136	CcrMagneto_gp259	Caulobacter virus Magneto	GCA_000903095.1
AFU86738.1	000932	Cluster326_1clades	180	CcrRogue_gp256	Caulobacter virus Rogue	GCA_000900555.1
AFU88575.1	000932	Cluster326_1clades	137	CcrSwift_gp257	Caulobacter virus Swift	GCA_000899655.1
AFU88576.1	000932	Cluster326_1clades	136	CcrSwift_gp258	Caulobacter virus Swift	GCA_000899655.1
AFU87083.1	000932	Cluster326_1clades	137	CbK_gp251	Caulobacter virus phiCbK	GCA_000900535.1
AFU87084.1	000932	Cluster326_1clades	136	CbK_gp252	Caulobacter virus phiCbK	GCA_000900535.1
ASV44697.1	000933	Cluster327_1clades	166	FDI40_gp079	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21728.1	000933	Cluster327_1clades	167	GAP32_278	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13909.1	000933	Cluster327_1clades	165	PBI_121Q_12	Escherichia phage 121Q	GCA_000926855.1
QAY00428.1	000933	Cluster327_1clades	165	Ecwhy1_148	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35172.1	000933	Cluster327_1clades	165	ACQ29_gp492	Escherichia phage PBECO4	GCA_001041035.1
BBM61601.1	000933	Cluster327_1clades	165	EO157G_0120	Escherichia phage SP27	GCA_008033345.1
AXC36744.1	000933	Cluster327_1clades	165	-	Escherichia phage UB	GCA_003341455.1
QBO61783.1	000933	Cluster327_1clades	165	G17_00294	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13827.1	000933	Cluster327_1clades	165	vBEcoMphAPEC6_gp198c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80504.1	000933	Cluster327_1clades	165	PSLUR01_00527	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44393.1	000933	Cluster327_1clades	165	RaK2_00120	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72767.1	000933	Cluster327_1clades	166	-	Myoviridae sp.	GCA_003657725.1
AMM43847.1	000933	Cluster327_1clades	167	CBB_283	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76098.1	000933	Cluster327_1clades	167	EST35_0217	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44160.1	000933	Cluster327_1clades	170	PBI_SCTP2_145	Salicola phage SCTP-2	GCA_002625545.1
QCW19006.1	000933	Cluster327_1clades	165	7t3_0486	Salmonella phage 7t3	GCA_006083215.1
AZU98253.1	000933	Cluster327_1clades	165	CPT_Munch_309	Salmonella phage Munch	GCA_004015485.1
QIG62731.1	000933	Cluster327_1clades	165	SEPL_118	Salmonella phage SE_PL	GCA_011067555.1
AQW88806.1	000933	Cluster327_1clades	167	BF_0281	Serratia phage BF	GCA_002619745.1
BBA65395.1	000933	Cluster327_1clades	162	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK59089.1	000933	Cluster327_1clades	167	g281	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58553.1	000933	Cluster327_1clades	167	g276	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22787.1	000934	Toast-rack	122	Ah1_00269	Aeromonas phage Ah1	GCA_002957415.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX98501.1	000934	Toast-rack	122	ASfcp2_165	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52964.1	000934	Toast-rack	122	PX29p245	Aeromonas phage PX29	GCA_000920195.1
ADM79890.1	000934	Toast-rack	129	phiAS5_ORF0047	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17912.1	000934	Toast-rack	122	Aeh1ORF250c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21550.1	000934	Toast-rack	146	GAP32_102	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43668.1	000934	Toast-rack	142	CBB_103	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88621.1	000934	Toast-rack	141	BF_0096	Serratia phage BF	GCA_002619745.1
AAQ64209.1	000934	Toast-rack	132	KVP40.0139	Vibrio phage KVP40	GCA_000843785.1
QIW90524.1	000934	Toast-rack	117	GCAPEGMB_00177	Vibrio phage V07	GCA_012361095.1
QIW90898.1	000934	Toast-rack	117	COHAPHLL_00035	Vibrio phage V09	GCA_012361135.1
QHJ74320.1	000934	Toast-rack	117	VH12019_00401	Vibrio phage VH1_2019	GCA_009931825.1
AGB06814.1	000934	Toast-rack	118	CF80_gp027	Vibrio phage VH7D	GCA_000914495.1
QBX06333.1	000934	Toast-rack	118	ValB1HC_380	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60963.1	000934	Toast-rack	118	AVU32_gp122	Vibrio phage ValKK3	GCA_001501635.1
AGN30188.1	000934	Toast-rack	120	VPFG_00188	Vibrio phage nt-1	GCA_000910195.2
ALP47165.1	000934	Toast-rack	118	phiGrn1_0250	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47552.1	000934	Toast-rack	118	phiST2_0005	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54576.1	000934	Toast-rack	118	vBValMR10Z_35	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37370.1	000934	Toast-rack	117	pp2_137	Vibriophage phi-pp2	GCA_002630725.1
SOK58897.1	000934	Toast-rack	141	g089	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58362.1	000934	Toast-rack	141	g085	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01620.1	000935	Cluster329_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
APU01630.1	000935	Cluster329_1clades	82	-	Aeromonas phage 65.2	GCA_002618145.1
APU01629.1	000935	Cluster329_1clades	85	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28847.1	000935	Cluster329_1clades	82	AP1_0140	Aeromonas phage AP1	GCA_014183365.1
QMV28849.1	000935	Cluster329_1clades	80	AP1_0142	Aeromonas phage AP1	GCA_014183365.1
QMV28853.1	000935	Cluster329_1clades	85	AP1_0146	Aeromonas phage AP1	GCA_014183365.1
ATI17282.1	000935	Cluster329_1clades	80	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17284.1	000935	Cluster329_1clades	82	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17288.1	000935	Cluster329_1clades	85	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00314.1	000935	Cluster329_1clades	80	HWB28_gp238	Aeromonas phage AS-zj	GCA_002627665.1
ASU00312.1	000935	Cluster329_1clades	82	HWB28_gp240	Aeromonas phage AS-zj	GCA_002627665.1
ASU00308.1	000935	Cluster329_1clades	85	HWB28_gp244	Aeromonas phage AS-zj	GCA_002627665.1
QAX97723.1	000935	Cluster329_1clades	80	ASswx1_77	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97726.1	000935	Cluster329_1clades	82	ASswx1_80	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97730.1	000935	Cluster329_1clades	85	ASswx1_84	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01426.1	000935	Cluster329_1clades	85	ASwh1_367	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39320.1	000935	Cluster329_1clades	85	CC2_028	Aeromonas phage CC2	GCA_000903495.1
AFN39321.1	000935	Cluster329_1clades	82	CC2_032	Aeromonas phage CC2	GCA_000903495.1
AFN39181.1	000935	Cluster329_1clades	80	CC2_035	Aeromonas phage CC2	GCA_000903495.1
ADQ53245.1	000935	Cluster329_1clades	88	65p237	Aeromonas virus 65	GCA_000893255.1
ADQ53254.1	000935	Cluster329_1clades	85	65p246	Aeromonas virus 65	GCA_000893255.1
ADQ53255.1	000935	Cluster329_1clades	82	65p247	Aeromonas virus 65	GCA_000893255.1
APU01631.1	000936	Cluster330_1clades	72	-	Aeromonas phage 65.2	GCA_002618145.1
APU01569.1	000936	Cluster330_1clades	73	-	Aeromonas phage 65.2	GCA_002618145.1
APU01758.1	000936	Cluster330_1clades	73	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28846.1	000936	Cluster330_1clades	72	AP1_0139	Aeromonas phage AP1	GCA_014183365.1
QMV28986.1	000936	Cluster330_1clades	75	AP1_0279	Aeromonas phage AP1	GCA_014183365.1
QMV29081.1	000936	Cluster330_1clades	75	AP1_0374	Aeromonas phage AP1	GCA_014183365.1
ATI17279.1	000936	Cluster330_1clades	72	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17537.1	000936	Cluster330_1clades	75	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17446.1	000936	Cluster330_1clades	75	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00315.1	000936	Cluster330_1clades	72	HWB28_gp237	Aeromonas phage AS-zj	GCA_002627665.1
QAX97886.1	000936	Cluster330_1clades	75	ASswx1_243	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97978.1	000936	Cluster330_1clades	75	ASswx1_337	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97720.1	000936	Cluster330_1clades	72	ASswx1_74	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01302.1	000936	Cluster330_1clades	71	ASwh1_239	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01451.1	000936	Cluster330_1clades	72	ASwh1_392	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01163.1	000936	Cluster330_1clades	73	ASwh1_97	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39322.1	000936	Cluster330_1clades	72	CC2_038	Aeromonas phage CC2	GCA_000903495.1
AFN39375.1	000936	Cluster330_1clades	75	CC2_196	Aeromonas phage CC2	GCA_000903495.1
AFN39305.1	000936	Cluster330_1clades	75	CC2_290	Aeromonas phage CC2	GCA_000903495.1
ADQ53192.1	000936	Cluster330_1clades	73	65p184	Aeromonas virus 65	GCA_000893255.1
ADQ53256.1	000936	Cluster330_1clades	72	65p248	Aeromonas virus 65	GCA_000893255.1
ADQ53401.1	000936	Cluster330_1clades	73	65p394	Aeromonas virus 65	GCA_000893255.1
AOO14214.1	000937	Cluster331_1clades	65	Sn110110_020	Cyanophage S-RIM14	GCA_002599065.1
AOO14866.1	000937	Cluster331_1clades	65	W1230910_020	Cyanophage S-RIM14	GCA_002599125.1
AMO43162.1	000937	Cluster331_1clades	72	R1080702_153	Cyanophage S-RIM32	GCA_001754165.1
AMO43386.1	000937	Cluster331_1clades	72	W270710_142	Cyanophage S-RIM44	GCA_002599145.1
AOO11631.1	000937	Cluster331_1clades	59	ES420910_150	Cyanophage S-RIM44	GCA_002599165.1
AOO11858.1	000937	Cluster331_1clades	72	Np050604_142	Cyanophage S-RIM44	GCA_002599185.1
AOO12096.1	000937	Cluster331_1clades	59	Np200711_150	Cyanophage S-RIM44	GCA_002599205.1
AOO12332.1	000937	Cluster331_1clades	61	Np420711_150	Cyanophage S-RIM44	GCA_002599225.1
AOO12559.1	000937	Cluster331_1clades	72	Sn080709_142	Cyanophage S-RIM44	GCA_002599245.1
AOO12797.1	000937	Cluster331_1clades	61	Sn130910_150	Cyanophage S-RIM44	GCA_002599265.1
AOO13025.1	000937	Cluster331_1clades	72	W2100709_143	Cyanophage S-RIM44	GCA_002599285.1
AGG54384.1	000937	Cluster331_1clades	54	CYWG_00100	Cyanophage S-SSM6b	GCA_002710425.1
AAX44542.1	000937	Cluster331_1clades	70	PSSM2_164	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12429.1	000937	Cluster331_1clades	62	PRTG_00279	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99244.1	000937	Cluster331_1clades	73	Syn1_143	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30497.1	000937	Cluster331_1clades	58	Syn7803US37_20	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54646.1	000937	Cluster331_1clades	56	b23_0018	Synechococcus phage B23	GCA_009745195.1
QGT54276.1	000937	Cluster331_1clades	56	b3_0018	Synechococcus phage B3	GCA_009745215.1
QCW22911.1	000937	Cluster331_1clades	52	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50547.1	000937	Cluster331_1clades	48	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70432.1	000937	Cluster331_1clades	58	HOU04_gp033	Synechococcus phage S-T4	GCA_003443335.1
QJT70148.1	000937	Cluster331_1clades	69	SynMITS9220M01_135	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFO71431.1	000938	Cluster333_1clades	480	CR5_211	Cronobacter phage CR5	GCA_000910235.1
AMR59895.1	000938	Cluster333_1clades	491	SEGD1_248	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07644.1	000938	Cluster333_1clades	480	DERBICUS_218	Erwinia phage Derbicus	GCA_004521655.1
ANZ49894.1	000938	Cluster333_1clades	487	MACHINA_256	Erwinia phage Machina	GCA_002758035.1
AXF51395.1	000938	Cluster333_1clades	486	WELLINGTON_269	Erwinia phage Wellington	GCA_003344985.1
AFQ96708.1	000938	Cluster333_1clades	491	G173_gp163	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48278.1	000938	Cluster333_1clades	491	ASESINO_265	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48550.1	000938	Cluster333_1clades	485	CAITLIN_255	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48828.1	000938	Cluster333_1clades	485	CHRISDB_266	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49068.1	000938	Cluster333_1clades	480	EARLPHILLIPIV_219	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49337.1	000938	Cluster333_1clades	487	HUXLEY_255	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49621.1	000938	Cluster333_1clades	486	KWAN_269	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50165.1	000938	Cluster333_1clades	487	PARSHIK_256	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50415.1	000938	Cluster333_1clades	480	PHOBOS_225	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50690.1	000938	Cluster333_1clades	491	STRATTON_265	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86084.1	000938	Cluster333_1clades	491	ACEC001_2410	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
BAS04830.1	000938	Cluster333_1clades	477	AVU11_gp038	Ralstonia phage RSF1	GCA_001500875.1
BAQ02563.1	000938	Cluster333_1clades	477	AVU38_gp035	Ralstonia phage RSL2	GCA_001503055.1
QNI20927.1	000938	Cluster333_1clades	491	-	Salmonella phage JN03	GCA_014319805.1
AWN09109.1	000938	Cluster333_1clades	491	MLDJOKPK_00197	Salmonella phage SPAsTU	GCA_003183805.1
AEP84076.1	000938	Cluster333_1clades	491	SPN3US_0243	Salmonella phage SPN3US	GCA_001042275.1
AFO71450.1	000939	Cluster335_1clades	392	CR5_230	Cronobacter phage CR5	GCA_000910235.1
AMR59915.1	000939	Cluster335_1clades	203	SEGD1_268	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59916.1	000939	Cluster335_1clades	153	SEGD1_269	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07663.1	000939	Cluster335_1clades	391	DERBICUS_237	Erwinia phage Derbicus	GCA_004521655.1
ANZ49913.1	000939	Cluster335_1clades	376	MACHINA_275	Erwinia phage Machina	GCA_002758035.1
AXF51414.1	000939	Cluster335_1clades	378	WELLINGTON_288	Erwinia phage Wellington	GCA_003344985.1
AFQ96725.1	000939	Cluster335_1clades	377	G173_gp180	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48297.1	000939	Cluster335_1clades	377	ASESINO_284	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48568.1	000939	Cluster335_1clades	375	CAITLIN_273	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48846.1	000939	Cluster335_1clades	375	CHRISDB_284	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49087.1	000939	Cluster335_1clades	391	EARLPHILLIPIV_238	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49356.1	000939	Cluster335_1clades	376	HUXLEY_274	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49639.1	000939	Cluster335_1clades	378	KWAN_287	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50184.1	000939	Cluster335_1clades	376	PARSHIK_275	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50434.1	000939	Cluster335_1clades	392	PHOBOS_244	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50708.1	000939	Cluster335_1clades	377	STRATTON_283	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86104.1	000939	Cluster335_1clades	377	ACEC001_2610	Escherichia phage vB_EcoM_EC001	GCA_014131305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNI20945.1	000939	Cluster335_1clades	377	-	Salmonella phage JN03	GCA_014319805.1
AWN09091.2	000939	Cluster335_1clades	377	MLDJOKPK_00177	Salmonella phage SPAsTU	GCA_003183805.1
AEP84096.1	000939	Cluster335_1clades	377	SPN3US_0263	Salmonella phage SPN3US	GCA_001042275.1
AQT28132.1	000939	Cluster335_1clades	253	pVa21_191	Vibrio phage pVa-21	GCA_002619305.1
ARB13595.1	000940	IES3	263	Ccr10_gp067	Caulobacter phage Ccr10	GCA_002619445.1
ARB13941.1	000940	IES3	263	Ccr2_gp066	Caulobacter phage Ccr2	GCA_002619465.1
ARB14630.1	000940	IES3	263	Ccr29_gp073	Caulobacter phage Ccr29	GCA_002619485.1
ARB14986.1	000940	IES3	263	Ccr32_gp067	Caulobacter phage Ccr32	GCA_002619505.1
ARB15317.1	000940	IES3	263	Ccr34_gp068	Caulobacter phage Ccr34	GCA_002619525.1
ARB14284.1	000940	IES3	263	Ccr5_gp066	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68251.1	000940	IES3	119	CcrBL10_gp047	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68268.1	000940	IES3	253	CcrBL10_gp064	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69145.1	000940	IES3	201	CcrBL9_gp121	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69146.1	000940	IES3	273	CcrBL9_gp122	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87950.1	000940	IES3	288	CcrColossus_gp080	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68622.1	000940	IES3	261	CcrPW_gp083	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69699.1	000940	IES3	201	CcrSC_gp117	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69700.1	000940	IES3	272	CcrSC_gp118	Caulobacter phage CcrSC	GCA_003443315.1
AFU87585.1	000940	IES3	263	CcrKarma_gp068	Caulobacter virus Karma	GCA_000901575.1
AFU87235.1	000940	IES3	263	CcrMagneto_gp065	Caulobacter virus Magneto	GCA_000903095.1
AFU86533.1	000940	IES3	130	CcrRogue_gp051	Caulobacter virus Rogue	GCA_000900555.1
AFU86551.1	000940	IES3	263	CcrRogue_gp069	Caulobacter virus Rogue	GCA_000900555.1
AFU88383.1	000940	IES3	263	CcrSwift_gp065	Caulobacter virus Swift	GCA_000899655.1
AFU86899.1	000940	IES3	263	CbK_gp067	Caulobacter virus phiCbK	GCA_000900535.1
QIW90745.1	000940	IES3	289	GCAPEGMB_00426	Vibrio phage V07	GCA_012361095.1
AUZ94919.1	000941	Cluster338_1clades	148	FDI40_gp124	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21653.1	000941	Cluster338_1clades	189	GAP32_203	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14446.1	000941	Cluster338_1clades	184	PBI_121Q_556	Escherichia phage 121Q	GCA_000926855.1
QAY00502.1	000941	Cluster338_1clades	185	Ecwhy1_223	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34697.1	000941	Cluster338_1clades	184	ACQ29_gp017	Escherichia phage PBECO4	GCA_001041035.1
BBM62119.1	000941	Cluster338_1clades	184	EO157G_5300	Escherichia phage SP27	GCA_008033345.1
AXC36817.1	000941	Cluster338_1clades	184	-	Escherichia phage UB	GCA_003341455.1
QBO61856.1	000941	Cluster338_1clades	184	G17_00367	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13896.1	000941	Cluster338_1clades	184	vBEcoMphAPEC6_gp271c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80431.1	000941	Cluster338_1clades	184	PSLUR01_00454	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44319.1	000941	Cluster338_1clades	185	RaK2_00046	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72760.1	000941	Cluster338_1clades	190	-	Myoviridae sp.	GCA_003657725.1
AMM43774.1	000941	Cluster338_1clades	187	CBB_209	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76082.1	000941	Cluster338_1clades	168	EST35_0201	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44313.1	000941	Cluster338_1clades	219	PBI_SCTP2_298	Salicola phage SCTP-2	GCA_002625545.1
QCW18922.1	000941	Cluster338_1clades	184	7t3_0401	Salmonella phage 7t3	GCA_006083215.1
AZU98179.1	000941	Cluster338_1clades	184	CPT_Munch_235	Salmonella phage Munch	GCA_004015485.1
QIG62805.1	000941	Cluster338_1clades	184	SEPL_192	Salmonella phage SE_PL	GCA_011067555.1
AQW88730.1	000941	Cluster338_1clades	185	BF_0205	Serratia phage BF	GCA_002619745.1
SOK59013.1	000941	Cluster338_1clades	187	g205	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58478.1	000941	Cluster338_1clades	187	g201	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ95072.1	000942	Cluster339_1clades	177	FDI40_gp306	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21779.1	000942	Cluster339_1clades	190	GAP32_329	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13959.1	000942	Cluster339_1clades	187	PBI_121Q_62	Escherichia phage 121Q	GCA_000926855.1
QAY00378.1	000942	Cluster339_1clades	188	Ecwhy1_97	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35123.1	000942	Cluster339_1clades	187	ACQ29_gp443	Escherichia phage PBECO4	GCA_001041035.1
BBM61651.1	000942	Cluster339_1clades	187	EO157G_0620	Escherichia phage SP27	GCA_008033345.1
AXC36697.1	000942	Cluster339_1clades	187	-	Escherichia phage UB	GCA_003341455.1
QBO61734.1	000942	Cluster339_1clades	187	G17_00245	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13779.1	000942	Cluster339_1clades	187	vBEcoMphAPEC6_gp150c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80553.1	000942	Cluster339_1clades	187	PSLUR01_00576	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44441.1	000942	Cluster339_1clades	181	RaK2_00168	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72571.1	000942	Cluster339_1clades	191	-	Myoviridae sp.	GCA_003657725.1
AMM43897.1	000942	Cluster339_1clades	189	CBB_334	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76176.1	000942	Cluster339_1clades	173	EST35_0295	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44089.1	000942	Cluster339_1clades	186	PBI_SCTP2_74	Salicola phage SCTP-2	GCA_002625545.1
QCW19056.1	000942	Cluster339_1clades	190	7t3_0536	Salmonella phage 7t3	GCA_006083215.1
AZU98303.1	000942	Cluster339_1clades	190	CPT_Munch_359	Salmonella phage Munch	GCA_004015485.1
QIG62681.1	000942	Cluster339_1clades	190	SEPL_068	Salmonella phage SE_PL	GCA_011067555.1
AQW88857.1	000942	Cluster339_1clades	189	BF_0332	Serratia phage BF	GCA_002619745.1
SOK59141.1	000942	Cluster339_1clades	186	g333	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58607.1	000942	Cluster339_1clades	186	g330	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMR59832.1	000943	Cluster340_1clades	167	SEGD1_185	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59833.1	000943	Cluster340_1clades	136	SEGD1_186	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49831.1	000943	Cluster340_1clades	133	MACHINA_193	Erwinia phage Machina	GCA_002758035.1
AFQ96651.1	000943	Cluster340_1clades	137	G173_gp106	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96650.1	000943	Cluster340_1clades	161	G173_gp105	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48215.1	000943	Cluster340_1clades	161	ASESINO_202	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48216.1	000943	Cluster340_1clades	137	ASESINO_203	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48487.1	000943	Cluster340_1clades	134	CAITLIN_192	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48766.1	000943	Cluster340_1clades	134	CHRISDB_204	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49275.1	000943	Cluster340_1clades	133	HUXLEY_193	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50103.1	000943	Cluster340_1clades	133	PARSHIK_194	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50627.1	000943	Cluster340_1clades	161	STRATTON_202	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50628.1	000943	Cluster340_1clades	137	STRATTON_203	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86022.1	000943	Cluster340_1clades	163	ACEC001_1810	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86023.1	000943	Cluster340_1clades	136	ACEC001_1820	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20878.1	000943	Cluster340_1clades	136	-	Salmonella phage JN03	GCA_014319805.1
QNI20877.1	000943	Cluster340_1clades	178	-	Salmonella phage JN03	GCA_014319805.1
AWN09156.1	000943	Cluster340_1clades	136	MLDJOKPK_00258	Salmonella phage SPAsTU	GCA_003183805.1
AXF51126.1	000943	Cluster340_1clades	165	MLDJOKPK_00259	Salmonella phage SPAsTU	GCA_003183805.1
AEP84014.1	000943	Cluster340_1clades	163	SPN3US_0181	Salmonella phage SPN3US	GCA_001042275.1
AEP84015.1	000943	Cluster340_1clades	136	SPN3US_0182	Salmonella phage SPN3US	GCA_001042275.1
AFO71369.1	000944	Peptidase_M15_3	174	CR5_149	Cronobacter phage CR5	GCA_000910235.1
AMR59808.1	000944	Peptidase_M15_3	171	SEGD1_161	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07579.1	000944	Peptidase_M15_3	174	DERBICUS_153	Erwinia phage Derbicus	GCA_004521655.1
ANZ49002.1	000944	Peptidase_M15_3	174	EARLPHILLIPIV_153	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50349.1	000944	Peptidase_M15_3	174	PHOBOS_159	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QKN85997.1	000944	Peptidase_M15_3	171	ACEC001_1570	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20856.1	000944	Peptidase_M15_3	171	-	Salmonella phage JN03	GCA_014319805.1
AWN09173.1	000944	Peptidase_M15_3	171	MLDJOKPK_00285	Salmonella phage SPAsTU	GCA_003183805.1
AEP83991.1	000944	Peptidase_M15_3	171	SPN3US_0158	Salmonella phage SPN3US	GCA_001042275.1
AAQ64361.1	000944	Peptidase_M15_3	161	KVP40.0291	Vibrio phage KVP40	GCA_000843785.1
QIW90675.1	000944	Peptidase_M15_3	161	GCAPEGMB_00328	Vibrio phage V07	GCA_012361095.1
QIW91123.1	000944	Peptidase_M15_3	161	COHAPHLL_00287	Vibrio phage V09	GCA_012361135.1
QHJ74470.1	000944	Peptidase_M15_3	161	VH12019_00143	Vibrio phage VH1_2019	GCA_009931825.1
AGB06964.1	000944	Peptidase_M15_3	161	CF80_gp177	Vibrio phage VH7D	GCA_000914495.1
QBX06181.1	000944	Peptidase_M15_3	161	ValB1HC_228	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61198.1	000944	Peptidase_M15_3	161	AVU32_gp357	Vibrio phage ValKK3	GCA_001501635.1
AGN30337.1	000944	Peptidase_M15_3	161	VPFG_00340	Vibrio phage nt-1	GCA_000910195.2
ALP47204.1	000944	Peptidase_M15_3	99	phiGrn1_0024	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47598.1	000944	Peptidase_M15_3	99	phiST2_0155	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54806.1	000944	Peptidase_M15_3	161	vBValMR10Z_266	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37522.1	000944	Peptidase_M15_3	161	pp2_289	Vibriophage phi-pp2	GCA_002630725.1
AFC21605.1	000945	Cluster342_1clades	137	GAP32_155	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21606.1	000945	Cluster342_1clades	168	GAP32_156	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21607.1	000945	Cluster342_1clades	158	GAP32_157	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44279.1	000945	Cluster342_1clades	154	RaK2_00006	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44280.1	000945	Cluster342_1clades	166	RaK2_00007	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72546.1	000945	Cluster342_1clades	156	-	Myoviridae sp.	GCA_003657725.1
AMM43725.1	000945	Cluster342_1clades	138	CBB_160	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43726.1	000945	Cluster342_1clades	167	CBB_161	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18861.1	000945	Cluster342_1clades	142	7t3_0340	Salmonella phage 7t3	GCA_006083215.1
QCW18862.1	000945	Cluster342_1clades	162	7t3_0341	Salmonella phage 7t3	GCA_006083215.1
AZU98122.1	000945	Cluster342_1clades	142	CPT_Munch_178	Salmonella phage Munch	GCA_004015485.1
AZU98123.1	000945	Cluster342_1clades	157	CPT_Munch_179	Salmonella phage Munch	GCA_004015485.1
QIG62859.1	000945	Cluster342_1clades	159	SEPL_246	Salmonella phage SE_PL	GCA_011067555.1
QIG62860.1	000945	Cluster342_1clades	142	SEPL_247	Salmonella phage SE_PL	GCA_011067555.1
AQW88679.1	000945	Cluster342_1clades	142	BF_0154	Serratia phage BF	GCA_002619745.1
AQW88680.1	000945	Cluster342_1clades	166	BF_0155	Serratia phage BF	GCA_002619745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQW88681.1	000945	Cluster342_1clades	157	BF_0156	Serratia phage BF	GCA_002619745.1
SOK58961.1	000945	Cluster342_1clades	148	g153	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58962.1	000945	Cluster342_1clades	157	g154	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58427.1	000945	Cluster342_1clades	148	g150	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58428.1	000945	Cluster342_1clades	157	g151	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01432.1	000946	Gly_radical	120	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22579.1	000946	Gly_radical	127	Ah1_00038	Aeromonas phage Ah1	GCA_002957415.1
QAX98615.1	000946	Gly_radical	125	ASfcp2_282	Aeromonas phage AsFcp_2	GCA_004146885.1
QAY01245.1	000946	Gly_radical	119	ASwh1_180	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ52752.1	000946	Gly_radical	125	PX29p033	Aeromonas phage PX29	GCA_000920195.1
ADM80008.1	000946	Gly_radical	125	phiAS5_ORF0165	Aeromonas phage phiAS5	GCA_000887715.1
AAR90897.1	000946	Gly_radical	120	65p041	Aeromonas virus 65	GCA_000893255.1
AAQ17694.1	000946	Gly_radical	125	vs.6	Aeromonas virus Aeh1	GCA_000843245.1
ANS06073.1	000946	Gly_radical	120	ABCD_0081	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64984.1	000946	Gly_radical	123	S13_187	Cronobacter phage S13	GCA_001503575.1
AON97093.1	000946	Gly_radical	120	E_085	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70937.1	000946	Gly_radical	120	phiC120_c232	Escherichia phage phiC120	GCA_002621185.1
AAX78603.1	000946	Gly_radical	120	RB43ORF081w	Escherichia virus RB43	GCA_000863505.1
AFA44807.1	000946	Gly_radical	120	RaK2_00521	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78951.1	000946	Gly_radical	123	-	Myoviridae sp.	GCA_012593985.1
QCW18850.1	000946	Gly_radical	120	7t3_0329	Salmonella phage 7t3	GCA_006083215.1
AZU98111.1	000946	Gly_radical	120	CPT_Munch_167	Salmonella phage Munch	GCA_004015485.1
QIG62871.1	000946	Gly_radical	120	SEPL_258	Salmonella phage SE_PL	GCA_011067555.1
AQW88662.1	000946	Gly_radical	120	BF_0137	Serratia phage BF	GCA_002619745.1
SOK58943.1	000946	Gly_radical	120	g135	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58409.1	000946	Gly_radical	120	g132	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AJK27456.1	000947	AdoMet_dc	114	PTIM40_29	Cyanophage P-TIM40	GCA_001470935.1
AMO43234.1	000947	AdoMet_dc	108	R1080702_229	Cyanophage S-RIM32	GCA_001754165.1
AMO43466.1	000947	AdoMet_dc	108	W270710_227	Cyanophage S-RIM44	GCA_002599145.1
AOO11706.1	000947	AdoMet_dc	108	ES420910_229	Cyanophage S-RIM44	GCA_002599165.1
AOO11938.1	000947	AdoMet_dc	108	Np050604_227	Cyanophage S-RIM44	GCA_002599185.1
AOO12172.1	000947	AdoMet_dc	108	Np200711_230	Cyanophage S-RIM44	GCA_002599205.1
AOO12407.1	000947	AdoMet_dc	108	Np420711_229	Cyanophage S-RIM44	GCA_002599225.1
AOO12639.1	000947	AdoMet_dc	108	Sn080709_227	Cyanophage S-RIM44	GCA_002599245.1
AOO12872.1	000947	AdoMet_dc	108	Sn130910_229	Cyanophage S-RIM44	GCA_002599265.1
AOO13105.1	000947	AdoMet_dc	108	W2100709_228	Cyanophage S-RIM44	GCA_002599285.1
AIR93468.1	000947	AdoMet_dc	117	AVU42_gp131	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99327.1	000947	AdoMet_dc	108	Syn1_231	Prochlorococcus phage Syn1	GCA_000892495.1
QGT54983.1	000947	AdoMet_dc	108	b23_0377	Synechococcus phage B23	GCA_009745195.1
QGT54618.1	000947	AdoMet_dc	108	b3_0383	Synechococcus phage B3	GCA_009745215.1
ASR76197.1	000947	AdoMet_dc	118	PBI_BELLAMY_152	Synechococcus phage Bellamy	GCA_002627525.1
QDH50581.1	000947	AdoMet_dc	111	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59608.1	000947	AdoMet_dc	57	S330809_147	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59370.1	000947	AdoMet_dc	57	C440309_147	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59846.1	000947	AdoMet_dc	57	N231010_147	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70557.1	000947	AdoMet_dc	115	HOU04_gp158	Synechococcus phage S-T4	GCA_003443335.1
QJT70144.1	000947	AdoMet_dc	111	SynMITS9220M01_131	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13625.1	000948	SIG+Phage-tail_3	1158	Ccr10_gp096	Caulobacter phage Ccr10	GCA_002619445.1
ARB13970.1	000948	SIG+Phage-tail_3	1158	Ccr2_gp095	Caulobacter phage Ccr2	GCA_002619465.1
ARB14659.1	000948	SIG+Phage-tail_3	1158	Ccr29_gp103	Caulobacter phage Ccr29	GCA_002619485.1
ARB15014.1	000948	SIG+Phage-tail_3	1158	Ccr32_gp096	Caulobacter phage Ccr32	GCA_002619505.1
ARB15346.1	000948	SIG+Phage-tail_3	869	Ccr34_gp104	Caulobacter phage Ccr34	GCA_002619525.1
ARB14314.1	000948	SIG+Phage-tail_3	1158	Ccr5_gp096	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68297.1	000948	SIG+Phage-tail_3	1160	CcrBL10_gp093	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69194.1	000948	SIG+Phage-tail_3	1201	CcrBL9_gp170	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69195.1	000948	SIG+Phage-tail_3	1199	CcrBL9_gp171	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87992.1	000948	SIG+Phage-tail_3	1198	CcrColossus_gp122	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87993.1	000948	SIG+Phage-tail_3	1196	CcrColossus_gp123	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68668.1	000948	SIG+Phage-tail_3	1198	CcrPW_gp129	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68669.1	000948	SIG+Phage-tail_3	1196	CcrPW_gp130	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69747.1	000948	SIG+Phage-tail_3	1201	CcrSC_gp165	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69748.1	000948	SIG+Phage-tail_3	1202	CcrSC_gp166	Caulobacter phage CcrSC	GCA_003443315.1
AFU87617.1	000948	SIG+Phage-tail_3	1158	CcrKarma_gp100	Caulobacter virus Karma	GCA_000901575.1
AFU87266.1	000948	SIG+Phage-tail_3	1158	CcrMagneto_gp096	Caulobacter virus Magneto	GCA_000903095.1
AFU86580.1	000948	SIG+Phage-tail_3	1158	CcrRogue_gp098	Caulobacter virus Rogue	GCA_000900555.1
AFU88413.1	000948	SIG+Phage-tail_3	1158	CcrSwift_gp095	Caulobacter virus Swift	GCA_000899655.1
AFU86931.1	000948	SIG+Phage-tail_3	1158	CbK_gp099	Caulobacter virus phiCbK	GCA_000900535.1
AHI60227.1	000949	Pectate_lyase_3	640	Ea357_076	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49785.1	000949	Pectate_lyase_3	600	MACHINA_147	Erwinia phage Machina	GCA_002758035.1
AGX01836.1	000949	Pectate_lyase_3	634	amsF	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07186.1	000949	Pectate_lyase_3	640	REBECCA_78	Erwinia phage Rebecca	GCA_004521635.1
AXF51286.1	000949	Pectate_lyase_3	632	WELLINGTON_157	Erwinia phage Wellington	GCA_003344985.1
AFQ96603.1	000949	Pectate_lyase_3	605	G173_gp058	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48167.1	000949	Pectate_lyase_3	604	ASESINO_154	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AUG85865.1	000949	Pectate_lyase_3	640	BOSOLAPHORUS_77	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52177.1	000949	Pectate_lyase_3	640	DM_79	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86184.1	000949	Pectate_lyase_3	640	DESERTFOX_76	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49229.1	000949	Pectate_lyase_3	600	HUXLEY_147	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49510.1	000949	Pectate_lyase_3	632	KWAN_158	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86506.1	000949	Pectate_lyase_3	640	MADMEL_78	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86827.1	000949	Pectate_lyase_3	640	MORTIMER_78	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50057.1	000949	Pectate_lyase_3	600	PARSHIK_148	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANH51857.1	000949	Pectate_lyase_3	640	RAY_76	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51541.1	000949	Pectate_lyase_3	640	SIMMY50_79	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64889.1	000949	Pectate_lyase_3	640	SPECIALG_79	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANZ50580.1	000949	Pectate_lyase_3	605	STRATTON_155	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AQT28720.1	000949	Pectate_lyase_3	604	YOLOSWAG_245	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01426.1	000950	Cluster354_1clades	482	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28759.1	000950	Cluster354_1clades	484	AP1_0041	Aeromonas phage AP1	GCA_014183365.1
ATI17472.1	000950	Cluster354_1clades	484	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00525.1	000950	Cluster354_1clades	484	HWB28_gp027	Aeromonas phage AS-zj	GCA_002627665.1
AUE22574.1	000950	Cluster354_1clades	479	Ah1_00033	Aeromonas phage Ah1	GCA_002957415.1
QAX98610.1	000950	Cluster354_1clades	480	ASfcp2_277	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97912.1	000950	Cluster354_1clades	484	ASswx1_269	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01238.1	000950	Cluster354_1clades	482	ASwh1_173	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39400.1	000950	Cluster354_1clades	484	CC2_263	Aeromonas phage CC2	GCA_000903495.1
ADQ52747.1	000950	Cluster354_1clades	480	PX29p028	Aeromonas phage PX29	GCA_000920195.1
ADM80003.1	000950	Cluster354_1clades	480	phiAS5_ORF0160	Aeromonas phage phiAS5	GCA_000887715.1
AAR90903.1	000950	Cluster354_1clades	481	65p035	Aeromonas virus 65	GCA_000893255.1
AAQ17689.1	000950	Cluster354_1clades	479	Aeh1ORF031c	Aeromonas virus Aeh1	GCA_000843245.1
ANS05949.1	000950	Cluster354_1clades	475	ABCD_0259	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65036.1	000950	Cluster354_1clades	479	S13_239	Cronobacter phage S13	GCA_001503575.1
AON97278.1	000950	Cluster354_1clades	475	E_270	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78799.1	000950	Cluster354_1clades	475	RB43ORF277w	Escherichia virus RB43	GCA_000863505.1
QHJ78896.1	000950	Cluster354_1clades	482	-	Myoviridae sp.	GCA_012593985.1
ASV44099.1	000950	Cluster354_1clades	488	PBI_SCTP2_84	Salicola phage SCTP-2	GCA_002625545.1
ALY07122.1	000950	Cluster354_1clades	476	VmeM32_00135	Vibrio phage vB_VmeM-32	GCA_002608825.1
ARB13537.1	000951	Cluster355_1clades	345	Ccr10_gp009	Caulobacter phage Ccr10	GCA_002619445.1
ARB13862.1	000951	Cluster355_1clades	345	Ccr10_gp332	Caulobacter phage Ccr10	GCA_002619445.1
ARB13884.1	000951	Cluster355_1clades	350	Ccr2_gp009	Caulobacter phage Ccr2	GCA_002619465.1
ARB14207.1	000951	Cluster355_1clades	350	Ccr2_gp331	Caulobacter phage Ccr2	GCA_002619465.1
ARB14566.1	000951	Cluster355_1clades	350	Ccr29_gp009	Caulobacter phage Ccr29	GCA_002619485.1
ARB14901.1	000951	Cluster355_1clades	350	Ccr29_gp345	Caulobacter phage Ccr29	GCA_002619485.1
ARB14927.1	000951	Cluster355_1clades	350	Ccr32_gp008	Caulobacter phage Ccr32	GCA_002619505.1
ARB15238.1	000951	Cluster355_1clades	350	Ccr32_gp320	Caulobacter phage Ccr32	GCA_002619505.1
ARB15258.1	000951	Cluster355_1clades	350	Ccr34_gp009	Caulobacter phage Ccr34	GCA_002619525.1
ARB15572.1	000951	Cluster355_1clades	350	Ccr34_gp330	Caulobacter phage Ccr34	GCA_002619525.1
ARB14225.1	000951	Cluster355_1clades	347	Ccr5_gp007	Caulobacter phage Ccr5	GCA_002619545.1
ARB14545.1	000951	Cluster355_1clades	347	Ccr5_gp325	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68211.1	000951	Cluster355_1clades	332	CcrBL10_gp007	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68529.1	000951	Cluster355_1clades	332	CcrBL10_gp325	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87525.1	000951	Cluster355_1clades	349	CcrKarma_gp008	Caulobacter virus Karma	GCA_000901575.1
AFU87858.1	000951	Cluster355_1clades	349	CcrKarma_gp341	Caulobacter virus Karma	GCA_000901575.1
AFU87178.1	000951	Cluster355_1clades	345	CcrMagneto_gp008	Caulobacter virus Magneto	GCA_000903095.1
AFU87506.1	000951	Cluster355_1clades	345	CcrMagneto_gp336	Caulobacter virus Magneto	GCA_000903095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU86840.1	000951	Cluster355_1clades	350	CbK_gp008	Caulobacter virus phiCbK	GCA_000900535.1
AFU87158.1	000951	Cluster355_1clades	350	CbK_gp326	Caulobacter virus phiCbK	GCA_000900535.1
AUZ94882.1	000952	Cluster356_1clades	239	FDI40_gp072	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21734.1	000952	Cluster356_1clades	323	GAP32_284	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13915.1	000952	Cluster356_1clades	309	PBI_121Q_18	Escherichia phage 121Q	GCA_000926855.1
QAY00423.1	000952	Cluster356_1clades	325	Ecwhy1_142	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35166.1	000952	Cluster356_1clades	330	ACQ29_gp486	Escherichia phage PBECO4	GCA_001041035.1
BBM61607.1	000952	Cluster356_1clades	325	EO157G_0180	Escherichia phage SP27	GCA_008033345.1
AXC36739.1	000952	Cluster356_1clades	264	-	Escherichia phage UB	GCA_003341455.1
QBO61777.1	000952	Cluster356_1clades	325	G17_00288	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13821.1	000952	Cluster356_1clades	325	vBEcoMphAPEC6_gp192c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80510.1	000952	Cluster356_1clades	325	PSLUR01_00533	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44399.1	000952	Cluster356_1clades	325	RaK2_00126	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72770.1	000952	Cluster356_1clades	287	-	Myoviridae sp.	GCA_003657725.1
AMM43853.1	000952	Cluster356_1clades	323	CBB_289	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76103.1	000952	Cluster356_1clades	289	EST35_0222	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW19012.1	000952	Cluster356_1clades	323	7t3_0492	Salmonella phage 7t3	GCA_006083215.1
AZU98259.1	000952	Cluster356_1clades	323	CPT_Munch_315	Salmonella phage Munch	GCA_004015485.1
QIG62725.1	000952	Cluster356_1clades	323	SEPL_112	Salmonella phage SE_PL	GCA_011067555.1
AQW88812.1	000952	Cluster356_1clades	323	BF_0287	Serratia phage BF	GCA_002619745.1
SOK59095.1	000952	Cluster356_1clades	323	g287	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58559.1	000952	Cluster356_1clades	323	g282	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70250.1	000953	Cluster357_1clades	292	CF8_0082	Aeromonas phage CF8	GCA_006384595.2
QDJ97229.1	000953	Cluster357_1clades	298	D6_0069	Aeromonas phage D6	GCA_007051205.2
QDH47093.1	000953	Cluster357_1clades	298	LAh10_2	Aeromonas phage LAh10	GCA_006863975.1
QDJ96839.1	000953	Cluster357_1clades	294	PS1_0080	Aeromonas phage PS1	GCA_007051165.2
QFR59469.1	000953	Cluster357_1clades	294	PS2_0078	Aeromonas phage PS2	GCA_009388305.2
QBZ70612.1	000953	Cluster357_1clades	292	pETSU_031	Edwardsiella virus pEt-SU	GCA_004800915.1
AGX01962.1	000953	Cluster357_1clades	280	CF95_gp240	Erwinia phage PhiEaH1	GCA_000914555.1
ASU03864.1	000953	Cluster357_1clades	302	JOAD_51	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03619.1	000953	Cluster357_1clades	302	RISINGSUN_51	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71928.1	000953	Cluster357_1clades	293	N1M2_65	Klebsiella phage N1M2	GCA_010092605.1
QGZ14391.1	000953	Cluster357_1clades	305	HWC77_gp028	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27139.1	000953	Cluster357_1clades	299	PPEV_gp045	Pseudomonas phage EL	GCA_000866825.1
AEV89528.1	000953	Cluster357_1clades	295	OBP_091	Pseudomonas phage OBP	GCA_000896635.1
ATA65338.1	000953	Cluster357_1clades	280	2050HW_00003	Serratia phage 2050HW	GCA_002628125.1
QDB71126.1	000953	Cluster357_1clades	280	CPT_Moabite_096	Serratia phage Moabite	GCA_006384735.1
QAU04345.1	000953	Cluster357_1clades	305	HWC03_gp190	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23231.1	000953	Cluster357_1clades	308	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80990.1	000953	Cluster357_1clades	308	Aphrodite1_0114	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47497.1	000953	Cluster357_1clades	308	HWC35_gp103	Vibrio phage USC-1	GCA_006864065.1
BAW98317.1	000953	Cluster357_1clades	287	FDH33_gp108	Vibrio phage pTD1	GCA_002618825.1
AFO71262.1	000954	Cluster359_1clades	287	CR5_042	Cronobacter phage CR5	GCA_000910235.1
AMR59692.1	000954	Cluster359_1clades	285	SEGD1_043	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07469.1	000954	Cluster359_1clades	287	DERBICUS_43	Erwinia phage Derbicus	GCA_004521655.1
ANZ49695.1	000954	Cluster359_1clades	284	MACHINA_57	Erwinia phage Machina	GCA_002758035.1
AXF51184.1	000954	Cluster359_1clades	281	WELLINGTON_53	Erwinia phage Wellington	GCA_003344985.1
AFQ96769.1	000954	Cluster359_1clades	287	G173_gp224	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48071.1	000954	Cluster359_1clades	287	ASESINO_58	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48346.1	000954	Cluster359_1clades	284	CAITLIN_51	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48619.1	000954	Cluster359_1clades	284	CHRISDB_57	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48893.1	000954	Cluster359_1clades	287	EARLPHILLIPIV_43	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49140.1	000954	Cluster359_1clades	284	HUXLEY_58	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49405.1	000954	Cluster359_1clades	281	KWAN_53	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49968.1	000954	Cluster359_1clades	284	PARSHIK_59	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50233.1	000954	Cluster359_1clades	287	PHOBOS_43	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50481.1	000954	Cluster359_1clades	287	STRATTON_56	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85882.1	000954	Cluster359_1clades	285	ACEC001_0440	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20757.1	000954	Cluster359_1clades	294	-	Salmonella phage JN03	GCA_014319805.1
AWN09056.1	000954	Cluster359_1clades	287	MLDJOKPK_00125	Salmonella phage SPAsTU	GCA_003183805.1
AEP83874.1	000954	Cluster359_1clades	285	SPN3US_0041	Salmonella phage SPN3US	GCA_001042275.1
AQT28168.1	000954	Cluster359_1clades	294	pVa21_227	Vibrio phage pVa-21	GCA_002619305.1
AFO71417.1	000955	Cluster360_1clades	273	CR5_197	Cronobacter phage CR5	GCA_000910235.1
AMR59873.1	000955	Cluster360_1clades	228	SEGD1_226	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07630.1	000955	Cluster360_1clades	279	DERBICUS_204	Erwinia phage Derbicus	GCA_004521655.1
ANZ49874.1	000955	Cluster360_1clades	286	MACHINA_236	Erwinia phage Machina	GCA_002758035.1
AXF51376.1	000955	Cluster360_1clades	275	WELLINGTON_250	Erwinia phage Wellington	GCA_003344985.1
AFQ96688.1	000955	Cluster360_1clades	274	G173_gp143	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48257.1	000955	Cluster360_1clades	274	ASESINO_244	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48531.1	000955	Cluster360_1clades	280	CAITLIN_236	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48807.1	000955	Cluster360_1clades	280	CHRISDB_245	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49054.1	000955	Cluster360_1clades	273	EARLPHILLIPIV_205	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49317.1	000955	Cluster360_1clades	286	HUXLEY_235	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49602.1	000955	Cluster360_1clades	275	KWAN_250	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50145.1	000955	Cluster360_1clades	286	PARSHIK_236	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50401.1	000955	Cluster360_1clades	282	PHOBOS_211	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50670.1	000955	Cluster360_1clades	274	STRATTON_245	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86063.1	000955	Cluster360_1clades	292	ACEC001_2200	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20909.1	000955	Cluster360_1clades	292	-	Salmonella phage JN03	GCA_014319805.1
AXF51113.1	000955	Cluster360_1clades	293	MLDJOKPK_00218	Salmonella phage SPAsTU	GCA_003183805.1
AEP84055.1	000955	Cluster360_1clades	292	SPN3US_0222	Salmonella phage SPN3US	GCA_001042275.1
AQT28097.1	000955	Cluster360_1clades	139	pVa21_156	Vibrio phage pVa-21	GCA_002619305.1
ASV44725.1	000956	Cluster361_1clades	235	FDI40_gp250	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21663.1	000956	Cluster361_1clades	228	GAP32_213	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14456.1	000956	Cluster361_1clades	218	PBI_121Q_566	Escherichia phage 121Q	GCA_000926855.1
QAY00492.1	000956	Cluster361_1clades	217	Ecwhy1_213	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34687.1	000956	Cluster361_1clades	218	ACQ29_gp007	Escherichia phage PBECO4	GCA_001041035.1
BBM62129.1	000956	Cluster361_1clades	218	EO157G_5400	Escherichia phage SP27	GCA_008033345.1
AXC36807.1	000956	Cluster361_1clades	218	-	Escherichia phage UB	GCA_003341455.1
QBO61846.1	000956	Cluster361_1clades	218	G17_00357	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13887.1	000956	Cluster361_1clades	218	vBEcoMphAPEC6_gp262c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80441.1	000956	Cluster361_1clades	218	PSLUR01_00464	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44329.1	000956	Cluster361_1clades	216	RaK2_00056	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72743.1	000956	Cluster361_1clades	292	-	Myoviridae sp.	GCA_003657725.1
AMM43784.1	000956	Cluster361_1clades	230	CBB_219	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76225.1	000956	Cluster361_1clades	246	EST35_0344	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18934.1	000956	Cluster361_1clades	214	7t3_0413	Salmonella phage 7t3	GCA_006083215.1
AZU98189.1	000956	Cluster361_1clades	214	CPT_Munch_245	Salmonella phage Munch	GCA_004015485.1
QIG62795.1	000956	Cluster361_1clades	214	SEPL_182	Salmonella phage SE_PL	GCA_011067555.1
AQW88740.1	000956	Cluster361_1clades	215	BF_0215	Serratia phage BF	GCA_002619745.1
SOK59023.1	000956	Cluster361_1clades	215	g215	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58488.1	000956	Cluster361_1clades	215	g211	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71334.1	000957	Cluster362_1clades	161	CR5_114	Cronobacter phage CR5	GCA_000910235.1
QBP07543.1	000957	Cluster362_1clades	155	DERBICUS_117	Erwinia phage Derbicus	GCA_004521655.1
AGX01831.1	000957	Cluster362_1clades	291	CF95_gp109	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ48966.1	000957	Cluster362_1clades	155	EARLPHILLIPIV_117	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50307.1	000957	Cluster362_1clades	148	PHOBOS_117	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ARM70809.1	000957	Cluster362_1clades	153	phiC120_c103	Escherichia phage phiC120	GCA_002621185.1
ABY63141.1	000957	Cluster362_1clades	157	201phi2-1p315	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45055.1	000957	Cluster362_1clades	144	KTN4_297	Pseudomonas phage KTN4	GCA_002607225.1
QBX32399.1	000957	Cluster362_1clades	154	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76945.1	000957	Cluster362_1clades	159	PHABIO_314	Pseudomonas phage Phabio	GCA_002624965.1
AEH03664.1	000957	Cluster362_1clades	148	241	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02799.1	000957	Cluster362_1clades	145	PSA21_273	Pseudomonas phage Psa21	GCA_004340405.1
ATN94660.1	000957	Cluster362_1clades	144	SL2_083	Pseudomonas phage SL2	GCA_002956015.1
QJB22930.1	000957	Cluster362_1clades	144	fnug_287	Pseudomonas phage fnug	GCA_012837215.1
QEM41969.1	000957	Cluster362_1clades	154	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83146.1	000957	Cluster362_1clades	144	PHIKZ245	Pseudomonas virus phiKZ	GCA_000842965.1
ASV44082.1	000957	Cluster362_1clades	88	PBI_SCTP2_67	Salicola phage SCTP-2	GCA_002625545.1
ATA65477.1	000957	Cluster362_1clades	157	2050HW_00142	Serratia phage 2050HW	GCA_002628125.1
QDB71247.1	000957	Cluster362_1clades	156	CPT_Moabite_217	Serratia phage Moabite	GCA_006384735.1
QFP93155.1	000957	Cluster362_1clades	207	-	Serratia phage PCH45	GCA_009187865.1
ASV44731.1	000958	Cluster363_1clades	265	FDI40_gp272	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21713.1	000958	Cluster363_1clades	239	GAP32_263	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14506.1	000958	Cluster363_1clades	241	PBI_121Q_616	Escherichia phage 121Q	GCA_000926855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY00443.1	000958	Cluster363_1clades	241	Ecwhy1_163	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35186.1	000958	Cluster363_1clades	241	ACQ29_gp506	Escherichia phage PBECO4	GCA_001041035.1
BBM62178.1	000958	Cluster363_1clades	241	EO157G_5890	Escherichia phage SP27	GCA_008033345.1
AXC36758.1	000958	Cluster363_1clades	241	-	Escherichia phage UB	GCA_003341455.1
QBO61797.1	000958	Cluster363_1clades	241	G17_00308	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13841.1	000958	Cluster363_1clades	241	vBEcoMphAPEC6_gp212c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80490.1	000958	Cluster363_1clades	241	PSLUR01_00513	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44378.1	000958	Cluster363_1clades	235	RaK2_00105	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72736.1	000958	Cluster363_1clades	274	-	Myoviridae sp.	GCA_003657725.1
AMM43833.1	000958	Cluster363_1clades	239	CBB_269	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76205.1	000958	Cluster363_1clades	203	EST35_0324	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18992.1	000958	Cluster363_1clades	240	7t3_0471	Salmonella phage 7t3	GCA_006083215.1
AZU98240.1	000958	Cluster363_1clades	233	CPT_Munch_296	Salmonella phage Munch	GCA_004015485.1
QIG62744.1	000958	Cluster363_1clades	233	SEPL_131	Salmonella phage SE_PL	GCA_011067555.1
AQW88792.1	000958	Cluster363_1clades	241	BF_0267	Serratia phage BF	GCA_002619745.1
SOK59073.1	000958	Cluster363_1clades	241	g265	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58539.1	000958	Cluster363_1clades	241	g262	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBX06455.1	000959	Cluster364_1clades	229	BcepSaruman_042	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74423.1	000959	Cluster364_1clades	229	BcepSauron_043	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13533.1	000959	Cluster364_1clades	267	Ccr10_gp005	Caulobacter phage Ccr10	GCA_002619445.1
ARB13858.1	000959	Cluster364_1clades	267	Ccr10_gp328	Caulobacter phage Ccr10	GCA_002619445.1
ARB13879.1	000959	Cluster364_1clades	267	Ccr2_gp004	Caulobacter phage Ccr2	GCA_002619465.1
ARB14202.1	000959	Cluster364_1clades	267	Ccr2_gp326	Caulobacter phage Ccr2	GCA_002619465.1
ARB14562.1	000959	Cluster364_1clades	267	Ccr29_gp005	Caulobacter phage Ccr29	GCA_002619485.1
ARB14897.1	000959	Cluster364_1clades	267	Ccr29_gp341	Caulobacter phage Ccr29	GCA_002619485.1
ARB14924.1	000959	Cluster364_1clades	267	Ccr32_gp005	Caulobacter phage Ccr32	GCA_002619505.1
ARB15235.1	000959	Cluster364_1clades	267	Ccr32_gp317	Caulobacter phage Ccr32	GCA_002619505.1
ARB15255.1	000959	Cluster364_1clades	267	Ccr34_gp006	Caulobacter phage Ccr34	GCA_002619525.1
ARB15569.1	000959	Cluster364_1clades	267	Ccr34_gp327	Caulobacter phage Ccr34	GCA_002619525.1
ARB14222.1	000959	Cluster364_1clades	267	Ccr5_gp004	Caulobacter phage Ccr5	GCA_002619545.1
ARB14542.1	000959	Cluster364_1clades	267	Ccr5_gp322	Caulobacter phage Ccr5	GCA_002619545.1
AFU87522.1	000959	Cluster364_1clades	267	CcrKarma_gp005	Caulobacter virus Karma	GCA_000901575.1
AFU87855.1	000959	Cluster364_1clades	267	CcrKarma_gp338	Caulobacter virus Karma	GCA_000901575.1
AFU87175.1	000959	Cluster364_1clades	267	CcrMagneto_gp005	Caulobacter virus Magneto	GCA_000903095.1
AFU87503.1	000959	Cluster364_1clades	267	CcrMagneto_gp333	Caulobacter virus Magneto	GCA_000903095.1
AFU86837.1	000959	Cluster364_1clades	267	CbK_gp005	Caulobacter virus phiCbK	GCA_000900535.1
AFU87155.1	000959	Cluster364_1clades	267	CbK_gp323	Caulobacter virus phiCbK	GCA_000900535.1
AFO71405.1	000960	DUF5051	242	CR5_185	Cronobacter phage CR5	GCA_000910235.1
AMR59857.1	000960	DUF5051	252	SEGD1_210	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07617.1	000960	DUF5051	250	DERBICUS_191	Erwinia phage Derbicus	GCA_004521655.1
ANZ49855.1	000960	DUF5051	251	MACHINA_217	Erwinia phage Machina	GCA_002758035.1
AXF51357.1	000960	DUF5051	237	WELLINGTON_231	Erwinia phage Wellington	GCA_003344985.1
AFQ96672.1	000960	DUF5051	245	G173_gp127	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48238.1	000960	DUF5051	243	ASESINO_225	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48512.1	000960	DUF5051	253	CAITLIN_217	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48789.1	000960	DUF5051	255	CHRISDB_227	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49041.1	000960	DUF5051	250	EARLPHILLIPIV_192	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49299.1	000960	DUF5051	251	HUXLEY_217	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49583.1	000960	DUF5051	237	KWAN_231	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50127.1	000960	DUF5051	251	PARSHIK_218	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50389.1	000960	DUF5051	243	PHOBOS_199	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50652.1	000960	DUF5051	248	STRATTON_227	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86046.1	000960	DUF5051	239	ACEC001_2030	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20894.1	000960	DUF5051	239	-	Salmonella phage JN03	GCA_014319805.1
AWN09141.1	000960	DUF5051	239	MLDJOKPK_00234	Salmonella phage SPAsTU	GCA_003183805.1
AEP84039.1	000960	DUF5051	239	SPN3US_0206	Salmonella phage SPN3US	GCA_001042275.1
AQT28080.1	000960	DUF5051	248	pVa21_139	Vibrio phage pVa-21	GCA_002619305.1
AFO71343.1	000961	Cluster368_1clades	248	CR5_123	Cronobacter phage CR5	GCA_000910235.1
AMR59766.1	000961	Cluster368_1clades	232	SEGD1_119	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07551.1	000961	Cluster368_1clades	249	DERBICUS_125	Erwinia phage Derbicus	GCA_004521655.1
ANZ49765.1	000961	Cluster368_1clades	254	MACHINA_127	Erwinia phage Machina	GCA_002758035.1
AXF51273.1	000961	Cluster368_1clades	207	WELLINGTON_143	Erwinia phage Wellington	GCA_003344985.1
AFQ96583.1	000961	Cluster368_1clades	233	G173_gp038	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48143.1	000961	Cluster368_1clades	232	ASESINO_130	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48420.1	000961	Cluster368_1clades	211	CAITLIN_125	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48692.1	000961	Cluster368_1clades	211	CHRISDB_130	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48974.1	000961	Cluster368_1clades	249	EARLPHILLIPIV_125	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49210.1	000961	Cluster368_1clades	220	HUXLEY_128	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49494.1	000961	Cluster368_1clades	207	KWAN_142	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50038.1	000961	Cluster368_1clades	220	PARSHIK_129	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50315.1	000961	Cluster368_1clades	245	PHOBOS_125	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50558.1	000961	Cluster368_1clades	233	STRATTON_133	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85956.1	000961	Cluster368_1clades	232	ACEC001_1180	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20822.1	000961	Cluster368_1clades	232	-	Salmonella phage JN03	GCA_014319805.1
AXF51072.1	000961	Cluster368_1clades	216	MLDJOKPK_00042	Salmonella phage SPAsTU	GCA_003183805.1
AEP83948.1	000961	Cluster368_1clades	232	SPN3US_0115	Salmonella phage SPN3US	GCA_001042275.1
AQT28009.1	000961	Cluster368_1clades	207	pVa21_068	Vibrio phage pVa-21	GCA_002619305.1
AUZ94910.1	000962	Cluster369_1clades	222	FDI40_gp113	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21654.1	000962	Cluster369_1clades	181	GAP32_204	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14447.1	000962	Cluster369_1clades	178	PBI_121Q_557	Escherichia phage 121Q	GCA_000926855.1
QAY00501.1	000962	Cluster369_1clades	177	Ecwhy1_222	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34696.1	000962	Cluster369_1clades	178	ACQ29_gp016	Escherichia phage PBECO4	GCA_001041035.1
BBM62120.1	000962	Cluster369_1clades	178	EO157G_5310	Escherichia phage SP27	GCA_008033345.1
AXC36816.1	000962	Cluster369_1clades	178	-	Escherichia phage UB	GCA_003341455.1
QBO61855.1	000962	Cluster369_1clades	178	G17_00366	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13895.1	000962	Cluster369_1clades	141	vBEcoMphAPEC6_gp270c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80432.1	000962	Cluster369_1clades	178	PSLUR01_00455	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44320.1	000962	Cluster369_1clades	206	RaK2_00047	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72761.1	000962	Cluster369_1clades	250	-	Myoviridae sp.	GCA_003657725.1
AMM43775.1	000962	Cluster369_1clades	181	CBB_210	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76083.1	000962	Cluster369_1clades	200	EST35_0202	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18923.1	000962	Cluster369_1clades	179	7t3_0402	Salmonella phage 7t3	GCA_006083215.1
AZU98180.1	000962	Cluster369_1clades	179	CPT_Munch_236	Salmonella phage Munch	GCA_004015485.1
QIG62804.1	000962	Cluster369_1clades	179	SEPL_191	Salmonella phage SE_PL	GCA_011067555.1
AQW88731.1	000962	Cluster369_1clades	181	BF_0206	Serratia phage BF	GCA_002619745.1
SOK59014.1	000962	Cluster369_1clades	181	g206	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58479.1	000962	Cluster369_1clades	181	g202	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIA64869.1	000963	Cluster370_1clades	181	S13_070	Cronobacter phage S13	GCA_001503575.1
AFC21914.1	000963	Cluster370_1clades	60	GAP32_457	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QHJ79070.1	000963	Cluster370_1clades	174	-	Myoviridae sp.	GCA_012593985.1
AMM44039.1	000963	Cluster370_1clades	158	CBB_476	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44040.1	000963	Cluster370_1clades	172	CBB_477	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88996.1	000963	Cluster370_1clades	178	BF_0471	Serratia phage BF	GCA_002619745.1
AAQ64296.1	000963	Cluster370_1clades	245	KVP40.0227	Vibrio phage KVP40	GCA_000843785.1
QIW90612.1	000963	Cluster370_1clades	245	GCAPEGMB_00265	Vibrio phage V07	GCA_012361095.1
QIW91187.1	000963	Cluster370_1clades	245	COHAPHLL_00351	Vibrio phage V09	GCA_012361135.1
QHJ74407.1	000963	Cluster370_1clades	245	VH12019_00080	Vibrio phage VH1_2019	GCA_009931825.1
AGB06914.1	000963	Cluster370_1clades	244	CF80_gp127	Vibrio phage VH7D	GCA_000914495.1
QBX06232.1	000963	Cluster370_1clades	244	ValB1HC_279	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60858.1	000963	Cluster370_1clades	244	AVU32_gp017	Vibrio phage ValKK3	GCA_001501635.1
AGN30287.1	000963	Cluster370_1clades	244	VPFG_00288	Vibrio phage nt-1	GCA_000910195.2
ALP47044.1	000963	Cluster370_1clades	244	phiGrn1_0350	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47423.1	000963	Cluster370_1clades	244	phiST2_0105	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54857.1	000963	Cluster370_1clades	244	vBValMR10Z_317	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37457.1	000963	Cluster370_1clades	245	pp2_224	Vibriophage phi-pp2	GCA_002630725.1
SOK59279.1	000963	Cluster370_1clades	178	g471	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58744.1	000963	Cluster370_1clades	178	g467	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44739.1	000964	Cluster371_1clades	240	FDI40_gp305	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21780.1	000964	Cluster371_1clades	227	GAP32_330	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13960.1	000964	Cluster371_1clades	226	PBI_121Q_63	Escherichia phage 121Q	GCA_000926855.1
QAY00377.1	000964	Cluster371_1clades	226	Ecwhy1_96	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35122.1	000964	Cluster371_1clades	226	ACQ29_gp442	Escherichia phage PBECO4	GCA_001041035.1
BBM61652.1	000964	Cluster371_1clades	226	EO157G_0630	Escherichia phage SP27	GCA_008033345.1
AXC36696.1	000964	Cluster371_1clades	226	-	Escherichia phage UB	GCA_003341455.1
QBO61733.1	000964	Cluster371_1clades	226	G17_00244	Escherichia phage vB_EcoM_G17	GCA_004521135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDF13778.1	000964	Cluster371_1clades	226	vBEcoMphAPEC6_gp149c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80554.1	000964	Cluster371_1clades	226	PSLUR01_00577	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44442.1	000964	Cluster371_1clades	225	RaK2_00169	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43898.1	000964	Cluster371_1clades	227	CBB_335	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76177.1	000964	Cluster371_1clades	233	EST35_0296	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44088.1	000964	Cluster371_1clades	146	PBI_SCTP2_73	Salicola phage SCTP-2	GCA_002625545.1
QCW19057.1	000964	Cluster371_1clades	226	7t3_0537	Salmonella phage 7t3	GCA_006083215.1
AZU98304.1	000964	Cluster371_1clades	226	CPT_Munch_360	Salmonella phage Munch	GCA_004015485.1
QIG62680.1	000964	Cluster371_1clades	226	SEPL_067	Salmonella phage SE_PL	GCA_011067555.1
AQW88858.1	000964	Cluster371_1clades	227	BF_0333	Serratia phage BF	GCA_002619745.1
SOK59142.1	000964	Cluster371_1clades	227	g334	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58608.1	000964	Cluster371_1clades	227	g331	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71264.1	000965	DUF3492	193	CR5_044	Cronobacter phage CR5	GCA_000910235.1
AMR59694.1	000965	DUF3492	166	SEGD1_045	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07471.1	000965	DUF3492	200	DERBICUS_45	Erwinia phage Derbicus	GCA_004521655.1
ANZ49697.1	000965	DUF3492	169	MACHINA_59	Erwinia phage Machina	GCA_002758035.1
AXF51186.1	000965	DUF3492	173	WELLINGTON_55	Erwinia phage Wellington	GCA_003344985.1
AFQ96771.1	000965	DUF3492	167	G173_gp226	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48073.1	000965	DUF3492	167	ASESINO_60	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48348.1	000965	DUF3492	169	CAITLIN_53	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48621.1	000965	DUF3492	185	CHRISDB_59	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48895.1	000965	DUF3492	200	EARLPHILLIPIV_45	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49142.1	000965	DUF3492	169	HUXLEY_60	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49407.1	000965	DUF3492	173	KWAN_55	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49970.1	000965	DUF3492	169	PARSHIK_61	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50235.1	000965	DUF3492	196	PHOBOS_45	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50483.1	000965	DUF3492	167	STRATTON_58	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85884.1	000965	DUF3492	166	ACEC001_0460	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20759.1	000965	DUF3492	166	-	Salmonella phage JN03	GCA_014319805.1
AWN09054.1	000965	DUF3492	166	MLDJOKPK_00123	Salmonella phage SPAsTU	GCA_003183805.1
AEP83876.1	000965	DUF3492	166	SPN3US_0043	Salmonella phage SPN3US	GCA_001042275.1
AQT28170.1	000965	DUF3492	211	pVa21_229	Vibrio phage pVa-21	GCA_002619305.1
AFC21990.1	000966	SIG+DUF1190	207	GAP32_529	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AHI60242.1	000966	SIG+DUF1190	205	Ea357_091	Erwinia phage Ea35-70	GCA_000914635.1
QBP07200.1	000966	SIG+DUF1190	205	REBECCA_93	Erwinia phage Rebecca	GCA_004521635.1
AUG85879.1	000966	SIG+DUF1190	205	BOSOLAPHORUS_92	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52194.1	000966	SIG+DUF1190	205	DM_96	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86198.1	000966	SIG+DUF1190	205	DESERTFOX_91	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03761.1	000966	SIG+DUF1190	189	JOAD_154	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86521.1	000966	SIG+DUF1190	205	MADMEL_93	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86844.1	000966	SIG+DUF1190	205	MORTIMER_95	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51872.1	000966	SIG+DUF1190	205	RAY_91	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03517.1	000966	SIG+DUF1190	189	RISINGSUN_153	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51556.1	000966	SIG+DUF1190	205	SIMMY50_94	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64904.1	000966	SIG+DUF1190	205	SPECIALG_94	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AFA44590.1	000966	SIG+DUF1190	198	RaK2_00317	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG65903.1	000966	SIG+DUF1190	175	phiOC_p242	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM44110.1	000966	SIG+DUF1190	207	CBB_547	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QKE54395.1	000966	SIG+DUF1190	194	ACSA002_0810	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AQW89063.1	000966	SIG+DUF1190	211	BF_0538	Serratia phage BF	GCA_002619745.1
SOK59341.1	000966	SIG+DUF1190	207	g533	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58803.1	000966	SIG+DUF1190	206	g526	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGX01949.1	000967	Cluster375_1clades	175	CF95_gp227	Erwinia phage PhiEaH1	GCA_000914555.1
QBO63852.1	000967	Cluster375_1clades	176	Goslar_00059	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ABY62983.1	000967	Cluster375_1clades	177	201phi2-1p153	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44876.1	000967	Cluster375_1clades	176	KTN4_118	Pseudomonas phage KTN4	GCA_002607225.1
ARV77262.1	000967	Cluster375_1clades	175	NOXIFER_92	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32249.1	000967	Cluster375_1clades	177	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76768.1	000967	Cluster375_1clades	178	PHABIO_137	Pseudomonas phage Phabio	GCA_002624965.1
AEH03518.1	000967	Cluster375_1clades	180	094	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02629.1	000967	Cluster375_1clades	173	PSA21_101	Pseudomonas phage Psa21	GCA_004340405.1
ATN94837.1	000967	Cluster375_1clades	181	SL2_260	Pseudomonas phage SL2	GCA_002956015.1
QJB22753.1	000967	Cluster375_1clades	176	fnug_110	Pseudomonas phage fnug	GCA_012837215.1
QEM41826.1	000967	Cluster375_1clades	177	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82992.2	000967	Cluster375_1clades	176	PHIKZ091	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19216.1	000967	Cluster375_1clades	199	FDH28_gp179	Ralstonia phage RP12	GCA_002617345.1
BAW19502.1	000967	Cluster375_1clades	199	-	Ralstonia phage RP31	GCA_002617365.1
BAS04973.1	000967	Cluster375_1clades	194	AVU11_gp181	Ralstonia phage RSF1	GCA_001500875.1
BAQ02699.1	000967	Cluster375_1clades	194	AVU38_gp171	Ralstonia phage RSL2	GCA_001503055.1
ATA65354.1	000967	Cluster375_1clades	137	2050HW_00019	Serratia phage 2050HW	GCA_002628125.1
QDB71141.1	000967	Cluster375_1clades	179	CPT_Moabite_111	Serratia phage Moabite	GCA_006384735.1
QFP93179.1	000967	Cluster375_1clades	175	-	Serratia phage PCH45	GCA_009187865.1
AFO71281.1	000968	Cluster376_1clades	182	CR5_061	Cronobacter phage CR5	GCA_000910235.1
AMR59713.1	000968	Cluster376_1clades	179	SEGD1_064	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07488.1	000968	Cluster376_1clades	178	DERBICUS_62	Erwinia phage Derbicus	GCA_004521655.1
ANZ49714.1	000968	Cluster376_1clades	180	MACHINA_76	Erwinia phage Machina	GCA_002758035.1
AXF51206.1	000968	Cluster376_1clades	181	WELLINGTON_76	Erwinia phage Wellington	GCA_003344985.1
AFQ96792.1	000968	Cluster376_1clades	182	G173_gp247	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48093.1	000968	Cluster376_1clades	183	ASESINO_80	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48366.1	000968	Cluster376_1clades	180	CAITLIN_71	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48639.1	000968	Cluster376_1clades	180	CHRISDB_77	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48912.1	000968	Cluster376_1clades	178	EARLPHILLIPIV_62	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49159.1	000968	Cluster376_1clades	180	HUXLEY_77	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49428.1	000968	Cluster376_1clades	181	KWAN_76	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49987.1	000968	Cluster376_1clades	180	PARSHIK_78	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50254.1	000968	Cluster376_1clades	178	PHOBOS_64	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50504.1	000968	Cluster376_1clades	182	STRATTON_79	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85904.1	000968	Cluster376_1clades	179	ACEC001_0660	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20779.1	000968	Cluster376_1clades	179	-	Salmonella phage JN03	GCA_014319805.1
AWN09037.1	000968	Cluster376_1clades	178	MLDJOKPK_00101	Salmonella phage SPAsTU	GCA_003183805.1
AEP83896.1	000968	Cluster376_1clades	179	SPN3US_0063	Salmonella phage SPN3US	GCA_001042275.1
AQT27945.1	000968	Cluster376_1clades	195	pVa21_003	Vibrio phage pVa-21	GCA_002619305.1
APU01663.1	000969	Cluster377_1clades	191	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01075.1	000969	Cluster377_1clades	96	ASwh1_7	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53295.1	000969	Cluster377_1clades	191	65p287	Aeromonas virus 65	GCA_000893255.1
AMM45073.1	000969	Cluster377_1clades	121	SP15_266	Bacillus phage SP-15	GCA_001754685.1
ARB13557.1	000969	Cluster377_1clades	100	Ccr10_gp029	Caulobacter phage Ccr10	GCA_002619445.1
ARB13903.1	000969	Cluster377_1clades	100	Ccr2_gp028	Caulobacter phage Ccr2	GCA_002619465.1
ARB14592.1	000969	Cluster377_1clades	100	Ccr29_gp035	Caulobacter phage Ccr29	GCA_002619485.1
ARB14947.1	000969	Cluster377_1clades	100	Ccr32_gp028	Caulobacter phage Ccr32	GCA_002619505.1
ARB15278.1	000969	Cluster377_1clades	100	Ccr34_gp029	Caulobacter phage Ccr34	GCA_002619525.1
ARB14246.1	000969	Cluster377_1clades	100	Ccr5_gp028	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68230.1	000969	Cluster377_1clades	160	CcrBL10_gp026	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87546.1	000969	Cluster377_1clades	100	CcrKarma_gp029	Caulobacter virus Karma	GCA_000901575.1
AFU87197.1	000969	Cluster377_1clades	100	CcrMagneto_gp027	Caulobacter virus Magneto	GCA_000903095.1
AFU86512.1	000969	Cluster377_1clades	96	CcrRogue_gp030	Caulobacter virus Rogue	GCA_000900555.1
AFU88343.1	000969	Cluster377_1clades	100	CcrSwift_gp025	Caulobacter virus Swift	GCA_000899655.1
AFU86860.1	000969	Cluster377_1clades	100	CbK_gp028	Caulobacter virus phiCbK	GCA_000900535.1
QHJ86011.1	000969	Cluster377_1clades	89	KKIINIFJ_00099	Pseudomonas phage PN05	GCA_009931935.1
AQW88929.1	000969	Cluster377_1clades	85	BF_0404	Serratia phage BF	GCA_002619745.1
SOK59218.1	000969	Cluster377_1clades	85	g410	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58684.1	000969	Cluster377_1clades	85	g407	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14392.1	000970	Cluster378_1clades	188	PBI_121Q_502	Escherichia phage 121Q	GCA_000926855.1
AIT14393.1	000970	Cluster378_1clades	171	PBI_121Q_503	Escherichia phage 121Q	GCA_000926855.1
QAY00555.1	000970	Cluster378_1clades	171	Ecwhy1_276	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00556.1	000970	Cluster378_1clades	188	Ecwhy1_277	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34749.1	000970	Cluster378_1clades	172	ACQ29_gp069	Escherichia phage PBECO4	GCA_001041035.1
AGC34750.1	000970	Cluster378_1clades	188	ACQ29_gp070	Escherichia phage PBECO4	GCA_001041035.1
BBM62063.1	000970	Cluster378_1clades	188	EO157G_4740	Escherichia phage SP27	GCA_008033345.1
BBM62064.1	000970	Cluster378_1clades	171	EO157G_4750	Escherichia phage SP27	GCA_008033345.1
AXC36864.1	000970	Cluster378_1clades	171	-	Escherichia phage UB	GCA_003341455.1
AXC36865.1	000970	Cluster378_1clades	188	-	Escherichia phage UB	GCA_003341455.1
QBO61909.1	000970	Cluster378_1clades	171	G17_00420	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61910.1	000970	Cluster378_1clades	188	G17_00421	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13944.1	000970	Cluster378_1clades	171	vBEcoMphAPEC6_gp320c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDF13945.1	000970	Cluster378_1clades	188	vBEcoMphAPEC6_gp321c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80381.1	000970	Cluster378_1clades	188	PSLUR01_00404	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80382.1	000970	Cluster378_1clades	171	PSLUR01_00405	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44274.1	000970	Cluster378_1clades	167	RaK2_00001	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18855.1	000970	Cluster378_1clades	191	7t3_0334	Salmonella phage 7t3	GCA_006083215.1
AZU98116.1	000970	Cluster378_1clades	191	CPT_Munch_172	Salmonella phage Munch	GCA_004015485.1
QIG62866.1	000970	Cluster378_1clades	191	SEPL_253	Salmonella phage SE_PL	GCA_011067555.1
AFO71273.1	000971	Cluster379_1clades	185	CR5_053	Cronobacter phage CR5	GCA_000910235.1
AMR59703.1	000971	Cluster379_1clades	162	SEGD1_054	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07480.1	000971	Cluster379_1clades	187	DERBICUS_54	Erwinia phage Derbicus	GCA_004521655.1
ANZ49706.1	000971	Cluster379_1clades	186	MACHINA_68	Erwinia phage Machina	GCA_002758035.1
AXF51196.1	000971	Cluster379_1clades	180	WELLINGTON_66	Erwinia phage Wellington	GCA_003344985.1
AFQ96781.1	000971	Cluster379_1clades	186	G173_gp236	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48082.1	000971	Cluster379_1clades	186	ASESINO_69	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48357.1	000971	Cluster379_1clades	187	CAITLIN_62	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48630.1	000971	Cluster379_1clades	187	CHRISDB_68	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48904.1	000971	Cluster379_1clades	180	EARLPHILLIPIV_54	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49151.1	000971	Cluster379_1clades	186	HUXLEY_69	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49418.1	000971	Cluster379_1clades	180	KWAN_66	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49979.1	000971	Cluster379_1clades	186	PARSHIK_70	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50245.1	000971	Cluster379_1clades	187	PHOBOS_55	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50493.1	000971	Cluster379_1clades	186	STRATTON_68	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85893.1	000971	Cluster379_1clades	185	ACEC001_0550	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20768.1	000971	Cluster379_1clades	185	-	Salmonella phage JN03	GCA_014319805.1
AWN09045.1	000971	Cluster379_1clades	185	MLDJOKPK_00113	Salmonella phage SPAsTU	GCA_003183805.1
AEP83885.1	000971	Cluster379_1clades	185	SPN3US_0052	Salmonella phage SPN3US	GCA_001042275.1
AQT28181.1	000971	Cluster379_1clades	164	pVa21_240	Vibrio phage pVa-21	GCA_002619305.1
AFO71297.1	000972	Cluster380_1clades	171	CR5_077	Cronobacter phage CR5	GCA_000910235.1
AMR59734.1	000972	Cluster380_1clades	175	SEGD1_085	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07506.1	000972	Cluster380_1clades	171	DERBICUS_80	Erwinia phage Derbicus	GCA_004521655.1
ANZ49733.1	000972	Cluster380_1clades	174	MACHINA_95	Erwinia phage Machina	GCA_002758035.1
AXF51233.1	000972	Cluster380_1clades	175	WELLINGTON_103	Erwinia phage Wellington	GCA_003344985.1
AFQ96552.1	000972	Cluster380_1clades	173	G173_gp007	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48112.1	000972	Cluster380_1clades	173	ASESINO_99	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48387.1	000972	Cluster380_1clades	173	CAITLIN_92	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48659.1	000972	Cluster380_1clades	173	CHRISDB_97	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48930.1	000972	Cluster380_1clades	171	EARLPHILLIPIV_80	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49178.1	000972	Cluster380_1clades	174	HUXLEY_96	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49454.1	000972	Cluster380_1clades	175	KWAN_102	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50006.1	000972	Cluster380_1clades	174	PARSHIK_97	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50270.1	000972	Cluster380_1clades	171	PHOBOS_80	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50526.1	000972	Cluster380_1clades	173	STRATTON_101	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85923.1	000972	Cluster380_1clades	175	ACEC001_0850	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20793.1	000972	Cluster380_1clades	175	-	Salmonella phage JN03	GCA_014319805.1
AWN09018.1	000972	Cluster380_1clades	175	MLDJOKPK_00076	Salmonella phage SPAsTU	GCA_003183805.1
AEP83916.1	000972	Cluster380_1clades	175	SPN3US_0083	Salmonella phage SPN3US	GCA_001042275.1
AQT27960.1	000972	Cluster380_1clades	162	pVa21_018	Vibrio phage pVa-21	GCA_002619305.1
APU01653.1	000973	Cluster381_1clades	166	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28890.1	000973	Cluster381_1clades	166	AP1_0183	Aeromonas phage AP1	GCA_014183365.1
ATI17232.1	000973	Cluster381_1clades	166	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00355.1	000973	Cluster381_1clades	166	HWB28_gp197	Aeromonas phage AS-zj	GCA_002627665.1
QAX97675.1	000973	Cluster381_1clades	166	ASswx1_29	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01175.1	000973	Cluster381_1clades	158	ASwh1_109	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39338.1	000973	Cluster381_1clades	166	CC2_086	Aeromonas phage CC2	GCA_000903495.1
ADM79921.1	000973	Cluster381_1clades	165	phiAS5_ORF0078	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53283.1	000973	Cluster381_1clades	166	65p275	Aeromonas virus 65	GCA_000893255.1
AIA64923.1	000973	Cluster381_1clades	133	S13_124	Cronobacter phage S13	GCA_001503575.1
AFC21869.1	000973	Cluster381_1clades	135	GAP32_416	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44515.1	000973	Cluster381_1clades	151	RaK2_00242	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ79011.1	000973	Cluster381_1clades	134	-	Myoviridae sp.	GCA_012593985.1
AMM43996.1	000973	Cluster381_1clades	135	CBB_433	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19122.1	000973	Cluster381_1clades	135	7t3_0606	Salmonella phage 7t3	GCA_006083215.1
AZU98359.1	000973	Cluster381_1clades	135	CPT_Munch_419	Salmonella phage Munch	GCA_004015485.1
QIG62623.1	000973	Cluster381_1clades	135	SEPL_010	Salmonella phage SE_PL	GCA_011067555.1
AQW88955.1	000973	Cluster381_1clades	135	BF_0430	Serratia phage BF	GCA_002619745.1
SOK59240.1	000973	Cluster381_1clades	137	g432	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58706.1	000973	Cluster381_1clades	137	g429	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AHI60424.1	000974	Cluster382_1clades	119	Ea357_270	Erwinia phage Ea35-70	GCA_000914635.1
AHI60425.1	000974	Cluster382_1clades	121	Ea357_271	Erwinia phage Ea35-70	GCA_000914635.1
QBP07381.1	000974	Cluster382_1clades	151	REBECCA_276	Erwinia phage Rebecca	GCA_004521635.1
QBP07382.1	000974	Cluster382_1clades	121	REBECCA_277	Erwinia phage Rebecca	GCA_004521635.1
AUG86063.1	000974	Cluster382_1clades	119	BOSOLAPHORUS_277	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86064.1	000974	Cluster382_1clades	121	BOSOLAPHORUS_278	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52379.2	000974	Cluster382_1clades	119	DM_280	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52380.2	000974	Cluster382_1clades	121	DM_281	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86383.1	000974	Cluster382_1clades	119	DESERTFOX_276	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86384.1	000974	Cluster382_1clades	121	DESERTFOX_277	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86704.1	000974	Cluster382_1clades	119	MADMEL_277	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86705.1	000974	Cluster382_1clades	121	MADMEL_278	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87029.1	000974	Cluster382_1clades	119	MORTIMER_281	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AUG87030.1	000974	Cluster382_1clades	121	MORTIMER_282	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52054.1	000974	Cluster382_1clades	119	RAY_274	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH52055.1	000974	Cluster382_1clades	121	RAY_275	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51737.1	000974	Cluster382_1clades	119	SIMMY50_279	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51738.1	000974	Cluster382_1clades	121	SIMMY50_280	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65089.2	000974	Cluster382_1clades	119	SPECIALG_278	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ANJ65090.2	000974	Cluster382_1clades	121	SPECIALG_279	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AFC21774.1	000975	Cluster383_1clades	124	GAP32_324	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13954.1	000975	Cluster383_1clades	114	PBI_121Q_57	Escherichia phage 121Q	GCA_000926855.1
QAY00383.1	000975	Cluster383_1clades	114	Ecwhy1_102	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35128.1	000975	Cluster383_1clades	114	ACQ29_gp448	Escherichia phage PBECO4	GCA_001041035.1
BBM61646.1	000975	Cluster383_1clades	114	EO157G_0570	Escherichia phage SP27	GCA_008033345.1
AXC36702.1	000975	Cluster383_1clades	114	-	Escherichia phage UB	GCA_003341455.1
QBO61739.1	000975	Cluster383_1clades	114	G17_00250	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13784.1	000975	Cluster383_1clades	114	vBEcoMphAPEC6_gp155c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80548.1	000975	Cluster383_1clades	114	PSLUR01_00571	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44436.1	000975	Cluster383_1clades	119	RaK2_00163	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72540.1	000975	Cluster383_1clades	115	-	Myoviridae sp.	GCA_003657725.1
AMM43892.1	000975	Cluster383_1clades	124	CBB_329	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76170.1	000975	Cluster383_1clades	113	EST35_0289	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44307.1	000975	Cluster383_1clades	150	PBI_SCTP2_292	Salicola phage SCTP-2	GCA_002625545.1
QCW19051.1	000975	Cluster383_1clades	130	7t3_0531	Salmonella phage 7t3	GCA_006083215.1
AZU98298.1	000975	Cluster383_1clades	130	CPT_Munch_354	Salmonella phage Munch	GCA_004015485.1
QIG62686.1	000975	Cluster383_1clades	130	SEPL_073	Salmonella phage SE_PL	GCA_011067555.1
AQW88852.1	000975	Cluster383_1clades	124	BF_0327	Serratia phage BF	GCA_002619745.1
SOK59136.1	000975	Cluster383_1clades	126	g328	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58602.1	000975	Cluster383_1clades	126	g325	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44694.1	000976	Cluster384_1clades	119	FDI40_gp073	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21733.1	000976	Cluster384_1clades	117	GAP32_283	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13914.1	000976	Cluster384_1clades	117	PBI_121Q_17	Escherichia phage 121Q	GCA_000926855.1
QAY00424.1	000976	Cluster384_1clades	117	Ecwhy1_143	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35167.1	000976	Cluster384_1clades	117	ACQ29_gp487	Escherichia phage PBECO4	GCA_001041035.1
BBM61606.1	000976	Cluster384_1clades	117	EO157G_0170	Escherichia phage SP27	GCA_008033345.1
AXC36740.1	000976	Cluster384_1clades	117	-	Escherichia phage UB	GCA_003341455.1
QBO61778.1	000976	Cluster384_1clades	117	G17_00289	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13822.1	000976	Cluster384_1clades	117	vBEcoMphAPEC6_gp193	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80509.1	000976	Cluster384_1clades	117	PSLUR01_00532	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44398.1	000976	Cluster384_1clades	118	RaK2_00125	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43852.1	000976	Cluster384_1clades	117	CBB_288	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76102.1	000976	Cluster384_1clades	132	EST35_0221	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44167.1	000976	Cluster384_1clades	124	PBI_SCTP2_152	Salicola phage SCTP-2	GCA_002625545.1
QCW19011.1	000976	Cluster384_1clades	117	7t3_0491	Salmonella phage 7t3	GCA_006083215.1
AZU98258.1	000976	Cluster384_1clades	117	CPT_Munch_314	Salmonella phage Munch	GCA_004015485.1
QIG62726.1	000976	Cluster384_1clades	117	SEPL_113	Salmonella phage SE_PL	GCA_011067555.1
AQW88811.1	000976	Cluster384_1clades	117	BF_0286	Serratia phage BF	GCA_002619745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK59094.1	000976	Cluster384_1clades	117	g286c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58558.1	000976	Cluster384_1clades	117	g281c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22686.1	000977	SIG+TM+TM	114	Ah1_00145	Aeromonas phage Ah1	GCA_002957415.1
QAX98411.1	000977	SIG+TM+TM	106	ASfcp2_67	Aeromonas phage AsFcp_2	GCA_004146885.1
ADM80127.1	000977	SIG+TM+TM	37	phiAS5_ORF0284	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17813.1	000977	SIG+TM+TM	114	Aeh1ORF148c	Aeromonas virus Aeh1	GCA_000843245.1
QIG65979.1	000977	SIG+TM+TM	126	phiOC_p337	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ANM44996.1	000977	SIG+TM+TM	120	KTN4_238	Pseudomonas phage KTN4	GCA_002607225.1
QBX32381.1	000977	SIG+TM+TM	120	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76921.1	000977	SIG+TM+TM	116	PHABIO_290	Pseudomonas phage Phabio	GCA_002624965.1
AEH03652.1	000977	SIG+TM+TM	120	229	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94718.1	000977	SIG+TM+TM	120	SL2_141	Pseudomonas phage SL2	GCA_002956015.1
QJB22874.1	000977	SIG+TM+TM	120	fnug_231	Pseudomonas phage fnug	GCA_012837215.1
QEM41954.1	000977	SIG+TM+TM	120	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83098.1	000977	SIG+TM+TM	120	PHIKZ197	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19236.1	000977	SIG+TM+TM	119	FDH28_gp159	Ralstonia phage RP12	GCA_002617345.1
BAW19522.1	000977	SIG+TM+TM	119	-	Ralstonia phage RP31	GCA_002617365.1
BAS04997.1	000977	SIG+TM+TM	127	AVU11_gp205	Ralstonia phage RSF1	GCA_001500875.1
BAQ02727.1	000977	SIG+TM+TM	120	AVU38_gp199	Ralstonia phage RSL2	GCA_001503055.1
AGR47838.1	000977	SIG+TM+TM	106	SmphiM12_206	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13045.1	000977	SIG+TM+TM	106	PHIM19_140	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12686.1	000977	SIG+TM+TM	106	PHIM7_140	Sinorhizobium phage phiM7	GCA_002622405.1
AGH56906.1	000978	Cluster386_1clades	78	CPXG_00103	Cyanophage P-RSM6	GCA_000906155.1
AJK27556.1	000978	Cluster386_1clades	41	PTIM40_129	Cyanophage P-TIM40	GCA_001470935.1
AMO43360.1	000978	Cluster386_1clades	79	W270710_116	Cyanophage S-RIM44	GCA_002599145.1
AOO11604.1	000978	Cluster386_1clades	79	ES420910_123	Cyanophage S-RIM44	GCA_002599165.1
AOO11832.1	000978	Cluster386_1clades	79	Np050604_116	Cyanophage S-RIM44	GCA_002599185.1
AOO12069.1	000978	Cluster386_1clades	79	Np200711_123	Cyanophage S-RIM44	GCA_002599205.1
AOO12305.1	000978	Cluster386_1clades	79	Np420711_123	Cyanophage S-RIM44	GCA_002599225.1
AOO12533.1	000978	Cluster386_1clades	79	Sn080709_116	Cyanophage S-RIM44	GCA_002599245.1
AOO12770.1	000978	Cluster386_1clades	79	Sn130910_123	Cyanophage S-RIM44	GCA_002599265.1
AOO12999.1	000978	Cluster386_1clades	79	W2100709_117	Cyanophage S-RIM44	GCA_002599285.1
AGH07454.1	000978	Cluster386_1clades	69	CYVG_00010	Cyanophage S-SSM6a	GCA_002710385.1
AAX44664.1	000978	Cluster386_1clades	121	PSSM2_287	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12312.1	000978	Cluster386_1clades	121	PRTG_00159	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93440.1	000978	Cluster386_1clades	76	AVU42_gp101	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99218.1	000978	Cluster386_1clades	79	Syn1_117	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76170.1	000978	Cluster386_1clades	75	PBI_BELLAMY_125	Synechococcus phage Bellamy	GCA_002627525.1
QCW22880.1	000978	Cluster386_1clades	76	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50477.1	000978	Cluster386_1clades	76	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70582.1	000978	Cluster386_1clades	74	HOU04_gp183	Synechococcus phage S-T4	GCA_003443335.1
QJT70112.1	000978	Cluster386_1clades	73	SynMITS9220M01_099	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13535.1	000979	Cluster387_1clades	93	Ccr10_gp007	Caulobacter phage Ccr10	GCA_002619445.1
ARB13860.1	000979	Cluster387_1clades	93	Ccr10_gp330	Caulobacter phage Ccr10	GCA_002619445.1
ARB13883.1	000979	Cluster387_1clades	90	Ccr2_gp008	Caulobacter phage Ccr2	GCA_002619465.1
ARB14206.1	000979	Cluster387_1clades	90	Ccr2_gp330	Caulobacter phage Ccr2	GCA_002619465.1
ARB14564.1	000979	Cluster387_1clades	93	Ccr29_gp007	Caulobacter phage Ccr29	GCA_002619485.1
ARB14899.1	000979	Cluster387_1clades	93	Ccr29_gp343	Caulobacter phage Ccr29	GCA_002619485.1
ARB14926.1	000979	Cluster387_1clades	93	Ccr32_gp007	Caulobacter phage Ccr32	GCA_002619505.1
ARB15237.1	000979	Cluster387_1clades	93	Ccr32_gp319	Caulobacter phage Ccr32	GCA_002619505.1
ARB15257.1	000979	Cluster387_1clades	93	Ccr34_gp008	Caulobacter phage Ccr34	GCA_002619525.1
ARB15571.1	000979	Cluster387_1clades	93	Ccr34_gp329	Caulobacter phage Ccr34	GCA_002619525.1
ARB14224.1	000979	Cluster387_1clades	93	Ccr5_gp006	Caulobacter phage Ccr5	GCA_002619545.1
ARB14544.1	000979	Cluster387_1clades	93	Ccr5_gp324	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68208.1	000979	Cluster387_1clades	95	CcrBL10_gp004	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68526.1	000979	Cluster387_1clades	95	CcrBL10_gp322	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87524.1	000979	Cluster387_1clades	93	CcrKarma_gp007	Caulobacter virus Karma	GCA_000901575.1
AFU87857.1	000979	Cluster387_1clades	93	CcrKarma_gp340	Caulobacter virus Karma	GCA_000901575.1
AFU87177.1	000979	Cluster387_1clades	93	CcrMagneto_gp007	Caulobacter virus Magneto	GCA_000903095.1
AFU87505.1	000979	Cluster387_1clades	93	CcrMagneto_gp335	Caulobacter virus Magneto	GCA_000903095.1
AFU86839.1	000979	Cluster387_1clades	93	CbK_gp007	Caulobacter virus phiCbK	GCA_000900535.1
AFU87157.1	000979	Cluster387_1clades	93	CbK_gp325	Caulobacter virus phiCbK	GCA_000900535.1
AUE22866.1	000980	Cluster388_1clades	38	Ah1_00348	Aeromonas phage Ah1	GCA_002957415.1
QAX98576.1	000980	Cluster388_1clades	41	ASfcp2_242	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53041.1	000980	Cluster388_1clades	41	PX29p324	Aeromonas phage PX29	GCA_000920195.1
ADM79964.1	000980	Cluster388_1clades	41	phiAS5_ORF0121	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17994.1	000980	Cluster388_1clades	38	Aeh1ORF324c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21507.1	000980	Cluster388_1clades	56	GAP32_059	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14300.1	000980	Cluster388_1clades	43	PBI_121Q_410	Escherichia phage 121Q	GCA_000926855.1
QAY00638.1	000980	Cluster388_1clades	43	Ecwhy1_363	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61974.1	000980	Cluster388_1clades	43	EO157G_3850	Escherichia phage SP27	GCA_008033345.1
AXC36943.1	000980	Cluster388_1clades	43	-	Escherichia phage UB	GCA_003341455.1
QBO62004.1	000980	Cluster388_1clades	43	G17_00515	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14025.1	000980	Cluster388_1clades	43	vBEcoMphAPEC6_gp401c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80287.1	000980	Cluster388_1clades	43	PSLUR01_00310	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43627.1	000980	Cluster388_1clades	56	CBB_62	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18757.1	000980	Cluster388_1clades	50	7t3_0236	Salmonella phage 7t3	GCA_006083215.1
AZU98026.1	000980	Cluster388_1clades	50	CPT_Munch_082	Salmonella phage Munch	GCA_004015485.1
QIG62954.1	000980	Cluster388_1clades	50	SEPL_341	Salmonella phage SE_PL	GCA_011067555.1
AQW88579.1	000980	Cluster388_1clades	55	BF_0054	Serratia phage BF	GCA_002619745.1
SOK58854.1	000980	Cluster388_1clades	53	g046	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58316.1	000980	Cluster388_1clades	53	g039	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOO14383.1	000981	Cluster389_1clades	55	Sn110110_189	Cyanophage S-RIM14	GCA_002599065.1
AOO15031.1	000981	Cluster389_1clades	55	W1230910_185	Cyanophage S-RIM14	GCA_002599125.1
AMO43468.1	000981	Cluster389_1clades	55	W270710_229	Cyanophage S-RIM44	GCA_002599145.1
AOO11708.1	000981	Cluster389_1clades	55	ES420910_231	Cyanophage S-RIM44	GCA_002599165.1
AOO11940.1	000981	Cluster389_1clades	55	Np050604_229	Cyanophage S-RIM44	GCA_002599185.1
AOO12174.1	000981	Cluster389_1clades	55	Np200711_232	Cyanophage S-RIM44	GCA_002599205.1
AOO12409.1	000981	Cluster389_1clades	55	Np420711_231	Cyanophage S-RIM44	GCA_002599225.1
AOO12641.1	000981	Cluster389_1clades	55	Sn080709_229	Cyanophage S-RIM44	GCA_002599245.1
AOO12874.1	000981	Cluster389_1clades	55	Sn130910_231	Cyanophage S-RIM44	GCA_002599265.1
AOO13107.1	000981	Cluster389_1clades	55	W2100709_230	Cyanophage S-RIM44	GCA_002599285.1
ADO99329.1	000981	Cluster389_1clades	55	Syn1_233	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30761.1	000981	Cluster389_1clades	55	Syn7803US37_284	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76310.1	000981	Cluster389_1clades	55	PBI_BELLAMY_274	Synechococcus phage Bellamy	GCA_002627525.1
QCW23058.1	000981	Cluster389_1clades	55	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50693.1	000981	Cluster389_1clades	55	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59689.1	000981	Cluster389_1clades	55	S330809_228	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59451.1	000981	Cluster389_1clades	55	C440309_228	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59926.1	000981	Cluster389_1clades	55	N231010_227	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70476.1	000981	Cluster389_1clades	54	HOU04_gp077	Synechococcus phage S-T4	GCA_003443335.1
QJT70255.1	000981	Cluster389_1clades	55	SynMITS9220M01_249	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUZ94962.1	000982	Cluster390_1clades	4449	FDI40_gp180	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21680.1	000982	Cluster390_1clades	3341	GAP32_230	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14472.1	000982	Cluster390_1clades	3323	PBI_121Q_582	Escherichia phage 121Q	GCA_000926855.1
QAY00475.1	000982	Cluster390_1clades	3323	Ecwhy1_196	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35218.1	000982	Cluster390_1clades	3333	ACQ29_gp538	Escherichia phage PBECO4	GCA_001041035.1
BBM62145.1	000982	Cluster390_1clades	3323	EO157G_5560	Escherichia phage SP27	GCA_008033345.1
AXC36790.1	000982	Cluster390_1clades	3323	-	Escherichia phage UB	GCA_003341455.1
QBO61830.1	000982	Cluster390_1clades	3323	G17_00341	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13874.1	000982	Cluster390_1clades	3323	vBEcoMphAPEC6_gp245	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80457.1	000982	Cluster390_1clades	3323	PSLUR01_00480	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44343.1	000982	Cluster390_1clades	3326	RaK2_0070	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72798.1	000982	Cluster390_1clades	3491	-	Myoviridae sp.	GCA_003657725.1
AMM43801.1	000982	Cluster390_1clades	3340	CBB_236	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18953.1	000982	Cluster390_1clades	3342	7t3_0432	Salmonella phage 7t3	GCA_006083215.1
AZU98206.1	000982	Cluster390_1clades	3342	CPT_Munch_262	Salmonella phage Munch	GCA_004015485.1
QIG62778.1	000982	Cluster390_1clades	3342	SEPL_165	Salmonella phage SE_PL	GCA_011067555.1
AQW88760.1	000982	Cluster390_1clades	3339	BF_0235	Serratia phage BF	GCA_002619745.1
SOK59041.1	000982	Cluster390_1clades	3339	g233c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58506.1	000982	Cluster390_1clades	3339	g229c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71252.1	000983	Cluster391_1clades	572	CR5_032	Cronobacter phage CR5	GCA_000910235.1
AMR59683.1	000983	Cluster391_1clades	430	SEGD1_034	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07459.1	000983	Cluster391_1clades	573	DERBICUS_33	Erwinia phage Derbicus	GCA_004521655.1
ANZ49685.1	000983	Cluster391_1clades	565	MACHINA_47	Erwinia phage Machina	GCA_002758035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXF51174.1	000983	Cluster391_1clades	557	WELLINGTON_43	Erwinia phage Wellington	GCA_003344985.1
AFQ96758.1	000983	Cluster391_1clades	587	G173_gp213	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48061.1	000983	Cluster391_1clades	584	ASESINO_48	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48336.1	000983	Cluster391_1clades	566	CAITLIN_41	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48609.1	000983	Cluster391_1clades	566	CHRISDB_47	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48883.1	000983	Cluster391_1clades	573	EARLPHILLIPIV_33	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49130.1	000983	Cluster391_1clades	565	HUXLEY_48	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49395.1	000983	Cluster391_1clades	557	KWAN_43	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49958.1	000983	Cluster391_1clades	565	PARSHIK_49	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50223.1	000983	Cluster391_1clades	570	PHOBOS_33	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50471.1	000983	Cluster391_1clades	585	STRATTON_46	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85872.1	000983	Cluster391_1clades	566	ACEC001_0340	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20747.1	000983	Cluster391_1clades	566	-	Salmonella phage JN03	GCA_014319805.1
AWN09064.2	000983	Cluster391_1clades	575	MLDJOKPK_00134	Salmonella phage SPAsTU	GCA_003183805.1
AEP83864.1	000983	Cluster391_1clades	566	SPN3US_0031	Salmonella phage SPN3US	GCA_001042275.1
QBP07475.1	000984	Cluster392_2clades	566	DERBICUS_49	Erwinia phage Derbicus	GCA_004521655.1
AFO71268.1	000984	Cluster392_2clades	566	CR5_048	Cronobacter phage CR5	GCA_000910235.1
AMR59698.1	000984	Cluster392_2clades	575	SEGD1_049	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49701.1	000984	Cluster392_2clades	585	MACHINA_63	Erwinia phage Machina	GCA_002758035.1
AXF51191.1	000984	Cluster392_2clades	565	WELLINGTON_61	Erwinia phage Wellington	GCA_003344985.1
AFQ96776.1	000984	Cluster392_2clades	566	G173_gp231	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48077.1	000984	Cluster392_2clades	562	ASESINO_64	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48352.1	000984	Cluster392_2clades	579	CAITLIN_57	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48625.1	000984	Cluster392_2clades	567	CHRISDB_63	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48899.1	000984	Cluster392_2clades	566	EARLPHILLIPIV_49	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49146.1	000984	Cluster392_2clades	585	HUXLEY_64	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49413.1	000984	Cluster392_2clades	565	KWAN_61	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49974.1	000984	Cluster392_2clades	585	PARSHIK_65	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50240.1	000984	Cluster392_2clades	571	PHOBOS_50	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50488.1	000984	Cluster392_2clades	562	STRATTON_63	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85888.1	000984	Cluster392_2clades	577	ACEC001_0500	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20763.1	000984	Cluster392_2clades	577	-	Salmonella phage JN03	GCA_014319805.1
AWN09050.2	000984	Cluster392_2clades	574	MLDJOKPK_00118	Salmonella phage SPAsTU	GCA_003183805.1
AEP83880.1	000984	Cluster392_2clades	573	SPN3US_0047	Salmonella phage SPN3US	GCA_001042275.1
AFO71294.1	000985	Cluster393_1clades	514	CR5_074	Cronobacter phage CR5	GCA_000910235.1
AMR59728.1	000985	Cluster393_1clades	558	SEGD1_079	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07502.1	000985	Cluster393_1clades	516	DERBICUS_76	Erwinia phage Derbicus	GCA_004521655.1
ANZ49728.1	000985	Cluster393_1clades	522	MACHINA_90	Erwinia phage Machina	GCA_002758035.1
AXF51225.1	000985	Cluster393_1clades	536	WELLINGTON_95	Erwinia phage Wellington	GCA_003344985.1
AFQ96548.1	000985	Cluster393_1clades	543	G173_gp003	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48108.1	000985	Cluster393_1clades	545	ASESINO_95	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48381.1	000985	Cluster393_1clades	534	CAITLIN_86	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48654.1	000985	Cluster393_1clades	531	CHRISDB_92	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48926.1	000985	Cluster393_1clades	516	EARLPHILLIPIV_76	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49173.1	000985	Cluster393_1clades	522	HUXLEY_91	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49446.1	000985	Cluster393_1clades	535	KWAN_94	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50001.1	000985	Cluster393_1clades	522	PARSHIK_92	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50267.1	000985	Cluster393_1clades	517	PHOBOS_77	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50522.1	000985	Cluster393_1clades	544	STRATTON_97	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85918.1	000985	Cluster393_1clades	556	ACEC001_0800	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20789.1	000985	Cluster393_1clades	556	-	Salmonella phage JN03	GCA_014319805.1
AWN09022.1	000985	Cluster393_1clades	554	MLDJOKPK_00081	Salmonella phage SPAsTU	GCA_003183805.1
AEP83911.1	000985	Cluster393_1clades	558	SPN3US_0078	Salmonella phage SPN3US	GCA_001042275.1
AFO71375.1	000986	Cluster394_1clades	313	CR5_155	Cronobacter phage CR5	GCA_000910235.1
AMR59815.1	000986	Cluster394_1clades	295	SEGD1_168	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07585.1	000986	Cluster394_1clades	312	DERBICUS_159	Erwinia phage Derbicus	GCA_004521655.1
ANZ49812.1	000986	Cluster394_1clades	292	MACHINA_174	Erwinia phage Machina	GCA_002758035.1
AXF51309.1	000986	Cluster394_1clades	308	WELLINGTON_180	Erwinia phage Wellington	GCA_003344985.1
AFQ96630.1	000986	Cluster394_1clades	295	G173_gp085	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48195.1	000986	Cluster394_1clades	295	ASESINO_182	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48468.1	000986	Cluster394_1clades	295	CAITLIN_173	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48747.1	000986	Cluster394_1clades	295	CHRISDB_185	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49008.1	000986	Cluster394_1clades	312	EARLPHILLIPIV_159	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49256.1	000986	Cluster394_1clades	292	HUXLEY_174	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49533.1	000986	Cluster394_1clades	308	KWAN_181	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50084.1	000986	Cluster394_1clades	292	PARSHIK_175	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50355.1	000986	Cluster394_1clades	327	PHOBOS_165	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50607.1	000986	Cluster394_1clades	295	STRATTON_182	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86004.1	000986	Cluster394_1clades	295	ACEC001_1640	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20863.1	000986	Cluster394_1clades	295	-	Salmonella phage JN03	GCA_014319805.1
AWN09168.1	000986	Cluster394_1clades	295	MLDJOKPK_00275	Salmonella phage SPAsTU	GCA_003183805.1
AEP83998.1	000986	Cluster394_1clades	295	SPN3US_0165	Salmonella phage SPN3US	GCA_001042275.1
QDB70362.1	000987	Cluster395_1clades	207	CF8_0194	Aeromonas phage CF8	GCA_006384595.2
QDJ96670.1	000987	Cluster395_1clades	198	PS1_0159	Aeromonas phage PS1	GCA_007051165.2
QFR59304.1	000987	Cluster395_1clades	198	PS2_0163	Aeromonas phage PS2	GCA_009388305.2
QBZ70682.1	000987	Cluster395_1clades	318	pETSU_101	Edwardsiella virus pEt-SU	GCA_004800915.1
AHI60203.1	000987	Cluster395_1clades	318	Ea357_053	Erwinia phage Ea35-70	GCA_000914635.1
QBP07162.1	000987	Cluster395_1clades	317	REBECCA_54	Erwinia phage Rebecca	GCA_004521635.1
AUG85842.1	000987	Cluster395_1clades	317	BOSOLAPHORUS_54	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52154.1	000987	Cluster395_1clades	317	DM_56	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86161.1	000987	Cluster395_1clades	317	DESERTFOX_53	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ASU03802.1	000987	Cluster395_1clades	196	JOAD_113	Erwinia phage vB_EamM_Joad	GCA_002629065.1
AUG86482.1	000987	Cluster395_1clades	317	MADMEL_54	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86803.1	000987	Cluster395_1clades	317	MORTIMER_54	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51834.1	000987	Cluster395_1clades	318	RAY_53	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASU03557.1	000987	Cluster395_1clades	196	RISINGSUN_113	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANH51517.1	000987	Cluster395_1clades	318	SIMMY50_55	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64865.1	000987	Cluster395_1clades	317	SPECIALG_55	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGH71997.1	000987	Cluster395_1clades	327	N1M2_134	Klebsiella phage N1M2	GCA_010092605.1
QMP24031.1	000987	Cluster395_1clades	201	-	Proteus phage 10	GCA_014071245.1
AEV89606.1	000987	Cluster395_1clades	325	OBP_169	Pseudomonas phage OBP	GCA_000896635.1
AFO71374.1	000988	RADICAL-SAM	259	CR5_154	Cronobacter phage CR5	GCA_000910235.1
AMR59814.1	000988	RADICAL-SAM	264	SEGD1_167	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07584.1	000988	RADICAL-SAM	291	DERBICUS_158	Erwinia phage Derbicus	GCA_004521655.1
ANZ49811.1	000988	RADICAL-SAM	297	MACHINA_173	Erwinia phage Machina	GCA_002758035.1
AXF51308.1	000988	RADICAL-SAM	294	WELLINGTON_179	Erwinia phage Wellington	GCA_003344985.1
AFQ96629.1	000988	RADICAL-SAM	301	G173_gp084	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48194.1	000988	RADICAL-SAM	301	ASESINO_181	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48467.1	000988	RADICAL-SAM	301	CAITLIN_172	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48746.1	000988	RADICAL-SAM	301	CHRISDB_184	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49007.1	000988	RADICAL-SAM	291	EARLPHILLIPIV_158	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49255.1	000988	RADICAL-SAM	297	HUXLEY_173	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49532.1	000988	RADICAL-SAM	294	KWAN_180	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50083.1	000988	RADICAL-SAM	297	PARSHIK_174	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50354.1	000988	RADICAL-SAM	290	PHOBOS_164	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50606.1	000988	RADICAL-SAM	301	STRATTON_181	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86003.1	000988	RADICAL-SAM	304	ACEC001_1630	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20862.1	000988	RADICAL-SAM	304	-	Salmonella phage JN03	GCA_014319805.1
AWN09169.2	000988	RADICAL-SAM	305	MLDJOKPK_00276	Salmonella phage SPAsTU	GCA_003183805.1
AEP83997.1	000988	RADICAL-SAM	264	SPN3US_0164	Salmonella phage SPN3US	GCA_001042275.1
AFO71283.1	000989	Cluster399_1clades	247	CR5_063	Cronobacter phage CR5	GCA_000910235.1
AMR59715.1	000989	Cluster399_1clades	265	SEGD1_066	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07490.1	000989	Cluster399_1clades	251	DERBICUS_64	Erwinia phage Derbicus	GCA_004521655.1
ANZ49716.1	000989	Cluster399_1clades	265	MACHINA_78	Erwinia phage Machina	GCA_002758035.1
AXF51208.1	000989	Cluster399_1clades	266	WELLINGTON_78	Erwinia phage Wellington	GCA_003344985.1
AFQ96794.1	000989	Cluster399_1clades	266	G173_gp249	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48095.1	000989	Cluster399_1clades	266	ASESINO_82	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48368.1	000989	Cluster399_1clades	269	CAITLIN_73	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48641.1	000989	Cluster399_1clades	265	CHRISDB_79	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48914.1	000989	Cluster399_1clades	251	EARLPHILLIPIV_64	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49161.1	000989	Cluster399_1clades	265	HUXLEY_79	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49430.1	000989	Cluster399_1clades	266	KWAN_78	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49989.1	000989	Cluster399_1clades	265	PARSHIK_80	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50256.1	000989	Cluster399_1clades	246	PHOBOS_66	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50506.1	000989	Cluster399_1clades	266	STRATTON_81	Erwinia phage vB_EamM_Stratton	GCA_002600675.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QKN85906.1	000989	Cluster399_1clades	265	ACEC001_0680	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20781.1	000989	Cluster399_1clades	265	-	Salmonella phage JN03	GCA_014319805.1
AWN09035.1	000989	Cluster399_1clades	265	MLDJOKPK_00099	Salmonella phage SPAsTU	GCA_003183805.1
AEP83898.1	000989	Cluster399_1clades	265	SPN3US_0065	Salmonella phage SPN3US	GCA_001042275.1
AFO71407.1	000990	Cluster400_1clades	258	CR5_187	Cronobacter phage CR5	GCA_000910235.1
AMR59860.1	000990	Cluster400_1clades	244	SEGD1_213	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07619.1	000990	Cluster400_1clades	258	DERBICUS_193	Erwinia phage Derbicus	GCA_004521655.1
ANZ49858.1	000990	Cluster400_1clades	244	MACHINA_220	Erwinia phage Machina	GCA_002758035.1
AXF51360.1	000990	Cluster400_1clades	239	WELLINGTON_234	Erwinia phage Wellington	GCA_003344985.1
AFQ96675.1	000990	Cluster400_1clades	244	G173_gp130	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48241.1	000990	Cluster400_1clades	244	ASESINO_228	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48515.1	000990	Cluster400_1clades	245	CAITLIN_220	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48792.1	000990	Cluster400_1clades	245	CHRISDB_230	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49043.1	000990	Cluster400_1clades	258	EARLPHILLIPIV_194	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49302.1	000990	Cluster400_1clades	244	HUXLEY_220	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49586.1	000990	Cluster400_1clades	239	KWAN_234	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50130.1	000990	Cluster400_1clades	244	PARSHIK_221	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50391.1	000990	Cluster400_1clades	258	PHOBOS_201	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50655.1	000990	Cluster400_1clades	244	STRATTON_230	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86049.1	000990	Cluster400_1clades	244	ACEC001_2060	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20897.1	000990	Cluster400_1clades	244	-	Salmonella phage JN03	GCA_014319805.1
AWN09138.1	000990	Cluster400_1clades	245	MLDJOKPK_00231	Salmonella phage SPAsTU	GCA_003183805.1
AEP84042.1	000990	Cluster400_1clades	244	SPN3US_0209	Salmonella phage SPN3US	GCA_001042275.1
AFO71410.1	000991	Cluster401_1clades	253	CR5_190	Cronobacter phage CR5	GCA_000910235.1
AMR59866.1	000991	Cluster401_1clades	251	SEGD1_219	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07623.1	000991	Cluster401_1clades	253	DERBICUS_197	Erwinia phage Derbicus	GCA_004521655.1
ANZ49865.1	000991	Cluster401_1clades	251	MACHINA_227	Erwinia phage Machina	GCA_002758035.1
AXF51369.1	000991	Cluster401_1clades	251	WELLINGTON_243	Erwinia phage Wellington	GCA_003344985.1
AFQ96682.1	000991	Cluster401_1clades	251	G173_gp137	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48249.1	000991	Cluster401_1clades	251	ASESINO_236	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48522.1	000991	Cluster401_1clades	252	CAITLIN_227	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48799.1	000991	Cluster401_1clades	251	CHRISDB_237	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49047.1	000991	Cluster401_1clades	253	EARLPHILLIPIV_198	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49309.1	000991	Cluster401_1clades	251	HUXLEY_227	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49595.1	000991	Cluster401_1clades	251	KWAN_243	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50137.1	000991	Cluster401_1clades	251	PARSHIK_228	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50394.1	000991	Cluster401_1clades	253	PHOBOS_204	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50662.1	000991	Cluster401_1clades	251	STRATTON_237	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86055.1	000991	Cluster401_1clades	251	ACEC001_2120	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20902.1	000991	Cluster401_1clades	251	-	Salmonella phage JN03	GCA_014319805.1
AWN09133.1	000991	Cluster401_1clades	251	MLDJOKPK_00226	Salmonella phage SPAsTU	GCA_003183805.1
AEP84047.1	000991	Cluster401_1clades	251	SPN3US_0214	Salmonella phage SPN3US	GCA_001042275.1
AHI60451.1	000992	Cluster403_1clades	233	Ea357_297	Erwinia phage Ea35-70	GCA_000914635.1
AGX01803.1	000992	Cluster403_1clades	241	CF95_gp081	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07408.1	000992	Cluster403_1clades	233	REBECCA_303	Erwinia phage Rebecca	GCA_004521635.1
AUG86090.1	000992	Cluster403_1clades	233	BOSOLAPHORUS_304	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52406.1	000992	Cluster403_1clades	233	DM_307	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86410.1	000992	Cluster403_1clades	233	DESERTFOX_303	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86731.1	000992	Cluster403_1clades	233	MADMEL_304	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87056.1	000992	Cluster403_1clades	233	MORTIMER_308	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52081.1	000992	Cluster403_1clades	233	RAY_301	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51764.1	000992	Cluster403_1clades	233	SIMMY50_306	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65116.1	000992	Cluster403_1clades	233	SPECIALG_305	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24210.1	000992	Cluster403_1clades	215	-	Proteus phage 10	GCA_014071245.1
CAG27248.1	000992	Cluster403_1clades	222	PPEV_gp154	Pseudomonas phage EL	GCA_000866825.1
ARV77306.1	000992	Cluster403_1clades	215	NOXIFER_137	Pseudomonas phage Noxifer	GCA_002625005.1
QBJ02728.1	000992	Cluster403_1clades	223	PSA21_202	Pseudomonas phage Psa21	GCA_004340405.1
BAS04960.1	000992	Cluster403_1clades	222	AVU11_gp168	Ralstonia phage RSF1	GCA_001500875.1
BAQ02685.1	000992	Cluster403_1clades	222	AVU38_gp157	Ralstonia phage RSL2	GCA_001503055.1
QKE54631.1	000992	Cluster403_1clades	224	ACSA002_3140	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFP93146.1	000992	Cluster403_1clades	221	-	Serratia phage PCH45	GCA_009187865.1
AFO71247.1	000993	Cluster404_1clades	207	CR5_027	Cronobacter phage CR5	GCA_000910235.1
AMR59677.1	000993	Cluster404_1clades	224	SEGD1_028	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07454.1	000993	Cluster404_1clades	200	DERBICUS_28	Erwinia phage Derbicus	GCA_004521655.1
ANZ49680.1	000993	Cluster404_1clades	223	MACHINA_42	Erwinia phage Machina	GCA_002758035.1
AXF51169.1	000993	Cluster404_1clades	219	WELLINGTON_38	Erwinia phage Wellington	GCA_003344985.1
AFQ96753.1	000993	Cluster404_1clades	230	G173_gp208	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48056.1	000993	Cluster404_1clades	237	ASESINO_43	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48331.1	000993	Cluster404_1clades	225	CAITLIN_36	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48604.1	000993	Cluster404_1clades	223	CHRISDB_42	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48878.1	000993	Cluster404_1clades	200	EARLPHILLIPIV_28	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49125.1	000993	Cluster404_1clades	223	HUXLEY_43	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49390.1	000993	Cluster404_1clades	219	KWAN_38	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49953.1	000993	Cluster404_1clades	223	PARSHIK_44	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50218.1	000993	Cluster404_1clades	214	PHOBOS_28	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50466.1	000993	Cluster404_1clades	230	STRATTON_41	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85867.1	000993	Cluster404_1clades	224	ACEC001_0290	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20742.1	000993	Cluster404_1clades	224	-	Salmonella phage JN03	GCA_014319805.1
AWN09069.1	000993	Cluster404_1clades	224	MLDJOKPK_00139	Salmonella phage SPAsTU	GCA_003183805.1
AEP83859.1	000993	Cluster404_1clades	224	SPN3US_0026	Salmonella phage SPN3US	GCA_001042275.1
AFC21452.1	000994	Cluster406_1clades	224	GAP32_005	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14167.1	000994	Cluster406_1clades	160	PBI_121Q_277	Escherichia phage 121Q	GCA_000926855.1
QAY00767.1	000994	Cluster406_1clades	160	Ecwhy1_493	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34947.1	000994	Cluster406_1clades	160	ACQ29_gp267	Escherichia phage PBECO4	GCA_001041035.1
BBM61843.1	000994	Cluster406_1clades	160	EO157G_2540	Escherichia phage SP27	GCA_008033345.1
AXC37049.1	000994	Cluster406_1clades	160	-	Escherichia phage UB	GCA_003341455.1
QBO61538.1	000994	Cluster406_1clades	160	G17_00042	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62144.1	000994	Cluster406_1clades	160	G17_00655	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14151.1	000994	Cluster406_1clades	160	vBEcoMphAPEC6_gp528c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80154.1	000994	Cluster406_1clades	160	PSLUR01_00177	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44605.1	000994	Cluster406_1clades	166	RaK2_00332	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43568.1	000994	Cluster406_1clades	225	CBB_3	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44119.1	000994	Cluster406_1clades	225	CBB_556	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18676.1	000994	Cluster406_1clades	195	7t3_0155	Salmonella phage 7t3	GCA_006083215.1
AZU97950.1	000994	Cluster406_1clades	195	CPT_Munch_006	Salmonella phage Munch	GCA_004015485.1
QIG63025.1	000994	Cluster406_1clades	195	SEPL_412	Salmonella phage SE_PL	GCA_011067555.1
AQW88526.1	000994	Cluster406_1clades	220	BF_0001	Serratia phage BF	GCA_002619745.1
SOK58809.1	000994	Cluster406_1clades	217	g001	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58278.1	000994	Cluster406_1clades	217	g001	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71371.1	000995	DUF4376	218	CR5_151	Cronobacter phage CR5	GCA_000910235.1
AMR59811.1	000995	DUF4376	223	SEGD1_164	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07581.1	000995	DUF4376	218	DERBICUS_155	Erwinia phage Derbicus	GCA_004521655.1
ANZ49808.1	000995	DUF4376	218	MACHINA_170	Erwinia phage Machina	GCA_002758035.1
AXF51305.1	000995	DUF4376	213	WELLINGTON_176	Erwinia phage Wellington	GCA_003344985.1
AFQ96626.1	000995	DUF4376	222	G173_gp081	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48191.1	000995	DUF4376	218	ASESINO_178	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48464.1	000995	DUF4376	217	CAITLIN_169	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48743.1	000995	DUF4376	218	CHRISDB_181	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49004.1	000995	DUF4376	218	EARLPHILLIPIV_155	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49252.1	000995	DUF4376	218	HUXLEY_170	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49529.1	000995	DUF4376	213	KWAN_177	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50080.1	000995	DUF4376	218	PARSHIK_171	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50351.1	000995	DUF4376	218	PHOBOS_161	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50603.1	000995	DUF4376	222	STRATTON_178	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86000.1	000995	DUF4376	223	ACEC001_1600	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20859.1	000995	DUF4376	223	-	Salmonella phage JN03	GCA_014319805.1
AWN09171.1	000995	DUF4376	223	MLDJOKPK_00279	Salmonella phage SPAsTU	GCA_003183805.1
AEP83994.1	000995	DUF4376	223	SPN3US_0161	Salmonella phage SPN3US	GCA_001042275.1
AFO71420.1	000996	Cluster408_1clades	221	CR5_200	Cronobacter phage CR5	GCA_000910235.1
AMR59876.1	000996	Cluster408_1clades	219	SEGD1_229	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07633.1	000996	Cluster408_1clades	222	DERBICUS_207	Erwinia phage Derbicus	GCA_004521655.1
ANZ49877.1	000996	Cluster408_1clades	219	MACHINA_239	Erwinia phage Machina	GCA_002758035.1
AXF51379.1	000996	Cluster408_1clades	220	WELLINGTON_253	Erwinia phage Wellington	GCA_003344985.1
AFQ96691.1	000996	Cluster408_1clades	219	G173_gp146	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48260.1	000996	Cluster408_1clades	219	ASESINO_247	Erwinia phage vB_EamM_Asesino	GCA_001744335.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48534.1	000996	Cluster408_1clades	219	CAITLIN_239	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48810.1	000996	Cluster408_1clades	219	CHRISDB_248	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49057.1	000996	Cluster408_1clades	222	EARLPHILLIPIV_208	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49320.1	000996	Cluster408_1clades	219	HUXLEY_238	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49605.1	000996	Cluster408_1clades	220	KWAN_253	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50148.1	000996	Cluster408_1clades	219	PARSHIK_239	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50404.1	000996	Cluster408_1clades	219	PHOBOS_214	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50673.1	000996	Cluster408_1clades	219	STRATTON_248	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86066.1	000996	Cluster408_1clades	219	ACEC001_2230	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20912.1	000996	Cluster408_1clades	220	-	Salmonella phage JN03	GCA_014319805.1
AWN09125.1	000996	Cluster408_1clades	219	MLDJOKPK_00215	Salmonella phage SPAsTU	GCA_003183805.1
AEP84058.1	000996	Cluster408_1clades	219	SPN3US_0225	Salmonella phage SPN3US	GCA_001042275.1
AFO71372.1	000997	Cluster410_1clades	187	CR5_152	Cronobacter phage CR5	GCA_000910235.1
AMR59812.1	000997	Cluster410_1clades	160	SEGD1_165	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07582.1	000997	Cluster410_1clades	187	DERBICUS_156	Erwinia phage Derbicus	GCA_004521655.1
ANZ49809.1	000997	Cluster410_1clades	185	MACHINA_171	Erwinia phage Machina	GCA_002758035.1
AXF51306.1	000997	Cluster410_1clades	182	WELLINGTON_177	Erwinia phage Wellington	GCA_003344985.1
AFQ96627.1	000997	Cluster410_1clades	196	G173_gp082	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48192.1	000997	Cluster410_1clades	196	ASESINO_179	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48465.1	000997	Cluster410_1clades	185	CAITLIN_170	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48744.1	000997	Cluster410_1clades	185	CHRISDB_182	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49005.1	000997	Cluster410_1clades	187	EARLPHILLIPIV_156	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49253.1	000997	Cluster410_1clades	185	HUXLEY_171	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49530.1	000997	Cluster410_1clades	182	KWAN_178	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50081.1	000997	Cluster410_1clades	185	PARSHIK_172	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50352.1	000997	Cluster410_1clades	187	PHOBOS_162	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50604.1	000997	Cluster410_1clades	196	STRATTON_179	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86001.1	000997	Cluster410_1clades	188	ACEC001_1610	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20860.1	000997	Cluster410_1clades	214	-	Salmonella phage JN03	GCA_014319805.1
AXF51131.1	000997	Cluster410_1clades	188	MLDJOKPK_00278	Salmonella phage SPAsTU	GCA_003183805.1
AEP83995.1	000997	Cluster410_1clades	188	SPN3US_0162	Salmonella phage SPN3US	GCA_001042275.1
AFO71236.1	000998	Cluster411_1clades	203	CR5_016	Cronobacter phage CR5	GCA_000910235.1
AMR59666.1	000998	Cluster411_1clades	199	SEGD1_015	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07442.1	000998	Cluster411_1clades	211	DERBICUS_16	Erwinia phage Derbicus	GCA_004521655.1
ANZ49669.1	000998	Cluster411_1clades	198	MACHINA_31	Erwinia phage Machina	GCA_002758035.1
AXF51157.1	000998	Cluster411_1clades	204	WELLINGTON_26	Erwinia phage Wellington	GCA_003344985.1
AFQ96743.1	000998	Cluster411_1clades	197	G173_gp198	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48046.1	000998	Cluster411_1clades	198	ASESINO_33	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48320.1	000998	Cluster411_1clades	198	CAITLIN_25	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48593.1	000998	Cluster411_1clades	198	CHRISDB_31	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48866.1	000998	Cluster411_1clades	203	EARLPHILLIPIV_16	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49114.1	000998	Cluster411_1clades	198	HUXLEY_32	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49378.1	000998	Cluster411_1clades	204	KWAN_26	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49942.1	000998	Cluster411_1clades	198	PARSHIK_33	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50206.1	000998	Cluster411_1clades	202	PHOBOS_16	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50456.1	000998	Cluster411_1clades	197	STRATTON_31	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85854.1	000998	Cluster411_1clades	199	ACEC001_0170	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20734.1	000998	Cluster411_1clades	199	-	Salmonella phage JN03	GCA_014319805.1
AWN09078.1	000998	Cluster411_1clades	199	MLDJOKPK_00151	Salmonella phage SPAsTU	GCA_003183805.1
AEP83849.1	000998	Cluster411_1clades	199	SPN3US_0016	Salmonella phage SPN3US	GCA_001042275.1
AXG67120.1	000999	Cluster412_1clades	199	AD1_076	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67122.1	000999	Cluster412_1clades	177	AD1_078	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67124.1	000999	Cluster412_1clades	174	AD1_080	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79877.1	000999	Cluster412_1clades	210	JA11_072	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79879.1	000999	Cluster412_1clades	184	JA11_074	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66476.1	000999	Cluster412_1clades	210	JA13_073	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66478.1	000999	Cluster412_1clades	184	JA13_075	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66801.1	000999	Cluster412_1clades	210	JA29_075	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66803.1	000999	Cluster412_1clades	184	JA29_077	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67446.1	000999	Cluster412_1clades	210	JA33_072	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67448.1	000999	Cluster412_1clades	184	JA33_074	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08356.1	000999	Cluster412_1clades	199	Alexandra_79	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08358.1	000999	Cluster412_1clades	177	Alexandra_81	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08360.1	000999	Cluster412_1clades	171	Alexandra_83	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58719.1	000999	Cluster412_1clades	199	Y3_079	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58721.1	000999	Cluster412_1clades	178	Y3_081	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58723.1	000999	Cluster412_1clades	173	Y3_083	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28553.1	000999	Cluster412_1clades	207	YOLOSWAG_70	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28555.1	000999	Cluster412_1clades	173	YOLOSWAG_72	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFO71259.1	001000	Cluster414_1clades	206	CR5_039	Cronobacter phage CR5	GCA_000910235.1
AMR59690.1	001000	Cluster414_1clades	206	SEGD1_041	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07466.1	001000	Cluster414_1clades	204	DERBICUS_40	Erwinia phage Derbicus	GCA_004521655.1
ANZ49692.1	001000	Cluster414_1clades	203	MACHINA_54	Erwinia phage Machina	GCA_002758035.1
AXF51181.1	001000	Cluster414_1clades	200	WELLINGTON_50	Erwinia phage Wellington	GCA_003344985.1
AFQ96766.1	001000	Cluster414_1clades	195	G173_gp221	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48068.1	001000	Cluster414_1clades	196	ASESINO_55	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48343.1	001000	Cluster414_1clades	197	CAITLIN_48	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48616.1	001000	Cluster414_1clades	202	CHRISDB_54	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48890.1	001000	Cluster414_1clades	204	EARLPHILLIPIV_40	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49137.1	001000	Cluster414_1clades	203	HUXLEY_55	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49402.1	001000	Cluster414_1clades	200	KWAN_50	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49965.1	001000	Cluster414_1clades	203	PARSHIK_56	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50230.1	001000	Cluster414_1clades	204	PHOBOS_40	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50478.1	001000	Cluster414_1clades	195	STRATTON_53	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85879.1	001000	Cluster414_1clades	206	ACEC001_0410	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20754.1	001000	Cluster414_1clades	206	-	Salmonella phage JN03	GCA_014319805.1
AWN09058.1	001000	Cluster414_1clades	205	MLDJOKPK_00128	Salmonella phage SPAsTU	GCA_003183805.1
AEP83871.1	001000	Cluster414_1clades	206	SPN3US_0038	Salmonella phage SPN3US	GCA_001042275.1
AFO71317.1	001001	Cluster415_1clades	200	CR5_097	Cronobacter phage CR5	GCA_000910235.1
AMR59750.1	001001	Cluster415_1clades	198	SEGD1_101	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07526.1	001001	Cluster415_1clades	194	DERBICUS_100	Erwinia phage Derbicus	GCA_004521655.1
ANZ49748.1	001001	Cluster415_1clades	199	MACHINA_110	Erwinia phage Machina	GCA_002758035.1
AXF51249.1	001001	Cluster415_1clades	196	WELLINGTON_119	Erwinia phage Wellington	GCA_003344985.1
AFQ96567.1	001001	Cluster415_1clades	199	G173_gp022	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48127.1	001001	Cluster415_1clades	199	ASESINO_114	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48401.1	001001	Cluster415_1clades	199	CAITLIN_106	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48674.1	001001	Cluster415_1clades	199	CHRISDB_112	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48949.1	001001	Cluster415_1clades	200	EARLPHILLIPIV_100	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49193.1	001001	Cluster415_1clades	199	HUXLEY_111	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49470.1	001001	Cluster415_1clades	196	KWAN_118	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50021.1	001001	Cluster415_1clades	199	PARSHIK_112	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50290.1	001001	Cluster415_1clades	200	PHOBOS_100	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50542.1	001001	Cluster415_1clades	199	STRATTON_117	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85939.1	001001	Cluster415_1clades	198	ACEC001_1010	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20807.1	001001	Cluster415_1clades	198	-	Salmonella phage JN03	GCA_014319805.1
AWN09007.1	001001	Cluster415_1clades	198	MLDJOKPK_00060	Salmonella phage SPAsTU	GCA_003183805.1
AEP83931.1	001001	Cluster415_1clades	198	SPN3US_0098	Salmonella phage SPN3US	GCA_001042275.1
AFO71300.1	001002	TM+TM	195	CR5_080	Cronobacter phage CR5	GCA_000910235.1
AMR59739.1	001002	TM+TM	121	SEGD1_090	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07509.1	001002	TM+TM	195	DERBICUS_83	Erwinia phage Derbicus	GCA_004521655.1
ANZ49736.1	001002	TM+TM	184	MACHINA_98	Erwinia phage Machina	GCA_002758035.1
AXF51236.1	001002	TM+TM	180	WELLINGTON_106	Erwinia phage Wellington	GCA_003344985.1
AFQ96555.1	001002	TM+TM	192	G173_gp010	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48115.1	001002	TM+TM	192	ASESINO_102	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48390.1	001002	TM+TM	191	CAITLIN_95	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48662.1	001002	TM+TM	191	CHRISDB_100	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48933.1	001002	TM+TM	195	EARLPHILLIPIV_83	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49181.1	001002	TM+TM	184	HUXLEY_99	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49457.1	001002	TM+TM	180	KWAN_105	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50009.1	001002	TM+TM	184	PARSHIK_100	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50273.1	001002	TM+TM	197	PHOBOS_83	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50529.1	001002	TM+TM	192	STRATTON_104	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85926.1	001002	TM+TM	190	ACEC001_0880	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20796.1	001002	TM+TM	190	-	Salmonella phage JN03	GCA_014319805.1
AWN09015.2	001002	TM+TM	191	MLDJOKPK_00073	Salmonella phage SPAsTU	GCA_003183805.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEP83919.1	001002	TM+TM	190	SPN3US_0086	Salmonella phage SPN3US	GCA_001042275.1
AFO71234.1	001003	Cluster417_1clades	182	CR5_014	Cronobacter phage CR5	GCA_000910235.1
AMR59664.1	001003	Cluster417_1clades	162	SEGD1_013	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07440.1	001003	Cluster417_1clades	181	DERBICUS_14	Erwinia phage Derbicus	GCA_004521655.1
ANZ49667.1	001003	Cluster417_1clades	190	MACHINA_29	Erwinia phage Machina	GCA_002758035.1
AXF51155.1	001003	Cluster417_1clades	189	WELLINGTON_24	Erwinia phage Wellington	GCA_003344985.1
AFQ96741.1	001003	Cluster417_1clades	194	G173_gp196	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48044.1	001003	Cluster417_1clades	196	ASESINO_31	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48318.1	001003	Cluster417_1clades	188	CAITLIN_23	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48591.1	001003	Cluster417_1clades	172	CHRISDB_29	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48864.1	001003	Cluster417_1clades	181	EARLPHILLIPIV_14	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49112.1	001003	Cluster417_1clades	190	HUXLEY_30	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49376.1	001003	Cluster417_1clades	189	KWAN_24	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49940.1	001003	Cluster417_1clades	190	PARSHIK_31	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50204.1	001003	Cluster417_1clades	181	PHOBOS_14	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50454.1	001003	Cluster417_1clades	194	STRATTON_29	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85852.1	001003	Cluster417_1clades	162	ACEC001_0150	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20732.1	001003	Cluster417_1clades	162	-	Salmonella phage JN03	GCA_014319805.1
AWN09080.1	001003	Cluster417_1clades	184	MLDJOKPK_00153	Salmonella phage SPAsTU	GCA_003183805.1
AEP83847.1	001003	Cluster417_1clades	162	SPN3US_0014	Salmonella phage SPN3US	GCA_001042275.1
AFO71404.1	001004	SIG+Bac_luciferase	148	CR5_184	Cronobacter phage CR5	GCA_000910235.1
QBP07616.1	001004	SIG+Bac_luciferase	148	DERBICUS_190	Erwinia phage Derbicus	GCA_004521655.1
ANZ49854.1	001004	SIG+Bac_luciferase	154	MACHINA_216	Erwinia phage Machina	GCA_002758035.1
AXF51356.1	001004	SIG+Bac_luciferase	156	WELLINGTON_230	Erwinia phage Wellington	GCA_003344985.1
AFQ96671.1	001004	SIG+Bac_luciferase	156	G173_gp126	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48237.1	001004	SIG+Bac_luciferase	156	ASESINO_224	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48511.1	001004	SIG+Bac_luciferase	156	CAITLIN_216	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48788.1	001004	SIG+Bac_luciferase	156	CHRISDB_226	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49040.1	001004	SIG+Bac_luciferase	148	EARLPHILLIPIV_191	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49298.1	001004	SIG+Bac_luciferase	154	HUXLEY_216	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49582.1	001004	SIG+Bac_luciferase	156	KWAN_230	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50126.1	001004	SIG+Bac_luciferase	154	PARSHIK_217	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50388.1	001004	SIG+Bac_luciferase	148	PHOBOS_198	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50651.1	001004	SIG+Bac_luciferase	156	STRATTON_226	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86045.1	001004	SIG+Bac_luciferase	159	ACEC001_2020	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20893.1	001004	SIG+Bac_luciferase	159	-	Salmonella phage JN03	GCA_014319805.1
AXF51116.1	001004	SIG+Bac_luciferase	157	MLDJOKPK_00235	Salmonella phage SPAsTU	GCA_003183805.1
AEP84038.1	001004	SIG+Bac_luciferase	159	SPN3US_0205	Salmonella phage SPN3US	GCA_001042275.1
AQT28079.1	001004	SIG+Bac_luciferase	194	pVa21_138	Vibrio phage pVa-21	GCA_002619305.1
AFO71290.1	001005	Cluster420_1clades	180	CR5_070	Cronobacter phage CR5	GCA_000910235.1
AMR59722.1	001005	Cluster420_1clades	174	SEGD1_073	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07498.1	001005	Cluster420_1clades	180	DERBICUS_72	Erwinia phage Derbicus	GCA_004521655.1
ANZ49723.1	001005	Cluster420_1clades	179	MACHINA_85	Erwinia phage Machina	GCA_002758035.1
AXF51218.1	001005	Cluster420_1clades	177	WELLINGTON_88	Erwinia phage Wellington	GCA_003344985.1
AFQ96804.1	001005	Cluster420_1clades	174	G173_gp259	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48103.1	001005	Cluster420_1clades	174	ASESINO_90	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48376.1	001005	Cluster420_1clades	179	CAITLIN_81	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48649.1	001005	Cluster420_1clades	179	CHRISDB_87	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48922.1	001005	Cluster420_1clades	180	EARLPHILLIPIV_72	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49168.1	001005	Cluster420_1clades	179	HUXLEY_86	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49439.1	001005	Cluster420_1clades	177	KWAN_87	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49996.1	001005	Cluster420_1clades	179	PARSHIK_87	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50263.1	001005	Cluster420_1clades	180	PHOBOS_73	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50517.1	001005	Cluster420_1clades	174	STRATTON_92	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85914.1	001005	Cluster420_1clades	174	ACEC001_0760	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20785.1	001005	Cluster420_1clades	174	-	Salmonella phage JN03	GCA_014319805.1
AWN09028.1	001005	Cluster420_1clades	180	MLDJOKPK_00088	Salmonella phage SPAsTU	GCA_003183805.1
AEP83907.1	001005	Cluster420_1clades	174	SPN3US_0074	Salmonella phage SPN3US	GCA_001042275.1
ANS06061.1	001006	Cluster421_1clades	134	ABCD_0239	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97257.1	001006	Cluster421_1clades	154	E_249	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78776.1	001006	Cluster421_1clades	136	RB43ORF254w	Escherichia virus RB43	GCA_000863505.1
ASV44439.1	001006	Cluster421_1clades	109	PBI_SCTP2_424	Salicola phage SCTP-2	GCA_002625545.1
AAQ64309.1	001006	Cluster421_1clades	175	KVP40.0240	Vibrio phage KVP40	GCA_000843785.1
QIW90625.1	001006	Cluster421_1clades	175	GCAPEGMB_00278	Vibrio phage V07	GCA_012361095.1
QIW91174.1	001006	Cluster421_1clades	175	COHAPHLL_00338	Vibrio phage V09	GCA_012361135.1
QHJ74420.1	001006	Cluster421_1clades	175	VH12019_00093	Vibrio phage VH1_2019	GCA_009931825.1
AGB06926.1	001006	Cluster421_1clades	177	CF80_gp139	Vibrio phage VH7D	GCA_000914495.1
QBX06220.1	001006	Cluster421_1clades	152	ValB1HC_267	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60846.1	001006	Cluster421_1clades	177	AVU32_gp005	Vibrio phage ValKK3	GCA_001501635.1
AGN30295.2	001006	Cluster421_1clades	171	VPFG_00296	Vibrio phage nt-1	GCA_000910195.2
ALP47126.1	001006	Cluster421_1clades	152	phiGrn1_0362	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47511.1	001006	Cluster421_1clades	152	phiST2_0117	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54845.1	001006	Cluster421_1clades	152	vBValMR10Z_305	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37469.1	001006	Cluster421_1clades	176	pp2_236	Vibriophage phi-pp2	GCA_002630725.1
BBA65636.1	001006	Cluster421_1clades	106	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65177.1	001006	Cluster421_1clades	106	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96209.1	001006	Cluster421_1clades	128	Xoosp13_22	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AFO71438.1	001007	Cluster422_1clades	154	CR5_218	Cronobacter phage CR5	GCA_000910235.1
AMR59904.1	001007	Cluster422_1clades	162	SEGD1_257	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07651.1	001007	Cluster422_1clades	158	DERBICUS_225	Erwinia phage Derbicus	GCA_004521655.1
ANZ49902.1	001007	Cluster422_1clades	166	MACHINA_264	Erwinia phage Machina	GCA_002758035.1
AXF51402.1	001007	Cluster422_1clades	169	WELLINGTON_276	Erwinia phage Wellington	GCA_003344985.1
AFQ96716.1	001007	Cluster422_1clades	161	G173_gp171	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48286.1	001007	Cluster422_1clades	161	ASESINO_273	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48558.1	001007	Cluster422_1clades	171	CAITLIN_263	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48835.1	001007	Cluster422_1clades	171	CHRISDB_273	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49075.1	001007	Cluster422_1clades	154	EARLPHILLIPIV_226	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49345.1	001007	Cluster422_1clades	166	HUXLEY_263	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49628.1	001007	Cluster422_1clades	169	KWAN_276	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50173.1	001007	Cluster422_1clades	166	PARSHIK_264	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50422.1	001007	Cluster422_1clades	158	PHOBOS_232	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50698.1	001007	Cluster422_1clades	177	STRATTON_273	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86093.1	001007	Cluster422_1clades	162	ACEC001_2500	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20936.1	001007	Cluster422_1clades	162	-	Salmonella phage JN03	GCA_014319805.1
AWN09101.1	001007	Cluster422_1clades	162	MLDJOKPK_00188	Salmonella phage SPAsTU	GCA_003183805.1
AEP84085.1	001007	Cluster422_1clades	162	SPN3US_0252	Salmonella phage SPN3US	GCA_001042275.1
AFO71350.1	001008	Cluster423_1clades	172	CR5_130	Cronobacter phage CR5	GCA_000910235.1
AMR59778.1	001008	Cluster423_1clades	172	SEGD1_131	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07558.1	001008	Cluster423_1clades	172	DERBICUS_132	Erwinia phage Derbicus	GCA_004521655.1
ANZ49776.1	001008	Cluster423_1clades	172	MACHINA_138	Erwinia phage Machina	GCA_002758035.1
AXF51282.1	001008	Cluster423_1clades	175	WELLINGTON_153	Erwinia phage Wellington	GCA_003344985.1
AFQ96591.1	001008	Cluster423_1clades	172	G173_gp046	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48156.1	001008	Cluster423_1clades	172	ASESINO_143	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48430.1	001008	Cluster423_1clades	175	CAITLIN_135	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48705.1	001008	Cluster423_1clades	175	CHRISDB_143	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48981.1	001008	Cluster423_1clades	172	EARLPHILLIPIV_132	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49220.1	001008	Cluster423_1clades	172	HUXLEY_138	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49505.1	001008	Cluster423_1clades	175	KWAN_153	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50048.1	001008	Cluster423_1clades	172	PARSHIK_139	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50323.1	001008	Cluster423_1clades	173	PHOBOS_133	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50568.1	001008	Cluster423_1clades	172	STRATTON_143	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85967.1	001008	Cluster423_1clades	172	ACEC001_1290	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20831.1	001008	Cluster423_1clades	168	-	Salmonella phage JN03	GCA_014319805.1
AWN08987.2	001008	Cluster423_1clades	174	MLDJOKPK_00026	Salmonella phage SPAsTU	GCA_003183805.1
AEP83960.1	001008	Cluster423_1clades	168	SPN3US_0127	Salmonella phage SPN3US	GCA_001042275.1
AFO71339.1	001009	Cluster424_1clades	162	CR5_119	Cronobacter phage CR5	GCA_000910235.1
AMR59760.1	001009	Cluster424_1clades	160	SEGD1_113	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07547.1	001009	Cluster424_1clades	175	DERBICUS_121	Erwinia phage Derbicus	GCA_004521655.1
ANZ49759.1	001009	Cluster424_1clades	166	MACHINA_121	Erwinia phage Machina	GCA_002758035.1
AXF51267.1	001009	Cluster424_1clades	152	WELLINGTON_137	Erwinia phage Wellington	GCA_003344985.1
AFQ96577.1	001009	Cluster424_1clades	161	G173_gp032	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48138.1	001009	Cluster424_1clades	161	ASESINO_125	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48416.1	001009	Cluster424_1clades	162	CAITLIN_121	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48688.1	001009	Cluster424_1clades	162	CHRISDB_126	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48970.1	001009	Cluster424_1clades	162	EARLPHILLIPIV_121	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ49203.1	001009	Cluster424_1clades	166	HUXLEY_121	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49488.1	001009	Cluster424_1clades	152	KWAN_136	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50031.1	001009	Cluster424_1clades	166	PARSHIK_122	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50311.1	001009	Cluster424_1clades	162	PHOBOS_121	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50552.1	001009	Cluster424_1clades	161	STRATTON_127	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85950.1	001009	Cluster424_1clades	160	ACEC001_1120	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20817.1	001009	Cluster424_1clades	160	-	Salmonella phage JN03	GCA_014319805.1
AWN09000.1	001009	Cluster424_1clades	160	MLDJOKPK_00048	Salmonella phage SPAsTU	GCA_003183805.1
AEP83942.1	001009	Cluster424_1clades	160	SPN3US_0109	Salmonella phage SPN3US	GCA_001042275.1
AFO71303.1	001010	Cluster425_1clades	174	CR5_083	Cronobacter phage CR5	GCA_000910235.1
AMR59742.1	001010	Cluster425_1clades	69	SEGD1_093	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07512.1	001010	Cluster425_1clades	174	DERBICUS_86	Erwinia phage Derbicus	GCA_004521655.1
ANZ49739.1	001010	Cluster425_1clades	161	MACHINA_101	Erwinia phage Machina	GCA_002758035.1
AXF51239.1	001010	Cluster425_1clades	164	WELLINGTON_109	Erwinia phage Wellington	GCA_003344985.1
AFQ96558.1	001010	Cluster425_1clades	68	G173_gp013	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48118.1	001010	Cluster425_1clades	158	ASESINO_105	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48393.1	001010	Cluster425_1clades	161	CAITLIN_98	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48665.1	001010	Cluster425_1clades	161	CHRISDB_103	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48936.1	001010	Cluster425_1clades	174	EARLPHILLIPIV_86	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49184.1	001010	Cluster425_1clades	161	HUXLEY_102	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49460.1	001010	Cluster425_1clades	164	KWAN_108	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50012.1	001010	Cluster425_1clades	161	PARSHIK_103	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50276.1	001010	Cluster425_1clades	173	PHOBOS_86	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50532.1	001010	Cluster425_1clades	158	STRATTON_107	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85929.1	001010	Cluster425_1clades	158	ACEC001_0910	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20799.1	001010	Cluster425_1clades	158	-	Salmonella phage JN03	GCA_014319805.1
AXF51081.1	001010	Cluster425_1clades	158	MLDJOKPK_00070	Salmonella phage SPAsTU	GCA_003183805.1
AEP83922.1	001010	Cluster425_1clades	158	SPN3US_0089	Salmonella phage SPN3US	GCA_001042275.1
AFO71233.1	001011	Cluster426_1clades	167	CR5_013	Cronobacter phage CR5	GCA_000910235.1
AMR59663.1	001011	Cluster426_1clades	169	SEGD1_012	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07439.1	001011	Cluster426_1clades	167	DERBICUS_13	Erwinia phage Derbicus	GCA_004521655.1
ANZ49666.1	001011	Cluster426_1clades	168	MACHINA_28	Erwinia phage Machina	GCA_002758035.1
AXF51154.1	001011	Cluster426_1clades	168	WELLINGTON_23	Erwinia phage Wellington	GCA_003344985.1
AFQ96740.1	001011	Cluster426_1clades	169	G173_gp195	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48043.1	001011	Cluster426_1clades	169	ASESINO_30	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48317.1	001011	Cluster426_1clades	168	CAITLIN_22	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48590.1	001011	Cluster426_1clades	168	CHRISDB_28	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48863.1	001011	Cluster426_1clades	167	EARLPHILLIPIV_13	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49111.1	001011	Cluster426_1clades	168	HUXLEY_29	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49375.1	001011	Cluster426_1clades	168	KWAN_23	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49939.1	001011	Cluster426_1clades	168	PARSHIK_30	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50203.1	001011	Cluster426_1clades	167	PHOBOS_13	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50453.1	001011	Cluster426_1clades	169	STRATTON_28	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85851.1	001011	Cluster426_1clades	169	ACEC001_0140	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20731.1	001011	Cluster426_1clades	169	-	Salmonella phage JN03	GCA_014319805.1
AWN09081.1	001011	Cluster426_1clades	168	MLDJOKPK_00154	Salmonella phage SPAsTU	GCA_003183805.1
AEP83846.1	001011	Cluster426_1clades	169	SPN3US_0013	Salmonella phage SPN3US	GCA_001042275.1
ASV44735.1	001012	Cluster428_1clades	138	FDI40_gp290	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21673.1	001012	Cluster428_1clades	146	GAP32_223	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14465.1	001012	Cluster428_1clades	165	PBI_121Q_575	Escherichia phage 121Q	GCA_000926855.1
QAY00482.1	001012	Cluster428_1clades	165	Ecwhy1_203	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35225.1	001012	Cluster428_1clades	165	ACQ29_gp545	Escherichia phage PBECO4	GCA_001041035.1
BBM62138.1	001012	Cluster428_1clades	165	EO157G_5490	Escherichia phage SP27	GCA_008033345.1
AXC36797.1	001012	Cluster428_1clades	165	-	Escherichia phage UB	GCA_003341455.1
QBO61837.1	001012	Cluster428_1clades	165	G17_00348	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80450.1	001012	Cluster428_1clades	165	PSLUR01_00473	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44336.1	001012	Cluster428_1clades	165	RaK2_00063	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72623.1	001012	Cluster428_1clades	139	-	Myoviridae sp.	GCA_003657725.1
AMM43794.1	001012	Cluster428_1clades	165	CBB_229	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76180.1	001012	Cluster428_1clades	144	EST35_0299	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18945.1	001012	Cluster428_1clades	165	7t3_0424	Salmonella phage 7t3	GCA_006083215.1
AZU98199.1	001012	Cluster428_1clades	165	CPT_Munch_255	Salmonella phage Munch	GCA_004015485.1
QIG62785.1	001012	Cluster428_1clades	165	SEPL_172	Salmonella phage SE_PL	GCA_011067555.1
AQW88753.1	001012	Cluster428_1clades	165	BF_0228	Serratia phage BF	GCA_002619745.1
SOK59033.1	001012	Cluster428_1clades	165	g225	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58498.1	001012	Cluster428_1clades	165	g221	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASV44747.1	001013	Cluster430_1clades	150	FDI40_gp658	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93378.1	001013	Cluster430_1clades	134	G_116	Bacillus virus G	GCA_000917535.1
AFC21628.1	001013	Cluster430_1clades	140	GAP32_178	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14421.1	001013	Cluster430_1clades	136	PBI_121Q_531	Escherichia phage 121Q	GCA_000926855.1
QAY00529.1	001013	Cluster430_1clades	136	Ecwhy1_250	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34721.1	001013	Cluster430_1clades	136	ACQ29_gp041	Escherichia phage PBECO4	GCA_001041035.1
BBM62093.1	001013	Cluster430_1clades	128	EO157G_5040	Escherichia phage SP27	GCA_008033345.1
AXC36839.1	001013	Cluster430_1clades	136	-	Escherichia phage UB	GCA_003341455.1
QBO61880.1	001013	Cluster430_1clades	136	G17_00391	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13919.1	001013	Cluster430_1clades	136	vBEcoMphAPEC6_gp294c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80407.1	001013	Cluster430_1clades	136	PSLUR01_00430	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44301.1	001013	Cluster430_1clades	135	RaK2_00028	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43750.1	001013	Cluster430_1clades	140	CBB_185	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18899.1	001013	Cluster430_1clades	138	7t3_0378	Salmonella phage 7t3	GCA_006083215.1
AZU98156.1	001013	Cluster430_1clades	138	CPT_Munch_212	Salmonella phage Munch	GCA_004015485.1
QIG62828.1	001013	Cluster430_1clades	138	SEPL_215	Salmonella phage SE_PL	GCA_011067555.1
AQW88708.1	001013	Cluster430_1clades	141	BF_0183	Serratia phage BF	GCA_002619745.1
SOK58990.1	001013	Cluster430_1clades	140	g182	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58455.1	001013	Cluster430_1clades	140	g178	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71267.1	001014	Cluster432_1clades	146	CR5_047	Cronobacter phage CR5	GCA_000910235.1
AMR59697.1	001014	Cluster432_1clades	141	SEGD1_048	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07474.1	001014	Cluster432_1clades	146	DERBICUS_48	Erwinia phage Derbicus	GCA_004521655.1
ANZ49700.1	001014	Cluster432_1clades	146	MACHINA_62	Erwinia phage Machina	GCA_002758035.1
AXF51190.1	001014	Cluster432_1clades	147	WELLINGTON_60	Erwinia phage Wellington	GCA_003344985.1
AFQ96775.1	001014	Cluster432_1clades	147	G173_gp230	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48076.1	001014	Cluster432_1clades	147	ASESINO_63	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48351.1	001014	Cluster432_1clades	145	CAITLIN_56	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48624.1	001014	Cluster432_1clades	145	CHRISDB_62	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48898.1	001014	Cluster432_1clades	146	EARLPHILLIPIV_48	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49145.1	001014	Cluster432_1clades	146	HUXLEY_63	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49412.1	001014	Cluster432_1clades	147	KWAN_60	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49973.1	001014	Cluster432_1clades	146	PARSHIK_64	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50239.1	001014	Cluster432_1clades	146	PHOBOS_49	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50487.1	001014	Cluster432_1clades	147	STRATTON_62	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85887.1	001014	Cluster432_1clades	147	ACEC001_0490	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20762.1	001014	Cluster432_1clades	147	-	Salmonella phage JN03	GCA_014319805.1
AWN09051.1	001014	Cluster432_1clades	147	MLDJOKPK_00119	Salmonella phage SPAsTU	GCA_003183805.1
AEP83879.1	001014	Cluster432_1clades	147	SPN3US_0046	Salmonella phage SPN3US	GCA_001042275.1
AFO71261.1	001015	Cluster433_1clades	74	CR5_041	Cronobacter phage CR5	GCA_000910235.1
QBP07468.1	001015	Cluster433_1clades	90	DERBICUS_42	Erwinia phage Derbicus	GCA_004521655.1
ANZ49694.1	001015	Cluster433_1clades	122	MACHINA_56	Erwinia phage Machina	GCA_002758035.1
AXF51183.1	001015	Cluster433_1clades	147	WELLINGTON_52	Erwinia phage Wellington	GCA_003344985.1
AFQ96768.1	001015	Cluster433_1clades	102	G173_gp223	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48070.1	001015	Cluster433_1clades	136	ASESINO_57	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48345.1	001015	Cluster433_1clades	97	CAITLIN_50	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48618.1	001015	Cluster433_1clades	89	CHRISDB_56	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48892.1	001015	Cluster433_1clades	90	EARLPHILLIPIV_42	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49139.1	001015	Cluster433_1clades	122	HUXLEY_57	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49404.1	001015	Cluster433_1clades	99	KWAN_52	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49967.1	001015	Cluster433_1clades	122	PARSHIK_58	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50232.1	001015	Cluster433_1clades	121	PHOBOS_42	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50480.1	001015	Cluster433_1clades	125	STRATTON_55	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85881.1	001015	Cluster433_1clades	123	ACEC001_0430	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20756.1	001015	Cluster433_1clades	123	-	Salmonella phage JN03	GCA_014319805.1
AXF51096.1	001015	Cluster433_1clades	126	MLDJOKPK_00126	Salmonella phage SPAsTU	GCA_003183805.1
AEP83873.1	001015	Cluster433_1clades	123	SPN3US_0040	Salmonella phage SPN3US	GCA_001042275.1
AQT28165.1	001015	Cluster433_1clades	122	pVa21_224	Vibrio phage pVa-21	GCA_002619305.1
AFO71231.1	001016	Cluster434_1clades	130	CR5_011	Cronobacter phage CR5	GCA_000910235.1
AMR59661.1	001016	Cluster434_1clades	99	SEGD1_010	Enterobacteria phage SEGD1	GCA_002601865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBP07437.1	001016	Cluster434_1clades	130	DERBICUS_11	Erwinia phage Derbicus	GCA_004521655.1
ANZ49664.1	001016	Cluster434_1clades	118	MACHINA_26	Erwinia phage Machina	GCA_002758035.1
AXF51152.1	001016	Cluster434_1clades	129	WELLINGTON_21	Erwinia phage Wellington	GCA_003344985.1
AFQ96738.1	001016	Cluster434_1clades	122	G173_gp193	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48041.1	001016	Cluster434_1clades	122	ASESINO_28	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48315.1	001016	Cluster434_1clades	119	CAITLIN_20	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48588.1	001016	Cluster434_1clades	113	CHRISDB_26	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48861.1	001016	Cluster434_1clades	130	EARLPHILLIPIV_11	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49109.1	001016	Cluster434_1clades	118	HUXLEY_27	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49373.1	001016	Cluster434_1clades	129	KWAN_21	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49937.1	001016	Cluster434_1clades	118	PARSHIK_28	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50201.1	001016	Cluster434_1clades	135	PHOBOS_11	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50451.1	001016	Cluster434_1clades	122	STRATTON_26	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85849.1	001016	Cluster434_1clades	145	ACEC001_0120	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20729.1	001016	Cluster434_1clades	102	-	Salmonella phage JN03	GCA_014319805.1
AWN09083.2	001016	Cluster434_1clades	124	MLDJOKPK_00156	Salmonella phage SPAsTU	GCA_003183805.1
AEP83844.1	001016	Cluster434_1clades	99	SPN3US_0011	Salmonella phage SPN3US	GCA_001042275.1
AFC21799.1	001017	Cluster435_1clades	82	GAP32_349	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13971.1	001017	Cluster435_1clades	92	PBI_121Q_74	Escherichia phage 121Q	GCA_000926855.1
AIT13972.1	001017	Cluster435_1clades	76	PBI_121Q_75	Escherichia phage 121Q	GCA_000926855.1
QAY00365.1	001017	Cluster435_1clades	78	Ecwhy1_84	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00366.1	001017	Cluster435_1clades	92	Ecwhy1_85	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35110.1	001017	Cluster435_1clades	76	ACQ29_gp430	Escherichia phage PBECO4	GCA_001041035.1
AGC35111.1	001017	Cluster435_1clades	92	ACQ29_gp431	Escherichia phage PBECO4	GCA_001041035.1
BBM61663.1	001017	Cluster435_1clades	92	EO157G_0740	Escherichia phage SP27	GCA_008033345.1
BBM61664.1	001017	Cluster435_1clades	76	EO157G_0750	Escherichia phage SP27	GCA_008033345.1
AXC36685.1	001017	Cluster435_1clades	76	-	Escherichia phage UB	GCA_003341455.1
QBO61720.1	001017	Cluster435_1clades	139	G17_00231	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13767.1	001017	Cluster435_1clades	92	vBEcoMphAPEC6_gp138c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80565.1	001017	Cluster435_1clades	92	PSLUR01_00588	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80566.1	001017	Cluster435_1clades	76	PSLUR01_00589	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44453.1	001017	Cluster435_1clades	79	RaK2_00180	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43920.1	001017	Cluster435_1clades	82	CBB_357	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88880.1	001017	Cluster435_1clades	81	BF_0355	Serratia phage BF	GCA_002619745.1
SOK59166.1	001017	Cluster435_1clades	79	g358	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58634.1	001017	Cluster435_1clades	79	g357	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71227.1	001018	Cluster436_1clades	129	CR5_007	Cronobacter phage CR5	GCA_000910235.1
AMR59656.1	001018	Cluster436_1clades	129	SEGD1_005	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07434.1	001018	Cluster436_1clades	133	DERBICUS_7	Erwinia phage Derbicus	GCA_004521655.1
ANZ49660.1	001018	Cluster436_1clades	128	MACHINA_22	Erwinia phage Machina	GCA_002758035.1
AXF51147.1	001018	Cluster436_1clades	128	WELLINGTON_16	Erwinia phage Wellington	GCA_003344985.1
AFQ96736.1	001018	Cluster436_1clades	129	G173_gp191	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48037.1	001018	Cluster436_1clades	129	ASESINO_24	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48311.1	001018	Cluster436_1clades	128	CAITLIN_16	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48584.1	001018	Cluster436_1clades	128	CHRISDB_22	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48857.1	001018	Cluster436_1clades	128	EARLPHILLIPIV_7	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49105.1	001018	Cluster436_1clades	128	HUXLEY_23	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49369.1	001018	Cluster436_1clades	128	KWAN_16	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49933.1	001018	Cluster436_1clades	128	PARSHIK_24	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50197.1	001018	Cluster436_1clades	127	PHOBOS_7	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50447.1	001018	Cluster436_1clades	129	STRATTON_22	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85845.1	001018	Cluster436_1clades	129	ACEC001_0080	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20725.1	001018	Cluster436_1clades	129	-	Salmonella phage JN03	GCA_014319805.1
AWN09086.1	001018	Cluster436_1clades	129	MLDJOKPK_00160	Salmonella phage SPAsTU	GCA_003183805.1
AEP83840.1	001018	Cluster436_1clades	129	SPN3US_0007	Salmonella phage SPN3US	GCA_001042275.1
ANZ50533.1	001019	Cluster437_2clades	130	STRATTON_108	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AFO71425.1	001019	Cluster437_2clades	127	CR5_205	Cronobacter phage CR5	GCA_000910235.1
AMR59743.1	001019	Cluster437_2clades	129	SEGD1_094	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07638.1	001019	Cluster437_2clades	127	DERBICUS_212	Erwinia phage Derbicus	GCA_004521655.1
ANZ49740.1	001019	Cluster437_2clades	130	MACHINA_102	Erwinia phage Machina	GCA_002758035.1
AXF51240.1	001019	Cluster437_2clades	130	WELLINGTON_110	Erwinia phage Wellington	GCA_003344985.1
AFQ96559.1	001019	Cluster437_2clades	130	G173_gp014	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48119.1	001019	Cluster437_2clades	130	ASESINO_106	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48394.1	001019	Cluster437_2clades	131	CAITLIN_99	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48666.1	001019	Cluster437_2clades	131	CHRISDB_104	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49062.1	001019	Cluster437_2clades	127	EARLPHILLIPIV_213	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49185.1	001019	Cluster437_2clades	130	HUXLEY_103	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49461.1	001019	Cluster437_2clades	130	KWAN_109	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50013.1	001019	Cluster437_2clades	130	PARSHIK_104	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50409.1	001019	Cluster437_2clades	127	PHOBOS_219	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QKN85930.1	001019	Cluster437_2clades	129	ACEC001_0920	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20800.1	001019	Cluster437_2clades	129	-	Salmonella phage JN03	GCA_014319805.1
AWN09013.1	001019	Cluster437_2clades	131	MLDJOKPK_00069	Salmonella phage SPAsTU	GCA_003183805.1
AEP83923.1	001019	Cluster437_2clades	129	SPN3US_0090	Salmonella phage SPN3US	GCA_001042275.1
ARB13600.1	001020	Cluster438_1clades	130	Ccr10_gp072	Caulobacter phage Ccr10	GCA_002619445.1
ARB13946.1	001020	Cluster438_1clades	130	Ccr2_gp071	Caulobacter phage Ccr2	GCA_002619465.1
ARB14636.1	001020	Cluster438_1clades	130	Ccr29_gp079	Caulobacter phage Ccr29	GCA_002619485.1
ARB14992.1	001020	Cluster438_1clades	130	Ccr32_gp073	Caulobacter phage Ccr32	GCA_002619505.1
ARB15322.1	001020	Cluster438_1clades	130	Ccr34_gp073	Caulobacter phage Ccr34	GCA_002619525.1
ARB14289.1	001020	Cluster438_1clades	130	Ccr5_gp071	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68273.1	001020	Cluster438_1clades	130	CcrBL10_gp069	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69151.1	001020	Cluster438_1clades	131	CcrBL9_gp127	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69156.1	001020	Cluster438_1clades	123	CcrBL9_gp132	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87956.1	001020	Cluster438_1clades	127	CcrColossus_gp086	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68578.1	001020	Cluster438_1clades	131	CcrPW_gp039	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68632.1	001020	Cluster438_1clades	127	CcrPW_gp093	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69705.1	001020	Cluster438_1clades	131	CcrSC_gp123	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69711.1	001020	Cluster438_1clades	123	CcrSC_gp129	Caulobacter phage CcrSC	GCA_003443315.1
AFU87590.1	001020	Cluster438_1clades	130	CcrKarma_gp073	Caulobacter virus Karma	GCA_000901575.1
AFU87240.1	001020	Cluster438_1clades	130	CcrMagneto_gp070	Caulobacter virus Magneto	GCA_000903095.1
AFU86556.1	001020	Cluster438_1clades	130	CcrRogue_gp074	Caulobacter virus Rogue	GCA_000900555.1
AFU88388.1	001020	Cluster438_1clades	130	CcrSwift_gp070	Caulobacter virus Swift	GCA_000899655.1
AFU86904.1	001020	Cluster438_1clades	130	CbK_gp072	Caulobacter virus phiCbK	GCA_000900535.1
AFO71258.1	001021	Cluster439_1clades	64	CR5_038	Cronobacter phage CR5	GCA_000910235.1
AMR59689.1	001021	Cluster439_1clades	37	SEGD1_040	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07465.1	001021	Cluster439_1clades	125	DERBICUS_39	Erwinia phage Derbicus	GCA_004521655.1
ANZ49691.1	001021	Cluster439_1clades	110	MACHINA_53	Erwinia phage Machina	GCA_002758035.1
AXF51180.1	001021	Cluster439_1clades	110	WELLINGTON_49	Erwinia phage Wellington	GCA_003344985.1
AFQ96765.1	001021	Cluster439_1clades	37	G173_gp220	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48067.1	001021	Cluster439_1clades	117	ASESINO_54	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48342.1	001021	Cluster439_1clades	111	CAITLIN_47	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48615.1	001021	Cluster439_1clades	111	CHRISDB_53	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48889.1	001021	Cluster439_1clades	125	EARLPHILLIPIV_39	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49136.1	001021	Cluster439_1clades	110	HUXLEY_54	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49401.1	001021	Cluster439_1clades	110	KWAN_49	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49964.1	001021	Cluster439_1clades	126	PARSHIK_55	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50229.1	001021	Cluster439_1clades	86	PHOBOS_39	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50477.1	001021	Cluster439_1clades	127	STRATTON_52	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85878.1	001021	Cluster439_1clades	127	ACEC001_0400	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20753.1	001021	Cluster439_1clades	127	-	Salmonella phage JN03	GCA_014319805.1
AEP83870.1	001021	Cluster439_1clades	127	SPN3US_0037	Salmonella phage SPN3US	GCA_001042275.1
AQT28164.1	001021	Cluster439_1clades	117	pVa21_223	Vibrio phage pVa-21	GCA_002619305.1
AFO71316.1	001022	Cluster440_1clades	67	CR5_096	Cronobacter phage CR5	GCA_000910235.1
AMR59749.1	001022	Cluster440_1clades	123	SEGD1_100	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07525.1	001022	Cluster440_1clades	123	DERBICUS_99	Erwinia phage Derbicus	GCA_004521655.1
ANZ49747.1	001022	Cluster440_1clades	122	MACHINA_109	Erwinia phage Machina	GCA_002758035.1
AXF51248.1	001022	Cluster440_1clades	125	WELLINGTON_118	Erwinia phage Wellington	GCA_003344985.1
AFQ96566.1	001022	Cluster440_1clades	123	G173_gp021	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48126.1	001022	Cluster440_1clades	123	ASESINO_113	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48400.1	001022	Cluster440_1clades	122	CAITLIN_105	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48673.1	001022	Cluster440_1clades	122	CHRISDB_111	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48948.1	001022	Cluster440_1clades	123	EARLPHILLIPIV_99	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49192.1	001022	Cluster440_1clades	122	HUXLEY_110	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49469.1	001022	Cluster440_1clades	125	KWAN_117	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50020.1	001022	Cluster440_1clades	122	PARSHIK_111	Erwinia phage vB_EamM_Parshik	GCA_002758055.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ50289.1	001022	Cluster440_1clades	123	PHOBOS_99	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50541.1	001022	Cluster440_1clades	123	STRATTON_116	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85938.1	001022	Cluster440_1clades	123	ACEC001_1000	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20806.1	001022	Cluster440_1clades	123	-	Salmonella phage JN03	GCA_014319805.1
AWN09008.1	001022	Cluster440_1clades	123	MLDJOKPK_00061	Salmonella phage SPAsTU	GCA_003183805.1
AEP83930.1	001022	Cluster440_1clades	123	SPN3US_0097	Salmonella phage SPN3US	GCA_001042275.1
APU01698.1	001023	Cluster442_1clades	104	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29127.1	001023	Cluster442_1clades	92	AP1_0424	Aeromonas phage AP1	GCA_014183365.1
ATI17229.1	001023	Cluster442_1clades	92	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00358.1	001023	Cluster442_1clades	92	HWB28_gp194	Aeromonas phage AS-zj	GCA_002627665.1
QAX97672.1	001023	Cluster442_1clades	92	ASswx1_26	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01109.1	001023	Cluster442_1clades	104	ASwh1_41	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39214.1	001023	Cluster442_1clades	92	CC2_089	Aeromonas phage CC2	GCA_000903495.1
ADQ53337.1	001023	Cluster442_1clades	104	65p329	Aeromonas virus 65	GCA_000893255.1
AIT14404.1	001023	Cluster442_1clades	118	PBI_121Q_514	Escherichia phage 121Q	GCA_000926855.1
QAY00547.1	001023	Cluster442_1clades	118	Ecwhy1_268	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34738.1	001023	Cluster442_1clades	118	ACQ29_gp058	Escherichia phage PBECO4	GCA_001041035.1
BBM62075.1	001023	Cluster442_1clades	118	EO157G_4860	Escherichia phage SP27	GCA_008033345.1
AXC36853.1	001023	Cluster442_1clades	118	-	Escherichia phage UB	GCA_003341455.1
QBO61898.1	001023	Cluster442_1clades	118	G17_00409	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13934.1	001023	Cluster442_1clades	118	vBEcoMphAPEC6_gp309c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80390.1	001023	Cluster442_1clades	118	PSLUR01_00413	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18868.1	001023	Cluster442_1clades	117	7t3_0347	Salmonella phage 7t3	GCA_006083215.1
AZU98129.1	001023	Cluster442_1clades	117	CPT_Munch_185	Salmonella phage Munch	GCA_004015485.1
QIG62853.1	001023	Cluster442_1clades	117	SEPL_240	Salmonella phage SE_PL	GCA_011067555.1
AFO71254.1	001024	Cluster443_1clades	107	CR5_034	Cronobacter phage CR5	GCA_000910235.1
AMR59685.1	001024	Cluster443_1clades	107	SEGD1_036	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07461.1	001024	Cluster443_1clades	106	DERBICUS_35	Erwinia phage Derbicus	GCA_004521655.1
ANZ49687.1	001024	Cluster443_1clades	107	MACHINA_49	Erwinia phage Machina	GCA_002758035.1
AXF51176.1	001024	Cluster443_1clades	106	WELLINGTON_45	Erwinia phage Wellington	GCA_003344985.1
AFQ96760.1	001024	Cluster443_1clades	107	G173_gp215	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48063.1	001024	Cluster443_1clades	107	ASESINO_50	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48338.1	001024	Cluster443_1clades	107	CAITLIN_43	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48611.1	001024	Cluster443_1clades	107	CHRISDB_49	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48885.1	001024	Cluster443_1clades	106	EARLPHILLIPIV_35	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49132.1	001024	Cluster443_1clades	107	HUXLEY_50	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49397.1	001024	Cluster443_1clades	106	KWAN_45	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49960.1	001024	Cluster443_1clades	107	PARSHIK_51	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50225.1	001024	Cluster443_1clades	106	PHOBOS_35	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50473.1	001024	Cluster443_1clades	107	STRATTON_48	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85874.1	001024	Cluster443_1clades	107	ACEC001_0360	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20749.1	001024	Cluster443_1clades	107	-	Salmonella phage JN03	GCA_014319805.1
AWN09062.1	001024	Cluster443_1clades	107	MLDJOKPK_00132	Salmonella phage SPAsTU	GCA_003183805.1
AEP83866.1	001024	Cluster443_1clades	107	SPN3US_0033	Salmonella phage SPN3US	GCA_001042275.1
QMV29021.1	001025	Cluster444_1clades	84	AP1_0314	Aeromonas phage AP1	GCA_014183365.1
ATI17630.1	001025	Cluster444_1clades	84	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00365.1	001025	Cluster444_1clades	84	HWB28_gp187	Aeromonas phage AS-zj	GCA_002627665.1
QAX97665.1	001025	Cluster444_1clades	84	ASswx1_19	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01069.1	001025	Cluster444_1clades	84	ASwh1_1	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39341.1	001025	Cluster444_1clades	84	CC2_096	Aeromonas phage CC2	GCA_000903495.1
AUZ95152.1	001025	Cluster444_1clades	103	FDI40_gp393	Agrobacterium phage Atu_ph07	GCA_002628245.1
QBX06758.1	001025	Cluster444_1clades	83	BcepSaruman_345	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74728.1	001025	Cluster444_1clades	83	BcepSauron_348	Burkholderia phage BcepSauron	GCA_005394215.1
ANS06131.1	001025	Cluster444_1clades	87	ABCD_0157	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97169.1	001025	Cluster444_1clades	87	E_161	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78685.1	001025	Cluster444_1clades	87	RB43ORF163c	Escherichia virus RB43	GCA_000863505.1
AGR47839.1	001025	Cluster444_1clades	84	SmphiM12_207	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13046.1	001025	Cluster444_1clades	84	PHIM19_141	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12687.1	001025	Cluster444_1clades	84	PHIM7_141	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13418.1	001025	Cluster444_1clades	84	PHIN3_155	Sinorhizobium phage phiN3	GCA_001501175.1
QAU04451.1	001025	Cluster444_1clades	85	ValB1MD_031	Vibrio phage ValB1MD	GCA_004138815.1
BBA65673.1	001025	Cluster444_1clades	82	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65214.1	001025	Cluster444_1clades	82	-	Xanthomonas phage XacN1	GCA_003173815.1
AFO71435.1	001026	Cluster445_1clades	98	CR5_215	Cronobacter phage CR5	GCA_000910235.1
AMR59899.1	001026	Cluster445_1clades	99	SEGD1_252	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07648.1	001026	Cluster445_1clades	98	DERBICUS_222	Erwinia phage Derbicus	GCA_004521655.1
ANZ49898.1	001026	Cluster445_1clades	98	MACHINA_260	Erwinia phage Machina	GCA_002758035.1
AXF51399.1	001026	Cluster445_1clades	100	WELLINGTON_273	Erwinia phage Wellington	GCA_003344985.1
AFQ96712.1	001026	Cluster445_1clades	99	G173_gp167	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48282.1	001026	Cluster445_1clades	99	ASESINO_269	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48554.1	001026	Cluster445_1clades	98	CAITLIN_259	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48832.1	001026	Cluster445_1clades	98	CHRISDB_270	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49072.1	001026	Cluster445_1clades	98	EARLPHILLIPIV_223	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49341.1	001026	Cluster445_1clades	98	HUXLEY_259	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49625.1	001026	Cluster445_1clades	100	KWAN_273	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50169.1	001026	Cluster445_1clades	98	PARSHIK_260	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50419.1	001026	Cluster445_1clades	98	PHOBOS_229	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50694.1	001026	Cluster445_1clades	99	STRATTON_269	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86088.1	001026	Cluster445_1clades	99	ACEC001_2450	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20931.1	001026	Cluster445_1clades	99	-	Salmonella phage JN03	GCA_014319805.1
AWN09106.1	001026	Cluster445_1clades	99	MLDJOKPK_00193	Salmonella phage SPAsTU	GCA_003183805.1
AEP84080.1	001026	Cluster445_1clades	99	SPN3US_0247	Salmonella phage SPN3US	GCA_001042275.1
AMO43310.1	001027	Cluster446_1clades	90	W270710_066	Cyanophage S-RIM44	GCA_002599145.1
AOO11544.1	001027	Cluster446_1clades	90	ES420910_063	Cyanophage S-RIM44	GCA_002599165.1
AOO11782.1	001027	Cluster446_1clades	90	Np050604_066	Cyanophage S-RIM44	GCA_002599185.1
AOO12009.1	001027	Cluster446_1clades	90	Np200711_063	Cyanophage S-RIM44	GCA_002599205.1
AOO12245.1	001027	Cluster446_1clades	90	Np420711_063	Cyanophage S-RIM44	GCA_002599225.1
AOO12483.1	001027	Cluster446_1clades	90	Sn080709_066	Cyanophage S-RIM44	GCA_002599245.1
AOO12710.1	001027	Cluster446_1clades	90	Sn130910_063	Cyanophage S-RIM44	GCA_002599265.1
AOO12948.1	001027	Cluster446_1clades	90	W2100709_066	Cyanophage S-RIM44	GCA_002599285.1
AGG54337.1	001027	Cluster446_1clades	97	CYWG_00053	Cyanophage S-SSM6b	GCA_002710425.1
ADO99164.1	001027	Cluster446_1clades	90	Syn1_063	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30519.1	001027	Cluster446_1clades	90	Syn7803US37_42	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76122.1	001027	Cluster446_1clades	98	PBI_BELLAMY_77	Synechococcus phage Bellamy	GCA_002627525.1
QCW23001.1	001027	Cluster446_1clades	95	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50653.1	001027	Cluster446_1clades	92	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59515.1	001027	Cluster446_1clades	93	S330809_054	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59277.1	001027	Cluster446_1clades	93	C440309_054	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59753.1	001027	Cluster446_1clades	93	N231010_054	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70413.1	001027	Cluster446_1clades	92	HOU04_gp014	Synechococcus phage S-T4	GCA_003443335.1
AXQ70615.1	001027	Cluster446_1clades	92	HOU04_gp014	Synechococcus phage S-T4	GCA_003443335.1
AJK27432.1	001028	Cluster447_1clades	50	PTIM40_5	Cyanophage P-TIM40	GCA_001470935.1
AOO14393.1	001028	Cluster447_1clades	49	Sn110110_200	Cyanophage S-RIM14	GCA_002599065.1
AOO15041.1	001028	Cluster447_1clades	49	W1230910_196	Cyanophage S-RIM14	GCA_002599125.1
AMO43449.1	001028	Cluster447_1clades	49	W270710_210	Cyanophage S-RIM44	GCA_002599145.1
AOO11690.1	001028	Cluster447_1clades	49	ES420910_213	Cyanophage S-RIM44	GCA_002599165.1
AOO11921.1	001028	Cluster447_1clades	49	Np050604_210	Cyanophage S-RIM44	GCA_002599185.1
AOO12156.1	001028	Cluster447_1clades	49	Np200711_214	Cyanophage S-RIM44	GCA_002599205.1
AOO12391.1	001028	Cluster447_1clades	49	Np420711_213	Cyanophage S-RIM44	GCA_002599225.1
AOO12622.1	001028	Cluster447_1clades	49	Sn080709_210	Cyanophage S-RIM44	GCA_002599245.1
AOO12856.1	001028	Cluster447_1clades	49	Sn130910_213	Cyanophage S-RIM44	GCA_002599265.1
AOO13088.1	001028	Cluster447_1clades	49	W2100709_211	Cyanophage S-RIM44	GCA_002599285.1
ADO99309.1	001028	Cluster447_1clades	93	Syn1_213	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30715.1	001028	Cluster447_1clades	49	Syn7803US37_238	Synechococcus phage ACG-2014f	GCA_002594065.1
QDH50667.1	001028	Cluster447_1clades	49	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59669.1	001028	Cluster447_1clades	49	S330809_208	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59431.1	001028	Cluster447_1clades	49	C440309_208	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59906.1	001028	Cluster447_1clades	49	N231010_207	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70499.1	001028	Cluster447_1clades	43	HOU04_gp100	Synechococcus phage S-T4	GCA_003443335.1
QJT70129.1	001028	Cluster447_1clades	48	SynMITS9220M01_116	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01453.1	001029	UvsW.1	90	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29069.1	001029	UvsW.1	56	AP1_0362	Aeromonas phage AP1	GCA_014183365.1
ATI17444.1	001029	UvsW.1	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00151.1	001029	UvsW.1	93	HWB28_gp401	Aeromonas phage AS-zj	GCA_002627665.1
AUE22778.1	001029	UvsW.1	85	Ah1_00260	Aeromonas phage Ah1	GCA_002957415.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX98494.1	001029	UvsW.1	83	ASfcp2_157	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97884.1	001029	UvsW.1	92	ASswx1_241	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01264.1	001029	UvsW.1	91	ASwh1_201	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39479.1	001029	UvsW.1	93	CC2_292	Aeromonas phage CC2	GCA_000903495.1
ADQ52956.1	001029	UvsW.1	75	PX29p237	Aeromonas phage PX29	GCA_000920195.1
ADM79881.1	001029	UvsW.1	85	phiAS5_ORF0038	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53073.1	001029	UvsW.1	90	65p063	Aeromonas virus 65	GCA_000893255.1
AAQ17903.1	001029	UvsW.1	85	uvsW.1	Aeromonas virus Aeh1	GCA_000843245.1
ANS06152.1	001029	UvsW.1	76	ABCD_0220	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64857.1	001029	UvsW.1	76	S13_058	Cronobacter phage S13	GCA_001503575.1
AON97237.1	001029	UvsW.1	76	E_229	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70743.1	001029	UvsW.1	76	phiC120_c36	Escherichia phage phiC120	GCA_002621185.1
AAX78754.1	001029	UvsW.1	76	RB43ORF232c	Escherichia virus RB43	GCA_000863505.1
QHJ79081.1	001029	UvsW.1	78	-	Myoviridae sp.	GCA_012593985.1
AFC21737.1	001030	Cluster449_1clades	89	GAP32_287	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13918.1	001030	Cluster449_1clades	90	PBI_121Q_21	Escherichia phage 121Q	GCA_000926855.1
QAY00420.1	001030	Cluster449_1clades	90	Ecwhy1_139	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35163.1	001030	Cluster449_1clades	90	ACQ29_gp483	Escherichia phage PBECO4	GCA_001041035.1
BBM61610.1	001030	Cluster449_1clades	90	EO157G_0210	Escherichia phage SP27	GCA_008033345.1
AXC36736.1	001030	Cluster449_1clades	90	-	Escherichia phage UB	GCA_003341455.1
QBO61774.1	001030	Cluster449_1clades	90	G17_00285	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13818.1	001030	Cluster449_1clades	90	vBEcoMphAPEC6_gp189c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80513.1	001030	Cluster449_1clades	90	PSLUR01_00536	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44402.1	001030	Cluster449_1clades	89	RaK2_00129	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43856.1	001030	Cluster449_1clades	89	CBB_292	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76106.1	001030	Cluster449_1clades	79	EST35_0225	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44171.1	001030	Cluster449_1clades	86	PBI_SCTP2_156	Salicola phage SCTP-2	GCA_002625545.1
QCW19015.1	001030	Cluster449_1clades	93	7t3_0495	Salmonella phage 7t3	GCA_006083215.1
AZU98262.1	001030	Cluster449_1clades	93	CPT_Munch_318	Salmonella phage Munch	GCA_004015485.1
QIG62722.1	001030	Cluster449_1clades	93	SEPL_109	Salmonella phage SE_PL	GCA_011067555.1
AQW88815.1	001030	Cluster449_1clades	89	BF_0290	Serratia phage BF	GCA_002619745.1
SOK59098.1	001030	Cluster449_1clades	89	g290	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58562.1	001030	Cluster449_1clades	89	g285	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01649.1	001031	Cluster450_1clades	70	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28887.1	001031	Cluster450_1clades	72	AP1_0180	Aeromonas phage AP1	GCA_014183365.1
ATI17236.1	001031	Cluster450_1clades	72	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00351.1	001031	Cluster450_1clades	72	HWB28_gp201	Aeromonas phage AS-zj	GCA_002627665.1
QAX97679.1	001031	Cluster450_1clades	72	ASswx1_33	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39335.1	001031	Cluster450_1clades	72	CC2_082	Aeromonas phage CC2	GCA_000903495.1
ADQ53278.1	001031	Cluster450_1clades	70	65p270	Aeromonas virus 65	GCA_000893255.1
AAQ64303.1	001031	Cluster450_1clades	92	KVP40.0234	Vibrio phage KVP40	GCA_000843785.1
QIW90619.1	001031	Cluster450_1clades	88	GCAPEGMB_00272	Vibrio phage V07	GCA_012361095.1
QIW91180.1	001031	Cluster450_1clades	88	COHAPHLL_00344	Vibrio phage V09	GCA_012361135.1
QHJ74414.1	001031	Cluster450_1clades	88	VH12019_00087	Vibrio phage VH1_2019	GCA_009931825.1
AGB06922.1	001031	Cluster450_1clades	58	CF80_gp135	Vibrio phage VH7D	GCA_000914495.1
QBX06224.1	001031	Cluster450_1clades	58	ValB1HC_271	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60850.1	001031	Cluster450_1clades	85	AVU32_gp009	Vibrio phage ValKK3	GCA_001501635.1
AGN30292.1	001031	Cluster450_1clades	91	VPFG_00293	Vibrio phage nt-1	GCA_000910195.2
ALP47316.1	001031	Cluster450_1clades	58	phiGrn1_0359	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47694.1	001031	Cluster450_1clades	58	phiST2_0113	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54849.1	001031	Cluster450_1clades	85	vBValMR10Z_309	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37464.1	001031	Cluster450_1clades	88	pp2_231	Vibriophage phi-pp2	GCA_002630725.1
AFC21453.1	001032	Cluster451_1clades	89	GAP32_006	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14173.1	001032	Cluster451_1clades	89	PBI_121Q_283	Escherichia phage 121Q	GCA_000926855.1
QAY00763.1	001032	Cluster451_1clades	89	Ecwhy1_489	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34943.1	001032	Cluster451_1clades	89	ACQ29_gp263	Escherichia phage PBECO4	GCA_001041035.1
BBM61847.1	001032	Cluster451_1clades	89	EO157G_2580	Escherichia phage SP27	GCA_008033345.1
AXC37046.1	001032	Cluster451_1clades	89	-	Escherichia phage UB	GCA_003341455.1
QBO61533.1	001032	Cluster451_1clades	89	G17_00037	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62139.1	001032	Cluster451_1clades	89	G17_00650	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14147.1	001032	Cluster451_1clades	89	vBEcoMphAPEC6_gp524c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80158.1	001032	Cluster451_1clades	89	PSLUR01_00181	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44607.1	001032	Cluster451_1clades	89	RaK2_00334	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44120.1	001032	Cluster451_1clades	89	CBB_4	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43569.1	001032	Cluster451_1clades	89	CBB_557	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18683.1	001032	Cluster451_1clades	84	7t3_0162	Salmonella phage 7t3	GCA_006083215.1
AZU97958.1	001032	Cluster451_1clades	84	CPT_Munch_014	Salmonella phage Munch	GCA_004015485.1
QIG63019.1	001032	Cluster451_1clades	84	SEPL_406	Salmonella phage SE_PL	GCA_011067555.1
AQW88527.1	001032	Cluster451_1clades	89	BF_0002	Serratia phage BF	GCA_002619745.1
SOK58810.1	001032	Cluster451_1clades	89	g002	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58279.1	001032	Cluster451_1clades	89	g002	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14221.1	001033	Cluster452_1clades	88	PBI_121Q_331	Escherichia phage 121Q	GCA_000926855.1
QAY00716.1	001033	Cluster452_1clades	87	Ecwhy1_441	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00718.1	001033	Cluster452_1clades	72	Ecwhy1_443	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34902.1	001033	Cluster452_1clades	72	ACQ29_gp222	Escherichia phage PBECO4	GCA_001041035.1
AGC34901.1	001033	Cluster452_1clades	79	ACQ29_gp221	Escherichia phage PBECO4	GCA_001041035.1
AGC34900.1	001033	Cluster452_1clades	85	ACQ29_gp220	Escherichia phage PBECO4	GCA_001041035.1
BBM61893.1	001033	Cluster452_1clades	72	EO157G_3040	Escherichia phage SP27	GCA_008033345.1
BBM61895.1	001033	Cluster452_1clades	79	EO157G_3060	Escherichia phage SP27	GCA_008033345.1
BBM61896.1	001033	Cluster452_1clades	87	EO157G_3070	Escherichia phage SP27	GCA_008033345.1
AXC37007.1	001033	Cluster452_1clades	87	-	Escherichia phage UB	GCA_003341455.1
QBO62086.1	001033	Cluster452_1clades	87	G17_00597	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62087.1	001033	Cluster452_1clades	79	G17_00598	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62089.1	001033	Cluster452_1clades	72	G17_00600	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14099.1	001033	Cluster452_1clades	89	vBEcoMphAPEC6_gp476c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14100.1	001033	Cluster452_1clades	79	vBEcoMphAPEC6_gp477c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14102.1	001033	Cluster452_1clades	70	vBEcoMphAPEC6_gp479c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80205.1	001033	Cluster452_1clades	72	PSLUR01_00228	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80207.1	001033	Cluster452_1clades	79	PSLUR01_00230	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80208.1	001033	Cluster452_1clades	87	PSLUR01_00231	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21488.1	001034	Cluster453_1clades	73	GAP32_041	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21491.1	001034	Cluster453_1clades	58	GAP32_044	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14189.1	001034	Cluster453_1clades	56	PBI_121Q_299	Escherichia phage 121Q	GCA_000926855.1
QAY00749.1	001034	Cluster453_1clades	57	Ecwhy1_475	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34929.1	001034	Cluster453_1clades	57	ACQ29_gp249	Escherichia phage PBECO4	GCA_001041035.1
BBM61863.1	001034	Cluster453_1clades	57	EO157G_2740	Escherichia phage SP27	GCA_008033345.1
AXC37032.1	001034	Cluster453_1clades	57	-	Escherichia phage UB	GCA_003341455.1
QBO61517.1	001034	Cluster453_1clades	57	G17_00021	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62123.1	001034	Cluster453_1clades	57	G17_00634	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14132.1	001034	Cluster453_1clades	56	vBEcoMphAPEC6_gp509c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80172.1	001034	Cluster453_1clades	57	PSLUR01_00195	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44622.1	001034	Cluster453_1clades	56	RaK2_00349	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44163.1	001034	Cluster453_1clades	76	CBB_47	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43615.1	001034	Cluster453_1clades	58	CBB_50	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43612.1	001034	Cluster453_1clades	76	CBB_600	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44166.1	001034	Cluster453_1clades	58	CBB_603	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88564.1	001034	Cluster453_1clades	59	BF_0039	Serratia phage BF	GCA_002619745.1
SOK58839.1	001034	Cluster453_1clades	60	g031	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58299.1	001034	Cluster453_1clades	60	g022	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56926.1	001035	DUF4815+DUF4815	2455	CPXG_00123	Cyanophage P-RSM6	GCA_000906155.1
AJK27531.1	001035	DUF4815+DUF4815	2479	PTIM40_104	Cyanophage P-TIM40	GCA_001470935.1
AOO14290.1	001035	DUF4815+DUF4815	2459	Sn110110_096	Cyanophage S-RIM14	GCA_002599065.1
AOO14939.1	001035	DUF4815+DUF4815	2459	W1230910_093	Cyanophage S-RIM14	GCA_002599125.1
AGH07722.1	001035	DUF4815+DUF4815	2505	CYVG_00279	Cyanophage S-SSM6a	GCA_002710385.1
AGG54294.1	001035	DUF4815+DUF4815	2488	CYWG_00010	Cyanophage S-SSM6b	GCA_002710425.1
AGH26134.1	001035	DUF4815+DUF4815	2169	CPMG_00033	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44491.1	001035	DUF4815+DUF4815	2506	PSSM2_113	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12475.1	001035	DUF4815+DUF4815	2506	PRTG_00328	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93430.1	001035	DUF4815+DUF4815	2624	AVU42_gp089	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30597.1	001035	DUF4815+DUF4815	2406	Syn7803US37_120	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54874.1	001035	DUF4815+DUF4815	2578	b23_0260	Synechococcus phage B23	GCA_009745195.1
QGT54509.1	001035	DUF4815+DUF4815	2578	b3_0267	Synechococcus phage B3	GCA_009745215.1
ASR76158.1	001035	DUF4815+DUF4815	2522	PBI_BELLAMY_113	Synechococcus phage Bellamy	GCA_002627525.1
QCW22828.1	001035	DUF4815+DUF4815	2539	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50493.1	001035	DUF4815+DUF4815	2539	-	Synechococcus phage S-B43	GCA_006869725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ70594.1	001035	DUF4815+DUF4815	2459	HOU04_gp195	Synechococcus phage S-T4	GCA_003443335.1
QJT70098.1	001035	DUF4815+DUF4815	2542	SynMITS9220M01_085	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56994.1	001036	Collar	1190	CPXG_00191	Cyanophage P-RSM6	GCA_000906155.1
AJK27466.1	001036	Collar	1190	PTIM40_39	Cyanophage P-TIM40	GCA_001470935.1
AOO14222.1	001036	Collar	1271	Sn110110_028	Cyanophage S-RIM14	GCA_002599065.1
AOO14874.1	001036	Collar	1271	W1230910_028	Cyanophage S-RIM14	GCA_002599125.1
AGG54343.1	001036	Collar	1270	CYWG_00059	Cyanophage S-SSM6b	GCA_002710425.1
AGH26184.1	001036	Collar	1580	CPMG_00083	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93405.1	001036	Collar	2011	AVU42_gp020	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30498.1	001036	Collar	1955	Syn7803US37_21	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54648.1	001036	Collar	2005	b23_0020	Synechococcus phage B23	GCA_009745195.1
QGT54278.1	001036	Collar	2005	b3_0020	Synechococcus phage B3	GCA_009745215.1
ASR76072.1	001036	Collar	1976	PBI_BELLAMY_27	Synechococcus phage Bellamy	GCA_002627525.1
QCW22909.1	001036	Collar	1633	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50550.1	001036	Collar	1633	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70431.1	001036	Collar	1949	HOU04_gp032	Synechococcus phage S-T4	GCA_003443335.1
QJT70040.1	001036	Collar	1963	SynMITS9220M01_027	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01438.1	001037	ILEI	1261	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28797.1	001037	ILEI	372	AP1_0090	Aeromonas phage AP1	GCA_014183365.1
QMV29013.1	001037	ILEI	884	AP1_0306	Aeromonas phage AP1	GCA_014183365.1
ATI17461.1	001037	ILEI	1259	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00135.1	001037	ILEI	1259	HWB28_gp015	Aeromonas phage AS-zj	GCA_002627665.1
AUE22855.1	001037	ILEI	1235	Ah1_00337	Aeromonas phage Ah1	GCA_002957415.1
QAX98566.1	001037	ILEI	1318	ASfcp2_232	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97901.1	001037	ILEI	1259	ASswx1_258	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01252.1	001037	ILEI	1259	ASwh1_187	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39406.1	001037	ILEI	1259	CC2_275	Aeromonas phage CC2	GCA_000903495.1
ADM79955.1	001037	ILEI	1305	phiAS5_ORF0112	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53058.1	001037	ILEI	1261	65p048	Aeromonas virus 65	GCA_000893255.1
AAQ17984.1	001037	ILEI	1312	35	Aeromonas virus Aeh1	GCA_000843245.1
ANS05942.1	001037	ILEI	528	ABCD_0261	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64808.1	001037	ILEI	501	S13_009	Cronobacter phage S13	GCA_001503575.1
AON97280.1	001037	ILEI	531	E_272	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78801.1	001037	ILEI	528	RB43ORF279w	Escherichia virus RB43	GCA_000863505.1
QHJ78856.1	001037	ILEI	512	-	Myoviridae sp.	GCA_012593985.1
AFO71243.1	001038	Cluster458_1clades	593	CR5_023	Cronobacter phage CR5	GCA_000910235.1
QBP07450.1	001038	Cluster458_1clades	595	DERBICUS_24	Erwinia phage Derbicus	GCA_004521655.1
ANZ49676.1	001038	Cluster458_1clades	603	MACHINA_38	Erwinia phage Machina	GCA_002758035.1
AXF51165.1	001038	Cluster458_1clades	603	WELLINGTON_34	Erwinia phage Wellington	GCA_003344985.1
AFQ96749.1	001038	Cluster458_1clades	618	G173_gp204	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48052.1	001038	Cluster458_1clades	618	ASESINO_39	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48327.1	001038	Cluster458_1clades	602	CAITLIN_32	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48600.1	001038	Cluster458_1clades	601	CHRISDB_38	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48874.1	001038	Cluster458_1clades	595	EARLPHILLIPIV_24	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49121.1	001038	Cluster458_1clades	603	HUXLEY_39	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49386.1	001038	Cluster458_1clades	603	KWAN_34	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49949.1	001038	Cluster458_1clades	603	PARSHIK_40	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50214.1	001038	Cluster458_1clades	591	PHOBOS_24	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50462.1	001038	Cluster458_1clades	618	STRATTON_37	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85862.1	001038	Cluster458_1clades	617	ACEC001_0240	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20738.1	001038	Cluster458_1clades	617	-	Salmonella phage JN03	GCA_014319805.1
AXF51099.1	001038	Cluster458_1clades	620	MLDJOKPK_00144	Salmonella phage SPAsTU	GCA_003183805.1
AEP83855.1	001038	Cluster458_1clades	617	SPN3US_0022	Salmonella phage SPN3US	GCA_001042275.1
AHI60266.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	Ea357_115	Erwinia phage Ea35-70	GCA_000914635.1
ANZ49767.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	578	MACHINA_129	Erwinia phage Machina	GCA_002758035.1
QBP07224.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	REBECCA_117	Erwinia phage Rebecca	GCA_004521635.1
AXF51277.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	580	WELLINGTON_148	Erwinia phage Wellington	GCA_003344985.1
AUG85904.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	BOSOLAPHORUS_117	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANZ48422.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	579	CAITLIN_127	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48694.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	580	CHRISDB_132	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANH52219.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	DM_121	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86223.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	DESERTFOX_116	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
ANZ49212.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	581	HUXLEY_130	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49500.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	580	KWAN_148	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86545.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	MADMEL_117	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86869.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	MORTIMER_120	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANZ50040.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	578	PARSHIK_131	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANH51897.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	RAY_116	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51581.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	SIMMY50_119	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64928.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	569	SPECIALG_118	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AXF51070.1	001039	HslUClpX-AAA+PARP+HslUClpX-AAA	586	MLDJOKPK_00040	Salmonella phage SPAsTU	GCA_003183805.1
AHI60431.1	001040	Cluster3667_1clades	526	Ea357_277	Erwinia phage Ea35-70	GCA_000914635.1
AGX01960.1	001040	Cluster3667_1clades	232	CF95_gp238	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07388.1	001040	Cluster3667_1clades	526	REBECCA_283	Erwinia phage Rebecca	GCA_004521635.1
AUG86070.1	001040	Cluster3667_1clades	526	BOSOLAPHORUS_284	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52386.1	001040	Cluster3667_1clades	526	DM_287	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86390.1	001040	Cluster3667_1clades	526	DESERTFOX_283	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86711.1	001040	Cluster3667_1clades	526	MADMEL_284	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87036.1	001040	Cluster3667_1clades	526	MORTIMER_288	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52061.1	001040	Cluster3667_1clades	526	RAY_281	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51744.1	001040	Cluster3667_1clades	526	SIMMY50_286	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65096.1	001040	Cluster3667_1clades	526	SPECIALG_285	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24185.1	001040	Cluster3667_1clades	220	-	Proteus phage 10	GCA_014071245.1
BAW19238.1	001040	Cluster3667_1clades	258	FDH28_gp157	Ralstonia phage RP12	GCA_002617345.1
BAW19524.1	001040	Cluster3667_1clades	258	-	Ralstonia phage RP31	GCA_002617365.1
QKE54609.1	001040	Cluster3667_1clades	242	ACSA002_2920	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65342.1	001040	Cluster3667_1clades	220	2050HW_00007	Serratia phage 2050HW	GCA_002628125.1
QDB71130.1	001040	Cluster3667_1clades	220	CPT_Moabite_100	Serratia phage Moabite	GCA_006384735.1
QFP93144.1	001040	Cluster3667_1clades	223	-	Serratia phage PCH45	GCA_009187865.1
AFC21720.1	001041	Cluster461_1clades	429	GAP32_270	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13902.1	001041	Cluster461_1clades	428	PBI_121Q_5	Escherichia phage 121Q	GCA_000926855.1
QAY00435.1	001041	Cluster461_1clades	434	Ecwhy1_155	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35179.1	001041	Cluster461_1clades	428	ACQ29_gp499	Escherichia phage PBECO4	GCA_001041035.1
BBM61594.1	001041	Cluster461_1clades	428	EO157G_0050	Escherichia phage SP27	GCA_008033345.1
AXC36751.1	001041	Cluster461_1clades	428	-	Escherichia phage UB	GCA_003341455.1
QBO61790.1	001041	Cluster461_1clades	428	G17_00301	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13834.1	001041	Cluster461_1clades	428	vBEcoMphAPEC6_gp205c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80497.1	001041	Cluster461_1clades	428	PSLUR01_00520	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44385.1	001041	Cluster461_1clades	426	RaK2_00112	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43840.1	001041	Cluster461_1clades	429	CBB_276	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCG76087.1	001041	Cluster461_1clades	496	EST35_0206	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCW18998.1	001041	Cluster461_1clades	426	7t3_0478	Salmonella phage 7t3	GCA_006083215.1
AZU98246.1	001041	Cluster461_1clades	426	CPT_Munch_302	Salmonella phage Munch	GCA_004015485.1
QIG62738.1	001041	Cluster461_1clades	426	SEPL_125	Salmonella phage SE_PL	GCA_011067555.1
AQW88799.1	001041	Cluster461_1clades	429	BF_0274	Serratia phage BF	GCA_002619745.1
SOK59081.1	001041	Cluster461_1clades	429	g273	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58546.1	001041	Cluster461_1clades	429	g269	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13596.1	001042	Cluster462_1clades	311	Ccr10_gp068	Caulobacter phage Ccr10	GCA_002619445.1
ARB13942.1	001042	Cluster462_1clades	311	Ccr2_gp067	Caulobacter phage Ccr2	GCA_002619465.1
ARB14631.1	001042	Cluster462_1clades	311	Ccr29_gp074	Caulobacter phage Ccr29	GCA_002619485.1
ARB14987.1	001042	Cluster462_1clades	311	Ccr32_gp068	Caulobacter phage Ccr32	GCA_002619505.1
ARB15318.1	001042	Cluster462_1clades	339	Ccr34_gp069	Caulobacter phage Ccr34	GCA_002619525.1
ARB14285.1	001042	Cluster462_1clades	311	Ccr5_gp067	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68269.1	001042	Cluster462_1clades	311	CcrBL10_gp065	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69147.1	001042	Cluster462_1clades	311	CcrBL9_gp123	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87906.1	001042	Cluster462_1clades	321	CcrColossus_gp036	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87951.1	001042	Cluster462_1clades	310	CcrColossus_gp081	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68623.1	001042	Cluster462_1clades	310	CcrPW_gp084	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69701.1	001042	Cluster462_1clades	311	CcrSC_gp119	Caulobacter phage CcrSC	GCA_003443315.1
AFU87586.1	001042	Cluster462_1clades	311	CcrKarma_gp069	Caulobacter virus Karma	GCA_000901575.1
AFU87236.1	001042	Cluster462_1clades	311	CcrMagneto_gp066	Caulobacter virus Magneto	GCA_000903095.1
AFU86505.1	001042	Cluster462_1clades	191	CcrRogue_gp023	Caulobacter virus Rogue	GCA_000900555.1
AFU86552.1	001042	Cluster462_1clades	311	CcrRogue_gp070	Caulobacter virus Rogue	GCA_000900555.1
AFU88384.1	001042	Cluster462_1clades	311	CcrSwift_gp066	Caulobacter virus Swift	GCA_000899655.1
AFU86900.1	001042	Cluster462_1clades	339	CbK_gp068	Caulobacter virus phiCbK	GCA_000900535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
APU01736.1	001043	PRTase	263	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28732.1	001043	PRTase	265	AP1_0014	Aeromonas phage AP1	GCA_014183365.1
ATI17562.1	001043	PRTase	265	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00434.1	001043	PRTase	265	HWB28_gp118	Aeromonas phage AS-zj	GCA_002627665.1
QAX98002.1	001043	PRTase	265	ASswx1_362	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01139.1	001043	PRTase	265	ASwh1_73	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39501.1	001043	PRTase	265	CC2_172	Aeromonas phage CC2	GCA_000903495.1
ADQ53378.1	001043	PRTase	263	65p370	Aeromonas virus 65	GCA_000893255.1
QIG57935.1	001043	PRTase	303	SEA_PAULODIABOLI_250	Microbacterium phage PauloDiaboli	GCA_011067425.1
QBX32438.1	001043	PRTase	295	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76974.1	001043	PRTase	293	PHABIO_343	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02829.1	001043	PRTase	314	PSA21_303	Pseudomonas phage Psa21	GCA_004340405.1
QEM42009.1	001043	PRTase	295	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAW19186.1	001043	PRTase	304	FDH28_gp209	Ralstonia phage RP12	GCA_002617345.1
BAW19472.1	001043	PRTase	304	-	Ralstonia phage RP31	GCA_002617365.1
CCE26092.1	001043	PRTase	274	g068	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000654	001043	PRTase	290	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000466	001043	PRTase	290	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFO71416.1	001044	Cluster465_1clades	173	CR5_196	Cronobacter phage CR5	GCA_000910235.1
QBP07629.1	001044	Cluster465_1clades	173	DERBICUS_203	Erwinia phage Derbicus	GCA_004521655.1
ANZ49873.1	001044	Cluster465_1clades	177	MACHINA_235	Erwinia phage Machina	GCA_002758035.1
AXF51375.1	001044	Cluster465_1clades	174	WELLINGTON_249	Erwinia phage Wellington	GCA_003344985.1
AFQ96687.1	001044	Cluster465_1clades	297	G173_gp142	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48256.1	001044	Cluster465_1clades	174	ASESINO_243	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48530.1	001044	Cluster465_1clades	177	CAITLIN_235	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48806.1	001044	Cluster465_1clades	178	CHRISDB_244	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49053.1	001044	Cluster465_1clades	173	EARLPHILLIPIV_204	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49316.1	001044	Cluster465_1clades	177	HUXLEY_234	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49601.1	001044	Cluster465_1clades	174	KWAN_249	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50144.1	001044	Cluster465_1clades	177	PARSHIK_235	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50400.1	001044	Cluster465_1clades	173	PHOBOS_210	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50669.1	001044	Cluster465_1clades	174	STRATTON_244	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86062.1	001044	Cluster465_1clades	176	ACEC001_2190	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20908.1	001044	Cluster465_1clades	176	-	Salmonella phage JN03	GCA_014319805.1
AWN09128.2	001044	Cluster465_1clades	176	MLDJOKPK_00219	Salmonella phage SPAsTU	GCA_003183805.1
AEP84054.1	001044	Cluster465_1clades	176	SPN3US_0221	Salmonella phage SPN3US	GCA_001042275.1
QDB70469.1	001045	Cluster466_1clades	110	CF8_0056	Aeromonas phage CF8	GCA_006384595.2
QDJ97208.1	001045	Cluster466_1clades	110	D6_0048	Aeromonas phage D6	GCA_007051205.2
QDH47228.1	001045	Cluster466_1clades	110	LAh10_215	Aeromonas phage LAh10	GCA_006863975.1
QDJ96813.1	001045	Cluster466_1clades	40	PS1_0054	Aeromonas phage PS1	GCA_007051165.2
QDJ96815.1	001045	Cluster466_1clades	108	PS1_0056	Aeromonas phage PS1	GCA_007051165.2
QFR59444.1	001045	Cluster466_1clades	108	PS2_0053	Aeromonas phage PS2	GCA_009388305.2
QGH71902.1	001045	Cluster466_1clades	141	N1M2_39	Klebsiella phage N1M2	GCA_010092605.1
ABY63107.1	001045	Cluster466_1clades	199	201phi2-1p280	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44982.1	001045	Cluster466_1clades	230	KTN4_224	Pseudomonas phage KTN4	GCA_002607225.1
ARV77369.1	001045	Cluster466_1clades	134	NOXIFER_200	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89497.1	001045	Cluster466_1clades	108	OBP_060	Pseudomonas phage OBP	GCA_000896635.1
QBX32373.1	001045	Cluster466_1clades	193	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76902.1	001045	Cluster466_1clades	203	PHABIO_271	Pseudomonas phage Phabio	GCA_002624965.1
AEH03640.1	001045	Cluster466_1clades	189	217	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94732.1	001045	Cluster466_1clades	230	SL2_155	Pseudomonas phage SL2	GCA_002956015.1
QJB22860.1	001045	Cluster466_1clades	230	fnug_217	Pseudomonas phage fnug	GCA_012837215.1
QEM41946.1	001045	Cluster466_1clades	193	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83085.1	001045	Cluster466_1clades	230	PHIKZ184	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71230.1	001046	Cluster467_1clades	202	CR5_010	Cronobacter phage CR5	GCA_000910235.1
AMR59660.1	001046	Cluster467_1clades	216	SEGD1_009	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07436.1	001046	Cluster467_1clades	202	DERBICUS_10	Erwinia phage Derbicus	GCA_004521655.1
ANZ49663.1	001046	Cluster467_1clades	217	MACHINA_25	Erwinia phage Machina	GCA_002758035.1
AXF51151.1	001046	Cluster467_1clades	179	WELLINGTON_20	Erwinia phage Wellington	GCA_003344985.1
ANZ48040.1	001046	Cluster467_1clades	188	ASESINO_27	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48314.1	001046	Cluster467_1clades	208	CAITLIN_19	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48587.1	001046	Cluster467_1clades	219	CHRISDB_25	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48860.1	001046	Cluster467_1clades	202	EARLPHILLIPIV_10	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49108.1	001046	Cluster467_1clades	217	HUXLEY_26	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49372.1	001046	Cluster467_1clades	179	KWAN_20	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49936.1	001046	Cluster467_1clades	217	PARSHIK_27	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50200.1	001046	Cluster467_1clades	202	PHOBOS_10	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50450.1	001046	Cluster467_1clades	188	STRATTON_25	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85848.1	001046	Cluster467_1clades	180	ACEC001_0110	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20728.1	001046	Cluster467_1clades	187	-	Salmonella phage JN03	GCA_014319805.1
AWN09084.1	001046	Cluster467_1clades	187	MLDJOKPK_00157	Salmonella phage SPAsTU	GCA_003183805.1
AEP83843.1	001046	Cluster467_1clades	180	SPN3US_0010	Salmonella phage SPN3US	GCA_001042275.1
AFC21583.1	001047	Cluster468_1clades	213	GAP32_133	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14379.1	001047	Cluster468_1clades	204	PBI_121Q_489	Escherichia phage 121Q	GCA_000926855.1
QAY00569.1	001047	Cluster468_1clades	204	Ecwhy1_290	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34761.1	001047	Cluster468_1clades	204	ACQ29_gp081	Escherichia phage PBECO4	GCA_001041035.1
BBM62050.1	001047	Cluster468_1clades	204	EO157G_4610	Escherichia phage SP27	GCA_008033345.1
AXC36876.1	001047	Cluster468_1clades	204	-	Escherichia phage UB	GCA_003341455.1
QBO61923.1	001047	Cluster468_1clades	204	G17_00434	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13955.1	001047	Cluster468_1clades	204	vBEcoMphAPEC6_gp331c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80368.1	001047	Cluster468_1clades	204	PSLUR01_00391	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44790.1	001047	Cluster468_1clades	218	RaK2_00517	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43699.1	001047	Cluster468_1clades	213	CBB_134	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18840.1	001047	Cluster468_1clades	212	7t3_0319	Salmonella phage 7t3	GCA_006083215.1
AZU98102.1	001047	Cluster468_1clades	212	CPT_Munch_158	Salmonella phage Munch	GCA_004015485.1
QIG62880.1	001047	Cluster468_1clades	212	SEPL_267	Salmonella phage SE_PL	GCA_011067555.1
AQW88655.1	001047	Cluster468_1clades	211	BF_0130	Serratia phage BF	GCA_002619745.1
ALY07018.1	001047	Cluster468_1clades	111	VmeM32_00024	Vibrio phage vB_VmeM-32	GCA_002608825.1
SOK58936.1	001047	Cluster468_1clades	210	g128	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58401.1	001047	Cluster468_1clades	210	g124	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMR59906.1	001048	Cluster470_1clades	180	SEGD1_259	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07652.1	001048	Cluster470_1clades	179	DERBICUS_226	Erwinia phage Derbicus	GCA_004521655.1
ANZ49904.1	001048	Cluster470_1clades	178	MACHINA_266	Erwinia phage Machina	GCA_002758035.1
AXF51405.1	001048	Cluster470_1clades	162	WELLINGTON_279	Erwinia phage Wellington	GCA_003344985.1
AFQ96717.1	001048	Cluster470_1clades	169	G173_gp172	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48288.1	001048	Cluster470_1clades	195	ASESINO_275	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48559.1	001048	Cluster470_1clades	177	CAITLIN_264	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48836.1	001048	Cluster470_1clades	175	CHRISDB_274	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49076.1	001048	Cluster470_1clades	174	EARLPHILLIPIV_227	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49347.1	001048	Cluster470_1clades	178	HUXLEY_265	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49630.1	001048	Cluster470_1clades	162	KWAN_278	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50175.1	001048	Cluster470_1clades	178	PARSHIK_266	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50423.1	001048	Cluster470_1clades	171	PHOBOS_233	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50699.1	001048	Cluster470_1clades	195	STRATTON_274	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86095.1	001048	Cluster470_1clades	180	ACEC001_2520	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20937.1	001048	Cluster470_1clades	196	-	Salmonella phage JN03	GCA_014319805.1
AWN09099.1	001048	Cluster470_1clades	202	MLDJOKPK_00186	Salmonella phage SPAsTU	GCA_003183805.1
AEP84087.1	001048	Cluster470_1clades	180	SPN3US_0254	Salmonella phage SPN3US	GCA_001042275.1
AFC21878.1	001049	CR-Kinase	169	GAP32_425	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14198.1	001049	CR-Kinase	194	PBI_121Q_308	Escherichia phage 121Q	GCA_000926855.1
QAY00741.1	001049	CR-Kinase	194	Ecwhy1_466	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34921.1	001049	CR-Kinase	147	ACQ29_gp241	Escherichia phage PBECO4	GCA_001041035.1
BBM61871.1	001049	CR-Kinase	194	EO157G_2820	Escherichia phage SP27	GCA_008033345.1
AXC37024.1	001049	CR-Kinase	194	-	Escherichia phage UB	GCA_003341455.1
QBO61508.1	001049	CR-Kinase	194	G17_00012	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62114.1	001049	CR-Kinase	194	G17_00625	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14123.1	001049	CR-Kinase	194	vBEcoMphAPEC6_gp500c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80181.1	001049	CR-Kinase	194	PSLUR01_00204	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44629.1	001049	CR-Kinase	194	RaK2_00356	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44007.1	001049	CR-Kinase	194	CBB_444	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44008.1	001049	CR-Kinase	168	CBB_445	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18717.1	001049	CR-Kinase	196	7t3_0196	Salmonella phage 7t3	GCA_006083215.1
AZU97990.1	001049	CR-Kinase	196	CPT_Munch_046	Salmonella phage Munch	GCA_004015485.1
QIG62989.1	001049	CR-Kinase	196	SEPL_376	Salmonella phage SE_PL	GCA_011067555.1
SOK59254.1	001049	CR-Kinase	169	g446	Yersinia phage fHe-Yen9-03	GCA_002990515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58719.1	001049	CR-Kinase	169	g442	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28855.1	001050	Cluster472_1clades	163	AP1_0148	Aeromonas phage AP1	GCA_014183365.1
ATI17308.1	001050	Cluster472_1clades	163	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00286.1	001050	Cluster472_1clades	163	HWB28_gp266	Aeromonas phage AS-zj	GCA_002627665.1
QAX97751.1	001050	Cluster472_1clades	163	ASswx1_106	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01404.1	001050	Cluster472_1clades	164	ASwh1_345	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39309.1	001050	Cluster472_1clades	163	CC2_003	Aeromonas phage CC2	GCA_000903495.1
AIA64974.1	001050	Cluster472_1clades	166	S13_175	Cronobacter phage S13	GCA_001503575.1
AFC21922.1	001050	Cluster472_1clades	160	GAP32_464	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ARM70965.1	001050	Cluster472_1clades	171	phiC120_c260	Escherichia phage phiC120	GCA_002621185.1
QHJ78958.1	001050	Cluster472_1clades	159	-	Myoviridae sp.	GCA_012593985.1
AMM44048.1	001050	Cluster472_1clades	161	CBB_485	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19123.1	001050	Cluster472_1clades	181	7t3_0608	Salmonella phage 7t3	GCA_006083215.1
AZU98360.1	001050	Cluster472_1clades	181	CPT_Munch_420	Salmonella phage Munch	GCA_004015485.1
QIG62622.1	001050	Cluster472_1clades	181	SEPL_009	Salmonella phage SE_PL	GCA_011067555.1
AGR47854.1	001050	Cluster472_1clades	149	SmphiM12_222	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13059.1	001050	Cluster472_1clades	149	PHIM19_154	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12700.1	001050	Cluster472_1clades	149	PHIM7_154	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13429.1	001050	Cluster472_1clades	149	PHIN3_166	Sinorhizobium phage phiN3	GCA_001501175.1
AFO71403.1	001051	SIG+TM	171	CR5_183	Cronobacter phage CR5	GCA_000910235.1
QBP07615.1	001051	SIG+TM	170	DERBICUS_189	Erwinia phage Derbicus	GCA_004521655.1
ANZ49853.1	001051	SIG+TM	162	MACHINA_215	Erwinia phage Machina	GCA_002758035.1
AXF51355.1	001051	SIG+TM	166	WELLINGTON_229	Erwinia phage Wellington	GCA_003344985.1
AFQ96670.1	001051	SIG+TM	165	G173_gp125	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48236.1	001051	SIG+TM	165	ASESINO_223	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48510.1	001051	SIG+TM	165	CAITLIN_215	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48787.1	001051	SIG+TM	165	CHRISDB_225	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49039.1	001051	SIG+TM	170	EARLPHILLIPIV_190	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49297.1	001051	SIG+TM	162	HUXLEY_215	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49581.1	001051	SIG+TM	166	KWAN_229	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50125.1	001051	SIG+TM	172	PARSHIK_216	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50387.1	001051	SIG+TM	174	PHOBOS_197	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50650.1	001051	SIG+TM	165	STRATTON_225	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86044.1	001051	SIG+TM	169	ACEC001_2010	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20892.1	001051	SIG+TM	169	-	Salmonella phage JN03	GCA_014319805.1
AXF51117.1	001051	SIG+TM	172	MLDJOKPK_00236	Salmonella phage SPAsTU	GCA_003183805.1
AEP84037.1	001051	SIG+TM	156	SPN3US_0204	Salmonella phage SPN3US	GCA_001042275.1
AUE22649.1	001052	Cluster475_1clades	140	Ah1_00108	Aeromonas phage Ah1	GCA_002957415.1
QAX98375.1	001052	Cluster475_1clades	140	ASfcp2_29	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52828.1	001052	Cluster475_1clades	140	PX29p109	Aeromonas phage PX29	GCA_000920195.1
ADM80088.1	001052	Cluster475_1clades	157	phiAS5_ORF0245	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17774.1	001052	Cluster475_1clades	140	Aeh1ORF112c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64084.1	001052	Cluster475_1clades	139	KVP40.0013	Vibrio phage KVP40	GCA_000843785.1
QIW90408.1	001052	Cluster475_1clades	139	GCAPEGMB_00061	Vibrio phage V07	GCA_012361095.1
QIW91021.1	001052	Cluster475_1clades	139	COHAPHLL_00158	Vibrio phage V09	GCA_012361135.1
QHJ74196.1	001052	Cluster475_1clades	139	VH12019_00277	Vibrio phage VH1_2019	GCA_009931825.1
AGB07020.1	001052	Cluster475_1clades	138	CF80_gp233	Vibrio phage VH7D	GCA_000914495.1
QBX06076.1	001052	Cluster475_1clades	138	ValB1HC_122	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04497.1	001052	Cluster475_1clades	137	ValB1MD_144	Vibrio phage ValB1MD	GCA_004138815.1
AJT61090.1	001052	Cluster475_1clades	138	AVU32_gp249	Vibrio phage ValKK3	GCA_001501635.1
AGN30063.1	001052	Cluster475_1clades	140	VPFG_00060	Vibrio phage nt-1	GCA_000910195.2
ALP47142.1	001052	Cluster475_1clades	138	phiGrn1_0128	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47529.1	001052	Cluster475_1clades	138	phiST2_0258	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54702.1	001052	Cluster475_1clades	138	vBValMR10Z_161	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37247.1	001052	Cluster475_1clades	139	pp2_013	Vibriophage phi-pp2	GCA_002630725.1
ARB13540.1	001053	Cluster476_1clades	139	Ccr10_gp012	Caulobacter phage Ccr10	GCA_002619445.1
ARB13865.1	001053	Cluster476_1clades	139	Ccr10_gp335	Caulobacter phage Ccr10	GCA_002619445.1
ARB13887.1	001053	Cluster476_1clades	139	Ccr2_gp012	Caulobacter phage Ccr2	GCA_002619465.1
ARB14210.1	001053	Cluster476_1clades	139	Ccr2_gp334	Caulobacter phage Ccr2	GCA_002619465.1
ARB14569.1	001053	Cluster476_1clades	139	Ccr29_gp012	Caulobacter phage Ccr29	GCA_002619485.1
ARB14904.1	001053	Cluster476_1clades	139	Ccr29_gp348	Caulobacter phage Ccr29	GCA_002619485.1
ARB14930.1	001053	Cluster476_1clades	139	Ccr32_gp011	Caulobacter phage Ccr32	GCA_002619505.1
ARB15241.1	001053	Cluster476_1clades	139	Ccr32_gp323	Caulobacter phage Ccr32	GCA_002619505.1
ARB15261.1	001053	Cluster476_1clades	139	Ccr34_gp012	Caulobacter phage Ccr34	GCA_002619525.1
ARB15575.1	001053	Cluster476_1clades	139	Ccr34_gp333	Caulobacter phage Ccr34	GCA_002619525.1
ARB14229.1	001053	Cluster476_1clades	140	Ccr5_gp011	Caulobacter phage Ccr5	GCA_002619545.1
ARB14549.1	001053	Cluster476_1clades	140	Ccr5_gp329	Caulobacter phage Ccr5	GCA_002619545.1
AFU87528.1	001053	Cluster476_1clades	139	CcrKarma_gp011	Caulobacter virus Karma	GCA_000901575.1
AFU87861.1	001053	Cluster476_1clades	139	CcrKarma_gp344	Caulobacter virus Karma	GCA_000901575.1
AFU87181.1	001053	Cluster476_1clades	139	CcrMagneto_gp011	Caulobacter virus Magneto	GCA_000903095.1
AFU87509.1	001053	Cluster476_1clades	139	CcrMagneto_gp339	Caulobacter virus Magneto	GCA_000903095.1
AFU86843.1	001053	Cluster476_1clades	139	CbK_gp011	Caulobacter virus phiCbK	GCA_000900535.1
AFU87161.1	001053	Cluster476_1clades	139	CbK_gp329	Caulobacter virus phiCbK	GCA_000900535.1
AIT14158.1	001054	Cluster477_1clades	88	PBI_121Q_268	Escherichia phage 121Q	GCA_000926855.1
AIT14194.1	001054	Cluster477_1clades	131	PBI_121Q_304	Escherichia phage 121Q	GCA_000926855.1
QAY00745.1	001054	Cluster477_1clades	131	Ecwhy1_470	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00777.1	001054	Cluster477_1clades	88	Ecwhy1_504	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34923.1	001054	Cluster477_1clades	131	ACQ29_gp243	Escherichia phage PBECO4	GCA_001041035.1
AGC34956.1	001054	Cluster477_1clades	88	ACQ29_gp276	Escherichia phage PBECO4	GCA_001041035.1
BBM61832.1	001054	Cluster477_1clades	88	EO157G_2430	Escherichia phage SP27	GCA_008033345.1
BBM61868.1	001054	Cluster477_1clades	131	EO157G_2790	Escherichia phage SP27	GCA_008033345.1
AXC37027.1	001054	Cluster477_1clades	131	-	Escherichia phage UB	GCA_003341455.1
QBO61512.1	001054	Cluster477_1clades	131	G17_00016	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61547.1	001054	Cluster477_1clades	88	G17_00051	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62118.1	001054	Cluster477_1clades	131	G17_00629	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62153.1	001054	Cluster477_1clades	88	G17_00664	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14127.1	001054	Cluster477_1clades	131	vBEcoMphAPEC6_gp504c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14160.1	001054	Cluster477_1clades	88	vBEcoMphAPEC6_gp537c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80147.1	001054	Cluster477_1clades	88	PSLUR01_00170	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80177.1	001054	Cluster477_1clades	131	PSLUR01_00200	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44626.1	001054	Cluster477_1clades	118	RaK2_00353	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ARB13539.1	001055	Cluster478_1clades	102	Ccr10_gp011	Caulobacter phage Ccr10	GCA_002619445.1
ARB13864.1	001055	Cluster478_1clades	102	Ccr10_gp334	Caulobacter phage Ccr10	GCA_002619445.1
ARB13886.1	001055	Cluster478_1clades	100	Ccr2_gp011	Caulobacter phage Ccr2	GCA_002619465.1
ARB14209.1	001055	Cluster478_1clades	100	Ccr2_gp333	Caulobacter phage Ccr2	GCA_002619465.1
ARB14568.1	001055	Cluster478_1clades	102	Ccr29_gp011	Caulobacter phage Ccr29	GCA_002619485.1
ARB14903.1	001055	Cluster478_1clades	102	Ccr29_gp347	Caulobacter phage Ccr29	GCA_002619485.1
ARB14929.1	001055	Cluster478_1clades	122	Ccr32_gp010	Caulobacter phage Ccr32	GCA_002619505.1
ARB15240.1	001055	Cluster478_1clades	122	Ccr32_gp322	Caulobacter phage Ccr32	GCA_002619505.1
ARB15260.1	001055	Cluster478_1clades	122	Ccr34_gp011	Caulobacter phage Ccr34	GCA_002619525.1
ARB15574.1	001055	Cluster478_1clades	122	Ccr34_gp332	Caulobacter phage Ccr34	GCA_002619525.1
ARB14228.1	001055	Cluster478_1clades	103	Ccr5_gp010	Caulobacter phage Ccr5	GCA_002619545.1
ARB14548.1	001055	Cluster478_1clades	103	Ccr5_gp328	Caulobacter phage Ccr5	GCA_002619545.1
AFU87527.1	001055	Cluster478_1clades	103	CcrKarma_gp010	Caulobacter virus Karma	GCA_000901575.1
AFU87860.1	001055	Cluster478_1clades	103	CcrKarma_gp343	Caulobacter virus Karma	GCA_000901575.1
AFU87180.1	001055	Cluster478_1clades	102	CcrMagneto_gp010	Caulobacter virus Magneto	GCA_000903095.1
AFU87508.1	001055	Cluster478_1clades	102	CcrMagneto_gp338	Caulobacter virus Magneto	GCA_000903095.1
AFU86842.1	001055	Cluster478_1clades	122	CbK_gp010	Caulobacter virus phiCbK	GCA_000900535.1
AFU87160.1	001055	Cluster478_1clades	122	CbK_gp328	Caulobacter virus phiCbK	GCA_000900535.1
AFO71322.1	001056	CyaA	88	CR5_102	Cronobacter phage CR5	GCA_000910235.1
AMR59759.1	001056	CyaA	92	SEGD1_112	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07531.1	001056	CyaA	88	DERBICUS_105	Erwinia phage Derbicus	GCA_004521655.1
ANZ49758.1	001056	CyaA	98	MACHINA_120	Erwinia phage Machina	GCA_002758035.1
AXF51266.1	001056	CyaA	92	WELLINGTON_136	Erwinia phage Wellington	GCA_003344985.1
AFQ96576.1	001056	CyaA	94	G173_gp031	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48137.1	001056	CyaA	96	ASESINO_124	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48415.1	001056	CyaA	90	CAITLIN_120	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48687.1	001056	CyaA	90	CHRISDB_125	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48954.1	001056	CyaA	88	EARLPHILLIPIV_105	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49202.1	001056	CyaA	98	HUXLEY_120	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49487.1	001056	CyaA	92	KWAN_135	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50030.1	001056	CyaA	98	PARSHIK_121	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50295.1	001056	CyaA	121	PHOBOS_105	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50551.1	001056	CyaA	94	STRATTON_126	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85949.1	001056	CyaA	92	ACEC001_1110	Escherichia phage vB_EcoM_EC001	GCA_014131305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AWN09001.1	001056	CyaA	92	MLDJOKPK_00049	Salmonella phage SPAsTU	GCA_003183805.1
AEP83941.1	001056	CyaA	92	SPN3US_0108	Salmonella phage SPN3US	GCA_001042275.1
APU01466.1	001057	RyR	93	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28950.1	001057	RyR	114	AP1_0243	Aeromonas phage AP1	GCA_014183365.1
ATI17431.1	001057	RyR	114	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00164.1	001057	RyR	114	HWB28_gp388	Aeromonas phage AS-zj	GCA_002627665.1
AUE22765.1	001057	RyR	113	Ah1_00247	Aeromonas phage Ah1	GCA_002957415.1
QAX98480.1	001057	RyR	113	ASfcp2_142	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97871.1	001057	RyR	114	ASswx1_228	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01278.1	001057	RyR	114	ASwh1_215	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39421.1	001057	RyR	114	CC2_306	Aeromonas phage CC2	GCA_000903495.1
ADQ52942.1	001057	RyR	113	PX29p223	Aeromonas phage PX29	GCA_000920195.1
ADM79864.1	001057	RyR	112	phiAS5_ORF0021	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53088.1	001057	RyR	93	65p078	Aeromonas virus 65	GCA_000893255.1
AAQ17888.1	001057	RyR	113	Aeh1ORF227c	Aeromonas virus Aeh1	GCA_000843245.1
AGX01925.1	001057	RyR	116	CF95_gp203	Erwinia phage PhiEaH1	GCA_000914555.1
BAW19019.1	001057	RyR	116	FDH28_gp045	Ralstonia phage RP12	GCA_002617345.1
BAW19305.1	001057	RyR	116	-	Ralstonia phage RP31	GCA_002617365.1
QFP93230.1	001057	RyR	118	-	Serratia phage PCH45	GCA_009187865.1
ALY07006.1	001057	RyR	116	VmeM32_00012	Vibrio phage vB_VmeM-32	GCA_002608825.1
APU01544.1	001058	Cluster481_1clades	98	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29048.1	001058	Cluster481_1clades	98	AP1_0341	Aeromonas phage AP1	GCA_014183365.1
ATI17366.1	001058	Cluster481_1clades	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00228.1	001058	Cluster481_1clades	99	HWB28_gp324	Aeromonas phage AS-zj	GCA_002627665.1
AUE22808.1	001058	Cluster481_1clades	96	Ah1_00290	Aeromonas phage Ah1	GCA_002957415.1
QAX98523.1	001058	Cluster481_1clades	97	ASfcp2_187	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97807.1	001058	Cluster481_1clades	99	ASswx1_163	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01354.1	001058	Cluster481_1clades	100	ASwh1_294	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39438.1	001058	Cluster481_1clades	89	CC2_373	Aeromonas phage CC2	GCA_000903495.1
ADQ52986.1	001058	Cluster481_1clades	97	PX29p267	Aeromonas phage PX29	GCA_000920195.1
ADM79910.1	001058	Cluster481_1clades	105	phiAS5_ORF0067	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53166.1	001058	Cluster481_1clades	98	65p158	Aeromonas virus 65	GCA_000893255.1
AAQ17936.1	001058	Cluster481_1clades	96	pseT.2	Aeromonas virus Aeh1	GCA_000843245.1
ANS06086.1	001058	Cluster481_1clades	108	ABCD_0069	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97082.1	001058	Cluster481_1clades	106	E_073	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70780.1	001058	Cluster481_1clades	96	phiC120_c74	Escherichia phage phiC120	GCA_002621185.1
AAX78592.1	001058	Cluster481_1clades	108	RB43ORF070w	Escherichia virus RB43	GCA_000863505.1
ALY07148.1	001058	Cluster481_1clades	102	VmeM32_00162	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFO71308.1	001059	Cluster482_1clades	90	CR5_088	Cronobacter phage CR5	GCA_000910235.1
AMR59746.1	001059	Cluster482_1clades	61	SEGD1_097	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07517.1	001059	Cluster482_1clades	101	DERBICUS_91	Erwinia phage Derbicus	GCA_004521655.1
ANZ49742.1	001059	Cluster482_1clades	90	MACHINA_104	Erwinia phage Machina	GCA_002758035.1
AXF51243.1	001059	Cluster482_1clades	87	WELLINGTON_113	Erwinia phage Wellington	GCA_003344985.1
AFQ96562.1	001059	Cluster482_1clades	65	G173_gp017	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48122.1	001059	Cluster482_1clades	88	ASESINO_109	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48396.1	001059	Cluster482_1clades	89	CAITLIN_101	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48668.1	001059	Cluster482_1clades	89	CHRISDB_106	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48940.1	001059	Cluster482_1clades	90	EARLPHILLIPIV_91	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49187.1	001059	Cluster482_1clades	90	HUXLEY_105	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49464.1	001059	Cluster482_1clades	87	KWAN_112	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50015.1	001059	Cluster482_1clades	90	PARSHIK_106	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50281.1	001059	Cluster482_1clades	89	PHOBOS_91	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50536.1	001059	Cluster482_1clades	88	STRATTON_111	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85933.1	001059	Cluster482_1clades	90	ACEC001_0950	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51080.1	001059	Cluster482_1clades	88	MLDJOKPK_00066	Salmonella phage SPAsTU	GCA_003183805.1
AEP83926.1	001059	Cluster482_1clades	90	SPN3US_0093	Salmonella phage SPN3US	GCA_001042275.1
ARB13538.1	001060	Cluster483_1clades	99	Ccr10_gp010	Caulobacter phage Ccr10	GCA_002619445.1
ARB13863.1	001060	Cluster483_1clades	99	Ccr10_gp333	Caulobacter phage Ccr10	GCA_002619445.1
ARB13885.1	001060	Cluster483_1clades	99	Ccr2_gp010	Caulobacter phage Ccr2	GCA_002619465.1
ARB14208.1	001060	Cluster483_1clades	99	Ccr2_gp332	Caulobacter phage Ccr2	GCA_002619465.1
ARB14567.1	001060	Cluster483_1clades	99	Ccr29_gp010	Caulobacter phage Ccr29	GCA_002619485.1
ARB14902.1	001060	Cluster483_1clades	99	Ccr29_gp346	Caulobacter phage Ccr29	GCA_002619485.1
ARB14928.1	001060	Cluster483_1clades	99	Ccr32_gp009	Caulobacter phage Ccr32	GCA_002619505.1
ARB15239.1	001060	Cluster483_1clades	99	Ccr32_gp321	Caulobacter phage Ccr32	GCA_002619505.1
ARB15259.1	001060	Cluster483_1clades	99	Ccr34_gp010	Caulobacter phage Ccr34	GCA_002619525.1
ARB15573.1	001060	Cluster483_1clades	99	Ccr34_gp331	Caulobacter phage Ccr34	GCA_002619525.1
ARB14227.1	001060	Cluster483_1clades	60	Ccr5_gp009	Caulobacter phage Ccr5	GCA_002619545.1
ARB14547.1	001060	Cluster483_1clades	60	Ccr5_gp327	Caulobacter phage Ccr5	GCA_002619545.1
AFU87526.1	001060	Cluster483_1clades	99	CcrKarma_gp009	Caulobacter virus Karma	GCA_000901575.1
AFU87859.1	001060	Cluster483_1clades	99	CcrKarma_gp342	Caulobacter virus Karma	GCA_000901575.1
AFU87179.1	001060	Cluster483_1clades	99	CcrMagneto_gp009	Caulobacter virus Magneto	GCA_000903095.1
AFU87507.1	001060	Cluster483_1clades	99	CcrMagneto_gp337	Caulobacter virus Magneto	GCA_000903095.1
AFU86841.1	001060	Cluster483_1clades	99	CbK_gp009	Caulobacter virus phiCbK	GCA_000900535.1
AFU87159.1	001060	Cluster483_1clades	99	CbK_gp327	Caulobacter virus phiCbK	GCA_000900535.1
AJK27462.1	001061	Cluster484_1clades	95	PTIM40_35	Cyanophage P-TIM40	GCA_001470935.1
AMO43035.1	001061	Cluster484_1clades	70	R1080702_021	Cyanophage S-RIM32	GCA_001754165.1
AMO43276.1	001061	Cluster484_1clades	90	W270710_031	Cyanophage S-RIM44	GCA_002599145.1
AOO11510.1	001061	Cluster484_1clades	90	ES420910_028	Cyanophage S-RIM44	GCA_002599165.1
AOO11748.1	001061	Cluster484_1clades	90	Np050604_031	Cyanophage S-RIM44	GCA_002599185.1
AOO11975.1	001061	Cluster484_1clades	90	Np200711_028	Cyanophage S-RIM44	GCA_002599205.1
AOO12211.1	001061	Cluster484_1clades	90	Np420711_028	Cyanophage S-RIM44	GCA_002599225.1
AOO12449.1	001061	Cluster484_1clades	90	Sn080709_031	Cyanophage S-RIM44	GCA_002599245.1
AOO12676.1	001061	Cluster484_1clades	90	Sn130910_028	Cyanophage S-RIM44	GCA_002599265.1
AOO12914.1	001061	Cluster484_1clades	90	W2100709_031	Cyanophage S-RIM44	GCA_002599285.1
ADO99129.1	001061	Cluster484_1clades	90	Syn1_027	Prochlorococcus phage Syn1	GCA_000892495.1
QGT54647.1	001061	Cluster484_1clades	98	b23_0019	Synechococcus phage B23	GCA_009745195.1
QGT54277.1	001061	Cluster484_1clades	98	b3_0019	Synechococcus phage B3	GCA_009745215.1
ASR76070.1	001061	Cluster484_1clades	90	PBI_BELLAMY_24	Synechococcus phage Bellamy	GCA_002627525.1
AOV59487.1	001061	Cluster484_1clades	93	S330809_026	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59249.1	001061	Cluster484_1clades	93	C440309_026	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59725.1	001061	Cluster484_1clades	93	N231010_026	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70038.1	001061	Cluster484_1clades	69	SynMITS9220M01_024	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFO71430.1	001062	Cluster485_1clades	96	CR5_210	Cronobacter phage CR5	GCA_000910235.1
AMR59894.1	001062	Cluster485_1clades	97	SEGD1_247	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07643.1	001062	Cluster485_1clades	96	DERBICUS_217	Erwinia phage Derbicus	GCA_004521655.1
ANZ49893.1	001062	Cluster485_1clades	97	MACHINA_255	Erwinia phage Machina	GCA_002758035.1
AXF51394.1	001062	Cluster485_1clades	97	WELLINGTON_268	Erwinia phage Wellington	GCA_003344985.1
AFQ96707.1	001062	Cluster485_1clades	97	G173_gp162	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48277.1	001062	Cluster485_1clades	97	ASESINO_264	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48549.1	001062	Cluster485_1clades	97	CAITLIN_254	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48827.1	001062	Cluster485_1clades	97	CHRISDB_265	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49067.1	001062	Cluster485_1clades	96	EARLPHILLIPIV_218	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49336.1	001062	Cluster485_1clades	97	HUXLEY_254	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49620.1	001062	Cluster485_1clades	97	KWAN_268	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50164.1	001062	Cluster485_1clades	97	PARSHIK_255	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50414.1	001062	Cluster485_1clades	94	PHOBOS_224	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50689.1	001062	Cluster485_1clades	97	STRATTON_264	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86083.1	001062	Cluster485_1clades	97	ACEC001_2400	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09110.1	001062	Cluster485_1clades	97	MLDJOKPK_00198	Salmonella phage SPAsTU	GCA_003183805.1
AEP84075.1	001062	Cluster485_1clades	97	SPN3US_0242	Salmonella phage SPN3US	GCA_001042275.1
AFC21485.1	001063	Cluster486_1clades	80	GAP32_037	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14187.1	001063	Cluster486_1clades	70	PBI_121Q_297	Escherichia phage 121Q	GCA_000926855.1
QAY00750.1	001063	Cluster486_1clades	70	Ecwhy1_476	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34930.1	001063	Cluster486_1clades	70	ACQ29_gp250	Escherichia phage PBECO4	GCA_001041035.1
BBM61862.1	001063	Cluster486_1clades	70	EO157G_2730	Escherichia phage SP27	GCA_008033345.1
AXC37033.1	001063	Cluster486_1clades	70	-	Escherichia phage UB	GCA_003341455.1
QBO61519.1	001063	Cluster486_1clades	70	G17_00023	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62125.1	001063	Cluster486_1clades	70	G17_00636	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14133.1	001063	Cluster486_1clades	70	vBEcoMphAPEC6_gp510c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80171.1	001063	Cluster486_1clades	70	PSLUR01_00194	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43609.1	001063	Cluster486_1clades	80	CBB_44	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44160.1	001063	Cluster486_1clades	80	CBB_597	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18718.1	001063	Cluster486_1clades	81	7t3_0197	Salmonella phage 7t3	GCA_006083215.1
AZU97991.1	001063	Cluster486_1clades	81	CPT_Munch_047	Salmonella phage Munch	GCA_004015485.1
QIG62988.1	001063	Cluster486_1clades	81	SEPL_375	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQW88560.1	001063	Cluster486_1clades	96	BF_0035	Serratia phage BF	GCA_002619745.1
SOK58835.1	001063	Cluster486_1clades	79	g027	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58295.1	001063	Cluster486_1clades	79	g018	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOO14215.1	001064	Cluster487_1clades	70	Sn110110_021	Cyanophage S-RIM14	GCA_002599065.1
AOO14867.1	001064	Cluster487_1clades	70	W1230910_021	Cyanophage S-RIM14	GCA_002599125.1
AMO43205.1	001064	Cluster487_1clades	65	R1080702_196	Cyanophage S-RIM32	GCA_001754165.1
AMO43435.1	001064	Cluster487_1clades	64	W270710_191	Cyanophage S-RIM44	GCA_002599145.1
AOO11679.1	001064	Cluster487_1clades	64	ES420910_198	Cyanophage S-RIM44	GCA_002599165.1
AOO11907.1	001064	Cluster487_1clades	64	Np050604_191	Cyanophage S-RIM44	GCA_002599185.1
AOO12145.1	001064	Cluster487_1clades	64	Np200711_199	Cyanophage S-RIM44	GCA_002599205.1
AOO12380.1	001064	Cluster487_1clades	64	Np420711_198	Cyanophage S-RIM44	GCA_002599225.1
AOO12608.1	001064	Cluster487_1clades	64	Sn080709_191	Cyanophage S-RIM44	GCA_002599245.1
AOO12845.1	001064	Cluster487_1clades	64	Sn130910_198	Cyanophage S-RIM44	GCA_002599265.1
AOO13074.1	001064	Cluster487_1clades	64	W2100709_192	Cyanophage S-RIM44	GCA_002599285.1
ADO99294.1	001064	Cluster487_1clades	64	Syn1_193	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30524.1	001064	Cluster487_1clades	66	Syn7803US37_47	Synechococcus phage ACG-2014f	GCA_002594065.1
QDH50610.1	001064	Cluster487_1clades	72	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59528.1	001064	Cluster487_1clades	95	S330809_067	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59290.1	001064	Cluster487_1clades	95	C440309_067	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59766.1	001064	Cluster487_1clades	95	N231010_067	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70525.1	001064	Cluster487_1clades	61	HOU04_gp126	Synechococcus phage S-T4	GCA_003443335.1
AOO14267.1	001065	Cluster488_1clades	94	Sn110110_073	Cyanophage S-RIM14	GCA_002599065.1
AOO14916.1	001065	Cluster488_1clades	94	W1230910_070	Cyanophage S-RIM14	GCA_002599125.1
AMO43100.1	001065	Cluster488_1clades	90	R1080702_091	Cyanophage S-RIM32	GCA_001754165.1
AMO43329.1	001065	Cluster488_1clades	73	W270710_085	Cyanophage S-RIM44	GCA_002599145.1
AOO11562.1	001065	Cluster488_1clades	73	ES420910_081	Cyanophage S-RIM44	GCA_002599165.1
AOO11801.1	001065	Cluster488_1clades	73	Np050604_085	Cyanophage S-RIM44	GCA_002599185.1
AOO12027.1	001065	Cluster488_1clades	73	Np200711_081	Cyanophage S-RIM44	GCA_002599205.1
AOO12263.1	001065	Cluster488_1clades	73	Np420711_081	Cyanophage S-RIM44	GCA_002599225.1
AOO12502.1	001065	Cluster488_1clades	73	Sn080709_085	Cyanophage S-RIM44	GCA_002599245.1
AOO12728.1	001065	Cluster488_1clades	73	Sn130910_081	Cyanophage S-RIM44	GCA_002599265.1
AOO12968.1	001065	Cluster488_1clades	73	W2100709_086	Cyanophage S-RIM44	GCA_002599285.1
ADO99185.1	001065	Cluster488_1clades	73	Syn1_084	Prochlorococcus phage Syn1	GCA_000892495.1
QCW22846.1	001065	Cluster488_1clades	83	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50600.1	001065	Cluster488_1clades	81	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50704.1	001065	Cluster488_1clades	83	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59539.1	001065	Cluster488_1clades	90	S330809_078	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59301.1	001065	Cluster488_1clades	90	C440309_078	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59777.1	001065	Cluster488_1clades	89	N231010_078	Synechococcus phage S-CAM4	GCA_002922155.1
AIT14223.1	001066	Cluster489_1clades	78	PBI_121Q_333	Escherichia phage 121Q	GCA_000926855.1
AIT14224.1	001066	Cluster489_1clades	77	PBI_121Q_334	Escherichia phage 121Q	GCA_000926855.1
QAY00712.1	001066	Cluster489_1clades	85	Ecwhy1_437	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00713.1	001066	Cluster489_1clades	76	Ecwhy1_438	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00714.1	001066	Cluster489_1clades	78	Ecwhy1_439	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34899.1	001066	Cluster489_1clades	83	ACQ29_gp219	Escherichia phage PBECO4	GCA_001041035.1
BBM61898.1	001066	Cluster489_1clades	84	EO157G_3090	Escherichia phage SP27	GCA_008033345.1
BBM61899.1	001066	Cluster489_1clades	83	EO157G_3100	Escherichia phage SP27	GCA_008033345.1
AXC37006.1	001066	Cluster489_1clades	78	-	Escherichia phage UB	GCA_003341455.1
AXC37005.1	001066	Cluster489_1clades	84	-	Escherichia phage UB	GCA_003341455.1
QBO62082.1	001066	Cluster489_1clades	83	G17_00593	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62083.1	001066	Cluster489_1clades	84	G17_00594	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62084.1	001066	Cluster489_1clades	76	G17_00595	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14096.1	001066	Cluster489_1clades	84	vBEcoMphAPEC6_gp473c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14097.1	001066	Cluster489_1clades	76	vBEcoMphAPEC6_gp474c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80210.1	001066	Cluster489_1clades	76	PSLUR01_00233	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80211.1	001066	Cluster489_1clades	84	PSLUR01_00234	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80212.1	001066	Cluster489_1clades	83	PSLUR01_00235	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMO43161.1	001067	Cluster490_1clades	64	R1080702_152	Cyanophage S-RIM32	GCA_001754165.1
AMO43385.1	001067	Cluster490_1clades	64	W270710_141	Cyanophage S-RIM44	GCA_002599145.1
AOO11630.1	001067	Cluster490_1clades	65	ES420910_149	Cyanophage S-RIM44	GCA_002599165.1
AOO11857.1	001067	Cluster490_1clades	64	Np050604_141	Cyanophage S-RIM44	GCA_002599185.1
AOO12095.1	001067	Cluster490_1clades	65	Np200711_149	Cyanophage S-RIM44	GCA_002599205.1
AOO12331.1	001067	Cluster490_1clades	65	Np420711_149	Cyanophage S-RIM44	GCA_002599225.1
AOO12558.1	001067	Cluster490_1clades	64	Sn080709_141	Cyanophage S-RIM44	GCA_002599245.1
AOO12796.1	001067	Cluster490_1clades	65	Sn130910_149	Cyanophage S-RIM44	GCA_002599265.1
AOO13024.1	001067	Cluster490_1clades	64	W2100709_142	Cyanophage S-RIM44	GCA_002599285.1
AGH26299.1	001067	Cluster490_1clades	55	CPMG_00199	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44381.1	001067	Cluster490_1clades	68	PSSM2_003	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12266.1	001067	Cluster490_1clades	68	PRTG_00112	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93387.1	001067	Cluster490_1clades	67	AVU42_gp001	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99243.1	001067	Cluster490_1clades	64	Syn1_142	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30556.1	001067	Cluster490_1clades	63	Syn7803US37_79	Synechococcus phage ACG-2014f	GCA_002594065.1
AOV59501.1	001067	Cluster490_1clades	70	S330809_040	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59263.1	001067	Cluster490_1clades	70	C440309_040	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59739.1	001067	Cluster490_1clades	81	N231010_040	Synechococcus phage S-CAM4	GCA_002922155.1
AFO71383.1	001068	DUF1471	68	CR5_163	Cronobacter phage CR5	GCA_000910235.1
AMR59824.1	001068	DUF1471	66	SEGD1_177	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07594.1	001068	DUF1471	80	DERBICUS_168	Erwinia phage Derbicus	GCA_004521655.1
ANZ49821.1	001068	DUF1471	69	MACHINA_183	Erwinia phage Machina	GCA_002758035.1
AXF51318.1	001068	DUF1471	73	WELLINGTON_190	Erwinia phage Wellington	GCA_003344985.1
AFQ96639.1	001068	DUF1471	69	G173_gp094	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48205.1	001068	DUF1471	69	ASESINO_192	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48477.1	001068	DUF1471	69	CAITLIN_182	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48756.1	001068	DUF1471	69	CHRISDB_194	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49017.1	001068	DUF1471	68	EARLPHILLIPIV_168	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49265.1	001068	DUF1471	69	HUXLEY_183	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49543.1	001068	DUF1471	73	KWAN_191	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50093.1	001068	DUF1471	69	PARSHIK_184	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50364.1	001068	DUF1471	67	PHOBOS_174	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50616.1	001068	DUF1471	69	STRATTON_191	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86013.1	001068	DUF1471	69	ACEC001_1720	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51130.1	001068	DUF1471	69	MLDJOKPK_00269	Salmonella phage SPAsTU	GCA_003183805.1
AEP84005.1	001068	DUF1471	69	SPN3US_0172	Salmonella phage SPN3US	GCA_001042275.1
AUZ94981.1	001069	Cluster492_1clades	77	FDI40_gp199	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21696.1	001069	Cluster492_1clades	76	GAP32_246	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14489.1	001069	Cluster492_1clades	75	PBI_121Q_599	Escherichia phage 121Q	GCA_000926855.1
QAY00460.1	001069	Cluster492_1clades	75	Ecwhy1_180	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35202.1	001069	Cluster492_1clades	75	ACQ29_gp522	Escherichia phage PBECO4	GCA_001041035.1
BBM62161.1	001069	Cluster492_1clades	75	EO157G_5720	Escherichia phage SP27	GCA_008033345.1
AXC36774.1	001069	Cluster492_1clades	75	-	Escherichia phage UB	GCA_003341455.1
QBO61814.1	001069	Cluster492_1clades	75	G17_00325	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13858.1	001069	Cluster492_1clades	75	vBEcoMphAPEC6_gp229c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80473.1	001069	Cluster492_1clades	75	PSLUR01_00496	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44363.1	001069	Cluster492_1clades	76	RaK2_00090	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43818.1	001069	Cluster492_1clades	76	CBB_253	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18973.1	001069	Cluster492_1clades	78	7t3_0452	Salmonella phage 7t3	GCA_006083215.1
AZU98223.1	001069	Cluster492_1clades	78	CPT_Munch_279	Salmonella phage Munch	GCA_004015485.1
QIG62762.1	001069	Cluster492_1clades	78	SEPL_149	Salmonella phage SE_PL	GCA_011067555.1
AQW88776.1	001069	Cluster492_1clades	77	BF_0251	Serratia phage BF	GCA_002619745.1
SOK59057.1	001069	Cluster492_1clades	77	g249	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58523.1	001069	Cluster492_1clades	77	g246	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13532.1	001070	Cluster493_1clades	61	Ccr10_gp004	Caulobacter phage Ccr10	GCA_002619445.1
ARB13857.1	001070	Cluster493_1clades	61	Ccr10_gp327	Caulobacter phage Ccr10	GCA_002619445.1
ARB13878.1	001070	Cluster493_1clades	61	Ccr2_gp003	Caulobacter phage Ccr2	GCA_002619465.1
ARB14201.1	001070	Cluster493_1clades	61	Ccr2_gp325	Caulobacter phage Ccr2	GCA_002619465.1
ARB14561.1	001070	Cluster493_1clades	61	Ccr29_gp004	Caulobacter phage Ccr29	GCA_002619485.1
ARB14896.1	001070	Cluster493_1clades	61	Ccr29_gp340	Caulobacter phage Ccr29	GCA_002619485.1
ARB14923.1	001070	Cluster493_1clades	61	Ccr32_gp004	Caulobacter phage Ccr32	GCA_002619505.1
ARB15234.1	001070	Cluster493_1clades	61	Ccr32_gp316	Caulobacter phage Ccr32	GCA_002619505.1
ARB15254.1	001070	Cluster493_1clades	61	Ccr34_gp005	Caulobacter phage Ccr34	GCA_002619525.1
ARB15568.1	001070	Cluster493_1clades	61	Ccr34_gp326	Caulobacter phage Ccr34	GCA_002619525.1
ARB14221.1	001070	Cluster493_1clades	61	Ccr5_gp003	Caulobacter phage Ccr5	GCA_002619545.1
ARB14541.1	001070	Cluster493_1clades	61	Ccr5_gp321	Caulobacter phage Ccr5	GCA_002619545.1
AFU87521.1	001070	Cluster493_1clades	61	CcrKarma_gp004	Caulobacter virus Karma	GCA_000901575.1
AFU87854.1	001070	Cluster493_1clades	61	CcrKarma_gp337	Caulobacter virus Karma	GCA_000901575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU87174.1	001070	Cluster493_1clades	61	CcrMagneto_gp004	Caulobacter virus Magneto	GCA_000903095.1
AFU87502.1	001070	Cluster493_1clades	61	CcrMagneto_gp332	Caulobacter virus Magneto	GCA_000903095.1
AFU86836.1	001070	Cluster493_1clades	61	CbK_gp004	Caulobacter virus phiCbK	GCA_000900535.1
AFU87154.1	001070	Cluster493_1clades	61	CbK_gp322	Caulobacter virus phiCbK	GCA_000900535.1
AIT14015.1	001071	Cluster434_1clades	58	PBI_121Q_118	Escherichia phage 121Q	GCA_000926855.1
AIT14017.1	001071	Cluster434_1clades	60	PBI_121Q_121	Escherichia phage 121Q	GCA_000926855.1
QAY00324.1	001071	Cluster434_1clades	56	Ecwhy1_43	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00326.1	001071	Cluster434_1clades	60	Ecwhy1_45	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35071.1	001071	Cluster434_1clades	58	ACQ29_gp391	Escherichia phage PBECO4	GCA_001041035.1
AGC35072.1	001071	Cluster434_1clades	59	ACQ29_gp392	Escherichia phage PBECO4	GCA_001041035.1
BBM61703.1	001071	Cluster434_1clades	59	EO157G_1140	Escherichia phage SP27	GCA_008033345.1
BBM61704.1	001071	Cluster434_1clades	58	EO157G_1150	Escherichia phage SP27	GCA_008033345.1
AXC36649.1	001071	Cluster434_1clades	58	-	Escherichia phage UB	GCA_003341455.1
AXC36650.1	001071	Cluster434_1clades	59	-	Escherichia phage UB	GCA_003341455.1
QBO61679.1	001071	Cluster434_1clades	60	G17_00189	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61681.1	001071	Cluster434_1clades	58	G17_00192	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61682.1	001071	Cluster434_1clades	59	G17_00193	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13729.1	001071	Cluster434_1clades	58	vBEcoMphAPEC6_gp099c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13730.1	001071	Cluster434_1clades	59	vBEcoMphAPEC6_gp100c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80015.1	001071	Cluster434_1clades	59	PSLUR01_00031	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80016.1	001071	Cluster434_1clades	58	PSLUR01_00032	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80018.1	001071	Cluster434_1clades	60	PSLUR01_00035	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21771.1	001072	Cluster495_1clades	790	GAP32_321	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13951.1	001072	Cluster495_1clades	797	PBI_121Q_54	Escherichia phage 121Q	GCA_000926855.1
QAY00386.1	001072	Cluster495_1clades	798	Ecwhy1_105	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35131.1	001072	Cluster495_1clades	797	ACQ29_gp451	Escherichia phage PBECO4	GCA_001041035.1
BBM61643.1	001072	Cluster495_1clades	797	EO157G_0540	Escherichia phage SP27	GCA_008033345.1
AXC36705.1	001072	Cluster495_1clades	797	-	Escherichia phage UB	GCA_003341455.1
QBO61742.1	001072	Cluster495_1clades	797	G17_00253	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13787.1	001072	Cluster495_1clades	797	vBEcoMphAPEC6_gp158c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80545.1	001072	Cluster495_1clades	797	PSLUR01_00568	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44433.1	001072	Cluster495_1clades	775	RaK2_00160	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43889.1	001072	Cluster495_1clades	789	CBB_326	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19048.1	001072	Cluster495_1clades	794	7t3_0528	Salmonella phage 7t3	GCA_006083215.1
AZU98295.1	001072	Cluster495_1clades	794	CPT_Munch_351	Salmonella phage Munch	GCA_004015485.1
QIG62689.1	001072	Cluster495_1clades	794	SEPL_076	Salmonella phage SE_PL	GCA_011067555.1
AQW88849.1	001072	Cluster495_1clades	1009	BF_0324	Serratia phage BF	GCA_002619745.1
SOK59133.1	001072	Cluster495_1clades	786	g325	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58599.1	001072	Cluster495_1clades	786	g322	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21685.1	001073	RCR	795	GAP32_235	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14478.1	001073	RCR	749	PBI_121Q_588	Escherichia phage 121Q	GCA_000926855.1
QAY00470.1	001073	RCR	751	Ecwhy1_191	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35213.1	001073	RCR	749	ACQ29_gp533	Escherichia phage PBECO4	GCA_001041035.1
BBM62150.1	001073	RCR	749	EO157G_5610	Escherichia phage SP27	GCA_008033345.1
AXC36785.1	001073	RCR	749	-	Escherichia phage UB	GCA_003341455.1
QBO61825.1	001073	RCR	749	G17_00336	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13869.1	001073	RCR	749	vBEcoMphAPEC6_gp240	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80462.1	001073	RCR	749	PSLUR01_00485	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44352.1	001073	RCR	777	RaK2_00079	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43806.1	001073	RCR	795	CBB_241	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18958.1	001073	RCR	780	7t3_0437	Salmonella phage 7t3	GCA_006083215.1
AZU98211.1	001073	RCR	780	CPT_Munch_267	Salmonella phage Munch	GCA_004015485.1
QIG62773.1	001073	RCR	780	SEPL_160	Salmonella phage SE_PL	GCA_011067555.1
AQW88765.1	001073	RCR	790	BF_0240	Serratia phage BF	GCA_002619745.1
SOK59046.1	001073	RCR	789	g238c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58511.1	001073	RCR	789	g234c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21694.1	001074	Cluster497_1clades	720	GAP32_244	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14487.1	001074	Cluster497_1clades	734	PBI_121Q_597	Escherichia phage 121Q	GCA_000926855.1
QAY00462.1	001074	Cluster497_1clades	732	Ecwhy1_182	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35204.1	001074	Cluster497_1clades	734	ACQ29_gp524	Escherichia phage PBECO4	GCA_001041035.1
BBM62159.1	001074	Cluster497_1clades	734	EO157G_5700	Escherichia phage SP27	GCA_008033345.1
AXC36776.1	001074	Cluster497_1clades	734	-	Escherichia phage UB	GCA_003341455.1
QBO61816.1	001074	Cluster497_1clades	734	G17_00327	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13860.1	001074	Cluster497_1clades	734	vBEcoMphAPEC6_gp231c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80471.1	001074	Cluster497_1clades	734	PSLUR01_00494	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44361.1	001074	Cluster497_1clades	720	RaK2_00088	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43816.1	001074	Cluster497_1clades	722	CBB_251	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18971.1	001074	Cluster497_1clades	742	7t3_0450	Salmonella phage 7t3	GCA_006083215.1
AZU98221.1	001074	Cluster497_1clades	742	CPT_Munch_277	Salmonella phage Munch	GCA_004015485.1
QIG62764.1	001074	Cluster497_1clades	742	SEPL_151	Salmonella phage SE_PL	GCA_011067555.1
AQW88774.1	001074	Cluster497_1clades	716	BF_0249	Serratia phage BF	GCA_002619745.1
SOK59055.1	001074	Cluster497_1clades	715	g247	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58521.1	001074	Cluster497_1clades	715	g244	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70465.1	001075	Cluster499_1clades	667	CF8_0052	Aeromonas phage CF8	GCA_006384595.2
QDJ97204.1	001075	Cluster499_1clades	662	D6_0044	Aeromonas phage D6	GCA_007051205.2
QDH47031.1	001075	Cluster499_1clades	662	LAh10_211	Aeromonas phage LAh10	GCA_006863975.1
QDJ96807.1	001075	Cluster499_1clades	633	PS1_0048	Aeromonas phage PS1	GCA_007051165.2
QFR59438.1	001075	Cluster499_1clades	633	PS2_0047	Aeromonas phage PS2	GCA_009388305.2
QBZ70583.1	001075	Cluster499_1clades	636	pETSU_002	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03887.1	001075	Cluster499_1clades	661	JOAD_28	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03642.1	001075	Cluster499_1clades	661	RISINGSUN_28	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71899.1	001075	Cluster499_1clades	638	N1M2_36	Klebsiella phage N1M2	GCA_010092605.1
QGZ14367.1	001075	Cluster499_1clades	688	HWC77_gp004	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27117.1	001075	Cluster499_1clades	670	PPEV_gp023	Pseudomonas phage EL	GCA_000866825.1
AEV89494.1	001075	Cluster499_1clades	635	OBP_057	Pseudomonas phage OBP	GCA_000896635.1
QAU04369.1	001075	Cluster499_1clades	688	HWC03_gp214	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23206.1	001075	Cluster499_1clades	688	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80931.1	001075	Cluster499_1clades	688	Aphrodite1_0138	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47522.1	001075	Cluster499_1clades	688	HWC35_gp128	Vibrio phage USC-1	GCA_006864065.1
BAW98339.1	001075	Cluster499_1clades	653	FDH33_gp130	Vibrio phage pTD1	GCA_002618825.1
ARB13619.1	001076	Cluster500_1clades	610	Ccr10_gp090	Caulobacter phage Ccr10	GCA_002619445.1
ARB13964.1	001076	Cluster500_1clades	610	Ccr2_gp089	Caulobacter phage Ccr2	GCA_002619465.1
ARB14653.1	001076	Cluster500_1clades	610	Ccr29_gp096	Caulobacter phage Ccr29	GCA_002619485.1
ARB15008.1	001076	Cluster500_1clades	610	Ccr32_gp089	Caulobacter phage Ccr32	GCA_002619505.1
ARB15339.1	001076	Cluster500_1clades	610	Ccr34_gp096	Caulobacter phage Ccr34	GCA_002619525.1
ARB14308.1	001076	Cluster500_1clades	610	Ccr5_gp090	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68290.1	001076	Cluster500_1clades	610	CcrBL10_gp086	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69187.1	001076	Cluster500_1clades	610	CcrBL9_gp163	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87985.1	001076	Cluster500_1clades	611	CcrColossus_gp115	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68661.1	001076	Cluster500_1clades	611	CcrPW_gp122	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69740.1	001076	Cluster500_1clades	610	CcrSC_gp158	Caulobacter phage CcrSC	GCA_003443315.1
AFU87610.1	001076	Cluster500_1clades	610	CcrKarma_gp093	Caulobacter virus Karma	GCA_000901575.1
AFU87259.1	001076	Cluster500_1clades	610	CcrMagneto_gp089	Caulobacter virus Magneto	GCA_000903095.1
AFU86573.1	001076	Cluster500_1clades	610	CcrRogue_gp091	Caulobacter virus Rogue	GCA_000900555.1
AFU88406.1	001076	Cluster500_1clades	610	CcrSwift_gp088	Caulobacter virus Swift	GCA_000899655.1
AFU86924.1	001076	Cluster500_1clades	610	CbK_gp092	Caulobacter virus phiCbK	GCA_000900535.1
QIW90753.1	001076	Cluster500_1clades	316	GCAPEGMB_00434	Vibrio phage V07	GCA_012361095.1
QDB70252.1	001077	Cluster501_1clades	545	CF8_0084	Aeromonas phage CF8	GCA_006384595.2
QDJ97231.1	001077	Cluster501_1clades	531	D6_0071	Aeromonas phage D6	GCA_007051205.2
QDH47041.1	001077	Cluster501_1clades	531	LAh10_4	Aeromonas phage LAh10	GCA_006863975.1
QDJ96841.1	001077	Cluster501_1clades	544	PS1_0082	Aeromonas phage PS1	GCA_007051165.2
QFR59471.1	001077	Cluster501_1clades	544	PS2_0080	Aeromonas phage PS2	GCA_009388305.2
QBZ70614.1	001077	Cluster501_1clades	539	pETSU_033	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03862.1	001077	Cluster501_1clades	604	JOAD_53	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03617.1	001077	Cluster501_1clades	604	RISINGSUN_53	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71930.1	001077	Cluster501_1clades	537	N1M2_67	Klebsiella phage N1M2	GCA_010092605.1
QGZ14393.1	001077	Cluster501_1clades	538	HWC77_gp030	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27141.1	001077	Cluster501_1clades	574	PPEV_gp047	Pseudomonas phage EL	GCA_000866825.1
AEV89530.1	001077	Cluster501_1clades	539	OBP_093	Pseudomonas phage OBP	GCA_000896635.1
QAU04343.1	001077	Cluster501_1clades	538	HWC03_gp188	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23233.1	001077	Cluster501_1clades	540	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80937.1	001077	Cluster501_1clades	540	Aphrodite1_0112	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47495.1	001077	Cluster501_1clades	540	HWC35_gp101	Vibrio phage USC-1	GCA_006864065.1
BAW98315.1	001077	Cluster501_1clades	541	FDH33_gp106	Vibrio phage pTD1	GCA_002618825.1
QDB70477.1	001078	Cluster504_1clades	510	CF8_0066	Aeromonas phage CF8	GCA_006384595.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ97217.1	001078	Cluster504_1clades	507	D6_0057	Aeromonas phage D6	GCA_007051205.2
QDH47047.1	001078	Cluster504_1clades	507	LAh10_223	Aeromonas phage LAh10	GCA_006863975.1
QDJ96825.1	001078	Cluster504_1clades	512	PS1_0066	Aeromonas phage PS1	GCA_007051165.2
QFR59455.1	001078	Cluster504_1clades	512	PS2_0064	Aeromonas phage PS2	GCA_009388305.2
QBZ70595.1	001078	Cluster504_1clades	513	pETSU_014	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03875.1	001078	Cluster504_1clades	479	JOAD_40	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03630.1	001078	Cluster504_1clades	479	RISINGSUN_40	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71911.1	001078	Cluster504_1clades	514	N1M2_48	Klebsiella phage N1M2	GCA_010092605.1
QGZ14379.1	001078	Cluster504_1clades	493	HWC77_gp016	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27128.1	001078	Cluster504_1clades	478	PPEV_gp034	Pseudomonas phage EL	GCA_000866825.1
AEV89507.1	001078	Cluster504_1clades	514	OBP_070	Pseudomonas phage OBP	GCA_000896635.1
QAU04357.1	001078	Cluster504_1clades	493	HWC03_gp202	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23219.1	001078	Cluster504_1clades	493	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80947.1	001078	Cluster504_1clades	493	Aphrodite1_0126	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47509.1	001078	Cluster504_1clades	493	HWC35_gp115	Vibrio phage USC-1	GCA_006864065.1
BAW98328.1	001078	Cluster504_1clades	488	FDH33_gp119	Vibrio phage pTD1	GCA_002618825.1
QDB70478.1	001079	Cluster505_1clades	496	CF8_0067	Aeromonas phage CF8	GCA_006384595.2
QDJ97228.2	001079	Cluster505_1clades	504	D6_0058	Aeromonas phage D6	GCA_007051205.2
QDH47049.1	001079	Cluster505_1clades	504	LAh10_224	Aeromonas phage LAh10	GCA_006863975.1
QDJ96826.1	001079	Cluster505_1clades	507	PS1_0067	Aeromonas phage PS1	GCA_007051165.2
QFR59456.1	001079	Cluster505_1clades	507	PS2_0065	Aeromonas phage PS2	GCA_009388305.2
QBZ70596.1	001079	Cluster505_1clades	509	pETSU_015	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03874.1	001079	Cluster505_1clades	469	JOAD_41	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03629.1	001079	Cluster505_1clades	468	RISINGSUN_41	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71912.1	001079	Cluster505_1clades	490	N1M2_49	Klebsiella phage N1M2	GCA_010092605.1
QGZ14380.1	001079	Cluster505_1clades	471	HWC77_gp017	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27129.1	001079	Cluster505_1clades	478	PPEV_gp035	Pseudomonas phage EL	GCA_000866825.1
AEV89508.1	001079	Cluster505_1clades	503	OBP_071	Pseudomonas phage OBP	GCA_000896635.1
QAU04356.1	001079	Cluster505_1clades	471	HWC03_gp201	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23220.1	001079	Cluster505_1clades	471	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80952.1	001079	Cluster505_1clades	471	Aphrodite1_0125	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47508.1	001079	Cluster505_1clades	471	HWC35_gp114	Vibrio phage USC-1	GCA_006864065.1
BAW98327.1	001079	Cluster505_1clades	471	FDH33_gp118	Vibrio phage pTD1	GCA_002618825.1
AFC21656.1	001080	Cluster506_1clades	473	GAP32_206	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14449.1	001080	Cluster506_1clades	505	PBI_121Q_559	Escherichia phage 121Q	GCA_000926855.1
QAY00499.1	001080	Cluster506_1clades	503	Ecwhy1_220	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34694.1	001080	Cluster506_1clades	505	ACQ29_gp014	Escherichia phage PBECO4	GCA_001041035.1
BBM62122.1	001080	Cluster506_1clades	505	EO157G_5330	Escherichia phage SP27	GCA_008033345.1
AXC36814.1	001080	Cluster506_1clades	505	-	Escherichia phage UB	GCA_003341455.1
QBO61853.1	001080	Cluster506_1clades	505	G17_00364	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13893.1	001080	Cluster506_1clades	456	vBEcoMphAPEC6_gp268c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80434.1	001080	Cluster506_1clades	502	PSLUR01_00457	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44322.1	001080	Cluster506_1clades	315	RaK2_00049	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43777.1	001080	Cluster506_1clades	478	CBB_212	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18925.1	001080	Cluster506_1clades	328	7t3_0404	Salmonella phage 7t3	GCA_006083215.1
AZU98182.1	001080	Cluster506_1clades	328	CPT_Munch_238	Salmonella phage Munch	GCA_004015485.1
QIG62802.1	001080	Cluster506_1clades	328	SEPL_189	Salmonella phage SE_PL	GCA_011067555.1
AQW88733.1	001080	Cluster506_1clades	331	BF_0208	Serratia phage BF	GCA_002619745.1
SOK59016.1	001080	Cluster506_1clades	470	g208	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58481.1	001080	Cluster506_1clades	451	g204	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70269.1	001081	Cluster507_1clades	422	CF8_0101	Aeromonas phage CF8	GCA_006384595.2
QDJ97247.1	001081	Cluster507_1clades	422	D6_0087	Aeromonas phage D6	GCA_007051205.2
QDH47061.1	001081	Cluster507_1clades	426	LAh10_19	Aeromonas phage LAh10	GCA_006863975.1
QDJ96860.1	001081	Cluster507_1clades	421	PS1_0101	Aeromonas phage PS1	GCA_007051165.2
QFR59492.1	001081	Cluster507_1clades	421	PS2_0101	Aeromonas phage PS2	GCA_009388305.2
QBZ70630.1	001081	Cluster507_1clades	423	pETSU_049	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03849.1	001081	Cluster507_1clades	431	JOAD_66	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03604.1	001081	Cluster507_1clades	431	RISINGSUN_66	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71946.1	001081	Cluster507_1clades	427	N1M2_83	Klebsiella phage N1M2	GCA_010092605.1
QGZ14407.1	001081	Cluster507_1clades	423	HWC77_gp044	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27155.1	001081	Cluster507_1clades	431	PPEV_gp061	Pseudomonas phage EL	GCA_000866825.1
AEV89546.1	001081	Cluster507_1clades	421	OBP_109	Pseudomonas phage OBP	GCA_000896635.1
QAU04329.1	001081	Cluster507_1clades	423	HWC03_gp174	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23247.1	001081	Cluster507_1clades	421	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80963.1	001081	Cluster507_1clades	421	Aphrodite1_0098	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47481.1	001081	Cluster507_1clades	421	HWC35_gp087	Vibrio phage USC-1	GCA_006864065.1
BAW98301.1	001081	Cluster507_1clades	423	FDH33_gp092	Vibrio phage pTD1	GCA_002618825.1
AFC21675.1	001082	Cluster508_1clades	369	GAP32_225	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14467.1	001082	Cluster508_1clades	366	PBI_121Q_577	Escherichia phage 121Q	GCA_000926855.1
QAY00480.1	001082	Cluster508_1clades	366	Ecwhy1_201	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35223.1	001082	Cluster508_1clades	366	ACQ29_gp543	Escherichia phage PBECO4	GCA_001041035.1
BBM62140.1	001082	Cluster508_1clades	366	EO157G_5510	Escherichia phage SP27	GCA_008033345.1
AXC36795.1	001082	Cluster508_1clades	366	-	Escherichia phage UB	GCA_003341455.1
QBO61835.1	001082	Cluster508_1clades	366	G17_00346	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13879.1	001082	Cluster508_1clades	366	vBEcoMphAPEC6_gp250c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80452.1	001082	Cluster508_1clades	366	PSLUR01_00475	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44338.1	001082	Cluster508_1clades	410	RaK2_00065	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43796.1	001082	Cluster508_1clades	368	CBB_231	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18947.1	001082	Cluster508_1clades	367	7t3_0426	Salmonella phage 7t3	GCA_006083215.1
AZU98201.1	001082	Cluster508_1clades	367	CPT_Munch_257	Salmonella phage Munch	GCA_004015485.1
QIG62783.1	001082	Cluster508_1clades	367	SEPL_170	Salmonella phage SE_PL	GCA_011067555.1
AQW88755.1	001082	Cluster508_1clades	367	BF_0230	Serratia phage BF	GCA_002619745.1
SOK59035.1	001082	Cluster508_1clades	368	g227	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58500.1	001082	Cluster508_1clades	368	g223	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21784.1	001083	Cluster509_1clades	396	GAP32_334	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13962.1	001083	Cluster509_1clades	375	PBI_121Q_65	Escherichia phage 121Q	GCA_000926855.1
QAY00375.1	001083	Cluster509_1clades	375	Ecwhy1_94	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35120.1	001083	Cluster509_1clades	375	ACQ29_gp440	Escherichia phage PBECO4	GCA_001041035.1
BBM61654.1	001083	Cluster509_1clades	375	EO157G_0650	Escherichia phage SP27	GCA_008033345.1
AXC36694.1	001083	Cluster509_1clades	375	-	Escherichia phage UB	GCA_003341455.1
QBO61731.1	001083	Cluster509_1clades	379	G17_00242	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13776.1	001083	Cluster509_1clades	375	vBEcoMphAPEC6_gp147c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80556.1	001083	Cluster509_1clades	375	PSLUR01_00579	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44444.1	001083	Cluster509_1clades	371	RaK2_00171	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43902.1	001083	Cluster509_1clades	398	CBB_339	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19061.1	001083	Cluster509_1clades	377	7t3_0541	Salmonella phage 7t3	GCA_006083215.1
AZU98307.1	001083	Cluster509_1clades	377	CPT_Munch_363	Salmonella phage Munch	GCA_004015485.1
QIG62677.1	001083	Cluster509_1clades	377	SEPL_064	Salmonella phage SE_PL	GCA_011067555.1
AQW88862.1	001083	Cluster509_1clades	386	BF_0337	Serratia phage BF	GCA_002619745.1
SOK59146.1	001083	Cluster509_1clades	378	g338	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58612.1	001083	Cluster509_1clades	378	g335	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21672.1	001084	Cluster510_1clades	379	GAP32_222	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14464.1	001084	Cluster510_1clades	371	PBI_121Q_574	Escherichia phage 121Q	GCA_000926855.1
QAY00483.1	001084	Cluster510_1clades	375	Ecwhy1_204	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35226.1	001084	Cluster510_1clades	371	ACQ29_gp546	Escherichia phage PBECO4	GCA_001041035.1
BBM62137.1	001084	Cluster510_1clades	375	EO157G_5480	Escherichia phage SP27	GCA_008033345.1
AXC36798.1	001084	Cluster510_1clades	371	-	Escherichia phage UB	GCA_003341455.1
QBO61838.1	001084	Cluster510_1clades	371	G17_00349	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13882.1	001084	Cluster510_1clades	375	vBEcoMphAPEC6_gp253	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80449.1	001084	Cluster510_1clades	375	PSLUR01_00472	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44335.1	001084	Cluster510_1clades	371	RaK2_00062	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43793.1	001084	Cluster510_1clades	380	CBB_228	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18944.1	001084	Cluster510_1clades	371	7t3_0423	Salmonella phage 7t3	GCA_006083215.1
AZU98198.1	001084	Cluster510_1clades	371	CPT_Munch_254	Salmonella phage Munch	GCA_004015485.1
QIG62786.1	001084	Cluster510_1clades	371	SEPL_173	Salmonella phage SE_PL	GCA_011067555.1
AQW88752.1	001084	Cluster510_1clades	372	BF_0227	Serratia phage BF	GCA_002619745.1
SOK59032.1	001084	Cluster510_1clades	372	g224c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58497.1	001084	Cluster510_1clades	372	g220c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70464.1	001085	Cluster511_1clades	365	CF8_0051	Aeromonas phage CF8	GCA_006384595.2
QDJ97203.1	001085	Cluster511_1clades	366	D6_0043	Aeromonas phage D6	GCA_007051205.2
QDH47073.1	001085	Cluster511_1clades	366	LAh10_210	Aeromonas phage LAh10	GCA_006863975.1
QDJ96806.1	001085	Cluster511_1clades	359	PS1_0047	Aeromonas phage PS1	GCA_007051165.2
QFR59437.1	001085	Cluster511_1clades	359	PS2_0046	Aeromonas phage PS2	GCA_009388305.2
QBZ70582.1	001085	Cluster511_1clades	363	pETSU_001	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03888.1	001085	Cluster511_1clades	368	JOAD_27	Erwinia phage vB_EamM_Joad	GCA_002629065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU03643.1	001085	Cluster511_1clades	368	RISINGSUN_27	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71898.1	001085	Cluster511_1clades	363	N1M2_35	Klebsiella phage N1M2	GCA_010092605.1
QGZ14366.1	001085	Cluster511_1clades	367	HWC77_gp003	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27116.1	001085	Cluster511_1clades	366	PPEV_gp022	Pseudomonas phage EL	GCA_000866825.1
AEV89493.1	001085	Cluster511_1clades	365	OBP_056	Pseudomonas phage OBP	GCA_000896635.1
QAU04370.1	001085	Cluster511_1clades	367	HWC03_gp215	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23205.1	001085	Cluster511_1clades	368	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80977.1	001085	Cluster511_1clades	368	Aphrodite1_0139	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47523.1	001085	Cluster511_1clades	368	HWC35_gp129	Vibrio phage USC-1	GCA_006864065.1
BAW98340.1	001085	Cluster511_1clades	368	FDH33_gp131	Vibrio phage pTD1	GCA_002618825.1
AFO71305.1	001086	Cluster512_1clades	176	CR5_085	Cronobacter phage CR5	GCA_000910235.1
AMR59744.1	001086	Cluster512_1clades	205	SEGD1_095	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07514.1	001086	Cluster512_1clades	176	DERBICUS_88	Erwinia phage Derbicus	GCA_004521655.1
AXF51241.1	001086	Cluster512_1clades	361	WELLINGTON_111	Erwinia phage Wellington	GCA_003344985.1
AFQ96560.1	001086	Cluster512_1clades	177	G173_gp015	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48120.1	001086	Cluster512_1clades	205	ASESINO_107	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48937.1	001086	Cluster512_1clades	176	EARLPHILLIPIV_88	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49462.1	001086	Cluster512_1clades	361	KWAN_110	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50278.1	001086	Cluster512_1clades	176	PHOBOS_88	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50534.1	001086	Cluster512_1clades	205	STRATTON_109	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85931.1	001086	Cluster512_1clades	205	ACEC001_0930	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20801.1	001086	Cluster512_1clades	216	-	Salmonella phage JN03	GCA_014319805.1
AWN09012.1	001086	Cluster512_1clades	205	MLDJOKPK_00068	Salmonella phage SPAsTU	GCA_003183805.1
AEP83924.1	001086	Cluster512_1clades	205	SPN3US_0091	Salmonella phage SPN3US	GCA_001042275.1
AQT27970.1	001086	Cluster512_1clades	193	pVa21_028	Vibrio phage pVa-21	GCA_002619305.1
AQT27971.1	001086	Cluster512_1clades	174	pVa21_029	Vibrio phage pVa-21	GCA_002619305.1
AQT27988.1	001086	Cluster512_1clades	273	pVa21_046	Vibrio phage pVa-21	GCA_002619305.1
QDB70472.1	001087	Cluster513_1clades	277	CF8_0060	Aeromonas phage CF8	GCA_006384595.2
QDJ97212.1	001087	Cluster513_1clades	266	D6_0052	Aeromonas phage D6	GCA_007051205.2
QDH47098.1	001087	Cluster513_1clades	285	LAh10_218	Aeromonas phage LAh10	GCA_006863975.1
QDJ96819.1	001087	Cluster513_1clades	270	PS1_0060	Aeromonas phage PS1	GCA_007051165.2
QFR59448.1	001087	Cluster513_1clades	270	PS2_0057	Aeromonas phage PS2	GCA_009388305.2
QBZ70590.1	001087	Cluster513_1clades	269	pETSU_009	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03880.1	001087	Cluster513_1clades	268	JOAD_35	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03635.1	001087	Cluster513_1clades	268	RISINGSUN_35	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71906.1	001087	Cluster513_1clades	267	N1M2_43	Klebsiella phage N1M2	GCA_010092605.1
QGZ14374.1	001087	Cluster513_1clades	316	HWC77_gp011	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27123.1	001087	Cluster513_1clades	277	PPEV_gp029	Pseudomonas phage EL	GCA_000866825.1
AEV89501.1	001087	Cluster513_1clades	266	OBP_064	Pseudomonas phage OBP	GCA_000896635.1
QAU04362.1	001087	Cluster513_1clades	321	HWC03_gp207	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23214.1	001087	Cluster513_1clades	295	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80995.1	001087	Cluster513_1clades	295	Aphrodite1_0131	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47514.1	001087	Cluster513_1clades	295	HWC35_gp120	Vibrio phage USC-1	GCA_006864065.1
BAW98333.1	001087	Cluster513_1clades	327	FDH33_gp124	Vibrio phage pTD1	GCA_002618825.1
AFC21740.1	001088	Neisseria_TspB	315	GAP32_290	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13921.1	001088	Neisseria_TspB	314	PBI_121Q_24	Escherichia phage 121Q	GCA_000926855.1
QAY00417.1	001088	Neisseria_TspB	320	Ecwhy1_136	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35160.1	001088	Neisseria_TspB	314	ACQ29_gp480	Escherichia phage PBECO4	GCA_001041035.1
BBM61613.1	001088	Neisseria_TspB	314	EO157G_0240	Escherichia phage SP27	GCA_008033345.1
AXC36733.1	001088	Neisseria_TspB	314	-	Escherichia phage UB	GCA_003341455.1
QBO61771.1	001088	Neisseria_TspB	314	G17_00282	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13815.1	001088	Neisseria_TspB	314	vBEcoMphAPEC6_gp186c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80516.1	001088	Neisseria_TspB	314	PSLUR01_00539	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44405.1	001088	Neisseria_TspB	323	RaK2_00132	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43859.1	001088	Neisseria_TspB	314	CBB_295	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19018.1	001088	Neisseria_TspB	311	7t3_0498	Salmonella phage 7t3	GCA_006083215.1
AZU98265.1	001088	Neisseria_TspB	311	CPT_Munch_321	Salmonella phage Munch	GCA_004015485.1
QIG62719.1	001088	Neisseria_TspB	311	SEPL_106	Salmonella phage SE_PL	GCA_011067555.1
AQW88818.1	001088	Neisseria_TspB	304	BF_0293	Serratia phage BF	GCA_002619745.1
SOK59101.1	001088	Neisseria_TspB	304	g293	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58565.1	001088	Neisseria_TspB	304	g288	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01671.1	001089	DUF4646	285	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29018.1	001089	DUF4646	175	AP1_0311	Aeromonas phage AP1	GCA_014183365.1
ATI17624.1	001089	DUF4646	291	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00372.1	001089	DUF4646	291	HWB28_gp180	Aeromonas phage AS-zj	GCA_002627665.1
AUE22609.1	001089	DUF4646	186	Ah1_00068	Aeromonas phage Ah1	GCA_002957415.1
QAX97658.1	001089	DUF4646	291	ASswx1_12	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01083.1	001089	DUF4646	183	ASwh1_15	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39344.1	001089	DUF4646	304	CC2_102	Aeromonas phage CC2	GCA_000903495.1
ADQ52793.1	001089	DUF4646	203	PX29p074	Aeromonas phage PX29	GCA_000920195.1
ADM80049.1	001089	DUF4646	188	phiAS5_ORF0206	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53302.1	001089	DUF4646	109	65p294	Aeromonas virus 65	GCA_000893255.1
ADQ53303.1	001089	DUF4646	125	65p295	Aeromonas virus 65	GCA_000893255.1
AAQ17736.1	001089	DUF4646	186	Aeh1ORF076c	Aeromonas virus Aeh1	GCA_000843245.1
ANS05986.1	001089	DUF4646	263	ABCD_0190	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97204.1	001089	DUF4646	261	E_196	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78722.1	001089	DUF4646	202	RB43ORF200w	Escherichia virus RB43	GCA_000863505.1
ALY07138.1	001089	DUF4646	166	VmeM32_00152	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFC21514.1	001090	Cluster516_1clades	260	GAP32_066	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14305.1	001090	Cluster516_1clades	284	PBI_121Q_415	Escherichia phage 121Q	GCA_000926855.1
QAY00633.1	001090	Cluster516_1clades	282	Ecwhy1_358	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34830.1	001090	Cluster516_1clades	285	ACQ29_gp150	Escherichia phage PBECO4	GCA_001041035.1
BBM61979.1	001090	Cluster516_1clades	282	EO157G_3900	Escherichia phage SP27	GCA_008033345.1
AXC36938.1	001090	Cluster516_1clades	284	-	Escherichia phage UB	GCA_003341455.1
QBO61999.1	001090	Cluster516_1clades	284	G17_00510	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14020.1	001090	Cluster516_1clades	284	vBEcoMphAPEC6_gp396c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80292.1	001090	Cluster516_1clades	282	PSLUR01_00315	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44718.1	001090	Cluster516_1clades	286	RaK2_00445	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43635.1	001090	Cluster516_1clades	264	CBB_70	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18763.1	001090	Cluster516_1clades	287	7t3_0242	Salmonella phage 7t3	GCA_006083215.1
AZU98032.1	001090	Cluster516_1clades	287	CPT_Munch_088	Salmonella phage Munch	GCA_004015485.1
QIG62948.1	001090	Cluster516_1clades	287	SEPL_335	Salmonella phage SE_PL	GCA_011067555.1
AQW88586.1	001090	Cluster516_1clades	261	BF_0061	Serratia phage BF	GCA_002619745.1
SOK58861.1	001090	Cluster516_1clades	269	g053	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58323.1	001090	Cluster516_1clades	269	g046	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70382.1	001091	Cluster517_1clades	260	CF8_0213	Aeromonas phage CF8	GCA_006384595.2
QDJ97381.1	001091	Cluster517_1clades	255	D6_0222	Aeromonas phage D6	GCA_007051205.2
QDH47106.1	001091	Cluster517_1clades	255	LAh10_136	Aeromonas phage LAh10	GCA_006863975.1
QDJ96724.1	001091	Cluster517_1clades	257	PS1_0213	Aeromonas phage PS1	GCA_007051165.2
QFR59357.1	001091	Cluster517_1clades	257	PS2_0215	Aeromonas phage PS2	GCA_009388305.2
QBZ70767.1	001091	Cluster517_1clades	259	pETSU_186	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03696.1	001091	Cluster517_1clades	281	JOAD_219	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03453.1	001091	Cluster517_1clades	281	RISINGSUN_217	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72073.1	001091	Cluster517_1clades	259	N1M2_210	Klebsiella phage N1M2	GCA_010092605.1
QGZ14499.1	001091	Cluster517_1clades	269	HWC77_gp136	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27266.1	001091	Cluster517_1clades	275	PPEV_gp172	Pseudomonas phage EL	GCA_000866825.1
AEV89702.1	001091	Cluster517_1clades	258	OBP_265	Pseudomonas phage OBP	GCA_000896635.1
QAU04235.1	001091	Cluster517_1clades	269	HWC03_gp080	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23128.1	001091	Cluster517_1clades	269	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81001.1	001091	Cluster517_1clades	269	Aphrodite1_0003	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47599.1	001091	Cluster517_1clades	280	HWC35_gp205	Vibrio phage USC-1	GCA_006864065.1
BAW98414.1	001091	Cluster517_1clades	266	FDH33_gp205	Vibrio phage pTD1	GCA_002618825.1
AFC21781.1	001092	Cluster518_1clades	259	GAP32_331	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13961.1	001092	Cluster518_1clades	267	PBI_121Q_64	Escherichia phage 121Q	GCA_000926855.1
QAY00376.1	001092	Cluster518_1clades	272	Ecwhy1_95	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35121.1	001092	Cluster518_1clades	267	ACQ29_gp441	Escherichia phage PBECO4	GCA_001041035.1
BBM61653.1	001092	Cluster518_1clades	272	EO157G_0640	Escherichia phage SP27	GCA_008033345.1
AXC36695.1	001092	Cluster518_1clades	267	-	Escherichia phage UB	GCA_003341455.1
QBO61732.1	001092	Cluster518_1clades	267	G17_00243	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13777.1	001092	Cluster518_1clades	272	vBEcoMphAPEC6_gp148c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80555.1	001092	Cluster518_1clades	267	PSLUR01_00578	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44443.1	001092	Cluster518_1clades	271	RaK2_00170	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43899.1	001092	Cluster518_1clades	264	CBB_336	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19058.1	001092	Cluster518_1clades	265	7t3_0538	Salmonella phage 7t3	GCA_006083215.1
AZU98305.1	001092	Cluster518_1clades	265	CPT_Munch_361	Salmonella phage Munch	GCA_004015485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG62679.1	001092	Cluster518_1clades	265	SEPL_066	Salmonella phage SE_PL	GCA_011067555.1
AQW88859.1	001092	Cluster518_1clades	264	BF_0334	Serratia phage BF	GCA_002619745.1
SOK59143.1	001092	Cluster518_1clades	264	g335	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58609.1	001092	Cluster518_1clades	264	g332	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21742.1	001093	Cluster519_1clades	267	GAP32_292	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13923.1	001093	Cluster519_1clades	223	PBI_121Q_26	Escherichia phage 121Q	GCA_000926855.1
QAY00415.1	001093	Cluster519_1clades	225	Ecwhy1_134	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35158.1	001093	Cluster519_1clades	223	ACQ29_gp478	Escherichia phage PBECO4	GCA_001041035.1
BBM61615.1	001093	Cluster519_1clades	223	EO157G_0260	Escherichia phage SP27	GCA_008033345.1
AXC36731.1	001093	Cluster519_1clades	225	-	Escherichia phage UB	GCA_003341455.1
QBO61769.1	001093	Cluster519_1clades	223	G17_00280	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13813.1	001093	Cluster519_1clades	223	vBEcoMphAPEC6_gp184c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80518.1	001093	Cluster519_1clades	223	PSLUR01_00541	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44406.1	001093	Cluster519_1clades	217	RaK2_00133	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43861.1	001093	Cluster519_1clades	267	CBB_297	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19020.1	001093	Cluster519_1clades	246	7t3_0500	Salmonella phage 7t3	GCA_006083215.1
AZU98267.1	001093	Cluster519_1clades	246	CPT_Munch_323	Salmonella phage Munch	GCA_004015485.1
QIG62717.1	001093	Cluster519_1clades	246	SEPL_104	Salmonella phage SE_PL	GCA_011067555.1
AQW88820.1	001093	Cluster519_1clades	267	BF_0295	Serratia phage BF	GCA_002619745.1
SOK59103.1	001093	Cluster519_1clades	265	g295	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58567.1	001093	Cluster519_1clades	265	g290	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70279.1	001094	Cluster523_1clades	220	CF8_0111	Aeromonas phage CF8	GCA_006384595.2
QDJ97257.1	001094	Cluster523_1clades	222	D6_0097	Aeromonas phage D6	GCA_007051205.2
QDH47133.1	001094	Cluster523_1clades	222	LAh10_29	Aeromonas phage LAh10	GCA_006863975.1
QDJ96870.1	001094	Cluster523_1clades	220	PS1_0111	Aeromonas phage PS1	GCA_007051165.2
QFR59502.1	001094	Cluster523_1clades	220	PS2_0111	Aeromonas phage PS2	GCA_009388305.2
QBZ70639.1	001094	Cluster523_1clades	207	pETSU_058	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03838.1	001094	Cluster523_1clades	235	JOAD_77	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03593.1	001094	Cluster523_1clades	235	RISINGSUN_77	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71956.1	001094	Cluster523_1clades	212	N1M2_93	Klebsiella phage N1M2	GCA_010092605.1
QGZ14417.1	001094	Cluster523_1clades	230	HWC77_gp054	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27164.1	001094	Cluster523_1clades	244	PPEV_gp070	Pseudomonas phage EL	GCA_000866825.1
AEV89557.1	001094	Cluster523_1clades	212	OBP_120	Pseudomonas phage OBP	GCA_000896635.1
QAU04319.1	001094	Cluster523_1clades	230	HWC03_gp164	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23259.1	001094	Cluster523_1clades	233	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81016.1	001094	Cluster523_1clades	233	Aphrodite1_0086	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47469.1	001094	Cluster523_1clades	237	HWC35_gp075	Vibrio phage USC-1	GCA_006864065.1
BAW98290.1	001094	Cluster523_1clades	206	FDH33_gp081	Vibrio phage pTD1	GCA_002618825.1
QBX06535.1	001095	Cluster524_1clades	226	BcepSaruman_122	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74501.1	001095	Cluster524_1clades	226	BcepSauron_121	Burkholderia phage BcepSauron	GCA_005394215.1
ARB13770.1	001095	Cluster524_1clades	240	Ccr10_gp240	Caulobacter phage Ccr10	GCA_002619445.1
ARB14115.1	001095	Cluster524_1clades	240	Ccr2_gp239	Caulobacter phage Ccr2	GCA_002619465.1
ARB14809.1	001095	Cluster524_1clades	240	Ccr29_gp253	Caulobacter phage Ccr29	GCA_002619485.1
ARB15149.1	001095	Cluster524_1clades	240	Ccr32_gp231	Caulobacter phage Ccr32	GCA_002619505.1
ARB15483.1	001095	Cluster524_1clades	240	Ccr34_gp241	Caulobacter phage Ccr34	GCA_002619525.1
ARB14457.1	001095	Cluster524_1clades	240	Ccr5_gp237	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68435.1	001095	Cluster524_1clades	240	CcrBL10_gp231	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69290.1	001095	Cluster524_1clades	243	CcrBL9_gp266c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69847.1	001095	Cluster524_1clades	243	CcrSC_gp265c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87765.1	001095	Cluster524_1clades	240	CcrKarma_gp248	Caulobacter virus Karma	GCA_000901575.1
AFU87412.1	001095	Cluster524_1clades	240	CcrMagneto_gp242	Caulobacter virus Magneto	GCA_000903095.1
AFU86721.1	001095	Cluster524_1clades	240	CcrRogue_gp239	Caulobacter virus Rogue	GCA_000900555.1
AFU88560.1	001095	Cluster524_1clades	240	CcrSwift_gp242	Caulobacter virus Swift	GCA_000899655.1
AFU87068.1	001095	Cluster524_1clades	240	CbK_gp236	Caulobacter virus phiCbK	GCA_000900535.1
CCE26178.1	001095	Cluster524_1clades	240	g154	Yersinia phage phiR1-37	GCA_000895615.1
AFC21756.1	001096	Cluster525_1clades	236	GAP32_306	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13937.1	001096	Cluster525_1clades	212	PBI_121Q_40	Escherichia phage 121Q	GCA_000926855.1
QAY00400.1	001096	Cluster525_1clades	220	Ecwhy1_119	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35145.1	001096	Cluster525_1clades	212	ACQ29_gp465	Escherichia phage PBECO4	GCA_001041035.1
BBM61629.1	001096	Cluster525_1clades	220	EO157G_0400	Escherichia phage SP27	GCA_008033345.1
AXC36718.1	001096	Cluster525_1clades	220	-	Escherichia phage UB	GCA_003341455.1
QBO61756.1	001096	Cluster525_1clades	225	G17_00267	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13801.1	001096	Cluster525_1clades	220	vBEcoMphAPEC6_gp172	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80531.1	001096	Cluster525_1clades	225	PSLUR01_00554	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44419.1	001096	Cluster525_1clades	240	RaK2_00146	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43874.1	001096	Cluster525_1clades	236	CBB_311	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19033.1	001096	Cluster525_1clades	239	7t3_0513	Salmonella phage 7t3	GCA_006083215.1
AZU98280.1	001096	Cluster525_1clades	239	CPT_Munch_336	Salmonella phage Munch	GCA_004015485.1
QIG62704.1	001096	Cluster525_1clades	239	SEPL_091	Salmonella phage SE_PL	GCA_011067555.1
AQW88833.1	001096	Cluster525_1clades	237	BF_0308	Serratia phage BF	GCA_002619745.1
SOK59117.1	001096	Cluster525_1clades	237	g309c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58583.1	001096	Cluster525_1clades	237	g306c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21787.1	001097	DUF5051	226	GAP32_337	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13964.1	001097	DUF5051	229	PBI_121Q_67	Escherichia phage 121Q	GCA_000926855.1
QAY00373.1	001097	DUF5051	229	Ecwhy1_92	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35118.1	001097	DUF5051	229	ACQ29_gp438	Escherichia phage PBECO4	GCA_001041035.1
BBM61656.1	001097	DUF5051	229	EO157G_0670	Escherichia phage SP27	GCA_008033345.1
AXC36692.1	001097	DUF5051	229	-	Escherichia phage UB	GCA_003341455.1
QBO61729.1	001097	DUF5051	229	G17_00240	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13774.1	001097	DUF5051	229	vBEcoMphAPEC6_gp145c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80558.1	001097	DUF5051	229	PSLUR01_00581	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44446.1	001097	DUF5051	226	RaK2_00173	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43905.1	001097	DUF5051	224	CBB_342	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19063.1	001097	DUF5051	232	7t3_0543	Salmonella phage 7t3	GCA_006083215.1
AZU98309.1	001097	DUF5051	232	CPT_Munch_365	Salmonella phage Munch	GCA_004015485.1
QIG62675.1	001097	DUF5051	232	SEPL_062	Salmonella phage SE_PL	GCA_011067555.1
AQW88865.1	001097	DUF5051	222	BF_0340	Serratia phage BF	GCA_002619745.1
SOK59149.1	001097	DUF5051	223	g341	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58615.1	001097	DUF5051	223	g338	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21714.1	001098	Cluster527_1clades	218	GAP32_264	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14507.1	001098	Cluster527_1clades	229	PBI_121Q_617	Escherichia phage 121Q	GCA_000926855.1
QAY00442.1	001098	Cluster527_1clades	229	Ecwhy1_162	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35185.1	001098	Cluster527_1clades	229	ACQ29_gp505	Escherichia phage PBECO4	GCA_001041035.1
BBM62179.1	001098	Cluster527_1clades	229	EO157G_5900	Escherichia phage SP27	GCA_008033345.1
AXC36757.1	001098	Cluster527_1clades	229	-	Escherichia phage UB	GCA_003341455.1
QBO61796.1	001098	Cluster527_1clades	229	G17_00307	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13840.1	001098	Cluster527_1clades	229	vBEcoMphAPEC6_gp211	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80491.1	001098	Cluster527_1clades	229	PSLUR01_00514	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44379.1	001098	Cluster527_1clades	231	RaK2_00106	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43834.1	001098	Cluster527_1clades	218	CBB_270	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18993.1	001098	Cluster527_1clades	217	7t3_0472	Salmonella phage 7t3	GCA_006083215.1
AZU98241.1	001098	Cluster527_1clades	217	CPT_Munch_297	Salmonella phage Munch	GCA_004015485.1
QIG62743.1	001098	Cluster527_1clades	217	SEPL_130	Salmonella phage SE_PL	GCA_011067555.1
AQW88793.1	001098	Cluster527_1clades	218	BF_0268	Serratia phage BF	GCA_002619745.1
SOK59074.1	001098	Cluster527_1clades	218	g266c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58540.1	001098	Cluster527_1clades	218	g263c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70254.1	001099	Cluster528_1clades	181	CF8_0086	Aeromonas phage CF8	GCA_006384595.2
QDJ97233.1	001099	Cluster528_1clades	181	D6_0073	Aeromonas phage D6	GCA_007051205.2
QDH47158.1	001099	Cluster528_1clades	181	LAh10_6	Aeromonas phage LAh10	GCA_006863975.1
QDJ96843.1	001099	Cluster528_1clades	182	PS1_0084	Aeromonas phage PS1	GCA_007051165.2
QFR59473.1	001099	Cluster528_1clades	182	PS2_0082	Aeromonas phage PS2	GCA_009388305.2
QBZ70616.1	001099	Cluster528_1clades	180	pETSU_035	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03860.1	001099	Cluster528_1clades	218	JOAD_55	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03615.1	001099	Cluster528_1clades	218	RISINGSUN_55	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71932.1	001099	Cluster528_1clades	180	N1M2_69	Klebsiella phage N1M2	GCA_010092605.1
QGZ14395.1	001099	Cluster528_1clades	186	HWC77_gp032	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27143.1	001099	Cluster528_1clades	202	PPEV_gp049	Pseudomonas phage EL	GCA_000866825.1
AEV89532.1	001099	Cluster528_1clades	175	OBP_095	Pseudomonas phage OBP	GCA_000896635.1
QAU04341.1	001099	Cluster528_1clades	186	HWC03_gp186	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23235.1	001099	Cluster528_1clades	185	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81035.1	001099	Cluster528_1clades	185	Aphrodite1_0110	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47493.1	001099	Cluster528_1clades	192	HWC35_gp099	Vibrio phage USC-1	GCA_006864065.1
BAW98313.1	001099	Cluster528_1clades	185	FDH33_gp104	Vibrio phage pTD1	GCA_002618825.1
AFC21515.1	001100	Cluster529_1clades	174	GAP32_067	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14306.1	001100	Cluster529_1clades	203	PBI_121Q_416	Escherichia phage 121Q	GCA_000926855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY00632.1	001100	Cluster529_1clades	180	Ecwhy1_357	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34829.1	001100	Cluster529_1clades	203	ACQ29_gp149	Escherichia phage PBECO4	GCA_001041035.1
BBM61980.1	001100	Cluster529_1clades	180	EO157G_3910	Escherichia phage SP27	GCA_008033345.1
AXC36937.1	001100	Cluster529_1clades	198	-	Escherichia phage UB	GCA_003341455.1
QBO61998.1	001100	Cluster529_1clades	180	G17_00509	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14019.1	001100	Cluster529_1clades	206	vBEcoMphAPEC6_gp395c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80293.1	001100	Cluster529_1clades	180	PSLUR01_00316	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44719.1	001100	Cluster529_1clades	203	RaK2_00446	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43636.1	001100	Cluster529_1clades	174	CBB_71	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18767.1	001100	Cluster529_1clades	176	7t3_0246	Salmonella phage 7t3	GCA_006083215.1
AZU98033.1	001100	Cluster529_1clades	176	CPT_Munch_089	Salmonella phage Munch	GCA_004015485.1
QIG62947.1	001100	Cluster529_1clades	176	SEPL_334	Salmonella phage SE_PL	GCA_011067555.1
AQW88587.1	001100	Cluster529_1clades	175	BF_0062	Serratia phage BF	GCA_002619745.1
SOK58863.1	001100	Cluster529_1clades	175	g055	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58326.1	001100	Cluster529_1clades	175	g049	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70388.1	001101	Cluster530_1clades	179	CF8_0219	Aeromonas phage CF8	GCA_006384595.2
QNH80853.1	001101	Cluster530_1clades	201	D6_0228	Aeromonas phage D6	GCA_007051205.2
QDH47146.1	001101	Cluster530_1clades	201	LAh10_142	Aeromonas phage LAh10	GCA_006863975.1
QDJ96731.1	001101	Cluster530_1clades	179	PS1_0220	Aeromonas phage PS1	GCA_007051165.2
QFR59364.1	001101	Cluster530_1clades	179	PS2_0222	Aeromonas phage PS2	GCA_009388305.2
QBZ70773.1	001101	Cluster530_1clades	202	pETSU_192	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03690.1	001101	Cluster530_1clades	165	JOAD_225	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03447.1	001101	Cluster530_1clades	165	RISINGSUN_223	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72079.1	001101	Cluster530_1clades	200	N1M2_216	Klebsiella phage N1M2	GCA_010092605.1
QGZ14506.1	001101	Cluster530_1clades	165	HWC77_gp143	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27272.1	001101	Cluster530_1clades	170	PPEV_gp178	Pseudomonas phage EL	GCA_000866825.1
AEV89708.1	001101	Cluster530_1clades	205	OBP_271	Pseudomonas phage OBP	GCA_000896635.1
QAU04228.1	001101	Cluster530_1clades	165	HWC03_gp073	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23134.1	001101	Cluster530_1clades	167	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81043.1	001101	Cluster530_1clades	167	Aphrodite1_0206	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47593.1	001101	Cluster530_1clades	167	HWC35_gp199	Vibrio phage USC-1	GCA_006864065.1
BAW98408.1	001101	Cluster530_1clades	167	FDH33_gp199	Vibrio phage pTD1	GCA_002618825.1
AFC21519.1	001102	Cluster531_1clades	191	GAP32_071	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14311.1	001102	Cluster531_1clades	204	PBI_121Q_421	Escherichia phage 121Q	GCA_000926855.1
QAY00627.1	001102	Cluster531_1clades	204	Ecwhy1_352	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34824.1	001102	Cluster531_1clades	204	ACQ29_gp144	Escherichia phage PBECO4	GCA_001041035.1
BBM61985.1	001102	Cluster531_1clades	204	EO157G_3960	Escherichia phage SP27	GCA_008033345.1
AXC36932.1	001102	Cluster531_1clades	204	-	Escherichia phage UB	GCA_003341455.1
QBO61993.1	001102	Cluster531_1clades	204	G17_00504	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14014.1	001102	Cluster531_1clades	158	vBEcoMphAPEC6_gp390c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80298.1	001102	Cluster531_1clades	204	PSLUR01_00321	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44724.1	001102	Cluster531_1clades	201	RaK2_00451	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43640.1	001102	Cluster531_1clades	182	CBB_75	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18772.1	001102	Cluster531_1clades	204	7t3_0251	Salmonella phage 7t3	GCA_006083215.1
AZU98038.1	001102	Cluster531_1clades	204	CPT_Munch_094	Salmonella phage Munch	GCA_004015485.1
QIG62942.1	001102	Cluster531_1clades	204	SEPL_329	Salmonella phage SE_PL	GCA_011067555.1
AQW88591.1	001102	Cluster531_1clades	193	BF_0066	Serratia phage BF	GCA_002619745.1
SOK58867.1	001102	Cluster531_1clades	189	g059	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58330.1	001102	Cluster531_1clades	191	g053	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14092.1	001103	Cluster532_1clades	83	PBI_121Q_202	Escherichia phage 121Q	GCA_000926855.1
AIT14093.1	001103	Cluster532_1clades	107	PBI_121Q_203	Escherichia phage 121Q	GCA_000926855.1
QAY00828.1	001103	Cluster532_1clades	83	Ecwhy1_556	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35001.1	001103	Cluster532_1clades	72	ACQ29_gp321	Escherichia phage PBECO4	GCA_001041035.1
AGC35002.1	001103	Cluster532_1clades	83	ACQ29_gp322	Escherichia phage PBECO4	GCA_001041035.1
BBM61774.1	001103	Cluster532_1clades	108	EO157G_1850	Escherichia phage SP27	GCA_008033345.1
BBM61775.1	001103	Cluster532_1clades	109	EO157G_1860	Escherichia phage SP27	GCA_008033345.1
AXC36580.1	001103	Cluster532_1clades	107	-	Escherichia phage UB	GCA_003341455.1
QBO61606.1	001103	Cluster532_1clades	107	G17_00110	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61607.1	001103	Cluster532_1clades	83	G17_00111	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13664.1	001103	Cluster532_1clades	107	vBEcoMphAPEC6_gp033c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13665.1	001103	Cluster532_1clades	108	vBEcoMphAPEC6_gp034c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80086.1	001103	Cluster532_1clades	83	PSLUR01_00109	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80087.1	001103	Cluster532_1clades	107	PSLUR01_00110	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18630.1	001103	Cluster532_1clades	202	7t3_0109	Salmonella phage 7t3	GCA_006083215.1
AZU98455.1	001103	Cluster532_1clades	204	CPT_Munch_523	Salmonella phage Munch	GCA_004015485.1
QIG63059.1	001103	Cluster532_1clades	202	SEPL_446	Salmonella phage SE_PL	GCA_011067555.1
QDB70268.1	001104	Cluster533_1clades	174	CF8_0100	Aeromonas phage CF8	GCA_006384595.2
QDJ97246.1	001104	Cluster533_1clades	174	D6_0086	Aeromonas phage D6	GCA_007051205.2
QDH47139.1	001104	Cluster533_1clades	204	LAh10_18	Aeromonas phage LAh10	GCA_006863975.1
QDJ96859.1	001104	Cluster533_1clades	174	PS1_0100	Aeromonas phage PS1	GCA_007051165.2
QFR59491.1	001104	Cluster533_1clades	174	PS2_0100	Aeromonas phage PS2	GCA_009388305.2
QBZ70629.1	001104	Cluster533_1clades	179	pETSU_048	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03850.1	001104	Cluster533_1clades	173	JOAD_65	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03605.1	001104	Cluster533_1clades	173	RISINGSUN_65	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71945.1	001104	Cluster533_1clades	176	N1M2_82	Klebsiella phage N1M2	GCA_010092605.1
QGZ14406.1	001104	Cluster533_1clades	169	HWC77_gp043	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27154.1	001104	Cluster533_1clades	170	PPEV_gp060	Pseudomonas phage EL	GCA_000866825.1
AEV89545.1	001104	Cluster533_1clades	176	OBP_108	Pseudomonas phage OBP	GCA_000896635.1
QAU04330.1	001104	Cluster533_1clades	169	HWC03_gp175	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23246.1	001104	Cluster533_1clades	169	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81041.1	001104	Cluster533_1clades	169	Aphrodite1_0099	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47482.1	001104	Cluster533_1clades	169	HWC35_gp088	Vibrio phage USC-1	GCA_006864065.1
BAW98302.1	001104	Cluster533_1clades	173	FDH33_gp093	Vibrio phage pTD1	GCA_002618825.1
AFC21715.1	001105	Cluster534_1clades	186	GAP32_265	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14508.1	001105	Cluster534_1clades	199	PBI_121Q_618	Escherichia phage 121Q	GCA_000926855.1
QAY00441.1	001105	Cluster534_1clades	199	Ecwhy1_161	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35184.1	001105	Cluster534_1clades	199	ACQ29_gp504	Escherichia phage PBECO4	GCA_001041035.1
BBM62180.1	001105	Cluster534_1clades	199	EO157G_5910	Escherichia phage SP27	GCA_008033345.1
AXC36756.1	001105	Cluster534_1clades	199	-	Escherichia phage UB	GCA_003341455.1
QBO61795.1	001105	Cluster534_1clades	199	G17_00306	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13839.1	001105	Cluster534_1clades	199	vBEcoMphAPEC6_gp210	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80492.1	001105	Cluster534_1clades	199	PSLUR01_00515	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44380.1	001105	Cluster534_1clades	202	RaK2_00107	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43835.1	001105	Cluster534_1clades	186	CBB_271	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18994.1	001105	Cluster534_1clades	187	7t3_0473	Salmonella phage 7t3	GCA_006083215.1
AZU98242.1	001105	Cluster534_1clades	187	CPT_Munch_298	Salmonella phage Munch	GCA_004015485.1
QIG62742.1	001105	Cluster534_1clades	187	SEPL_129	Salmonella phage SE_PL	GCA_011067555.1
AQW88794.1	001105	Cluster534_1clades	186	BF_0269	Serratia phage BF	GCA_002619745.1
SOK59075.1	001105	Cluster534_1clades	182	g267c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58541.1	001105	Cluster534_1clades	182	g264c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH07724.1	001106	Cluster535_1clades	111	CYVG_00281	Cyanophage S-SSM6a	GCA_002710385.1
AGH26132.1	001106	Cluster535_1clades	112	CPMG_00031	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44591.1	001106	Cluster535_1clades	115	PSSM2_214	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44593.1	001106	Cluster535_1clades	196	PSSM2_216	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12378.1	001106	Cluster535_1clades	196	PRTG_00225	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12380.1	001106	Cluster535_1clades	115	PRTG_00227	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93431.1	001106	Cluster535_1clades	128	AVU42_gp091	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30599.1	001106	Cluster535_1clades	177	Syn7803US37_122	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54933.1	001106	Cluster535_1clades	187	b23_0320	Synechococcus phage B23	GCA_009745195.1
QGT54934.1	001106	Cluster535_1clades	97	b23_0321	Synechococcus phage B23	GCA_009745195.1
QGT54568.1	001106	Cluster535_1clades	187	b3_0327	Synechococcus phage B3	GCA_009745215.1
QGT54569.1	001106	Cluster535_1clades	97	b3_0328	Synechococcus phage B3	GCA_009745215.1
ASR76161.1	001106	Cluster535_1clades	128	PBI_BELLAMY_116	Synechococcus phage Bellamy	GCA_002627525.1
QCW22871.1	001106	Cluster535_1clades	111	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50487.1	001106	Cluster535_1clades	111	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70592.1	001106	Cluster535_1clades	112	HOU04_gp193	Synechococcus phage S-T4	GCA_003443335.1
QJT70101.1	001106	Cluster535_1clades	139	SynMITS9220M01_088	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFC21761.1	001107	Cluster536_1clades	181	GAP32_311	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13942.1	001107	Cluster536_1clades	188	PBI_121Q_45	Escherichia phage 121Q	GCA_000926855.1
QAY00395.1	001107	Cluster536_1clades	188	Ecwhy1_114	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35140.1	001107	Cluster536_1clades	196	ACQ29_gp460	Escherichia phage PBECO4	GCA_001041035.1
BBM61634.1	001107	Cluster536_1clades	188	EO157G_0450	Escherichia phage SP27	GCA_008033345.1
AXC36714.1	001107	Cluster536_1clades	188	-	Escherichia phage UB	GCA_003341455.1
QBO61751.1	001107	Cluster536_1clades	188	G17_00262	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13796.1	001107	Cluster536_1clades	188	vBEcoMphAPEC6_gp167c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SCA80536.1	001107	Cluster536_1clades	188	PSLUR01_00559	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44424.1	001107	Cluster536_1clades	186	RaK2_00151	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43879.1	001107	Cluster536_1clades	181	CBB_316	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19039.1	001107	Cluster536_1clades	179	7t3_0519	Salmonella phage 7t3	GCA_006083215.1
AZU98286.1	001107	Cluster536_1clades	179	CPT_Munch_342	Salmonella phage Munch	GCA_004015485.1
QIG62698.1	001107	Cluster536_1clades	179	SEPL_085	Salmonella phage SE_PL	GCA_011067555.1
AQW88839.1	001107	Cluster536_1clades	180	BF_0314	Serratia phage BF	GCA_002619745.1
SOK59123.1	001107	Cluster536_1clades	180	g315	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58589.1	001107	Cluster536_1clades	180	g312	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21934.1	001108	Cluster537_1clades	192	GAP32_476	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14046.1	001108	Cluster537_1clades	194	PBI_121Q_156	Escherichia phage 121Q	GCA_000926855.1
QAY00297.1	001108	Cluster537_1clades	194	Ecwhy1_15	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35047.1	001108	Cluster537_1clades	194	ACQ29_gp367	Escherichia phage PBECO4	GCA_001041035.1
BBM61729.1	001108	Cluster537_1clades	194	EO157G_1400	Escherichia phage SP27	GCA_008033345.1
AXC36624.1	001108	Cluster537_1clades	194	-	Escherichia phage UB	GCA_003341455.1
QBO61653.1	001108	Cluster537_1clades	194	G17_00157	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13706.1	001108	Cluster537_1clades	194	vBEcoMphAPEC6_gp076c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80041.1	001108	Cluster537_1clades	194	PSLUR01_00064	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44507.1	001108	Cluster537_1clades	194	RaK2_00234	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44060.1	001108	Cluster537_1clades	191	CBB_497	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18580.1	001108	Cluster537_1clades	190	7t3_059	Salmonella phage 7t3	GCA_006083215.1
AZU98408.1	001108	Cluster537_1clades	190	CPT_Munch_476	Salmonella phage Munch	GCA_004015485.1
QIG63105.1	001108	Cluster537_1clades	190	SEPL_492	Salmonella phage SE_PL	GCA_011067555.1
AQW89014.1	001108	Cluster537_1clades	192	BF_0489	Serratia phage BF	GCA_002619745.1
SOK59295.1	001108	Cluster537_1clades	192	g487	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58760.1	001108	Cluster537_1clades	192	g483	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21747.1	001109	Cluster538_1clades	192	GAP32_297	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13928.1	001109	Cluster538_1clades	193	PBI_121Q_31	Escherichia phage 121Q	GCA_000926855.1
QAY00410.1	001109	Cluster538_1clades	193	Ecwhy1_129	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35153.1	001109	Cluster538_1clades	193	ACQ29_gp473	Escherichia phage PBECO4	GCA_001041035.1
BBM61620.1	001109	Cluster538_1clades	193	EO157G_0310	Escherichia phage SP27	GCA_008033345.1
AXC36726.1	001109	Cluster538_1clades	193	-	Escherichia phage UB	GCA_003341455.1
QBO61764.1	001109	Cluster538_1clades	193	G17_00275	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13808.1	001109	Cluster538_1clades	193	vBEcoMphAPEC6_gp179c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80523.1	001109	Cluster538_1clades	193	PSLUR01_00546	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44412.1	001109	Cluster538_1clades	191	RaK2_00139	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43865.1	001109	Cluster538_1clades	192	CBB_302	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19025.1	001109	Cluster538_1clades	190	7t3_0505	Salmonella phage 7t3	GCA_006083215.1
AZU98272.1	001109	Cluster538_1clades	190	CPT_Munch_328	Salmonella phage Munch	GCA_004015485.1
QIG62712.1	001109	Cluster538_1clades	190	SEPL_099	Salmonella phage SE_PL	GCA_011067555.1
AQW88825.1	001109	Cluster538_1clades	192	BF_0300	Serratia phage BF	GCA_002619745.1
SOK59108.1	001109	Cluster538_1clades	192	g300	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58572.1	001109	Cluster538_1clades	192	g295	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21655.1	001110	Cluster539_1clades	191	GAP32_205	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14448.1	001110	Cluster539_1clades	180	PBI_121Q_558	Escherichia phage 121Q	GCA_000926855.1
QAY00500.1	001110	Cluster539_1clades	181	Ecwhy1_221	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34695.1	001110	Cluster539_1clades	180	ACQ29_gp015	Escherichia phage PBECO4	GCA_001041035.1
BBM62121.1	001110	Cluster539_1clades	180	EO157G_5320	Escherichia phage SP27	GCA_008033345.1
AXC36815.1	001110	Cluster539_1clades	180	-	Escherichia phage UB	GCA_003341455.1
QBO61854.1	001110	Cluster539_1clades	180	G17_00365	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13894.1	001110	Cluster539_1clades	180	vBEcoMphAPEC6_gp269c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80433.1	001110	Cluster539_1clades	180	PSLUR01_00456	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44321.1	001110	Cluster539_1clades	181	RaK2_00048	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43776.1	001110	Cluster539_1clades	186	CBB_211	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18924.1	001110	Cluster539_1clades	184	7t3_0403	Salmonella phage 7t3	GCA_006083215.1
AZU98181.1	001110	Cluster539_1clades	184	CPT_Munch_237	Salmonella phage Munch	GCA_004015485.1
QIG62803.1	001110	Cluster539_1clades	184	SEPL_190	Salmonella phage SE_PL	GCA_011067555.1
AQW88732.1	001110	Cluster539_1clades	185	BF_0207	Serratia phage BF	GCA_002619745.1
SOK59015.1	001110	Cluster539_1clades	182	g207	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58480.1	001110	Cluster539_1clades	184	g203	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14239.1	001111	TM	181	PBI_121Q_349	Escherichia phage 121Q	GCA_000926855.1
AIT14241.1	001111	TM	185	PBI_121Q_351	Escherichia phage 121Q	GCA_000926855.1
QAY00690.1	001111	TM	189	Ecwhy1_415	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00693.1	001111	TM	186	Ecwhy1_418	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34888.1	001111	TM	144	ACQ29_gp208	Escherichia phage PBECO4	GCA_001041035.1
AGC34886.1	001111	TM	188	ACQ29_gp206	Escherichia phage PBECO4	GCA_001041035.1
BBM61917.1	001111	TM	182	EO157G_3280	Escherichia phage SP27	GCA_008033345.1
BBM61919.1	001111	TM	188	EO157G_3300	Escherichia phage SP27	GCA_008033345.1
AXC36993.1	001111	TM	182	-	Escherichia phage UB	GCA_003341455.1
AXC36991.1	001111	TM	188	-	Escherichia phage UB	GCA_003341455.1
QBO62063.1	001111	TM	188	G17_00574	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62065.1	001111	TM	182	G17_00576	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14081.1	001111	TM	188	vBEcoMphAPEC6_gp458c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14083.1	001111	TM	182	vBEcoMphAPEC6_gp460c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80228.1	001111	TM	182	PSLUR01_00251	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80229.1	001111	TM	168	PSLUR01_00252	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80231.1	001111	TM	188	PSLUR01_00254	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21576.1	001112	Cluster541_1clades	180	GAP32_126	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14372.1	001112	Cluster541_1clades	185	PBI_121Q_482	Escherichia phage 121Q	GCA_000926855.1
QAY00576.1	001112	Cluster541_1clades	185	Ecwhy1_297	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34769.1	001112	Cluster541_1clades	185	ACQ29_gp089	Escherichia phage PBECO4	GCA_001041035.1
BBM62043.1	001112	Cluster541_1clades	185	EO157G_4540	Escherichia phage SP27	GCA_008033345.1
AXC36884.1	001112	Cluster541_1clades	185	-	Escherichia phage UB	GCA_003341455.1
QBO61932.1	001112	Cluster541_1clades	185	G17_00443	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13963.1	001112	Cluster541_1clades	185	vBEcoMphAPEC6_gp339c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80359.1	001112	Cluster541_1clades	185	PSLUR01_00382	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44781.1	001112	Cluster541_1clades	187	RaK2_00508	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43693.1	001112	Cluster541_1clades	181	CBB_128	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18832.1	001112	Cluster541_1clades	183	7t3_0311	Salmonella phage 7t3	GCA_006083215.1
AZU98095.1	001112	Cluster541_1clades	183	CPT_Munch_151	Salmonella phage Munch	GCA_004015485.1
QIG62887.1	001112	Cluster541_1clades	183	SEPL_274	Salmonella phage SE_PL	GCA_011067555.1
AQW88646.1	001112	Cluster541_1clades	180	BF_0121	Serratia phage BF	GCA_002619745.1
SOK58926.1	001112	Cluster541_1clades	180	g118	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58391.1	001112	Cluster541_1clades	180	g114	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21746.1	001113	Cluster544_1clades	183	GAP32_296	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13927.1	001113	Cluster544_1clades	184	PBI_121Q_30	Escherichia phage 121Q	GCA_000926855.1
QAY00411.1	001113	Cluster544_1clades	185	Ecwhy1_130	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35154.1	001113	Cluster544_1clades	178	ACQ29_gp474	Escherichia phage PBECO4	GCA_001041035.1
BBM61619.1	001113	Cluster544_1clades	178	EO157G_0300	Escherichia phage SP27	GCA_008033345.1
AXC36727.1	001113	Cluster544_1clades	178	-	Escherichia phage UB	GCA_003341455.1
QBO61765.1	001113	Cluster544_1clades	184	G17_00276	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13809.1	001113	Cluster544_1clades	184	vBEcoMphAPEC6_gp180c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80522.1	001113	Cluster544_1clades	184	PSLUR01_00545	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44411.1	001113	Cluster544_1clades	178	RaK2_00138	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44170.1	001113	Cluster544_1clades	183	CBB_301	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19024.1	001113	Cluster544_1clades	185	7t3_0504	Salmonella phage 7t3	GCA_006083215.1
AZU98271.1	001113	Cluster544_1clades	185	CPT_Munch_327	Salmonella phage Munch	GCA_004015485.1
QIG62713.1	001113	Cluster544_1clades	185	SEPL_100	Salmonella phage SE_PL	GCA_011067555.1
AQW88824.1	001113	Cluster544_1clades	179	BF_0299	Serratia phage BF	GCA_002619745.1
SOK59107.1	001113	Cluster544_1clades	184	g299	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58571.1	001113	Cluster544_1clades	184	g294	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21555.1	001114	Cluster546_1clades	175	GAP32_107	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14357.1	001114	Cluster546_1clades	182	PBI_121Q_467	Escherichia phage 121Q	GCA_000926855.1
QAY00587.1	001114	Cluster546_1clades	172	Ecwhy1_310	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34782.1	001114	Cluster546_1clades	182	ACQ29_gp102	Escherichia phage PBECO4	GCA_001041035.1
BBM62028.1	001114	Cluster546_1clades	182	EO157G_4390	Escherichia phage SP27	GCA_008033345.1
AXC36897.1	001114	Cluster546_1clades	182	-	Escherichia phage UB	GCA_003341455.1
QBO61947.1	001114	Cluster546_1clades	182	G17_00458	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13974.1	001114	Cluster546_1clades	182	vBEcoMphAPEC6_gp350c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80344.1	001114	Cluster546_1clades	182	PSLUR01_00367	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44767.1	001114	Cluster546_1clades	175	RaK2_00494	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43673.1	001114	Cluster546_1clades	175	CBB_108	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18808.1	001114	Cluster546_1clades	174	7t3_0287	Salmonella phage 7t3	GCA_006083215.1
AZU98073.1	001114	Cluster546_1clades	174	CPT_Munch_129	Salmonella phage Munch	GCA_004015485.1
QIG62909.1	001114	Cluster546_1clades	174	SEPL_296	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQW88626.1	001114	Cluster546_1clades	175	BF_0101	Serratia phage BF	GCA_002619745.1
SOK58902.1	001114	Cluster546_1clades	174	g094	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58367.1	001114	Cluster546_1clades	174	g090	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01573.1	001115	SIG+TM	104	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28947.1	001115	SIG+TM	144	AP1_0240	Aeromonas phage AP1	GCA_014183365.1
ATI17334.1	001115	SIG+TM	144	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00260.1	001115	SIG+TM	144	HWB28_gp292	Aeromonas phage AS-zj	GCA_002627665.1
QAX97778.1	001115	SIG+TM	144	ASswx1_133	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39453.1	001115	SIG+TM	144	CC2_405	Aeromonas phage CC2	GCA_000903495.1
ADQ53197.1	001115	SIG+TM	139	65p189	Aeromonas virus 65	GCA_000893255.1
AIA64861.1	001115	SIG+TM	178	S13_062	Cronobacter phage S13	GCA_001503575.1
AFC21942.1	001115	SIG+TM	148	GAP32_484	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ARM70918.1	001115	SIG+TM	157	phiC120_c213	Escherichia phage phiC120	GCA_002621185.1
QHJ79077.1	001115	SIG+TM	170	-	Myoviridae sp.	GCA_012593985.1
AMM44069.1	001115	SIG+TM	144	CBB_506	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89024.1	001115	SIG+TM	159	BF_0499	Serratia phage BF	GCA_002619745.1
QAU04474.1	001115	SIG+TM	182	ValB1MD_075	Vibrio phage ValB1MD	GCA_004138815.1
SOK59305.1	001115	SIG+TM	159	g497	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58770.1	001115	SIG+TM	159	g493	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26288.1	001115	SIG+TM	166	g265	Yersinia phage phiR1-37	GCA_000895615.1
AGH57003.1	001116	CpeT	158	CPXG_00200	Cyanophage P-RSM6	GCA_000906155.1
AJK27458.1	001116	CpeT	155	PTIM40_31	Cyanophage P-TIM40	GCA_001470935.1
AMO43036.1	001116	CpeT	177	R1080702_022	Cyanophage S-RIM32	GCA_001754165.1
AMO43277.1	001116	CpeT	179	W270710_032	Cyanophage S-RIM44	GCA_002599145.1
AOO11511.1	001116	CpeT	179	ES420910_029	Cyanophage S-RIM44	GCA_002599165.1
AOO11749.1	001116	CpeT	179	Np050604_032	Cyanophage S-RIM44	GCA_002599185.1
AOO11976.1	001116	CpeT	179	Np200711_029	Cyanophage S-RIM44	GCA_002599205.1
AOO12212.1	001116	CpeT	179	Np420711_029	Cyanophage S-RIM44	GCA_002599225.1
AOO12450.1	001116	CpeT	179	Sn080709_032	Cyanophage S-RIM44	GCA_002599245.1
AOO12677.1	001116	CpeT	179	Sn130910_029	Cyanophage S-RIM44	GCA_002599265.1
AOO12915.1	001116	CpeT	179	W2100709_032	Cyanophage S-RIM44	GCA_002599285.1
AGH26187.1	001116	CpeT	138	CPMG_00086	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99130.1	001116	CpeT	179	Syn1_028	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30689.1	001116	CpeT	139	Syn7803US37_212	Synechococcus phage ACG-2014f	GCA_002594065.1
AOV59488.1	001116	CpeT	174	S330809_027	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59250.1	001116	CpeT	174	C440309_027	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59726.1	001116	CpeT	174	N231010_027	Synechococcus phage S-CAM4	GCA_002922155.1
AFC21937.1	001117	Cluster549_1clades	175	GAP32_479	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14050.1	001117	Cluster549_1clades	152	PBI_121Q_160	Escherichia phage 121Q	GCA_000926855.1
QAY00293.1	001117	Cluster549_1clades	152	Ecwhy1_11	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35043.1	001117	Cluster549_1clades	152	ACQ29_gp363	Escherichia phage PBECO4	GCA_001041035.1
BBM61733.1	001117	Cluster549_1clades	152	EO157G_1440	Escherichia phage SP27	GCA_008033345.1
AXC36620.1	001117	Cluster549_1clades	152	-	Escherichia phage UB	GCA_003341455.1
QBO61649.1	001117	Cluster549_1clades	152	G17_00153	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13703.1	001117	Cluster549_1clades	152	vBEcoMphAPEC6_gp073c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80045.1	001117	Cluster549_1clades	152	PSLUR01_00068	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44511.1	001117	Cluster549_1clades	155	RaK2_00238	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44063.1	001117	Cluster549_1clades	173	CBB_500	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18583.1	001117	Cluster549_1clades	160	7t3_062	Salmonella phage 7t3	GCA_006083215.1
AZU98411.1	001117	Cluster549_1clades	160	CPT_Munch_479	Salmonella phage Munch	GCA_004015485.1
QIG63102.1	001117	Cluster549_1clades	160	SEPL_489	Salmonella phage SE_PL	GCA_011067555.1
AQW89018.1	001117	Cluster549_1clades	166	BF_0493	Serratia phage BF	GCA_002619745.1
SOK59299.1	001117	Cluster549_1clades	166	g491	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58764.1	001117	Cluster549_1clades	166	g487	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21556.1	001118	Cluster550_1clades	164	GAP32_108	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14358.1	001118	Cluster550_1clades	174	PBI_121Q_468	Escherichia phage 121Q	GCA_000926855.1
QAY00586.1	001118	Cluster550_1clades	175	Ecwhy1_309	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34780.1	001118	Cluster550_1clades	68	ACQ29_gp100	Escherichia phage PBECO4	GCA_001041035.1
AGC34781.1	001118	Cluster550_1clades	86	ACQ29_gp101	Escherichia phage PBECO4	GCA_001041035.1
BBM62029.1	001118	Cluster550_1clades	174	EO157G_4400	Escherichia phage SP27	GCA_008033345.1
AXC36896.1	001118	Cluster550_1clades	174	-	Escherichia phage UB	GCA_003341455.1
QBO61946.1	001118	Cluster550_1clades	174	G17_00457	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13973.1	001118	Cluster550_1clades	174	vBEcoMphAPEC6_gp349c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80345.1	001118	Cluster550_1clades	174	PSLUR01_00368	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43674.1	001118	Cluster550_1clades	160	CBB_109	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18809.1	001118	Cluster550_1clades	166	7t3_0288	Salmonella phage 7t3	GCA_006083215.1
AZU98074.1	001118	Cluster550_1clades	166	CPT_Munch_130	Salmonella phage Munch	GCA_004015485.1
QIG62908.1	001118	Cluster550_1clades	166	SEPL_295	Salmonella phage SE_PL	GCA_011067555.1
AQW88627.1	001118	Cluster550_1clades	164	BF_0102	Serratia phage BF	GCA_002619745.1
SOK58903.1	001118	Cluster550_1clades	167	g095	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58368.1	001118	Cluster550_1clades	162	g091	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21717.1	001119	Cluster551_1clades	166	GAP32_267	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13899.1	001119	Cluster551_1clades	161	PBI_121Q_2	Escherichia phage 121Q	GCA_000926855.1
QAY00439.1	001119	Cluster551_1clades	161	Ecwhy1_159	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35182.1	001119	Cluster551_1clades	164	ACQ29_gp502	Escherichia phage PBECO4	GCA_001041035.1
BBM61591.1	001119	Cluster551_1clades	161	EO157G_0020	Escherichia phage SP27	GCA_008033345.1
AXC36754.1	001119	Cluster551_1clades	161	-	Escherichia phage UB	GCA_003341455.1
QBO61793.1	001119	Cluster551_1clades	161	G17_00304	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13837.1	001119	Cluster551_1clades	161	vBEcoMphAPEC6_gp208c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80494.1	001119	Cluster551_1clades	161	PSLUR01_00517	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44382.1	001119	Cluster551_1clades	161	RaK2_00109	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43837.1	001119	Cluster551_1clades	166	CBB_273	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18996.1	001119	Cluster551_1clades	169	7t3_0476	Salmonella phage 7t3	GCA_006083215.1
AZU98244.1	001119	Cluster551_1clades	169	CPT_Munch_300	Salmonella phage Munch	GCA_004015485.1
QIG62740.1	001119	Cluster551_1clades	169	SEPL_127	Salmonella phage SE_PL	GCA_011067555.1
AQW88796.1	001119	Cluster551_1clades	166	BF_0271	Serratia phage BF	GCA_002619745.1
SOK59078.1	001119	Cluster551_1clades	166	g270	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58543.1	001119	Cluster551_1clades	166	g266	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21881.1	001120	Cluster552_1clades	156	GAP32_428	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14004.1	001120	Cluster552_1clades	168	PBI_121Q_107	Escherichia phage 121Q	GCA_000926855.1
QAY00334.1	001120	Cluster552_1clades	168	Ecwhy1_53	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35080.1	001120	Cluster552_1clades	168	ACQ29_gp400	Escherichia phage PBECO4	GCA_001041035.1
BBM61695.1	001120	Cluster552_1clades	168	EO157G_1060	Escherichia phage SP27	GCA_008033345.1
AXC36657.1	001120	Cluster552_1clades	168	-	Escherichia phage UB	GCA_003341455.1
QBO61689.1	001120	Cluster552_1clades	168	G17_00200	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13738.1	001120	Cluster552_1clades	168	vBEcoMphAPEC6_gp108c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80008.1	001120	Cluster552_1clades	168	PSLUR01_00024	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44484.1	001120	Cluster552_1clades	167	RaK2_00211	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44011.1	001120	Cluster552_1clades	156	CBB_448	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18538.1	001120	Cluster552_1clades	163	7t3_05	Salmonella phage 7t3	GCA_006083215.1
AZU98371.1	001120	Cluster552_1clades	163	CPT_Munch_431	Salmonella phage Munch	GCA_004015485.1
QIG63142.1	001120	Cluster552_1clades	163	SEPL_529	Salmonella phage SE_PL	GCA_011067555.1
AQW88968.1	001120	Cluster552_1clades	153	BF_0443	Serratia phage BF	GCA_002619745.1
SOK59257.1	001120	Cluster552_1clades	156	g449	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58722.1	001120	Cluster552_1clades	152	g445	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21807.1	001121	Cluster553_1clades	140	GAP32_357	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13974.1	001121	Cluster553_1clades	140	PBI_121Q_77	Escherichia phage 121Q	GCA_000926855.1
QAY00363.1	001121	Cluster553_1clades	140	Ecwhy1_82	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35109.1	001121	Cluster553_1clades	140	ACQ29_gp429	Escherichia phage PBECO4	GCA_001041035.1
BBM61666.1	001121	Cluster553_1clades	140	EO157G_0770	Escherichia phage SP27	GCA_008033345.1
AXC36684.1	001121	Cluster553_1clades	140	-	Escherichia phage UB	GCA_003341455.1
QBO61718.1	001121	Cluster553_1clades	140	G17_00229	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13765.1	001121	Cluster553_1clades	140	vBEcoMphAPEC6_gp136c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80568.1	001121	Cluster553_1clades	140	PSLUR01_00591	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44454.1	001121	Cluster553_1clades	146	RaK2_00181	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43929.1	001121	Cluster553_1clades	145	CBB_366	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19077.1	001121	Cluster553_1clades	164	7t3_0557	Salmonella phage 7t3	GCA_006083215.1
AZU98320.1	001121	Cluster553_1clades	164	CPT_Munch_376	Salmonella phage Munch	GCA_004015485.1
QIG62664.1	001121	Cluster553_1clades	164	SEPL_051	Salmonella phage SE_PL	GCA_011067555.1
AQW88888.1	001121	Cluster553_1clades	140	BF_0363	Serratia phage BF	GCA_002619745.1
SOK59175.1	001121	Cluster553_1clades	142	g367	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58641.1	001121	Cluster553_1clades	142	g364	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGY75125.1	001122	Cluster554_1clades	83	CF8_0128	Aeromonas phage CF8	GCA_006384595.2
QDJ97273.1	001122	Cluster554_1clades	96	D6_0113	Aeromonas phage D6	GCA_007051205.2
QDH47176.1	001122	Cluster554_1clades	156	LAh10_45	Aeromonas phage LAh10	GCA_006863975.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ96890.1	001122	Cluster554_1clades	68	PS1_0131	Aeromonas phage PS1	GCA_007051165.2
QFR59520.1	001122	Cluster554_1clades	68	PS2_0129	Aeromonas phage PS2	GCA_009388305.2
QBZ70659.1	001122	Cluster554_1clades	58	pETSU_078	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03820.1	001122	Cluster554_1clades	144	JOAD_95	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03575.1	001122	Cluster554_1clades	144	RISINGSUN_95	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71975.1	001122	Cluster554_1clades	82	N1M2_112	Klebsiella phage N1M2	GCA_010092605.1
QGZ14447.1	001122	Cluster554_1clades	143	HWC77_gp084	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27204.1	001122	Cluster554_1clades	77	PPEV_gp110	Pseudomonas phage EL	GCA_000866825.1
AEV89576.1	001122	Cluster554_1clades	157	OBP_139	Pseudomonas phage OBP	GCA_000896635.1
QAU04287.1	001122	Cluster554_1clades	164	HWC03_gp132	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23290.1	001122	Cluster554_1clades	146	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81101.1	001122	Cluster554_1clades	48	Aphrodite1_0055	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47438.1	001122	Cluster554_1clades	146	HWC35_gp044	Vibrio phage USC-1	GCA_006864065.1
BAW98259.1	001122	Cluster554_1clades	107	FDH33_gp050	Vibrio phage pTD1	GCA_002618825.1
QGY75131.1	001123	TM	151	CF8_0208	Aeromonas phage CF8	GCA_006384595.2
QDJ97376.1	001123	TM	136	D6_0217	Aeromonas phage D6	GCA_007051205.2
QDH47195.1	001123	TM	136	LAh10_131	Aeromonas phage LAh10	GCA_006863975.1
QDJ96719.1	001123	TM	140	PS1_0208	Aeromonas phage PS1	GCA_007051165.2
QFR59352.1	001123	TM	140	PS2_0210	Aeromonas phage PS2	GCA_009388305.2
QBZ70761.1	001123	TM	156	pETSU_180	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03698.1	001123	TM	163	JOAD_217	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03455.1	001123	TM	163	RISINGSUN_215	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72068.1	001123	TM	134	N1M2_205	Klebsiella phage N1M2	GCA_010092605.1
QGZ14497.1	001123	TM	143	HWC77_gp134	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27264.1	001123	TM	151	PPEV_gp170	Pseudomonas phage EL	GCA_000866825.1
AEV89697.1	001123	TM	135	OBP_260	Pseudomonas phage OBP	GCA_000896635.1
QAU04237.1	001123	TM	143	HWC03_gp082	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23126.1	001123	TM	143	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81063.1	001123	TM	143	Aphrodite1_0005	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47601.1	001123	TM	143	HWC35_gp207	Vibrio phage USC-1	GCA_006864065.1
BAW98416.1	001123	TM	141	FDH33_gp207	Vibrio phage pTD1	GCA_002618825.1
AFC21505.1	001124	Cluster556_1clades	147	GAP32_057	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14296.1	001124	Cluster556_1clades	157	PBI_121Q_406	Escherichia phage 121Q	GCA_000926855.1
QAY00642.1	001124	Cluster556_1clades	157	Ecwhy1_367	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34838.1	001124	Cluster556_1clades	157	ACQ29_gp158	Escherichia phage PBECO4	GCA_001041035.1
BBM61970.1	001124	Cluster556_1clades	157	EO157G_3810	Escherichia phage SP27	GCA_008033345.1
AXC36947.1	001124	Cluster556_1clades	157	-	Escherichia phage UB	GCA_003341455.1
QBO62008.1	001124	Cluster556_1clades	157	G17_00519	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14029.1	001124	Cluster556_1clades	157	vBEcoMphAPEC6_gp406c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80283.1	001124	Cluster556_1clades	157	PSLUR01_00306	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44710.1	001124	Cluster556_1clades	162	RaK2_00437	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43625.1	001124	Cluster556_1clades	147	CBB_60	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18753.1	001124	Cluster556_1clades	154	7t3_0232	Salmonella phage 7t3	GCA_006083215.1
AZU98022.1	001124	Cluster556_1clades	154	CPT_Munch_078	Salmonella phage Munch	GCA_004015485.1
QIG62958.1	001124	Cluster556_1clades	154	SEPL_345	Salmonella phage SE_PL	GCA_011067555.1
AQW88577.1	001124	Cluster556_1clades	148	BF_0052	Serratia phage BF	GCA_002619745.1
SOK58852.1	001124	Cluster556_1clades	148	g044	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58314.1	001124	Cluster556_1clades	148	g037	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21911.1	001125	Cluster557_1clades	148	GAP32_454	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14040.1	001125	Cluster557_1clades	139	PBI_121Q_150	Escherichia phage 121Q	GCA_000926855.1
QAY00303.1	001125	Cluster557_1clades	139	Ecwhy1_21	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35053.1	001125	Cluster557_1clades	139	ACQ29_gp373	Escherichia phage PBECO4	GCA_001041035.1
BBM61723.1	001125	Cluster557_1clades	139	EO157G_1340	Escherichia phage SP27	GCA_008033345.1
AXC36629.1	001125	Cluster557_1clades	139	-	Escherichia phage UB	GCA_003341455.1
QBO61659.1	001125	Cluster557_1clades	139	G17_00163	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13711.1	001125	Cluster557_1clades	139	vBEcoMphAPEC6_gp081c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80035.1	001125	Cluster557_1clades	139	PSLUR01_00058	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44503.1	001125	Cluster557_1clades	161	RaK2_00230	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44035.1	001125	Cluster557_1clades	147	CBB_472	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18572.1	001125	Cluster557_1clades	136	7t3_051	Salmonella phage 7t3	GCA_006083215.1
AZU98401.1	001125	Cluster557_1clades	136	CPT_Munch_469	Salmonella phage Munch	GCA_004015485.1
QIG63112.1	001125	Cluster557_1clades	136	SEPL_499	Salmonella phage SE_PL	GCA_011067555.1
AQW88995.1	001125	Cluster557_1clades	145	BF_0470	Serratia phage BF	GCA_002619745.1
SOK59276.1	001125	Cluster557_1clades	144	g468	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58741.1	001125	Cluster557_1clades	144	g464	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01626.1	001126	Inhibitor_I24	115	-	Aeromonas phage 65.2	GCA_002618145.1
APU01628.1	001126	Inhibitor_I24	159	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29035.1	001126	Inhibitor_I24	128	AP1_0328	Aeromonas phage AP1	GCA_014183365.1
ATI17257.1	001126	Inhibitor_I24	128	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17283.1	001126	Inhibitor_I24	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00334.1	001126	Inhibitor_I24	128	HWB28_gp218	Aeromonas phage AS-zj	GCA_002627665.1
ASU00313.1	001126	Inhibitor_I24	79	HWB28_gp239	Aeromonas phage AS-zj	GCA_002627665.1
QAX97698.1	001126	Inhibitor_I24	128	ASswx1_52	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97724.1	001126	Inhibitor_I24	79	ASswx1_78	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01439.1	001126	Inhibitor_I24	130	ASwh1_380	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01440.1	001126	Inhibitor_I24	84	ASwh1_381	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01443.1	001126	Inhibitor_I24	110	ASwh1_384	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39180.1	001126	Inhibitor_I24	79	CC2_034	Aeromonas phage CC2	GCA_000903495.1
AFN39467.1	001126	Inhibitor_I24	110	CC2_059	Aeromonas phage CC2	GCA_000903495.1
AFN39327.1	001126	Inhibitor_I24	130	CC2_060	Aeromonas phage CC2	GCA_000903495.1
ADQ53251.1	001126	Inhibitor_I24	115	65p243	Aeromonas virus 65	GCA_000893255.1
ADQ53253.1	001126	Inhibitor_I24	159	65p245	Aeromonas virus 65	GCA_000893255.1
AFC21506.1	001127	Cluster559_1clades	158	GAP32_058	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14299.1	001127	Cluster559_1clades	157	PBI_121Q_409	Escherichia phage 121Q	GCA_000926855.1
QAY00639.1	001127	Cluster559_1clades	157	Ecwhy1_364	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34835.1	001127	Cluster559_1clades	157	ACQ29_gp155	Escherichia phage PBECO4	GCA_001041035.1
BBM61973.1	001127	Cluster559_1clades	157	EO157G_3840	Escherichia phage SP27	GCA_008033345.1
AXC36944.1	001127	Cluster559_1clades	157	-	Escherichia phage UB	GCA_003341455.1
QBO62005.1	001127	Cluster559_1clades	157	G17_00516	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14026.1	001127	Cluster559_1clades	157	vBEcoMphAPEC6_gp402c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80286.1	001127	Cluster559_1clades	157	PSLUR01_00309	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44713.1	001127	Cluster559_1clades	158	RaK2_00440	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43626.1	001127	Cluster559_1clades	158	CBB_61	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18756.1	001127	Cluster559_1clades	157	7t3_0235	Salmonella phage 7t3	GCA_006083215.1
AZU98025.1	001127	Cluster559_1clades	157	CPT_Munch_081	Salmonella phage Munch	GCA_004015485.1
QIG62955.1	001127	Cluster559_1clades	157	SEPL_342	Salmonella phage SE_PL	GCA_011067555.1
AQW88578.1	001127	Cluster559_1clades	159	BF_0053	Serratia phage BF	GCA_002619745.1
SOK58853.1	001127	Cluster559_1clades	159	g045	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58315.1	001127	Cluster559_1clades	159	g038	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01738.1	001128	Cluster561_1clades	143	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28730.1	001128	Cluster561_1clades	141	AP1_0012	Aeromonas phage AP1	GCA_014183365.1
ATI17560.1	001128	Cluster561_1clades	141	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00437.1	001128	Cluster561_1clades	141	HWB28_gp115	Aeromonas phage AS-zj	GCA_002627665.1
QAX98000.1	001128	Cluster561_1clades	141	ASswx1_360	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01142.1	001128	Cluster561_1clades	138	ASwh1_76	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39369.1	001128	Cluster561_1clades	141	CC2_175	Aeromonas phage CC2	GCA_000903495.1
ADQ53381.1	001128	Cluster561_1clades	143	65p373	Aeromonas virus 65	GCA_000893255.1
AIT13992.1	001128	Cluster561_1clades	127	PBI_121Q_95	Escherichia phage 121Q	GCA_000926855.1
QAY00346.1	001128	Cluster561_1clades	127	Ecwhy1_65	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35092.1	001128	Cluster561_1clades	127	ACQ29_gp412	Escherichia phage PBECO4	GCA_001041035.1
BBM61683.1	001128	Cluster561_1clades	127	EO157G_0940	Escherichia phage SP27	GCA_008033345.1
AXC36669.1	001128	Cluster561_1clades	127	-	Escherichia phage UB	GCA_003341455.1
QBO61701.1	001128	Cluster561_1clades	127	G17_00212	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13748.1	001128	Cluster561_1clades	127	vBEcoMphAPEC6_gp119c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79996.1	001128	Cluster561_1clades	127	PSLUR01_00012	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ASV44524.1	001128	Cluster561_1clades	156	PBI_SCTP2_509	Salicola phage SCTP-2	GCA_002625545.1
AFC21553.1	001129	Cluster562_1clades	152	GAP32_105	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14356.1	001129	Cluster562_1clades	148	PBI_121Q_466	Escherichia phage 121Q	GCA_000926855.1
QAY00588.1	001129	Cluster562_1clades	148	Ecwhy1_311	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34783.1	001129	Cluster562_1clades	148	ACQ29_gp103	Escherichia phage PBECO4	GCA_001041035.1
BBM62027.1	001129	Cluster562_1clades	148	EO157G_4380	Escherichia phage SP27	GCA_008033345.1
AXC36898.1	001129	Cluster562_1clades	148	-	Escherichia phage UB	GCA_003341455.1
QBO61948.1	001129	Cluster562_1clades	148	G17_00459	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13975.1	001129	Cluster562_1clades	148	vBEcoMphAPEC6_gp351c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80343.1	001129	Cluster562_1clades	148	PSLUR01_00366	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFA44764.1	001129	Cluster562_1clades	154	RaK2_00491	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43671.1	001129	Cluster562_1clades	151	CBB_106	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18806.1	001129	Cluster562_1clades	147	7t3_0285	Salmonella phage 7t3	GCA_006083215.1
AZU98071.1	001129	Cluster562_1clades	147	CPT_Munch_127	Salmonella phage Munch	GCA_004015485.1
QIG62911.1	001129	Cluster562_1clades	147	SEPL_298	Salmonella phage SE_PL	GCA_011067555.1
AQW88624.1	001129	Cluster562_1clades	148	BF_0099	Serratia phage BF	GCA_002619745.1
SOK58900.1	001129	Cluster562_1clades	148	g092	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58365.1	001129	Cluster562_1clades	148	g088	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70404.1	001130	Cluster563_1clades	141	CF8_0235	Aeromonas phage CF8	GCA_006384595.2
QDJ97408.1	001130	Cluster563_1clades	148	D6_0249	Aeromonas phage D6	GCA_007051205.2
QDH47186.1	001130	Cluster563_1clades	148	LAh10_161	Aeromonas phage LAh10	GCA_006863975.1
QDJ96751.1	001130	Cluster563_1clades	144	PS1_0240	Aeromonas phage PS1	GCA_007051165.2
QFR59384.1	001130	Cluster563_1clades	144	PS2_0242	Aeromonas phage PS2	GCA_009388305.2
QBZ70794.1	001130	Cluster563_1clades	152	pETSU_213	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03676.1	001130	Cluster563_1clades	146	JOAD_239	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03433.1	001130	Cluster563_1clades	146	RISINGSUN_237	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72097.1	001130	Cluster563_1clades	145	N1M2_234	Klebsiella phage N1M2	GCA_010092605.1
QGZ14522.1	001130	Cluster563_1clades	148	HWC77_gp159	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27288.1	001130	Cluster563_1clades	146	PPEV_gp194	Pseudomonas phage EL	GCA_000866825.1
AEV89732.1	001130	Cluster563_1clades	152	OBP_295	Pseudomonas phage OBP	GCA_000896635.1
QAU04212.1	001130	Cluster563_1clades	148	HWC03_gp057	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23148.1	001130	Cluster563_1clades	148	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81057.1	001130	Cluster563_1clades	148	Aphrodite1_0192	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47579.1	001130	Cluster563_1clades	148	HWC35_gp185	Vibrio phage USC-1	GCA_006864065.1
BAW98394.1	001130	Cluster563_1clades	148	FDH33_gp185	Vibrio phage pTD1	GCA_002618825.1
QDB70261.1	001131	Cluster564_1clades	141	CF8_0093	Aeromonas phage CF8	GCA_006384595.2
QDJ97239.1	001131	Cluster564_1clades	149	D6_0079	Aeromonas phage D6	GCA_007051205.2
QDH47185.1	001131	Cluster564_1clades	149	LAh10_11	Aeromonas phage LAh10	GCA_006863975.1
QDJ96852.1	001131	Cluster564_1clades	142	PS1_0093	Aeromonas phage PS1	GCA_007051165.2
QFR59484.1	001131	Cluster564_1clades	142	PS2_0093	Aeromonas phage PS2	GCA_009388305.2
QBZ70622.1	001131	Cluster564_1clades	141	pETSU_041	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03857.1	001131	Cluster564_1clades	136	JOAD_58	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03612.1	001131	Cluster564_1clades	136	RISINGSUN_58	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71938.1	001131	Cluster564_1clades	144	N1M2_75	Klebsiella phage N1M2	GCA_010092605.1
QGZ14399.1	001131	Cluster564_1clades	136	HWC77_gp036	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27147.1	001131	Cluster564_1clades	148	PPEV_gp053	Pseudomonas phage EL	GCA_000866825.1
AEV89538.1	001131	Cluster564_1clades	143	OBP_101	Pseudomonas phage OBP	GCA_000896635.1
QAU04337.1	001131	Cluster564_1clades	136	HWC03_gp182	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23239.1	001131	Cluster564_1clades	136	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81066.1	001131	Cluster564_1clades	136	Aphrodite1_0106	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47489.1	001131	Cluster564_1clades	136	HWC35_gp095	Vibrio phage USC-1	GCA_006864065.1
BAW98309.1	001131	Cluster564_1clades	134	FDH33_gp100	Vibrio phage pTD1	GCA_002618825.1
AFC21727.1	001132	Cluster565_1clades	146	GAP32_277	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13908.1	001132	Cluster565_1clades	142	PBI_121Q_11	Escherichia phage 121Q	GCA_000926855.1
QAY00429.1	001132	Cluster565_1clades	142	Ecwhy1_149	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35173.1	001132	Cluster565_1clades	142	ACQ29_gp493	Escherichia phage PBECO4	GCA_001041035.1
BBM61600.1	001132	Cluster565_1clades	142	EO157G_0110	Escherichia phage SP27	GCA_008033345.1
AXC36745.1	001132	Cluster565_1clades	142	-	Escherichia phage UB	GCA_003341455.1
QBO61784.1	001132	Cluster565_1clades	142	G17_00295	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13828.1	001132	Cluster565_1clades	142	vBEcoMphAPEC6_gp199c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80503.1	001132	Cluster565_1clades	142	PSLUR01_00526	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44392.1	001132	Cluster565_1clades	140	RaK2_00119	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43846.1	001132	Cluster565_1clades	145	CBB_282	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19005.1	001132	Cluster565_1clades	144	7t3_0485	Salmonella phage 7t3	GCA_006083215.1
AZU98252.1	001132	Cluster565_1clades	144	CPT_Munch_308	Salmonella phage Munch	GCA_004015485.1
QIG62732.1	001132	Cluster565_1clades	144	SEPL_119	Salmonella phage SE_PL	GCA_011067555.1
AQW88805.1	001132	Cluster565_1clades	145	BF_0280	Serratia phage BF	GCA_002619745.1
SOK59088.1	001132	Cluster565_1clades	146	g280	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58552.1	001132	Cluster565_1clades	146	g275	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13667.1	001133	Cluster566_1clades	135	Ccr10_gp138	Caulobacter phage Ccr10	GCA_002619445.1
ARB14012.1	001133	Cluster566_1clades	135	Ccr2_gp137	Caulobacter phage Ccr2	GCA_002619465.1
ARB14699.1	001133	Cluster566_1clades	135	Ccr29_gp143	Caulobacter phage Ccr29	GCA_002619485.1
ARB14753.1	001133	Cluster566_1clades	118	Ccr29_gp197	Caulobacter phage Ccr29	GCA_002619485.1
ARB15054.1	001133	Cluster566_1clades	135	Ccr32_gp136	Caulobacter phage Ccr32	GCA_002619505.1
ARB15388.1	001133	Cluster566_1clades	94	Ccr34_gp146	Caulobacter phage Ccr34	GCA_002619525.1
ARB14355.1	001133	Cluster566_1clades	135	Ccr5_gp136	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68335.1	001133	Cluster566_1clades	141	CcrBL10_gp131	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69241.1	001133	Cluster566_1clades	135	CcrBL9_gp217	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88050.1	001133	Cluster566_1clades	145	CcrColossus_gp180	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68729.1	001133	Cluster566_1clades	89	CcrPW_gp190	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69795.1	001133	Cluster566_1clades	81	CcrSC_gp213	Caulobacter phage CcrSC	GCA_003443315.1
AFU87660.1	001133	Cluster566_1clades	135	CcrKarma_gp143	Caulobacter virus Karma	GCA_000901575.1
AFU87309.1	001133	Cluster566_1clades	135	CcrMagneto_gp139	Caulobacter virus Magneto	GCA_000903095.1
AFU86620.1	001133	Cluster566_1clades	135	CcrRogue_gp138	Caulobacter virus Rogue	GCA_000900555.1
AFU88456.1	001133	Cluster566_1clades	135	CcrSwift_gp138	Caulobacter virus Swift	GCA_000899655.1
AFU86973.1	001133	Cluster566_1clades	135	CbK_gp141	Caulobacter virus phiCbK	GCA_000900535.1
QDB70390.1	001134	Cluster567_1clades	142	CF8_0221	Aeromonas phage CF8	GCA_006384595.2
QDJ97389.1	001134	Cluster567_1clades	140	D6_0230	Aeromonas phage D6	GCA_007051205.2
QDH47191.1	001134	Cluster567_1clades	140	LAh10_144	Aeromonas phage LAh10	GCA_006863975.1
QDJ96733.1	001134	Cluster567_1clades	140	PS1_0222	Aeromonas phage PS1	GCA_007051165.2
QFR59366.1	001134	Cluster567_1clades	140	PS2_0224	Aeromonas phage PS2	GCA_009388305.2
QBZ70775.1	001134	Cluster567_1clades	139	pETSU_194	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03688.1	001134	Cluster567_1clades	145	JOAD_227	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03445.1	001134	Cluster567_1clades	145	RISINGSUN_225	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72081.1	001134	Cluster567_1clades	136	N1M2_218	Klebsiella phage N1M2	GCA_010092605.1
QGZ14508.1	001134	Cluster567_1clades	138	HWC77_gp145	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27274.1	001134	Cluster567_1clades	144	PPEV_gp180	Pseudomonas phage EL	GCA_000866825.1
AEV89710.1	001134	Cluster567_1clades	136	OBP_273	Pseudomonas phage OBP	GCA_000896635.1
QAU04226.1	001134	Cluster567_1clades	138	HWC03_gp071	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23136.1	001134	Cluster567_1clades	137	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81070.1	001134	Cluster567_1clades	133	Aphrodite1_0204	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47591.1	001134	Cluster567_1clades	137	HWC35_gp197	Vibrio phage USC-1	GCA_006864065.1
BAW98406.1	001134	Cluster567_1clades	60	FDH33_gp197	Vibrio phage pTD1	GCA_002618825.1
AFC21702.1	001135	Cluster568_1clades	138	GAP32_252	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14495.1	001135	Cluster568_1clades	116	PBI_121Q_605	Escherichia phage 121Q	GCA_000926855.1
QAY00454.1	001135	Cluster568_1clades	116	Ecwhy1_174	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35197.1	001135	Cluster568_1clades	116	ACQ29_gp517	Escherichia phage PBECO4	GCA_001041035.1
BBM62167.1	001135	Cluster568_1clades	116	EO157G_5780	Escherichia phage SP27	GCA_008033345.1
AXC36768.1	001135	Cluster568_1clades	116	-	Escherichia phage UB	GCA_003341455.1
QBO61808.1	001135	Cluster568_1clades	116	G17_00319	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13852.1	001135	Cluster568_1clades	116	vBEcoMphAPEC6_gp223c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80479.1	001135	Cluster568_1clades	116	PSLUR01_00502	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44369.1	001135	Cluster568_1clades	117	RaK2_00096	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43822.1	001135	Cluster568_1clades	138	CBB_258	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18981.1	001135	Cluster568_1clades	106	7t3_0460	Salmonella phage 7t3	GCA_006083215.1
AZU98229.1	001135	Cluster568_1clades	134	CPT_Munch_285	Salmonella phage Munch	GCA_004015485.1
QIG62755.1	001135	Cluster568_1clades	135	SEPL_142	Salmonella phage SE_PL	GCA_011067555.1
AQW88781.1	001135	Cluster568_1clades	142	BF_0256	Serratia phage BF	GCA_002619745.1
SOK59062.1	001135	Cluster568_1clades	143	g254	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58528.1	001135	Cluster568_1clades	143	g251	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21503.1	001136	Cluster569_1clades	142	GAP32_055	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14294.1	001136	Cluster569_1clades	137	PBI_121Q_404	Escherichia phage 121Q	GCA_000926855.1
QAY00644.1	001136	Cluster569_1clades	137	Ecwhy1_369	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34840.1	001136	Cluster569_1clades	137	ACQ29_gp160	Escherichia phage PBECO4	GCA_001041035.1
BBM61968.1	001136	Cluster569_1clades	137	EO157G_3790	Escherichia phage SP27	GCA_008033345.1
AXC36949.1	001136	Cluster569_1clades	137	-	Escherichia phage UB	GCA_003341455.1
QBO62010.1	001136	Cluster569_1clades	137	G17_00521	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14031.1	001136	Cluster569_1clades	137	vBEcoMphAPEC6_gp408c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80281.1	001136	Cluster569_1clades	137	PSLUR01_00304	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44708.1	001136	Cluster569_1clades	136	RaK2_00435	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43624.1	001136	Cluster569_1clades	137	CBB_59	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18750.1	001136	Cluster569_1clades	134	7t3_0229	Salmonella phage 7t3	GCA_006083215.1
AZU98019.1	001136	Cluster569_1clades	134	CPT_Munch_075	Salmonella phage Munch	GCA_004015485.1
QIG62961.1	001136	Cluster569_1clades	134	SEPL_348	Salmonella phage SE_PL	GCA_011067555.1
AQW88575.1	001136	Cluster569_1clades	142	BF_0050	Serratia phage BF	GCA_002619745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58850.1	001136	Cluster569_1clades	142	g042	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58312.1	001136	Cluster569_1clades	142	g035	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AND75444.1	001137	Cluster570_1clades	138	ME3_283	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ARB13808.1	001137	Cluster570_1clades	140	Ccr10_gp278	Caulobacter phage Ccr10	GCA_002619445.1
ARB14153.1	001137	Cluster570_1clades	140	Ccr2_gp277	Caulobacter phage Ccr2	GCA_002619465.1
ARB14847.1	001137	Cluster570_1clades	140	Ccr29_gp291	Caulobacter phage Ccr29	GCA_002619485.1
ARB15187.1	001137	Cluster570_1clades	140	Ccr32_gp269	Caulobacter phage Ccr32	GCA_002619505.1
ARB15521.1	001137	Cluster570_1clades	140	Ccr34_gp279	Caulobacter phage Ccr34	GCA_002619525.1
ARB14496.1	001137	Cluster570_1clades	140	Ccr5_gp276	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68473.1	001137	Cluster570_1clades	138	CcrBL10_gp269	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87806.1	001137	Cluster570_1clades	140	CcrKarma_gp289	Caulobacter virus Karma	GCA_000901575.1
AFU87453.1	001137	Cluster570_1clades	140	CcrMagneto_gp283	Caulobacter virus Magneto	GCA_000903095.1
AFU86758.1	001137	Cluster570_1clades	138	CcrRogue_gp276	Caulobacter virus Rogue	GCA_000900555.1
AFU88598.1	001137	Cluster570_1clades	140	CcrSwift_gp280	Caulobacter virus Swift	GCA_000899655.1
AFU87106.1	001137	Cluster570_1clades	140	CbK_gp274	Caulobacter virus phiCbK	GCA_000900535.1
AXH72497.1	001137	Cluster570_1clades	137	-	Myoviridae sp.	GCA_003657725.1
AFH14889.1	001137	Cluster570_1clades	136	Lu11_0351	Pseudomonas phage Lu11	GCA_000897175.1
BAG41504.1	001137	Cluster570_1clades	137	RSL1_ORF058	Ralstonia phage phiRSL1	GCA_000879455.1
ALY07175.1	001137	Cluster570_1clades	135	VmeM32_00189	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFC21658.1	001138	Cluster571_1clades	134	GAP32_208	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14451.1	001138	Cluster571_1clades	131	PBI_121Q_561	Escherichia phage 121Q	GCA_000926855.1
QAY00497.1	001138	Cluster571_1clades	130	Ecwhy1_218	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34692.1	001138	Cluster571_1clades	131	ACQ29_gp012	Escherichia phage PBECO4	GCA_001041035.1
BBM62124.1	001138	Cluster571_1clades	131	EO157G_5350	Escherichia phage SP27	GCA_008033345.1
AXC36812.1	001138	Cluster571_1clades	131	-	Escherichia phage UB	GCA_003341455.1
QBO61851.1	001138	Cluster571_1clades	131	G17_00362	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13891.1	001138	Cluster571_1clades	131	vBEcoMphAPEC6_gp266c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80436.1	001138	Cluster571_1clades	131	PSLUR01_00459	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44324.1	001138	Cluster571_1clades	134	RaK2_00051	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43779.1	001138	Cluster571_1clades	136	CBB_214	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18927.1	001138	Cluster571_1clades	136	7t3_0406	Salmonella phage 7t3	GCA_006083215.1
AZU98184.1	001138	Cluster571_1clades	136	CPT_Munch_240	Salmonella phage Munch	GCA_004015485.1
QIG62800.1	001138	Cluster571_1clades	136	SEPL_187	Salmonella phage SE_PL	GCA_011067555.1
AQW88735.1	001138	Cluster571_1clades	125	BF_0210	Serratia phage BF	GCA_002619745.1
SOK59018.1	001138	Cluster571_1clades	130	g210	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58483.1	001138	Cluster571_1clades	130	g206	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21739.1	001139	Cluster573_1clades	132	GAP32_289	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13920.1	001139	Cluster573_1clades	130	PBI_121Q_23	Escherichia phage 121Q	GCA_000926855.1
QAY00418.1	001139	Cluster573_1clades	130	Ecwhy1_137	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35161.1	001139	Cluster573_1clades	130	ACQ29_gp481	Escherichia phage PBECO4	GCA_001041035.1
BBM61612.1	001139	Cluster573_1clades	130	EO157G_0230	Escherichia phage SP27	GCA_008033345.1
AXC36734.1	001139	Cluster573_1clades	130	-	Escherichia phage UB	GCA_003341455.1
QBO61772.1	001139	Cluster573_1clades	130	G17_00283	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13816.1	001139	Cluster573_1clades	130	vBEcoMphAPEC6_gp187c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80515.1	001139	Cluster573_1clades	130	PSLUR01_00538	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44404.1	001139	Cluster573_1clades	130	RaK2_00131	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43858.1	001139	Cluster573_1clades	132	CBB_294	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19017.1	001139	Cluster573_1clades	133	7t3_0497	Salmonella phage 7t3	GCA_006083215.1
AZU98264.1	001139	Cluster573_1clades	133	CPT_Munch_320	Salmonella phage Munch	GCA_004015485.1
QIG62720.1	001139	Cluster573_1clades	133	SEPL_107	Salmonella phage SE_PL	GCA_011067555.1
AQW88817.1	001139	Cluster573_1clades	132	BF_0292	Serratia phage BF	GCA_002619745.1
SOK59100.1	001139	Cluster573_1clades	132	g292	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58564.1	001139	Cluster573_1clades	132	g287	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21612.1	001140	Cluster574_1clades	129	GAP32_162	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14405.1	001140	Cluster574_1clades	132	PBI_121Q_515	Escherichia phage 121Q	GCA_000926855.1
QAY00546.1	001140	Cluster574_1clades	132	Ecwhy1_267	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34737.1	001140	Cluster574_1clades	132	ACQ29_gp057	Escherichia phage PBECO4	GCA_001041035.1
BBM62076.1	001140	Cluster574_1clades	132	EO157G_4870	Escherichia phage SP27	GCA_008033345.1
AXC36852.1	001140	Cluster574_1clades	132	-	Escherichia phage UB	GCA_003341455.1
QBO61897.1	001140	Cluster574_1clades	132	G17_00408	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13933.1	001140	Cluster574_1clades	132	vBEcoMphAPEC6_gp308c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80391.1	001140	Cluster574_1clades	132	PSLUR01_00414	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44286.1	001140	Cluster574_1clades	131	RaK2_00013	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43731.1	001140	Cluster574_1clades	129	CBB_166	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18869.1	001140	Cluster574_1clades	129	7t3_0348	Salmonella phage 7t3	GCA_006083215.1
AZU98130.1	001140	Cluster574_1clades	129	CPT_Munch_186	Salmonella phage Munch	GCA_004015485.1
QIG62852.1	001140	Cluster574_1clades	129	SEPL_239	Salmonella phage SE_PL	GCA_011067555.1
AQW88686.1	001140	Cluster574_1clades	129	BF_0161	Serratia phage BF	GCA_002619745.1
SOK58968.1	001140	Cluster574_1clades	129	g160	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58434.1	001140	Cluster574_1clades	129	g157	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21510.1	001141	Cluster575_1clades	131	GAP32_062	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14303.1	001141	Cluster575_1clades	128	PBI_121Q_413	Escherichia phage 121Q	GCA_000926855.1
QAY00635.1	001141	Cluster575_1clades	128	Ecwhy1_360	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34832.1	001141	Cluster575_1clades	128	ACQ29_gp152	Escherichia phage PBECO4	GCA_001041035.1
BBM61977.1	001141	Cluster575_1clades	128	EO157G_3880	Escherichia phage SP27	GCA_008033345.1
AXC36940.1	001141	Cluster575_1clades	128	-	Escherichia phage UB	GCA_003341455.1
QBO62001.1	001141	Cluster575_1clades	128	G17_00512	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14022.1	001141	Cluster575_1clades	128	vBEcoMphAPEC6_gp398c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80290.1	001141	Cluster575_1clades	128	PSLUR01_00313	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44716.1	001141	Cluster575_1clades	128	RaK2_00443	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43631.1	001141	Cluster575_1clades	132	CBB_66	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18760.1	001141	Cluster575_1clades	127	7t3_0239	Salmonella phage 7t3	GCA_006083215.1
AZU98029.1	001141	Cluster575_1clades	127	CPT_Munch_085	Salmonella phage Munch	GCA_004015485.1
QIG62951.1	001141	Cluster575_1clades	127	SEPL_338	Salmonella phage SE_PL	GCA_011067555.1
AQW88582.1	001141	Cluster575_1clades	131	BF_0057	Serratia phage BF	GCA_002619745.1
SOK58857.1	001141	Cluster575_1clades	131	g049	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58319.1	001141	Cluster575_1clades	131	g042	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21610.1	001142	Cluster577_1clades	125	GAP32_160	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14401.1	001142	Cluster577_1clades	124	PBI_121Q_511	Escherichia phage 121Q	GCA_000926855.1
QAY00550.1	001142	Cluster577_1clades	124	Ecwhy1_271	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34741.1	001142	Cluster577_1clades	124	ACQ29_gp061	Escherichia phage PBECO4	GCA_001041035.1
BBM62072.1	001142	Cluster577_1clades	124	EO157G_4830	Escherichia phage SP27	GCA_008033345.1
AXC36856.1	001142	Cluster577_1clades	124	-	Escherichia phage UB	GCA_003341455.1
QBO61901.1	001142	Cluster577_1clades	124	G17_00412	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13937.1	001142	Cluster577_1clades	124	vBEcoMphAPEC6_gp312c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80387.1	001142	Cluster577_1clades	124	PSLUR01_00410	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44283.1	001142	Cluster577_1clades	122	RaK2_00010	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43729.1	001142	Cluster577_1clades	122	CBB_164	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18865.1	001142	Cluster577_1clades	117	7t3_0344	Salmonella phage 7t3	GCA_006083215.1
AZU98126.1	001142	Cluster577_1clades	117	CPT_Munch_182	Salmonella phage Munch	GCA_004015485.1
QIG62856.1	001142	Cluster577_1clades	117	SEPL_243	Salmonella phage SE_PL	GCA_011067555.1
AQW88684.1	001142	Cluster577_1clades	121	BF_0159	Serratia phage BF	GCA_002619745.1
SOK58965.1	001142	Cluster577_1clades	120	g157	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58431.1	001142	Cluster577_1clades	120	g154	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70384.1	001143	Cluster578_1clades	117	CF8_0215	Aeromonas phage CF8	GCA_006384595.2
QDJ97383.1	001143	Cluster578_1clades	122	D6_0224	Aeromonas phage D6	GCA_007051205.2
QDH47212.1	001143	Cluster578_1clades	122	LAh10_138	Aeromonas phage LAh10	GCA_006863975.1
QDJ96726.1	001143	Cluster578_1clades	117	PS1_0215	Aeromonas phage PS1	GCA_007051165.2
QFR59359.1	001143	Cluster578_1clades	117	PS2_0217	Aeromonas phage PS2	GCA_009388305.2
QBZ70769.1	001143	Cluster578_1clades	121	pETSU_188	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03694.1	001143	Cluster578_1clades	124	JOAD_221	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03451.1	001143	Cluster578_1clades	124	RISINGSUN_219	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72075.1	001143	Cluster578_1clades	120	N1M2_212	Klebsiella phage N1M2	GCA_010092605.1
QGZ14501.1	001143	Cluster578_1clades	121	HWC77_gp138	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27268.1	001143	Cluster578_1clades	124	PPEV_gp174	Pseudomonas phage EL	GCA_000866825.1
AEV89704.1	001143	Cluster578_1clades	120	OBP_267	Pseudomonas phage OBP	GCA_000896635.1
QAU04233.1	001143	Cluster578_1clades	121	HWC03_gp078	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23130.1	001143	Cluster578_1clades	121	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81077.1	001143	Cluster578_1clades	121	Aphrodite1_0001	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47597.1	001143	Cluster578_1clades	121	HWC35_gp203	Vibrio phage USC-1	GCA_006864065.1
BAW98412.1	001143	Cluster578_1clades	123	FDH33_gp203	Vibrio phage pTD1	GCA_002618825.1
AFC21744.1	001144	Cluster579_1clades	111	GAP32_294	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13925.1	001144	Cluster579_1clades	111	PBI_121Q_28	Escherichia phage 121Q	GCA_000926855.1
QAY00413.1	001144	Cluster579_1clades	109	Ecwhy1_132	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35156.1	001144	Cluster579_1clades	111	ACQ29_gp476	Escherichia phage PBECO4	GCA_001041035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBM61617.1	001144	Cluster579_1clades	111	EO157G_0280	Escherichia phage SP27	GCA_008033345.1
AXC36729.1	001144	Cluster579_1clades	111	-	Escherichia phage UB	GCA_003341455.1
QBO61767.1	001144	Cluster579_1clades	111	G17_00278	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13811.1	001144	Cluster579_1clades	111	vBEcoMphAPEC6_gp182c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80520.1	001144	Cluster579_1clades	111	PSLUR01_00543	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44409.1	001144	Cluster579_1clades	116	RaK2_00136	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43863.1	001144	Cluster579_1clades	111	CBB_299	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19022.1	001144	Cluster579_1clades	109	7t3_0502	Salmonella phage 7t3	GCA_006083215.1
AZU98269.1	001144	Cluster579_1clades	109	CPT_Munch_325	Salmonella phage Munch	GCA_004015485.1
QIG62715.1	001144	Cluster579_1clades	109	SEPL_102	Salmonella phage SE_PL	GCA_011067555.1
AQW88822.1	001144	Cluster579_1clades	111	BF_0297	Serratia phage BF	GCA_002619745.1
SOK59105.1	001144	Cluster579_1clades	111	g297	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58569.1	001144	Cluster579_1clades	111	g292	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21511.1	001145	Cluster580_1clades	116	GAP32_063	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14304.1	001145	Cluster580_1clades	101	PBI_121Q_414	Escherichia phage 121Q	GCA_000926855.1
QAY00634.1	001145	Cluster580_1clades	101	Ecwhy1_359	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34831.1	001145	Cluster580_1clades	101	ACQ29_gp151	Escherichia phage PBECO4	GCA_001041035.1
BBM61978.1	001145	Cluster580_1clades	101	EO157G_3890	Escherichia phage SP27	GCA_008033345.1
AXC36939.1	001145	Cluster580_1clades	101	-	Escherichia phage UB	GCA_003341455.1
QBO62000.1	001145	Cluster580_1clades	101	G17_00511	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14021.1	001145	Cluster580_1clades	101	vBEcoMphAPEC6_gp397c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80291.1	001145	Cluster580_1clades	101	PSLUR01_00314	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44717.1	001145	Cluster580_1clades	95	RaK2_00444	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43632.1	001145	Cluster580_1clades	116	CBB_67	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18761.1	001145	Cluster580_1clades	100	7t3_0240	Salmonella phage 7t3	GCA_006083215.1
AZU98030.1	001145	Cluster580_1clades	100	CPT_Munch_086	Salmonella phage Munch	GCA_004015485.1
QIG62950.1	001145	Cluster580_1clades	100	SEPL_337	Salmonella phage SE_PL	GCA_011067555.1
AQW88583.1	001145	Cluster580_1clades	116	BF_0058	Serratia phage BF	GCA_002619745.1
SOK58858.1	001145	Cluster580_1clades	115	g050	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58320.1	001145	Cluster580_1clades	115	g043	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71229.1	001146	Cluster581_1clades	115	CR5_009	Cronobacter phage CR5	GCA_000910235.1
QBP07667.1	001146	Cluster581_1clades	115	DERBICUS_9	Erwinia phage Derbicus	GCA_004521655.1
ANZ49662.1	001146	Cluster581_1clades	90	MACHINA_24	Erwinia phage Machina	GCA_002758035.1
AXF51150.1	001146	Cluster581_1clades	99	WELLINGTON_19	Erwinia phage Wellington	GCA_003344985.1
ANZ48039.1	001146	Cluster581_1clades	107	ASESINO_26	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48313.1	001146	Cluster581_1clades	110	CAITLIN_18	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48586.1	001146	Cluster581_1clades	107	CHRISDB_24	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48859.1	001146	Cluster581_1clades	115	EARLPHILLIPIV_9	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49107.1	001146	Cluster581_1clades	90	HUXLEY_25	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49646.1	001146	Cluster581_1clades	99	KWAN_19	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49935.1	001146	Cluster581_1clades	90	PARSHIK_26	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50199.1	001146	Cluster581_1clades	115	PHOBOS_9	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50449.1	001146	Cluster581_1clades	107	STRATTON_24	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85847.1	001146	Cluster581_1clades	106	ACEC001_0100	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20727.1	001146	Cluster581_1clades	106	-	Salmonella phage JN03	GCA_014319805.1
AXF51103.1	001146	Cluster581_1clades	106	MLDJOKPK_00158	Salmonella phage SPAsTU	GCA_003183805.1
AEP83842.1	001146	Cluster581_1clades	106	SPN3US_0009	Salmonella phage SPN3US	GCA_001042275.1
AIT14172.1	001147	Cluster582_1clades	107	PBI_121Q_282	Escherichia phage 121Q	GCA_000926855.1
AIT14193.1	001147	Cluster582_1clades	107	PBI_121Q_303	Escherichia phage 121Q	GCA_000926855.1
QAY00746.1	001147	Cluster582_1clades	107	Ecwhy1_471	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00764.1	001147	Cluster582_1clades	107	Ecwhy1_490	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34944.1	001147	Cluster582_1clades	107	ACQ29_gp264	Escherichia phage PBECO4	GCA_001041035.1
AGC34924.1	001147	Cluster582_1clades	71	ACQ29_gp244	Escherichia phage PBECO4	GCA_001041035.1
BBM61846.1	001147	Cluster582_1clades	114	EO157G_2570	Escherichia phage SP27	GCA_008033345.1
BBM61867.1	001147	Cluster582_1clades	107	EO157G_2780	Escherichia phage SP27	GCA_008033345.1
AXC37028.1	001147	Cluster582_1clades	42	-	Escherichia phage UB	GCA_003341455.1
QBO61513.1	001147	Cluster582_1clades	107	G17_00017	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61534.1	001147	Cluster582_1clades	107	G17_00038	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62119.1	001147	Cluster582_1clades	107	G17_00630	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62140.1	001147	Cluster582_1clades	107	G17_00651	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14128.1	001147	Cluster582_1clades	107	vBEcoMphAPEC6_gp505c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14148.1	001147	Cluster582_1clades	114	vBEcoMphAPEC6_gp525c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80157.1	001147	Cluster582_1clades	107	PSLUR01_00180	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80176.1	001147	Cluster582_1clades	107	PSLUR01_00199	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21611.1	001148	Cluster583_1clades	98	GAP32_161	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14402.1	001148	Cluster583_1clades	102	PBI_121Q_512	Escherichia phage 121Q	GCA_000926855.1
QAY00549.1	001148	Cluster583_1clades	104	Ecwhy1_270	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34740.1	001148	Cluster583_1clades	102	ACQ29_gp060	Escherichia phage PBECO4	GCA_001041035.1
BBM62073.1	001148	Cluster583_1clades	102	EO157G_4840	Escherichia phage SP27	GCA_008033345.1
AXC36855.1	001148	Cluster583_1clades	102	-	Escherichia phage UB	GCA_003341455.1
QBO61900.1	001148	Cluster583_1clades	102	G17_00411	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13936.1	001148	Cluster583_1clades	102	vBEcoMphAPEC6_gp311c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80388.1	001148	Cluster583_1clades	102	PSLUR01_00411	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44284.1	001148	Cluster583_1clades	105	RaK2_00011	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43730.1	001148	Cluster583_1clades	104	CBB_165	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18866.1	001148	Cluster583_1clades	112	7t3_0345	Salmonella phage 7t3	GCA_006083215.1
AZU98127.1	001148	Cluster583_1clades	112	CPT_Munch_183	Salmonella phage Munch	GCA_004015485.1
QIG62855.1	001148	Cluster583_1clades	112	SEPL_242	Salmonella phage SE_PL	GCA_011067555.1
AQW88685.1	001148	Cluster583_1clades	103	BF_0160	Serratia phage BF	GCA_002619745.1
SOK58966.1	001148	Cluster583_1clades	104	g158	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58432.1	001148	Cluster583_1clades	104	g155	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21643.1	001149	Cluster585_1clades	108	GAP32_193	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14435.1	001149	Cluster585_1clades	102	PBI_121Q_545	Escherichia phage 121Q	GCA_000926855.1
QAY00513.1	001149	Cluster585_1clades	102	Ecwhy1_234	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34707.1	001149	Cluster585_1clades	102	ACQ29_gp027	Escherichia phage PBECO4	GCA_001041035.1
BBM62107.1	001149	Cluster585_1clades	102	EO157G_5180	Escherichia phage SP27	GCA_008033345.1
AXC36826.1	001149	Cluster585_1clades	102	-	Escherichia phage UB	GCA_003341455.1
QBO61866.1	001149	Cluster585_1clades	102	G17_00377	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13907.1	001149	Cluster585_1clades	102	vBEcoMphAPEC6_gp282c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80421.1	001149	Cluster585_1clades	102	PSLUR01_00444	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44309.1	001149	Cluster585_1clades	104	RaK2_00036	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43764.1	001149	Cluster585_1clades	109	CBB_199	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18913.1	001149	Cluster585_1clades	107	7t3_0392	Salmonella phage 7t3	GCA_006083215.1
AZU98170.1	001149	Cluster585_1clades	107	CPT_Munch_226	Salmonella phage Munch	GCA_004015485.1
QIG62814.1	001149	Cluster585_1clades	107	SEPL_201	Salmonella phage SE_PL	GCA_011067555.1
AQW88720.1	001149	Cluster585_1clades	107	BF_0195	Serratia phage BF	GCA_002619745.1
SOK59002.1	001149	Cluster585_1clades	106	g194	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58467.1	001149	Cluster585_1clades	106	g190	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21662.1	001150	Cluster586_1clades	78	GAP32_212	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14455.1	001150	Cluster586_1clades	81	PBI_121Q_565	Escherichia phage 121Q	GCA_000926855.1
QAY00493.1	001150	Cluster586_1clades	109	Ecwhy1_214	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34688.1	001150	Cluster586_1clades	86	ACQ29_gp008	Escherichia phage PBECO4	GCA_001041035.1
BBM62128.1	001150	Cluster586_1clades	81	EO157G_5390	Escherichia phage SP27	GCA_008033345.1
AXC36808.1	001150	Cluster586_1clades	81	-	Escherichia phage UB	GCA_003341455.1
QBO61847.1	001150	Cluster586_1clades	81	G17_00358	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13888.1	001150	Cluster586_1clades	81	vBEcoMphAPEC6_gp263c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80440.1	001150	Cluster586_1clades	81	PSLUR01_00463	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44328.1	001150	Cluster586_1clades	73	RaK2_00055	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43783.1	001150	Cluster586_1clades	78	CBB_218	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18933.1	001150	Cluster586_1clades	84	7t3_0412	Salmonella phage 7t3	GCA_006083215.1
AZU98188.1	001150	Cluster586_1clades	84	CPT_Munch_244	Salmonella phage Munch	GCA_004015485.1
QIG62796.1	001150	Cluster586_1clades	84	SEPL_183	Salmonella phage SE_PL	GCA_011067555.1
AQW88739.1	001150	Cluster586_1clades	77	BF_0214	Serratia phage BF	GCA_002619745.1
SOK59022.1	001150	Cluster586_1clades	76	g214	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58487.1	001150	Cluster586_1clades	76	g210	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71412.1	001151	Cluster587_1clades	103	CR5_192	Cronobacter phage CR5	GCA_000910235.1
AMR59869.1	001151	Cluster587_1clades	91	SEGD1_222	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07625.1	001151	Cluster587_1clades	103	DERBICUS_199	Erwinia phage Derbicus	GCA_004521655.1
ANZ49868.1	001151	Cluster587_1clades	105	MACHINA_230	Erwinia phage Machina	GCA_002758035.1
AXF51371.1	001151	Cluster587_1clades	98	WELLINGTON_245	Erwinia phage Wellington	GCA_003344985.1
ANZ48252.1	001151	Cluster587_1clades	94	ASESINO_239	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48525.1	001151	Cluster587_1clades	96	CAITLIN_230	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48802.1	001151	Cluster587_1clades	108	CHRISDB_240	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49049.1	001151	Cluster587_1clades	103	EARLPHILLIPIV_200	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49312.1	001151	Cluster587_1clades	105	HUXLEY_230	Erwinia phage vB_EamM_Huxley	GCA_001745635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ49597.1	001151	Cluster587_1clades	98	KWAN_245	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50140.1	001151	Cluster587_1clades	105	PARSHIK_231	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50396.1	001151	Cluster587_1clades	103	PHOBOS_206	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50665.1	001151	Cluster587_1clades	94	STRATTON_240	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86058.1	001151	Cluster587_1clades	91	ACEC001_2150	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51115.1	001151	Cluster587_1clades	91	MLDJOKPK_00223	Salmonella phage SPAsTU	GCA_003183805.1
AEP84050.1	001151	Cluster587_1clades	91	SPN3US_0217	Salmonella phage SPN3US	GCA_001042275.1
AFC21776.1	001152	Cluster588_1clades	96	GAP32_326	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13956.1	001152	Cluster588_1clades	89	PBI_121Q_59	Escherichia phage 121Q	GCA_000926855.1
QAY00381.1	001152	Cluster588_1clades	89	Ecwhy1_100	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35126.1	001152	Cluster588_1clades	89	ACQ29_gp446	Escherichia phage PBECO4	GCA_001041035.1
BBM61648.1	001152	Cluster588_1clades	89	EO157G_0590	Escherichia phage SP27	GCA_008033345.1
AXC36700.1	001152	Cluster588_1clades	89	-	Escherichia phage UB	GCA_003341455.1
QBO61737.1	001152	Cluster588_1clades	89	G17_00248	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13782.1	001152	Cluster588_1clades	67	vBEcoMphAPEC6_gp153c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80550.1	001152	Cluster588_1clades	89	PSLUR01_00573	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44438.1	001152	Cluster588_1clades	89	RaK2_00165	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43894.1	001152	Cluster588_1clades	96	CBB_331	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19053.1	001152	Cluster588_1clades	91	7t3_0533	Salmonella phage 7t3	GCA_006083215.1
AZU98300.1	001152	Cluster588_1clades	91	CPT_Munch_356	Salmonella phage Munch	GCA_004015485.1
QIG62684.1	001152	Cluster588_1clades	91	SEPL_071	Salmonella phage SE_PL	GCA_011067555.1
AQW88854.1	001152	Cluster588_1clades	106	BF_0329	Serratia phage BF	GCA_002619745.1
SOK59138.1	001152	Cluster588_1clades	99	g330	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58604.1	001152	Cluster588_1clades	99	g327	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21772.1	001153	Cluster590_1clades	101	GAP32_322	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13952.1	001153	Cluster590_1clades	103	PBI_121Q_55	Escherichia phage 121Q	GCA_000926855.1
QAY00385.1	001153	Cluster590_1clades	103	Ecwhy1_104	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35130.1	001153	Cluster590_1clades	103	ACQ29_gp450	Escherichia phage PBECO4	GCA_001041035.1
BBM61644.1	001153	Cluster590_1clades	103	EO157G_0550	Escherichia phage SP27	GCA_008033345.1
AXC36704.1	001153	Cluster590_1clades	103	-	Escherichia phage UB	GCA_003341455.1
QBO61741.1	001153	Cluster590_1clades	103	G17_00252	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13786.1	001153	Cluster590_1clades	103	vBEcoMphAPEC6_gp157c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80546.1	001153	Cluster590_1clades	103	PSLUR01_00569	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44434.1	001153	Cluster590_1clades	102	RaK2_00161	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43890.1	001153	Cluster590_1clades	101	CBB_327	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19049.1	001153	Cluster590_1clades	102	7t3_0529	Salmonella phage 7t3	GCA_006083215.1
AZU98296.1	001153	Cluster590_1clades	102	CPT_Munch_352	Salmonella phage Munch	GCA_004015485.1
QIG62688.1	001153	Cluster590_1clades	102	SEPL_075	Salmonella phage SE_PL	GCA_011067555.1
AQW88850.1	001153	Cluster590_1clades	100	BF_0325	Serratia phage BF	GCA_002619745.1
SOK59134.1	001153	Cluster590_1clades	100	g326	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58600.1	001153	Cluster590_1clades	100	g323	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21518.1	001154	Cluster591_1clades	93	GAP32_070	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14309.1	001154	Cluster591_1clades	97	PBI_121Q_419	Escherichia phage 121Q	GCA_000926855.1
QAY00629.1	001154	Cluster591_1clades	97	Ecwhy1_354	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34826.1	001154	Cluster591_1clades	97	ACQ29_gp146	Escherichia phage PBECO4	GCA_001041035.1
BBM61983.1	001154	Cluster591_1clades	97	EO157G_3940	Escherichia phage SP27	GCA_008033345.1
AXC36934.1	001154	Cluster591_1clades	97	-	Escherichia phage UB	GCA_003341455.1
QBO61995.1	001154	Cluster591_1clades	97	G17_00506	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14016.1	001154	Cluster591_1clades	97	vBEcoMphAPEC6_gp392c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80296.1	001154	Cluster591_1clades	97	PSLUR01_00319	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44722.1	001154	Cluster591_1clades	96	RaK2_00449	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43639.1	001154	Cluster591_1clades	93	CBB_74	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18770.1	001154	Cluster591_1clades	95	7t3_0249	Salmonella phage 7t3	GCA_006083215.1
AZU98036.1	001154	Cluster591_1clades	95	CPT_Munch_092	Salmonella phage Munch	GCA_004015485.1
QIG62944.1	001154	Cluster591_1clades	95	SEPL_331	Salmonella phage SE_PL	GCA_011067555.1
AQW88590.1	001154	Cluster591_1clades	93	BF_0065	Serratia phage BF	GCA_002619745.1
SOK58866.1	001154	Cluster591_1clades	103	g058	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58329.1	001154	Cluster591_1clades	103	g052	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56854.1	001155	Cluster593_1clades	79	CPXG_00051	Cyanophage P-RSM6	GCA_000906155.1
AJK27601.1	001155	Cluster593_1clades	73	PTIM40_174	Cyanophage P-TIM40	GCA_001470935.1
AOO14357.1	001155	Cluster593_1clades	88	Sn110110_163	Cyanophage S-RIM14	GCA_002599065.1
AOO15006.1	001155	Cluster593_1clades	88	W1230910_160	Cyanophage S-RIM14	GCA_002599125.1
AGH07496.1	001155	Cluster593_1clades	86	CYVG_00052	Cyanophage S-SSM6a	GCA_002710385.1
AGG54451.1	001155	Cluster593_1clades	79	CYWG_00167	Cyanophage S-SSM6b	GCA_002710425.1
AGH26289.1	001155	Cluster593_1clades	79	CPMG_00189	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44559.1	001155	Cluster593_1clades	82	PSSM2_181	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12413.1	001155	Cluster593_1clades	82	PRTG_00261	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93484.1	001155	Cluster593_1clades	88	AVU42_gp146	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30646.1	001155	Cluster593_1clades	93	Syn7803US37_169	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54914.1	001155	Cluster593_1clades	83	b23_0301	Synechococcus phage B23	GCA_009745195.1
QGT54549.1	001155	Cluster593_1clades	83	b3_0308	Synechococcus phage B3	GCA_009745215.1
ASR76316.1	001155	Cluster593_1clades	85	PBI_BELLAMY_160	Synechococcus phage Bellamy	GCA_002627525.1
QDH50572.1	001155	Cluster593_1clades	84	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70546.1	001155	Cluster593_1clades	81	HOU04_gp147	Synechococcus phage S-T4	GCA_003443335.1
QJT70155.1	001155	Cluster593_1clades	86	SynMITS9220M01_142	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AOO14255.1	001156	Cluster594_1clades	89	Sn110110_061	Cyanophage S-RIM14	GCA_002599065.1
AOO14907.1	001156	Cluster594_1clades	89	W1230910_061	Cyanophage S-RIM14	GCA_002599125.1
AMO43151.1	001156	Cluster594_1clades	72	R1080702_142	Cyanophage S-RIM32	GCA_001754165.1
AMO43375.1	001156	Cluster594_1clades	92	W270710_131	Cyanophage S-RIM44	GCA_002599145.1
AOO11619.1	001156	Cluster594_1clades	92	ES420910_138	Cyanophage S-RIM44	GCA_002599165.1
AOO11847.1	001156	Cluster594_1clades	92	Np050604_131	Cyanophage S-RIM44	GCA_002599185.1
AOO12084.1	001156	Cluster594_1clades	92	Np200711_138	Cyanophage S-RIM44	GCA_002599205.1
AOO12320.1	001156	Cluster594_1clades	92	Np420711_138	Cyanophage S-RIM44	GCA_002599225.1
AOO12548.1	001156	Cluster594_1clades	92	Sn080709_131	Cyanophage S-RIM44	GCA_002599245.1
AOO12785.1	001156	Cluster594_1clades	92	Sn130910_138	Cyanophage S-RIM44	GCA_002599265.1
AOO13014.1	001156	Cluster594_1clades	92	W2100709_132	Cyanophage S-RIM44	GCA_002599285.1
ADO99233.1	001156	Cluster594_1clades	92	Syn1_132	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76110.1	001156	Cluster594_1clades	81	PBI_BELLAMY_65	Synechococcus phage Bellamy	GCA_002627525.1
QCW22939.1	001156	Cluster594_1clades	88	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50624.1	001156	Cluster594_1clades	88	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70568.1	001156	Cluster594_1clades	78	HOU04_gp169	Synechococcus phage S-T4	GCA_003443335.1
QJT70055.1	001156	Cluster594_1clades	71	SynMITS9220M01_042	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56997.1	001157	Cluster595_1clades	78	CPXG_00194	Cyanophage P-RSM6	GCA_000906155.1
AOO14217.1	001157	Cluster595_1clades	86	Sn110110_023	Cyanophage S-RIM14	GCA_002599065.1
AOO14869.1	001157	Cluster595_1clades	86	W1230910_023	Cyanophage S-RIM14	GCA_002599125.1
AMO43055.1	001157	Cluster595_1clades	81	R1080702_046	Cyanophage S-RIM32	GCA_001754165.1
AMO43294.1	001157	Cluster595_1clades	91	W270710_050	Cyanophage S-RIM44	GCA_002599145.1
AOO11528.1	001157	Cluster595_1clades	91	ES420910_047	Cyanophage S-RIM44	GCA_002599165.1
AOO11766.1	001157	Cluster595_1clades	91	Np050604_050	Cyanophage S-RIM44	GCA_002599185.1
AOO11993.1	001157	Cluster595_1clades	91	Np200711_047	Cyanophage S-RIM44	GCA_002599205.1
AOO12229.1	001157	Cluster595_1clades	91	Np420711_047	Cyanophage S-RIM44	GCA_002599225.1
AOO12467.1	001157	Cluster595_1clades	91	Sn080709_050	Cyanophage S-RIM44	GCA_002599245.1
AOO12694.1	001157	Cluster595_1clades	91	Sn130910_047	Cyanophage S-RIM44	GCA_002599265.1
AOO12932.1	001157	Cluster595_1clades	91	W2100709_050	Cyanophage S-RIM44	GCA_002599285.1
AGG54346.1	001157	Cluster595_1clades	78	CYWG_00062	Cyanophage S-SSM6b	GCA_002710425.1
ADO99148.1	001157	Cluster595_1clades	91	Syn1_047	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59504.1	001157	Cluster595_1clades	82	S330809_043	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59266.1	001157	Cluster595_1clades	82	C440309_043	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59742.1	001157	Cluster595_1clades	82	N231010_043	Synechococcus phage S-CAM4	GCA_002922155.1
AFC21752.1	001158	Cluster596_1clades	77	GAP32_302	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13932.1	001158	Cluster596_1clades	87	PBI_121Q_35	Escherichia phage 121Q	GCA_000926855.1
QAY00405.1	001158	Cluster596_1clades	77	Ecwhy1_124	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35149.1	001158	Cluster596_1clades	87	ACQ29_gp469	Escherichia phage PBECO4	GCA_001041035.1
BBM61624.1	001158	Cluster596_1clades	77	EO157G_0350	Escherichia phage SP27	GCA_008033345.1
AXC36722.1	001158	Cluster596_1clades	77	-	Escherichia phage UB	GCA_003341455.1
QBO61761.1	001158	Cluster596_1clades	77	G17_00272	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13805.1	001158	Cluster596_1clades	77	vBEcoMphAPEC6_gp176c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80526.1	001158	Cluster596_1clades	77	PSLUR01_00549	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44415.1	001158	Cluster596_1clades	80	RaK2_00142	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43870.1	001158	Cluster596_1clades	77	CBB_307	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19029.1	001158	Cluster596_1clades	77	7t3_0509	Salmonella phage 7t3	GCA_006083215.1
AZU98276.1	001158	Cluster596_1clades	77	CPT_Munch_332	Salmonella phage Munch	GCA_004015485.1
QIG62708.1	001158	Cluster596_1clades	77	SEPL_095	Salmonella phage SE_PL	GCA_011067555.1
AQW88829.1	001158	Cluster596_1clades	77	BF_0304	Serratia phage BF	GCA_002619745.1
SOK59113.1	001158	Cluster596_1clades	76	g305	Yersinia phage fHe-Yen9-03	GCA_002990515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58579.1	001158	Cluster596_1clades	76	g302	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21839.1	001159	Cluster597_1clades	84	GAP32_387	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13986.1	001159	Cluster597_1clades	86	PBI_121Q_89	Escherichia phage 121Q	GCA_000926855.1
QAY00352.1	001159	Cluster597_1clades	86	Ecwhy1_71	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35098.1	001159	Cluster597_1clades	86	ACQ29_gp418	Escherichia phage PBECO4	GCA_001041035.1
BBM61677.1	001159	Cluster597_1clades	86	EO157G_0880	Escherichia phage SP27	GCA_008033345.1
AXC36675.1	001159	Cluster597_1clades	86	-	Escherichia phage UB	GCA_003341455.1
QBO61707.1	001159	Cluster597_1clades	86	G17_00218	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13755.1	001159	Cluster597_1clades	86	vBEcoMphAPEC6_gp126c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79990.1	001159	Cluster597_1clades	86	PSLUR01_00006	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44465.1	001159	Cluster597_1clades	84	RaK2_00192	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43959.1	001159	Cluster597_1clades	84	CBB_396	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19097.1	001159	Cluster597_1clades	74	7t3_0579	Salmonella phage 7t3	GCA_006083215.1
AZU98336.1	001159	Cluster597_1clades	83	CPT_Munch_394	Salmonella phage Munch	GCA_004015485.1
QIG62647.1	001159	Cluster597_1clades	83	SEPL_034	Salmonella phage SE_PL	GCA_011067555.1
AQW88921.1	001159	Cluster597_1clades	84	BF_0396	Serratia phage BF	GCA_002619745.1
SOK59210.1	001159	Cluster597_1clades	84	g402	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58676.1	001159	Cluster597_1clades	84	g399	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21479.1	001160	Cluster598_1clades	80	GAP32_031	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14195.1	001160	Cluster598_1clades	84	PBI_121Q_305	Escherichia phage 121Q	GCA_000926855.1
QAY00744.1	001160	Cluster598_1clades	84	Ecwhy1_469	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61869.1	001160	Cluster598_1clades	84	EO157G_2800	Escherichia phage SP27	GCA_008033345.1
QBO61511.1	001160	Cluster598_1clades	84	G17_00015	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62117.1	001160	Cluster598_1clades	84	G17_00628	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14126.1	001160	Cluster598_1clades	84	vBEcoMphAPEC6_gp503c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80178.1	001160	Cluster598_1clades	84	PSLUR01_00201	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44627.1	001160	Cluster598_1clades	72	RaK2_00354	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44153.1	001160	Cluster598_1clades	80	CBB_37	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43602.1	001160	Cluster598_1clades	80	CBB_590	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18709.1	001160	Cluster598_1clades	83	7t3_0188	Salmonella phage 7t3	GCA_006083215.1
AZU97981.1	001160	Cluster598_1clades	83	CPT_Munch_037	Salmonella phage Munch	GCA_004015485.1
QIG62997.1	001160	Cluster598_1clades	83	SEPL_384	Salmonella phage SE_PL	GCA_011067555.1
AQW88551.1	001160	Cluster598_1clades	80	BF_0026	Serratia phage BF	GCA_002619745.1
SOK58824.1	001160	Cluster598_1clades	80	g016	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58291.1	001160	Cluster598_1clades	80	g014	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21879.1	001161	Cluster599_1clades	71	GAP32_426	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14003.1	001161	Cluster599_1clades	69	PBI_121Q_106	Escherichia phage 121Q	GCA_000926855.1
QAY00335.1	001161	Cluster599_1clades	69	Ecwhy1_54	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35081.1	001161	Cluster599_1clades	69	ACQ29_gp401	Escherichia phage PBECO4	GCA_001041035.1
BBM61694.1	001161	Cluster599_1clades	69	EO157G_1050	Escherichia phage SP27	GCA_008033345.1
AXC36658.1	001161	Cluster599_1clades	69	-	Escherichia phage UB	GCA_003341455.1
QBO61690.1	001161	Cluster599_1clades	69	G17_00201	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13739.1	001161	Cluster599_1clades	69	vBEcoMphAPEC6_gp109c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80007.1	001161	Cluster599_1clades	69	PSLUR01_00023	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44483.1	001161	Cluster599_1clades	81	RaK2_00210	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44009.1	001161	Cluster599_1clades	71	CBB_446	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18536.1	001161	Cluster599_1clades	72	7t3_03	Salmonella phage 7t3	GCA_006083215.1
AZU98369.1	001161	Cluster599_1clades	72	CPT_Munch_429	Salmonella phage Munch	GCA_004015485.1
QIG63144.1	001161	Cluster599_1clades	72	SEPL_531	Salmonella phage SE_PL	GCA_011067555.1
AQW88966.1	001161	Cluster599_1clades	73	BF_0441	Serratia phage BF	GCA_002619745.1
SOK59255.1	001161	Cluster599_1clades	74	g447	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58720.1	001161	Cluster599_1clades	74	g443	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13760.1	001162	Cluster600_1clades	69	Ccr10_gp230	Caulobacter phage Ccr10	GCA_002619445.1
ARB14105.1	001162	Cluster600_1clades	69	Ccr2_gp229	Caulobacter phage Ccr2	GCA_002619465.1
ARB14794.1	001162	Cluster600_1clades	70	Ccr29_gp238	Caulobacter phage Ccr29	GCA_002619485.1
ARB14798.1	001162	Cluster600_1clades	70	Ccr29_gp242	Caulobacter phage Ccr29	GCA_002619485.1
ARB15138.1	001162	Cluster600_1clades	70	Ccr32_gp220	Caulobacter phage Ccr32	GCA_002619505.1
ARB15472.1	001162	Cluster600_1clades	70	Ccr34_gp230	Caulobacter phage Ccr34	GCA_002619525.1
ARB14447.1	001162	Cluster600_1clades	69	Ccr5_gp227	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68427.1	001162	Cluster600_1clades	70	CcrBL10_gp223	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87754.1	001162	Cluster600_1clades	69	CcrKarma_gp237	Caulobacter virus Karma	GCA_000901575.1
AFU87402.1	001162	Cluster600_1clades	69	CcrMagneto_gp232	Caulobacter virus Magneto	GCA_000903095.1
AFU86713.1	001162	Cluster600_1clades	70	CcrRogue_gp231	Caulobacter virus Rogue	GCA_000900555.1
AFU88550.1	001162	Cluster600_1clades	69	CcrSwift_gp232	Caulobacter virus Swift	GCA_000899655.1
AFU87057.1	001162	Cluster600_1clades	69	CbK_gp225	Caulobacter virus phiCbK	GCA_000900535.1
AGR48067.1	001162	Cluster600_1clades	66	SmphiM12_435	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13243.1	001162	Cluster600_1clades	66	PHIM19_338	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12883.1	001162	Cluster600_1clades	66	PHIM7_338	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13606.1	001162	Cluster600_1clades	66	PHIN3_343	Sinorhizobium phage phiN3	GCA_001501175.1
AOO14266.1	001163	Cluster603_1clades	61	Sn110110_072	Cyanophage S-RIM14	GCA_002599065.1
AOO14915.1	001163	Cluster603_1clades	61	W1230910_069	Cyanophage S-RIM14	GCA_002599125.1
AMO43095.1	001163	Cluster603_1clades	37	R1080702_086	Cyanophage S-RIM32	GCA_001754165.1
AMO43323.1	001163	Cluster603_1clades	62	W270710_079	Cyanophage S-RIM44	GCA_002599145.1
AOO11557.1	001163	Cluster603_1clades	63	ES420910_076	Cyanophage S-RIM44	GCA_002599165.1
AOO11795.1	001163	Cluster603_1clades	63	Np050604_079	Cyanophage S-RIM44	GCA_002599185.1
AOO12022.1	001163	Cluster603_1clades	63	Np200711_076	Cyanophage S-RIM44	GCA_002599205.1
AOO12258.1	001163	Cluster603_1clades	63	Np420711_076	Cyanophage S-RIM44	GCA_002599225.1
AOO12496.1	001163	Cluster603_1clades	63	Sn080709_079	Cyanophage S-RIM44	GCA_002599245.1
AOO12723.1	001163	Cluster603_1clades	63	Sn130910_076	Cyanophage S-RIM44	GCA_002599265.1
AOO12961.1	001163	Cluster603_1clades	62	W2100709_079	Cyanophage S-RIM44	GCA_002599285.1
ADO99179.1	001163	Cluster603_1clades	63	Syn1_078	Prochlorococcus phage Syn1	GCA_000892495.1
QDH50605.1	001163	Cluster603_1clades	46	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59534.1	001163	Cluster603_1clades	63	S330809_073	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59296.1	001163	Cluster603_1clades	63	C440309_073	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59772.1	001163	Cluster603_1clades	63	N231010_073	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70084.1	001163	Cluster603_1clades	59	SynMITS9220M01_071	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AOO14237.1	001164	Cluster604_1clades	56	Sn110110_043	Cyanophage S-RIM14	GCA_002599065.1
AOO14889.1	001164	Cluster604_1clades	56	W1230910_043	Cyanophage S-RIM14	GCA_002599125.1
AMO43428.1	001164	Cluster604_1clades	53	W270710_184	Cyanophage S-RIM44	GCA_002599145.1
AOO11672.1	001164	Cluster604_1clades	53	ES420910_191	Cyanophage S-RIM44	GCA_002599165.1
AOO11900.1	001164	Cluster604_1clades	53	Np050604_184	Cyanophage S-RIM44	GCA_002599185.1
AOO12138.1	001164	Cluster604_1clades	53	Np200711_192	Cyanophage S-RIM44	GCA_002599205.1
AOO12373.1	001164	Cluster604_1clades	53	Np420711_191	Cyanophage S-RIM44	GCA_002599225.1
AOO12601.1	001164	Cluster604_1clades	53	Sn080709_184	Cyanophage S-RIM44	GCA_002599245.1
AOO12838.1	001164	Cluster604_1clades	53	Sn130910_191	Cyanophage S-RIM44	GCA_002599265.1
AOO13067.1	001164	Cluster604_1clades	53	W2100709_185	Cyanophage S-RIM44	GCA_002599285.1
ADO99287.1	001164	Cluster604_1clades	53	Syn1_186	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76286.1	001164	Cluster604_1clades	54	PBI_BELLAMY_250	Synechococcus phage Bellamy	GCA_002627525.1
QCW23035.1	001164	Cluster604_1clades	46	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59578.1	001164	Cluster604_1clades	51	S330809_117	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59340.1	001164	Cluster604_1clades	51	C440309_117	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59816.1	001164	Cluster604_1clades	52	N231010_117	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70480.1	001164	Cluster604_1clades	39	HOU04_gp081	Synechococcus phage S-T4	GCA_003443335.1
AOO14382.1	001165	Cluster605_1clades	54	Sn110110_188	Cyanophage S-RIM14	GCA_002599065.1
AOO15030.1	001165	Cluster605_1clades	54	W1230910_184	Cyanophage S-RIM14	GCA_002599125.1
AMO43467.1	001165	Cluster605_1clades	55	W270710_228	Cyanophage S-RIM44	GCA_002599145.1
AOO11707.1	001165	Cluster605_1clades	55	ES420910_230	Cyanophage S-RIM44	GCA_002599165.1
AOO11939.1	001165	Cluster605_1clades	55	Np050604_228	Cyanophage S-RIM44	GCA_002599185.1
AOO12173.1	001165	Cluster605_1clades	55	Np200711_231	Cyanophage S-RIM44	GCA_002599205.1
AOO12408.1	001165	Cluster605_1clades	55	Np420711_230	Cyanophage S-RIM44	GCA_002599225.1
AOO12640.1	001165	Cluster605_1clades	55	Sn080709_228	Cyanophage S-RIM44	GCA_002599245.1
AOO12873.1	001165	Cluster605_1clades	55	Sn130910_230	Cyanophage S-RIM44	GCA_002599265.1
AOO13106.1	001165	Cluster605_1clades	55	W2100709_229	Cyanophage S-RIM44	GCA_002599285.1
AGH07596.1	001165	Cluster605_1clades	54	CYVG_00152	Cyanophage S-SSM6a	GCA_002710385.1
AGG54419.1	001165	Cluster605_1clades	53	CYWG_00135	Cyanophage S-SSM6b	GCA_002710425.1
ADO99328.1	001165	Cluster605_1clades	55	Syn1_232	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59688.1	001165	Cluster605_1clades	54	S330809_227	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59450.1	001165	Cluster605_1clades	54	C440309_227	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59925.1	001165	Cluster605_1clades	54	N231010_226	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70254.1	001165	Cluster605_1clades	53	SynMITS9220M01_248	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27564.1	001166	Cluster606_1clades	55	PTIM40_137	Cyanophage P-TIM40	GCA_001470935.1
AOO14384.1	001166	Cluster606_1clades	54	Sn110110_190	Cyanophage S-RIM14	GCA_002599065.1
AOO15032.1	001166	Cluster606_1clades	54	W1230910_186	Cyanophage S-RIM14	GCA_002599125.1
AMO43142.1	001166	Cluster606_1clades	49	R1080702_133	Cyanophage S-RIM32	GCA_001754165.1
AMO43368.1	001166	Cluster606_1clades	49	W270710_124	Cyanophage S-RIM44	GCA_002599145.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO11612.1	001166	Cluster606_1clades	49	ES420910_131	Cyanophage S-RIM44	GCA_002599165.1
AOO11840.1	001166	Cluster606_1clades	49	Np050604_124	Cyanophage S-RIM44	GCA_002599185.1
AOO12077.1	001166	Cluster606_1clades	49	Np200711_131	Cyanophage S-RIM44	GCA_002599205.1
AOO12313.1	001166	Cluster606_1clades	49	Np420711_131	Cyanophage S-RIM44	GCA_002599225.1
AOO12541.1	001166	Cluster606_1clades	49	Sn080709_124	Cyanophage S-RIM44	GCA_002599245.1
AOO12778.1	001166	Cluster606_1clades	49	Sn130910_131	Cyanophage S-RIM44	GCA_002599265.1
AOO13007.1	001166	Cluster606_1clades	49	W2100709_125	Cyanophage S-RIM44	GCA_002599285.1
ADO99226.1	001166	Cluster606_1clades	54	Syn1_125	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59592.1	001166	Cluster606_1clades	55	S330809_131	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59354.1	001166	Cluster606_1clades	55	C440309_131	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59830.1	001166	Cluster606_1clades	55	N231010_131	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70479.1	001166	Cluster606_1clades	54	HOU04_gp080	Synechococcus phage S-T4	GCA_003443335.1
ARB13627.1	001167	SUN+SUN	1412	Ccr10_gp098	Caulobacter phage Ccr10	GCA_002619445.1
ARB13972.1	001167	SUN+SUN	1412	Ccr2_gp097	Caulobacter phage Ccr2	GCA_002619465.1
ARB14661.1	001167	SUN+SUN	1412	Ccr29_gp105	Caulobacter phage Ccr29	GCA_002619485.1
ARB15016.1	001167	SUN+SUN	1412	Ccr32_gp098	Caulobacter phage Ccr32	GCA_002619505.1
ARB15348.1	001167	SUN+SUN	1412	Ccr34_gp106	Caulobacter phage Ccr34	GCA_002619525.1
ARB14316.1	001167	SUN+SUN	1412	Ccr5_gp098	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68299.1	001167	SUN+SUN	1578	CcrBL10_gp095	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69197.1	001167	SUN+SUN	1616	CcrBL9_gp173	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87995.1	001167	SUN+SUN	1665	CcrColossus_gp125	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68671.1	001167	SUN+SUN	1666	CcrPW_gp132	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69750.1	001167	SUN+SUN	1620	CcrSC_gp168	Caulobacter phage CcrSC	GCA_003443315.1
AFU87619.1	001167	SUN+SUN	1412	CcrKarma_gp102	Caulobacter virus Karma	GCA_000901575.1
AFU87268.1	001167	SUN+SUN	1412	CcrMagneto_gp098	Caulobacter virus Magneto	GCA_000903095.1
AFU86582.1	001167	SUN+SUN	1579	CcrRogue_gp100	Caulobacter virus Rogue	GCA_000900555.1
AFU88415.1	001167	SUN+SUN	1412	CcrSwift_gp097	Caulobacter virus Swift	GCA_000899655.1
AFU86933.1	001167	SUN+SUN	1412	CbK_gp101	Caulobacter virus phiCbK	GCA_000900535.1
ARB13672.1	001168	Cluster609_1clades	1218	Ccr10_gp143	Caulobacter phage Ccr10	GCA_002619445.1
ARB14017.1	001168	Cluster609_1clades	1218	Ccr2_gp142	Caulobacter phage Ccr2	GCA_002619465.1
ARB14705.1	001168	Cluster609_1clades	1218	Ccr29_gp149	Caulobacter phage Ccr29	GCA_002619485.1
ARB15060.1	001168	Cluster609_1clades	1218	Ccr32_gp142	Caulobacter phage Ccr32	GCA_002619505.1
ARB15394.1	001168	Cluster609_1clades	1218	Ccr34_gp152	Caulobacter phage Ccr34	GCA_002619525.1
ARB14360.1	001168	Cluster609_1clades	1218	Ccr5_gp141	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68342.1	001168	Cluster609_1clades	1218	CcrBL10_gp138	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69245.1	001168	Cluster609_1clades	1234	CcrBL9_gp221	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88053.1	001168	Cluster609_1clades	1213	CcrColossus_gp183	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68732.1	001168	Cluster609_1clades	1200	CcrPW_gp193	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69800.1	001168	Cluster609_1clades	1234	CcrSC_gp218	Caulobacter phage CcrSC	GCA_003443315.1
AFU87665.1	001168	Cluster609_1clades	1218	CcrKarma_gp148	Caulobacter virus Karma	GCA_000901575.1
AFU87314.1	001168	Cluster609_1clades	1218	CcrMagneto_gp144	Caulobacter virus Magneto	GCA_000903095.1
AFU86626.1	001168	Cluster609_1clades	1218	CcrRogue_gp144	Caulobacter virus Rogue	GCA_000900555.1
AFU88461.1	001168	Cluster609_1clades	1214	CcrSwift_gp143	Caulobacter virus Swift	GCA_000899655.1
AFU86978.1	001168	Cluster609_1clades	1218	CbK_gp146	Caulobacter virus phiCbK	GCA_000900535.1
QBX06170.1	001169	ValB1HC_217	512	ValB1HC_217	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61187.1	001169	ValB1HC_217	512	AVU32_gp346	Vibrio phage ValKK3	GCA_001501635.1
ALP46978.1	001169	ValB1HC_217	512	phiGrn1_0035	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47361.1	001169	ValB1HC_217	511	phiST2_0167	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54796.1	001169	ValB1HC_217	512	vBValMR10Z_256	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AUZ94870.1	001170	Cluster614_1clades	252	FDI40_gp058	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94874.1	001170	Cluster614_1clades	252	FDI40_gp062	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94872.1	001170	Cluster614_1clades	253	FDI40_gp060	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94867.1	001170	Cluster614_1clades	256	FDI40_gp055	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95167.1	001170	Cluster614_1clades	258	FDI40_gp408	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94873.1	001170	Cluster614_1clades	258	FDI40_gp061	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94869.1	001170	Cluster614_1clades	259	FDI40_gp057	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94868.1	001170	Cluster614_1clades	264	FDI40_gp056	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94871.1	001170	Cluster614_1clades	267	FDI40_gp059	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94875.1	001170	Cluster614_1clades	362	FDI40_gp063	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94866.1	001170	Cluster614_1clades	490	FDI40_gp054	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94865.1	001170	Cluster614_1clades	778	FDI40_gp053	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44338.1	001170	Cluster614_1clades	257	PBI_SCTP2_323	Salicola phage SCTP-2	GCA_002625545.1
ASV44400.1	001170	Cluster614_1clades	247	PBI_SCTP2_385	Salicola phage SCTP-2	GCA_002625545.1
ASV44425.1	001170	Cluster614_1clades	311	PBI_SCTP2_410	Salicola phage SCTP-2	GCA_002625545.1
ASV44460.1	001170	Cluster614_1clades	219	PBI_SCTP2_445	Salicola phage SCTP-2	GCA_002625545.1
AXG67217.1	001171	Trypan_PARP	325	AD1_173	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67288.1	001171	Trypan_PARP	512	AD1_244	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79967.1	001171	Trypan_PARP	105	JA11_162	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80033.1	001171	Trypan_PARP	605	JA11_228	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66565.1	001171	Trypan_PARP	105	JA13_162	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66632.1	001171	Trypan_PARP	605	JA13_229	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66890.1	001171	Trypan_PARP	105	JA29_164	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66956.1	001171	Trypan_PARP	605	JA29_230	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67536.1	001171	Trypan_PARP	105	JA33_162	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67603.1	001171	Trypan_PARP	605	JA33_229	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08447.1	001171	Trypan_PARP	248	Alexandra_178	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08511.1	001171	Trypan_PARP	699	Alexandra_254	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58814.1	001171	Trypan_PARP	408	Y3_174	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58889.1	001171	Trypan_PARP	310	Y3_249	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28648.1	001171	Trypan_PARP	382	YOLOSWAG_169	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28719.1	001171	Trypan_PARP	485	YOLOSWAG_243	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14459.1	001172	Cluster616_2clades	654	PBI_121Q_569	Escherichia phage 121Q	GCA_000926855.1
AFC21668.1	001172	Cluster616_2clades	645	GAP32_218	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QAY00489.1	001172	Cluster616_2clades	654	Ecwhy1_210	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34684.1	001172	Cluster616_2clades	654	ACQ29_gp004	Escherichia phage PBECO4	GCA_001041035.1
BBM62132.1	001172	Cluster616_2clades	654	EO157G_5430	Escherichia phage SP27	GCA_008033345.1
AXC36804.1	001172	Cluster616_2clades	654	-	Escherichia phage UB	GCA_003341455.1
QBO61843.1	001172	Cluster616_2clades	654	G17_00354	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80444.1	001172	Cluster616_2clades	654	PSLUR01_00467	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44333.1	001172	Cluster616_2clades	510	RaK2_00060	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43789.1	001172	Cluster616_2clades	640	CBB_224	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18939.1	001172	Cluster616_2clades	650	7t3_0418	Salmonella phage 7t3	GCA_006083215.1
AZU98194.1	001172	Cluster616_2clades	650	CPT_Munch_250	Salmonella phage Munch	GCA_004015485.1
QIG62791.1	001172	Cluster616_2clades	650	SEPL_178	Salmonella phage SE_PL	GCA_011067555.1
AQW88745.1	001172	Cluster616_2clades	648	BF_0220	Serratia phage BF	GCA_002619745.1
SOK59028.1	001172	Cluster616_2clades	666	g220c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58493.1	001172	Cluster616_2clades	666	g216c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13570.1	001173	DUF4055	632	Ccr10_gp042	Caulobacter phage Ccr10	GCA_002619445.1
ARB13916.1	001173	DUF4055	632	Ccr2_gp041	Caulobacter phage Ccr2	GCA_002619465.1
ARB14605.1	001173	DUF4055	632	Ccr29_gp048	Caulobacter phage Ccr29	GCA_002619485.1
ARB14961.1	001173	DUF4055	632	Ccr32_gp042	Caulobacter phage Ccr32	GCA_002619505.1
ARB15292.1	001173	DUF4055	407	Ccr34_gp043	Caulobacter phage Ccr34	GCA_002619525.1
ARB14259.1	001173	DUF4055	632	Ccr5_gp041	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68246.1	001173	DUF4055	635	CcrBL10_gp042	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69106.1	001173	DUF4055	601	CcrBL9_gp082	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87908.1	001173	DUF4055	661	CcrColossus_gp038	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68581.1	001173	DUF4055	640	CcrPW_gp042	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69660.1	001173	DUF4055	602	CcrSC_gp078	Caulobacter phage CcrSC	GCA_003443315.1
AFU87560.1	001173	DUF4055	609	CcrKarma_gp043	Caulobacter virus Karma	GCA_000901575.1
AFU87210.1	001173	DUF4055	610	CcrMagneto_gp040	Caulobacter virus Magneto	GCA_000903095.1
AFU86528.1	001173	DUF4055	612	CcrRogue_gp046	Caulobacter virus Rogue	GCA_000900555.1
AFU88358.1	001173	DUF4055	609	CcrSwift_gp040	Caulobacter virus Swift	GCA_000899655.1
AFU86874.1	001173	DUF4055	609	CbK_gp042	Caulobacter virus phiCbK	GCA_000900535.1
QDH83678.1	001174	Cluster619_1clades	590	H1O15_gp133	Achromobacter phage Motura	GCA_006964305.1
QBX06675.1	001174	Cluster619_1clades	595	BcepSaruman_262	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74645.1	001174	Cluster619_1clades	609	BcepSauron_265	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67155.1	001174	Cluster619_1clades	487	AD1_111	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79905.1	001174	Cluster619_1clades	487	JA11_100	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66504.1	001174	Cluster619_1clades	487	JA13_101	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66829.1	001174	Cluster619_1clades	487	JA29_103	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67474.1	001174	Cluster619_1clades	487	JA33_100	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08389.1	001174	Cluster619_1clades	487	Alexandra_117	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58753.1	001174	Cluster619_1clades	488	Y3_113	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28587.1	001174	Cluster619_1clades	487	YOLOSWAG_105	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38308.1	001174	Cluster619_1clades	443	BN7874_139	Phage NCTB	GCA_900092385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFH14763.1	001174	Cluster619_1clades	485	Lu11_0226	Pseudomonas phage Lu11	GCA_000897175.1
QHJ85933.1	001174	Cluster619_1clades	467	KKIINIFJ_00021	Pseudomonas phage PN05	GCA_009931935.1
AGS82114.1	001174	Cluster619_1clades	487	PaBG_00240	Pseudomonas phage PaBG	GCA_000912555.1
BAG41647.1	001174	Cluster619_1clades	594	RSL1_ORF198	Ralstonia phage phiRSL1	GCA_000879455.1
AMS01281.1	001175	Cluster620_1clades	292	AR9_g197	Bacillus phage AR9	GCA_001743835.1
AMS01361.1	001175	Cluster620_1clades	195	AR9_g277	Bacillus phage AR9	GCA_001743835.1
ALN97703.1	001175	Cluster620_1clades	197	Bp8pS_024	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99991.1	001175	Cluster620_1clades	195	PBI_PBS1_170	Bacillus virus PBS1	GCA_002601325.1
AST99909.1	001175	Cluster620_1clades	292	PBI_PBS1_87	Bacillus virus PBS1	GCA_002601325.1
AXG67139.1	001175	Cluster620_1clades	539	AD1_095	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79888.1	001175	Cluster620_1clades	458	JA11_083	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66487.1	001175	Cluster620_1clades	458	JA13_084	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66812.1	001175	Cluster620_1clades	458	JA29_086	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67457.1	001175	Cluster620_1clades	458	JA33_083	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08375.1	001175	Cluster620_1clades	540	Alexandra_100	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58738.1	001175	Cluster620_1clades	537	Y3_098	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28571.1	001175	Cluster620_1clades	529	YOLOSWAG_88	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38290.1	001175	Cluster620_1clades	564	BN7874_121	Phage NCTB	GCA_900092385.1
AFH14786.1	001175	Cluster620_1clades	330	Lu11_0250	Pseudomonas phage Lu11	GCA_000897175.1
AGS82132.1	001175	Cluster620_1clades	560	PaBG_00257	Pseudomonas phage PaBG	GCA_000912555.1
ARB13623.1	001176	DUF2163+Phage_BR0599	541	Ccr10_gp094	Caulobacter phage Ccr10	GCA_002619445.1
ARB13968.1	001176	DUF2163+Phage_BR0599	541	Ccr2_gp093	Caulobacter phage Ccr2	GCA_002619465.1
ARB14657.1	001176	DUF2163+Phage_BR0599	541	Ccr29_gp101	Caulobacter phage Ccr29	GCA_002619485.1
ARB15012.1	001176	DUF2163+Phage_BR0599	533	Ccr32_gp094	Caulobacter phage Ccr32	GCA_002619505.1
ARB15343.1	001176	DUF2163+Phage_BR0599	533	Ccr34_gp101	Caulobacter phage Ccr34	GCA_002619525.1
ARB14312.1	001176	DUF2163+Phage_BR0599	541	Ccr5_gp094	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68295.1	001176	DUF2163+Phage_BR0599	541	CcrBL10_gp091	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69192.1	001176	DUF2163+Phage_BR0599	549	CcrBL9_gp168	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87990.1	001176	DUF2163+Phage_BR0599	542	CcrColossus_gp120	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68666.1	001176	DUF2163+Phage_BR0599	520	CcrPW_gp127	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69745.1	001176	DUF2163+Phage_BR0599	549	CcrSC_gp163	Caulobacter phage CcrSC	GCA_003443315.1
AFU87615.1	001176	DUF2163+Phage_BR0599	541	CcrKarma_gp098	Caulobacter virus Karma	GCA_000901575.1
AFU87264.1	001176	DUF2163+Phage_BR0599	533	CcrMagneto_gp094	Caulobacter virus Magneto	GCA_000903095.1
AFU86578.1	001176	DUF2163+Phage_BR0599	541	CcrRogue_gp096	Caulobacter virus Rogue	GCA_000900555.1
AFU88411.1	001176	DUF2163+Phage_BR0599	533	CcrSwift_gp093	Caulobacter virus Swift	GCA_000899655.1
AFU86929.1	001176	DUF2163+Phage_BR0599	541	CbK_gp097	Caulobacter virus phiCbK	GCA_000900535.1
AHI60439.1	001177	Cluster625_1clades	418	Ea357_285	Erwinia phage Ea35-70	GCA_000914635.1
AGX01954.1	001177	Cluster625_1clades	456	CF95_gp232	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07396.1	001177	Cluster625_1clades	418	REBECCA_291	Erwinia phage Rebecca	GCA_004521635.1
AUG86078.1	001177	Cluster625_1clades	418	BOSOLAPHORUS_292	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52394.1	001177	Cluster625_1clades	418	DM_295	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86398.1	001177	Cluster625_1clades	418	DESERTFOX_291	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86719.1	001177	Cluster625_1clades	418	MADMEL_292	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87044.1	001177	Cluster625_1clades	418	MORTIMER_296	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52069.1	001177	Cluster625_1clades	418	RAY_289	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51752.1	001177	Cluster625_1clades	418	SIMMY50_294	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65104.1	001177	Cluster625_1clades	418	SPECIALG_293	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24192.1	001177	Cluster625_1clades	419	-	Proteus phage 10	GCA_014071245.1
QKE54616.1	001177	Cluster625_1clades	419	ACSA002_2990	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65349.1	001177	Cluster625_1clades	405	2050HW_00014	Serratia phage 2050HW	GCA_002628125.1
QDB71136.1	001177	Cluster625_1clades	405	CPT_Moabite_106	Serratia phage Moabite	GCA_006384735.1
QFP93081.1	001177	Cluster625_1clades	460	-	Serratia phage PCH45	GCA_009187865.1
AMR59852.1	001178	Cluster626_1clades	142	SEGD1_205	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59853.1	001178	Cluster626_1clades	123	SEGD1_206	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49850.1	001178	Cluster626_1clades	293	MACHINA_212	Erwinia phage Machina	GCA_002758035.1
AXF51352.1	001178	Cluster626_1clades	306	WELLINGTON_226	Erwinia phage Wellington	GCA_003344985.1
AFQ96667.1	001178	Cluster626_1clades	408	G173_gp122	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48233.1	001178	Cluster626_1clades	397	ASESINO_220	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48507.1	001178	Cluster626_1clades	313	CAITLIN_212	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48784.1	001178	Cluster626_1clades	315	CHRISDB_222	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49294.1	001178	Cluster626_1clades	293	HUXLEY_212	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49578.1	001178	Cluster626_1clades	306	KWAN_226	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50122.1	001178	Cluster626_1clades	293	PARSHIK_213	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50647.1	001178	Cluster626_1clades	408	STRATTON_222	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86041.1	001178	Cluster626_1clades	377	ACEC001_1980	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20889.1	001178	Cluster626_1clades	377	-	Salmonella phage JN03	GCA_014319805.1
AXF51118.1	001178	Cluster626_1clades	302	MLDJOKPK_00239	Salmonella phage SPAsTU	GCA_003183805.1
AEP84034.1	001178	Cluster626_1clades	377	SPN3US_0201	Salmonella phage SPN3US	GCA_001042275.1
ARB13646.1	001179	Cluster627_1clades	378	Ccr10_gp117c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13991.1	001179	Cluster627_1clades	378	Ccr2_gp116c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14679.1	001179	Cluster627_1clades	378	Ccr29_gp123	Caulobacter phage Ccr29	GCA_002619485.1
ARB15034.1	001179	Cluster627_1clades	378	Ccr32_gp116	Caulobacter phage Ccr32	GCA_002619505.1
ARB15366.1	001179	Cluster627_1clades	378	Ccr34_gp124	Caulobacter phage Ccr34	GCA_002619525.1
ARB14335.1	001179	Cluster627_1clades	378	Ccr5_gp117c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68315.1	001179	Cluster627_1clades	378	CcrBL10_gp111c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69215.1	001179	Cluster627_1clades	363	CcrBL9_gp191	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88025.1	001179	Cluster627_1clades	365	CcrColossus_gp155	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68702.1	001179	Cluster627_1clades	365	CcrPW_gp163c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69769.1	001179	Cluster627_1clades	363	CcrSC_gp187	Caulobacter phage CcrSC	GCA_003443315.1
AFU87638.1	001179	Cluster627_1clades	378	CcrKarma_gp121	Caulobacter virus Karma	GCA_000901575.1
AFU87287.1	001179	Cluster627_1clades	378	CcrMagneto_gp117	Caulobacter virus Magneto	GCA_000903095.1
AFU86599.1	001179	Cluster627_1clades	378	CcrRogue_gp117	Caulobacter virus Rogue	GCA_000900555.1
AFU88434.1	001179	Cluster627_1clades	378	CcrSwift_gp116	Caulobacter virus Swift	GCA_000899655.1
AFU86952.1	001179	Cluster627_1clades	378	CbK_gp120	Caulobacter virus phiCbK	GCA_000900535.1
QDH83600.1	001180	Cluster629_1clades	361	H1O15_gp188	Achromobacter phage Motura	GCA_006964305.1
AEO93298.1	001180	Cluster629_1clades	282	G_27	Bacillus virus G	GCA_000917535.1
QBX06495.1	001180	Cluster629_1clades	362	BcepSaruman_082	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74462.1	001180	Cluster629_1clades	362	BcepSauron_082	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67182.1	001180	Cluster629_1clades	366	AD1_138	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79932.1	001180	Cluster629_1clades	364	JA11_127	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66531.1	001180	Cluster629_1clades	364	JA13_128	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66856.1	001180	Cluster629_1clades	364	JA29_130	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67501.1	001180	Cluster629_1clades	364	JA33_127	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08415.1	001180	Cluster629_1clades	366	Alexandra_143	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58779.1	001180	Cluster629_1clades	366	Y3_139	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28617.1	001180	Cluster629_1clades	370	YOLOSWAG_137	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38404.1	001180	Cluster629_1clades	360	BN7874_220	Phage NCTB	GCA_900092385.1
AFH14596.1	001180	Cluster629_1clades	364	Lu11_0065	Pseudomonas phage Lu11	GCA_000897175.1
AGS81964.1	001180	Cluster629_1clades	368	PaBG_00080	Pseudomonas phage PaBG	GCA_000912555.1
BAG41581.1	001180	Cluster629_1clades	362	RSL1_ORF136	Ralstonia phage phiRSL1	GCA_000879455.1
AGH07644.1	001181	Cluster634_1clades	278	CYVG_00201	Cyanophage S-SSM6a	GCA_002710385.1
AIR93403.1	001181	Cluster634_1clades	266	AVU42_gp017	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93404.1	001181	Cluster634_1clades	78	AVU42_gp018	Prochlorococcus phage P-TIM68	GCA_001503075.1
QGT54642.1	001181	Cluster634_1clades	261	b23_0014	Synechococcus phage B23	GCA_009745195.1
QGT54643.1	001181	Cluster634_1clades	218	b23_0015	Synechococcus phage B23	GCA_009745195.1
QGT54272.1	001181	Cluster634_1clades	261	b3_0014	Synechococcus phage B3	GCA_009745215.1
QGT54273.1	001181	Cluster634_1clades	218	b3_0015	Synechococcus phage B3	GCA_009745215.1
ASR76066.1	001181	Cluster634_1clades	264	PBI_BELLAMY_19	Synechococcus phage Bellamy	GCA_002627525.1
ASR76067.1	001181	Cluster634_1clades	220	PBI_BELLAMY_20	Synechococcus phage Bellamy	GCA_002627525.1
QCW22913.1	001181	Cluster634_1clades	230	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22914.1	001181	Cluster634_1clades	257	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50543.1	001181	Cluster634_1clades	225	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50544.1	001181	Cluster634_1clades	280	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70435.1	001181	Cluster634_1clades	296	HOU04_gp036	Synechococcus phage S-T4	GCA_003443335.1
QJT70034.1	001181	Cluster634_1clades	264	SynMITS9220M01_018	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70035.1	001181	Cluster634_1clades	258	SynMITS9220M01_019	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ANS06029.1	001182	CR-HNH3	176	ABCD_0234	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97252.1	001182	CR-HNH3	175	E_244	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78770.1	001182	CR-HNH3	175	RB43ORF248w	Escherichia virus RB43	GCA_000863505.1
AAQ64111.1	001182	CR-HNH3	235	KVP40.0040	Vibrio phage KVP40	GCA_000843785.1
QIW90434.1	001182	CR-HNH3	235	GCAPEGMB_00087	Vibrio phage V07	GCA_012361095.1
QIW90995.1	001182	CR-HNH3	235	COHAPHLL_00132	Vibrio phage V09	GCA_012361135.1
QHJ74223.1	001182	CR-HNH3	235	VH12019_00304	Vibrio phage VH1_2019	GCA_009931825.1
AGB07047.1	001182	CR-HNH3	235	CF80_gp260	Vibrio phage VH7D	GCA_000914495.1
QBX06049.1	001182	CR-HNH3	235	ValB1HC_095	Vibrio phage ValB1 HC	GCA_004771355.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN30089.1	001182	CR-HNH3	235	VPFG_00087	Vibrio phage nt-1	GCA_000910195.2
ALP47428.1	001182	CR-HNH3	235	phiST2_0285	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54675.1	001182	CR-HNH3	235	vBValMR10Z_134	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QAX96828.1	001182	CR-HNH3	274	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96193.1	001182	CR-HNH3	274	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96511.1	001182	CR-HNH3	274	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFN37273.1	001182	CR-HNH3	235	pp2_039	Vibriophage phi-pp2	GCA_002630725.1
ARB13606.1	001183	Cluster639_1clades	258	Ccr10_gp078	Caulobacter phage Ccr10	GCA_002619445.1
ARB13952.1	001183	Cluster639_1clades	258	Ccr2_gp077	Caulobacter phage Ccr2	GCA_002619465.1
ARB14643.1	001183	Cluster639_1clades	258	Ccr29_gp086	Caulobacter phage Ccr29	GCA_002619485.1
ARB14998.1	001183	Cluster639_1clades	258	Ccr32_gp079	Caulobacter phage Ccr32	GCA_002619505.1
ARB15329.1	001183	Cluster639_1clades	258	Ccr34_gp085	Caulobacter phage Ccr34	GCA_002619525.1
ARB14295.1	001183	Cluster639_1clades	258	Ccr5_gp077	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68280.1	001183	Cluster639_1clades	258	CcrBL10_gp076	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69163.1	001183	Cluster639_1clades	260	CcrBL9_gp139	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87963.1	001183	Cluster639_1clades	255	CcrColossus_gp093	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68639.1	001183	Cluster639_1clades	255	CcrPW_gp100	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69718.1	001183	Cluster639_1clades	260	CcrSC_gp136	Caulobacter phage CcrSC	GCA_003443315.1
AFU87596.1	001183	Cluster639_1clades	219	CcrKarma_gp079	Caulobacter virus Karma	GCA_000901575.1
AFU87246.1	001183	Cluster639_1clades	258	CcrMagneto_gp076	Caulobacter virus Magneto	GCA_000903095.1
AFU86562.1	001183	Cluster639_1clades	219	CcrRogue_gp080	Caulobacter virus Rogue	GCA_000900555.1
AFU88394.1	001183	Cluster639_1clades	258	CcrSwift_gp076	Caulobacter virus Swift	GCA_000899655.1
AFU86910.1	001183	Cluster639_1clades	219	CbK_gp078	Caulobacter virus phiCbK	GCA_000900535.1
AFC21525.1	001184	Cluster641_1clades	243	GAP32_077	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14322.1	001184	Cluster641_1clades	242	PBI_121Q_432	Escherichia phage 121Q	GCA_000926855.1
AGC34815.1	001184	Cluster641_1clades	245	ACQ29_gp135	Escherichia phage PBECO4	GCA_001041035.1
BBM61995.1	001184	Cluster641_1clades	242	EO157G_4060	Escherichia phage SP27	GCA_008033345.1
AXC36925.1	001184	Cluster641_1clades	242	-	Escherichia phage UB	GCA_003341455.1
QBO61982.1	001184	Cluster641_1clades	242	G17_00493	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14006.1	001184	Cluster641_1clades	242	vBEcoMphAPEC6_gp382c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80309.1	001184	Cluster641_1clades	242	PSLUR01_00332	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44732.1	001184	Cluster641_1clades	242	RaK2_00459	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43645.1	001184	Cluster641_1clades	243	CBB_80	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18777.1	001184	Cluster641_1clades	243	7t3_0256	Salmonella phage 7t3	GCA_006083215.1
AZU98042.1	001184	Cluster641_1clades	243	CPT_Munch_098	Salmonella phage Munch	GCA_004015485.1
QIG62938.1	001184	Cluster641_1clades	243	SEPL_325	Salmonella phage SE_PL	GCA_011067555.1
AQW88595.1	001184	Cluster641_1clades	243	BF_0070	Serratia phage BF	GCA_002619745.1
SOK58871.1	001184	Cluster641_1clades	243	g063	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58334.1	001184	Cluster641_1clades	243	g057	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13669.1	001185	SIG+Phage_integrase	208	Ccr10_gp140	Caulobacter phage Ccr10	GCA_002619445.1
ARB14014.1	001185	SIG+Phage_integrase	208	Ccr2_gp139	Caulobacter phage Ccr2	GCA_002619465.1
ARB14701.1	001185	SIG+Phage_integrase	208	Ccr29_gp145	Caulobacter phage Ccr29	GCA_002619485.1
ARB15056.1	001185	SIG+Phage_integrase	208	Ccr32_gp138	Caulobacter phage Ccr32	GCA_002619505.1
ARB15390.1	001185	SIG+Phage_integrase	208	Ccr34_gp148	Caulobacter phage Ccr34	GCA_002619525.1
ARB14357.1	001185	SIG+Phage_integrase	208	Ccr5_gp138	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68337.1	001185	SIG+Phage_integrase	208	CcrBL10_gp133	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69243.1	001185	SIG+Phage_integrase	242	CcrBL9_gp219	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88052.1	001185	SIG+Phage_integrase	220	CcrColossus_gp182	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68731.1	001185	SIG+Phage_integrase	220	CcrPW_gp192	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69797.1	001185	SIG+Phage_integrase	242	CcrSC_gp215	Caulobacter phage CcrSC	GCA_003443315.1
AFU87662.1	001185	SIG+Phage_integrase	208	CcrKarma_gp145	Caulobacter virus Karma	GCA_000901575.1
AFU87311.1	001185	SIG+Phage_integrase	208	CcrMagneto_gp141	Caulobacter virus Magneto	GCA_000903095.1
AFU86622.1	001185	SIG+Phage_integrase	208	CcrRogue_gp140	Caulobacter virus Rogue	GCA_000900555.1
AFU88458.1	001185	SIG+Phage_integrase	208	CcrSwift_gp140	Caulobacter virus Swift	GCA_000899655.1
AFU86975.1	001185	SIG+Phage_integrase	208	CbK_gp143	Caulobacter virus phiCbK	GCA_000900535.1
ARB13848.1	001186	Cluster643_1clades	234	Ccr10_gp318	Caulobacter phage Ccr10	GCA_002619445.1
ARB14193.1	001186	Cluster643_1clades	234	Ccr2_gp317	Caulobacter phage Ccr2	GCA_002619465.1
ARB14887.1	001186	Cluster643_1clades	234	Ccr29_gp331	Caulobacter phage Ccr29	GCA_002619485.1
ARB15225.1	001186	Cluster643_1clades	234	Ccr32_gp307	Caulobacter phage Ccr32	GCA_002619505.1
ARB15559.1	001186	Cluster643_1clades	234	Ccr34_gp317	Caulobacter phage Ccr34	GCA_002619525.1
ARB14533.1	001186	Cluster643_1clades	234	Ccr5_gp313	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68516.1	001186	Cluster643_1clades	236	CcrBL10_gp312	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69521.1	001186	Cluster643_1clades	241	CcrBL9_gp497	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88311.1	001186	Cluster643_1clades	190	CcrColossus_gp441	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68982.1	001186	Cluster643_1clades	159	CcrPW_gp443	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70066.1	001186	Cluster643_1clades	241	CcrSC_gp484	Caulobacter phage CcrSC	GCA_003443315.1
AFU87844.1	001186	Cluster643_1clades	236	CcrKarma_gp327	Caulobacter virus Karma	GCA_000901575.1
AFU87492.1	001186	Cluster643_1clades	236	CcrMagneto_gp322	Caulobacter virus Magneto	GCA_000903095.1
AFU86806.1	001186	Cluster643_1clades	236	CcrRogue_gp324	Caulobacter virus Rogue	GCA_000900555.1
AFU88637.1	001186	Cluster643_1clades	234	CcrSwift_gp319	Caulobacter virus Swift	GCA_000899655.1
AFU87144.1	001186	Cluster643_1clades	234	CbK_gp312	Caulobacter virus phiCbK	GCA_000900535.1
ARB13820.1	001187	Cluster644_1clades	125	Ccr10_gp290	Caulobacter phage Ccr10	GCA_002619445.1
ARB14165.1	001187	Cluster644_1clades	125	Ccr2_gp289	Caulobacter phage Ccr2	GCA_002619465.1
ARB14859.1	001187	Cluster644_1clades	125	Ccr29_gp303	Caulobacter phage Ccr29	GCA_002619485.1
ARB15198.1	001187	Cluster644_1clades	125	Ccr32_gp280	Caulobacter phage Ccr32	GCA_002619505.1
ARB15532.1	001187	Cluster644_1clades	125	Ccr34_gp290	Caulobacter phage Ccr34	GCA_002619525.1
ARB14507.1	001187	Cluster644_1clades	125	Ccr5_gp287	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68487.1	001187	Cluster644_1clades	159	CcrBL10_gp283	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69334.1	001187	Cluster644_1clades	143	CcrBL9_gp310	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88131.1	001187	Cluster644_1clades	236	CcrColossus_gp261	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68808.1	001187	Cluster644_1clades	236	CcrPW_gp269	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69895.1	001187	Cluster644_1clades	143	CcrSC_gp313	Caulobacter phage CcrSC	GCA_003443315.1
AFU87817.1	001187	Cluster644_1clades	125	CcrKarma_gp300	Caulobacter virus Karma	GCA_000901575.1
AFU87464.1	001187	Cluster644_1clades	125	CcrMagneto_gp294	Caulobacter virus Magneto	GCA_000903095.1
AFU86775.1	001187	Cluster644_1clades	163	CcrRogue_gp293	Caulobacter virus Rogue	GCA_000900555.1
AFU88609.1	001187	Cluster644_1clades	125	CcrSwift_gp291	Caulobacter virus Swift	GCA_000899655.1
AFU87117.1	001187	Cluster644_1clades	125	CbK_gp285	Caulobacter virus phiCbK	GCA_000900535.1
AND75327.1	001188	Cluster645_1clades	102	ME3_166	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ95395.1	001188	Cluster645_1clades	102	FDI40_gp636	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21897.1	001188	Cluster645_1clades	161	GAP32_442	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXH72424.1	001188	Cluster645_1clades	228	-	Myoviridae sp.	GCA_003657725.1
AMM44026.1	001188	Cluster645_1clades	161	CBB_463	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QHJ85952.1	001188	Cluster645_1clades	92	KKIINIFJ_00040	Pseudomonas phage PN05	GCA_009931935.1
QCW18553.1	001188	Cluster645_1clades	85	7t3_028	Salmonella phage 7t3	GCA_006083215.1
AZU98382.1	001188	Cluster645_1clades	85	CPT_Munch_448	Salmonella phage Munch	GCA_004015485.1
QIG63130.1	001188	Cluster645_1clades	85	SEPL_517	Salmonella phage SE_PL	GCA_011067555.1
ATA65547.1	001188	Cluster645_1clades	183	2050HW_00212	Serratia phage 2050HW	GCA_002628125.1
AQW88983.1	001188	Cluster645_1clades	84	BF_0458	Serratia phage BF	GCA_002619745.1
QDB71312.1	001188	Cluster645_1clades	183	CPT_Moabite_282	Serratia phage Moabite	GCA_006384735.1
AGR48003.1	001188	Cluster645_1clades	96	SmphiM12_371	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13189.1	001188	Cluster645_1clades	96	PHIM19_284	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12829.1	001188	Cluster645_1clades	96	PHIM7_284	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13551.1	001188	Cluster645_1clades	96	PHIN3_288	Sinorhizobium phage phiN3	GCA_001501175.1
ARB13561.1	001189	Cluster646_1clades	221	Ccr10_gp033	Caulobacter phage Ccr10	GCA_002619445.1
ARB13907.1	001189	Cluster646_1clades	221	Ccr2_gp032	Caulobacter phage Ccr2	GCA_002619465.1
ARB14596.1	001189	Cluster646_1clades	221	Ccr29_gp039	Caulobacter phage Ccr29	GCA_002619485.1
ARB14951.1	001189	Cluster646_1clades	221	Ccr32_gp032	Caulobacter phage Ccr32	GCA_002619505.1
ARB15282.1	001189	Cluster646_1clades	221	Ccr34_gp033	Caulobacter phage Ccr34	GCA_002619525.1
ARB14250.1	001189	Cluster646_1clades	221	Ccr5_gp032	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68233.1	001189	Cluster646_1clades	225	CcrBL10_gp029	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69488.1	001189	Cluster646_1clades	224	CcrBL9_gp464	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88241.1	001189	Cluster646_1clades	210	CcrColossus_gp371	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68916.1	001189	Cluster646_1clades	210	CcrPW_gp377c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70036.1	001189	Cluster646_1clades	224	CcrSC_gp454	Caulobacter phage CcrSC	GCA_003443315.1
AFU87550.1	001189	Cluster646_1clades	221	CcrKarma_gp033	Caulobacter virus Karma	GCA_000901575.1
AFU87201.1	001189	Cluster646_1clades	221	CcrMagneto_gp031	Caulobacter virus Magneto	GCA_000903095.1
AFU86515.1	001189	Cluster646_1clades	225	CcrRogue_gp033	Caulobacter virus Rogue	GCA_000900555.1
AFU88347.1	001189	Cluster646_1clades	221	CcrSwift_gp029	Caulobacter virus Swift	GCA_000899655.1
AFU86864.1	001189	Cluster646_1clades	221	CbK_gp032	Caulobacter virus phiCbK	GCA_000900535.1
ARB13605.1	001190	Cluster647_1clades	222	Ccr10_gp077	Caulobacter phage Ccr10	GCA_002619445.1
ARB13951.1	001190	Cluster647_1clades	222	Ccr2_gp076	Caulobacter phage Ccr2	GCA_002619465.1
ARB14642.1	001190	Cluster647_1clades	222	Ccr29_gp085	Caulobacter phage Ccr29	GCA_002619485.1
ARB14997.1	001190	Cluster647_1clades	222	Ccr32_gp078	Caulobacter phage Ccr32	GCA_002619505.1
ARB15328.1	001190	Cluster647_1clades	222	Ccr34_gp084	Caulobacter phage Ccr34	GCA_002619525.1
ARB14294.1	001190	Cluster647_1clades	222	Ccr5_gp076	Caulobacter phage Ccr5	GCA_002619545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ68279.1	001190	Cluster647_1clades	222	CcrBL10_gp075	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69162.1	001190	Cluster647_1clades	224	CcrBL9_gp138	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87962.1	001190	Cluster647_1clades	225	CcrColossus_gp092	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68638.1	001190	Cluster647_1clades	225	CcrPW_gp099	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69717.1	001190	Cluster647_1clades	224	CcrSC_gp135	Caulobacter phage CcrSC	GCA_003443315.1
AFU87595.1	001190	Cluster647_1clades	222	CcrKarma_gp078	Caulobacter virus Karma	GCA_000901575.1
AFU87245.1	001190	Cluster647_1clades	222	CcrMagneto_gp075	Caulobacter virus Magneto	GCA_000903095.1
AFU86561.1	001190	Cluster647_1clades	222	CcrRogue_gp079	Caulobacter virus Rogue	GCA_000900555.1
AFU88393.1	001190	Cluster647_1clades	222	CcrSwift_gp075	Caulobacter virus Swift	GCA_000899655.1
AFU86909.1	001190	Cluster647_1clades	222	CbK_gp077	Caulobacter virus phiCbK	GCA_000900535.1
ARB13622.1	001191	DUF2460	216	Ccr10_gp093	Caulobacter phage Ccr10	GCA_002619445.1
ARB13967.1	001191	DUF2460	216	Ccr2_gp092	Caulobacter phage Ccr2	GCA_002619465.1
ARB14656.1	001191	DUF2460	216	Ccr29_gp100	Caulobacter phage Ccr29	GCA_002619485.1
ARB15011.1	001191	DUF2460	216	Ccr32_gp093	Caulobacter phage Ccr32	GCA_002619505.1
ARB15342.1	001191	DUF2460	216	Ccr34_gp100	Caulobacter phage Ccr34	GCA_002619525.1
ARB14311.1	001191	DUF2460	216	Ccr5_gp093	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68294.1	001191	DUF2460	222	CcrBL10_gp090	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69191.1	001191	DUF2460	216	CcrBL9_gp167	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87989.1	001191	DUF2460	215	CcrColossus_gp119	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68665.1	001191	DUF2460	215	CcrPW_gp126	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69744.1	001191	DUF2460	216	CcrSC_gp162	Caulobacter phage CcrSC	GCA_003443315.1
AFU87614.1	001191	DUF2460	216	CcrKarma_gp097	Caulobacter virus Karma	GCA_000901575.1
AFU87263.1	001191	DUF2460	216	CcrMagneto_gp093	Caulobacter virus Magneto	GCA_000903095.1
AFU86577.1	001191	DUF2460	222	CcrRogue_gp095	Caulobacter virus Rogue	GCA_000900555.1
AFU88410.1	001191	DUF2460	216	CcrSwift_gp092	Caulobacter virus Swift	GCA_000899655.1
AFU86928.1	001191	DUF2460	216	CbK_gp096	Caulobacter virus phiCbK	GCA_000900535.1
AIT14365.1	001192	Cluster649_1clades	198	PBI_121Q_475	Escherichia phage 121Q	GCA_000926855.1
QAY00583.1	001192	Cluster649_1clades	197	Ecwhy1_304	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34776.1	001192	Cluster649_1clades	197	ACQ29_gp096	Escherichia phage PBECO4	GCA_001041035.1
BBM62035.1	001192	Cluster649_1clades	197	EO157G_4460	Escherichia phage SP27	GCA_008033345.1
AXC36891.1	001192	Cluster649_1clades	197	-	Escherichia phage UB	GCA_003341455.1
QBO61940.1	001192	Cluster649_1clades	197	G17_00451	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13969.1	001192	Cluster649_1clades	197	vBEcoMphAPEC6_gp345c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80351.1	001192	Cluster649_1clades	197	PSLUR01_00374	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG65802.1	001192	Cluster649_1clades	219	phiOC_p137	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ASV44484.1	001192	Cluster649_1clades	188	PBI_SCTP2_469	Salicola phage SCTP-2	GCA_002625545.1
QCW18819.1	001192	Cluster649_1clades	197	7t3_0298	Salmonella phage 7t3	GCA_006083215.1
AZU98083.1	001192	Cluster649_1clades	197	CPT_Munch_139	Salmonella phage Munch	GCA_004015485.1
QIG62899.1	001192	Cluster649_1clades	197	SEPL_286	Salmonella phage SE_PL	GCA_011067555.1
BAV39416.1	001192	Cluster649_1clades	198	BPT24_298	Tenacibaculum phage pT24	GCA_002611925.1
BBA65351.1	001192	Cluster649_1clades	196	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96383.1	001192	Cluster649_1clades	192	Xoosp13_197	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ARB13851.1	001193	Cluster650_1clades	211	Ccr10_gp321	Caulobacter phage Ccr10	GCA_002619445.1
ARB14196.1	001193	Cluster650_1clades	211	Ccr2_gp320	Caulobacter phage Ccr2	GCA_002619465.1
ARB14890.1	001193	Cluster650_1clades	211	Ccr29_gp334	Caulobacter phage Ccr29	GCA_002619485.1
ARB15228.1	001193	Cluster650_1clades	211	Ccr32_gp310	Caulobacter phage Ccr32	GCA_002619505.1
ARB15562.1	001193	Cluster650_1clades	211	Ccr34_gp320	Caulobacter phage Ccr34	GCA_002619525.1
ARB14536.1	001193	Cluster650_1clades	211	Ccr5_gp316	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68520.1	001193	Cluster650_1clades	217	CcrBL10_gp316	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69534.1	001193	Cluster650_1clades	169	CcrBL9_gp510	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88315.1	001193	Cluster650_1clades	180	CcrColossus_gp445	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68986.1	001193	Cluster650_1clades	180	CcrPW_gp447	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70077.1	001193	Cluster650_1clades	169	CcrSC_gp495	Caulobacter phage CcrSC	GCA_003443315.1
AFU87847.1	001193	Cluster650_1clades	214	CcrKarma_gp330	Caulobacter virus Karma	GCA_000901575.1
AFU87495.1	001193	Cluster650_1clades	211	CcrMagneto_gp325	Caulobacter virus Magneto	GCA_000903095.1
AFU86810.1	001193	Cluster650_1clades	217	CcrRogue_gp328	Caulobacter virus Rogue	GCA_000900555.1
AFU88640.1	001193	Cluster650_1clades	211	CcrSwift_gp322	Caulobacter virus Swift	GCA_000899655.1
AFU87147.1	001193	Cluster650_1clades	211	CbK_gp315	Caulobacter virus phiCbK	GCA_000900535.1
AFO71315.1	001194	Cluster651_1clades	210	CR5_095	Cronobacter phage CR5	GCA_000910235.1
QBP07524.1	001194	Cluster651_1clades	210	DERBICUS_98	Erwinia phage Derbicus	GCA_004521655.1
ANZ49746.1	001194	Cluster651_1clades	201	MACHINA_108	Erwinia phage Machina	GCA_002758035.1
AXF51247.1	001194	Cluster651_1clades	196	WELLINGTON_117	Erwinia phage Wellington	GCA_003344985.1
ANZ48125.1	001194	Cluster651_1clades	202	ASESINO_112	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48399.1	001194	Cluster651_1clades	215	CAITLIN_104	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48672.1	001194	Cluster651_1clades	215	CHRISDB_110	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48947.1	001194	Cluster651_1clades	210	EARLPHILLIPIV_98	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49191.1	001194	Cluster651_1clades	201	HUXLEY_109	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49468.1	001194	Cluster651_1clades	196	KWAN_116	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50019.1	001194	Cluster651_1clades	201	PARSHIK_110	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50288.1	001194	Cluster651_1clades	211	PHOBOS_98	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50540.1	001194	Cluster651_1clades	202	STRATTON_115	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85937.1	001194	Cluster651_1clades	202	ACEC001_0990	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51078.1	001194	Cluster651_1clades	202	MLDJOKPK_00062	Salmonella phage SPAsTU	GCA_003183805.1
AEP83929.1	001194	Cluster651_1clades	202	SPN3US_0096	Salmonella phage SPN3US	GCA_001042275.1
AMR59863.1	001195	Cluster653_1clades	60	SEGD1_216	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59864.1	001195	Cluster653_1clades	120	SEGD1_217	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49862.1	001195	Cluster653_1clades	179	MACHINA_224	Erwinia phage Machina	GCA_002758035.1
AXF51364.1	001195	Cluster653_1clades	200	WELLINGTON_238	Erwinia phage Wellington	GCA_003344985.1
AFQ96679.1	001195	Cluster653_1clades	178	G173_gp134	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48245.1	001195	Cluster653_1clades	178	ASESINO_232	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48519.1	001195	Cluster653_1clades	181	CAITLIN_224	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48796.1	001195	Cluster653_1clades	181	CHRISDB_234	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49306.1	001195	Cluster653_1clades	179	HUXLEY_224	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49590.1	001195	Cluster653_1clades	200	KWAN_238	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50134.1	001195	Cluster653_1clades	179	PARSHIK_225	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50659.1	001195	Cluster653_1clades	178	STRATTON_234	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86052.1	001195	Cluster653_1clades	179	ACEC001_2090	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20900.1	001195	Cluster653_1clades	179	-	Salmonella phage JN03	GCA_014319805.1
AWN09135.2	001195	Cluster653_1clades	179	MLDJOKPK_00228	Salmonella phage SPAsTU	GCA_003183805.1
AEP84045.1	001195	Cluster653_1clades	179	SPN3US_0212	Salmonella phage SPN3US	GCA_001042275.1
AMR59754.1	001196	Cluster656_1clades	128	SEGD1_105	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49753.1	001196	Cluster656_1clades	154	MACHINA_115	Erwinia phage Machina	GCA_002758035.1
AFQ96572.1	001196	Cluster656_1clades	126	G173_gp027	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48133.1	001196	Cluster656_1clades	128	ASESINO_120	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48408.1	001196	Cluster656_1clades	125	CAITLIN_113	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48680.1	001196	Cluster656_1clades	124	CHRISDB_118	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49197.1	001196	Cluster656_1clades	154	HUXLEY_115	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50025.1	001196	Cluster656_1clades	154	PARSHIK_116	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50547.1	001196	Cluster656_1clades	126	STRATTON_122	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85943.1	001196	Cluster656_1clades	128	ACEC001_1050	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
BAS04964.1	001196	Cluster656_1clades	136	AVU11_gp172	Ralstonia phage RSF1	GCA_001500875.1
BAQ02689.1	001196	Cluster656_1clades	196	AVU38_gp161	Ralstonia phage RSL2	GCA_001503055.1
QNI20811.1	001196	Cluster656_1clades	128	-	Salmonella phage JN03	GCA_014319805.1
AWN09004.1	001196	Cluster656_1clades	127	MLDJOKPK_00055	Salmonella phage SPAsTU	GCA_003183805.1
AEP83935.1	001196	Cluster656_1clades	128	SPN3US_0102	Salmonella phage SPN3US	GCA_001042275.1
AQT28129.1	001196	Cluster656_1clades	125	pVa21_188	Vibrio phage pVa-21	GCA_002619305.1
AFC21708.1	001197	Cluster657_1clades	169	GAP32_258	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14502.1	001197	Cluster657_1clades	98	PBI_121Q_612	Escherichia phage 121Q	GCA_000926855.1
QAY00447.1	001197	Cluster657_1clades	100	Ecwhy1_167	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35190.1	001197	Cluster657_1clades	98	ACQ29_gp510	Escherichia phage PBECO4	GCA_001041035.1
BBM62174.1	001197	Cluster657_1clades	99	EO157G_5850	Escherichia phage SP27	GCA_008033345.1
AXC36761.1	001197	Cluster657_1clades	98	-	Escherichia phage UB	GCA_003341455.1
QBO61801.1	001197	Cluster657_1clades	98	G17_00312	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13845.1	001197	Cluster657_1clades	98	vBEcoMphAPEC6_gp216c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80486.1	001197	Cluster657_1clades	99	PSLUR01_00509	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43828.1	001197	Cluster657_1clades	170	CBB_264	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18987.1	001197	Cluster657_1clades	196	7t3_0466	Salmonella phage 7t3	GCA_006083215.1
AZU98235.1	001197	Cluster657_1clades	190	CPT_Munch_291	Salmonella phage Munch	GCA_004015485.1
QIG62749.1	001197	Cluster657_1clades	190	SEPL_136	Salmonella phage SE_PL	GCA_011067555.1
AQW88787.1	001197	Cluster657_1clades	154	BF_0262	Serratia phage BF	GCA_002619745.1
SOK59068.1	001197	Cluster657_1clades	150	g260	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58534.1	001197	Cluster657_1clades	150	g257	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22860.1	001198	Cluster658_1clades	174	Ah1_00342	Aeromonas phage Ah1	GCA_002957415.1
QAX98570.1	001198	Cluster658_1clades	176	ASfcp2_236	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53035.1	001198	Cluster658_1clades	174	PX29p318	Aeromonas phage PX29	GCA_000920195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADM79959.1	001198	Cluster658_1clades	175	phiAS5_ORF0116	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17988.1	001198	Cluster658_1clades	177	Aeh1ORF319w	Aeromonas virus Aeh1	GCA_000843245.1
ANS06018.1	001198	Cluster658_1clades	188	ABCD_0080	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64972.1	001198	Cluster658_1clades	170	S13_173	Cronobacter phage S13	GCA_001503575.1
AON97092.1	001198	Cluster658_1clades	189	E_084	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78602.1	001198	Cluster658_1clades	188	RB43ORF080w	Escherichia virus RB43	GCA_000863505.1
QIG66002.1	001198	Cluster658_1clades	184	phiOC_p360	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ATA65568.1	001198	Cluster658_1clades	72	2050HW_00233	Serratia phage 2050HW	GCA_002628125.1
QDB71331.1	001198	Cluster658_1clades	180	CPT_Moabite_301	Serratia phage Moabite	GCA_006384735.1
QAX96827.1	001198	Cluster658_1clades	183	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96192.1	001198	Cluster658_1clades	183	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96510.1	001198	Cluster658_1clades	183	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
CCE26286.1	001198	Cluster658_1clades	191	g263	Yersinia phage phiR1-37	GCA_000895615.1
ARB13710.1	001199	Cluster659_1clades	96	Ccr10_gp180c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14055.1	001199	Cluster659_1clades	96	Ccr2_gp179c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14742.1	001199	Cluster659_1clades	96	Ccr29_gp186	Caulobacter phage Ccr29	GCA_002619485.1
ARB15097.1	001199	Cluster659_1clades	96	Ccr32_gp179	Caulobacter phage Ccr32	GCA_002619505.1
ARB15431.1	001199	Cluster659_1clades	96	Ccr34_gp189	Caulobacter phage Ccr34	GCA_002619525.1
ARB14398.1	001199	Cluster659_1clades	96	Ccr5_gp178c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68380.1	001199	Cluster659_1clades	185	CcrBL10_gp176c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69228.1	001199	Cluster659_1clades	92	CcrBL9_gp204	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88129.1	001199	Cluster659_1clades	93	CcrColossus_gp259	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68806.1	001199	Cluster659_1clades	93	CcrPW_gp267	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69782.1	001199	Cluster659_1clades	93	CcrSC_gp200	Caulobacter phage CcrSC	GCA_003443315.1
AFU87703.1	001199	Cluster659_1clades	96	CcrKarma_gp186	Caulobacter virus Karma	GCA_000901575.1
AFU87352.1	001199	Cluster659_1clades	96	CcrMagneto_gp182	Caulobacter virus Magneto	GCA_000903095.1
AFU86663.1	001199	Cluster659_1clades	185	CcrRogue_gp181	Caulobacter virus Rogue	GCA_000900555.1
AFU88499.1	001199	Cluster659_1clades	96	CcrSwift_gp181	Caulobacter virus Swift	GCA_000899655.1
AFU87016.1	001199	Cluster659_1clades	96	CbK_gp184	Caulobacter virus phiCbK	GCA_000900535.1
AMR59809.1	001200	Cluster660_1clades	126	SEGD1_162	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49802.1	001200	Cluster660_1clades	150	MACHINA_164	Erwinia phage Machina	GCA_002758035.1
AXF51301.1	001200	Cluster660_1clades	178	WELLINGTON_172	Erwinia phage Wellington	GCA_003344985.1
AFQ96623.1	001200	Cluster660_1clades	171	G173_gp078	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48187.1	001200	Cluster660_1clades	171	ASESINO_174	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48458.1	001200	Cluster660_1clades	157	CAITLIN_163	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48736.1	001200	Cluster660_1clades	156	CHRISDB_174	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49246.1	001200	Cluster660_1clades	151	HUXLEY_164	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49525.1	001200	Cluster660_1clades	178	KWAN_173	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50074.1	001200	Cluster660_1clades	156	PARSHIK_165	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50600.1	001200	Cluster660_1clades	171	STRATTON_175	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85998.1	001200	Cluster660_1clades	163	ACEC001_1580	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63881.1	001200	Cluster660_1clades	167	Goslar_00088	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QNI20857.1	001200	Cluster660_1clades	182	-	Salmonella phage JN03	GCA_014319805.1
AXF51135.1	001200	Cluster660_1clades	170	MLDJOKPK_00284	Salmonella phage SPAsTU	GCA_003183805.1
AEP83992.1	001200	Cluster660_1clades	163	SPN3US_0159	Salmonella phage SPN3US	GCA_001042275.1
ARB13614.1	001201	Cluster661_1clades	173	Ccr10_gp085	Caulobacter phage Ccr10	GCA_002619445.1
ARB13959.1	001201	Cluster661_1clades	173	Ccr2_gp084	Caulobacter phage Ccr2	GCA_002619465.1
ARB14649.1	001201	Cluster661_1clades	173	Ccr29_gp092	Caulobacter phage Ccr29	GCA_002619485.1
ARB15004.1	001201	Cluster661_1clades	173	Ccr32_gp085	Caulobacter phage Ccr32	GCA_002619505.1
ARB15335.1	001201	Cluster661_1clades	173	Ccr34_gp092	Caulobacter phage Ccr34	GCA_002619525.1
ARB14303.1	001201	Cluster661_1clades	173	Ccr5_gp085	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68285.1	001201	Cluster661_1clades	173	CcrBL10_gp081	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69183.1	001201	Cluster661_1clades	180	CcrBL9_gp159	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87980.1	001201	Cluster661_1clades	173	CcrColossus_gp110	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68657.1	001201	Cluster661_1clades	168	CcrPW_gp118	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69736.1	001201	Cluster661_1clades	180	CcrSC_gp154	Caulobacter phage CcrSC	GCA_003443315.1
AFU87605.1	001201	Cluster661_1clades	123	CcrKarma_gp088	Caulobacter virus Karma	GCA_000901575.1
AFU87254.1	001201	Cluster661_1clades	173	CcrMagneto_gp084	Caulobacter virus Magneto	GCA_000903095.1
AFU86569.1	001201	Cluster661_1clades	173	CcrRogue_gp087	Caulobacter virus Rogue	GCA_000900555.1
AFU88401.1	001201	Cluster661_1clades	173	CcrSwift_gp083	Caulobacter virus Swift	GCA_000899655.1
AFU86919.1	001201	Cluster661_1clades	173	CbK_gp087	Caulobacter virus phiCbK	GCA_000900535.1
ARB13631.1	001202	-	162	Ccr10_gp102	Caulobacter phage Ccr10	GCA_002619445.1
ARB13976.1	001202	-	162	Ccr2_gp101	Caulobacter phage Ccr2	GCA_002619465.1
ARB14665.1	001202	-	162	Ccr29_gp109	Caulobacter phage Ccr29	GCA_002619485.1
ARB15020.1	001202	-	162	Ccr32_gp102	Caulobacter phage Ccr32	GCA_002619505.1
ARB15352.1	001202	-	162	Ccr34_gp110	Caulobacter phage Ccr34	GCA_002619525.1
ARB14320.1	001202	-	162	Ccr5_gp102	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68301.1	001202	-	162	CcrBL10_gp097	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69206.1	001202	-	176	CcrBL9_gp182	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88006.1	001202	-	168	CcrColossus_gp136	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68682.1	001202	-	166	CcrPW_gp143	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69759.1	001202	-	176	CcrSC_gp177	Caulobacter phage CcrSC	GCA_003443315.1
AFU87623.1	001202	-	162	CcrKarma_gp106	Caulobacter virus Karma	GCA_000901575.1
AFU87272.1	001202	-	162	CcrMagneto_gp102	Caulobacter virus Magneto	GCA_000903095.1
AFU86584.1	001202	-	162	CcrRogue_gp102	Caulobacter virus Rogue	GCA_000900555.1
AFU88419.1	001202	-	162	CcrSwift_gp101	Caulobacter virus Swift	GCA_000899655.1
AFU86937.1	001202	-	162	CbK_gp105	Caulobacter virus phiCbK	GCA_000900535.1
APU01606.1	001203	Cluster664_1clades	152	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01407.1	001203	Cluster664_1clades	152	ASwh1_348	Aeromonas phage Aswh_1	GCA_004146945.1
QDJ97319.1	001203	Cluster664_1clades	152	D6_0159	Aeromonas phage D6	GCA_007051205.2
QDH47180.1	001203	Cluster664_1clades	152	LAh10_81	Aeromonas phage LAh10	GCA_006863975.1
ADQ53230.1	001203	Cluster664_1clades	137	65p222	Aeromonas virus 65	GCA_000893255.1
ASV44534.1	001203	Cluster664_1clades	153	PBI_SCTP2_519	Salicola phage SCTP-2	GCA_002625545.1
AXH70947.1	001203	Cluster664_1clades	171	-	Vibrio phage BONAISHI	GCA_003441475.1
QIW90799.1	001203	Cluster664_1clades	157	GCAPEGMB_00481	Vibrio phage V07	GCA_012361095.1
AGB06940.1	001203	Cluster664_1clades	167	CF80_gp153	Vibrio phage VH7D	GCA_000914495.1
QBX06206.1	001203	Cluster664_1clades	167	ValB1HC_253	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61223.1	001203	Cluster664_1clades	167	AVU32_gp382	Vibrio phage ValKK3	GCA_001501635.1
ALP47102.1	001203	Cluster664_1clades	167	phiGrn1_0376	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47485.1	001203	Cluster664_1clades	167	phiST2_0131	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54831.1	001203	Cluster664_1clades	167	vBValMR10Z_291	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07250.1	001203	Cluster664_1clades	166	VmeM32_00151	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07142.1	001203	Cluster664_1clades	139	VmeM32_00156	Vibrio phage vB_VmeM-32	GCA_002608825.1
ARB13616.1	001204	Cluster665_1clades	157	Ccr10_gp087	Caulobacter phage Ccr10	GCA_002619445.1
ARB13961.1	001204	Cluster665_1clades	157	Ccr2_gp086	Caulobacter phage Ccr2	GCA_002619465.1
ARB14651.1	001204	Cluster665_1clades	157	Ccr29_gp094	Caulobacter phage Ccr29	GCA_002619485.1
ARB15006.1	001204	Cluster665_1clades	157	Ccr32_gp087	Caulobacter phage Ccr32	GCA_002619505.1
ARB15337.1	001204	Cluster665_1clades	157	Ccr34_gp094	Caulobacter phage Ccr34	GCA_002619525.1
ARB14305.1	001204	Cluster665_1clades	157	Ccr5_gp087	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68287.1	001204	Cluster665_1clades	71	CcrBL10_gp083	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69185.1	001204	Cluster665_1clades	168	CcrBL9_gp161	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87982.1	001204	Cluster665_1clades	165	CcrColossus_gp112	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68659.1	001204	Cluster665_1clades	165	CcrPW_gp120	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69738.1	001204	Cluster665_1clades	168	CcrSC_gp156	Caulobacter phage CcrSC	GCA_003443315.1
AFU87607.1	001204	Cluster665_1clades	157	CcrKarma_gp090	Caulobacter virus Karma	GCA_000901575.1
AFU87256.1	001204	Cluster665_1clades	157	CcrMagneto_gp086	Caulobacter virus Magneto	GCA_000903095.1
AFU86571.1	001204	Cluster665_1clades	157	CcrRogue_gp089	Caulobacter virus Rogue	GCA_000900555.1
AFU88403.1	001204	Cluster665_1clades	157	CcrSwift_gp085	Caulobacter virus Swift	GCA_000899655.1
AFU86921.1	001204	Cluster665_1clades	157	CbK_gp089	Caulobacter virus phiCbK	GCA_000900535.1
ARB13747.1	001205	Cluster666_1clades	120	Ccr10_gp217c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14092.1	001205	Cluster666_1clades	120	Ccr2_gp216c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14781.1	001205	Cluster666_1clades	95	Ccr29_gp225	Caulobacter phage Ccr29	GCA_002619485.1
ARB15125.1	001205	Cluster666_1clades	95	Ccr32_gp207	Caulobacter phage Ccr32	GCA_002619505.1
ARB15459.1	001205	Cluster666_1clades	95	Ccr34_gp217	Caulobacter phage Ccr34	GCA_002619525.1
ARB14434.1	001205	Cluster666_1clades	120	Ccr5_gp214c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68414.1	001205	Cluster666_1clades	52	CcrBL10_gp210c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69257.1	001205	Cluster666_1clades	95	CcrBL9_gp233c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88149.1	001205	Cluster666_1clades	166	CcrColossus_gp279	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68825.1	001205	Cluster666_1clades	95	CcrPW_gp286	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69813.1	001205	Cluster666_1clades	95	CcrSC_gp231c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87741.1	001205	Cluster666_1clades	118	CcrKarma_gp224	Caulobacter virus Karma	GCA_000901575.1
AFU88537.1	001205	Cluster666_1clades	118	CcrSwift_gp219	Caulobacter virus Swift	GCA_000899655.1
AFU87044.1	001205	Cluster666_1clades	122	CbK_gp212	Caulobacter virus phiCbK	GCA_000900535.1
BBA65560.1	001205	Cluster666_1clades	109	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96553.1	001205	Cluster666_1clades	107	Xoosp13_367	Xanthomonas phage Xoo-sp13	GCA_013364725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFO71335.1	001206	A18	151	CR5_115	Cronobacter phage CR5	GCA_000910235.1
AMR59884.1	001206	A18	159	SEGD1_237	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49883.1	001206	A18	150	MACHINA_245	Erwinia phage Machina	GCA_002758035.1
AXF51386.1	001206	A18	152	WELLINGTON_260	Erwinia phage Wellington	GCA_003344985.1
AFQ96697.1	001206	A18	157	G173_gp152	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48267.1	001206	A18	159	ASESINO_254	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48540.1	001206	A18	150	CAITLIN_245	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48817.1	001206	A18	147	CHRISDB_255	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49326.1	001206	A18	150	HUXLEY_244	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49612.1	001206	A18	152	KWAN_260	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50154.1	001206	A18	150	PARSHIK_245	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50679.1	001206	A18	159	STRATTON_254	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86074.1	001206	A18	159	ACEC001_2310	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20919.1	001206	A18	159	-	Salmonella phage JN03	GCA_014319805.1
AWN09119.1	001206	A18	159	MLDJOKPK_00207	Salmonella phage SPAsTU	GCA_003183805.1
AEP84066.1	001206	A18	159	SPN3US_0233	Salmonella phage SPN3US	GCA_001042275.1
ARB13597.1	001207	Cluster668_1clades	148	Ccr10_gp069	Caulobacter phage Ccr10	GCA_002619445.1
ARB13943.1	001207	Cluster668_1clades	148	Ccr2_gp068	Caulobacter phage Ccr2	GCA_002619465.1
ARB14632.1	001207	Cluster668_1clades	148	Ccr29_gp075	Caulobacter phage Ccr29	GCA_002619485.1
ARB14988.1	001207	Cluster668_1clades	148	Ccr32_gp069	Caulobacter phage Ccr32	GCA_002619505.1
ARB15319.1	001207	Cluster668_1clades	148	Ccr34_gp070	Caulobacter phage Ccr34	GCA_002619525.1
ARB14286.1	001207	Cluster668_1clades	148	Ccr5_gp068	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68270.1	001207	Cluster668_1clades	148	CcrBL10_gp066	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69148.1	001207	Cluster668_1clades	146	CcrBL9_gp124	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87952.1	001207	Cluster668_1clades	159	CcrColossus_gp082	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68624.1	001207	Cluster668_1clades	159	CcrPW_gp085	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69702.1	001207	Cluster668_1clades	146	CcrSC_gp120	Caulobacter phage CcrSC	GCA_003443315.1
AFU87587.1	001207	Cluster668_1clades	148	CcrKarma_gp070	Caulobacter virus Karma	GCA_000901575.1
AFU87237.1	001207	Cluster668_1clades	148	CcrMagneto_gp067	Caulobacter virus Magneto	GCA_000903095.1
AFU86553.1	001207	Cluster668_1clades	148	CcrRogue_gp071	Caulobacter virus Rogue	GCA_000900555.1
AFU88385.1	001207	Cluster668_1clades	148	CcrSwift_gp067	Caulobacter virus Swift	GCA_000899655.1
AFU86901.1	001207	Cluster668_1clades	148	CbK_gp069	Caulobacter virus phiCbK	GCA_000900535.1
ARB13618.1	001208	Cluster669_1clades	151	Ccr10_gp089	Caulobacter phage Ccr10	GCA_002619445.1
ARB13963.1	001208	Cluster669_1clades	151	Ccr2_gp088	Caulobacter phage Ccr2	GCA_002619465.1
ARB14652.1	001208	Cluster669_1clades	151	Ccr29_gp095	Caulobacter phage Ccr29	GCA_002619485.1
ARB15007.1	001208	Cluster669_1clades	151	Ccr32_gp088	Caulobacter phage Ccr32	GCA_002619505.1
ARB15338.1	001208	Cluster669_1clades	151	Ccr34_gp095	Caulobacter phage Ccr34	GCA_002619525.1
ARB14307.1	001208	Cluster669_1clades	151	Ccr5_gp089	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68288.1	001208	Cluster669_1clades	151	CcrBL10_gp084	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69186.1	001208	Cluster669_1clades	149	CcrBL9_gp162	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87984.1	001208	Cluster669_1clades	151	CcrColossus_gp114	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68660.1	001208	Cluster669_1clades	151	CcrPW_gp121	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69739.1	001208	Cluster669_1clades	149	CcrSC_gp157	Caulobacter phage CcrSC	GCA_003443315.1
AFU87609.1	001208	Cluster669_1clades	151	CcrKarma_gp092	Caulobacter virus Karma	GCA_000901575.1
AFU87258.1	001208	Cluster669_1clades	151	CcrMagneto_gp088	Caulobacter virus Magneto	GCA_000903095.1
AFU86572.1	001208	Cluster669_1clades	151	CcrRogue_gp090	Caulobacter virus Rogue	GCA_000900555.1
AFU88405.1	001208	Cluster669_1clades	151	CcrSwift_gp087	Caulobacter virus Swift	GCA_000899655.1
AFU86923.1	001208	Cluster669_1clades	151	CbK_gp091	Caulobacter virus phiCbK	GCA_000900535.1
ARB13663.1	001209	Cluster670_1clades	149	Ccr10_gp134c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14008.1	001209	Cluster670_1clades	149	Ccr2_gp133c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14696.1	001209	Cluster670_1clades	149	Ccr29_gp140	Caulobacter phage Ccr29	GCA_002619485.1
ARB15050.1	001209	Cluster670_1clades	149	Ccr32_gp132	Caulobacter phage Ccr32	GCA_002619505.1
ARB15383.1	001209	Cluster670_1clades	149	Ccr34_gp141	Caulobacter phage Ccr34	GCA_002619525.1
ARB14351.1	001209	Cluster670_1clades	149	Ccr5_gp132c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68332.1	001209	Cluster670_1clades	149	CcrBL10_gp128c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69240.1	001209	Cluster670_1clades	137	CcrBL9_gp216c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88047.1	001209	Cluster670_1clades	139	CcrColossus_gp177	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68724.1	001209	Cluster670_1clades	139	CcrPW_gp185c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69794.1	001209	Cluster670_1clades	137	CcrSC_gp212c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87655.1	001209	Cluster670_1clades	149	CcrKarma_gp138	Caulobacter virus Karma	GCA_000901575.1
AFU87304.1	001209	Cluster670_1clades	149	CcrMagneto_gp134	Caulobacter virus Magneto	GCA_000903095.1
AFU86616.1	001209	Cluster670_1clades	149	CcrRogue_gp134	Caulobacter virus Rogue	GCA_000900555.1
AFU88451.1	001209	Cluster670_1clades	149	CcrSwift_gp133	Caulobacter virus Swift	GCA_000899655.1
AFU86968.1	001209	Cluster670_1clades	149	CbK_gp136	Caulobacter virus phiCbK	GCA_000900535.1
AIT14031.1	001210	Cluster671_1clades	147	PBI_121Q_141	Escherichia phage 121Q	GCA_000926855.1
AIT14032.1	001210	Cluster671_1clades	121	PBI_121Q_142	Escherichia phage 121Q	GCA_000926855.1
QAY00309.1	001210	Cluster671_1clades	119	Ecwhy1_27	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00310.1	001210	Cluster671_1clades	138	Ecwhy1_28	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35059.1	001210	Cluster671_1clades	113	ACQ29_gp379	Escherichia phage PBECO4	GCA_001041035.1
AGC35060.1	001210	Cluster671_1clades	141	ACQ29_gp380	Escherichia phage PBECO4	GCA_001041035.1
BBM61715.1	001210	Cluster671_1clades	141	EO157G_1260	Escherichia phage SP27	GCA_008033345.1
BBM61716.1	001210	Cluster671_1clades	121	EO157G_1270	Escherichia phage SP27	GCA_008033345.1
AXC36636.1	001210	Cluster671_1clades	141	-	Escherichia phage UB	GCA_003341455.1
AXC36635.1	001210	Cluster671_1clades	86	-	Escherichia phage UB	GCA_003341455.1
QBO61667.1	001210	Cluster671_1clades	121	G17_00171	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61668.1	001210	Cluster671_1clades	141	G17_00172	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13717.1	001210	Cluster671_1clades	121	vBEcoMphAPEC6_gp087c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13718.1	001210	Cluster671_1clades	141	vBEcoMphAPEC6_gp088c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80027.1	001210	Cluster671_1clades	141	PSLUR01_00050	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80028.1	001210	Cluster671_1clades	121	PSLUR01_00051	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ARB13675.1	001211	HTH	138	Ccr10_gp146	Caulobacter phage Ccr10	GCA_002619445.1
ARB14020.1	001211	HTH	138	Ccr2_gp145	Caulobacter phage Ccr2	GCA_002619465.1
ARB14708.1	001211	HTH	138	Ccr29_gp152	Caulobacter phage Ccr29	GCA_002619485.1
ARB15063.1	001211	HTH	138	Ccr32_gp145	Caulobacter phage Ccr32	GCA_002619505.1
ARB15397.1	001211	HTH	138	Ccr34_gp155	Caulobacter phage Ccr34	GCA_002619525.1
ARB14363.1	001211	HTH	138	Ccr5_gp144	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68345.1	001211	HTH	103	CcrBL10_gp141	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69250.1	001211	HTH	121	CcrBL9_gp226c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88057.1	001211	HTH	144	CcrColossus_gp187	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68736.1	001211	HTH	144	CcrPW_gp197	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69806.1	001211	HTH	119	CcrSC_gp224c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87668.1	001211	HTH	138	CcrKarma_gp151	Caulobacter virus Karma	GCA_000901575.1
AFU87317.1	001211	HTH	138	CcrMagneto_gp147	Caulobacter virus Magneto	GCA_000903095.1
AFU86629.1	001211	HTH	138	CcrRogue_gp147	Caulobacter virus Rogue	GCA_000900555.1
AFU88464.1	001211	HTH	138	CcrSwift_gp146	Caulobacter virus Swift	GCA_000899655.1
AFU86981.1	001211	HTH	138	CbK_gp149	Caulobacter virus phiCbK	GCA_000900535.1
ARB13693.1	001212	Cluster673_1clades	141	Ccr10_gp163c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14038.1	001212	Cluster673_1clades	141	Ccr2_gp162c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14725.1	001212	Cluster673_1clades	141	Ccr29_gp169	Caulobacter phage Ccr29	GCA_002619485.1
ARB15080.1	001212	Cluster673_1clades	141	Ccr32_gp162	Caulobacter phage Ccr32	GCA_002619505.1
ARB15414.1	001212	Cluster673_1clades	141	Ccr34_gp172	Caulobacter phage Ccr34	GCA_002619525.1
ARB14381.1	001212	Cluster673_1clades	141	Ccr5_gp161c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68363.1	001212	Cluster673_1clades	143	CcrBL10_gp159c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69260.1	001212	Cluster673_1clades	136	CcrBL9_gp236c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88081.1	001212	Cluster673_1clades	140	CcrColossus_gp211	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68757.1	001212	Cluster673_1clades	140	CcrPW_gp218c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69817.1	001212	Cluster673_1clades	137	CcrSC_gp235c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87686.1	001212	Cluster673_1clades	141	CcrKarma_gp169	Caulobacter virus Karma	GCA_000901575.1
AFU87335.1	001212	Cluster673_1clades	141	CcrMagneto_gp165	Caulobacter virus Magneto	GCA_000903095.1
AFU86646.1	001212	Cluster673_1clades	137	CcrRogue_gp164	Caulobacter virus Rogue	GCA_000900555.1
AFU88482.1	001212	Cluster673_1clades	141	CcrSwift_gp164	Caulobacter virus Swift	GCA_000899655.1
AFU86999.1	001212	Cluster673_1clades	141	CbK_gp167	Caulobacter virus phiCbK	GCA_000900535.1
ARB13603.1	001213	Cluster676_1clades	138	Ccr10_gp075	Caulobacter phage Ccr10	GCA_002619445.1
ARB13949.1	001213	Cluster676_1clades	138	Ccr2_gp074	Caulobacter phage Ccr2	GCA_002619465.1
ARB14639.1	001213	Cluster676_1clades	138	Ccr29_gp082	Caulobacter phage Ccr29	GCA_002619485.1
ARB14995.1	001213	Cluster676_1clades	138	Ccr32_gp076	Caulobacter phage Ccr32	GCA_002619505.1
ARB15325.1	001213	Cluster676_1clades	138	Ccr34_gp076	Caulobacter phage Ccr34	GCA_002619525.1
ARB14292.1	001213	Cluster676_1clades	138	Ccr5_gp074	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68276.1	001213	Cluster676_1clades	138	CcrBL10_gp072	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69160.1	001213	Cluster676_1clades	138	CcrBL9_gp136	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87960.1	001213	Cluster676_1clades	140	CcrColossus_gp090	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68636.1	001213	Cluster676_1clades	140	CcrPW_gp097	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69715.1	001213	Cluster676_1clades	138	CcrSC_gp133	Caulobacter phage CcrSC	GCA_003443315.1
AFU87593.1	001213	Cluster676_1clades	138	CcrKarma_gp076	Caulobacter virus Karma	GCA_000901575.1
AFU87243.1	001213	Cluster676_1clades	138	CcrMagneto_gp073	Caulobacter virus Magneto	GCA_000903095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU86559.1	001213	Cluster676_1clades	138	CcrRogue_gp077	Caulobacter virus Rogue	GCA_000900555.1
AFU88391.1	001213	Cluster676_1clades	138	CcrSwift_gp073	Caulobacter virus Swift	GCA_000899655.1
AFU86907.1	001213	Cluster676_1clades	138	CbK_gp075	Caulobacter virus phiCbK	GCA_000900535.1
ARB13639.1	001214	Cluster677_1clades	45	Ccr10_gp110c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13984.1	001214	Cluster677_1clades	45	Ccr2_gp109c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14672.1	001214	Cluster677_1clades	83	Ccr29_gp116	Caulobacter phage Ccr29	GCA_002619485.1
ARB15027.1	001214	Cluster677_1clades	45	Ccr32_gp109	Caulobacter phage Ccr32	GCA_002619505.1
ARB15359.1	001214	Cluster677_1clades	78	Ccr34_gp117	Caulobacter phage Ccr34	GCA_002619525.1
ARB14328.1	001214	Cluster677_1clades	45	Ccr5_gp110c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68308.1	001214	Cluster677_1clades	67	CcrBL10_gp104c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69226.1	001214	Cluster677_1clades	139	CcrBL9_gp202	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88014.1	001214	Cluster677_1clades	74	CcrColossus_gp144	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68691.1	001214	Cluster677_1clades	74	CcrPW_gp152c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69780.1	001214	Cluster677_1clades	140	CcrSC_gp198	Caulobacter phage CcrSC	GCA_003443315.1
AFU87631.1	001214	Cluster677_1clades	78	CcrKarma_gp114	Caulobacter virus Karma	GCA_000901575.1
AFU87280.1	001214	Cluster677_1clades	78	CcrMagneto_gp110	Caulobacter virus Magneto	GCA_000903095.1
AFU86592.1	001214	Cluster677_1clades	78	CcrRogue_gp110	Caulobacter virus Rogue	GCA_000900555.1
AFU88427.1	001214	Cluster677_1clades	78	CcrSwift_gp109	Caulobacter virus Swift	GCA_000899655.1
AFU86945.1	001214	Cluster677_1clades	78	CbK_gp113	Caulobacter virus phiCbK	GCA_000900535.1
QDH83665.1	001215	SIG+TM	139	H1O15_gp085	Achromobacter phage Motura	GCA_006964305.1
APU01673.1	001215	SIG+TM	100	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29015.1	001215	SIG+TM	128	AP1_0308	Aeromonas phage AP1	GCA_014183365.1
ATI17621.1	001215	SIG+TM	128	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00375.1	001215	SIG+TM	128	HWB28_gp177	Aeromonas phage AS-zj	GCA_002627665.1
QAX97655.1	001215	SIG+TM	128	ASswx1_9	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01396.1	001215	SIG+TM	124	ASwh1_337	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39487.1	001215	SIG+TM	128	CC2_105	Aeromonas phage CC2	GCA_000903495.1
ADQ53306.1	001215	SIG+TM	130	65p298	Aeromonas virus 65	GCA_000893255.1
AXQ69380.1	001215	SIG+TM	132	CcrBL9_gp356	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69940.1	001215	SIG+TM	132	CcrSC_gp358	Caulobacter phage CcrSC	GCA_003443315.1
AFC21768.1	001215	SIG+TM	121	GAP32_318	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43886.1	001215	SIG+TM	94	CBB_323	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88846.1	001215	SIG+TM	94	BF_0321	Serratia phage BF	GCA_002619745.1
SOK59130.1	001215	SIG+TM	121	g322	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58596.1	001215	SIG+TM	121	g319	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13769.1	001216	Cluster679_1clades	131	Ccr10_gp239	Caulobacter phage Ccr10	GCA_002619445.1
ARB14114.1	001216	Cluster679_1clades	131	Ccr2_gp238	Caulobacter phage Ccr2	GCA_002619465.1
ARB14808.1	001216	Cluster679_1clades	131	Ccr29_gp252	Caulobacter phage Ccr29	GCA_002619485.1
ARB15148.1	001216	Cluster679_1clades	131	Ccr32_gp230	Caulobacter phage Ccr32	GCA_002619505.1
ARB15482.1	001216	Cluster679_1clades	131	Ccr34_gp240	Caulobacter phage Ccr34	GCA_002619525.1
ARB14456.1	001216	Cluster679_1clades	131	Ccr5_gp236	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68434.1	001216	Cluster679_1clades	133	CcrBL10_gp230	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69295.1	001216	Cluster679_1clades	136	CcrBL9_gp271c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88098.1	001216	Cluster679_1clades	117	CcrColossus_gp228	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68775.1	001216	Cluster679_1clades	134	CcrPW_gp236	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69854.1	001216	Cluster679_1clades	136	CcrSC_gp272c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87764.1	001216	Cluster679_1clades	131	CcrKarma_gp247	Caulobacter virus Karma	GCA_000901575.1
AFU87411.1	001216	Cluster679_1clades	131	CcrMagneto_gp241	Caulobacter virus Magneto	GCA_000903095.1
AFU86720.1	001216	Cluster679_1clades	133	CcrRogue_gp238	Caulobacter virus Rogue	GCA_000900555.1
AFU88559.1	001216	Cluster679_1clades	131	CcrSwift_gp241	Caulobacter virus Swift	GCA_000899655.1
AFU87067.1	001216	Cluster679_1clades	131	CbK_gp235	Caulobacter virus phiCbK	GCA_000900535.1
APU01766.1	001217	WYL	117	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28980.1	001217	WYL	134	AP1_0273	Aeromonas phage AP1	GCA_014183365.1
ATI17531.1	001217	WYL	134	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00465.1	001217	WYL	134	HWB28_gp087	Aeromonas phage AS-zj	GCA_002627665.1
AUE22799.1	001217	WYL	109	Ah1_00281	Aeromonas phage Ah1	GCA_002957415.1
QAX98514.1	001217	WYL	109	ASfcp2_178	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97973.1	001217	WYL	134	ASswx1_331	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01167.1	001217	WYL	109	ASwh1_101	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39505.1	001217	WYL	134	CC2_202	Aeromonas phage CC2	GCA_000903495.1
ADQ52977.1	001217	WYL	109	PX29p258	Aeromonas phage PX29	GCA_000920195.1
ADM79902.1	001217	WYL	109	phiAS5_ORF0059	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53409.1	001217	WYL	117	65p402	Aeromonas virus 65	GCA_000893255.1
AAQ17926.1	001217	WYL	109	31.1	Aeromonas virus Aeh1	GCA_000843245.1
AIA64836.1	001217	WYL	109	S13_037	Cronobacter phage S13	GCA_001503575.1
ARM70769.1	001217	WYL	98	phiC120_c63	Escherichia phage phiC120	GCA_002621185.1
QHJ78826.1	001217	WYL	109	-	Myoviridae sp.	GCA_012593985.1
ARB13668.1	001218	Cluster681_1clades	124	Ccr10_gp139	Caulobacter phage Ccr10	GCA_002619445.1
ARB14013.1	001218	Cluster681_1clades	124	Ccr2_gp138	Caulobacter phage Ccr2	GCA_002619465.1
ARB14700.1	001218	Cluster681_1clades	124	Ccr29_gp144	Caulobacter phage Ccr29	GCA_002619485.1
ARB15055.1	001218	Cluster681_1clades	124	Ccr32_gp137	Caulobacter phage Ccr32	GCA_002619505.1
ARB15389.1	001218	Cluster681_1clades	124	Ccr34_gp147	Caulobacter phage Ccr34	GCA_002619525.1
ARB14356.1	001218	Cluster681_1clades	124	Ccr5_gp137	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68336.1	001218	Cluster681_1clades	123	CcrBL10_gp132	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69242.1	001218	Cluster681_1clades	132	CcrBL9_gp218	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88051.1	001218	Cluster681_1clades	124	CcrColossus_gp181	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68730.1	001218	Cluster681_1clades	124	CcrPW_gp191	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69796.1	001218	Cluster681_1clades	132	CcrSC_gp214	Caulobacter phage CcrSC	GCA_003443315.1
AFU87661.1	001218	Cluster681_1clades	124	CcrKarma_gp144	Caulobacter virus Karma	GCA_000901575.1
AFU87310.1	001218	Cluster681_1clades	124	CcrMagneto_gp140	Caulobacter virus Magneto	GCA_000903095.1
AFU86621.1	001218	Cluster681_1clades	123	CcrRogue_gp139	Caulobacter virus Rogue	GCA_000900555.1
AFU88457.1	001218	Cluster681_1clades	124	CcrSwift_gp139	Caulobacter virus Swift	GCA_000899655.1
AFU86974.1	001218	Cluster681_1clades	124	CbK_gp142	Caulobacter virus phiCbK	GCA_000900535.1
ARB13615.1	001219	Cluster682_1clades	130	Ccr10_gp086	Caulobacter phage Ccr10	GCA_002619445.1
ARB13960.1	001219	Cluster682_1clades	130	Ccr2_gp085	Caulobacter phage Ccr2	GCA_002619465.1
ARB14650.1	001219	Cluster682_1clades	130	Ccr29_gp093	Caulobacter phage Ccr29	GCA_002619485.1
ARB15005.1	001219	Cluster682_1clades	130	Ccr32_gp086	Caulobacter phage Ccr32	GCA_002619505.1
ARB15336.1	001219	Cluster682_1clades	130	Ccr34_gp093	Caulobacter phage Ccr34	GCA_002619525.1
ARB14304.1	001219	Cluster682_1clades	130	Ccr5_gp086	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68286.1	001219	Cluster682_1clades	130	CcrBL10_gp082	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69184.1	001219	Cluster682_1clades	126	CcrBL9_gp160	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87981.1	001219	Cluster682_1clades	124	CcrColossus_gp111	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68658.1	001219	Cluster682_1clades	124	CcrPW_gp119	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69737.1	001219	Cluster682_1clades	126	CcrSC_gp155	Caulobacter phage CcrSC	GCA_003443315.1
AFU87606.1	001219	Cluster682_1clades	89	CcrKarma_gp089	Caulobacter virus Karma	GCA_000901575.1
AFU87255.1	001219	Cluster682_1clades	130	CcrMagneto_gp085	Caulobacter virus Magneto	GCA_000903095.1
AFU86570.1	001219	Cluster682_1clades	130	CcrRogue_gp088	Caulobacter virus Rogue	GCA_000900555.1
AFU88402.1	001219	Cluster682_1clades	130	CcrSwift_gp084	Caulobacter virus Swift	GCA_000899655.1
AFU86920.1	001219	Cluster682_1clades	130	CbK_gp088	Caulobacter virus phiCbK	GCA_000900535.1
APU01543.1	001220	Cluster683_1clades	125	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29049.1	001220	Cluster683_1clades	125	AP1_0342	Aeromonas phage AP1	GCA_014183365.1
ATI17365.1	001220	Cluster683_1clades	125	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00229.1	001220	Cluster683_1clades	125	HWB28_gp323	Aeromonas phage AS-zj	GCA_002627665.1
AUE22809.1	001220	Cluster683_1clades	128	Ah1_00291	Aeromonas phage Ah1	GCA_002957415.1
QAX98524.1	001220	Cluster683_1clades	128	ASfcp2_188	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97806.1	001220	Cluster683_1clades	125	ASswx1_162	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01353.1	001220	Cluster683_1clades	126	ASwh1_293	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39439.1	001220	Cluster683_1clades	125	CC2_374	Aeromonas phage CC2	GCA_000903495.1
ADQ52987.1	001220	Cluster683_1clades	128	PX29p268	Aeromonas phage PX29	GCA_000920195.1
ADM79911.1	001220	Cluster683_1clades	128	phiAS5_ORF0068	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53165.1	001220	Cluster683_1clades	125	65p157	Aeromonas virus 65	GCA_000893255.1
AAQ17937.1	001220	Cluster683_1clades	128	pseT.3	Aeromonas virus Aeh1	GCA_000843245.1
AIA64829.1	001220	Cluster683_1clades	123	S13_030	Cronobacter phage S13	GCA_001503575.1
QHJ78833.1	001220	Cluster683_1clades	121	-	Myoviridae sp.	GCA_012593985.1
ALY07149.1	001220	Cluster683_1clades	128	VmeM32_00163	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFC21659.1	001221	Cluster684_1clades	124	GAP32_209	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14452.1	001221	Cluster684_1clades	126	PBI_121Q_562	Escherichia phage 121Q	GCA_000926855.1
QAY00496.1	001221	Cluster684_1clades	125	Ecwhy1_217	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34691.1	001221	Cluster684_1clades	126	ACQ29_gp011	Escherichia phage PBECO4	GCA_001041035.1
BBM62125.1	001221	Cluster684_1clades	126	EO157G_5360	Escherichia phage SP27	GCA_008033345.1
AXC36811.1	001221	Cluster684_1clades	126	-	Escherichia phage UB	GCA_003341455.1
QBO61850.1	001221	Cluster684_1clades	126	G17_00361	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80437.1	001221	Cluster684_1clades	126	PSLUR01_00460	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44325.1	001221	Cluster684_1clades	125	RaK2_00052	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43780.1	001221	Cluster684_1clades	124	CBB_215	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW18928.1	001221	Cluster684_1clades	124	7t3_0407	Salmonella phage 7t3	GCA_006083215.1
AZU98185.1	001221	Cluster684_1clades	124	CPT_Munch_241	Salmonella phage Munch	GCA_004015485.1
QIG62799.1	001221	Cluster684_1clades	124	SEPL_186	Salmonella phage SE_PL	GCA_011067555.1
AQW88736.1	001221	Cluster684_1clades	124	BF_0211	Serratia phage BF	GCA_002619745.1
SOK59019.1	001221	Cluster684_1clades	124	g211	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58484.1	001221	Cluster684_1clades	124	g207	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22674.1	001222	TM	121	Ah1_00133	Aeromonas phage Ah1	GCA_002957415.1
QAX98400.1	001222	TM	121	ASfcp2_56	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52856.1	001222	TM	121	PX29p137	Aeromonas phage PX29	GCA_000920195.1
ADM80115.1	001222	TM	112	phiAS5_ORF0272	Aeromonas phage phiAS5	GCA_000887715.1
AAQ64172.1	001222	TM	115	KVP40.0101	Vibrio phage KVP40	GCA_000843785.1
QIW90495.1	001222	TM	125	GCAPEGMB_00148	Vibrio phage V07	GCA_012361095.1
QIW90934.1	001222	TM	125	COHAPHLL_00071	Vibrio phage V09	GCA_012361135.1
QHJ74283.1	001222	TM	125	VH12019_00364	Vibrio phage VH1_2019	GCA_009931825.1
AGB07107.1	001222	TM	115	CF80_gp320	Vibrio phage VH7D	GCA_000914495.1
QBX05988.1	001222	TM	125	ValB1HC_034	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61001.1	001222	TM	125	AVU32_gp160	Vibrio phage ValKK3	GCA_001501635.1
AGN30150.2	001222	TM	125	VPFG_00148	Vibrio phage nt-1	GCA_000910195.2
ALP47219.1	001222	TM	95	phiGrn1_0214	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47569.1	001222	TM	109	phiST2_0347	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54613.1	001222	TM	125	vBValMR10Z_72	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37331.1	001222	TM	125	pp2_098	Vibriophage phi-pp2	GCA_002630725.1
AFC21791.1	001223	SIG+TM	115	GAP32_341	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13969.1	001223	SIG+TM	117	PBI_121Q_72	Escherichia phage 121Q	GCA_000926855.1
QAY00368.1	001223	SIG+TM	117	Ecwhy1_87	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35113.1	001223	SIG+TM	117	ACQ29_gp433	Escherichia phage PBECO4	GCA_001041035.1
BBM61661.1	001223	SIG+TM	117	EO157G_0720	Escherichia phage SP27	GCA_008033345.1
AXC36687.1	001223	SIG+TM	117	-	Escherichia phage UB	GCA_003341455.1
QBO61723.1	001223	SIG+TM	78	G17_00234	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80563.1	001223	SIG+TM	117	PSLUR01_00586	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44451.1	001223	SIG+TM	120	RaK2_00178	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43909.1	001223	SIG+TM	115	CBB_346	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19068.1	001223	SIG+TM	125	7t3_0548	Salmonella phage 7t3	GCA_006083215.1
AZU98314.1	001223	SIG+TM	125	CPT_Munch_370	Salmonella phage Munch	GCA_004015485.1
QIG62670.1	001223	SIG+TM	125	SEPL_057	Salmonella phage SE_PL	GCA_011067555.1
AQW88871.1	001223	SIG+TM	118	BF_0346	Serratia phage BF	GCA_002619745.1
SOK59155.1	001223	SIG+TM	121	g347	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58621.1	001223	SIG+TM	121	g344	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01616.1	001224	Cluster687_1clades	106	-	Aeromonas phage 65.2	GCA_002618145.1
APU01612.1	001224	Cluster687_1clades	106	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28867.1	001224	Cluster687_1clades	115	AP1_0160	Aeromonas phage AP1	GCA_014183365.1
ATI17292.1	001224	Cluster687_1clades	102	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17297.1	001224	Cluster687_1clades	115	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00304.1	001224	Cluster687_1clades	102	HWB28_gp248	Aeromonas phage AS-zj	GCA_002627665.1
ASU00297.1	001224	Cluster687_1clades	115	HWB28_gp255	Aeromonas phage AS-zj	GCA_002627665.1
QAX97734.1	001224	Cluster687_1clades	102	ASswx1_88	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97740.1	001224	Cluster687_1clades	115	ASswx1_95	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01416.1	001224	Cluster687_1clades	114	ASwh1_357	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01417.1	001224	Cluster687_1clades	100	ASwh1_358	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01442.1	001224	Cluster687_1clades	107	ASwh1_383	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39316.1	001224	Cluster687_1clades	115	CC2_016	Aeromonas phage CC2	GCA_000903495.1
AFN39318.1	001224	Cluster687_1clades	102	CC2_023	Aeromonas phage CC2	GCA_000903495.1
ADQ53237.1	001224	Cluster687_1clades	106	65p229	Aeromonas virus 65	GCA_000893255.1
ADQ53241.1	001224	Cluster687_1clades	106	65p233	Aeromonas virus 65	GCA_000893255.1
AFC21640.1	001225	Cluster688_1clades	114	GAP32_190	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14432.1	001225	Cluster688_1clades	80	PBI_121Q_542	Escherichia phage 121Q	GCA_000926855.1
QAY00516.1	001225	Cluster688_1clades	80	Ecwhy1_237	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34710.1	001225	Cluster688_1clades	80	ACQ29_gp030	Escherichia phage PBECO4	GCA_001041035.1
BBM62104.1	001225	Cluster688_1clades	80	EO157G_5150	Escherichia phage SP27	GCA_008033345.1
AXC36829.1	001225	Cluster688_1clades	80	-	Escherichia phage UB	GCA_003341455.1
QBO61869.1	001225	Cluster688_1clades	80	G17_00380	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13909.1	001225	Cluster688_1clades	80	vBEcoMphAPEC6_gp284c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80418.1	001225	Cluster688_1clades	80	PSLUR01_00441	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43761.1	001225	Cluster688_1clades	114	CBB_196	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18910.1	001225	Cluster688_1clades	82	7t3_0389	Salmonella phage 7t3	GCA_006083215.1
AZU98167.1	001225	Cluster688_1clades	82	CPT_Munch_223	Salmonella phage Munch	GCA_004015485.1
QIG62817.1	001225	Cluster688_1clades	82	SEPL_204	Salmonella phage SE_PL	GCA_011067555.1
AQW88717.1	001225	Cluster688_1clades	114	BF_0192	Serratia phage BF	GCA_002619745.1
SOK58999.1	001225	Cluster688_1clades	114	g191	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58464.1	001225	Cluster688_1clades	114	g187	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71353.1	001226	Cluster689_1clades	94	CR5_133	Cronobacter phage CR5	GCA_000910235.1
AMR59782.1	001226	Cluster689_1clades	101	SEGD1_135	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07561.1	001226	Cluster689_1clades	94	DERBICUS_135	Erwinia phage Derbicus	GCA_004521655.1
ANZ49778.1	001226	Cluster689_1clades	108	MACHINA_140	Erwinia phage Machina	GCA_002758035.1
AXF51283.1	001226	Cluster689_1clades	99	WELLINGTON_154	Erwinia phage Wellington	GCA_003344985.1
ANZ48160.1	001226	Cluster689_1clades	64	ASESINO_147	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48435.1	001226	Cluster689_1clades	107	CAITLIN_140	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48710.1	001226	Cluster689_1clades	107	CHRISDB_148	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48984.1	001226	Cluster689_1clades	94	EARLPHILLIPIV_135	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49222.1	001226	Cluster689_1clades	108	HUXLEY_140	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49506.1	001226	Cluster689_1clades	99	KWAN_154	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50050.1	001226	Cluster689_1clades	108	PARSHIK_141	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50326.1	001226	Cluster689_1clades	94	PHOBOS_136	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QKN85971.1	001226	Cluster689_1clades	101	ACEC001_1330	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51059.1	001226	Cluster689_1clades	101	MLDJOKPK_00022	Salmonella phage SPAsTU	GCA_003183805.1
AEP83964.1	001226	Cluster689_1clades	101	SPN3US_0131	Salmonella phage SPN3US	GCA_001042275.1
AFC21570.1	001227	Cluster691_1clades	100	GAP32_121	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14369.1	001227	Cluster691_1clades	100	PBI_121Q_479	Escherichia phage 121Q	GCA_000926855.1
QAY00579.1	001227	Cluster691_1clades	100	Ecwhy1_300	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34772.1	001227	Cluster691_1clades	100	ACQ29_gp092	Escherichia phage PBECO4	GCA_001041035.1
BBM62040.1	001227	Cluster691_1clades	100	EO157G_4510	Escherichia phage SP27	GCA_008033345.1
AXC36887.1	001227	Cluster691_1clades	46	-	Escherichia phage UB	GCA_003341455.1
QBO61935.1	001227	Cluster691_1clades	100	G17_00446	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80356.1	001227	Cluster691_1clades	100	PSLUR01_00379	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44778.1	001227	Cluster691_1clades	105	RaK2_00505	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43687.1	001227	Cluster691_1clades	100	CBB_122	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18826.1	001227	Cluster691_1clades	100	7t3_0305	Salmonella phage 7t3	GCA_006083215.1
AZU98090.1	001227	Cluster691_1clades	100	CPT_Munch_146	Salmonella phage Munch	GCA_004015485.1
QIG62892.1	001227	Cluster691_1clades	100	SEPL_279	Salmonella phage SE_PL	GCA_011067555.1
AQW88639.1	001227	Cluster691_1clades	100	BF_0114	Serratia phage BF	GCA_002619745.1
SOK58919.1	001227	Cluster691_1clades	100	g111	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58384.1	001227	Cluster691_1clades	100	g107	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOO14257.1	001228	Cluster692_1clades	90	Sn110110_063	Cyanophage S-RIM14	GCA_002599065.1
AOO14909.1	001228	Cluster692_1clades	89	W1230910_063	Cyanophage S-RIM14	GCA_002599125.1
AMO43307.1	001228	Cluster692_1clades	83	W270710_063	Cyanophage S-RIM44	GCA_002599145.1
AOO11541.1	001228	Cluster692_1clades	84	ES420910_060	Cyanophage S-RIM44	GCA_002599165.1
AOO11779.1	001228	Cluster692_1clades	83	Np050604_063	Cyanophage S-RIM44	GCA_002599185.1
AOO12006.1	001228	Cluster692_1clades	84	Np200711_060	Cyanophage S-RIM44	GCA_002599205.1
AOO12242.1	001228	Cluster692_1clades	84	Np420711_060	Cyanophage S-RIM44	GCA_002599225.1
AOO12480.1	001228	Cluster692_1clades	83	Sn080709_063	Cyanophage S-RIM44	GCA_002599245.1
AOO12707.1	001228	Cluster692_1clades	84	Sn130910_060	Cyanophage S-RIM44	GCA_002599265.1
AOO12945.1	001228	Cluster692_1clades	83	W2100709_063	Cyanophage S-RIM44	GCA_002599285.1
ADO99161.1	001228	Cluster692_1clades	83	Syn1_060	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76139.1	001228	Cluster692_1clades	88	PBI_BELLAMY_94	Synechococcus phage Bellamy	GCA_002627525.1
AOV59512.1	001228	Cluster692_1clades	84	S330809_051	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59274.1	001228	Cluster692_1clades	84	C440309_051	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59750.1	001228	Cluster692_1clades	84	N231010_051	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70078.1	001228	Cluster692_1clades	88	SynMITS9220M01_065	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFC21641.1	001229	Cluster693_1clades	80	GAP32_191	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14433.1	001229	Cluster693_1clades	85	PBI_121Q_543	Escherichia phage 121Q	GCA_000926855.1
QAY00515.1	001229	Cluster693_1clades	80	Ecwhy1_236	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34709.1	001229	Cluster693_1clades	80	ACQ29_gp029	Escherichia phage PBECO4	GCA_001041035.1
BBM62105.1	001229	Cluster693_1clades	80	EO157G_5160	Escherichia phage SP27	GCA_008033345.1
AXC36828.1	001229	Cluster693_1clades	80	-	Escherichia phage UB	GCA_003341455.1
QBO61868.1	001229	Cluster693_1clades	80	G17_00379	Escherichia phage vB_EcoM_G17	GCA_004521135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SCA80419.1	001229	Cluster693_1clades	80	PSLUR01_00442	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44307.1	001229	Cluster693_1clades	79	RaK2_00034	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43762.1	001229	Cluster693_1clades	80	CBB_197	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18911.1	001229	Cluster693_1clades	80	7t3_0390	Salmonella phage 7t3	GCA_006083215.1
AZU98168.1	001229	Cluster693_1clades	80	CPT_Munch_224	Salmonella phage Munch	GCA_004015485.1
QIG62816.1	001229	Cluster693_1clades	80	SEPL_203	Salmonella phage SE_PL	GCA_011067555.1
AQW88718.1	001229	Cluster693_1clades	80	BF_0193	Serratia phage BF	GCA_002619745.1
SOK59000.1	001229	Cluster693_1clades	80	g192	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58465.1	001229	Cluster693_1clades	80	g188	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21531.1	001230	Cluster694_1clades	74	GAP32_083	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14330.1	001230	Cluster694_1clades	76	PBI_121Q_440	Escherichia phage 121Q	GCA_000926855.1
QAY00611.1	001230	Cluster694_1clades	78	Ecwhy1_335	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34807.1	001230	Cluster694_1clades	78	ACQ29_gp127	Escherichia phage PBECO4	GCA_001041035.1
BBM62003.1	001230	Cluster694_1clades	78	EO157G_4140	Escherichia phage SP27	GCA_008033345.1
AXC36919.1	001230	Cluster694_1clades	78	-	Escherichia phage UB	GCA_003341455.1
QBO61974.1	001230	Cluster694_1clades	76	G17_00485	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13998.1	001230	Cluster694_1clades	78	vBEcoMphAPEC6_gp374c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80317.1	001230	Cluster694_1clades	76	PSLUR01_00340	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44739.1	001230	Cluster694_1clades	70	RaK2_00466	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43651.1	001230	Cluster694_1clades	74	CBB_86	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18786.1	001230	Cluster694_1clades	84	7t3_0265	Salmonella phage 7t3	GCA_006083215.1
AZU98051.1	001230	Cluster694_1clades	84	CPT_Munch_107	Salmonella phage Munch	GCA_004015485.1
AQW88600.1	001230	Cluster694_1clades	74	BF_0075	Serratia phage BF	GCA_002619745.1
SOK58877.1	001230	Cluster694_1clades	74	g069	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58340.1	001230	Cluster694_1clades	74	g063	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21939.1	001231	Cluster695_1clades	81	GAP32_481	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14053.1	001231	Cluster695_1clades	83	PBI_121Q_163	Escherichia phage 121Q	GCA_000926855.1
QAY00290.1	001231	Cluster695_1clades	83	Ecwhy1_8	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35040.1	001231	Cluster695_1clades	83	ACQ29_gp360	Escherichia phage PBECO4	GCA_001041035.1
BBM61736.1	001231	Cluster695_1clades	83	EO157G_1470	Escherichia phage SP27	GCA_008033345.1
AXC36617.1	001231	Cluster695_1clades	83	-	Escherichia phage UB	GCA_003341455.1
QBO61646.1	001231	Cluster695_1clades	83	G17_00150	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13700.1	001231	Cluster695_1clades	83	vBEcoMphAPEC6_gp070c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80048.1	001231	Cluster695_1clades	83	PSLUR01_00071	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM44066.1	001231	Cluster695_1clades	81	CBB_503	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18588.1	001231	Cluster695_1clades	82	7t3_067	Salmonella phage 7t3	GCA_006083215.1
AZU98416.1	001231	Cluster695_1clades	82	CPT_Munch_484	Salmonella phage Munch	GCA_004015485.1
QIG63097.1	001231	Cluster695_1clades	82	SEPL_484	Salmonella phage SE_PL	GCA_011067555.1
AQW89021.1	001231	Cluster695_1clades	82	BF_0496	Serratia phage BF	GCA_002619745.1
SOK59302.1	001231	Cluster695_1clades	81	g494	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58767.1	001231	Cluster695_1clades	81	g490	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28831.1	001232	Cluster696_1clades	72	AP1_0124	Aeromonas phage AP1	GCA_014183365.1
QMV28848.1	001232	Cluster696_1clades	69	AP1_0141	Aeromonas phage AP1	GCA_014183365.1
QMV29118.1	001232	Cluster696_1clades	57	AP1_0415	Aeromonas phage AP1	GCA_014183365.1
ATI17253.1	001232	Cluster696_1clades	69	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17251.1	001232	Cluster696_1clades	70	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17254.1	001232	Cluster696_1clades	70	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17265.1	001232	Cluster696_1clades	72	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00337.1	001232	Cluster696_1clades	70	HWB28_gp215	Aeromonas phage AS-zj	GCA_002627665.1
ASU00327.1	001232	Cluster696_1clades	72	HWB28_gp225	Aeromonas phage AS-zj	GCA_002627665.1
QAX97704.1	001232	Cluster696_1clades	72	ASswx1_58	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97725.1	001232	Cluster696_1clades	71	ASswx1_79	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01374.1	001232	Cluster696_1clades	79	ASwh1_314	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01433.1	001232	Cluster696_1clades	75	ASwh1_374	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01444.1	001232	Cluster696_1clades	80	ASwh1_385	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39179.1	001232	Cluster696_1clades	70	CC2_033	Aeromonas phage CC2	GCA_000903495.1
AFN39192.1	001232	Cluster696_1clades	72	CC2_052	Aeromonas phage CC2	GCA_000903495.1
AFC21741.1	001233	Cluster697_1clades	72	GAP32_291	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13922.1	001233	Cluster697_1clades	72	PBI_121Q_25	Escherichia phage 121Q	GCA_000926855.1
QAY00416.1	001233	Cluster697_1clades	72	Ecwhy1_135	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35159.1	001233	Cluster697_1clades	72	ACQ29_gp479	Escherichia phage PBECO4	GCA_001041035.1
BBM61614.1	001233	Cluster697_1clades	72	EO157G_0250	Escherichia phage SP27	GCA_008033345.1
AXC36732.1	001233	Cluster697_1clades	72	-	Escherichia phage UB	GCA_003341455.1
QBO61770.1	001233	Cluster697_1clades	72	G17_00281	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13814.1	001233	Cluster697_1clades	72	vBEcoMphAPEC6_gp185c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80517.1	001233	Cluster697_1clades	72	PSLUR01_00540	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43860.1	001233	Cluster697_1clades	72	CBB_296	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19019.1	001233	Cluster697_1clades	73	7t3_0499	Salmonella phage 7t3	GCA_006083215.1
AZU98266.1	001233	Cluster697_1clades	73	CPT_Munch_322	Salmonella phage Munch	GCA_004015485.1
QIG62718.1	001233	Cluster697_1clades	73	SEPL_105	Salmonella phage SE_PL	GCA_011067555.1
AQW88819.1	001233	Cluster697_1clades	72	BF_0294	Serratia phage BF	GCA_002619745.1
SOK59102.1	001233	Cluster697_1clades	72	g294	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58566.1	001233	Cluster697_1clades	72	g289	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13565.1	001234	Cluster698_1clades	72	Ccr10_gp037	Caulobacter phage Ccr10	GCA_002619445.1
ARB13911.1	001234	Cluster698_1clades	72	Ccr2_gp036	Caulobacter phage Ccr2	GCA_002619465.1
ARB14600.1	001234	Cluster698_1clades	72	Ccr29_gp043	Caulobacter phage Ccr29	GCA_002619485.1
ARB14956.1	001234	Cluster698_1clades	72	Ccr32_gp037	Caulobacter phage Ccr32	GCA_002619505.1
ARB15287.1	001234	Cluster698_1clades	72	Ccr34_gp038	Caulobacter phage Ccr34	GCA_002619525.1
ARB14254.1	001234	Cluster698_1clades	72	Ccr5_gp036	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68239.1	001234	Cluster698_1clades	72	CcrBL10_gp035	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69127.1	001234	Cluster698_1clades	72	CcrBL9_gp103	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87944.1	001234	Cluster698_1clades	72	CcrColossus_gp074	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68616.1	001234	Cluster698_1clades	72	CcrPW_gp077	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69681.1	001234	Cluster698_1clades	72	CcrSC_gp099	Caulobacter phage CcrSC	GCA_003443315.1
AFU87555.1	001234	Cluster698_1clades	72	CcrKarma_gp038	Caulobacter virus Karma	GCA_000901575.1
AFU87205.1	001234	Cluster698_1clades	72	CcrMagneto_gp035	Caulobacter virus Magneto	GCA_000903095.1
AFU86521.1	001234	Cluster698_1clades	72	CcrRogue_gp039	Caulobacter virus Rogue	GCA_000900555.1
AFU88352.1	001234	Cluster698_1clades	72	CcrSwift_gp034	Caulobacter virus Swift	GCA_000899655.1
AFU86869.1	001234	Cluster698_1clades	72	CbK_gp037	Caulobacter virus phiCbK	GCA_000900535.1
AFC21692.1	001235	Cluster699_1clades	58	GAP32_242	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14485.1	001235	Cluster699_1clades	69	PBI_121Q_595	Escherichia phage 121Q	GCA_000926855.1
QAY00464.1	001235	Cluster699_1clades	69	Ecwhy1_184	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35206.1	001235	Cluster699_1clades	69	ACQ29_gp526	Escherichia phage PBECO4	GCA_001041035.1
BBM62157.1	001235	Cluster699_1clades	69	EO157G_5680	Escherichia phage SP27	GCA_008033345.1
AXC36778.1	001235	Cluster699_1clades	69	-	Escherichia phage UB	GCA_003341455.1
QBO61818.1	001235	Cluster699_1clades	69	G17_00329	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13862.1	001235	Cluster699_1clades	69	vBEcoMphAPEC6_gp233	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80469.1	001235	Cluster699_1clades	69	PSLUR01_00492	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43814.1	001235	Cluster699_1clades	58	CBB_249	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18969.1	001235	Cluster699_1clades	52	7t3_0448	Salmonella phage 7t3	GCA_006083215.1
AZU98219.1	001235	Cluster699_1clades	52	CPT_Munch_275	Salmonella phage Munch	GCA_004015485.1
QIG62766.1	001235	Cluster699_1clades	52	SEPL_153	Salmonella phage SE_PL	GCA_011067555.1
AQW88772.1	001235	Cluster699_1clades	59	BF_0247	Serratia phage BF	GCA_002619745.1
SOK59053.1	001235	Cluster699_1clades	59	g245c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58519.1	001235	Cluster699_1clades	58	g242c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOO14239.1	001236	Cluster700_1clades	62	Sn110110_045	Cyanophage S-RIM14	GCA_002599065.1
AOO14891.1	001236	Cluster700_1clades	62	W1230910_045	Cyanophage S-RIM14	GCA_002599125.1
AMO43239.1	001236	Cluster700_1clades	60	R1080702_234	Cyanophage S-RIM32	GCA_001754165.1
AMO43469.1	001236	Cluster700_1clades	58	W270710_230	Cyanophage S-RIM44	GCA_002599145.1
AOO11709.1	001236	Cluster700_1clades	58	ES420910_232	Cyanophage S-RIM44	GCA_002599165.1
AOO11941.1	001236	Cluster700_1clades	58	Np050604_230	Cyanophage S-RIM44	GCA_002599185.1
AOO12175.1	001236	Cluster700_1clades	58	Np200711_233	Cyanophage S-RIM44	GCA_002599205.1
AOO12410.1	001236	Cluster700_1clades	58	Np420711_232	Cyanophage S-RIM44	GCA_002599225.1
AOO12642.1	001236	Cluster700_1clades	58	Sn080709_230	Cyanophage S-RIM44	GCA_002599245.1
AOO12875.1	001236	Cluster700_1clades	58	Sn130910_232	Cyanophage S-RIM44	GCA_002599265.1
AOO13108.1	001236	Cluster700_1clades	58	W2100709_231	Cyanophage S-RIM44	GCA_002599285.1
AGG54385.1	001236	Cluster700_1clades	69	CYWG_00101	Cyanophage S-SSM6b	GCA_002710425.1
ADO99330.1	001236	Cluster700_1clades	58	Syn1_234	Prochlorococcus phage Syn1	GCA_000892495.1
QGT54985.1	001236	Cluster700_1clades	53	b23_0379	Synechococcus phage B23	GCA_009745195.1
QGT54620.1	001236	Cluster700_1clades	53	b3_0385	Synechococcus phage B3	GCA_009745215.1
AXQ70456.1	001236	Cluster700_1clades	59	HOU04_gp057	Synechococcus phage S-T4	GCA_003443335.1
AOO14305.1	001237	Cluster701_1clades	51	Sn110110_111	Cyanophage S-RIM14	GCA_002599065.1
AOO14954.1	001237	Cluster701_1clades	51	W1230910_108	Cyanophage S-RIM14	GCA_002599125.1
AMO43424.1	001237	Cluster701_1clades	56	W270710_180	Cyanophage S-RIM44	GCA_002599145.1
AOO11668.1	001237	Cluster701_1clades	56	ES420910_187	Cyanophage S-RIM44	GCA_002599165.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO11896.1	001237	Cluster701_1clades	56	Np050604_180	Cyanophage S-RIM44	GCA_002599185.1
AOO12134.1	001237	Cluster701_1clades	56	Np200711_188	Cyanophage S-RIM44	GCA_002599205.1
AOO12369.1	001237	Cluster701_1clades	56	Np420711_187	Cyanophage S-RIM44	GCA_002599225.1
AOO12597.1	001237	Cluster701_1clades	56	Sn080709_180	Cyanophage S-RIM44	GCA_002599245.1
AOO12834.1	001237	Cluster701_1clades	56	Sn130910_187	Cyanophage S-RIM44	GCA_002599265.1
AOO13063.1	001237	Cluster701_1clades	56	W2100709_181	Cyanophage S-RIM44	GCA_002599285.1
AIX30728.1	001237	Cluster701_1clades	55	Syn7803US37_251	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW22940.1	001237	Cluster701_1clades	54	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50625.1	001237	Cluster701_1clades	54	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59580.1	001237	Cluster701_1clades	58	S330809_119	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59342.1	001237	Cluster701_1clades	52	C440309_119	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59818.1	001237	Cluster701_1clades	52	N231010_119	Synechococcus phage S-CAM4	GCA_002922155.1
AFC21738.1	001238	Cluster702_1clades	52	GAP32_288	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13919.1	001238	Cluster702_1clades	54	PBI_121Q_22	Escherichia phage 121Q	GCA_000926855.1
QAY00419.1	001238	Cluster702_1clades	55	Ecwhy1_138	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35162.1	001238	Cluster702_1clades	54	ACQ29_gp482	Escherichia phage PBECO4	GCA_001041035.1
BBM61611.1	001238	Cluster702_1clades	54	EO157G_0220	Escherichia phage SP27	GCA_008033345.1
AXC36735.1	001238	Cluster702_1clades	54	-	Escherichia phage UB	GCA_003341455.1
QBO61773.1	001238	Cluster702_1clades	54	G17_00284	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13817.1	001238	Cluster702_1clades	54	vBEcoMphAPEC6_gp188c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80514.1	001238	Cluster702_1clades	54	PSLUR01_00537	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43857.1	001238	Cluster702_1clades	52	CBB_293	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19016.1	001238	Cluster702_1clades	54	7t3_0496	Salmonella phage 7t3	GCA_006083215.1
AZU98263.1	001238	Cluster702_1clades	54	CPT_Munch_319	Salmonella phage Munch	GCA_004015485.1
QIG62721.1	001238	Cluster702_1clades	54	SEPL_108	Salmonella phage SE_PL	GCA_011067555.1
AQW88816.1	001238	Cluster702_1clades	54	BF_0291	Serratia phage BF	GCA_002619745.1
SOK59099.1	001238	Cluster702_1clades	54	g291	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58563.1	001238	Cluster702_1clades	54	g286	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMO43164.1	001239	Cluster703_1clades	46	R1080702_155	Cyanophage S-RIM32	GCA_001754165.1
AMO43388.1	001239	Cluster703_1clades	47	W270710_144	Cyanophage S-RIM44	GCA_002599145.1
AOO11633.1	001239	Cluster703_1clades	47	ES420910_152	Cyanophage S-RIM44	GCA_002599165.1
AOO11860.1	001239	Cluster703_1clades	47	Np050604_144	Cyanophage S-RIM44	GCA_002599185.1
AOO12098.1	001239	Cluster703_1clades	47	Np200711_152	Cyanophage S-RIM44	GCA_002599205.1
AOO12334.1	001239	Cluster703_1clades	47	Np420711_152	Cyanophage S-RIM44	GCA_002599225.1
AOO12561.1	001239	Cluster703_1clades	47	Sn080709_144	Cyanophage S-RIM44	GCA_002599245.1
AOO12799.1	001239	Cluster703_1clades	47	Sn130910_152	Cyanophage S-RIM44	GCA_002599265.1
AOO13027.1	001239	Cluster703_1clades	47	W2100709_145	Cyanophage S-RIM44	GCA_002599285.1
ADO99246.1	001239	Cluster703_1clades	47	Syn1_145	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76138.1	001239	Cluster703_1clades	48	PBI_BELLAMY_93	Synechococcus phage Bellamy	GCA_002627525.1
AOV59613.1	001239	Cluster703_1clades	47	S330809_152	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59375.1	001239	Cluster703_1clades	47	C440309_152	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59851.1	001239	Cluster703_1clades	47	N231010_152	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70551.1	001239	Cluster703_1clades	46	HOU04_gp152	Synechococcus phage S-T4	GCA_003443335.1
QJT70075.1	001239	Cluster703_1clades	46	SynMITS9220M01_062	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ATA65450.1	001240	Cluster708_1clades	738	2050HW_00115	Serratia phage 2050HW	GCA_002628125.1
ATA65451.1	001240	Cluster708_1clades	345	2050HW_00116	Serratia phage 2050HW	GCA_002628125.1
ATA65453.1	001240	Cluster708_1clades	710	2050HW_00118	Serratia phage 2050HW	GCA_002628125.1
ATA65454.1	001240	Cluster708_1clades	670	2050HW_00119	Serratia phage 2050HW	GCA_002628125.1
ATA65456.1	001240	Cluster708_1clades	731	2050HW_00121	Serratia phage 2050HW	GCA_002628125.1
ATA65458.1	001240	Cluster708_1clades	662	2050HW_00123	Serratia phage 2050HW	GCA_002628125.1
ATA65565.1	001240	Cluster708_1clades	608	2050HW_00230	Serratia phage 2050HW	GCA_002628125.1
QDB71221.1	001240	Cluster708_1clades	738	CPT_Moabite_191	Serratia phage Moabite	GCA_006384735.1
QDB71222.1	001240	Cluster708_1clades	806	CPT_Moabite_192	Serratia phage Moabite	GCA_006384735.1
QDB71223.1	001240	Cluster708_1clades	710	CPT_Moabite_193	Serratia phage Moabite	GCA_006384735.1
QDB71224.1	001240	Cluster708_1clades	691	CPT_Moabite_194	Serratia phage Moabite	GCA_006384735.1
QDB71226.1	001240	Cluster708_1clades	731	CPT_Moabite_196	Serratia phage Moabite	GCA_006384735.1
QDB71227.1	001240	Cluster708_1clades	729	CPT_Moabite_197	Serratia phage Moabite	GCA_006384735.1
QDB71228.1	001240	Cluster708_1clades	672	CPT_Moabite_198	Serratia phage Moabite	GCA_006384735.1
QDB71330.1	001240	Cluster708_1clades	725	CPT_Moabite_300	Serratia phage Moabite	GCA_006384735.1
QDH83641.1	001241	Cluster709_1clades	614	H1O15_gp147	Achromobacter phage Motura	GCA_006964305.1
QBX06662.1	001241	Cluster709_1clades	651	BcepSaruman_249	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74631.1	001241	Cluster709_1clades	651	BcepSauron_251	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67050.1	001241	Cluster709_1clades	647	AD1_006	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79810.1	001241	Cluster709_1clades	647	JA11_005	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66408.1	001241	Cluster709_1clades	647	JA13_005	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66731.1	001241	Cluster709_1clades	647	JA29_005	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67379.1	001241	Cluster709_1clades	647	JA33_005	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08288.1	001241	Cluster709_1clades	644	Alexandra_6	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58646.1	001241	Cluster709_1clades	646	Y3_006	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28493.1	001241	Cluster709_1clades	647	YOLOSWAG_6	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38265.1	001241	Cluster709_1clades	597	BN7874_096	Phage NCTB	GCA_900092385.1
AFH14722.1	001241	Cluster709_1clades	660	Lu11_0185	Pseudomonas phage Lu11	GCA_000897175.1
AGS81991.2	001241	Cluster709_1clades	625	PaBG_00106	Pseudomonas phage PaBG	GCA_000912555.1
BAG41660.1	001241	Cluster709_1clades	635	RSL1_ORF211	Ralstonia phage phiRSL1	GCA_000879455.1
QDH83622.1	001242	Cluster710_1clades	518	H1O15_gp166	Achromobacter phage Motura	GCA_006964305.1
QBX06506.1	001242	Cluster710_1clades	517	BcepSaruman_093	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74472.1	001242	Cluster710_1clades	517	BcepSauron_092	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67225.1	001242	Cluster710_1clades	387	AD1_181	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79975.1	001242	Cluster710_1clades	386	JA11_170	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66573.1	001242	Cluster710_1clades	386	JA13_170	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66898.1	001242	Cluster710_1clades	386	JA29_172	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67544.1	001242	Cluster710_1clades	386	JA33_170	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08454.1	001242	Cluster710_1clades	387	Alexandra_186	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58822.1	001242	Cluster710_1clades	386	Y3_182	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28656.1	001242	Cluster710_1clades	387	YOLOSWAG_177	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38497.1	001242	Cluster710_1clades	405	BN7874_278	Phage NCTB	GCA_900092385.1
AFH14638.1	001242	Cluster710_1clades	404	Lu11_0106	Pseudomonas phage Lu11	GCA_000897175.1
AGS82071.1	001242	Cluster710_1clades	406	PaBG_00195	Pseudomonas phage PaBG	GCA_000912555.1
BAG41563.1	001242	Cluster710_1clades	537	RSL1_ORF118	Ralstonia phage phiRSL1	GCA_000879455.1
AMR59655.1	001243	Cluster718_1clades	315	SEGD1_004	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49658.1	001243	Cluster718_1clades	326	MACHINA_20	Erwinia phage Machina	GCA_002758035.1
AXF51145.1	001243	Cluster718_1clades	351	WELLINGTON_14	Erwinia phage Wellington	GCA_003344985.1
AFQ96734.1	001243	Cluster718_1clades	325	G173_gp189	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48035.1	001243	Cluster718_1clades	323	ASESINO_22	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48309.1	001243	Cluster718_1clades	330	CAITLIN_14	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48582.1	001243	Cluster718_1clades	337	CHRISDB_20	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49103.1	001243	Cluster718_1clades	326	HUXLEY_21	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49367.1	001243	Cluster718_1clades	351	KWAN_14	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49931.1	001243	Cluster718_1clades	326	PARSHIK_22	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50445.1	001243	Cluster718_1clades	325	STRATTON_20	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85843.1	001243	Cluster718_1clades	316	ACEC001_0060	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20723.1	001243	Cluster718_1clades	315	-	Salmonella phage JN03	GCA_014319805.1
AWN09087.1	001243	Cluster718_1clades	319	MLDJOKPK_00162	Salmonella phage SPAsTU	GCA_003183805.1
AEP83838.1	001243	Cluster718_1clades	315	SPN3US_0005	Salmonella phage SPN3US	GCA_001042275.1
QDB70270.1	001244	Cluster719_1clades	322	CF8_0102	Aeromonas phage CF8	GCA_006384595.2
QDJ97248.1	001244	Cluster719_1clades	320	D6_0088	Aeromonas phage D6	GCA_007051205.2
QDH47085.1	001244	Cluster719_1clades	320	LAh10_20	Aeromonas phage LAh10	GCA_006863975.1
QDJ96861.1	001244	Cluster719_1clades	327	PS1_0102	Aeromonas phage PS1	GCA_007051165.2
QFR59493.1	001244	Cluster719_1clades	327	PS2_0102	Aeromonas phage PS2	GCA_009388305.2
ASU03848.1	001244	Cluster719_1clades	346	JOAD_67	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03603.1	001244	Cluster719_1clades	346	RISINGSUN_67	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71947.1	001244	Cluster719_1clades	320	N1M2_84	Klebsiella phage N1M2	GCA_010092605.1
QGZ14408.1	001244	Cluster719_1clades	317	HWC77_gp045	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27156.1	001244	Cluster719_1clades	337	PPEV_gp062	Pseudomonas phage EL	GCA_000866825.1
QAU04328.1	001244	Cluster719_1clades	317	HWC03_gp173	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23248.1	001244	Cluster719_1clades	317	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80989.1	001244	Cluster719_1clades	317	Aphrodite1_0097	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47480.1	001244	Cluster719_1clades	317	HWC35_gp086	Vibrio phage USC-1	GCA_006864065.1
BAW98300.1	001244	Cluster719_1clades	319	FDH33_gp091	Vibrio phage pTD1	GCA_002618825.1
AMR59878.1	001245	Cluster721_1clades	232	SEGD1_231	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49879.1	001245	Cluster721_1clades	294	MACHINA_241	Erwinia phage Machina	GCA_002758035.1
AXF51382.1	001245	Cluster721_1clades	191	WELLINGTON_256	Erwinia phage Wellington	GCA_003344985.1
AFQ96694.1	001245	Cluster721_1clades	303	G173_gp149	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48263.1	001245	Cluster721_1clades	303	ASESINO_250	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48536.1	001245	Cluster721_1clades	224	CAITLIN_241	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48812.1	001245	Cluster721_1clades	303	CHRISDB_250	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49322.1	001245	Cluster721_1clades	294	HUXLEY_240	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49609.1	001245	Cluster721_1clades	191	KWAN_257	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50150.1	001245	Cluster721_1clades	294	PARSHIK_241	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50676.1	001245	Cluster721_1clades	303	STRATTON_251	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86069.1	001245	Cluster721_1clades	286	ACEC001_2260	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20915.1	001245	Cluster721_1clades	286	-	Salmonella phage JN03	GCA_014319805.1
AXF51111.1	001245	Cluster721_1clades	295	MLDJOKPK_00212	Salmonella phage SPAsTU	GCA_003183805.1
AEP84061.1	001245	Cluster721_1clades	289	SPN3US_0228	Salmonella phage SPN3US	GCA_001042275.1
QDH83590.1	001246	Cluster722_1clades	253	H1O15_gp198	Achromobacter phage Motura	GCA_006964305.1
QBX06487.1	001246	Cluster722_1clades	246	BcepSaruman_074	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74454.1	001246	Cluster722_1clades	246	BcepSauron_074	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67224.1	001246	Cluster722_1clades	266	AD1_180	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79974.1	001246	Cluster722_1clades	267	JA11_169	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66572.1	001246	Cluster722_1clades	267	JA13_169	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66897.1	001246	Cluster722_1clades	267	JA29_171	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67543.1	001246	Cluster722_1clades	267	JA33_169	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08453.1	001246	Cluster722_1clades	266	Alexandra_185	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58821.1	001246	Cluster722_1clades	268	Y3_181	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28655.1	001246	Cluster722_1clades	265	YOLOSWAG_176	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38494.1	001246	Cluster722_1clades	274	BN7874_277	Phage NCTB	GCA_900092385.1
AFH14636.1	001246	Cluster722_1clades	286	Lu11_0104	Pseudomonas phage Lu11	GCA_000897175.1
AGS82073.1	001246	Cluster722_1clades	286	PaBG_00197	Pseudomonas phage PaBG	GCA_000912555.1
BAG41592.1	001246	Cluster722_1clades	193	RSL1_ORF146	Ralstonia phage phiRSL1	GCA_000879455.1
AMR59757.1	001247	Cluster723_1clades	267	SEGD1_110	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49756.1	001247	Cluster723_1clades	264	MACHINA_118	Erwinia phage Machina	GCA_002758035.1
AXF51264.1	001247	Cluster723_1clades	276	WELLINGTON_134	Erwinia phage Wellington	GCA_003344985.1
AFQ96574.1	001247	Cluster723_1clades	268	G173_gp029	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48135.1	001247	Cluster723_1clades	268	ASESINO_122	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48412.1	001247	Cluster723_1clades	267	CAITLIN_117	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48684.1	001247	Cluster723_1clades	267	CHRISDB_122	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49200.1	001247	Cluster723_1clades	264	HUXLEY_118	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49485.1	001247	Cluster723_1clades	276	KWAN_133	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50028.1	001247	Cluster723_1clades	264	PARSHIK_119	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50549.1	001247	Cluster723_1clades	268	STRATTON_124	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85947.1	001247	Cluster723_1clades	267	ACEC001_1090	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20815.1	001247	Cluster723_1clades	267	-	Salmonella phage JN03	GCA_014319805.1
AXF51073.1	001247	Cluster723_1clades	269	MLDJOKPK_00051	Salmonella phage SPAsTU	GCA_003183805.1
AEP83939.1	001247	Cluster723_1clades	267	SPN3US_0106	Salmonella phage SPN3US	GCA_001042275.1
QDH83417.1	001248	Cluster724_1clades	225	H1O15_gp008	Achromobacter phage Motura	GCA_006964305.1
QBX06723.1	001248	Cluster724_1clades	258	BcepSaruman_310	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74691.1	001248	Cluster724_1clades	258	BcepSauron_311	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67205.1	001248	Cluster724_1clades	206	AD1_161	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79956.1	001248	Cluster724_1clades	210	JA11_151	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66555.1	001248	Cluster724_1clades	210	JA13_152	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66880.1	001248	Cluster724_1clades	210	JA29_154	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67525.1	001248	Cluster724_1clades	210	JA33_151	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08437.1	001248	Cluster724_1clades	206	Alexandra_166	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58802.1	001248	Cluster724_1clades	204	Y3_162	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28640.1	001248	Cluster724_1clades	206	YOLOSWAG_160	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38460.1	001248	Cluster724_1clades	210	BN7874_257	Phage NCTB	GCA_900092385.1
AFH14615.1	001248	Cluster724_1clades	248	Lu11_0083	Pseudomonas phage Lu11	GCA_000897175.1
AGS82086.1	001248	Cluster724_1clades	269	PaBG_00211	Pseudomonas phage PaBG	GCA_000912555.1
BAG41597.1	001248	Cluster724_1clades	241	RSL1_ORF151	Ralstonia phage phiRSL1	GCA_000879455.1
AMR59859.1	001249	Cluster725_1clades	218	SEGD1_212	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49857.1	001249	Cluster725_1clades	250	MACHINA_219	Erwinia phage Machina	GCA_002758035.1
AXF51359.1	001249	Cluster725_1clades	245	WELLINGTON_233	Erwinia phage Wellington	GCA_003344985.1
AFQ96674.1	001249	Cluster725_1clades	210	G173_gp129	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48240.1	001249	Cluster725_1clades	244	ASESINO_227	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48514.1	001249	Cluster725_1clades	252	CAITLIN_219	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48791.1	001249	Cluster725_1clades	252	CHRISDB_229	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49301.1	001249	Cluster725_1clades	250	HUXLEY_219	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49585.1	001249	Cluster725_1clades	245	KWAN_233	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50129.1	001249	Cluster725_1clades	250	PARSHIK_220	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50654.1	001249	Cluster725_1clades	244	STRATTON_229	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86048.1	001249	Cluster725_1clades	246	ACEC001_2050	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20896.1	001249	Cluster725_1clades	266	-	Salmonella phage JN03	GCA_014319805.1
AWN09139.2	001249	Cluster725_1clades	244	MLDJOKPK_00232	Salmonella phage SPAsTU	GCA_003183805.1
AEP84041.1	001249	Cluster725_1clades	246	SPN3US_0208	Salmonella phage SPN3US	GCA_001042275.1
QDH83400.1	001250	SIG+MmcB-like	147	H1O15_gp062	Achromobacter phage Motura	GCA_006964305.1
QBX06661.1	001250	SIG+MmcB-like	164	BcepSaruman_248	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74630.1	001250	SIG+MmcB-like	158	BcepSauron_250	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67162.1	001250	SIG+MmcB-like	163	AD1_118	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79912.1	001250	SIG+MmcB-like	145	JA11_107	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66511.1	001250	SIG+MmcB-like	145	JA13_108	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66836.1	001250	SIG+MmcB-like	162	JA29_110	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67481.1	001250	SIG+MmcB-like	145	JA33_107	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08395.1	001250	SIG+MmcB-like	162	Alexandra_123	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58759.1	001250	SIG+MmcB-like	163	Y3_119	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28597.1	001250	SIG+MmcB-like	162	YOLOSWAG_115	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38347.1	001250	SIG+MmcB-like	266	BN7874_178	Phage NCTB	GCA_900092385.1
AFH14731.1	001250	SIG+MmcB-like	184	Lu11_0194	Pseudomonas phage Lu11	GCA_000897175.1
AGS81973.1	001250	SIG+MmcB-like	162	PaBG_00088	Pseudomonas phage PaBG	GCA_000912555.1
BAG41661.1	001250	SIG+MmcB-like	150	RSL1_ORF212	Ralstonia phage phiRSL1	GCA_000879455.1
AGX01889.1	001251	Cluster727_1clades	263	CF95_gp166	Erwinia phage PhiEaH1	GCA_000914555.1
ABY63085.1	001251	Cluster727_1clades	251	201phi2-1p257	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44969.1	001251	Cluster727_1clades	253	KTN4_211	Pseudomonas phage KTN4	GCA_002607225.1
ARV77356.1	001251	Cluster727_1clades	256	NOXIFER_187	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32359.1	001251	Cluster727_1clades	251	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76877.1	001251	Cluster727_1clades	251	PHABIO_246	Pseudomonas phage Phabio	GCA_002624965.1
AEH03623.1	001251	Cluster727_1clades	251	200	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02759.1	001251	Cluster727_1clades	248	PSA21_233	Pseudomonas phage Psa21	GCA_004340405.1
ATN94745.1	001251	Cluster727_1clades	253	SL2_168	Pseudomonas phage SL2	GCA_002956015.1
QJB22847.1	001251	Cluster727_1clades	253	fnug_204	Pseudomonas phage fnug	GCA_012837215.1
QEM41933.1	001251	Cluster727_1clades	251	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83072.1	001251	Cluster727_1clades	253	PHIKZ171	Pseudomonas virus phiKZ	GCA_000842965.1
ATA65422.1	001251	Cluster727_1clades	202	2050HW_00087	Serratia phage 2050HW	GCA_002628125.1
QDB71199.1	001251	Cluster727_1clades	252	CPT_Moabite_169	Serratia phage Moabite	GCA_006384735.1
QFP93156.1	001251	Cluster727_1clades	205	-	Serratia phage PCH45	GCA_009187865.1
AFC21669.1	001252	DUF4376	212	GAP32_219	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14460.1	001252	DUF4376	259	PBI_121Q_570	Escherichia phage 121Q	GCA_000926855.1
QAY00488.1	001252	DUF4376	259	Ecwhy1_209	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34682.1	001252	DUF4376	259	ACQ29_gp002	Escherichia phage PBECO4	GCA_001041035.1
BBM62133.1	001252	DUF4376	259	EO157G_5440	Escherichia phage SP27	GCA_008033345.1
AXC36802.1	001252	DUF4376	259	-	Escherichia phage UB	GCA_003341455.1
QBO61842.1	001252	DUF4376	259	G17_00353	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80445.1	001252	DUF4376	259	PSLUR01_00468	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43790.1	001252	DUF4376	212	CBB_225	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18941.1	001252	DUF4376	210	7t3_0420	Salmonella phage 7t3	GCA_006083215.1
AZU98195.1	001252	DUF4376	210	CPT_Munch_251	Salmonella phage Munch	GCA_004015485.1
QIG62789.1	001252	DUF4376	210	SEPL_176	Salmonella phage SE_PL	GCA_011067555.1
AQW88749.1	001252	DUF4376	212	BF_0224	Serratia phage BF	GCA_002619745.1
SOK59029.1	001252	DUF4376	212	g221c	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58494.1	001252	DUF4376	212	g217c	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDH83601.1	001253	Cluster729_1clades	226	H1O15_gp187	Achromobacter phage Motura	GCA_006964305.1
QBX06496.1	001253	Cluster729_1clades	236	BcepSaruman_083	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74463.1	001253	Cluster729_1clades	236	BcepSauron_083	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67183.1	001253	Cluster729_1clades	235	AD1_139	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79933.1	001253	Cluster729_1clades	234	JA11_128	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66532.1	001253	Cluster729_1clades	234	JA13_129	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66857.1	001253	Cluster729_1clades	234	JA29_131	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67502.1	001253	Cluster729_1clades	234	JA33_128	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08416.1	001253	Cluster729_1clades	235	Alexandra_144	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58780.1	001253	Cluster729_1clades	235	Y3_140	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28618.1	001253	Cluster729_1clades	235	YOLOSWAG_138	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SBV38405.1	001253	Cluster729_1clades	233	BN7874_221	Phage NCTB	GCA_900092385.1
AFH14597.1	001253	Cluster729_1clades	247	Lu11_0066	Pseudomonas phage Lu11	GCA_000897175.1
AGS81965.1	001253	Cluster729_1clades	228	PaBG_00081	Pseudomonas phage PaBG	GCA_000912555.1
BAG41580.1	001253	Cluster729_1clades	248	RSL1_ORF135	Ralstonia phage phiRSL1	GCA_000879455.1
QDH83450.1	001254	Cluster730_1clades	225	H1O15_gp042	Achromobacter phage Motura	GCA_006964305.1
QBX06601.1	001254	Cluster730_1clades	241	BcepSaruman_188	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74566.1	001254	Cluster730_1clades	241	BcepSauron_186	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67265.1	001254	Cluster730_1clades	216	AD1_221	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80012.1	001254	Cluster730_1clades	225	JA11_207	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66610.1	001254	Cluster730_1clades	225	JA13_207	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66935.1	001254	Cluster730_1clades	226	JA29_209	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67582.1	001254	Cluster730_1clades	225	JA33_208	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08494.1	001254	Cluster730_1clades	217	Alexandra_231	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58866.1	001254	Cluster730_1clades	219	Y3_226	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28698.1	001254	Cluster730_1clades	216	YOLOSWAG_220	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38176.1	001254	Cluster730_1clades	212	BN7874_007	Phage NCTB	GCA_900092385.1
AFH14670.1	001254	Cluster730_1clades	223	Lu11_0136	Pseudomonas phage Lu11	GCA_000897175.1
AGS82037.2	001254	Cluster730_1clades	223	PaBG_00154	Pseudomonas phage PaBG	GCA_000912555.1
BAG41745.1	001254	Cluster730_1clades	238	RSL1_ORF299	Ralstonia phage phiRSL1	GCA_000879455.1
AMR59740.1	001255	Cluster731_1clades	189	SEGD1_091	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49737.1	001255	Cluster731_1clades	207	MACHINA_99	Erwinia phage Machina	GCA_002758035.1
AXF51237.1	001255	Cluster731_1clades	230	WELLINGTON_107	Erwinia phage Wellington	GCA_003344985.1
AFQ96556.1	001255	Cluster731_1clades	218	G173_gp011	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48116.1	001255	Cluster731_1clades	218	ASESINO_103	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48391.1	001255	Cluster731_1clades	199	CAITLIN_96	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48663.1	001255	Cluster731_1clades	201	CHRISDB_101	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49182.1	001255	Cluster731_1clades	207	HUXLEY_100	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49458.1	001255	Cluster731_1clades	230	KWAN_106	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50010.1	001255	Cluster731_1clades	207	PARSHIK_101	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50530.1	001255	Cluster731_1clades	218	STRATTON_105	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85927.1	001255	Cluster731_1clades	212	ACEC001_0890	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20797.1	001255	Cluster731_1clades	212	-	Salmonella phage JN03	GCA_014319805.1
AXF51082.1	001255	Cluster731_1clades	217	MLDJOKPK_00072	Salmonella phage SPAsTU	GCA_003183805.1
AEP83920.1	001255	Cluster731_1clades	212	SPN3US_0087	Salmonella phage SPN3US	GCA_001042275.1
AMR59865.1	001256	Cluster732_1clades	180	SEGD1_218	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49863.1	001256	Cluster732_1clades	200	MACHINA_225	Erwinia phage Machina	GCA_002758035.1
AXF51365.1	001256	Cluster732_1clades	225	WELLINGTON_239	Erwinia phage Wellington	GCA_003344985.1
AFQ96680.1	001256	Cluster732_1clades	172	G173_gp135	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48246.1	001256	Cluster732_1clades	172	ASESINO_233	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48520.1	001256	Cluster732_1clades	174	CAITLIN_225	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48797.1	001256	Cluster732_1clades	168	CHRISDB_235	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49307.1	001256	Cluster732_1clades	200	HUXLEY_225	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49592.1	001256	Cluster732_1clades	213	KWAN_240	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50135.1	001256	Cluster732_1clades	200	PARSHIK_226	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50660.1	001256	Cluster732_1clades	172	STRATTON_235	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86053.1	001256	Cluster732_1clades	180	ACEC001_2100	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20901.1	001256	Cluster732_1clades	180	-	Salmonella phage JN03	GCA_014319805.1
AWN09134.1	001256	Cluster732_1clades	180	MLDJOKPK_00227	Salmonella phage SPAsTU	GCA_003183805.1
AEP84046.1	001256	Cluster732_1clades	180	SPN3US_0213	Salmonella phage SPN3US	GCA_001042275.1
ABY62993.1	001257	Cluster733_1clades	199	201phi2-1p163	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44885.1	001257	Cluster733_1clades	193	KTN4_127	Pseudomonas phage KTN4	GCA_002607225.1
ARV77268.1	001257	Cluster733_1clades	185	NOXIFER_99	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32262.1	001257	Cluster733_1clades	190	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76777.1	001257	Cluster733_1clades	192	PHABIO_146	Pseudomonas phage Phabio	GCA_002624965.1
AEH03529.1	001257	Cluster733_1clades	195	105	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02640.1	001257	Cluster733_1clades	191	PSA21_112	Pseudomonas phage Psa21	GCA_004340405.1
ATN94828.1	001257	Cluster733_1clades	193	SL2_251	Pseudomonas phage SL2	GCA_002956015.1
QJB22762.1	001257	Cluster733_1clades	193	fnug_119	Pseudomonas phage fnug	GCA_012837215.1
QEM41836.1	001257	Cluster733_1clades	190	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83001.1	001257	Cluster733_1clades	193	PHIKZ100	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19206.1	001257	Cluster733_1clades	225	FDH28_gp189	Ralstonia phage RP12	GCA_002617345.1
BAW19492.1	001257	Cluster733_1clades	225	-	Ralstonia phage RP31	GCA_002617365.1
BAS04967.2	001257	Cluster733_1clades	174	AVU11_agp36	Ralstonia phage RSF1	GCA_001500875.1
BAQ02692.2	001257	Cluster733_1clades	205	-	Ralstonia phage RSL2	GCA_001503055.1
QDH83440.1	001258	Cluster734_1clades	139	H1O15_gp032	Achromobacter phage Motura	GCA_006964305.1
QBX06651.1	001258	Cluster734_1clades	223	BcepSaruman_238	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74619.1	001258	Cluster734_1clades	223	BcepSauron_239	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67273.1	001258	Cluster734_1clades	218	AD1_229	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80017.1	001258	Cluster734_1clades	220	JA11_212	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66616.1	001258	Cluster734_1clades	220	JA13_213	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66940.1	001258	Cluster734_1clades	220	JA29_214	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67587.1	001258	Cluster734_1clades	220	JA33_213	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08612.1	001258	Cluster734_1clades	222	Alexandra_238	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58873.1	001258	Cluster734_1clades	181	Y3_233	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28705.1	001258	Cluster734_1clades	219	YOLOSWAG_227	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38184.1	001258	Cluster734_1clades	203	BN7874_015	Phage NCTB	GCA_900092385.1
AFH14700.1	001258	Cluster734_1clades	219	Lu11_0166	Pseudomonas phage Lu11	GCA_000897175.1
AGS82004.1	001258	Cluster734_1clades	218	PaBG_00120	Pseudomonas phage PaBG	GCA_000912555.1
BAG41676.1	001258	Cluster734_1clades	143	RSL1_ORF226	Ralstonia phage phiRSL1	GCA_000879455.1
ARB13536.1	001259	Cluster735_1clades	172	Ccr10_gp008	Caulobacter phage Ccr10	GCA_002619445.1
ARB13861.1	001259	Cluster735_1clades	172	Ccr10_gp331	Caulobacter phage Ccr10	GCA_002619445.1
ARB14565.1	001259	Cluster735_1clades	172	Ccr29_gp008	Caulobacter phage Ccr29	GCA_002619485.1
ARB14900.1	001259	Cluster735_1clades	172	Ccr29_gp344	Caulobacter phage Ccr29	GCA_002619485.1
AXQ69062.1	001259	Cluster735_1clades	218	CcrBL9_gp038	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69578.1	001259	Cluster735_1clades	218	CcrBL9_gp554	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69622.1	001259	Cluster735_1clades	187	CcrSC_gp040	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70122.1	001259	Cluster735_1clades	187	CcrSC_gp540	Caulobacter phage CcrSC	GCA_003443315.1
AFU86491.1	001259	Cluster735_1clades	172	CcrRogue_gp009	Caulobacter virus Rogue	GCA_000900555.1
AFU86822.1	001259	Cluster735_1clades	172	CcrRogue_gp340	Caulobacter virus Rogue	GCA_000900555.1
AFU88326.1	001259	Cluster735_1clades	192	CcrSwift_gp008	Caulobacter virus Swift	GCA_000899655.1
AFU88651.1	001259	Cluster735_1clades	192	CcrSwift_gp333	Caulobacter virus Swift	GCA_000899655.1
QAY00739.1	001259	Cluster735_1clades	135	Ecwhy1_464	Escherichia phage Ecwhy_1	GCA_004146585.1
QBO61506.1	001259	Cluster735_1clades	135	G17_00010	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62112.1	001259	Cluster735_1clades	135	G17_00623	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AFC21596.1	001260	Cluster737_1clades	190	GAP32_146	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21600.1	001260	Cluster737_1clades	159	GAP32_150	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21601.1	001260	Cluster737_1clades	206	GAP32_151	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43715.1	001260	Cluster737_1clades	186	CBB_150	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43720.1	001260	Cluster737_1clades	159	CBB_155	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43721.1	001260	Cluster737_1clades	210	CBB_156	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88669.1	001260	Cluster737_1clades	185	BF_0144	Serratia phage BF	GCA_002619745.1
AQW88674.1	001260	Cluster737_1clades	159	BF_0149	Serratia phage BF	GCA_002619745.1
AQW88675.1	001260	Cluster737_1clades	187	BF_0150	Serratia phage BF	GCA_002619745.1
SOK58951.1	001260	Cluster737_1clades	182	g143	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58956.1	001260	Cluster737_1clades	148	g148	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58957.1	001260	Cluster737_1clades	186	g149	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58417.1	001260	Cluster737_1clades	182	g140	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58422.1	001260	Cluster737_1clades	148	g145	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58423.1	001260	Cluster737_1clades	186	g146	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGT54716.1	001261	Cluster738_1clades	188	b23_0101	Synechococcus phage B23	GCA_009745195.1
QGT54727.1	001261	Cluster738_1clades	182	b23_0112	Synechococcus phage B23	GCA_009745195.1
QGT54819.1	001261	Cluster738_1clades	192	b23_0204	Synechococcus phage B23	GCA_009745195.1
QGT54837.1	001261	Cluster738_1clades	179	b23_0222	Synechococcus phage B23	GCA_009745195.1
QGT54838.1	001261	Cluster738_1clades	176	b23_0223	Synechococcus phage B23	GCA_009745195.1
QGT54853.1	001261	Cluster738_1clades	209	b23_0239	Synechococcus phage B23	GCA_009745195.1
QGT54854.1	001261	Cluster738_1clades	177	b23_0240	Synechococcus phage B23	GCA_009745195.1
QGT54346.1	001261	Cluster738_1clades	188	b3_0102	Synechococcus phage B3	GCA_009745215.1
QGT54357.1	001261	Cluster738_1clades	182	b3_0113	Synechococcus phage B3	GCA_009745215.1
QGT54449.1	001261	Cluster738_1clades	192	b3_0206	Synechococcus phage B3	GCA_009745215.1
QGT54467.1	001261	Cluster738_1clades	186	b3_0224	Synechococcus phage B3	GCA_009745215.1
QGT54471.1	001261	Cluster738_1clades	177	b3_0228	Synechococcus phage B3	GCA_009745215.1
QGT54472.1	001261	Cluster738_1clades	176	b3_0229	Synechococcus phage B3	GCA_009745215.1
QGT54487.1	001261	Cluster738_1clades	209	b3_0245	Synechococcus phage B3	GCA_009745215.1
QGT54488.1	001261	Cluster738_1clades	177	b3_0246	Synechococcus phage B3	GCA_009745215.1
AMR59836.1	001262	Cluster739_1clades	208	SEGD1_189	Enterobacteria phage SEGD1	GCA_002601865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ49834.1	001262	Cluster739_1clades	207	MACHINA_196	Erwinia phage Machina	GCA_002758035.1
AXF51333.1	001262	Cluster739_1clades	182	WELLINGTON_205	Erwinia phage Wellington	GCA_003344985.1
AFQ96654.1	001262	Cluster739_1clades	202	G173_gp109	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48219.1	001262	Cluster739_1clades	202	ASESINO_206	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48490.1	001262	Cluster739_1clades	199	CAITLIN_195	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48769.1	001262	Cluster739_1clades	199	CHRISDB_207	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49278.1	001262	Cluster739_1clades	207	HUXLEY_196	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49558.1	001262	Cluster739_1clades	182	KWAN_206	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50106.1	001262	Cluster739_1clades	207	PARSHIK_197	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50631.1	001262	Cluster739_1clades	202	STRATTON_206	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86026.1	001262	Cluster739_1clades	208	ACEC001_1850	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20881.1	001262	Cluster739_1clades	208	-	Salmonella phage JN03	GCA_014319805.1
AWN09153.1	001262	Cluster739_1clades	208	MLDJOKPK_00255	Salmonella phage SPAsTU	GCA_003183805.1
AEP84018.1	001262	Cluster739_1clades	208	SPN3US_0185	Salmonella phage SPN3US	GCA_001042275.1
AMR59849.1	001263	Cluster741_1clades	197	SEGD1_202	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49847.1	001263	Cluster741_1clades	170	MACHINA_209	Erwinia phage Machina	GCA_002758035.1
AXF51349.1	001263	Cluster741_1clades	171	WELLINGTON_223	Erwinia phage Wellington	GCA_003344985.1
AFQ96666.1	001263	Cluster741_1clades	192	G173_gp121	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48232.1	001263	Cluster741_1clades	192	ASESINO_219	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48504.1	001263	Cluster741_1clades	173	CAITLIN_209	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48782.1	001263	Cluster741_1clades	173	CHRISDB_220	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49291.1	001263	Cluster741_1clades	170	HUXLEY_209	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49576.1	001263	Cluster741_1clades	173	KWAN_224	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50119.1	001263	Cluster741_1clades	170	PARSHIK_210	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50646.1	001263	Cluster741_1clades	192	STRATTON_221	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86040.1	001263	Cluster741_1clades	197	ACEC001_1970	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20888.1	001263	Cluster741_1clades	100	-	Salmonella phage JN03	GCA_014319805.1
AXF51120.1	001263	Cluster741_1clades	197	MLDJOKPK_00241	Salmonella phage SPAsTU	GCA_003183805.1
AEP84032.1	001263	Cluster741_1clades	197	SPN3US_0199	Salmonella phage SPN3US	GCA_001042275.1
AMR59917.1	001264	Cluster742_1clades	169	SEGD1_270	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49914.1	001264	Cluster742_1clades	173	MACHINA_276	Erwinia phage Machina	GCA_002758035.1
AXF51415.1	001264	Cluster742_1clades	167	WELLINGTON_289	Erwinia phage Wellington	GCA_003344985.1
AFQ96726.1	001264	Cluster742_1clades	136	G173_gp181	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48298.1	001264	Cluster742_1clades	188	ASESINO_285	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48569.1	001264	Cluster742_1clades	170	CAITLIN_274	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48847.1	001264	Cluster742_1clades	169	CHRISDB_285	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49357.1	001264	Cluster742_1clades	173	HUXLEY_275	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49640.1	001264	Cluster742_1clades	167	KWAN_288	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50185.1	001264	Cluster742_1clades	173	PARSHIK_276	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50709.1	001264	Cluster742_1clades	188	STRATTON_284	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86105.1	001264	Cluster742_1clades	169	ACEC001_2620	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20946.1	001264	Cluster742_1clades	184	-	Salmonella phage JN03	GCA_014319805.1
AWN09090.1	001264	Cluster742_1clades	169	MLDJOKPK_00176	Salmonella phage SPAsTU	GCA_003183805.1
AEP84097.1	001264	Cluster742_1clades	169	SPN3US_0264	Salmonella phage SPN3US	GCA_001042275.1
QDH83414.1	001265	Cluster743_1clades	173	H1O15_gp005	Achromobacter phage Motura	GCA_006964305.1
QBX06717.1	001265	Cluster743_1clades	180	BcepSaruman_304	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74685.1	001265	Cluster743_1clades	180	BcepSauron_305	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67212.1	001265	Cluster743_1clades	181	AD1_168	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79962.1	001265	Cluster743_1clades	187	JA11_157	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66560.1	001265	Cluster743_1clades	187	JA13_157	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66885.1	001265	Cluster743_1clades	186	JA29_159	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67531.1	001265	Cluster743_1clades	187	JA33_157	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08443.1	001265	Cluster743_1clades	182	Alexandra_173	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58809.1	001265	Cluster743_1clades	181	Y3_169	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28644.1	001265	Cluster743_1clades	182	YOLOSWAG_164	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38470.1	001265	Cluster743_1clades	179	BN7874_265	Phage NCTB	GCA_900092385.1
AFH14623.1	001265	Cluster743_1clades	178	Lu11_0091	Pseudomonas phage Lu11	GCA_000897175.1
AGS82084.1	001265	Cluster743_1clades	176	PaBG_00209	Pseudomonas phage PaBG	GCA_000912555.1
BAG41601.1	001265	Cluster743_1clades	186	RSL1_ORF155	Ralstonia phage phiRSL1	GCA_000879455.1
AFO71332.1	001266	Cluster745_1clades	176	CR5_112	Cronobacter phage CR5	GCA_000910235.1
AMR59881.1	001266	Cluster745_1clades	178	SEGD1_234	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07541.1	001266	Cluster745_1clades	177	DERBICUS_115	Erwinia phage Derbicus	GCA_004521655.1
ANZ49881.1	001266	Cluster745_1clades	166	MACHINA_243	Erwinia phage Machina	GCA_002758035.1
ANZ48265.1	001266	Cluster745_1clades	178	ASESINO_252	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48538.1	001266	Cluster745_1clades	153	CAITLIN_243	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48815.1	001266	Cluster745_1clades	153	CHRISDB_253	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48964.1	001266	Cluster745_1clades	177	EARLPHILLIPIV_115	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49324.1	001266	Cluster745_1clades	166	HUXLEY_242	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50152.1	001266	Cluster745_1clades	166	PARSHIK_243	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50305.1	001266	Cluster745_1clades	175	PHOBOS_115	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QKN86071.1	001266	Cluster745_1clades	178	ACEC001_2280	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20917.1	001266	Cluster745_1clades	178	-	Salmonella phage JN03	GCA_014319805.1
AWN09122.1	001266	Cluster745_1clades	179	MLDJOKPK_00210	Salmonella phage SPAsTU	GCA_003183805.1
AEP84063.1	001266	Cluster745_1clades	178	SPN3US_0230	Salmonella phage SPN3US	GCA_001042275.1
AMO43116.1	001267	Cluster746_1clades	171	R1080702_107	Cyanophage S-RIM32	GCA_001754165.1
AMO43343.1	001267	Cluster746_1clades	170	W270710_099	Cyanophage S-RIM44	GCA_002599145.1
AOO11576.1	001267	Cluster746_1clades	169	ES420910_095	Cyanophage S-RIM44	GCA_002599165.1
AOO11815.1	001267	Cluster746_1clades	170	Np050604_099	Cyanophage S-RIM44	GCA_002599185.1
AOO12041.1	001267	Cluster746_1clades	169	Np200711_095	Cyanophage S-RIM44	GCA_002599205.1
AOO12277.1	001267	Cluster746_1clades	169	Np420711_095	Cyanophage S-RIM44	GCA_002599225.1
AOO12516.1	001267	Cluster746_1clades	170	Sn080709_099	Cyanophage S-RIM44	GCA_002599245.1
AOO12742.1	001267	Cluster746_1clades	169	Sn130910_095	Cyanophage S-RIM44	GCA_002599265.1
AOO12982.1	001267	Cluster746_1clades	170	W2100709_100	Cyanophage S-RIM44	GCA_002599285.1
AGH26126.1	001267	Cluster746_1clades	177	CPMG_00025	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99201.1	001267	Cluster746_1clades	170	Syn1_100	Prochlorococcus phage Syn1	GCA_000892495.1
QDH50633.1	001267	Cluster746_1clades	166	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59555.1	001267	Cluster746_1clades	166	S330809_094	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59317.1	001267	Cluster746_1clades	166	C440309_094	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59793.1	001267	Cluster746_1clades	166	N231010_094	Synechococcus phage S-CAM4	GCA_002922155.1
AJK27436.1	001268	DUF4385	153	PTIM40_9	Cyanophage P-TIM40	GCA_001470935.1
AMO43306.1	001268	DUF4385	171	W270710_062	Cyanophage S-RIM44	GCA_002599145.1
AOO11540.1	001268	DUF4385	171	ES420910_059	Cyanophage S-RIM44	GCA_002599165.1
AOO11778.1	001268	DUF4385	171	Np050604_062	Cyanophage S-RIM44	GCA_002599185.1
AOO12005.1	001268	DUF4385	171	Np200711_059	Cyanophage S-RIM44	GCA_002599205.1
AOO12241.1	001268	DUF4385	171	Np420711_059	Cyanophage S-RIM44	GCA_002599225.1
AOO12479.1	001268	DUF4385	171	Sn080709_062	Cyanophage S-RIM44	GCA_002599245.1
AOO12706.1	001268	DUF4385	171	Sn130910_059	Cyanophage S-RIM44	GCA_002599265.1
AOO12944.1	001268	DUF4385	171	W2100709_062	Cyanophage S-RIM44	GCA_002599285.1
AGH07482.1	001268	DUF4385	154	CYVG_00038	Cyanophage S-SSM6a	GCA_002710385.1
AGH26207.1	001268	DUF4385	161	CPMG_00106	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93470.1	001268	DUF4385	154	AVU42_gp132	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99160.1	001268	DUF4385	171	Syn1_059	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76108.1	001268	DUF4385	153	PBI_BELLAMY_63	Synechococcus phage Bellamy	GCA_002627525.1
QJT70143.1	001268	DUF4385	154	SynMITS9220M01_130	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUE22661.1	001269	Cluster749_1clades	108	Ah1_00120	Aeromonas phage Ah1	GCA_002957415.1
QAX98387.1	001269	Cluster749_1clades	108	ASfcp2_42	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52841.1	001269	Cluster749_1clades	108	PX29p122	Aeromonas phage PX29	GCA_000920195.1
ADM80101.1	001269	Cluster749_1clades	156	phiAS5_ORF0258	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17788.1	001269	Cluster749_1clades	108	Aeh1ORF125c	Aeromonas virus Aeh1	GCA_000843245.1
AIT14065.1	001269	Cluster749_1clades	83	PBI_121Q_175	Escherichia phage 121Q	GCA_000926855.1
QAY00857.1	001269	Cluster749_1clades	83	Ecwhy1_586	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35028.1	001269	Cluster749_1clades	81	ACQ29_gp348	Escherichia phage PBECO4	GCA_001041035.1
BBM61748.1	001269	Cluster749_1clades	81	EO157G_1590	Escherichia phage SP27	GCA_008033345.1
AXC36605.1	001269	Cluster749_1clades	81	-	Escherichia phage UB	GCA_003341455.1
QBO61634.1	001269	Cluster749_1clades	83	G17_00138	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80060.1	001269	Cluster749_1clades	81	PSLUR01_00083	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AQW88609.1	001269	Cluster749_1clades	80	BF_0084	Serratia phage BF	GCA_002619745.1
SOK58886.1	001269	Cluster749_1clades	79	g078	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58349.1	001269	Cluster749_1clades	79	g072	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMR59877.1	001270	Cluster750_1clades	140	SEGD1_230	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49878.1	001270	Cluster750_1clades	142	MACHINA_240	Erwinia phage Machina	GCA_002758035.1
AXF51381.1	001270	Cluster750_1clades	133	WELLINGTON_255	Erwinia phage Wellington	GCA_003344985.1
AFQ96693.1	001270	Cluster750_1clades	142	G173_gp148	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48262.1	001270	Cluster750_1clades	141	ASESINO_249	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48535.1	001270	Cluster750_1clades	152	CAITLIN_240	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48811.1	001270	Cluster750_1clades	149	CHRISDB_249	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49321.1	001270	Cluster750_1clades	142	HUXLEY_239	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49608.1	001270	Cluster750_1clades	133	KWAN_256	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50149.1	001270	Cluster750_1clades	142	PARSHIK_240	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50675.1	001270	Cluster750_1clades	141	STRATTON_250	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86068.1	001270	Cluster750_1clades	139	ACEC001_2250	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20914.1	001270	Cluster750_1clades	139	-	Salmonella phage JN03	GCA_014319805.1
AWN09124.1	001270	Cluster750_1clades	141	MLDJOKPK_00213	Salmonella phage SPAsTU	GCA_003183805.1
AEP84060.1	001270	Cluster750_1clades	140	SPN3US_0227	Salmonella phage SPN3US	GCA_001042275.1
AMR59665.1	001271	Cluster751_1clades	143	SEGD1_014	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49668.1	001271	Cluster751_1clades	144	MACHINA_30	Erwinia phage Machina	GCA_002758035.1
AXF51156.1	001271	Cluster751_1clades	145	WELLINGTON_25	Erwinia phage Wellington	GCA_003344985.1
AFQ96742.1	001271	Cluster751_1clades	143	G173_gp197	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48045.1	001271	Cluster751_1clades	143	ASESINO_32	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48319.1	001271	Cluster751_1clades	145	CAITLIN_24	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48592.1	001271	Cluster751_1clades	145	CHRISDB_30	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49113.1	001271	Cluster751_1clades	144	HUXLEY_31	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49377.1	001271	Cluster751_1clades	145	KWAN_25	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49941.1	001271	Cluster751_1clades	144	PARSHIK_32	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50455.1	001271	Cluster751_1clades	143	STRATTON_30	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85853.1	001271	Cluster751_1clades	143	ACEC001_0160	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20733.1	001271	Cluster751_1clades	143	-	Salmonella phage JN03	GCA_014319805.1
AWN09079.1	001271	Cluster751_1clades	143	MLDJOKPK_00152	Salmonella phage SPAsTU	GCA_003183805.1
AEP83848.1	001271	Cluster751_1clades	143	SPN3US_0015	Salmonella phage SPN3US	GCA_001042275.1
AMR59831.1	001272	Cluster752_1clades	133	SEGD1_184	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49830.1	001272	Cluster752_1clades	127	MACHINA_192	Erwinia phage Machina	GCA_002758035.1
AXF51327.1	001272	Cluster752_1clades	126	WELLINGTON_199	Erwinia phage Wellington	GCA_003344985.1
AFQ96649.1	001272	Cluster752_1clades	144	G173_gp104	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48214.1	001272	Cluster752_1clades	144	ASESINO_201	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48486.1	001272	Cluster752_1clades	125	CAITLIN_191	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48765.1	001272	Cluster752_1clades	125	CHRISDB_203	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49274.1	001272	Cluster752_1clades	127	HUXLEY_192	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49552.1	001272	Cluster752_1clades	126	KWAN_200	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50102.1	001272	Cluster752_1clades	127	PARSHIK_193	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50626.1	001272	Cluster752_1clades	144	STRATTON_201	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86021.1	001272	Cluster752_1clades	133	ACEC001_1800	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20876.1	001272	Cluster752_1clades	133	-	Salmonella phage JN03	GCA_014319805.1
AWN09157.1	001272	Cluster752_1clades	136	MLDJOKPK_00260	Salmonella phage SPAsTU	GCA_003183805.1
AEP84013.1	001272	Cluster752_1clades	133	SPN3US_0180	Salmonella phage SPN3US	GCA_001042275.1
AMR59662.1	001273	Cluster753_1clades	133	SEGD1_011	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49665.1	001273	Cluster753_1clades	129	MACHINA_27	Erwinia phage Machina	GCA_002758035.1
AXF51153.1	001273	Cluster753_1clades	143	WELLINGTON_22	Erwinia phage Wellington	GCA_003344985.1
AFQ96739.1	001273	Cluster753_1clades	89	G173_gp194	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48042.1	001273	Cluster753_1clades	131	ASESINO_29	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48316.1	001273	Cluster753_1clades	129	CAITLIN_21	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48589.1	001273	Cluster753_1clades	129	CHRISDB_27	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49110.1	001273	Cluster753_1clades	129	HUXLEY_28	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49374.1	001273	Cluster753_1clades	143	KWAN_22	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49938.1	001273	Cluster753_1clades	129	PARSHIK_29	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50452.1	001273	Cluster753_1clades	132	STRATTON_27	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85850.1	001273	Cluster753_1clades	135	ACEC001_0130	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20730.1	001273	Cluster753_1clades	135	-	Salmonella phage JN03	GCA_014319805.1
AWN09082.1	001273	Cluster753_1clades	133	MLDJOKPK_00155	Salmonella phage SPAsTU	GCA_003183805.1
AEP83845.1	001273	Cluster753_1clades	132	SPN3US_0012	Salmonella phage SPN3US	GCA_001042275.1
ARB13748.1	001274	Cluster754_1clades	128	Ccr10_gp218c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14093.1	001274	Cluster754_1clades	128	Ccr2_gp217c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14782.1	001274	Cluster754_1clades	128	Ccr29_gp226	Caulobacter phage Ccr29	GCA_002619485.1
ARB15126.1	001274	Cluster754_1clades	128	Ccr32_gp208	Caulobacter phage Ccr32	GCA_002619505.1
ARB15460.1	001274	Cluster754_1clades	128	Ccr34_gp218	Caulobacter phage Ccr34	GCA_002619525.1
ARB14435.1	001274	Cluster754_1clades	128	Ccr5_gp215c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68415.1	001274	Cluster754_1clades	128	CcrBL10_gp211c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88145.1	001274	Cluster754_1clades	135	CcrColossus_gp275	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68821.1	001274	Cluster754_1clades	135	CcrPW_gp282	Caulobacter phage CcrPW	GCA_003443275.1
AFU87742.1	001274	Cluster754_1clades	128	CcrKarma_gp225	Caulobacter virus Karma	GCA_000901575.1
AFU87390.1	001274	Cluster754_1clades	128	CcrMagneto_gp220	Caulobacter virus Magneto	GCA_000903095.1
AFU86701.1	001274	Cluster754_1clades	128	CcrRogue_gp219	Caulobacter virus Rogue	GCA_000900555.1
AFU88538.1	001274	Cluster754_1clades	128	CcrSwift_gp220	Caulobacter virus Swift	GCA_000899655.1
AFU87045.1	001274	Cluster754_1clades	128	CbK_gp213	Caulobacter virus phiCbK	GCA_000900535.1
ASV44385.1	001274	Cluster754_1clades	125	PBI_SCTP2_370	Salicola phage SCTP-2	GCA_002625545.1
AMR59834.1	001275	Cluster755_1clades	127	SEGD1_187	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49832.1	001275	Cluster755_1clades	129	MACHINA_194	Erwinia phage Machina	GCA_002758035.1
AXF51329.1	001275	Cluster755_1clades	132	WELLINGTON_201	Erwinia phage Wellington	GCA_003344985.1
AFQ96652.1	001275	Cluster755_1clades	131	G173_gp107	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48217.1	001275	Cluster755_1clades	132	ASESINO_204	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48488.1	001275	Cluster755_1clades	126	CAITLIN_193	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48767.1	001275	Cluster755_1clades	125	CHRISDB_205	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49276.1	001275	Cluster755_1clades	129	HUXLEY_194	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49554.1	001275	Cluster755_1clades	132	KWAN_202	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50104.1	001275	Cluster755_1clades	129	PARSHIK_195	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50629.1	001275	Cluster755_1clades	131	STRATTON_204	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86024.1	001275	Cluster755_1clades	127	ACEC001_1830	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20879.1	001275	Cluster755_1clades	127	-	Salmonella phage JN03	GCA_014319805.1
AWN09155.1	001275	Cluster755_1clades	127	MLDJOKPK_00257	Salmonella phage SPAsTU	GCA_003183805.1
AEP84016.1	001275	Cluster755_1clades	127	SPN3US_0183	Salmonella phage SPN3US	GCA_001042275.1
APU01598.1	001276	Cluster756_1clades	61	-	Aeromonas phage 65.2	GCA_002618145.1
APU01603.1	001276	Cluster756_1clades	67	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29046.1	001276	Cluster756_1clades	132	AP1_0339	Aeromonas phage AP1	GCA_014183365.1
ATI17313.1	001276	Cluster756_1clades	69	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17314.1	001276	Cluster756_1clades	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00280.1	001276	Cluster756_1clades	65	HWB28_gp272	Aeromonas phage AS-zj	GCA_002627665.1
ASU00281.1	001276	Cluster756_1clades	69	HWB28_gp271	Aeromonas phage AS-zj	GCA_002627665.1
QAX97756.1	001276	Cluster756_1clades	69	ASswx1_111	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97757.1	001276	Cluster756_1clades	79	ASswx1_112	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01398.1	001276	Cluster756_1clades	65	ASwh1_339	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01399.1	001276	Cluster756_1clades	71	ASwh1_340	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39297.1	001276	Cluster756_1clades	79	CC2_425	Aeromonas phage CC2	GCA_000903495.1
AFN39298.1	001276	Cluster756_1clades	69	CC2_426	Aeromonas phage CC2	GCA_000903495.1
ADQ53222.1	001276	Cluster756_1clades	61	65p214	Aeromonas virus 65	GCA_000893255.1
ADQ53227.1	001276	Cluster756_1clades	71	65p219	Aeromonas virus 65	GCA_000893255.1
AOO14329.1	001277	Cluster757_1clades	99	Sn110110_135	Cyanophage S-RIM14	GCA_002599065.1
AOO14978.1	001277	Cluster757_1clades	99	W1230910_132	Cyanophage S-RIM14	GCA_002599125.1
AMO43265.1	001277	Cluster757_1clades	97	W270710_020	Cyanophage S-RIM44	GCA_002599145.1
AOO11502.1	001277	Cluster757_1clades	99	ES420910_020	Cyanophage S-RIM44	GCA_002599165.1
AOO11737.1	001277	Cluster757_1clades	97	Np050604_020	Cyanophage S-RIM44	GCA_002599185.1
AOO11967.1	001277	Cluster757_1clades	99	Np200711_020	Cyanophage S-RIM44	GCA_002599205.1
AOO12203.1	001277	Cluster757_1clades	99	Np420711_020	Cyanophage S-RIM44	GCA_002599225.1
AOO12438.1	001277	Cluster757_1clades	97	Sn080709_020	Cyanophage S-RIM44	GCA_002599245.1
AOO12668.1	001277	Cluster757_1clades	99	Sn130910_020	Cyanophage S-RIM44	GCA_002599265.1
AOO12903.1	001277	Cluster757_1clades	97	W2100709_020	Cyanophage S-RIM44	GCA_002599285.1
ADO99122.1	001277	Cluster757_1clades	131	Syn1_020	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30732.1	001277	Cluster757_1clades	93	Syn7803US37_255	Synechococcus phage ACG-2014f	GCA_002594065.1
AOV59479.1	001277	Cluster757_1clades	99	S330809_018	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59241.1	001277	Cluster757_1clades	99	C440309_018	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59717.1	001277	Cluster757_1clades	99	N231010_018	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67068.1	001278	Cluster758_1clades	60	AD1_024	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79819.1	001278	Cluster758_1clades	88	JA11_014	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66417.1	001278	Cluster758_1clades	88	JA13_014	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66740.1	001278	Cluster758_1clades	88	JA29_014	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67388.1	001278	Cluster758_1clades	88	JA33_014	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBP07156.1	001278	Cluster758_1clades	92	REBECCA_48	Erwinia phage Rebecca	GCA_004521635.1
AWY08304.1	001278	Cluster758_1clades	87	Alexandra_24	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AUG85836.1	001278	Cluster758_1clades	92	BOSOLAPHORUS_48	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52147.1	001278	Cluster758_1clades	121	DM_49	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86476.1	001278	Cluster758_1clades	92	MADMEL_48	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86797.1	001278	Cluster758_1clades	92	MORTIMER_48	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASB43074.1	001278	Cluster758_1clades	122	SIMMY50_49	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64858.1	001278	Cluster758_1clades	121	SPECIALG_48	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARW58664.1	001278	Cluster758_1clades	83	Y3_024	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QKE54418.1	001278	Cluster758_1clades	109	ACSA002_1040	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AFC21731.1	001279	PseuCD	116	GAP32_281	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13912.1	001279	PseuCD	109	PBI_121Q_15	Escherichia phage 121Q	GCA_000926855.1
QAY00426.1	001279	PseuCD	109	Ecwhy1_145	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35169.1	001279	PseuCD	109	ACQ29_gp489	Escherichia phage PBECO4	GCA_001041035.1
BBM61604.1	001279	PseuCD	109	EO157G_0150	Escherichia phage SP27	GCA_008033345.1
QBO61780.1	001279	PseuCD	109	G17_00291	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80507.1	001279	PseuCD	109	PSLUR01_00530	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44396.1	001279	PseuCD	121	RaK2_00123	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43850.1	001279	PseuCD	115	CBB_286	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19009.1	001279	PseuCD	118	7t3_0489	Salmonella phage 7t3	GCA_006083215.1
AZU98256.1	001279	PseuCD	118	CPT_Munch_312	Salmonella phage Munch	GCA_004015485.1
QIG62728.1	001279	PseuCD	118	SEPL_115	Salmonella phage SE_PL	GCA_011067555.1
AQW88809.1	001279	PseuCD	116	BF_0284	Serratia phage BF	GCA_002619745.1
SOK59092.1	001279	PseuCD	116	g284	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58556.1	001279	PseuCD	116	g279	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70479.1	001280	Cluster760_1clades	111	CF8_0068	Aeromonas phage CF8	GCA_006384595.2
QDJ97219.1	001280	Cluster760_1clades	113	D6_0059	Aeromonas phage D6	GCA_007051205.2
QDJ96827.1	001280	Cluster760_1clades	112	PS1_0068	Aeromonas phage PS1	GCA_007051165.2
QFR59457.1	001280	Cluster760_1clades	112	PS2_0066	Aeromonas phage PS2	GCA_009388305.2
QBZ70597.1	001280	Cluster760_1clades	113	pETSU_016	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03873.1	001280	Cluster760_1clades	108	JOAD_42	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03628.1	001280	Cluster760_1clades	108	RISINGSUN_42	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71913.1	001280	Cluster760_1clades	111	N1M2_50	Klebsiella phage N1M2	GCA_010092605.1
QGZ14382.1	001280	Cluster760_1clades	106	HWC77_gp019	Photobacterium phage PDCC-1	GCA_009800445.1
AEV89509.1	001280	Cluster760_1clades	111	OBP_072	Pseudomonas phage OBP	GCA_000896635.1
QAU04354.1	001280	Cluster760_1clades	106	HWC03_gp199	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23222.1	001280	Cluster760_1clades	106	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81090.1	001280	Cluster760_1clades	106	Aphrodite1_0123	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47506.1	001280	Cluster760_1clades	106	HWC35_gp112	Vibrio phage USC-1	GCA_006864065.1
BAW98325.1	001280	Cluster760_1clades	100	FDH33_gp116	Vibrio phage pTD1	GCA_002618825.1
AMR59761.1	001281	Cluster761_1clades	105	SEGD1_114	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49760.1	001281	Cluster761_1clades	111	MACHINA_122	Erwinia phage Machina	GCA_002758035.1
AXF51268.1	001281	Cluster761_1clades	108	WELLINGTON_138	Erwinia phage Wellington	GCA_003344985.1
AFQ96578.1	001281	Cluster761_1clades	111	G173_gp033	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48139.1	001281	Cluster761_1clades	111	ASESINO_126	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48417.1	001281	Cluster761_1clades	111	CAITLIN_122	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48689.1	001281	Cluster761_1clades	111	CHRISDB_127	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49204.1	001281	Cluster761_1clades	111	HUXLEY_122	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49489.1	001281	Cluster761_1clades	108	KWAN_137	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50032.1	001281	Cluster761_1clades	111	PARSHIK_123	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50553.1	001281	Cluster761_1clades	111	STRATTON_128	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85951.1	001281	Cluster761_1clades	105	ACEC001_1130	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20818.1	001281	Cluster761_1clades	105	-	Salmonella phage JN03	GCA_014319805.1
AWN08999.1	001281	Cluster761_1clades	112	MLDJOKPK_00047	Salmonella phage SPAsTU	GCA_003183805.1
AEP83943.1	001281	Cluster761_1clades	105	SPN3US_0110	Salmonella phage SPN3US	GCA_001042275.1
AMO43144.1	001282	Cluster762_1clades	59	R1080702_135	Cyanophage S-RIM32	GCA_001754165.1
AMO43369.1	001282	Cluster762_1clades	73	W270710_125	Cyanophage S-RIM44	GCA_002599145.1
AOO11613.1	001282	Cluster762_1clades	73	ES420910_132	Cyanophage S-RIM44	GCA_002599165.1
AOO11841.1	001282	Cluster762_1clades	73	Np050604_125	Cyanophage S-RIM44	GCA_002599185.1
AOO12078.1	001282	Cluster762_1clades	73	Np200711_132	Cyanophage S-RIM44	GCA_002599205.1
AOO12314.1	001282	Cluster762_1clades	73	Np420711_132	Cyanophage S-RIM44	GCA_002599225.1
AOO12542.1	001282	Cluster762_1clades	71	Sn080709_125	Cyanophage S-RIM44	GCA_002599245.1
AOO12779.1	001282	Cluster762_1clades	71	Sn130910_132	Cyanophage S-RIM44	GCA_002599265.1
AOO13008.1	001282	Cluster762_1clades	71	W2100709_126	Cyanophage S-RIM44	GCA_002599285.1
AIR93577.1	001282	Cluster762_1clades	110	AVU42_gp241	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99227.1	001282	Cluster762_1clades	73	Syn1_126	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76274.1	001282	Cluster762_1clades	73	PBI_BELLAMY_238	Synechococcus phage Bellamy	GCA_002627525.1
QCW23060.1	001282	Cluster762_1clades	68	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50691.1	001282	Cluster762_1clades	80	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70224.1	001282	Cluster762_1clades	70	SynMITS9220M01_218	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14371.1	001283	Cluster763_1clades	62	PBI_121Q_481	Escherichia phage 121Q	GCA_000926855.1
QAY00577.1	001283	Cluster763_1clades	65	Ecwhy1_298	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34770.1	001283	Cluster763_1clades	62	ACQ29_gp090	Escherichia phage PBECO4	GCA_001041035.1
BBM62042.1	001283	Cluster763_1clades	62	EO157G_4530	Escherichia phage SP27	GCA_008033345.1
AXC36885.1	001283	Cluster763_1clades	62	-	Escherichia phage UB	GCA_003341455.1
QBO61933.1	001283	Cluster763_1clades	62	G17_00444	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13964.1	001283	Cluster763_1clades	62	vBEcoMphAPEC6_gp340c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80358.1	001283	Cluster763_1clades	62	PSLUR01_00381	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44780.1	001283	Cluster763_1clades	98	RaK2_00507	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18829.1	001283	Cluster763_1clades	82	7t3_0308	Salmonella phage 7t3	GCA_006083215.1
AZU98093.1	001283	Cluster763_1clades	82	CPT_Munch_149	Salmonella phage Munch	GCA_004015485.1
QIG62889.1	001283	Cluster763_1clades	82	SEPL_276	Salmonella phage SE_PL	GCA_011067555.1
AQW88642.1	001283	Cluster763_1clades	84	BF_0117	Serratia phage BF	GCA_002619745.1
SOK58922.1	001283	Cluster763_1clades	85	g114	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58387.1	001283	Cluster763_1clades	85	g110	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71333.1	001284	Cluster764_1clades	78	CR5_113	Cronobacter phage CR5	GCA_000910235.1
AMR59885.1	001284	Cluster764_1clades	62	SEGD1_238	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07542.1	001284	Cluster764_1clades	86	DERBICUS_116	Erwinia phage Derbicus	GCA_004521655.1
ANZ49884.1	001284	Cluster764_1clades	54	MACHINA_246	Erwinia phage Machina	GCA_002758035.1
AFQ96698.1	001284	Cluster764_1clades	51	G173_gp153	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48268.1	001284	Cluster764_1clades	51	ASESINO_255	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48541.1	001284	Cluster764_1clades	51	CAITLIN_246	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48965.1	001284	Cluster764_1clades	86	EARLPHILLIPIV_116	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49327.1	001284	Cluster764_1clades	54	HUXLEY_245	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50155.1	001284	Cluster764_1clades	56	PARSHIK_246	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50306.1	001284	Cluster764_1clades	97	PHOBOS_116	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50680.1	001284	Cluster764_1clades	51	STRATTON_255	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86075.1	001284	Cluster764_1clades	62	ACEC001_2320	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09118.1	001284	Cluster764_1clades	67	MLDJOKPK_00206	Salmonella phage SPAsTU	GCA_003183805.1
AEP84067.1	001284	Cluster764_1clades	62	SPN3US_0234	Salmonella phage SPN3US	GCA_001042275.1
APU01394.1	001285	Cluster765_1clades	87	-	Aeromonas phage 65.2	GCA_002618145.1
APU01393.1	001285	Cluster765_1clades	90	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28875.1	001285	Cluster765_1clades	90	AP1_0168	Aeromonas phage AP1	GCA_014183365.1
QMV28876.1	001285	Cluster765_1clades	95	AP1_0169	Aeromonas phage AP1	GCA_014183365.1
ATI17501.1	001285	Cluster765_1clades	90	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17502.1	001285	Cluster765_1clades	95	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00496.1	001285	Cluster765_1clades	90	HWB28_gp056	Aeromonas phage AS-zj	GCA_002627665.1
ASU00495.1	001285	Cluster765_1clades	95	HWB28_gp057	Aeromonas phage AS-zj	GCA_002627665.1
QAX97940.1	001285	Cluster765_1clades	90	ASswx1_298	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97941.1	001285	Cluster765_1clades	95	ASswx1_299	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01206.1	001285	Cluster765_1clades	90	ASwh1_141	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39267.1	001285	Cluster765_1clades	95	CC2_232	Aeromonas phage CC2	GCA_000903495.1
AFN39265.1	001285	Cluster765_1clades	90	CC2_233	Aeromonas phage CC2	GCA_000903495.1
ADQ53051.1	001285	Cluster765_1clades	90	65p002	Aeromonas virus 65	GCA_000893255.1
ADQ53052.1	001285	Cluster765_1clades	87	65p003	Aeromonas virus 65	GCA_000893255.1
AGH56925.1	001286	Cluster766_1clades	87	CPXG_00122	Cyanophage P-RSM6	GCA_000906155.1
AJK27533.1	001286	Cluster766_1clades	81	PTIM40_105	Cyanophage P-TIM40	GCA_001470935.1
AGH07723.1	001286	Cluster766_1clades	69	CYVG_00280	Cyanophage S-SSM6a	GCA_002710385.1
AGG54293.1	001286	Cluster766_1clades	80	CYWG_00009	Cyanophage S-SSM6b	GCA_002710425.1
AGH26133.1	001286	Cluster766_1clades	72	CPMG_00032	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44494.1	001286	Cluster766_1clades	67	PSSM2_116	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12472.1	001286	Cluster766_1clades	67	PRTG_00325	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93632.1	001286	Cluster766_1clades	76	AVU42_gp090	Prochlorococcus phage P-TIM68	GCA_001503075.1
QGT54875.1	001286	Cluster766_1clades	76	b23_0261	Synechococcus phage B23	GCA_009745195.1
QGT54510.1	001286	Cluster766_1clades	76	b3_0268	Synechococcus phage B3	GCA_009745215.1
ASR76159.1	001286	Cluster766_1clades	75	PBI_BELLAMY_114	Synechococcus phage Bellamy	GCA_002627525.1
QCW22827.1	001286	Cluster766_1clades	77	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50492.1	001286	Cluster766_1clades	77	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70593.1	001286	Cluster766_1clades	68	HOU04_gp194	Synechococcus phage S-T4	GCA_003443335.1
QJT70099.1	001286	Cluster766_1clades	74	SynMITS9220M01_086	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27619.1	001287	Cluster768_1clades	70	PTIM40_206	Cyanophage P-TIM40	GCA_001470935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO14387.1	001287	Cluster768_1clades	66	Sn110110_194	Cyanophage S-RIM14	GCA_002599065.1
AOO15035.1	001287	Cluster768_1clades	66	W1230910_190	Cyanophage S-RIM14	GCA_002599125.1
AGH07558.1	001287	Cluster768_1clades	71	CYVG_00114	Cyanophage S-SSM6a	GCA_002710385.1
AGG54403.1	001287	Cluster768_1clades	66	CYWG_00119	Cyanophage S-SSM6b	GCA_002710425.1
AAX44631.1	001287	Cluster768_1clades	71	PSSM2_254	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12340.1	001287	Cluster768_1clades	71	PRTG_00187	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIX30697.1	001287	Cluster768_1clades	71	Syn7803US37_220	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54951.1	001287	Cluster768_1clades	82	b23_0345	Synechococcus phage B23	GCA_009745195.1
QGT54586.1	001287	Cluster768_1clades	82	b3_0351	Synechococcus phage B3	GCA_009745215.1
ASR76233.1	001287	Cluster768_1clades	70	PBI_BELLAMY_197	Synechococcus phage Bellamy	GCA_002627525.1
QCW23024.1	001287	Cluster768_1clades	71	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50521.1	001287	Cluster768_1clades	71	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70522.1	001287	Cluster768_1clades	71	HOU04_gp123	Synechococcus phage S-T4	GCA_003443335.1
QJT70190.1	001287	Cluster768_1clades	72	SynMITS9220M01_184	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AOO14367.1	001288	Cluster769_1clades	68	Sn110110_173	Cyanophage S-RIM14	GCA_002599065.1
AOO15015.1	001288	Cluster769_1clades	68	W1230910_169	Cyanophage S-RIM14	GCA_002599125.1
AMO43175.1	001288	Cluster769_1clades	66	R1080702_166	Cyanophage S-RIM32	GCA_001754165.1
AMO43400.1	001288	Cluster769_1clades	65	W270710_156	Cyanophage S-RIM44	GCA_002599145.1
AOO11644.1	001288	Cluster769_1clades	65	ES420910_163	Cyanophage S-RIM44	GCA_002599165.1
AOO11872.1	001288	Cluster769_1clades	65	Np050604_156	Cyanophage S-RIM44	GCA_002599185.1
AOO12110.1	001288	Cluster769_1clades	65	Np200711_164	Cyanophage S-RIM44	GCA_002599205.1
AOO12345.1	001288	Cluster769_1clades	65	Np420711_163	Cyanophage S-RIM44	GCA_002599225.1
AOO12573.1	001288	Cluster769_1clades	65	Sn080709_156	Cyanophage S-RIM44	GCA_002599245.1
AOO12810.1	001288	Cluster769_1clades	65	Sn130910_163	Cyanophage S-RIM44	GCA_002599265.1
AOO13039.1	001288	Cluster769_1clades	65	W2100709_157	Cyanophage S-RIM44	GCA_002599285.1
ADO99259.1	001288	Cluster769_1clades	65	Syn1_158	Prochlorococcus phage Syn1	GCA_000892495.1
QCW22941.1	001288	Cluster769_1clades	69	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50626.1	001288	Cluster769_1clades	69	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70483.1	001288	Cluster769_1clades	67	HOU04_gp084	Synechococcus phage S-T4	GCA_003443335.1
AMO43081.1	001289	Cluster770_1clades	49	R1080702_072	Cyanophage S-RIM32	GCA_001754165.1
AMO43309.1	001289	Cluster770_1clades	49	W270710_065	Cyanophage S-RIM44	GCA_002599145.1
AOO11543.1	001289	Cluster770_1clades	49	ES420910_062	Cyanophage S-RIM44	GCA_002599165.1
AOO11781.1	001289	Cluster770_1clades	49	Np050604_065	Cyanophage S-RIM44	GCA_002599185.1
AOO12008.1	001289	Cluster770_1clades	49	Np200711_062	Cyanophage S-RIM44	GCA_002599205.1
AOO12244.1	001289	Cluster770_1clades	49	Np420711_062	Cyanophage S-RIM44	GCA_002599225.1
AOO12482.1	001289	Cluster770_1clades	49	Sn080709_065	Cyanophage S-RIM44	GCA_002599245.1
AOO12709.1	001289	Cluster770_1clades	49	Sn130910_062	Cyanophage S-RIM44	GCA_002599265.1
AOO12947.1	001289	Cluster770_1clades	49	W2100709_065	Cyanophage S-RIM44	GCA_002599285.1
ADO99163.1	001289	Cluster770_1clades	25	Syn1_062	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59514.1	001289	Cluster770_1clades	58	S330809_053	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59276.1	001289	Cluster770_1clades	58	C440309_053	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59752.1	001289	Cluster770_1clades	58	N231010_053	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70610.1	001289	Cluster770_1clades	48	HOU04_gp009	Synechococcus phage S-T4	GCA_003443335.1
AXQ70408.1	001289	Cluster770_1clades	48	HOU04_gp009	Synechococcus phage S-T4	GCA_003443335.1
ARB13531.1	001290	Cluster771_1clades	38	Ccr10_gp003	Caulobacter phage Ccr10	GCA_002619445.1
ARB13856.1	001290	Cluster771_1clades	38	Ccr10_gp326	Caulobacter phage Ccr10	GCA_002619445.1
ARB13877.1	001290	Cluster771_1clades	38	Ccr2_gp343	Caulobacter phage Ccr2	GCA_002619465.1
ARB14560.1	001290	Cluster771_1clades	38	Ccr29_gp003	Caulobacter phage Ccr29	GCA_002619485.1
ARB14895.1	001290	Cluster771_1clades	38	Ccr29_gp339	Caulobacter phage Ccr29	GCA_002619485.1
ARB14922.1	001290	Cluster771_1clades	38	Ccr32_gp003	Caulobacter phage Ccr32	GCA_002619505.1
ARB15233.1	001290	Cluster771_1clades	38	Ccr32_gp315	Caulobacter phage Ccr32	GCA_002619505.1
ARB15253.1	001290	Cluster771_1clades	34	Ccr34_gp004	Caulobacter phage Ccr34	GCA_002619525.1
ARB15567.1	001290	Cluster771_1clades	38	Ccr34_gp325	Caulobacter phage Ccr34	GCA_002619525.1
AFU87520.1	001290	Cluster771_1clades	34	CcrKarma_gp003	Caulobacter virus Karma	GCA_000901575.1
AFU87853.1	001290	Cluster771_1clades	34	CcrKarma_gp336	Caulobacter virus Karma	GCA_000901575.1
AFU87173.1	001290	Cluster771_1clades	34	CcrMagneto_gp003	Caulobacter virus Magneto	GCA_000903095.1
AFU87501.1	001290	Cluster771_1clades	34	CcrMagneto_gp331	Caulobacter virus Magneto	GCA_000903095.1
AFU86835.1	001290	Cluster771_1clades	34	CbK_gp003	Caulobacter virus phiCbK	GCA_000900535.1
AFU87153.1	001290	Cluster771_1clades	34	CbK_gp321	Caulobacter virus phiCbK	GCA_000900535.1
AMO43117.1	001291	Cluster772_1clades	3496	R1080702_108	Cyanophage S-RIM32	GCA_001754165.1
AMO43344.1	001291	Cluster772_1clades	3380	W270710_100	Cyanophage S-RIM44	GCA_002599145.1
AOO11577.1	001291	Cluster772_1clades	3496	ES420910_096	Cyanophage S-RIM44	GCA_002599165.1
AOO11816.1	001291	Cluster772_1clades	3380	Np050604_100	Cyanophage S-RIM44	GCA_002599185.1
AOO12042.1	001291	Cluster772_1clades	3496	Np200711_096	Cyanophage S-RIM44	GCA_002599205.1
AOO12278.1	001291	Cluster772_1clades	3496	Np420711_096	Cyanophage S-RIM44	GCA_002599225.1
AOO12517.1	001291	Cluster772_1clades	3380	Sn080709_100	Cyanophage S-RIM44	GCA_002599245.1
AOO12743.1	001291	Cluster772_1clades	3496	Sn130910_096	Cyanophage S-RIM44	GCA_002599265.1
AOO12983.1	001291	Cluster772_1clades	3380	W2100709_101	Cyanophage S-RIM44	GCA_002599285.1
AGH26125.1	001291	Cluster772_1clades	3763	CPMG_00024	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99202.1	001291	Cluster772_1clades	3380	Syn1_101	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59556.1	001291	Cluster772_1clades	3031	S330809_095	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59318.1	001291	Cluster772_1clades	3031	C440309_095	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59794.1	001291	Cluster772_1clades	3031	N231010_095	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43113.1	001292	DUF4815+DUF4815	2760	R1080702_104	Cyanophage S-RIM32	GCA_001754165.1
AMO43340.1	001292	DUF4815+DUF4815	2757	W270710_096	Cyanophage S-RIM44	GCA_002599145.1
AOO11573.1	001292	DUF4815+DUF4815	2757	ES420910_092	Cyanophage S-RIM44	GCA_002599165.1
AOO11812.1	001292	DUF4815+DUF4815	2757	Np050604_096	Cyanophage S-RIM44	GCA_002599185.1
AOO12038.1	001292	DUF4815+DUF4815	2757	Np200711_092	Cyanophage S-RIM44	GCA_002599205.1
AOO12274.1	001292	DUF4815+DUF4815	2757	Np420711_092	Cyanophage S-RIM44	GCA_002599225.1
AOO12513.1	001292	DUF4815+DUF4815	2757	Sn080709_096	Cyanophage S-RIM44	GCA_002599245.1
AOO12739.1	001292	DUF4815+DUF4815	2757	Sn130910_092	Cyanophage S-RIM44	GCA_002599265.1
AOO12979.1	001292	DUF4815+DUF4815	2757	W2100709_097	Cyanophage S-RIM44	GCA_002599285.1
ADO99198.1	001292	DUF4815+DUF4815	2757	Syn1_097	Prochlorococcus phage Syn1	GCA_000892495.1
QDH50587.1	001292	DUF4815+DUF4815	1928	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59552.1	001292	DUF4815+DUF4815	2704	S330809_091	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59314.1	001292	DUF4815+DUF4815	2704	C440309_091	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59790.1	001292	DUF4815+DUF4815	2704	N231010_091	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43115.1	001293	Cluster774_1clades	1626	R1080702_106	Cyanophage S-RIM32	GCA_001754165.1
AMO43342.1	001293	Cluster774_1clades	1618	W270710_098	Cyanophage S-RIM44	GCA_002599145.1
AOO11575.1	001293	Cluster774_1clades	1278	ES420910_094	Cyanophage S-RIM44	GCA_002599165.1
AOO11814.1	001293	Cluster774_1clades	1618	Np050604_098	Cyanophage S-RIM44	GCA_002599185.1
AOO12040.1	001293	Cluster774_1clades	1278	Np200711_094	Cyanophage S-RIM44	GCA_002599205.1
AOO12276.1	001293	Cluster774_1clades	1278	Np420711_094	Cyanophage S-RIM44	GCA_002599225.1
AOO12515.1	001293	Cluster774_1clades	1618	Sn080709_098	Cyanophage S-RIM44	GCA_002599245.1
AOO12741.1	001293	Cluster774_1clades	1278	Sn130910_094	Cyanophage S-RIM44	GCA_002599265.1
AOO12981.1	001293	Cluster774_1clades	1618	W2100709_099	Cyanophage S-RIM44	GCA_002599285.1
ADO99200.1	001293	Cluster774_1clades	1618	Syn1_099	Prochlorococcus phage Syn1	GCA_000892495.1
QDH50632.1	001293	Cluster774_1clades	1092	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59554.1	001293	Cluster774_1clades	1701	S330809_093	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59316.1	001293	Cluster774_1clades	1701	C440309_093	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59792.1	001293	Cluster774_1clades	1701	N231010_093	Synechococcus phage S-CAM4	GCA_002922155.1
AMR59775.1	001294	Cluster775_1clades	945	SEGD1_128	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ48154.1	001294	Cluster775_1clades	1000	ASESINO_141	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AIT14399.1	001294	Cluster775_1clades	929	PBI_121Q_509	Escherichia phage 121Q	GCA_000926855.1
AGC34743.1	001294	Cluster775_1clades	929	ACQ29_gp063	Escherichia phage PBECO4	GCA_001041035.1
BBM62070.1	001294	Cluster775_1clades	929	EO157G_4810	Escherichia phage SP27	GCA_008033345.1
AXC36858.1	001294	Cluster775_1clades	929	-	Escherichia phage UB	GCA_003341455.1
QKN85964.1	001294	Cluster775_1clades	1005	ACEC001_1260	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61903.1	001294	Cluster775_1clades	929	G17_00414	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO63885.1	001294	Cluster775_1clades	1198	Goslar_00092	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13939.1	001294	Cluster775_1clades	929	vBEcoMphAPEC6_gp314c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QNI20828.1	001294	Cluster775_1clades	1005	-	Salmonella phage JN03	GCA_014319805.1
AWN08990.2	001294	Cluster775_1clades	1002	MLDJOKPK_00029	Salmonella phage SPAsTU	GCA_003183805.1
AEP83957.1	001294	Cluster775_1clades	1005	SPN3US_0124	Salmonella phage SPN3US	GCA_001042275.1
QFP93042.1	001294	Cluster775_1clades	1332	-	Serratia phage PCH45	GCA_009187865.1
AHI60448.1	001295	Cluster776_1clades	462	Ea357_294	Erwinia phage Ea35-70	GCA_000914635.1
QBP07405.1	001295	Cluster776_1clades	451	REBECCA_300	Erwinia phage Rebecca	GCA_004521635.1
AUG86087.1	001295	Cluster776_1clades	451	BOSOLAPHORUS_301	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52403.1	001295	Cluster776_1clades	451	DM_304	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86407.1	001295	Cluster776_1clades	451	DESERTFOX_300	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86728.1	001295	Cluster776_1clades	451	MADMEL_301	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87053.1	001295	Cluster776_1clades	451	MORTIMER_305	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52078.1	001295	Cluster776_1clades	451	RAY_298	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51761.1	001295	Cluster776_1clades	451	SIMMY50_303	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65113.1	001295	Cluster776_1clades	451	SPECIALG_302	Erwinia phage vB_EamM_Special G	GCA_002624385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QMP24053.1	001295	Cluster776_1clades	444	-	Proteus phage 10	GCA_014071245.1
QMP24201.1	001295	Cluster776_1clades	448	-	Proteus phage 10	GCA_014071245.1
QKE54512.1	001295	Cluster776_1clades	464	ACSA002_1980	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54625.1	001295	Cluster776_1clades	563	ACSA002_3080	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QDB70262.1	001296	Cluster777_1clades	515	CF8_0094	Aeromonas phage CF8	GCA_006384595.2
QDJ97240.1	001296	Cluster777_1clades	515	D6_0080	Aeromonas phage D6	GCA_007051205.2
QDH47045.1	001296	Cluster777_1clades	515	LAh10_12	Aeromonas phage LAh10	GCA_006863975.1
QDJ96853.1	001296	Cluster777_1clades	511	PS1_0094	Aeromonas phage PS1	GCA_007051165.2
QFR59485.1	001296	Cluster777_1clades	511	PS2_0094	Aeromonas phage PS2	GCA_009388305.2
QBZ70623.1	001296	Cluster777_1clades	521	pETSU_042	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71939.1	001296	Cluster777_1clades	526	N1M2_76	Klebsiella phage N1M2	GCA_010092605.1
QGZ14400.1	001296	Cluster777_1clades	487	HWC77_gp037	Photobacterium phage PDCC-1	GCA_009800445.1
AEV89539.1	001296	Cluster777_1clades	527	OBP_102	Pseudomonas phage OBP	GCA_000896635.1
QAU04336.1	001296	Cluster777_1clades	487	HWC03_gp181	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23240.1	001296	Cluster777_1clades	487	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80948.1	001296	Cluster777_1clades	487	Aphrodite1_0105	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47488.1	001296	Cluster777_1clades	478	HWC35_gp094	Vibrio phage USC-1	GCA_006864065.1
BAW98308.1	001296	Cluster777_1clades	482	FDH33_gp099	Vibrio phage pTD1	GCA_002618825.1
CCH63668.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	264	CP21_206	Campylobacter virus CP21	GCA_000902535.1
BAE47706.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	493	CST008	Clostridium phage c-st	GCA_000865225.1
BAE47719.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	493	CST021	Clostridium phage c-st	GCA_000865225.1
BAE47743.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	365	CST045	Clostridium phage c-st	GCA_000865225.1
BAE47811.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	376	CST113	Clostridium phage c-st	GCA_000865225.1
BAE47830.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	392	CST132	Clostridium phage c-st	GCA_000865225.1
BAE47844.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	389	CST146	Clostridium phage c-st	GCA_000865225.1
BAE47869.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	493	CST171	Clostridium phage c-st	GCA_000865225.1
BAE47873.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	389	CST175	Clostridium phage c-st	GCA_000865225.1
BAE47879.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	489	CST181	Clostridium phage c-st	GCA_000865225.1
CAG27131.1	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	380	PPEV_gp037	Pseudomonas phage EL	GCA_000866825.1
prev15ph1000000085	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	378	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000235	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	378	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000376	001297	HTH_OrfB_IS605+OrfB_IS605+OrfB_Zn_ribbon	377	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ARB13847.1	001298	Cluster779_1clades	373	Ccr10_gp317	Caulobacter phage Ccr10	GCA_002619445.1
ARB14192.1	001298	Cluster779_1clades	373	Ccr2_gp316	Caulobacter phage Ccr2	GCA_002619465.1
ARB14886.1	001298	Cluster779_1clades	373	Ccr29_gp330	Caulobacter phage Ccr29	GCA_002619485.1
ARB15224.1	001298	Cluster779_1clades	373	Ccr32_gp306	Caulobacter phage Ccr32	GCA_002619505.1
ARB15558.1	001298	Cluster779_1clades	373	Ccr34_gp316	Caulobacter phage Ccr34	GCA_002619525.1
ARB14532.1	001298	Cluster779_1clades	376	Ccr5_gp312	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68515.1	001298	Cluster779_1clades	376	CcrBL10_gp311	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69520.1	001298	Cluster779_1clades	382	CcrBL9_gp496	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70065.1	001298	Cluster779_1clades	390	CcrSC_gp483	Caulobacter phage CcrSC	GCA_003443315.1
AFU87843.1	001298	Cluster779_1clades	373	CcrKarma_gp326	Caulobacter virus Karma	GCA_000901575.1
AFU87491.1	001298	Cluster779_1clades	373	CcrMagneto_gp321	Caulobacter virus Magneto	GCA_000903095.1
AFU86805.1	001298	Cluster779_1clades	372	CcrRogue_gp323	Caulobacter virus Rogue	GCA_000900555.1
AFU88636.1	001298	Cluster779_1clades	373	CcrSwift_gp318	Caulobacter virus Swift	GCA_000899655.1
AFU87143.1	001298	Cluster779_1clades	373	CbK_gp311	Caulobacter virus phiCbK	GCA_000900535.1
ARB13767.1	001299	Cluster780_1clades	339	Ccr10_gp237	Caulobacter phage Ccr10	GCA_002619445.1
ARB14112.1	001299	Cluster780_1clades	339	Ccr2_gp236	Caulobacter phage Ccr2	GCA_002619465.1
ARB14806.1	001299	Cluster780_1clades	339	Ccr29_gp250	Caulobacter phage Ccr29	GCA_002619485.1
ARB15146.1	001299	Cluster780_1clades	339	Ccr32_gp228	Caulobacter phage Ccr32	GCA_002619505.1
ARB15480.1	001299	Cluster780_1clades	339	Ccr34_gp238	Caulobacter phage Ccr34	GCA_002619525.1
ARB14454.1	001299	Cluster780_1clades	339	Ccr5_gp234	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68433.1	001299	Cluster780_1clades	387	CcrBL10_gp229	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88096.1	001299	Cluster780_1clades	342	CcrColossus_gp226	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68773.1	001299	Cluster780_1clades	343	CcrPW_gp234	Caulobacter phage CcrPW	GCA_003443275.1
AFU87762.1	001299	Cluster780_1clades	339	CcrKarma_gp245	Caulobacter virus Karma	GCA_000901575.1
AFU87409.1	001299	Cluster780_1clades	339	CcrMagneto_gp239	Caulobacter virus Magneto	GCA_000903095.1
AFU86719.1	001299	Cluster780_1clades	387	CcrRogue_gp237	Caulobacter virus Rogue	GCA_000900555.1
AFU88557.1	001299	Cluster780_1clades	339	CcrSwift_gp239	Caulobacter virus Swift	GCA_000899655.1
AFU87065.1	001299	Cluster780_1clades	339	CbK_gp233	Caulobacter virus phiCbK	GCA_000900535.1
QDB70272.1	001300	Cluster781_1clades	361	CF8_0104	Aeromonas phage CF8	GCA_006384595.2
QDJ97250.1	001300	Cluster781_1clades	367	D6_0090	Aeromonas phage D6	GCA_007051205.2
QDH47072.1	001300	Cluster781_1clades	367	LAh10_22	Aeromonas phage LAh10	GCA_006863975.1
QDJ96863.1	001300	Cluster781_1clades	363	PS1_0104	Aeromonas phage PS1	GCA_007051165.2
QFR59495.1	001300	Cluster781_1clades	363	PS2_0104	Aeromonas phage PS2	GCA_009388305.2
QBZ70632.1	001300	Cluster781_1clades	345	pETSU_051	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71949.1	001300	Cluster781_1clades	353	N1M2_86	Klebsiella phage N1M2	GCA_010092605.1
QGZ14413.1	001300	Cluster781_1clades	364	HWC77_gp050	Photobacterium phage PDCC-1	GCA_009800445.1
AEV89550.1	001300	Cluster781_1clades	361	OBP_113	Pseudomonas phage OBP	GCA_000896635.1
QAU04323.1	001300	Cluster781_1clades	364	HWC03_gp168	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23255.1	001300	Cluster781_1clades	362	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80979.1	001300	Cluster781_1clades	362	Aphrodite1_0090	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47473.1	001300	Cluster781_1clades	362	HWC35_gp079	Vibrio phage USC-1	GCA_006864065.1
BAW98294.1	001300	Cluster781_1clades	361	FDH33_gp085	Vibrio phage pTD1	GCA_002618825.1
AOO14235.1	001301	NAD_binding_2+6PGD	340	Sn110110_041	Cyanophage S-RIM14	GCA_002599065.1
AOO14887.1	001301	NAD_binding_2+6PGD	340	W1230910_041	Cyanophage S-RIM14	GCA_002599125.1
AMO43431.1	001301	NAD_binding_2+6PGD	341	W270710_187	Cyanophage S-RIM44	GCA_002599145.1
AOO11675.1	001301	NAD_binding_2+6PGD	341	ES420910_194	Cyanophage S-RIM44	GCA_002599165.1
AOO11903.1	001301	NAD_binding_2+6PGD	341	Np050604_187	Cyanophage S-RIM44	GCA_002599185.1
AOO12141.1	001301	NAD_binding_2+6PGD	341	Np200711_195	Cyanophage S-RIM44	GCA_002599205.1
AOO12376.1	001301	NAD_binding_2+6PGD	341	Np420711_194	Cyanophage S-RIM44	GCA_002599225.1
AOO12604.1	001301	NAD_binding_2+6PGD	341	Sn080709_187	Cyanophage S-RIM44	GCA_002599245.1
AOO12841.1	001301	NAD_binding_2+6PGD	341	Sn130910_194	Cyanophage S-RIM44	GCA_002599265.1
AOO13070.1	001301	NAD_binding_2+6PGD	341	W2100709_188	Cyanophage S-RIM44	GCA_002599285.1
AGG54412.1	001301	NAD_binding_2+6PGD	339	CYWG_00128	Cyanophage S-SSM6b	GCA_002710425.1
ADO99290.1	001301	NAD_binding_2+6PGD	345	Syn1_189	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76282.1	001301	NAD_binding_2+6PGD	345	PBI_BELLAMY_246	Synechococcus phage Bellamy	GCA_002627525.1
QJT70183.1	001301	NAD_binding_2+6PGD	345	SynMITS9220M01_175	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13562.1	001302	Cluster783_1clades	203	Ccr10_gp034	Caulobacter phage Ccr10	GCA_002619445.1
ARB13908.1	001302	Cluster783_1clades	203	Ccr2_gp033	Caulobacter phage Ccr2	GCA_002619465.1
ARB14597.1	001302	Cluster783_1clades	203	Ccr29_gp040	Caulobacter phage Ccr29	GCA_002619485.1
ARB14952.1	001302	Cluster783_1clades	203	Ccr32_gp033	Caulobacter phage Ccr32	GCA_002619505.1
ARB15283.1	001302	Cluster783_1clades	203	Ccr34_gp034	Caulobacter phage Ccr34	GCA_002619525.1
ARB14251.1	001302	Cluster783_1clades	203	Ccr5_gp033	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68234.1	001302	Cluster783_1clades	199	CcrBL10_gp030	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69509.1	001302	Cluster783_1clades	245	CcrBL9_gp485	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70057.1	001302	Cluster783_1clades	300	CcrSC_gp475	Caulobacter phage CcrSC	GCA_003443315.1
AFU87551.1	001302	Cluster783_1clades	204	CcrKarma_gp034	Caulobacter virus Karma	GCA_000901575.1
AFU87202.1	001302	Cluster783_1clades	206	CcrMagneto_gp032	Caulobacter virus Magneto	GCA_000903095.1
AFU86516.1	001302	Cluster783_1clades	284	CcrRogue_gp034	Caulobacter virus Rogue	GCA_000900555.1
AFU88348.1	001302	Cluster783_1clades	204	CcrSwift_gp030	Caulobacter virus Swift	GCA_000899655.1
AFU86865.1	001302	Cluster783_1clades	203	CbK_gp033	Caulobacter virus phiCbK	GCA_000900535.1
ARB13652.1	001303	Cluster785_1clades	262	Ccr10_gp123c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13997.1	001303	Cluster785_1clades	262	Ccr2_gp122c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14685.1	001303	Cluster785_1clades	262	Ccr29_gp129	Caulobacter phage Ccr29	GCA_002619485.1
ARB15039.1	001303	Cluster785_1clades	262	Ccr32_gp121	Caulobacter phage Ccr32	GCA_002619505.1
ARB15372.1	001303	Cluster785_1clades	262	Ccr34_gp130	Caulobacter phage Ccr34	GCA_002619525.1
ARB14340.1	001303	Cluster785_1clades	262	Ccr5_gp122c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68320.1	001303	Cluster785_1clades	268	CcrBL10_gp116c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88030.1	001303	Cluster785_1clades	256	CcrColossus_gp160	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68707.1	001303	Cluster785_1clades	256	CcrPW_gp168c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87644.1	001303	Cluster785_1clades	262	CcrKarma_gp127	Caulobacter virus Karma	GCA_000901575.1
AFU87293.1	001303	Cluster785_1clades	262	CcrMagneto_gp123	Caulobacter virus Magneto	GCA_000903095.1
AFU86604.1	001303	Cluster785_1clades	252	CcrRogue_gp122	Caulobacter virus Rogue	GCA_000900555.1
AFU88440.1	001303	Cluster785_1clades	262	CcrSwift_gp122	Caulobacter virus Swift	GCA_000899655.1
AFU86957.1	001303	Cluster785_1clades	262	CbK_gp125	Caulobacter virus phiCbK	GCA_000900535.1
ABY62895.1	001304	DSPc	179	201phi2-1p062	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63171.1	001304	DSPc	114	201phi2-1p345	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44811.1	001304	DSPc	160	KTN4_053	Pseudomonas phage KTN4	GCA_002607225.1
ARV77413.1	001304	DSPc	152	NOXIFER_248	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32396.1	001304	DSPc	138	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76679.1	001304	DSPc	183	PHABIO_48	Pseudomonas phage Phabio	GCA_002624965.1
ARV76727.1	001304	DSPc	104	PHABIO_96	Pseudomonas phage Phabio	GCA_002624965.1
AEH03709.1	001304	DSPc	155	286	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02559.1	001304	DSPc	239	PSA21_29	Pseudomonas phage Psa21	GCA_004340405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATN94900.1	001304	DSPc	160	SL2_323	Pseudomonas phage SL2	GCA_002956015.1
QJB22690.1	001304	DSPc	160	fnug_47	Pseudomonas phage fnug	GCA_012837215.1
QCG75936.1	001304	DSPc	155	EST35_0053	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM41966.1	001304	DSPc	138	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82941.1	001304	DSPc	160	PHIKZ040	Pseudomonas virus phiKZ	GCA_000842965.1
AMO43184.1	001305	Cluster793_1clades	237	R1080702_175	Cyanophage S-RIM32	GCA_001754165.1
AMO43410.1	001305	Cluster793_1clades	237	W270710_166	Cyanophage S-RIM44	GCA_002599145.1
AOO11654.1	001305	Cluster793_1clades	237	ES420910_173	Cyanophage S-RIM44	GCA_002599165.1
AOO11882.1	001305	Cluster793_1clades	237	Np050604_166	Cyanophage S-RIM44	GCA_002599185.1
AOO12120.1	001305	Cluster793_1clades	237	Np200711_174	Cyanophage S-RIM44	GCA_002599205.1
AOO12355.1	001305	Cluster793_1clades	237	Np420711_173	Cyanophage S-RIM44	GCA_002599225.1
AOO12583.1	001305	Cluster793_1clades	237	Sn080709_166	Cyanophage S-RIM44	GCA_002599245.1
AOO12820.1	001305	Cluster793_1clades	237	Sn130910_173	Cyanophage S-RIM44	GCA_002599265.1
AOO13049.1	001305	Cluster793_1clades	237	W2100709_167	Cyanophage S-RIM44	GCA_002599285.1
AGH26272.1	001305	Cluster793_1clades	234	CPMG_00172	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99269.1	001305	Cluster793_1clades	237	Syn1_168	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59635.1	001305	Cluster793_1clades	236	S330809_174	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59397.1	001305	Cluster793_1clades	236	C440309_174	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59873.1	001305	Cluster793_1clades	236	N231010_174	Synechococcus phage S-CAM4	GCA_002922155.1
QAY01449.1	001306	Cluster794_1clades	114	ASwh1_390	Aeromonas phage Aswh_1	GCA_004146945.1
ARV77401.1	001306	Cluster794_1clades	233	NOXIFER_236	Pseudomonas phage Noxifer	GCA_002625005.1
AAQ64249.1	001306	Cluster794_1clades	116	KVP40.0180	Vibrio phage KVP40	GCA_000843785.1
QIW90565.1	001306	Cluster794_1clades	116	GCAPEGMB_00218	Vibrio phage V07	GCA_012361095.1
QIW91234.1	001306	Cluster794_1clades	115	COHAPHLL_00398	Vibrio phage V09	GCA_012361135.1
QHJ74363.1	001306	Cluster794_1clades	115	VH12019_00036	Vibrio phage VH1_2019	GCA_009931825.1
AGB06858.1	001306	Cluster794_1clades	116	CF80_gp071	Vibrio phage VH7D	GCA_000914495.1
QBX06287.1	001306	Cluster794_1clades	116	ValB1HC_334	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60916.1	001306	Cluster794_1clades	117	AVU32_gp075	Vibrio phage ValKK3	GCA_001501635.1
AGN30238.1	001306	Cluster794_1clades	116	VPFG_00239	Vibrio phage nt-1	GCA_000910195.2
ALP47170.1	001306	Cluster794_1clades	116	phiGrn1_0298	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47558.1	001306	Cluster794_1clades	116	phiST2_0054	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54914.1	001306	Cluster794_1clades	116	vBValMR10Z_374	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37410.1	001306	Cluster794_1clades	116	pp2_177	Vibriophage phi-pp2	GCA_002630725.1
ARB13792.1	001307	Cluster795_1clades	206	Ccr10_gp262	Caulobacter phage Ccr10	GCA_002619445.1
ARB14137.1	001307	Cluster795_1clades	210	Ccr2_gp261	Caulobacter phage Ccr2	GCA_002619465.1
ARB14831.1	001307	Cluster795_1clades	206	Ccr29_gp275	Caulobacter phage Ccr29	GCA_002619485.1
ARB15171.1	001307	Cluster795_1clades	206	Ccr32_gp253	Caulobacter phage Ccr32	GCA_002619505.1
ARB15505.1	001307	Cluster795_1clades	206	Ccr34_gp263	Caulobacter phage Ccr34	GCA_002619525.1
ARB14479.1	001307	Cluster795_1clades	206	Ccr5_gp259	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68456.1	001307	Cluster795_1clades	209	CcrBL10_gp252	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88144.1	001307	Cluster795_1clades	199	CcrColossus_gp274	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68820.1	001307	Cluster795_1clades	199	CcrPW_gp281	Caulobacter phage CcrPW	GCA_003443275.1
AFU87789.1	001307	Cluster795_1clades	206	CcrKarma_gp272	Caulobacter virus Karma	GCA_000901575.1
AFU87436.1	001307	Cluster795_1clades	206	CcrMagneto_gp266	Caulobacter virus Magneto	GCA_000903095.1
AFU86743.1	001307	Cluster795_1clades	213	CcrRogue_gp261	Caulobacter virus Rogue	GCA_000900555.1
AFU88582.1	001307	Cluster795_1clades	206	CcrSwift_gp264	Caulobacter virus Swift	GCA_000899655.1
AFU87090.1	001307	Cluster795_1clades	206	CbK_gp258	Caulobacter virus phiCbK	GCA_000900535.1
ARB13576.1	001308	Cluster796_1clades	192	Ccr10_gp048	Caulobacter phage Ccr10	GCA_002619445.1
ARB13922.1	001308	Cluster796_1clades	192	Ccr2_gp047	Caulobacter phage Ccr2	GCA_002619465.1
ARB14611.1	001308	Cluster796_1clades	192	Ccr29_gp054	Caulobacter phage Ccr29	GCA_002619485.1
ARB14967.1	001308	Cluster796_1clades	192	Ccr32_gp048	Caulobacter phage Ccr32	GCA_002619505.1
ARB15298.1	001308	Cluster796_1clades	192	Ccr34_gp049	Caulobacter phage Ccr34	GCA_002619525.1
ARB14265.1	001308	Cluster796_1clades	65	Ccr5_gp047	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68250.1	001308	Cluster796_1clades	208	CcrBL10_gp046	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88015.1	001308	Cluster796_1clades	136	CcrColossus_gp145	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68692.1	001308	Cluster796_1clades	120	CcrPW_gp153c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87566.1	001308	Cluster796_1clades	192	CcrKarma_gp049	Caulobacter virus Karma	GCA_000901575.1
AFU87216.1	001308	Cluster796_1clades	194	CcrMagneto_gp046	Caulobacter virus Magneto	GCA_000903095.1
AFU86532.1	001308	Cluster796_1clades	212	CcrRogue_gp050	Caulobacter virus Rogue	GCA_000900555.1
AFU88364.1	001308	Cluster796_1clades	194	CcrSwift_gp046	Caulobacter virus Swift	GCA_000899655.1
AFU86880.1	001308	Cluster796_1clades	192	CbK_gp048	Caulobacter virus phiCbK	GCA_000900535.1
ARB13680.1	001309	DUF1643	212	Ccr10_gp151c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14025.1	001309	DUF1643	212	Ccr2_gp150c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14713.1	001309	DUF1643	101	Ccr29_gp157	Caulobacter phage Ccr29	GCA_002619485.1
ARB15068.1	001309	DUF1643	212	Ccr32_gp150	Caulobacter phage Ccr32	GCA_002619505.1
ARB15402.1	001309	DUF1643	212	Ccr34_gp160	Caulobacter phage Ccr34	GCA_002619525.1
ARB14368.1	001309	DUF1643	212	Ccr5_gp149c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68351.1	001309	DUF1643	210	CcrBL10_gp147c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88065.1	001309	DUF1643	143	CcrColossus_gp195	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68742.1	001309	DUF1643	139	CcrPW_gp203c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87673.1	001309	DUF1643	212	CcrKarma_gp156	Caulobacter virus Karma	GCA_000901575.1
AFU87322.1	001309	DUF1643	212	CcrMagneto_gp152	Caulobacter virus Magneto	GCA_000903095.1
AFU86635.1	001309	DUF1643	210	CcrRogue_gp153	Caulobacter virus Rogue	GCA_000900555.1
AFU88469.1	001309	DUF1643	212	CcrSwift_gp151	Caulobacter virus Swift	GCA_000899655.1
AFU86986.1	001309	DUF1643	212	CbK_gp154	Caulobacter virus phiCbK	GCA_000900535.1
ARB13740.1	001310	Cluster798_1clades	195	Ccr10_gp210c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14085.1	001310	Cluster798_1clades	195	Ccr2_gp209c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14774.1	001310	Cluster798_1clades	195	Ccr29_gp218	Caulobacter phage Ccr29	GCA_002619485.1
ARB15118.1	001310	Cluster798_1clades	195	Ccr32_gp200	Caulobacter phage Ccr32	GCA_002619505.1
ARB15452.1	001310	Cluster798_1clades	195	Ccr34_gp210	Caulobacter phage Ccr34	GCA_002619525.1
ARB14427.1	001310	Cluster798_1clades	195	Ccr5_gp207c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68406.1	001310	Cluster798_1clades	190	CcrBL10_gp202c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88166.1	001310	Cluster798_1clades	203	CcrColossus_gp296	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68842.1	001310	Cluster798_1clades	202	CcrPW_gp303	Caulobacter phage CcrPW	GCA_003443275.1
AFU87733.1	001310	Cluster798_1clades	195	CcrKarma_gp216	Caulobacter virus Karma	GCA_000901575.1
AFU87382.1	001310	Cluster798_1clades	195	CcrMagneto_gp212	Caulobacter virus Magneto	GCA_000903095.1
AFU86692.1	001310	Cluster798_1clades	190	CcrRogue_gp210	Caulobacter virus Rogue	GCA_000900555.1
AFU88529.1	001310	Cluster798_1clades	195	CcrSwift_gp211	Caulobacter virus Swift	GCA_000899655.1
AFU87037.1	001310	Cluster798_1clades	195	CbK_gp205	Caulobacter virus phiCbK	GCA_000900535.1
ARB13797.1	001311	Cluster799_1clades	178	Ccr10_gp267	Caulobacter phage Ccr10	GCA_002619445.1
ARB14142.1	001311	Cluster799_1clades	178	Ccr2_gp266	Caulobacter phage Ccr2	GCA_002619465.1
ARB14836.1	001311	Cluster799_1clades	178	Ccr29_gp280	Caulobacter phage Ccr29	GCA_002619485.1
ARB15176.1	001311	Cluster799_1clades	178	Ccr32_gp258	Caulobacter phage Ccr32	GCA_002619505.1
ARB15510.1	001311	Cluster799_1clades	178	Ccr34_gp268	Caulobacter phage Ccr34	GCA_002619525.1
ARB14484.1	001311	Cluster799_1clades	177	Ccr5_gp264	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68462.1	001311	Cluster799_1clades	178	CcrBL10_gp258	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69142.1	001311	Cluster799_1clades	199	CcrBL9_gp118	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69696.1	001311	Cluster799_1clades	195	CcrSC_gp114	Caulobacter phage CcrSC	GCA_003443315.1
AFU87794.1	001311	Cluster799_1clades	178	CcrKarma_gp277	Caulobacter virus Karma	GCA_000901575.1
AFU87441.1	001311	Cluster799_1clades	178	CcrMagneto_gp271	Caulobacter virus Magneto	GCA_000903095.1
AFU86748.1	001311	Cluster799_1clades	179	CcrRogue_gp266	Caulobacter virus Rogue	GCA_000900555.1
AFU88587.1	001311	Cluster799_1clades	178	CcrSwift_gp269	Caulobacter virus Swift	GCA_000899655.1
AFU87095.1	001311	Cluster799_1clades	178	CbK_gp263	Caulobacter virus phiCbK	GCA_000900535.1
ARB13661.1	001312	ENDO3	189	Ccr10_gp132c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14006.1	001312	ENDO3	189	Ccr2_gp131c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14694.1	001312	ENDO3	189	Ccr29_gp138	Caulobacter phage Ccr29	GCA_002619485.1
ARB15048.1	001312	ENDO3	190	Ccr32_gp130	Caulobacter phage Ccr32	GCA_002619505.1
ARB15381.1	001312	ENDO3	190	Ccr34_gp139	Caulobacter phage Ccr34	GCA_002619525.1
ARB14349.1	001312	ENDO3	190	Ccr5_gp130c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68330.1	001312	ENDO3	190	CcrBL10_gp126c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88060.1	001312	ENDO3	189	CcrColossus_gp190	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68738.1	001312	ENDO3	189	CcrPW_gp199c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87653.1	001312	ENDO3	190	CcrKarma_gp136	Caulobacter virus Karma	GCA_000901575.1
AFU87302.1	001312	ENDO3	189	CcrMagneto_gp132	Caulobacter virus Magneto	GCA_000903095.1
AFU86614.1	001312	ENDO3	190	CcrRogue_gp132	Caulobacter virus Rogue	GCA_000900555.1
AFU88449.1	001312	ENDO3	190	CcrSwift_gp131	Caulobacter virus Swift	GCA_000899655.1
AFU86966.1	001312	ENDO3	190	CbK_gp134	Caulobacter virus phiCbK	GCA_000900535.1
AIT13997.1	001313	Cluster802_1clades	190	PBI_121Q_100	Escherichia phage 121Q	GCA_000926855.1
QAY00341.1	001313	Cluster802_1clades	190	Ecwhy1_60	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35087.1	001313	Cluster802_1clades	190	ACQ29_gp407	Escherichia phage PBECO4	GCA_001041035.1
BBM61688.1	001313	Cluster802_1clades	190	EO157G_0990	Escherichia phage SP27	GCA_008033345.1
AXC36664.1	001313	Cluster802_1clades	190	-	Escherichia phage UB	GCA_003341455.1
QBO61696.1	001313	Cluster802_1clades	190	G17_00207	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13745.1	001313	Cluster802_1clades	190	vBEcoMphAPEC6_gp115c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80001.1	001313	Cluster802_1clades	190	PSLUR01_00017	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFA44477.1	001313	Cluster802_1clades	180	RaK2_00204	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72620.1	001313	Cluster802_1clades	157	-	Myoviridae sp.	GCA_003657725.1
AFH14821.1	001313	Cluster802_1clades	175	Lu11_0283	Pseudomonas phage Lu11	GCA_000897175.1
QCW18612.1	001313	Cluster802_1clades	184	7t3_091	Salmonella phage 7t3	GCA_006083215.1
AZU98437.1	001313	Cluster802_1clades	184	CPT_Munch_505	Salmonella phage Munch	GCA_004015485.1
QIG63076.1	001313	Cluster802_1clades	184	SEPL_463	Salmonella phage SE_PL	GCA_011067555.1
ARB13686.1	001314	Cluster803_1clades	178	Ccr10_gp156c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14031.1	001314	Cluster803_1clades	178	Ccr2_gp155c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14718.1	001314	Cluster803_1clades	178	Ccr29_gp162	Caulobacter phage Ccr29	GCA_002619485.1
ARB15073.1	001314	Cluster803_1clades	178	Ccr32_gp155	Caulobacter phage Ccr32	GCA_002619505.1
ARB15407.1	001314	Cluster803_1clades	178	Ccr34_gp165	Caulobacter phage Ccr34	GCA_002619525.1
ARB14374.1	001314	Cluster803_1clades	178	Ccr5_gp154c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68355.1	001314	Cluster803_1clades	183	CcrBL10_gp151c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88068.1	001314	Cluster803_1clades	147	CcrColossus_gp198	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68745.1	001314	Cluster803_1clades	147	CcrPW_gp206c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87679.1	001314	Cluster803_1clades	178	CcrKarma_gp162	Caulobacter virus Karma	GCA_000901575.1
AFU87328.1	001314	Cluster803_1clades	178	CcrMagneto_gp158	Caulobacter virus Magneto	GCA_000903095.1
AFU86639.1	001314	Cluster803_1clades	183	CcrRogue_gp157	Caulobacter virus Rogue	GCA_000900555.1
AFU88475.1	001314	Cluster803_1clades	178	CcrSwift_gp157	Caulobacter virus Swift	GCA_000899655.1
AFU86992.1	001314	Cluster803_1clades	178	CbK_gp160	Caulobacter virus phiCbK	GCA_000900535.1
ARB13790.1	001315	Cluster804_1clades	151	Ccr10_gp260	Caulobacter phage Ccr10	GCA_002619445.1
ARB14135.1	001315	Cluster804_1clades	151	Ccr2_gp259	Caulobacter phage Ccr2	GCA_002619465.1
ARB14829.1	001315	Cluster804_1clades	151	Ccr29_gp273	Caulobacter phage Ccr29	GCA_002619485.1
ARB15169.1	001315	Cluster804_1clades	151	Ccr32_gp251	Caulobacter phage Ccr32	GCA_002619505.1
ARB15503.1	001315	Cluster804_1clades	151	Ccr34_gp261	Caulobacter phage Ccr34	GCA_002619525.1
ARB14477.1	001315	Cluster804_1clades	151	Ccr5_gp257	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68454.1	001315	Cluster804_1clades	150	CcrBL10_gp250	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88226.1	001315	Cluster804_1clades	180	CcrColossus_gp356	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68903.1	001315	Cluster804_1clades	174	CcrPW_gp364	Caulobacter phage CcrPW	GCA_003443275.1
AFU87787.1	001315	Cluster804_1clades	151	CcrKarma_gp270	Caulobacter virus Karma	GCA_000901575.1
AFU87434.1	001315	Cluster804_1clades	151	CcrMagneto_gp264	Caulobacter virus Magneto	GCA_000903095.1
AFU86741.1	001315	Cluster804_1clades	149	CcrRogue_gp259	Caulobacter virus Rogue	GCA_000900555.1
AFU88580.1	001315	Cluster804_1clades	151	CcrSwift_gp262	Caulobacter virus Swift	GCA_000899655.1
AFU87088.1	001315	Cluster804_1clades	151	CbK_gp256	Caulobacter virus phiCbK	GCA_000900535.1
ARB13659.1	001316	Cluster805_1clades	99	Ccr10_gp130	Caulobacter phage Ccr10	GCA_002619445.1
ARB14004.1	001316	Cluster805_1clades	99	Ccr2_gp129	Caulobacter phage Ccr2	GCA_002619465.1
ARB14692.1	001316	Cluster805_1clades	99	Ccr29_gp136	Caulobacter phage Ccr29	GCA_002619485.1
ARB15046.1	001316	Cluster805_1clades	99	Ccr32_gp128	Caulobacter phage Ccr32	GCA_002619505.1
ARB15379.1	001316	Cluster805_1clades	99	Ccr34_gp137	Caulobacter phage Ccr34	GCA_002619525.1
ARB14347.1	001316	Cluster805_1clades	99	Ccr5_gp128	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68327.1	001316	Cluster805_1clades	99	CcrBL10_gp123	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69178.1	001316	Cluster805_1clades	176	CcrBL9_gp154	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69731.1	001316	Cluster805_1clades	178	CcrSC_gp149	Caulobacter phage CcrSC	GCA_003443315.1
AFU87651.1	001316	Cluster805_1clades	99	CcrKarma_gp134	Caulobacter virus Karma	GCA_000901575.1
AFU87300.1	001316	Cluster805_1clades	99	CcrMagneto_gp130	Caulobacter virus Magneto	GCA_000903095.1
AFU86612.1	001316	Cluster805_1clades	99	CcrRogue_gp130	Caulobacter virus Rogue	GCA_000900555.1
AFU88447.1	001316	Cluster805_1clades	99	CcrSwift_gp129	Caulobacter virus Swift	GCA_000899655.1
AFU86964.1	001316	Cluster805_1clades	99	CbK_gp132	Caulobacter virus phiCbK	GCA_000900535.1
ARB13749.1	001317	Cluster806_1clades	153	Ccr10_gp219c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14094.1	001317	Cluster806_1clades	153	Ccr2_gp218c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14783.1	001317	Cluster806_1clades	153	Ccr29_gp227	Caulobacter phage Ccr29	GCA_002619485.1
ARB15127.1	001317	Cluster806_1clades	153	Ccr32_gp209	Caulobacter phage Ccr32	GCA_002619505.1
ARB15461.1	001317	Cluster806_1clades	153	Ccr34_gp219	Caulobacter phage Ccr34	GCA_002619525.1
ARB14436.1	001317	Cluster806_1clades	153	Ccr5_gp216c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68416.1	001317	Cluster806_1clades	154	CcrBL10_gp212c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69401.1	001317	Cluster806_1clades	153	CcrBL9_gp377	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69958.1	001317	Cluster806_1clades	177	CcrSC_gp376	Caulobacter phage CcrSC	GCA_003443315.1
AFU87743.1	001317	Cluster806_1clades	153	CcrKarma_gp226	Caulobacter virus Karma	GCA_000901575.1
AFU87391.1	001317	Cluster806_1clades	153	CcrMagneto_gp221	Caulobacter virus Magneto	GCA_000903095.1
AFU86702.1	001317	Cluster806_1clades	154	CcrRogue_gp220	Caulobacter virus Rogue	GCA_000900555.1
AFU88539.1	001317	Cluster806_1clades	153	CcrSwift_gp221	Caulobacter virus Swift	GCA_000899655.1
AFU87046.1	001317	Cluster806_1clades	153	CbK_gp214	Caulobacter virus phiCbK	GCA_000900535.1
ARB13578.1	001318	Cluster808_1clades	120	Ccr10_gp050	Caulobacter phage Ccr10	GCA_002619445.1
ARB13924.1	001318	Cluster808_1clades	109	Ccr2_gp049	Caulobacter phage Ccr2	GCA_002619465.1
ARB14613.1	001318	Cluster808_1clades	127	Ccr29_gp056	Caulobacter phage Ccr29	GCA_002619485.1
ARB14969.1	001318	Cluster808_1clades	120	Ccr32_gp050	Caulobacter phage Ccr32	GCA_002619505.1
ARB15300.1	001318	Cluster808_1clades	109	Ccr34_gp051	Caulobacter phage Ccr34	GCA_002619525.1
ARB14267.1	001318	Cluster808_1clades	120	Ccr5_gp049	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68252.1	001318	Cluster808_1clades	121	CcrBL10_gp048	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87921.1	001318	Cluster808_1clades	173	CcrColossus_gp051	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68594.1	001318	Cluster808_1clades	175	CcrPW_gp055	Caulobacter phage CcrPW	GCA_003443275.1
AFU87568.1	001318	Cluster808_1clades	127	CcrKarma_gp051	Caulobacter virus Karma	GCA_000901575.1
AFU87218.1	001318	Cluster808_1clades	127	CcrMagneto_gp048	Caulobacter virus Magneto	GCA_000903095.1
AFU86534.1	001318	Cluster808_1clades	121	CcrRogue_gp052	Caulobacter virus Rogue	GCA_000900555.1
AFU88366.1	001318	Cluster808_1clades	127	CcrSwift_gp048	Caulobacter virus Swift	GCA_000899655.1
AFU86882.1	001318	Cluster808_1clades	127	CbK_gp050	Caulobacter virus phiCbK	GCA_000900535.1
AGH56890.1	001319	Cluster809_1clades	132	CPXG_00087	Cyanophage P-RSM6	GCA_000906155.1
AJK27611.1	001319	Cluster809_1clades	144	PTIM40_196	Cyanophage P-TIM40	GCA_001470935.1
AMO43189.1	001319	Cluster809_1clades	174	R1080702_180	Cyanophage S-RIM32	GCA_001754165.1
AMO43415.1	001319	Cluster809_1clades	70	W270710_171	Cyanophage S-RIM44	GCA_002599145.1
AOO11659.1	001319	Cluster809_1clades	70	ES420910_178	Cyanophage S-RIM44	GCA_002599165.1
AOO11887.1	001319	Cluster809_1clades	70	Np050604_171	Cyanophage S-RIM44	GCA_002599185.1
AOO12125.1	001319	Cluster809_1clades	70	Np200711_179	Cyanophage S-RIM44	GCA_002599205.1
AOO12360.1	001319	Cluster809_1clades	70	Np420711_178	Cyanophage S-RIM44	GCA_002599225.1
AOO12588.1	001319	Cluster809_1clades	70	Sn080709_171	Cyanophage S-RIM44	GCA_002599245.1
AOO12825.1	001319	Cluster809_1clades	70	Sn130910_178	Cyanophage S-RIM44	GCA_002599265.1
AOO13054.1	001319	Cluster809_1clades	70	W2100709_172	Cyanophage S-RIM44	GCA_002599285.1
AGH07590.1	001319	Cluster809_1clades	128	CYVG_00146	Cyanophage S-SSM6a	GCA_002710385.1
AGG54487.1	001319	Cluster809_1clades	130	CYWG_00203	Cyanophage S-SSM6b	GCA_002710425.1
ADO99274.1	001319	Cluster809_1clades	96	Syn1_173	Prochlorococcus phage Syn1	GCA_000892495.1
APU01554.1	001320	Phage_T4_Ndd	134	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29085.1	001320	Phage_T4_Ndd	134	AP1_0378	Aeromonas phage AP1	GCA_014183365.1
ATI17347.1	001320	Phage_T4_Ndd	134	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00246.1	001320	Phage_T4_Ndd	134	HWB28_gp306	Aeromonas phage AS-zj	GCA_002627665.1
AUE22870.1	001320	Phage_T4_Ndd	170	Ah1_00352	Aeromonas phage Ah1	GCA_002957415.1
QAX98580.1	001320	Phage_T4_Ndd	166	ASfcp2_246	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97792.1	001320	Phage_T4_Ndd	134	ASswx1_147	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01362.1	001320	Phage_T4_Ndd	134	ASwh1_302	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39447.1	001320	Phage_T4_Ndd	134	CC2_390	Aeromonas phage CC2	GCA_000903495.1
ADQ53045.1	001320	Phage_T4_Ndd	166	PX29p328	Aeromonas phage PX29	GCA_000920195.1
ADM79968.1	001320	Phage_T4_Ndd	168	phiAS5_ORF0125	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53177.1	001320	Phage_T4_Ndd	134	65p169	Aeromonas virus 65	GCA_000893255.1
AAQ17998.1	001320	Phage_T4_Ndd	170	Aeh1ORF328c	Aeromonas virus Aeh1	GCA_000843245.1
ALY07204.1	001320	Phage_T4_Ndd	150	VmeM32_00218	Vibrio phage vB_VmeM-32	GCA_002608825.1
APU01655.1	001321	Cluster811_1clades	77	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22838.1	001321	Cluster811_1clades	77	Ah1_00320	Aeromonas phage Ah1	GCA_002957415.1
QAX98551.1	001321	Cluster811_1clades	77	ASfcp2_216	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53015.1	001321	Cluster811_1clades	79	PX29p296	Aeromonas phage PX29	GCA_000920195.1
ADQ53285.1	001321	Cluster811_1clades	77	65p277	Aeromonas virus 65	GCA_000893255.1
AAQ17968.1	001321	Cluster811_1clades	77	Aeh1ORF299c	Aeromonas virus Aeh1	GCA_000843245.1
QBX06856.1	001321	Cluster811_1clades	70	BcepSaruman_443	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74825.1	001321	Cluster811_1clades	70	BcepSauron_445	Burkholderia phage BcepSauron	GCA_005394215.1
ANS06135.1	001321	Cluster811_1clades	85	ABCD_0176	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64842.1	001321	Cluster811_1clades	102	S13_043	Cronobacter phage S13	GCA_001503575.1
AON97189.1	001321	Cluster811_1clades	86	E_181	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78706.1	001321	Cluster811_1clades	85	RB43ORF184c	Escherichia virus RB43	GCA_000863505.1
QHJ78820.1	001321	Cluster811_1clades	93	-	Myoviridae sp.	GCA_012593985.1
QHJ85958.1	001321	Cluster811_1clades	166	KKIINIFJ_00046	Pseudomonas phage PN05	GCA_009931935.1
AIA64841.1	001322	Cluster812_1clades	133	S13_042	Cronobacter phage S13	GCA_001503575.1
QHJ78821.1	001322	Cluster812_1clades	133	-	Myoviridae sp.	GCA_012593985.1
AAQ64345.1	001322	Cluster812_1clades	163	KVP40.0276	Vibrio phage KVP40	GCA_000843785.1
QIW90659.1	001322	Cluster812_1clades	158	GCAPEGMB_00312	Vibrio phage V07	GCA_012361095.1
QIW91139.1	001322	Cluster812_1clades	158	COHAPHLL_00303	Vibrio phage V09	GCA_012361135.1
QHJ74454.1	001322	Cluster812_1clades	158	VH12019_00127	Vibrio phage VH1_2019	GCA_009931825.1
AGB06948.1	001322	Cluster812_1clades	158	CF80_gp161	Vibrio phage VH7D	GCA_000914495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06197.1	001322	Cluster812_1clades	158	ValB1HC_244	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61214.1	001322	Cluster812_1clades	158	AVU32_gp373	Vibrio phage ValKK3	GCA_001501635.1
AGN30322.2	001322	Cluster812_1clades	158	VPFG_00324	Vibrio phage nt-1	GCA_000910195.2
ALP47117.1	001322	Cluster812_1clades	158	phiGrn1_0008	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47499.1	001322	Cluster812_1clades	158	phiST2_0140	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54822.1	001322	Cluster812_1clades	158	vBValMR10Z_282	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37505.1	001322	Cluster812_1clades	158	pp2_272	Vibriophage phi-pp2	GCA_002630725.1
AHI60411.1	001323	Cluster813_1clades	146	Ea357_257	Erwinia phage Ea35-70	GCA_000914635.1
QBP07368.1	001323	Cluster813_1clades	146	REBECCA_263	Erwinia phage Rebecca	GCA_004521635.1
AUG86050.1	001323	Cluster813_1clades	146	BOSOLAPHORUS_264	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52366.1	001323	Cluster813_1clades	146	DM_267	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86370.1	001323	Cluster813_1clades	146	DESERTFOX_263	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86691.1	001323	Cluster813_1clades	146	MADMEL_264	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87016.1	001323	Cluster813_1clades	146	MORTIMER_268	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52041.1	001323	Cluster813_1clades	146	RAY_261	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51724.1	001323	Cluster813_1clades	146	SIMMY50_266	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65076.1	001323	Cluster813_1clades	146	SPECIALG_265	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24169.1	001323	Cluster813_1clades	143	-	Proteus phage 10	GCA_014071245.1
QMP24173.1	001323	Cluster813_1clades	147	-	Proteus phage 10	GCA_014071245.1
QMP24172.1	001323	Cluster813_1clades	161	-	Proteus phage 10	GCA_014071245.1
QKE54589.1	001323	Cluster813_1clades	144	ACSA002_2730	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13633.1	001324	SIG+TM+TM	159	Ccr10_gp104	Caulobacter phage Ccr10	GCA_002619445.1
ARB13978.1	001324	SIG+TM+TM	159	Ccr2_gp103	Caulobacter phage Ccr2	GCA_002619465.1
ARB14666.1	001324	SIG+TM+TM	159	Ccr29_gp110	Caulobacter phage Ccr29	GCA_002619485.1
ARB15021.1	001324	SIG+TM+TM	159	Ccr32_gp103	Caulobacter phage Ccr32	GCA_002619505.1
ARB15353.1	001324	SIG+TM+TM	159	Ccr34_gp111	Caulobacter phage Ccr34	GCA_002619525.1
ARB14322.1	001324	SIG+TM+TM	159	Ccr5_gp104	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68302.1	001324	SIG+TM+TM	158	CcrBL10_gp098	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88005.1	001324	SIG+TM+TM	157	CcrColossus_gp135	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68681.1	001324	SIG+TM+TM	156	CcrPW_gp142	Caulobacter phage CcrPW	GCA_003443275.1
AFU87625.1	001324	SIG+TM+TM	159	CcrKarma_gp108	Caulobacter virus Karma	GCA_000901575.1
AFU87274.1	001324	SIG+TM+TM	159	CcrMagneto_gp104	Caulobacter virus Magneto	GCA_000903095.1
AFU86586.1	001324	SIG+TM+TM	158	CcrRogue_gp104	Caulobacter virus Rogue	GCA_000900555.1
AFU88421.1	001324	SIG+TM+TM	159	CcrSwift_gp103	Caulobacter virus Swift	GCA_000899655.1
AFU86939.1	001324	SIG+TM+TM	159	CbK_gp107	Caulobacter virus phiCbK	GCA_000900535.1
AFC21938.1	001325	SIG+TM+TM	152	GAP32_480	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14051.1	001325	SIG+TM+TM	140	PBI_121Q_161	Escherichia phage 121Q	GCA_000926855.1
QAY00292.1	001325	SIG+TM+TM	140	Ecwhy1_10	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35042.1	001325	SIG+TM+TM	140	ACQ29_gp362	Escherichia phage PBECO4	GCA_001041035.1
BBM61734.1	001325	SIG+TM+TM	140	EO157G_1450	Escherichia phage SP27	GCA_008033345.1
AXC36619.1	001325	SIG+TM+TM	140	-	Escherichia phage UB	GCA_003341455.1
QBO61648.1	001325	SIG+TM+TM	140	G17_00152	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13702.1	001325	SIG+TM+TM	140	vBEcoMphAPEC6_gp072c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80046.1	001325	SIG+TM+TM	140	PSLUR01_00069	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44512.1	001325	SIG+TM+TM	154	RaK2_00239	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM44064.1	001325	SIG+TM+TM	156	CBB_501	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89019.1	001325	SIG+TM+TM	148	BF_0494	Serratia phage BF	GCA_002619745.1
SOK59300.1	001325	SIG+TM+TM	144	g492	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58765.1	001325	SIG+TM+TM	144	g488	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14207.1	001326	Cluster816_1clades	144	PBI_121Q_317	Escherichia phage 121Q	GCA_000926855.1
QAY00731.1	001326	Cluster816_1clades	154	Ecwhy1_456	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34913.1	001326	Cluster816_1clades	144	ACQ29_gp233	Escherichia phage PBECO4	GCA_001041035.1
BBM61880.1	001326	Cluster816_1clades	133	EO157G_2910	Escherichia phage SP27	GCA_008033345.1
AXC37016.1	001326	Cluster816_1clades	133	-	Escherichia phage UB	GCA_003341455.1
QBO61498.1	001326	Cluster816_1clades	144	G17_00002	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62104.1	001326	Cluster816_1clades	144	G17_00615	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14114.1	001326	Cluster816_1clades	133	vBEcoMphAPEC6_gp491c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80190.1	001326	Cluster816_1clades	144	PSLUR01_00213	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44634.1	001326	Cluster816_1clades	132	RaK2_00361	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18725.1	001326	Cluster816_1clades	133	7t3_0204	Salmonella phage 7t3	GCA_006083215.1
AZU97996.1	001326	Cluster816_1clades	133	CPT_Munch_052	Salmonella phage Munch	GCA_004015485.1
QIG62983.1	001326	Cluster816_1clades	133	SEPL_370	Salmonella phage SE_PL	GCA_011067555.1
AQW88566.1	001326	Cluster816_1clades	133	BF_0041	Serratia phage BF	GCA_002619745.1
ARB13690.1	001327	Cluster817_1clades	146	Ccr10_gp160c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14035.1	001327	Cluster817_1clades	146	Ccr2_gp159c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14722.1	001327	Cluster817_1clades	146	Ccr29_gp166	Caulobacter phage Ccr29	GCA_002619485.1
ARB15077.1	001327	Cluster817_1clades	146	Ccr32_gp159	Caulobacter phage Ccr32	GCA_002619505.1
ARB15411.1	001327	Cluster817_1clades	146	Ccr34_gp169	Caulobacter phage Ccr34	GCA_002619525.1
ARB14378.1	001327	Cluster817_1clades	146	Ccr5_gp158c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68360.1	001327	Cluster817_1clades	151	CcrBL10_gp156c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88075.1	001327	Cluster817_1clades	152	CcrColossus_gp205	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68752.1	001327	Cluster817_1clades	129	CcrPW_gp213c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87683.1	001327	Cluster817_1clades	142	CcrKarma_gp166	Caulobacter virus Karma	GCA_000901575.1
AFU87332.1	001327	Cluster817_1clades	142	CcrMagneto_gp162	Caulobacter virus Magneto	GCA_000903095.1
AFU86643.1	001327	Cluster817_1clades	151	CcrRogue_gp161	Caulobacter virus Rogue	GCA_000900555.1
AFU88479.1	001327	Cluster817_1clades	142	CcrSwift_gp161	Caulobacter virus Swift	GCA_000899655.1
AFU86996.1	001327	Cluster817_1clades	146	CbK_gp164	Caulobacter virus phiCbK	GCA_000900535.1
ANZ49659.1	001328	Cluster818_1clades	146	MACHINA_21	Erwinia phage Machina	GCA_002758035.1
AXF51146.1	001328	Cluster818_1clades	132	WELLINGTON_15	Erwinia phage Wellington	GCA_003344985.1
AFQ96735.1	001328	Cluster818_1clades	65	G173_gp190	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48036.1	001328	Cluster818_1clades	135	ASESINO_23	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48310.1	001328	Cluster818_1clades	149	CAITLIN_15	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48583.1	001328	Cluster818_1clades	150	CHRISDB_21	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49104.1	001328	Cluster818_1clades	146	HUXLEY_22	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49368.1	001328	Cluster818_1clades	132	KWAN_15	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49932.1	001328	Cluster818_1clades	146	PARSHIK_23	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50446.1	001328	Cluster818_1clades	135	STRATTON_21	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85844.1	001328	Cluster818_1clades	138	ACEC001_0070	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20724.1	001328	Cluster818_1clades	138	-	Salmonella phage JN03	GCA_014319805.1
AXF51104.1	001328	Cluster818_1clades	137	MLDJOKPK_00161	Salmonella phage SPAsTU	GCA_003183805.1
AEP83839.1	001328	Cluster818_1clades	138	SPN3US_0006	Salmonella phage SPN3US	GCA_001042275.1
ARB13800.1	001329	Cluster819_1clades	139	Ccr10_gp270	Caulobacter phage Ccr10	GCA_002619445.1
ARB14145.1	001329	Cluster819_1clades	139	Ccr2_gp269	Caulobacter phage Ccr2	GCA_002619465.1
ARB14839.1	001329	Cluster819_1clades	139	Ccr29_gp283	Caulobacter phage Ccr29	GCA_002619485.1
ARB15179.1	001329	Cluster819_1clades	139	Ccr32_gp261	Caulobacter phage Ccr32	GCA_002619505.1
ARB15513.1	001329	Cluster819_1clades	139	Ccr34_gp271	Caulobacter phage Ccr34	GCA_002619525.1
ARB14487.1	001329	Cluster819_1clades	139	Ccr5_gp267	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68465.1	001329	Cluster819_1clades	139	CcrBL10_gp261	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88208.1	001329	Cluster819_1clades	142	CcrColossus_gp338	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68885.1	001329	Cluster819_1clades	142	CcrPW_gp346	Caulobacter phage CcrPW	GCA_003443275.1
AFU87797.1	001329	Cluster819_1clades	139	CcrKarma_gp280	Caulobacter virus Karma	GCA_000901575.1
AFU87444.1	001329	Cluster819_1clades	139	CcrMagneto_gp274	Caulobacter virus Magneto	GCA_000903095.1
AFU86751.1	001329	Cluster819_1clades	139	CcrRogue_gp269	Caulobacter virus Rogue	GCA_000900555.1
AFU88590.1	001329	Cluster819_1clades	139	CcrSwift_gp272	Caulobacter virus Swift	GCA_000899655.1
AFU87098.1	001329	Cluster819_1clades	139	CbK_gp266	Caulobacter virus phiCbK	GCA_000900535.1
ARB13598.1	001330	Cluster820_1clades	128	Ccr10_gp070	Caulobacter phage Ccr10	GCA_002619445.1
ARB13944.1	001330	Cluster820_1clades	128	Ccr2_gp069	Caulobacter phage Ccr2	GCA_002619465.1
ARB14634.1	001330	Cluster820_1clades	128	Ccr29_gp077	Caulobacter phage Ccr29	GCA_002619485.1
ARB14990.1	001330	Cluster820_1clades	128	Ccr32_gp071	Caulobacter phage Ccr32	GCA_002619505.1
ARB15320.1	001330	Cluster820_1clades	128	Ccr34_gp071	Caulobacter phage Ccr34	GCA_002619525.1
ARB14287.1	001330	Cluster820_1clades	128	Ccr5_gp069	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68271.1	001330	Cluster820_1clades	122	CcrBL10_gp067	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69149.1	001330	Cluster820_1clades	136	CcrBL9_gp125	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69703.1	001330	Cluster820_1clades	136	CcrSC_gp121	Caulobacter phage CcrSC	GCA_003443315.1
AFU87588.1	001330	Cluster820_1clades	127	CcrKarma_gp071	Caulobacter virus Karma	GCA_000901575.1
AFU87238.1	001330	Cluster820_1clades	127	CcrMagneto_gp068	Caulobacter virus Magneto	GCA_000903095.1
AFU86554.1	001330	Cluster820_1clades	119	CcrRogue_gp072	Caulobacter virus Rogue	GCA_000900555.1
AFU88386.1	001330	Cluster820_1clades	127	CcrSwift_gp068	Caulobacter virus Swift	GCA_000899655.1
AFU86902.1	001330	Cluster820_1clades	128	CbK_gp070	Caulobacter virus phiCbK	GCA_000900535.1
AFC21886.1	001331	Cluster821_1clades	133	GAP32_432	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14022.1	001331	Cluster821_1clades	117	PBI_121Q_128	Escherichia phage 121Q	GCA_000926855.1
QAY00317.1	001331	Cluster821_1clades	121	Ecwhy1_35	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35065.1	001331	Cluster821_1clades	117	ACQ29_gp385	Escherichia phage PBECO4	GCA_001041035.1
BBM61710.1	001331	Cluster821_1clades	117	EO157G_1210	Escherichia phage SP27	GCA_008033345.1
QBO61674.1	001331	Cluster821_1clades	117	G17_00182	Escherichia phage vB_EcoM_G17	GCA_004521135.1

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QDF13723.1	001331	Cluster821_1clades	117	vBEcoMphAPEC6_gp093c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80022.1	001331	Cluster821_1clades	117	PSLUR01_00041	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM44014.1	001331	Cluster821_1clades	133	CBB_451	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18542.1	001331	Cluster821_1clades	119	7t3_012	Salmonella phage 7t3	GCA_006083215.1
AZU98374.1	001331	Cluster821_1clades	131	CPT_Munch_435	Salmonella phage Munch	GCA_004015485.1
QIG63139.1	001331	Cluster821_1clades	119	SEPL_526	Salmonella phage SE_PL	GCA_011067555.1
SOK59258.1	001331	Cluster821_1clades	134	g450	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58723.1	001331	Cluster821_1clades	134	g446	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01699.1	001332	Cluster822_1clades	130	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53338.1	001332	Cluster822_1clades	130	65p330	Aeromonas virus 65	GCA_000893255.1
AAQ64201.1	001332	Cluster822_1clades	129	KVP40.0130	Vibrio phage KVP40	GCA_000843785.1
QIW90516.1	001332	Cluster822_1clades	129	GCAPEGMB_00169	Vibrio phage V07	GCA_012361095.1
QIW90906.1	001332	Cluster822_1clades	129	COHAPHLL_00043	Vibrio phage V09	GCA_012361135.1
QHJ74312.1	001332	Cluster822_1clades	129	VH12019_00393	Vibrio phage VH1_2019	GCA_009931825.1
AGB06807.1	001332	Cluster822_1clades	129	CF80_gp020	Vibrio phage VH7D	GCA_000914495.1
QBX05959.1	001332	Cluster822_1clades	129	ValB1HC_005	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60971.1	001332	Cluster822_1clades	129	AVU32_gp130	Vibrio phage ValKK3	GCA_001501635.1
AGN30180.1	001332	Cluster822_1clades	129	VPFG_00178	Vibrio phage nt-1	GCA_000910195.2
ALP47155.1	001332	Cluster822_1clades	129	phiGrn1_0242	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47540.1	001332	Cluster822_1clades	129	phiST2_0380	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54584.1	001332	Cluster822_1clades	129	vBValMR10Z_43	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37361.1	001332	Cluster822_1clades	129	pp2_128	Vibriophage phi-pp2	GCA_002630725.1
ARB13714.1	001333	Cluster823_1clades	75	Ccr10_gp184c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14059.1	001333	Cluster823_1clades	75	Ccr2_gp183c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14746.1	001333	Cluster823_1clades	75	Ccr29_gp190	Caulobacter phage Ccr29	GCA_002619485.1
ARB15101.1	001333	Cluster823_1clades	75	Ccr32_gp183	Caulobacter phage Ccr32	GCA_002619505.1
ARB15435.1	001333	Cluster823_1clades	75	Ccr34_gp193	Caulobacter phage Ccr34	GCA_002619525.1
ARB14402.1	001333	Cluster823_1clades	75	Ccr5_gp182c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68383.1	001333	Cluster823_1clades	76	CcrBL10_gp179c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69460.1	001333	Cluster823_1clades	91	CcrBL9_gp436	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70009.1	001333	Cluster823_1clades	106	CcrSC_gp427	Caulobacter phage CcrSC	GCA_003443315.1
AFU87707.1	001333	Cluster823_1clades	75	CcrKarma_gp190	Caulobacter virus Karma	GCA_000901575.1
AFU87356.1	001333	Cluster823_1clades	75	CcrMagneto_gp186	Caulobacter virus Magneto	GCA_000903095.1
AFU86668.1	001333	Cluster823_1clades	76	CcrRogue_gp186	Caulobacter virus Rogue	GCA_000900555.1
AFU88503.1	001333	Cluster823_1clades	76	CcrSwift_gp185	Caulobacter virus Swift	GCA_000899655.1
AFU87020.1	001333	Cluster823_1clades	75	CbK_gp188	Caulobacter virus phiCbK	GCA_000900535.1
ARB13641.1	001334	Cluster824_1clades	101	Ccr10_gp112c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13986.1	001334	Cluster824_1clades	101	Ccr2_gp111c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14674.1	001334	Cluster824_1clades	101	Ccr29_gp118	Caulobacter phage Ccr29	GCA_002619485.1
ARB15029.1	001334	Cluster824_1clades	101	Ccr32_gp111	Caulobacter phage Ccr32	GCA_002619505.1
ARB15361.1	001334	Cluster824_1clades	101	Ccr34_gp119	Caulobacter phage Ccr34	GCA_002619525.1
ARB14330.1	001334	Cluster824_1clades	101	Ccr5_gp112c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68310.1	001334	Cluster824_1clades	99	CcrBL10_gp106c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88017.1	001334	Cluster824_1clades	96	CcrColossus_gp147	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68694.1	001334	Cluster824_1clades	96	CcrPW_gp155c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87633.1	001334	Cluster824_1clades	101	CcrKarma_gp116	Caulobacter virus Karma	GCA_000901575.1
AFU87282.1	001334	Cluster824_1clades	101	CcrMagneto_gp112	Caulobacter virus Magneto	GCA_000903095.1
AFU86594.1	001334	Cluster824_1clades	99	CcrRogue_gp112	Caulobacter virus Rogue	GCA_000900555.1
AFU88429.1	001334	Cluster824_1clades	101	CcrSwift_gp111	Caulobacter virus Swift	GCA_000899655.1
AFU86947.1	001334	Cluster824_1clades	101	CbK_gp115	Caulobacter virus phiCbK	GCA_000900535.1
ARB13743.1	001335	Cluster825_1clades	97	Ccr10_gp213c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14088.1	001335	Cluster825_1clades	97	Ccr2_gp212c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14777.1	001335	Cluster825_1clades	97	Ccr29_gp221	Caulobacter phage Ccr29	GCA_002619485.1
ARB15121.1	001335	Cluster825_1clades	97	Ccr32_gp203	Caulobacter phage Ccr32	GCA_002619505.1
ARB15455.1	001335	Cluster825_1clades	97	Ccr34_gp213	Caulobacter phage Ccr34	GCA_002619525.1
ARB14430.1	001335	Cluster825_1clades	97	Ccr5_gp210c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68409.1	001335	Cluster825_1clades	97	CcrBL10_gp205c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88203.1	001335	Cluster825_1clades	100	CcrColossus_gp333	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68880.1	001335	Cluster825_1clades	96	CcrPW_gp341	Caulobacter phage CcrPW	GCA_003443275.1
AFU87737.1	001335	Cluster825_1clades	97	CcrKarma_gp220	Caulobacter virus Karma	GCA_000901575.1
AFU87385.1	001335	Cluster825_1clades	97	CcrMagneto_gp215	Caulobacter virus Magneto	GCA_000903095.1
AFU86696.1	001335	Cluster825_1clades	96	CcrRogue_gp214	Caulobacter virus Rogue	GCA_000900555.1
AFU88533.1	001335	Cluster825_1clades	96	CcrSwift_gp215	Caulobacter virus Swift	GCA_000899655.1
AFU87040.1	001335	Cluster825_1clades	97	CbK_gp208	Caulobacter virus phiCbK	GCA_000900535.1
AFC21558.1	001336	Cluster826_1clades	88	GAP32_110	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14360.1	001336	Cluster826_1clades	84	PBI_121Q_470	Escherichia phage 121Q	GCA_000926855.1
BBM62031.1	001336	Cluster826_1clades	85	EO157G_4420	Escherichia phage SP27	GCA_008033345.1
AXC36894.1	001336	Cluster826_1clades	62	-	Escherichia phage UB	GCA_003341455.1
QBO61944.1	001336	Cluster826_1clades	85	G17_00455	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13972.1	001336	Cluster826_1clades	85	vBEcoMphAPEC6_gp348c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80347.1	001336	Cluster826_1clades	85	PSLUR01_00370	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43676.1	001336	Cluster826_1clades	89	CBB_111	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18811.1	001336	Cluster826_1clades	91	7t3_0290	Salmonella phage 7t3	GCA_006083215.1
AZU98076.1	001336	Cluster826_1clades	91	CPT_Munch_132	Salmonella phage Munch	GCA_004015485.1
QIG62906.1	001336	Cluster826_1clades	91	SEPL_293	Salmonella phage SE_PL	GCA_011067555.1
AQW88629.1	001336	Cluster826_1clades	90	BF_0104	Serratia phage BF	GCA_002619745.1
SOK58905.1	001336	Cluster826_1clades	90	g097	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58370.1	001336	Cluster826_1clades	90	g093	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOO14334.1	001337	Cluster827_1clades	89	Sn110110_140	Cyanophage S-RIM14	GCA_002599065.1
AOO14983.1	001337	Cluster827_1clades	89	W1230910_137	Cyanophage S-RIM14	GCA_002599125.1
AMO43269.1	001337	Cluster827_1clades	90	W270710_024	Cyanophage S-RIM44	GCA_002599145.1
AOO11505.1	001337	Cluster827_1clades	89	ES420910_023	Cyanophage S-RIM44	GCA_002599165.1
AOO11741.1	001337	Cluster827_1clades	90	Np050604_024	Cyanophage S-RIM44	GCA_002599185.1
AOO11970.1	001337	Cluster827_1clades	89	Np200711_023	Cyanophage S-RIM44	GCA_002599205.1
AOO12206.1	001337	Cluster827_1clades	89	Np420711_023	Cyanophage S-RIM44	GCA_002599225.1
AOO12442.1	001337	Cluster827_1clades	90	Sn080709_024	Cyanophage S-RIM44	GCA_002599245.1
AOO12671.1	001337	Cluster827_1clades	89	Sn130910_023	Cyanophage S-RIM44	GCA_002599265.1
AOO12907.1	001337	Cluster827_1clades	90	W2100709_024	Cyanophage S-RIM44	GCA_002599285.1
ADO99126.1	001337	Cluster827_1clades	90	Syn1_024	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59679.1	001337	Cluster827_1clades	71	S330809_218	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59441.1	001337	Cluster827_1clades	90	C440309_218	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59916.1	001337	Cluster827_1clades	90	N231010_217	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13592.1	001338	Cluster828_1clades	81	Ccr10_gp064	Caulobacter phage Ccr10	GCA_002619445.1
ARB13938.1	001338	Cluster828_1clades	81	Ccr2_gp063	Caulobacter phage Ccr2	GCA_002619465.1
ARB14627.1	001338	Cluster828_1clades	89	Ccr29_gp070	Caulobacter phage Ccr29	GCA_002619485.1
ARB14983.1	001338	Cluster828_1clades	81	Ccr32_gp064	Caulobacter phage Ccr32	GCA_002619505.1
ARB15314.1	001338	Cluster828_1clades	81	Ccr34_gp065	Caulobacter phage Ccr34	GCA_002619525.1
ARB14281.1	001338	Cluster828_1clades	81	Ccr5_gp063	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68265.1	001338	Cluster828_1clades	68	CcrBL10_gp061	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87946.1	001338	Cluster828_1clades	90	CcrColossus_gp076	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68619.1	001338	Cluster828_1clades	90	CcrPW_gp080	Caulobacter phage CcrPW	GCA_003443275.1
AFU87582.1	001338	Cluster828_1clades	50	CcrKarma_gp065	Caulobacter virus Karma	GCA_000901575.1
AFU87232.1	001338	Cluster828_1clades	50	CcrMagneto_gp062	Caulobacter virus Magneto	GCA_000903095.1
AFU86548.1	001338	Cluster828_1clades	49	CcrRogue_gp066	Caulobacter virus Rogue	GCA_000900555.1
AFU88380.1	001338	Cluster828_1clades	50	CcrSwift_gp062	Caulobacter virus Swift	GCA_000899655.1
AFU86896.1	001338	Cluster828_1clades	50	CbK_gp064	Caulobacter virus phiCbK	GCA_000900535.1
AUE22768.1	001339	HIN-HTH	75	Ah1_00250	Aeromonas phage Ah1	GCA_002957415.1
AUE22835.1	001339	HIN-HTH	85	Ah1_00317	Aeromonas phage Ah1	GCA_002957415.1
QAX98484.1	001339	HIN-HTH	75	ASfcp2_146	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98549.1	001339	HIN-HTH	85	ASfcp2_214	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98392.1	001339	HIN-HTH	89	ASfcp2_47	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52847.1	001339	HIN-HTH	89	PX29p128	Aeromonas phage PX29	GCA_000920195.1
ADQ52946.1	001339	HIN-HTH	75	PX29p227	Aeromonas phage PX29	GCA_000920195.1
ADQ53013.1	001339	HIN-HTH	85	PX29p294	Aeromonas phage PX29	GCA_000920195.1
ADM79870.1	001339	HIN-HTH	75	phiAS5_ORF0027	Aeromonas phage phiAS5	GCA_000887715.1
ADM79936.1	001339	HIN-HTH	85	phiAS5_ORF0093	Aeromonas phage phiAS5	GCA_000887715.1
ADM80106.1	001339	HIN-HTH	75	phiAS5_ORF0263	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17794.1	001339	HIN-HTH	89	Aeh1ORF129c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17892.1	001339	HIN-HTH	75	Aeh1ORF231c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17964.1	001339	HIN-HTH	85	Aeh1ORF295c	Aeromonas virus Aeh1	GCA_000843245.1
AMO43470.1	001340	Cluster830_1clades	76	W270710_231	Cyanophage S-RIM44	GCA_002599145.1
AOO11710.1	001340	Cluster830_1clades	76	ES420910_233	Cyanophage S-RIM44	GCA_002599165.1
AOO11942.1	001340	Cluster830_1clades	76	Np050604_231	Cyanophage S-RIM44	GCA_002599185.1
AOO12176.1	001340	Cluster830_1clades	76	Np200711_234	Cyanophage S-RIM44	GCA_002599205.1
AOO12411.1	001340	Cluster830_1clades	76	Np420711_233	Cyanophage S-RIM44	GCA_002599225.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12643.1	001340	Cluster830_1clades	76	Sn080709_231	Cyanophage S-RIM44	GCA_002599245.1
AOO12876.1	001340	Cluster830_1clades	76	Sn130910_233	Cyanophage S-RIM44	GCA_002599265.1
AOO13109.1	001340	Cluster830_1clades	76	W2100709_232	Cyanophage S-RIM44	GCA_002599285.1
AAX44444.1	001340	Cluster830_1clades	88	PSSM2_066	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12208.1	001340	Cluster830_1clades	88	PRTG_00050	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADO99331.1	001340	Cluster830_1clades	76	Syn1_235	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30509.1	001340	Cluster830_1clades	65	Syn7803US37_32	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23000.1	001340	Cluster830_1clades	66	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50651.1	001340	Cluster830_1clades	66	-	Synechococcus phage S-B43	GCA_006869725.1
ARB13766.1	001341	Cluster831_1clades	84	Ccr10_gp236	Caulobacter phage Ccr10	GCA_002619445.1
ARB14111.1	001341	Cluster831_1clades	84	Ccr2_gp235	Caulobacter phage Ccr2	GCA_002619465.1
ARB14805.1	001341	Cluster831_1clades	84	Ccr29_gp249	Caulobacter phage Ccr29	GCA_002619485.1
ARB15145.1	001341	Cluster831_1clades	84	Ccr32_gp227	Caulobacter phage Ccr32	GCA_002619505.1
ARB15479.1	001341	Cluster831_1clades	84	Ccr34_gp237	Caulobacter phage Ccr34	GCA_002619525.1
ARB14453.1	001341	Cluster831_1clades	84	Ccr5_gp233	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68432.1	001341	Cluster831_1clades	63	CcrBL10_gp228	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88095.1	001341	Cluster831_1clades	61	CcrColossus_gp225	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68772.1	001341	Cluster831_1clades	42	CcrPW_gp233	Caulobacter phage CcrPW	GCA_003443275.1
AFU87761.1	001341	Cluster831_1clades	84	CcrKarma_gp244	Caulobacter virus Karma	GCA_000901575.1
AFU87408.1	001341	Cluster831_1clades	84	CcrMagneto_gp238	Caulobacter virus Magneto	GCA_000903095.1
AFU86718.1	001341	Cluster831_1clades	62	CcrRogue_gp236	Caulobacter virus Rogue	GCA_000900555.1
AFU88556.1	001341	Cluster831_1clades	84	CcrSwift_gp238	Caulobacter virus Swift	GCA_000899655.1
AFU87064.1	001341	Cluster831_1clades	84	CbK_gp232	Caulobacter virus phiCbK	GCA_000900535.1
AMO43074.1	001342	Cluster832_1clades	67	R1080702_065	Cyanophage S-RIM32	GCA_001754165.1
AMO43271.1	001342	Cluster832_1clades	66	W270710_026	Cyanophage S-RIM44	GCA_002599145.1
AOO11743.1	001342	Cluster832_1clades	66	Np050604_026	Cyanophage S-RIM44	GCA_002599185.1
AOO12444.1	001342	Cluster832_1clades	66	Sn080709_026	Cyanophage S-RIM44	GCA_002599245.1
AOO12909.1	001342	Cluster832_1clades	66	W2100709_026	Cyanophage S-RIM44	GCA_002599285.1
AGH07612.1	001342	Cluster832_1clades	69	CYVG_00169	Cyanophage S-SSM6a	GCA_002710385.1
AAX44442.1	001342	Cluster832_1clades	78	PSSM2_064	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12210.1	001342	Cluster832_1clades	78	PRTG_00052	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIX30652.1	001342	Cluster832_1clades	77	Syn7803US37_175	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54975.1	001342	Cluster832_1clades	76	b23_0369	Synechococcus phage B23	GCA_009745195.1
QGT54610.1	001342	Cluster832_1clades	76	b3_0375	Synechococcus phage B3	GCA_009745215.1
AOV59485.1	001342	Cluster832_1clades	66	S330809_024	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59247.1	001342	Cluster832_1clades	66	C440309_024	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59723.1	001342	Cluster832_1clades	66	N231010_024	Synechococcus phage S-CAM4	GCA_002922155.1
AOO14326.1	001343	Cluster833_1clades	58	Sn110110_132	Cyanophage S-RIM14	GCA_002599065.1
AOO14975.1	001343	Cluster833_1clades	58	W1230910_129	Cyanophage S-RIM14	GCA_002599125.1
AMO43430.1	001343	Cluster833_1clades	68	W270710_186	Cyanophage S-RIM44	GCA_002599145.1
AOO11674.1	001343	Cluster833_1clades	68	ES420910_193	Cyanophage S-RIM44	GCA_002599165.1
AOO11902.1	001343	Cluster833_1clades	68	Np050604_186	Cyanophage S-RIM44	GCA_002599185.1
AOO12140.1	001343	Cluster833_1clades	68	Np200711_194	Cyanophage S-RIM44	GCA_002599205.1
AOO12375.1	001343	Cluster833_1clades	68	Np420711_193	Cyanophage S-RIM44	GCA_002599225.1
AOO12603.1	001343	Cluster833_1clades	68	Sn080709_186	Cyanophage S-RIM44	GCA_002599245.1
AOO12840.1	001343	Cluster833_1clades	68	Sn130910_193	Cyanophage S-RIM44	GCA_002599265.1
AOO13069.1	001343	Cluster833_1clades	68	W2100709_187	Cyanophage S-RIM44	GCA_002599285.1
ADO99289.1	001343	Cluster833_1clades	78	Syn1_188	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59477.1	001343	Cluster833_1clades	58	S330809_016	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59239.1	001343	Cluster833_1clades	58	C440309_016	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59715.1	001343	Cluster833_1clades	58	N231010_016	Synechococcus phage S-CAM4	GCA_002922155.1
AOO15045.1	001344	Cluster834_1clades	75	W1230910_200	Cyanophage S-RIM14	GCA_002599125.1
AMO43456.1	001344	Cluster834_1clades	73	W270710_217	Cyanophage S-RIM44	GCA_002599145.1
AOO11928.1	001344	Cluster834_1clades	73	Np050604_217	Cyanophage S-RIM44	GCA_002599185.1
AOO12629.1	001344	Cluster834_1clades	73	Sn080709_217	Cyanophage S-RIM44	GCA_002599245.1
AOO13095.1	001344	Cluster834_1clades	73	W2100709_218	Cyanophage S-RIM44	GCA_002599285.1
ADO99317.1	001344	Cluster834_1clades	73	Syn1_221	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30720.1	001344	Cluster834_1clades	76	Syn7803US37_243	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76269.1	001344	Cluster834_1clades	74	PBI_BELLAMY_233	Synechococcus phage Bellamy	GCA_002627525.1
QCW22955.1	001344	Cluster834_1clades	69	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50670.1	001344	Cluster834_1clades	69	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59674.1	001344	Cluster834_1clades	72	S330809_213	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59436.1	001344	Cluster834_1clades	72	C440309_213	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59911.1	001344	Cluster834_1clades	72	N231010_212	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70237.1	001344	Cluster834_1clades	76	SynMITS9220M01_231	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27545.1	001345	Cluster835_1clades	73	PTIM40_118	Cyanophage P-TIM40	GCA_001470935.1
AMO43198.1	001345	Cluster835_1clades	48	R1080702_189	Cyanophage S-RIM32	GCA_001754165.1
AMO43427.1	001345	Cluster835_1clades	75	W270710_183	Cyanophage S-RIM44	GCA_002599145.1
AOO11671.1	001345	Cluster835_1clades	75	ES420910_190	Cyanophage S-RIM44	GCA_002599165.1
AOO11899.1	001345	Cluster835_1clades	75	Np050604_183	Cyanophage S-RIM44	GCA_002599185.1
AOO12137.1	001345	Cluster835_1clades	75	Np200711_191	Cyanophage S-RIM44	GCA_002599205.1
AOO12372.1	001345	Cluster835_1clades	75	Np420711_190	Cyanophage S-RIM44	GCA_002599225.1
AOO12600.1	001345	Cluster835_1clades	75	Sn080709_183	Cyanophage S-RIM44	GCA_002599245.1
AOO12837.1	001345	Cluster835_1clades	75	Sn130910_190	Cyanophage S-RIM44	GCA_002599265.1
AOO13066.1	001345	Cluster835_1clades	75	W2100709_184	Cyanophage S-RIM44	GCA_002599285.1
AGG54410.1	001345	Cluster835_1clades	56	CYWG_00126	Cyanophage S-SSM6b	GCA_002710425.1
ADO99286.1	001345	Cluster835_1clades	75	Syn1_185	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30734.1	001345	Cluster835_1clades	50	Syn7803US37_257	Synechococcus phage ACG-2014f	GCA_002594065.1
QJT70185.1	001345	Cluster835_1clades	50	SynMITS9220M01_177	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH57005.1	001346	CP12	75	CPXG_00202	Cyanophage P-RSM6	GCA_000906155.1
AJK27450.1	001346	CP12	75	PTIM40_23	Cyanophage P-TIM40	GCA_001470935.1
AOO14208.1	001346	CP12	75	Sn110110_014	Cyanophage S-RIM14	GCA_002599065.1
AOO14860.1	001346	CP12	75	W1230910_014	Cyanophage S-RIM14	GCA_002599125.1
AGH07641.1	001346	CP12	75	CYVG_00198	Cyanophage S-SSM6a	GCA_002710385.1
AGG54357.1	001346	CP12	75	CYWG_00073	Cyanophage S-SSM6b	GCA_002710425.1
AGH26226.1	001346	CP12	70	CPMG_00125	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93425.1	001346	CP12	75	AVU42_gp083	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76062.1	001346	CP12	75	PBI_BELLAMY_15	Synechococcus phage Bellamy	GCA_002627525.1
AOV59472.1	001346	CP12	75	S330809_011	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59234.1	001346	CP12	75	C440309_011	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59710.1	001346	CP12	75	N231010_011	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70438.1	001346	CP12	70	HOU04_gp039	Synechococcus phage S-T4	GCA_003443335.1
QJT70030.1	001346	CP12	72	SynMITS9220M01_014	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AOO14300.1	001347	Cluster837_1clades	72	Sn110110_106	Cyanophage S-RIM14	GCA_002599065.1
AOO14949.1	001347	Cluster837_1clades	72	W1230910_103	Cyanophage S-RIM14	GCA_002599125.1
AMO43132.1	001347	Cluster837_1clades	70	R1080702_123	Cyanophage S-RIM32	GCA_001754165.1
AMO43357.1	001347	Cluster837_1clades	73	W270710_113	Cyanophage S-RIM44	GCA_002599145.1
AOO11601.1	001347	Cluster837_1clades	73	ES420910_120	Cyanophage S-RIM44	GCA_002599165.1
AOO11829.1	001347	Cluster837_1clades	73	Np050604_113	Cyanophage S-RIM44	GCA_002599185.1
AOO12066.1	001347	Cluster837_1clades	73	Np200711_120	Cyanophage S-RIM44	GCA_002599205.1
AOO12302.1	001347	Cluster837_1clades	73	Np420711_120	Cyanophage S-RIM44	GCA_002599225.1
AOO12530.1	001347	Cluster837_1clades	73	Sn080709_113	Cyanophage S-RIM44	GCA_002599245.1
AOO12767.1	001347	Cluster837_1clades	73	Sn130910_120	Cyanophage S-RIM44	GCA_002599265.1
AOO12996.1	001347	Cluster837_1clades	73	W2100709_114	Cyanophage S-RIM44	GCA_002599285.1
ADO99215.1	001347	Cluster837_1clades	73	Syn1_114	Prochlorococcus phage Syn1	GCA_000892495.1
QCW23039.1	001347	Cluster837_1clades	72	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50726.1	001347	Cluster837_1clades	72	-	Synechococcus phage S-B43	GCA_006869725.1
AIT14212.1	001348	Cluster838_1clades	70	PBI_121Q_322	Escherichia phage 121Q	GCA_000926855.1
AIT14213.1	001348	Cluster838_1clades	71	PBI_121Q_323	Escherichia phage 121Q	GCA_000926855.1
QAY00725.1	001348	Cluster838_1clades	70	Ecwhy1_450	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00726.1	001348	Cluster838_1clades	70	Ecwhy1_451	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34907.1	001348	Cluster838_1clades	70	ACQ29_gp227	Escherichia phage PBECO4	GCA_001041035.1
BBM61885.1	001348	Cluster838_1clades	70	EO157G_2960	Escherichia phage SP27	GCA_008033345.1
BBM61886.1	001348	Cluster838_1clades	70	EO157G_2970	Escherichia phage SP27	GCA_008033345.1
AXC37012.1	001348	Cluster838_1clades	70	-	Escherichia phage UB	GCA_003341455.1
QBO62098.1	001348	Cluster838_1clades	70	G17_00609	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62099.1	001348	Cluster838_1clades	71	G17_00610	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14108.1	001348	Cluster838_1clades	70	vBEcoMphAPEC6_gp485c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14109.1	001348	Cluster838_1clades	71	vBEcoMphAPEC6_gp486c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80195.1	001348	Cluster838_1clades	71	PSLUR01_00218	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80196.1	001348	Cluster838_1clades	70	PSLUR01_00219	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMO43107.1	001349	Cluster839_1clades	64	R1080702_098	Cyanophage S-RIM32	GCA_001754165.1
AMO43334.1	001349	Cluster839_1clades	48	W270710_090	Cyanophage S-RIM44	GCA_002599145.1
AOO11567.1	001349	Cluster839_1clades	48	ES420910_086	Cyanophage S-RIM44	GCA_002599165.1
AOO11806.1	001349	Cluster839_1clades	48	Np050604_090	Cyanophage S-RIM44	GCA_002599185.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12032.1	001349	Cluster839_1clades	48	Np200711_086	Cyanophage S-RIM44	GCA_002599205.1
AOO12268.1	001349	Cluster839_1clades	48	Np420711_086	Cyanophage S-RIM44	GCA_002599225.1
AOO12507.1	001349	Cluster839_1clades	48	Sn080709_090	Cyanophage S-RIM44	GCA_002599245.1
AOO12733.1	001349	Cluster839_1clades	48	Sn130910_086	Cyanophage S-RIM44	GCA_002599265.1
AOO12973.1	001349	Cluster839_1clades	48	W2100709_091	Cyanophage S-RIM44	GCA_002599285.1
ADO99192.1	001349	Cluster839_1clades	48	Syn1_091	Prochlorococcus phage Syn1	GCA_000892495.1
QDH50591.1	001349	Cluster839_1clades	71	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59547.1	001349	Cluster839_1clades	63	S330809_086	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59309.1	001349	Cluster839_1clades	63	C440309_086	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59785.1	001349	Cluster839_1clades	63	N231010_086	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13572.1	001350	Cluster840_1clades	59	Ccr10_gp044	Caulobacter phage Ccr10	GCA_002619445.1
ARB13918.1	001350	Cluster840_1clades	59	Ccr2_gp043	Caulobacter phage Ccr2	GCA_002619465.1
ARB14607.1	001350	Cluster840_1clades	59	Ccr29_gp050	Caulobacter phage Ccr29	GCA_002619485.1
ARB14963.1	001350	Cluster840_1clades	48	Ccr32_gp044	Caulobacter phage Ccr32	GCA_002619505.1
ARB15294.1	001350	Cluster840_1clades	59	Ccr34_gp045	Caulobacter phage Ccr34	GCA_002619525.1
ARB14261.1	001350	Cluster840_1clades	59	Ccr5_gp043	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68247.1	001350	Cluster840_1clades	60	CcrBL10_gp043	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87912.1	001350	Cluster840_1clades	65	CcrColossus_gp042	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68584.1	001350	Cluster840_1clades	66	CcrPW_gp045	Caulobacter phage CcrPW	GCA_003443275.1
AFU87562.1	001350	Cluster840_1clades	59	CcrKarma_gp045	Caulobacter virus Karma	GCA_000901575.1
AFU87212.1	001350	Cluster840_1clades	59	CcrMagneto_gp042	Caulobacter virus Magneto	GCA_000903095.1
AFU86529.1	001350	Cluster840_1clades	60	CcrRogue_gp047	Caulobacter virus Rogue	GCA_000900555.1
AFU88360.1	001350	Cluster840_1clades	59	CcrSwift_gp042	Caulobacter virus Swift	GCA_000899655.1
AFU86876.1	001350	Cluster840_1clades	59	CbK_gp044	Caulobacter virus phiCbK	GCA_000900535.1
ARB13746.1	001351	Cluster841_1clades	65	Ccr10_gp216c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14091.1	001351	Cluster841_1clades	65	Ccr2_gp215c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14780.1	001351	Cluster841_1clades	65	Ccr29_gp224	Caulobacter phage Ccr29	GCA_002619485.1
ARB15124.1	001351	Cluster841_1clades	65	Ccr32_gp206	Caulobacter phage Ccr32	GCA_002619505.1
ARB15458.1	001351	Cluster841_1clades	65	Ccr34_gp216	Caulobacter phage Ccr34	GCA_002619525.1
ARB14433.1	001351	Cluster841_1clades	65	Ccr5_gp213c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68413.1	001351	Cluster841_1clades	65	CcrBL10_gp209c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88150.1	001351	Cluster841_1clades	65	CcrColossus_gp280	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68826.1	001351	Cluster841_1clades	65	CcrPW_gp287	Caulobacter phage CcrPW	GCA_003443275.1
AFU87740.1	001351	Cluster841_1clades	65	CcrKarma_gp223	Caulobacter virus Karma	GCA_000901575.1
AFU87388.1	001351	Cluster841_1clades	65	CcrMagneto_gp218	Caulobacter virus Magneto	GCA_000903095.1
AFU86700.1	001351	Cluster841_1clades	65	CcrRogue_gp218	Caulobacter virus Rogue	GCA_000900555.1
AFU88536.1	001351	Cluster841_1clades	65	CcrSwift_gp218	Caulobacter virus Swift	GCA_000899655.1
AFU87043.1	001351	Cluster841_1clades	65	CbK_gp211	Caulobacter virus phiCbK	GCA_000900535.1
AIT14182.1	001352	Cluster842_1clades	65	PBI_121Q_292	Escherichia phage 121Q	GCA_000926855.1
QAY00755.1	001352	Cluster842_1clades	65	Ecwhy1_481	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34934.1	001352	Cluster842_1clades	62	ACQ29_gp254	Escherichia phage PBECO4	GCA_001041035.1
BBM61857.1	001352	Cluster842_1clades	65	EO157G_2680	Escherichia phage SP27	GCA_008033345.1
AXC37037.1	001352	Cluster842_1clades	65	-	Escherichia phage UB	GCA_003341455.1
QBO61523.1	001352	Cluster842_1clades	65	G17_00027	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62129.1	001352	Cluster842_1clades	65	G17_00640	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14137.1	001352	Cluster842_1clades	65	vBEcoMphAPEC6_gp514c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80167.1	001352	Cluster842_1clades	65	PSLUR01_00190	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18682.1	001352	Cluster842_1clades	63	7t3_0161	Salmonella phage 7t3	GCA_006083215.1
AZU97957.1	001352	Cluster842_1clades	63	CPT_Munch_013	Salmonella phage Munch	GCA_004015485.1
QIG63020.1	001352	Cluster842_1clades	63	SEPL_407	Salmonella phage SE_PL	GCA_011067555.1
SOK58827.1	001352	Cluster842_1clades	65	g019	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58294.1	001352	Cluster842_1clades	65	g017	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13543.1	001353	Cluster843_1clades	60	Ccr10_gp015	Caulobacter phage Ccr10	GCA_002619445.1
ARB13868.1	001353	Cluster843_1clades	60	Ccr10_gp338	Caulobacter phage Ccr10	GCA_002619445.1
ARB14572.1	001353	Cluster843_1clades	60	Ccr29_gp015	Caulobacter phage Ccr29	GCA_002619485.1
ARB14578.1	001353	Cluster843_1clades	60	Ccr29_gp021	Caulobacter phage Ccr29	GCA_002619485.1
ARB14907.1	001353	Cluster843_1clades	60	Ccr29_gp351	Caulobacter phage Ccr29	GCA_002619485.1
ARB14913.1	001353	Cluster843_1clades	60	Ccr29_gp357	Caulobacter phage Ccr29	GCA_002619485.1
ARB14933.1	001353	Cluster843_1clades	60	Ccr32_gp014	Caulobacter phage Ccr32	GCA_002619505.1
ARB15244.1	001353	Cluster843_1clades	60	Ccr32_gp326	Caulobacter phage Ccr32	GCA_002619505.1
ARB15264.1	001353	Cluster843_1clades	60	Ccr34_gp015	Caulobacter phage Ccr34	GCA_002619525.1
ARB15578.1	001353	Cluster843_1clades	60	Ccr34_gp336	Caulobacter phage Ccr34	GCA_002619525.1
ARB14232.1	001353	Cluster843_1clades	61	Ccr5_gp014	Caulobacter phage Ccr5	GCA_002619545.1
ARB14552.1	001353	Cluster843_1clades	61	Ccr5_gp332	Caulobacter phage Ccr5	GCA_002619545.1
AFU86846.1	001353	Cluster843_1clades	60	CbK_gp014	Caulobacter virus phiCbK	GCA_000900535.1
AFU87164.1	001353	Cluster843_1clades	60	CbK_gp332	Caulobacter virus phiCbK	GCA_000900535.1
AOO14331.1	001354	Cluster844_1clades	47	Sn110110_137	Cyanophage S-RIM14	GCA_002599065.1
AOO14980.1	001354	Cluster844_1clades	47	W1230910_134	Cyanophage S-RIM14	GCA_002599125.1
AMO43267.1	001354	Cluster844_1clades	49	W270710_022	Cyanophage S-RIM44	GCA_002599145.1
AOO11503.1	001354	Cluster844_1clades	49	ES420910_021	Cyanophage S-RIM44	GCA_002599165.1
AOO11739.1	001354	Cluster844_1clades	49	Np050604_022	Cyanophage S-RIM44	GCA_002599185.1
AOO11968.1	001354	Cluster844_1clades	49	Np200711_021	Cyanophage S-RIM44	GCA_002599205.1
AOO12204.1	001354	Cluster844_1clades	49	Np420711_021	Cyanophage S-RIM44	GCA_002599225.1
AOO12440.1	001354	Cluster844_1clades	49	Sn080709_022	Cyanophage S-RIM44	GCA_002599245.1
AOO12669.1	001354	Cluster844_1clades	49	Sn130910_021	Cyanophage S-RIM44	GCA_002599265.1
AOO12905.1	001354	Cluster844_1clades	49	W2100709_022	Cyanophage S-RIM44	GCA_002599285.1
ADO99124.1	001354	Cluster844_1clades	49	Syn1_022	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59480.1	001354	Cluster844_1clades	49	S330809_019	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59242.1	001354	Cluster844_1clades	49	C440309_019	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59718.1	001354	Cluster844_1clades	49	N231010_019	Synechococcus phage S-CAM4	GCA_002922155.1
AOO14261.1	001355	Cluster845_1clades	44	Sn110110_067	Cyanophage S-RIM14	GCA_002599065.1
AOO14910.1	001355	Cluster845_1clades	44	W1230910_064	Cyanophage S-RIM14	GCA_002599125.1
AMO43308.1	001355	Cluster845_1clades	47	W270710_064	Cyanophage S-RIM44	GCA_002599145.1
AOO11542.1	001355	Cluster845_1clades	44	ES420910_061	Cyanophage S-RIM44	GCA_002599165.1
AOO11780.1	001355	Cluster845_1clades	47	Np050604_064	Cyanophage S-RIM44	GCA_002599185.1
AOO12007.1	001355	Cluster845_1clades	44	Np200711_061	Cyanophage S-RIM44	GCA_002599205.1
AOO12243.1	001355	Cluster845_1clades	44	Np420711_061	Cyanophage S-RIM44	GCA_002599225.1
AOO12481.1	001355	Cluster845_1clades	47	Sn080709_064	Cyanophage S-RIM44	GCA_002599245.1
AOO12708.1	001355	Cluster845_1clades	44	Sn130910_061	Cyanophage S-RIM44	GCA_002599265.1
AOO12946.1	001355	Cluster845_1clades	47	W2100709_064	Cyanophage S-RIM44	GCA_002599285.1
ADO99162.1	001355	Cluster845_1clades	47	Syn1_061	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59513.1	001355	Cluster845_1clades	46	S330809_052	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59275.1	001355	Cluster845_1clades	46	C440309_052	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59751.1	001355	Cluster845_1clades	46	N231010_052	Synechococcus phage S-CAM4	GCA_002922155.1
AMR59716.1	001356	Cluster846_1clades	47	SEGD1_067	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49718.1	001356	Cluster846_1clades	45	MACHINA_80	Erwinia phage Machina	GCA_002758035.1
AXF51211.1	001356	Cluster846_1clades	47	WELLINGTON_81	Erwinia phage Wellington	GCA_003344985.1
AFQ96798.1	001356	Cluster846_1clades	47	G173_gp253	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48097.1	001356	Cluster846_1clades	47	ASESINO_84	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48371.1	001356	Cluster846_1clades	46	CAITLIN_76	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48644.1	001356	Cluster846_1clades	46	CHRISDB_82	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49163.1	001356	Cluster846_1clades	45	HUXLEY_81	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49433.1	001356	Cluster846_1clades	47	KWAN_81	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49991.1	001356	Cluster846_1clades	45	PARSHIK_82	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50511.1	001356	Cluster846_1clades	47	STRATTON_86	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85907.1	001356	Cluster846_1clades	47	ACEC001_0690	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09034.1	001356	Cluster846_1clades	47	MLDJOKPK_00096	Salmonella phage SPAsTU	GCA_003183805.1
AEP83899.1	001356	Cluster846_1clades	47	SPN3US_0066	Salmonella phage SPN3US	GCA_001042275.1
AMO43039.1	001357	Cluster847_1clades	4021	R1080702_030	Cyanophage S-RIM32	GCA_001754165.1
AMO43279.1	001357	Cluster847_1clades	4017	W270710_035	Cyanophage S-RIM44	GCA_002599145.1
AOO11513.1	001357	Cluster847_1clades	4017	ES420910_032	Cyanophage S-RIM44	GCA_002599165.1
AOO11751.1	001357	Cluster847_1clades	4017	Np050604_035	Cyanophage S-RIM44	GCA_002599185.1
AOO11978.1	001357	Cluster847_1clades	4017	Np200711_032	Cyanophage S-RIM44	GCA_002599205.1
AOO12214.1	001357	Cluster847_1clades	4017	Np420711_032	Cyanophage S-RIM44	GCA_002599225.1
AOO12452.1	001357	Cluster847_1clades	4017	Sn080709_035	Cyanophage S-RIM44	GCA_002599245.1
AOO12679.1	001357	Cluster847_1clades	4017	Sn130910_032	Cyanophage S-RIM44	GCA_002599265.1
AOO12917.1	001357	Cluster847_1clades	4017	W2100709_035	Cyanophage S-RIM44	GCA_002599285.1
ADO99133.1	001357	Cluster847_1clades	4017	Syn1_032	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59489.1	001357	Cluster847_1clades	4057	S330809_028	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59251.1	001357	Cluster847_1clades	4057	C440309_028	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59727.1	001357	Cluster847_1clades	4057	N231010_028	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43221.1	001358	Cluster848_1clades	1219	R1080702_216	Cyanophage S-RIM32	GCA_001754165.1
AMO43454.1	001358	Cluster848_1clades	1222	W270710_215	Cyanophage S-RIM44	GCA_002599145.1
AOO11695.1	001358	Cluster848_1clades	1177	ES420910_218	Cyanophage S-RIM44	GCA_002599165.1
AOO11926.1	001358	Cluster848_1clades	1222	Np050604_215	Cyanophage S-RIM44	GCA_002599185.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12161.1	001358	Cluster848_1clades	1177	Np200711_219	Cyanophage S-RIM44	GCA_002599205.1
AOO12396.1	001358	Cluster848_1clades	1177	Np420711_218	Cyanophage S-RIM44	GCA_002599225.1
AOO12627.1	001358	Cluster848_1clades	1222	Sn080709_215	Cyanophage S-RIM44	GCA_002599245.1
AOO12861.1	001358	Cluster848_1clades	1177	Sn130910_218	Cyanophage S-RIM44	GCA_002599265.1
AOO13093.1	001358	Cluster848_1clades	1222	W2100709_216	Cyanophage S-RIM44	GCA_002599285.1
ADO99314.1	001358	Cluster848_1clades	1222	Syn1_219	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59652.1	001358	Cluster848_1clades	1252	S330809_191	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59414.1	001358	Cluster848_1clades	1252	C440309_191	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59890.1	001358	Cluster848_1clades	1370	N231010_191	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43045.1	001359	Collar	1054	R1080702_036	Cyanophage S-RIM32	GCA_001754165.1
AMO43285.1	001359	Collar	1057	W270710_041	Cyanophage S-RIM44	GCA_002599145.1
AOO11519.1	001359	Collar	1057	ES420910_038	Cyanophage S-RIM44	GCA_002599165.1
AOO11757.1	001359	Collar	1057	Np050604_041	Cyanophage S-RIM44	GCA_002599185.1
AOO11984.1	001359	Collar	1057	Np200711_038	Cyanophage S-RIM44	GCA_002599205.1
AOO12220.1	001359	Collar	1057	Np420711_038	Cyanophage S-RIM44	GCA_002599225.1
AOO12458.1	001359	Collar	1057	Sn080709_041	Cyanophage S-RIM44	GCA_002599245.1
AOO12685.1	001359	Collar	1057	Sn130910_038	Cyanophage S-RIM44	GCA_002599265.1
AOO12923.1	001359	Collar	1057	W2100709_041	Cyanophage S-RIM44	GCA_002599285.1
ADO99139.1	001359	Collar	1057	Syn1_038	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59494.1	001359	Collar	981	S330809_033	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59256.1	001359	Collar	981	C440309_033	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59732.1	001359	Collar	981	N231010_033	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43028.1	001360	Calx-beta	979	R1080702_013	Cyanophage S-RIM32	GCA_001754165.1
AMO43259.1	001360	Calx-beta	973	W270710_014	Cyanophage S-RIM44	GCA_002599145.1
AOO11496.1	001360	Calx-beta	973	ES420910_014	Cyanophage S-RIM44	GCA_002599165.1
AOO11731.1	001360	Calx-beta	973	Np050604_014	Cyanophage S-RIM44	GCA_002599185.1
AOO11961.1	001360	Calx-beta	973	Np200711_014	Cyanophage S-RIM44	GCA_002599205.1
AOO12197.1	001360	Calx-beta	973	Np420711_014	Cyanophage S-RIM44	GCA_002599225.1
AOO12432.1	001360	Calx-beta	973	Sn080709_014	Cyanophage S-RIM44	GCA_002599245.1
AOO12662.1	001360	Calx-beta	973	Sn130910_014	Cyanophage S-RIM44	GCA_002599265.1
AOO12897.1	001360	Calx-beta	973	W2100709_014	Cyanophage S-RIM44	GCA_002599285.1
ADO99117.1	001360	Calx-beta	973	Syn1_015	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59473.1	001360	Calx-beta	945	S330809_012	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59235.1	001360	Calx-beta	945	C440309_012	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59711.1	001360	Calx-beta	945	N231010_012	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43040.1	001361	Collar	440	R1080702_031	Cyanophage S-RIM32	GCA_001754165.1
AMO43280.1	001361	Collar	567	W270710_036	Cyanophage S-RIM44	GCA_002599145.1
AOO11514.1	001361	Collar	567	ES420910_033	Cyanophage S-RIM44	GCA_002599165.1
AOO11752.1	001361	Collar	567	Np050604_036	Cyanophage S-RIM44	GCA_002599185.1
AOO11979.1	001361	Collar	567	Np200711_033	Cyanophage S-RIM44	GCA_002599205.1
AOO12215.1	001361	Collar	567	Np420711_033	Cyanophage S-RIM44	GCA_002599225.1
AOO12453.1	001361	Collar	567	Sn080709_036	Cyanophage S-RIM44	GCA_002599245.1
AOO12680.1	001361	Collar	567	Sn130910_033	Cyanophage S-RIM44	GCA_002599265.1
AOO12918.1	001361	Collar	567	W2100709_036	Cyanophage S-RIM44	GCA_002599285.1
ADO99134.1	001361	Collar	567	Syn1_033	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59490.1	001361	Collar	432	S330809_029	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59252.1	001361	Collar	423	C440309_029	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59728.1	001361	Collar	432	N231010_029	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67234.1	001362	Cluster853_1clades	303	AD1_190	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67235.1	001362	Cluster853_1clades	153	AD1_191	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79984.1	001362	Cluster853_1clades	188	JA11_179	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66582.1	001362	Cluster853_1clades	188	JA13_179	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66907.1	001362	Cluster853_1clades	188	JA29_181	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67553.1	001362	Cluster853_1clades	188	JA33_179	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08465.1	001362	Cluster853_1clades	243	Alexandra_200	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08608.1	001362	Cluster853_1clades	201	Alexandra_201	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58827.1	001362	Cluster853_1clades	331	Y3_187	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58834.1	001362	Cluster853_1clades	351	Y3_194	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58835.1	001362	Cluster853_1clades	200	Y3_195	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58846.1	001362	Cluster853_1clades	256	Y3_206	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28666.1	001362	Cluster853_1clades	545	YOLOSWAG_187	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01529.1	001363	IG	264	-	Aeromonas phage 65.2	GCA_002618145.1
APU01532.1	001363	IG	273	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29037.1	001363	IG	255	AP1_0330	Aeromonas phage AP1	GCA_014183365.1
ATI17371.1	001363	IG	255	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00223.1	001363	IG	255	HWB28_gp329	Aeromonas phage AS-zj	GCA_002627665.1
QAX97812.1	001363	IG	255	ASswx1_168	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01339.1	001363	IG	258	ASwh1_278	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39435.1	001363	IG	255	CC2_368	Aeromonas phage CC2	GCA_000903495.1
ADQ53151.1	001363	IG	264	65p143	Aeromonas virus 65	GCA_000893255.1
ADQ53154.1	001363	IG	273	65p146	Aeromonas virus 65	GCA_000893255.1
AIA64866.1	001363	IG	272	S13_067	Cronobacter phage S13	GCA_001503575.1
ARM70740.1	001363	IG	471	phiC120_c33	Escherichia phage phiC120	GCA_002621185.1
QHJ79074.1	001363	IG	265	-	Myoviridae sp.	GCA_012593985.1
SBV38375.1	001364	Cluster856_1clades	354	BN7874_204	Phage NCTB	GCA_900092385.1
AAQ64191.1	001364	Cluster856_1clades	308	KVP40.0120	Vibrio phage KVP40	GCA_000843785.1
QIW90834.1	001364	Cluster856_1clades	308	GCAPEGMB_00519	Vibrio phage V07	GCA_012361095.1
QIW90915.1	001364	Cluster856_1clades	308	COHAPHLL_00052	Vibrio phage V09	GCA_012361135.1
QHJ74303.1	001364	Cluster856_1clades	308	VH12019_00384	Vibrio phage VH1_2019	GCA_009931825.1
AGB06797.1	001364	Cluster856_1clades	310	CF80_gp010	Vibrio phage VH7D	GCA_000914495.1
QBX05969.1	001364	Cluster856_1clades	310	ValB1HC_015	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60981.1	001364	Cluster856_1clades	310	AVU32_gp140	Vibrio phage ValKK3	GCA_001501635.1
AGN30170.2	001364	Cluster856_1clades	310	VPFG_00168	Vibrio phage nt-1	GCA_000910195.2
ALP47016.1	001364	Cluster856_1clades	310	phiGrn1_0232	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47397.1	001364	Cluster856_1clades	310	phiST2_0367	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54594.1	001364	Cluster856_1clades	310	vBValMR10Z_53	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37350.1	001364	Cluster856_1clades	308	pp2_117	Vibriophage phi-pp2	GCA_002630725.1
AMO43272.1	001365	AIRS+AIRS_C	311	W270710_027	Cyanophage S-RIM44	GCA_002599145.1
AOO11506.1	001365	AIRS+AIRS_C	311	ES420910_024	Cyanophage S-RIM44	GCA_002599165.1
AOO11744.1	001365	AIRS+AIRS_C	311	Np050604_027	Cyanophage S-RIM44	GCA_002599185.1
AOO11971.1	001365	AIRS+AIRS_C	311	Np200711_024	Cyanophage S-RIM44	GCA_002599205.1
AOO12207.1	001365	AIRS+AIRS_C	311	Np420711_024	Cyanophage S-RIM44	GCA_002599225.1
AOO12445.1	001365	AIRS+AIRS_C	311	Sn080709_027	Cyanophage S-RIM44	GCA_002599245.1
AOO12672.1	001365	AIRS+AIRS_C	311	Sn130910_024	Cyanophage S-RIM44	GCA_002599265.1
AOO12910.1	001365	AIRS+AIRS_C	311	W2100709_027	Cyanophage S-RIM44	GCA_002599285.1
AAX44554.1	001365	AIRS+AIRS_C	331	PSSM2_176	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12417.1	001365	AIRS+AIRS_C	331	PRTG_00266	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59681.1	001365	AIRS+AIRS_C	309	S330809_220	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59443.1	001365	AIRS+AIRS_C	309	C440309_220	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59918.1	001365	AIRS+AIRS_C	309	N231010_219	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43047.1	001366	Phage_tail_APC	312	R1080702_038	Cyanophage S-RIM32	GCA_001754165.1
AMO43287.1	001366	Phage_tail_APC	293	W270710_043	Cyanophage S-RIM44	GCA_002599145.1
AOO11521.1	001366	Phage_tail_APC	293	ES420910_040	Cyanophage S-RIM44	GCA_002599165.1
AOO11759.1	001366	Phage_tail_APC	293	Np050604_043	Cyanophage S-RIM44	GCA_002599185.1
AOO11986.1	001366	Phage_tail_APC	293	Np200711_040	Cyanophage S-RIM44	GCA_002599205.1
AOO12222.1	001366	Phage_tail_APC	293	Np420711_040	Cyanophage S-RIM44	GCA_002599225.1
AOO12460.1	001366	Phage_tail_APC	293	Sn080709_043	Cyanophage S-RIM44	GCA_002599245.1
AOO12687.1	001366	Phage_tail_APC	293	Sn130910_040	Cyanophage S-RIM44	GCA_002599265.1
AOO12925.1	001366	Phage_tail_APC	293	W2100709_043	Cyanophage S-RIM44	GCA_002599285.1
ADO99141.1	001366	Phage_tail_APC	315	Syn1_040	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59496.1	001366	Phage_tail_APC	315	S330809_035	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59258.1	001366	Phage_tail_APC	315	C440309_035	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59734.1	001366	Phage_tail_APC	315	N231010_035	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43041.1	001367	Collar	298	R1080702_032	Cyanophage S-RIM32	GCA_001754165.1
AMO43281.1	001367	Collar	294	W270710_037	Cyanophage S-RIM44	GCA_002599145.1
AOO11515.1	001367	Collar	294	ES420910_034	Cyanophage S-RIM44	GCA_002599165.1
AOO11753.1	001367	Collar	294	Np050604_037	Cyanophage S-RIM44	GCA_002599185.1
AOO11980.1	001367	Collar	294	Np200711_034	Cyanophage S-RIM44	GCA_002599205.1
AOO12216.1	001367	Collar	294	Np420711_034	Cyanophage S-RIM44	GCA_002599225.1
AOO12454.1	001367	Collar	294	Sn080709_037	Cyanophage S-RIM44	GCA_002599245.1
AOO12681.1	001367	Collar	294	Sn130910_034	Cyanophage S-RIM44	GCA_002599265.1
AOO12919.1	001367	Collar	294	W2100709_037	Cyanophage S-RIM44	GCA_002599285.1
ADO99135.1	001367	Collar	294	Syn1_034	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59491.1	001367	Collar	295	S330809_030	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59253.1	001367	Collar	295	C440309_030	Synechococcus phage S-CAM4	GCA_002922145.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59729.1	001367	Collar	295	N231010_030	Synechococcus phage S-CAM4	GCA_002922155.1
AMR59720.1	001368	ZNR	286	SEGD1_071	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49719.1	001368	ZNR	238	MACHINA_81	Erwinia phage Machina	GCA_002758035.1
AFQ96802.1	001368	ZNR	292	G173_gp257	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48101.1	001368	ZNR	294	ASESINO_88	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48373.1	001368	ZNR	240	CAITLIN_78	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48646.1	001368	ZNR	242	CHRISDB_84	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49164.1	001368	ZNR	238	HUXLEY_82	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49992.1	001368	ZNR	238	PARSHIK_83	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50515.1	001368	ZNR	292	STRATTON_90	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85911.1	001368	ZNR	286	ACEC001_0730	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20783.1	001368	ZNR	286	-	Salmonella phage JN03	GCA_014319805.1
AWN09030.1	001368	ZNR	286	MLDJOKPK_00091	Salmonella phage SPAsTU	GCA_003183805.1
AEP83903.1	001368	ZNR	286	SPN3US_0070	Salmonella phage SPN3US	GCA_001042275.1
AGH07577.1	001369	Glyco_transf_25	269	CYVG_00133	Cyanophage S-SSM6a	GCA_002710385.1
AAX44648.1	001369	Glyco_transf_25	263	PSSM2_271	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12323.1	001369	Glyco_transf_25	263	PRTG_00170	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93534.1	001369	Glyco_transf_25	265	AVU42_gp197	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30712.1	001369	Glyco_transf_25	292	Syn7803US37_235	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54965.1	001369	Glyco_transf_25	265	b23_0359	Synechococcus phage B23	GCA_009745195.1
QGT54600.1	001369	Glyco_transf_25	265	b3_0365	Synechococcus phage B3	GCA_009745215.1
ASR76264.1	001369	Glyco_transf_25	278	PBI_BELLAMY_228	Synechococcus phage Bellamy	GCA_002627525.1
QCW22960.1	001369	Glyco_transf_25	266	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50570.1	001369	Glyco_transf_25	137	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50675.1	001369	Glyco_transf_25	266	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70503.1	001369	Glyco_transf_25	262	HOU04_gp104	Synechococcus phage S-T4	GCA_003443335.1
QJT70218.1	001369	Glyco_transf_25	276	SynMITS9220M01_212	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMR59883.1	001370	Cluster863_1clades	255	SEGD1_236	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49882.1	001370	Cluster863_1clades	291	MACHINA_244	Erwinia phage Machina	GCA_002758035.1
AFQ96696.1	001370	Cluster863_1clades	265	G173_gp151	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48266.1	001370	Cluster863_1clades	265	ASESINO_253	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48539.1	001370	Cluster863_1clades	272	CAITLIN_244	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48816.1	001370	Cluster863_1clades	277	CHRISDB_254	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49325.1	001370	Cluster863_1clades	291	HUXLEY_243	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50153.1	001370	Cluster863_1clades	291	PARSHIK_244	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50678.1	001370	Cluster863_1clades	265	STRATTON_253	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86073.1	001370	Cluster863_1clades	255	ACEC001_2300	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20918.1	001370	Cluster863_1clades	255	-	Salmonella phage JN03	GCA_014319805.1
AWN09120.1	001370	Cluster863_1clades	255	MLDJOKPK_00208	Salmonella phage SPAsTU	GCA_003183805.1
AEP84065.1	001370	Cluster863_1clades	255	SPN3US_0232	Salmonella phage SPN3US	GCA_001042275.1
AJK27631.1	001371	Cluster865_1clades	222	PTIM40_225	Cyanophage P-TIM40	GCA_001470935.1
AGG54348.1	001371	Cluster865_1clades	238	CYWG_00064	Cyanophage S-SSM6b	GCA_002710425.1
AGH26265.1	001371	Cluster865_1clades	219	CPMG_00164	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44553.1	001371	Cluster865_1clades	222	PSSM2_175	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12418.1	001371	Cluster865_1clades	222	PRTG_00267	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93460.1	001371	Cluster865_1clades	241	AVU42_gp122	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76152.1	001371	Cluster865_1clades	224	PBI_BELLAMY_107	Synechococcus phage Bellamy	GCA_002627525.1
QCW22835.1	001371	Cluster865_1clades	208	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50501.1	001371	Cluster865_1clades	208	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59546.1	001371	Cluster865_1clades	219	S330809_085	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59308.1	001371	Cluster865_1clades	219	C440309_085	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59784.1	001371	Cluster865_1clades	219	N231010_085	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70092.1	001371	Cluster865_1clades	238	SynMITS9220M01_079	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AHI60377.1	001372	Cluster866_1clades	233	Ea357_224	Erwinia phage Ea35-70	GCA_000914635.1
QBP07334.1	001372	Cluster866_1clades	233	REBECCA_229	Erwinia phage Rebecca	GCA_004521635.1
AUG86015.1	001372	Cluster866_1clades	233	BOSOLAPHORUS_229	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52332.1	001372	Cluster866_1clades	198	DM_232	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86334.1	001372	Cluster866_1clades	233	DESERTFOX_227	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86657.1	001372	Cluster866_1clades	233	MADMEL_229	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86980.1	001372	Cluster866_1clades	233	MORTIMER_232	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52007.1	001372	Cluster866_1clades	233	RAY_227	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51691.1	001372	Cluster866_1clades	233	SIMMY50_232	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65041.1	001372	Cluster866_1clades	233	SPECIALG_230	Erwinia phage vB_EamM_Special G	GCA_002624385.1
BAW19099.1	001372	Cluster866_1clades	211	FDH28_gp125	Ralstonia phage RP12	GCA_002617345.1
BAW19385.1	001372	Cluster866_1clades	211	-	Ralstonia phage RP31	GCA_002617365.1
QKE54551.1	001372	Cluster866_1clades	228	ACSA002_2350	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AFC21449.1	001373	Cluster867_1clades	210	GAP32_002	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21992.1	001373	Cluster867_1clades	171	GAP32_531	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AGX01725.1	001373	Cluster867_1clades	213	CF95_gp003	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01724.1	001373	Cluster867_1clades	226	CF95_gp002	Erwinia phage PhiEaH1	GCA_000914555.1
AMM44112.1	001373	Cluster867_1clades	223	CBB_549	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44116.1	001373	Cluster867_1clades	223	CBB_553	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAS04895.2	001373	Cluster867_1clades	134	AVU11_gp103	Ralstonia phage RSF1	GCA_001500875.1
QCW18647.1	001373	Cluster867_1clades	233	7t3_0126	Salmonella phage 7t3	GCA_006083215.1
AZU98472.1	001373	Cluster867_1clades	233	CPT_Munch_540	Salmonella phage Munch	GCA_004015485.1
QIG63042.1	001373	Cluster867_1clades	233	SEPL_429	Salmonella phage SE_PL	GCA_011067555.1
AQW89073.1	001373	Cluster867_1clades	221	BF_0548	Serratia phage BF	GCA_002619745.1
QFP93149.1	001373	Cluster867_1clades	217	-	Serratia phage PCH45	GCA_009187865.1
QFP93145.1	001373	Cluster867_1clades	220	-	Serratia phage PCH45	GCA_009187865.1
AWY08348.1	001374	FamBDNAPol	115	Alexandra_68	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58710.1	001374	FamBDNAPol	112	Y3_070	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AIT14378.1	001374	FamBDNAPol	119	PBI_121Q_488	Escherichia phage 121Q	GCA_000926855.1
QAY00570.1	001374	FamBDNAPol	119	Ecwhy1_291	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34762.1	001374	FamBDNAPol	119	ACQ29_gp082	Escherichia phage PBECO4	GCA_001041035.1
BBM62049.1	001374	FamBDNAPol	119	EO157G_4600	Escherichia phage SP27	GCA_008033345.1
AXC36877.1	001374	FamBDNAPol	119	-	Escherichia phage UB	GCA_003341455.1
QBO61924.1	001374	FamBDNAPol	119	G17_00435	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13956.1	001374	FamBDNAPol	119	vBEcoMphAPEC6_gp332c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80367.1	001374	FamBDNAPol	119	PSLUR01_00390	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44786.1	001374	FamBDNAPol	124	RaK2_00513	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFH14676.1	001374	FamBDNAPol	146	Lu11_0143	Pseudomonas phage Lu11	GCA_000897175.1
AGS81981.1	001374	FamBDNAPol	232	PaBG_00097	Pseudomonas phage PaBG	GCA_000912555.1
AND75347.1	001375	Cluster869_1clades	201	ME3_186	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AEO93788.1	001375	Cluster869_1clades	231	G_530	Bacillus virus G	GCA_000917535.1
AHI60351.1	001375	Cluster869_1clades	217	Ea357_199	Erwinia phage Ea35-70	GCA_000914635.1
QBP07309.1	001375	Cluster869_1clades	217	REBECCA_204	Erwinia phage Rebecca	GCA_004521635.1
AUG85990.1	001375	Cluster869_1clades	217	BOSOLAPHORUS_204	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52305.1	001375	Cluster869_1clades	217	DM_207	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86309.1	001375	Cluster869_1clades	217	DESERTFOX_202	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86632.1	001375	Cluster869_1clades	217	MADMEL_204	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86955.1	001375	Cluster869_1clades	217	MORTIMER_207	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51982.1	001375	Cluster869_1clades	217	RAY_202	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51666.1	001375	Cluster869_1clades	217	SIMMY50_205	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65014.1	001375	Cluster869_1clades	217	SPECIALG_205	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54519.1	001375	Cluster869_1clades	219	ACSA002_2050	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64170.1	001376	Cluster871_1clades	219	KVP40.0099	Vibrio phage KVP40	GCA_000843785.1
QIW90493.1	001376	Cluster871_1clades	207	GCAPEGMB_00146	Vibrio phage V07	GCA_012361095.1
QIW90814.1	001376	Cluster871_1clades	102	GCAPEGMB_00496	Vibrio phage V07	GCA_012361095.1
QIW90936.1	001376	Cluster871_1clades	207	COHAPHLL_00073	Vibrio phage V09	GCA_012361135.1
QHJ74281.1	001376	Cluster871_1clades	207	VH12019_00362	Vibrio phage VH1_2019	GCA_009931825.1
AGB07106.1	001376	Cluster871_1clades	207	CF80_gp319	Vibrio phage VH7D	GCA_000914495.1
QBX05989.1	001376	Cluster871_1clades	207	ValB1HC_035	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61002.1	001376	Cluster871_1clades	207	AVU32_gp161	Vibrio phage ValKK3	GCA_001501635.1
AGN30149.1	001376	Cluster871_1clades	210	VPFG_00147	Vibrio phage nt-1	GCA_000910195.2
ALP47064.1	001376	Cluster871_1clades	207	phiGrn1_0213	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47444.1	001376	Cluster871_1clades	207	phiST2_0346	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54614.1	001376	Cluster871_1clades	207	vBValMR10Z_73	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37329.1	001376	Cluster871_1clades	207	pp2_096	Vibriophage phi-pp2	GCA_002630725.1
AMR59828.1	001377	Cluster872_1clades	193	SEGD1_181	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49826.1	001377	Cluster872_1clades	177	MACHINA_188	Erwinia phage Machina	GCA_002758035.1
AFQ96643.1	001377	Cluster872_1clades	193	G173_gp098	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48209.1	001377	Cluster872_1clades	193	ASESINO_196	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48481.1	001377	Cluster872_1clades	188	CAITLIN_186	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48760.1	001377	Cluster872_1clades	188	CHRISDB_198	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49270.1	001377	Cluster872_1clades	177	HUXLEY_188	Erwinia phage vB_EamM_Huxley	GCA_001745635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ50098.1	001377	Cluster872_1clades	177	PARSHIK_189	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50620.1	001377	Cluster872_1clades	193	STRATTON_195	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86017.1	001377	Cluster872_1clades	193	ACEC001_1760	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20872.1	001377	Cluster872_1clades	193	-	Salmonella phage JN03	GCA_014319805.1
AWN09160.1	001377	Cluster872_1clades	194	MLDJOKPK_00265	Salmonella phage SPAsTU	GCA_003183805.1
AEP84009.1	001377	Cluster872_1clades	193	SPN3US_0176	Salmonella phage SPN3US	GCA_001042275.1
AIA64995.1	001378	Cluster873_1clades	57	S13_198	Cronobacter phage S13	GCA_001503575.1
QHJ78935.1	001378	Cluster873_1clades	123	-	Myoviridae sp.	GCA_012593985.1
AAQ64387.1	001378	Cluster873_1clades	186	KVP40.0317	Vibrio phage KVP40	GCA_000843785.1
QIW90701.1	001378	Cluster873_1clades	173	GCAPEGMB_00381	Vibrio phage V07	GCA_012361095.1
QIW91097.1	001378	Cluster873_1clades	173	COHAPHLL_00235	Vibrio phage V09	GCA_012361135.1
QHJ74500.1	001378	Cluster873_1clades	173	VH12019_00199	Vibrio phage VH1_2019	GCA_009931825.1
QBX06155.1	001378	Cluster873_1clades	173	ValB1HC_201	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61167.1	001378	Cluster873_1clades	174	AVU32_gp326	Vibrio phage ValKK3	GCA_001501635.1
AGN30369.1	001378	Cluster873_1clades	175	VPFG_00372	Vibrio phage nt-1	GCA_000910195.2
ALP47095.1	001378	Cluster873_1clades	174	phiGrn1_0379	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47476.1	001378	Cluster873_1clades	173	phiST2_0184	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54780.1	001378	Cluster873_1clades	173	vBValMR10Z_240	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37550.1	001378	Cluster873_1clades	173	pp2_318	Vibriophage phi-pp2	GCA_002630725.1
AIT14009.1	001379	Cluster874_1clades	162	PBI_121Q_112	Escherichia phage 121Q	GCA_000926855.1
QAY00325.1	001379	Cluster874_1clades	167	Ecwhy1_44	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00329.1	001379	Cluster874_1clades	162	Ecwhy1_48	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35075.1	001379	Cluster874_1clades	162	ACQ29_gp395	Escherichia phage PBECO4	GCA_001041035.1
BBM61700.1	001379	Cluster874_1clades	162	EO157G_1110	Escherichia phage SP27	GCA_008033345.1
AXC36652.1	001379	Cluster874_1clades	162	-	Escherichia phage UB	GCA_003341455.1
QBO61684.1	001379	Cluster874_1clades	162	G17_00195	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13733.1	001379	Cluster874_1clades	162	vBEcoMphAPEC6_gp103c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80013.1	001379	Cluster874_1clades	162	PSLUR01_00029	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44487.1	001379	Cluster874_1clades	159	RaK2_00214	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW19092.1	001379	Cluster874_1clades	182	7t3_0574	Salmonella phage 7t3	GCA_006083215.1
AZU98331.1	001379	Cluster874_1clades	182	CPT_Munch_389	Salmonella phage Munch	GCA_004015485.1
QIG62652.1	001379	Cluster874_1clades	182	SEPL_039	Salmonella phage SE_PL	GCA_011067555.1
AHI60207.1	001380	Cluster875_1clades	172	Ea357_057	Erwinia phage Ea35-70	GCA_000914635.1
AGX01838.1	001380	Cluster875_1clades	180	CF95_gp116	Erwinia phage PhiEaH1	GCA_000914555.1
QBP07166.1	001380	Cluster875_1clades	172	REBECCA_58	Erwinia phage Rebecca	GCA_004521635.1
AUG85846.1	001380	Cluster875_1clades	172	BOSOLAPHORUS_58	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52158.1	001380	Cluster875_1clades	172	DM_60	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86165.1	001380	Cluster875_1clades	172	DESERTFOX_57	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86486.1	001380	Cluster875_1clades	170	MADMEL_58	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86807.1	001380	Cluster875_1clades	172	MORTIMER_58	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51838.1	001380	Cluster875_1clades	170	RAY_57	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51521.1	001380	Cluster875_1clades	172	SIMMY50_59	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64869.1	001380	Cluster875_1clades	170	SPECIALG_59	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ATA65583.1	001380	Cluster875_1clades	154	2050HW_00248	Serratia phage 2050HW	GCA_002628125.1
QDB71348.1	001380	Cluster875_1clades	159	CPT_Moabite_318	Serratia phage Moabite	GCA_006384735.1
AMR59846.1	001381	Cluster876_1clades	140	SEGD1_199	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49843.1	001381	Cluster876_1clades	130	MACHINA_205	Erwinia phage Machina	GCA_002758035.1
AXF51343.1	001381	Cluster876_1clades	128	WELLINGTON_217	Erwinia phage Wellington	GCA_003344985.1
AFQ96661.1	001381	Cluster876_1clades	172	G173_gp116	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48227.1	001381	Cluster876_1clades	145	ASESINO_214	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ49287.1	001381	Cluster876_1clades	130	HUXLEY_205	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49570.1	001381	Cluster876_1clades	128	KWAN_218	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50115.1	001381	Cluster876_1clades	130	PARSHIK_206	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50640.1	001381	Cluster876_1clades	173	STRATTON_215	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86036.1	001381	Cluster876_1clades	140	ACEC001_1930	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20885.1	001381	Cluster876_1clades	140	-	Salmonella phage JN03	GCA_014319805.1
AXF51124.1	001381	Cluster876_1clades	180	MLDJOKPK_00246	Salmonella phage SPAsTU	GCA_003183805.1
AEP84027.1	001381	Cluster876_1clades	140	SPN3US_0194	Salmonella phage SPN3US	GCA_001042275.1
ARB13826.1	001382	Cluster877_1clades	145	Ccr10_gp296	Caulobacter phage Ccr10	GCA_002619445.1
ARB14171.1	001382	Cluster877_1clades	145	Ccr2_gp295	Caulobacter phage Ccr2	GCA_002619465.1
ARB14865.1	001382	Cluster877_1clades	145	Ccr29_gp309	Caulobacter phage Ccr29	GCA_002619485.1
ARB15203.1	001382	Cluster877_1clades	143	Ccr32_gp285	Caulobacter phage Ccr32	GCA_002619505.1
ARB15537.1	001382	Cluster877_1clades	143	Ccr34_gp295	Caulobacter phage Ccr34	GCA_002619525.1
ARB14512.1	001382	Cluster877_1clades	144	Ccr5_gp292	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68493.1	001382	Cluster877_1clades	162	CcrBL10_gp289	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88255.1	001382	Cluster877_1clades	142	CcrColossus_gp385	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87822.1	001382	Cluster877_1clades	143	CcrKarma_gp305	Caulobacter virus Karma	GCA_000901575.1
AFU87469.1	001382	Cluster877_1clades	143	CcrMagneto_gp299	Caulobacter virus Magneto	GCA_000903095.1
AFU86781.1	001382	Cluster877_1clades	142	CcrRogue_gp299	Caulobacter virus Rogue	GCA_000900555.1
AFU88614.1	001382	Cluster877_1clades	143	CcrSwift_gp296	Caulobacter virus Swift	GCA_000899655.1
AFU87122.1	001382	Cluster877_1clades	143	CbK_gp290	Caulobacter virus phiCbK	GCA_000900535.1
APU01643.1	001383	Cluster878_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
APU01641.1	001383	Cluster878_1clades	88	-	Aeromonas phage 65.2	GCA_002618145.1
APU01645.1	001383	Cluster878_1clades	98	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28883.1	001383	Cluster878_1clades	93	AP1_0176	Aeromonas phage AP1	GCA_014183365.1
ATI17240.1	001383	Cluster878_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00347.1	001383	Cluster878_1clades	98	HWB28_gp205	Aeromonas phage AS-zj	GCA_002627665.1
QAX97683.1	001383	Cluster878_1clades	93	ASswx1_37	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01464.1	001383	Cluster878_1clades	160	ASwh1_405	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39333.1	001383	Cluster878_1clades	83	CC2_077	Aeromonas phage CC2	GCA_000903495.1
AFN39468.1	001383	Cluster878_1clades	93	CC2_078	Aeromonas phage CC2	GCA_000903495.1
ADQ53267.1	001383	Cluster878_1clades	88	65p259	Aeromonas virus 65	GCA_000893255.1
ADQ53270.1	001383	Cluster878_1clades	78	65p262	Aeromonas virus 65	GCA_000893255.1
ADQ53272.1	001383	Cluster878_1clades	98	65p264	Aeromonas virus 65	GCA_000893255.1
AAQ64316.1	001384	Cluster879_1clades	159	KVP40.0247	Vibrio phage KVP40	GCA_000843785.1
QIW90631.1	001384	Cluster879_1clades	154	GCAPEGMB_00284	Vibrio phage V07	GCA_012361095.1
QIW91168.1	001384	Cluster879_1clades	154	COHAPHLL_00332	Vibrio phage V09	GCA_012361135.1
QHJ74426.1	001384	Cluster879_1clades	154	VH12019_00099	Vibrio phage VH1_2019	GCA_009931825.1
AGB06932.1	001384	Cluster879_1clades	156	CF80_gp145	Vibrio phage VH7D	GCA_000914495.1
QBX06214.1	001384	Cluster879_1clades	154	ValB1HC_261	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04472.1	001384	Cluster879_1clades	143	ValB1MD_071	Vibrio phage ValB1MD	GCA_004138815.1
AJT61231.1	001384	Cluster879_1clades	154	AVU32_gp390	Vibrio phage ValKK3	GCA_001501635.1
AGN30302.2	001384	Cluster879_1clades	149	VPFG_00303	Vibrio phage nt-1	GCA_000910195.2
ALP47123.1	001384	Cluster879_1clades	154	phiGrn1_0368	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47506.1	001384	Cluster879_1clades	154	phiST2_0123	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54839.1	001384	Cluster879_1clades	154	vBValMR10Z_299	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37475.1	001384	Cluster879_1clades	154	pp2_242	Vibriophage phi-pp2	GCA_002630725.1
AXQ69030.1	001385	Cluster880_1clades	157	CcrBL9_gp006	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69546.1	001385	Cluster880_1clades	157	CcrBL9_gp522	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69591.1	001385	Cluster880_1clades	128	CcrSC_gp009	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70091.1	001385	Cluster880_1clades	128	CcrSC_gp509	Caulobacter phage CcrSC	GCA_003443315.1
AFC21487.1	001385	Cluster880_1clades	112	GAP32_040	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21489.1	001385	Cluster880_1clades	115	GAP32_042	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44162.1	001385	Cluster880_1clades	112	CBB_46	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44164.1	001385	Cluster880_1clades	115	CBB_48	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43611.1	001385	Cluster880_1clades	112	CBB_599	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43613.1	001385	Cluster880_1clades	115	CBB_601	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88562.1	001385	Cluster880_1clades	115	BF_0037	Serratia phage BF	GCA_002619745.1
SOK58837.1	001385	Cluster880_1clades	111	g029	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58297.1	001385	Cluster880_1clades	111	g020	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01677.1	001386	Cluster881_1clades	63	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29062.1	001386	Cluster881_1clades	156	AP1_0355	Aeromonas phage AP1	GCA_014183365.1
ATI17617.1	001386	Cluster881_1clades	156	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00379.1	001386	Cluster881_1clades	156	HWB28_gp173	Aeromonas phage AS-zj	GCA_002627665.1
AUE22632.1	001386	Cluster881_1clades	153	Ah1_00091	Aeromonas phage Ah1	GCA_002957415.1
QAX98362.1	001386	Cluster881_1clades	153	ASfcp2_16	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97651.1	001386	Cluster881_1clades	156	ASswx1_5	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01090.1	001386	Cluster881_1clades	155	ASwh1_22	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39347.1	001386	Cluster881_1clades	156	CC2_109	Aeromonas phage CC2	GCA_000903495.1
ADQ52816.1	001386	Cluster881_1clades	153	PX29p097	Aeromonas phage PX29	GCA_000920195.1
ADM80072.1	001386	Cluster881_1clades	155	phiAS5_ORF0229	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53311.1	001386	Cluster881_1clades	156	65p303	Aeromonas virus 65	GCA_000893255.1
AAQ17759.1	001386	Cluster881_1clades	153	Aeh1ORF098c	Aeromonas virus Aeh1	GCA_000843245.1
AHI60323.1	001387	Cluster882_1clades	148	Ea357_172	Erwinia phage Ea35-70	GCA_000914635.1
QBP07282.1	001387	Cluster882_1clades	148	REBECCA_175	Erwinia phage Rebecca	GCA_004521635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG85962.1	001387	Cluster882_1clades	148	BOSOLAPHORUS_175	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52277.1	001387	Cluster882_1clades	148	DM_179	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86281.1	001387	Cluster882_1clades	148	DESERTFOX_174	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86603.1	001387	Cluster882_1clades	148	MADMEL_175	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86927.1	001387	Cluster882_1clades	148	MORTIMER_178	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51954.1	001387	Cluster882_1clades	148	RAY_173	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51638.1	001387	Cluster882_1clades	148	SIMMY50_176	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64985.1	001387	Cluster882_1clades	148	SPECIALG_175	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24104.1	001387	Cluster882_1clades	145	-	Proteus phage 10	GCA_014071245.1
QKE54481.1	001387	Cluster882_1clades	149	ACSA002_1670	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AXH70775.1	001387	Cluster882_1clades	148	-	Vibrio phage BONAISHI	GCA_003441475.1
AMR59887.1	001388	Cluster883_1clades	140	SEGD1_240	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49888.1	001388	Cluster883_1clades	147	MACHINA_250	Erwinia phage Machina	GCA_002758035.1
AXF51389.1	001388	Cluster883_1clades	136	WELLINGTON_263	Erwinia phage Wellington	GCA_003344985.1
AFQ96701.1	001388	Cluster883_1clades	145	G173_gp156	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48271.1	001388	Cluster883_1clades	143	ASESINO_258	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ49331.1	001388	Cluster883_1clades	147	HUXLEY_249	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49615.1	001388	Cluster883_1clades	136	KWAN_263	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50159.1	001388	Cluster883_1clades	147	PARSHIK_250	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50683.1	001388	Cluster883_1clades	145	STRATTON_258	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86077.1	001388	Cluster883_1clades	140	ACEC001_2340	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20921.1	001388	Cluster883_1clades	145	-	Salmonella phage JN03	GCA_014319805.1
AWN09116.1	001388	Cluster883_1clades	140	MLDJOKPK_00204	Salmonella phage SPAsTU	GCA_003183805.1
AEP84069.1	001388	Cluster883_1clades	140	SPN3US_0236	Salmonella phage SPN3US	GCA_001042275.1
APU01621.1	001389	Cluster884_1clades	122	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28837.1	001389	Cluster884_1clades	145	AP1_0130	Aeromonas phage AP1	GCA_014183365.1
ATI17270.1	001389	Cluster884_1clades	139	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00323.1	001389	Cluster884_1clades	137	HWB28_gp229	Aeromonas phage AS-zj	GCA_002627665.1
AUE22605.1	001389	Cluster884_1clades	137	Ah1_00064	Aeromonas phage Ah1	GCA_002957415.1
QAX98642.1	001389	Cluster884_1clades	133	ASfcp2_309	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97710.1	001389	Cluster884_1clades	137	ASswx1_64	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01455.1	001389	Cluster884_1clades	143	ASwh1_396	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39326.1	001389	Cluster884_1clades	138	CC2_047	Aeromonas phage CC2	GCA_000903495.1
ADQ52782.1	001389	Cluster884_1clades	133	PX29p063	Aeromonas phage PX29	GCA_000920195.1
ADM80037.1	001389	Cluster884_1clades	145	phiAS5_ORF0194	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53246.1	001389	Cluster884_1clades	122	65p238	Aeromonas virus 65	GCA_000893255.1
AAQ17726.1	001389	Cluster884_1clades	145	Aeh1ORF066c	Aeromonas virus Aeh1	GCA_000843245.1
AMR59708.1	001390	Cluster885_1clades	123	SEGD1_059	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49710.1	001390	Cluster885_1clades	141	MACHINA_72	Erwinia phage Machina	GCA_002758035.1
AFQ96786.1	001390	Cluster885_1clades	116	G173_gp241	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48087.1	001390	Cluster885_1clades	116	ASESINO_74	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48361.1	001390	Cluster885_1clades	116	CAITLIN_66	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48634.1	001390	Cluster885_1clades	116	CHRISDB_72	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49155.1	001390	Cluster885_1clades	141	HUXLEY_73	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49983.1	001390	Cluster885_1clades	141	PARSHIK_74	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50498.1	001390	Cluster885_1clades	116	STRATTON_73	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85898.1	001390	Cluster885_1clades	123	ACEC001_0600	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20773.1	001390	Cluster885_1clades	126	-	Salmonella phage JN03	GCA_014319805.1
AWN09041.1	001390	Cluster885_1clades	126	MLDJOKPK_00108	Salmonella phage SPAsTU	GCA_003183805.1
AEP83890.1	001390	Cluster885_1clades	123	SPN3US_0057	Salmonella phage SPN3US	GCA_001042275.1
AND75463.1	001391	SIG+TM+TM	130	ME3_302	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AAQ64318.1	001391	SIG+TM+TM	109	KVP40.0249	Vibrio phage KVP40	GCA_000843785.1
QIW90633.1	001391	SIG+TM+TM	109	GCAPEGMB_00286	Vibrio phage V07	GCA_012361095.1
QIW91166.1	001391	SIG+TM+TM	109	COHAPHLL_00330	Vibrio phage V09	GCA_012361135.1
QHJ74428.1	001391	SIG+TM+TM	109	VH12019_00101	Vibrio phage VH1_2019	GCA_009931825.1
AGB06934.1	001391	SIG+TM+TM	109	CF80_gp147	Vibrio phage VH7D	GCA_000914495.1
QBX06212.1	001391	SIG+TM+TM	109	ValB1HC_259	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61229.1	001391	SIG+TM+TM	109	AVU32_gp388	Vibrio phage ValKK3	GCA_001501635.1
AGN30304.1	001391	SIG+TM+TM	109	VPFG_00305	Vibrio phage nt-1	GCA_000910195.2
ALP47184.1	001391	SIG+TM+TM	109	phiGrn1_0370	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47571.1	001391	SIG+TM+TM	109	phiST2_0125	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54837.1	001391	SIG+TM+TM	109	vBValMR10Z_297	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37477.1	001391	SIG+TM+TM	109	pp2_244	Vibriophage phi-pp2	GCA_002630725.1
ARB13802.1	001392	TrmB	127	Ccr10_gp272	Caulobacter phage Ccr10	GCA_002619445.1
ARB14147.1	001392	TrmB	127	Ccr2_gp271	Caulobacter phage Ccr2	GCA_002619465.1
ARB14841.1	001392	TrmB	127	Ccr29_gp285	Caulobacter phage Ccr29	GCA_002619485.1
ARB15181.1	001392	TrmB	127	Ccr32_gp263	Caulobacter phage Ccr32	GCA_002619505.1
ARB15515.1	001392	TrmB	127	Ccr34_gp273	Caulobacter phage Ccr34	GCA_002619525.1
ARB14489.1	001392	TrmB	127	Ccr5_gp269	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68467.1	001392	TrmB	125	CcrBL10_gp263	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88210.1	001392	TrmB	124	CcrColossus_gp340	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68887.1	001392	TrmB	127	CcrPW_gp348	Caulobacter phage CcrPW	GCA_003443275.1
AFU87799.1	001392	TrmB	127	CcrKarma_gp282	Caulobacter virus Karma	GCA_000901575.1
AFU87446.1	001392	TrmB	127	CcrMagneto_gp276	Caulobacter virus Magneto	GCA_000903095.1
AFU86753.1	001392	TrmB	125	CcrRogue_gp271	Caulobacter virus Rogue	GCA_000900555.1
AFU87100.1	001392	TrmB	127	CbK_gp268	Caulobacter virus phiCbK	GCA_000900535.1
AFC21619.1	001393	DUF3271	99	GAP32_169	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14414.1	001393	DUF3271	112	PBI_121Q_524	Escherichia phage 121Q	GCA_000926855.1
QAY00537.1	001393	DUF3271	112	Ecwhy1_258	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34728.1	001393	DUF3271	112	ACQ29_gp048	Escherichia phage PBECO4	GCA_001041035.1
BBM62086.1	001393	DUF3271	112	EO157G_4970	Escherichia phage SP27	GCA_008033345.1
AXC36844.1	001393	DUF3271	112	-	Escherichia phage UB	GCA_003341455.1
QBO61887.1	001393	DUF3271	112	G17_00398	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13924.1	001393	DUF3271	112	vBEcoMphAPEC6_gp299c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80400.1	001393	DUF3271	112	PSLUR01_00423	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44292.1	001393	DUF3271	108	RaK2_00019	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18882.1	001393	DUF3271	122	7t3_0361	Salmonella phage 7t3	GCA_006083215.1
AZU98140.1	001393	DUF3271	122	CPT_Munch_196	Salmonella phage Munch	GCA_004015485.1
QIG62842.1	001393	DUF3271	122	SEPL_229	Salmonella phage SE_PL	GCA_011067555.1
APU01395.1	001394	Cluster889_1clades	109	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28874.1	001394	Cluster889_1clades	108	AP1_0167	Aeromonas phage AP1	GCA_014183365.1
ATI17500.1	001394	Cluster889_1clades	108	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00497.1	001394	Cluster889_1clades	108	HWB28_gp055	Aeromonas phage AS-zj	GCA_002627665.1
AUE22544.1	001394	Cluster889_1clades	103	Ah1_00003	Aeromonas phage Ah1	GCA_002957415.1
QAX98585.1	001394	Cluster889_1clades	103	ASfcp2_252	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97939.1	001394	Cluster889_1clades	108	ASswx1_297	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01207.1	001394	Cluster889_1clades	121	ASwh1_142	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39266.1	001394	Cluster889_1clades	108	CC2_234	Aeromonas phage CC2	GCA_000903495.1
ADQ52721.1	001394	Cluster889_1clades	103	PX29p002	Aeromonas phage PX29	GCA_000920195.1
ADM79973.1	001394	Cluster889_1clades	103	phiAS5_ORF0130	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53053.1	001394	Cluster889_1clades	42	65p004	Aeromonas virus 65	GCA_000893255.1
AAQ17658.1	001394	Cluster889_1clades	103	Aeh1ORF003c	Aeromonas virus Aeh1	GCA_000843245.1
ARB13724.1	001395	Cluster890_1clades	78	Ccr10_gp194c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14069.1	001395	Cluster890_1clades	78	Ccr2_gp193c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14758.1	001395	Cluster890_1clades	78	Ccr29_gp202	Caulobacter phage Ccr29	GCA_002619485.1
ARB14412.1	001395	Cluster890_1clades	78	Ccr5_gp192c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68391.1	001395	Cluster890_1clades	83	CcrBL10_gp187c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69294.1	001395	Cluster890_1clades	110	CcrBL9_gp270c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88272.1	001395	Cluster890_1clades	112	CcrColossus_gp402	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68948.1	001395	Cluster890_1clades	112	CcrPW_gp409c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69852.1	001395	Cluster890_1clades	110	CcrSC_gp270c	Caulobacter phage CcrSC	GCA_003443315.1
AFU87717.1	001395	Cluster890_1clades	78	CcrKarma_gp200	Caulobacter virus Karma	GCA_000901575.1
AFU87366.1	001395	Cluster890_1clades	78	CcrMagneto_gp196	Caulobacter virus Magneto	GCA_000903095.1
AFU86676.1	001395	Cluster890_1clades	119	CcrRogue_gp194	Caulobacter virus Rogue	GCA_000900555.1
AFU88513.1	001395	Cluster890_1clades	78	CcrSwift_gp195	Caulobacter virus Swift	GCA_000899655.1
AMO43050.1	001396	Cluster891_1clades	117	R1080702_041	Cyanophage S-RIM32	GCA_001754165.1
AMO43290.1	001396	Cluster891_1clades	117	W270710_046	Cyanophage S-RIM44	GCA_002599145.1
AOO11524.1	001396	Cluster891_1clades	117	ES420910_043	Cyanophage S-RIM44	GCA_002599165.1
AOO11762.1	001396	Cluster891_1clades	117	Np050604_046	Cyanophage S-RIM44	GCA_002599185.1
AOO11989.1	001396	Cluster891_1clades	117	Np200711_043	Cyanophage S-RIM44	GCA_002599205.1
AOO12225.1	001396	Cluster891_1clades	117	Np420711_043	Cyanophage S-RIM44	GCA_002599225.1
AOO12463.1	001396	Cluster891_1clades	117	Sn080709_046	Cyanophage S-RIM44	GCA_002599245.1
AOO12690.1	001396	Cluster891_1clades	117	Sn130910_043	Cyanophage S-RIM44	GCA_002599265.1
AOO12928.1	001396	Cluster891_1clades	117	W2100709_046	Cyanophage S-RIM44	GCA_002599285.1
ADO99144.1	001396	Cluster891_1clades	117	Syn1_043	Prochlorococcus phage Syn1	GCA_000892495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59499.1	001396	Cluster891_1clades	115	S330809_038	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59261.1	001396	Cluster891_1clades	115	C440309_038	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59737.1	001396	Cluster891_1clades	115	N231010_038	Synechococcus phage S-CAM4	GCA_002922155.1
AIT13975.1	001397	Cluster892_1clades	111	PBI_121Q_78	Escherichia phage 121Q	GCA_000926855.1
QAY00362.1	001397	Cluster892_1clades	111	Ecwhy1_81	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35108.1	001397	Cluster892_1clades	111	ACQ29_gp428	Escherichia phage PBECO4	GCA_001041035.1
BBM61667.1	001397	Cluster892_1clades	111	EO157G_0780	Escherichia phage SP27	GCA_008033345.1
AXC36683.1	001397	Cluster892_1clades	111	-	Escherichia phage UB	GCA_003341455.1
QBO61717.1	001397	Cluster892_1clades	111	G17_00228	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13764.1	001397	Cluster892_1clades	111	vBEcoMphAPEC6_gp135c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80569.1	001397	Cluster892_1clades	111	PSLUR01_00592	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44455.1	001397	Cluster892_1clades	111	RaK2_00182	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43933.1	001397	Cluster892_1clades	117	CBB_370	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88892.1	001397	Cluster892_1clades	114	BF_0367	Serratia phage BF	GCA_002619745.1
SOK59178.1	001397	Cluster892_1clades	113	g370	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58644.1	001397	Cluster892_1clades	113	g367	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AHI60279.1	001398	Cluster893_1clades	96	Ea357_128	Erwinia phage Ea35-70	GCA_000914635.1
QBP07237.1	001398	Cluster893_1clades	96	REBECCA_130	Erwinia phage Rebecca	GCA_004521635.1
AUG85917.1	001398	Cluster893_1clades	96	BOSOLAPHORUS_130	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52232.1	001398	Cluster893_1clades	96	DM_134	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86236.1	001398	Cluster893_1clades	96	DESERTFOX_129	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86558.1	001398	Cluster893_1clades	96	MADMEL_130	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86882.1	001398	Cluster893_1clades	96	MORTIMER_133	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51910.1	001398	Cluster893_1clades	96	RAY_129	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51594.1	001398	Cluster893_1clades	96	SIMMY50_132	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64941.1	001398	Cluster893_1clades	96	SPECIALG_131	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54433.1	001398	Cluster893_1clades	96	ACSA002_1190	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65561.1	001398	Cluster893_1clades	115	2050HW_00226	Serratia phage 2050HW	GCA_002628125.1
QDB71326.1	001398	Cluster893_1clades	115	CPT_Moabite_296	Serratia phage Moabite	GCA_006384735.1
AIT14114.1	001399	SIG+TM+TM	113	PBI_121Q_224	Escherichia phage 121Q	GCA_000926855.1
AIT14115.1	001399	SIG+TM+TM	112	PBI_121Q_225	Escherichia phage 121Q	GCA_000926855.1
QAY00809.1	001399	SIG+TM+TM	112	Ecwhy1_536	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34983.1	001399	SIG+TM+TM	112	ACQ29_gp303	Escherichia phage PBECO4	GCA_001041035.1
BBM61793.1	001399	SIG+TM+TM	113	EO157G_2040	Escherichia phage SP27	GCA_008033345.1
BBM61794.1	001399	SIG+TM+TM	112	EO157G_2050	Escherichia phage SP27	GCA_008033345.1
AXC36561.1	001399	SIG+TM+TM	112	-	Escherichia phage UB	GCA_003341455.1
AXC36562.1	001399	SIG+TM+TM	42	-	Escherichia phage UB	GCA_003341455.1
QBO61585.1	001399	SIG+TM+TM	112	G17_00089	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61586.1	001399	SIG+TM+TM	113	G17_00090	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13648.1	001399	SIG+TM+TM	112	vBEcoMphAPEC6_gp017c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80106.1	001399	SIG+TM+TM	112	PSLUR01_00129	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44584.1	001399	SIG+TM+TM	114	RaK2_00311	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
APU01407.1	001400	Phage_head_chap	93	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28897.1	001400	Phage_head_chap	96	AP1_0190	Aeromonas phage AP1	GCA_014183365.1
ATI17488.1	001400	Phage_head_chap	96	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00509.1	001400	Phage_head_chap	96	HWB28_gp043	Aeromonas phage AS-zj	GCA_002627665.1
AUE22557.1	001400	Phage_head_chap	94	Ah1_00016	Aeromonas phage Ah1	GCA_002957415.1
QAX97928.1	001400	Phage_head_chap	96	ASswx1_285	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01220.1	001400	Phage_head_chap	94	ASwh1_155	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39397.1	001400	Phage_head_chap	96	CC2_245	Aeromonas phage CC2	GCA_000903495.1
AAR90923.1	001400	Phage_head_chap	93	65p015	Aeromonas virus 65	GCA_000893255.1
AAQ17669.1	001400	Phage_head_chap	105	40	Aeromonas virus Aeh1	GCA_000843245.1
ANS06098.1	001400	Phage_head_chap	101	ABCD_0036	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97046.1	001400	Phage_head_chap	101	E_037	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78558.1	001400	Phage_head_chap	101	RB43ORF036c	Escherichia virus RB43	GCA_000863505.1
APU01719.1	001401	Cluster896_1clades	100	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28747.1	001401	Cluster896_1clades	97	AP1_0029	Aeromonas phage AP1	GCA_014183365.1
ATI17576.1	001401	Cluster896_1clades	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00420.1	001401	Cluster896_1clades	98	HWB28_gp132	Aeromonas phage AS-zj	GCA_002627665.1
AUE22844.1	001401	Cluster896_1clades	99	Ah1_00326	Aeromonas phage Ah1	GCA_002957415.1
QAX98556.1	001401	Cluster896_1clades	104	ASfcp2_222	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98016.1	001401	Cluster896_1clades	97	ASswx1_376	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01127.1	001401	Cluster896_1clades	91	ASwh1_60	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39362.1	001401	Cluster896_1clades	97	CC2_156	Aeromonas phage CC2	GCA_000903495.1
ADQ53021.1	001401	Cluster896_1clades	104	PX29p302	Aeromonas phage PX29	GCA_000920195.1
ADM79945.1	001401	Cluster896_1clades	99	phiAS5_ORF0102	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53359.1	001401	Cluster896_1clades	100	65p351	Aeromonas virus 65	GCA_000893255.1
AAQ17974.1	001401	Cluster896_1clades	99	Aeh1ORF305c	Aeromonas virus Aeh1	GCA_000843245.1
APU01769.1	001402	Cluster897_1clades	103	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28977.1	001402	Cluster897_1clades	93	AP1_0270	Aeromonas phage AP1	GCA_014183365.1
ATI17528.1	001402	Cluster897_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00468.1	001402	Cluster897_1clades	93	HWB28_gp084	Aeromonas phage AS-zj	GCA_002627665.1
AUE22804.1	001402	Cluster897_1clades	95	Ah1_00286	Aeromonas phage Ah1	GCA_002957415.1
QAX98519.1	001402	Cluster897_1clades	95	ASfcp2_183	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97970.1	001402	Cluster897_1clades	93	ASswx1_328	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01170.1	001402	Cluster897_1clades	93	ASwh1_104	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39379.1	001402	Cluster897_1clades	93	CC2_205	Aeromonas phage CC2	GCA_000903495.1
ADQ52982.1	001402	Cluster897_1clades	95	PX29p263	Aeromonas phage PX29	GCA_000920195.1
ADM79906.1	001402	Cluster897_1clades	95	phiAS5_ORF0063	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53412.1	001402	Cluster897_1clades	95	65p405	Aeromonas virus 65	GCA_000893255.1
AAQ17931.1	001402	Cluster897_1clades	95	Aeh1ORF267c	Aeromonas virus Aeh1	GCA_000843245.1
AMR59730.1	001403	Cluster898_1clades	100	SEGD1_081	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49730.1	001403	Cluster898_1clades	101	MACHINA_92	Erwinia phage Machina	GCA_002758035.1
AFQ96549.1	001403	Cluster898_1clades	102	G173_gp004	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48109.1	001403	Cluster898_1clades	102	ASESINO_96	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48384.1	001403	Cluster898_1clades	101	CAITLIN_89	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48656.1	001403	Cluster898_1clades	100	CHRISDB_94	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49175.1	001403	Cluster898_1clades	101	HUXLEY_93	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50003.1	001403	Cluster898_1clades	101	PARSHIK_94	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50523.1	001403	Cluster898_1clades	102	STRATTON_98	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85920.1	001403	Cluster898_1clades	100	ACEC001_0820	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20790.1	001403	Cluster898_1clades	100	-	Salmonella phage JN03	GCA_014319805.1
AWN09021.1	001403	Cluster898_1clades	101	MLDJOKPK_00079	Salmonella phage SPAsTU	GCA_003183805.1
AEP83913.1	001403	Cluster898_1clades	100	SPN3US_0080	Salmonella phage SPN3US	GCA_001042275.1
ARB13759.1	001404	TM	102	Ccr10_gp229	Caulobacter phage Ccr10	GCA_002619445.1
ARB14104.1	001404	TM	102	Ccr2_gp228	Caulobacter phage Ccr2	GCA_002619465.1
ARB14793.1	001404	TM	102	Ccr29_gp237	Caulobacter phage Ccr29	GCA_002619485.1
ARB14797.1	001404	TM	48	Ccr29_gp241	Caulobacter phage Ccr29	GCA_002619485.1
ARB15137.1	001404	TM	102	Ccr32_gp219	Caulobacter phage Ccr32	GCA_002619505.1
ARB15471.1	001404	TM	102	Ccr34_gp229	Caulobacter phage Ccr34	GCA_002619525.1
ARB14446.1	001404	TM	102	Ccr5_gp226	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68426.1	001404	TM	99	CcrBL10_gp222	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87753.1	001404	TM	102	CcrKarma_gp236	Caulobacter virus Karma	GCA_000901575.1
AFU87401.1	001404	TM	102	CcrMagneto_gp231	Caulobacter virus Magneto	GCA_000903095.1
AFU86712.1	001404	TM	99	CcrRogue_gp230	Caulobacter virus Rogue	GCA_000900555.1
AFU88549.1	001404	TM	102	CcrSwift_gp231	Caulobacter virus Swift	GCA_000899655.1
AFU87056.1	001404	TM	102	CbK_gp224	Caulobacter virus phiCbK	GCA_000900535.1
AOO14236.1	001405	Cluster900_1clades	101	Sn110110_042	Cyanophage S-RIM14	GCA_002599065.1
AOO14888.1	001405	Cluster900_1clades	101	W1230910_042	Cyanophage S-RIM14	GCA_002599125.1
AMO43429.1	001405	Cluster900_1clades	100	W270710_185	Cyanophage S-RIM44	GCA_002599145.1
AOO11673.1	001405	Cluster900_1clades	100	ES420910_192	Cyanophage S-RIM44	GCA_002599165.1
AOO11901.1	001405	Cluster900_1clades	100	Np050604_185	Cyanophage S-RIM44	GCA_002599185.1
AOO12139.1	001405	Cluster900_1clades	100	Np200711_193	Cyanophage S-RIM44	GCA_002599205.1
AOO12374.1	001405	Cluster900_1clades	100	Np420711_192	Cyanophage S-RIM44	GCA_002599225.1
AOO12602.1	001405	Cluster900_1clades	100	Sn080709_185	Cyanophage S-RIM44	GCA_002599245.1
AOO12839.1	001405	Cluster900_1clades	100	Sn130910_192	Cyanophage S-RIM44	GCA_002599265.1
AOO13068.1	001405	Cluster900_1clades	100	W2100709_186	Cyanophage S-RIM44	GCA_002599285.1
ADO99288.1	001405	Cluster900_1clades	100	Syn1_187	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30684.1	001405	Cluster900_1clades	71	Syn7803US37_207	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23034.1	001405	Cluster900_1clades	58	-	Synechococcus phage S-B05	GCA_006083695.1
AMR59867.1	001406	Cluster901_1clades	99	SEGD1_220	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49866.1	001406	Cluster901_1clades	91	MACHINA_228	Erwinia phage Machina	GCA_002758035.1
AFQ96683.1	001406	Cluster901_1clades	99	G173_gp138	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48250.1	001406	Cluster901_1clades	99	ASESINO_237	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48523.1	001406	Cluster901_1clades	89	CAITLIN_228	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48800.1	001406	Cluster901_1clades	90	CHRISDB_238	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49310.1	001406	Cluster901_1clades	91	HUXLEY_228	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50138.1	001406	Cluster901_1clades	91	PARSHIK_229	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50663.1	001406	Cluster901_1clades	99	STRATTON_238	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86056.1	001406	Cluster901_1clades	99	ACEC001_2130	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20903.1	001406	Cluster901_1clades	99	-	Salmonella phage JN03	GCA_014319805.1
AWN09132.1	001406	Cluster901_1clades	99	MLDJOKPK_00225	Salmonella phage SPAsTU	GCA_003183805.1
AEP84048.1	001406	Cluster901_1clades	99	SPN3US_0215	Salmonella phage SPN3US	GCA_001042275.1
AGS82060.1	001407	DUF2829	77	PaBG_00184	Pseudomonas phage PaBG	GCA_000912555.1
AAQ64366.1	001407	DUF2829	98	KVP40.0296	Vibrio phage KVP40	GCA_000843785.1
QIW90681.1	001407	DUF2829	98	GCAPEGMB_00334	Vibrio phage V07	GCA_012361095.1
QIW91117.1	001407	DUF2829	98	COHAPHLL_00281	Vibrio phage V09	GCA_012361135.1
QHJ74476.1	001407	DUF2829	98	VH12019_00149	Vibrio phage VH1_2019	GCA_009931825.1
AGB06969.1	001407	DUF2829	98	CF80_gp182	Vibrio phage VH7D	GCA_000914495.1
QBX06175.1	001407	DUF2829	98	ValB1HC_222	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61192.1	001407	DUF2829	98	AVU32_gp351	Vibrio phage ValKK3	GCA_001501635.1
AGN30342.1	001407	DUF2829	97	VPFG_00345	Vibrio phage nt-1	GCA_000910195.2
ALP47210.1	001407	DUF2829	98	phiGrn1_0029	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47601.1	001407	DUF2829	98	phiST2_0162	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54801.1	001407	DUF2829	98	vBValMR10Z_261	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37527.1	001407	DUF2829	98	pp2_294	Vibriophage phi-pp2	GCA_002630725.1
ARB13761.1	001408	Cluster903_1clades	90	Ccr10_gp231	Caulobacter phage Ccr10	GCA_002619445.1
ARB14106.1	001408	Cluster903_1clades	90	Ccr2_gp230	Caulobacter phage Ccr2	GCA_002619465.1
ARB14795.1	001408	Cluster903_1clades	90	Ccr29_gp239	Caulobacter phage Ccr29	GCA_002619485.1
ARB14800.1	001408	Cluster903_1clades	90	Ccr29_gp244	Caulobacter phage Ccr29	GCA_002619485.1
ARB15140.1	001408	Cluster903_1clades	90	Ccr32_gp222	Caulobacter phage Ccr32	GCA_002619505.1
ARB15474.1	001408	Cluster903_1clades	90	Ccr34_gp232	Caulobacter phage Ccr34	GCA_002619525.1
ARB14448.1	001408	Cluster903_1clades	90	Ccr5_gp228	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68428.1	001408	Cluster903_1clades	96	CcrBL10_gp224	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87756.1	001408	Cluster903_1clades	90	CcrKarma_gp239	Caulobacter virus Karma	GCA_000901575.1
AFU87403.1	001408	Cluster903_1clades	90	CcrMagneto_gp233	Caulobacter virus Magneto	GCA_000903095.1
AFU86714.1	001408	Cluster903_1clades	94	CcrRogue_gp232	Caulobacter virus Rogue	GCA_000900555.1
AFU88551.1	001408	Cluster903_1clades	90	CcrSwift_gp233	Caulobacter virus Swift	GCA_000899655.1
AFU87059.1	001408	Cluster903_1clades	90	CbK_gp227	Caulobacter virus phiCbK	GCA_000900535.1
ARB13599.1	001409	Cluster904_1clades	93	Ccr10_gp071	Caulobacter phage Ccr10	GCA_002619445.1
ARB13945.1	001409	Cluster904_1clades	92	Ccr2_gp070	Caulobacter phage Ccr2	GCA_002619465.1
ARB14635.1	001409	Cluster904_1clades	93	Ccr29_gp078	Caulobacter phage Ccr29	GCA_002619485.1
ARB14991.1	001409	Cluster904_1clades	93	Ccr32_gp072	Caulobacter phage Ccr32	GCA_002619505.1
ARB15321.1	001409	Cluster904_1clades	93	Ccr34_gp072	Caulobacter phage Ccr34	GCA_002619525.1
ARB14288.1	001409	Cluster904_1clades	93	Ccr5_gp070	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68272.1	001409	Cluster904_1clades	93	CcrBL10_gp068	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68577.1	001409	Cluster904_1clades	94	CcrPW_gp038	Caulobacter phage CcrPW	GCA_003443275.1
AFU87589.1	001409	Cluster904_1clades	93	CcrKarma_gp072	Caulobacter virus Karma	GCA_000901575.1
AFU87239.1	001409	Cluster904_1clades	93	CcrMagneto_gp069	Caulobacter virus Magneto	GCA_000903095.1
AFU86555.1	001409	Cluster904_1clades	93	CcrRogue_gp073	Caulobacter virus Rogue	GCA_000900555.1
AFU88387.1	001409	Cluster904_1clades	93	CcrSwift_gp069	Caulobacter virus Swift	GCA_000899655.1
AFU86903.1	001409	Cluster904_1clades	93	CbK_gp071	Caulobacter virus phiCbK	GCA_000900535.1
AMO43179.1	001410	Cluster905_1clades	93	R1080702_170	Cyanophage S-RIM32	GCA_001754165.1
AMO43404.1	001410	Cluster905_1clades	92	W270710_160	Cyanophage S-RIM44	GCA_002599145.1
AOO11648.1	001410	Cluster905_1clades	92	ES420910_167	Cyanophage S-RIM44	GCA_002599165.1
AOO11876.1	001410	Cluster905_1clades	92	Np050604_160	Cyanophage S-RIM44	GCA_002599185.1
AOO12114.1	001410	Cluster905_1clades	92	Np200711_168	Cyanophage S-RIM44	GCA_002599205.1
AOO12349.1	001410	Cluster905_1clades	92	Np420711_167	Cyanophage S-RIM44	GCA_002599225.1
AOO12577.1	001410	Cluster905_1clades	92	Sn080709_160	Cyanophage S-RIM44	GCA_002599245.1
AOO12814.1	001410	Cluster905_1clades	92	Sn130910_167	Cyanophage S-RIM44	GCA_002599265.1
AOO13043.1	001410	Cluster905_1clades	92	W2100709_161	Cyanophage S-RIM44	GCA_002599285.1
ADO99263.1	001410	Cluster905_1clades	92	Syn1_162	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59629.1	001410	Cluster905_1clades	85	S330809_168	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59391.1	001410	Cluster905_1clades	85	C440309_168	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59867.1	001410	Cluster905_1clades	85	N231010_168	Synechococcus phage S-CAM4	GCA_002922155.1
AIT14192.1	001411	Cluster906_1clades	91	PBI_121Q_302	Escherichia phage 121Q	GCA_000926855.1
QAY00747.1	001411	Cluster906_1clades	91	Ecwhy1_473	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34926.1	001411	Cluster906_1clades	91	ACQ29_gp246	Escherichia phage PBECO4	GCA_001041035.1
BBM61865.1	001411	Cluster906_1clades	91	EO157G_2760	Escherichia phage SP27	GCA_008033345.1
AXC37030.1	001411	Cluster906_1clades	91	-	Escherichia phage UB	GCA_003341455.1
QBO61515.1	001411	Cluster906_1clades	91	G17_00019	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62121.1	001411	Cluster906_1clades	91	G17_00632	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14129.1	001411	Cluster906_1clades	91	vBEcoMphAPEC6_gp506c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80174.1	001411	Cluster906_1clades	91	PSLUR01_00197	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44624.1	001411	Cluster906_1clades	91	RaK2_00351	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18678.1	001411	Cluster906_1clades	90	7t3_0157	Salmonella phage 7t3	GCA_006083215.1
AZU97952.1	001411	Cluster906_1clades	90	CPT_Munch_008	Salmonella phage Munch	GCA_004015485.1
QIG63024.1	001411	Cluster906_1clades	90	SEPL_411	Salmonella phage SE_PL	GCA_011067555.1
ARB13762.1	001412	Cluster907_1clades	88	Ccr10_gp232	Caulobacter phage Ccr10	GCA_002619445.1
ARB14107.1	001412	Cluster907_1clades	88	Ccr2_gp231	Caulobacter phage Ccr2	GCA_002619465.1
ARB14796.1	001412	Cluster907_1clades	88	Ccr29_gp240	Caulobacter phage Ccr29	GCA_002619485.1
ARB14801.1	001412	Cluster907_1clades	85	Ccr29_gp245	Caulobacter phage Ccr29	GCA_002619485.1
ARB15141.1	001412	Cluster907_1clades	85	Ccr32_gp223	Caulobacter phage Ccr32	GCA_002619505.1
ARB15475.1	001412	Cluster907_1clades	85	Ccr34_gp233	Caulobacter phage Ccr34	GCA_002619525.1
ARB14449.1	001412	Cluster907_1clades	85	Ccr5_gp229	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68429.1	001412	Cluster907_1clades	87	CcrBL10_gp225	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87757.1	001412	Cluster907_1clades	85	CcrKarma_gp240	Caulobacter virus Karma	GCA_000901575.1
AFU87404.1	001412	Cluster907_1clades	85	CcrMagneto_gp234	Caulobacter virus Magneto	GCA_000903095.1
AFU86715.1	001412	Cluster907_1clades	87	CcrRogue_gp233	Caulobacter virus Rogue	GCA_000900555.1
AFU88552.1	001412	Cluster907_1clades	88	CcrSwift_gp234	Caulobacter virus Swift	GCA_000899655.1
AFU87060.1	001412	Cluster907_1clades	85	CbK_gp228	Caulobacter virus phiCbK	GCA_000900535.1
APU01790.1	001413	Cluster908_1clades	84	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28992.1	001413	Cluster908_1clades	87	AP1_0285	Aeromonas phage AP1	GCA_014183365.1
ATI17515.1	001413	Cluster908_1clades	87	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00481.1	001413	Cluster908_1clades	87	HWB28_gp071	Aeromonas phage AS-zj	GCA_002627665.1
AUE22608.1	001413	Cluster908_1clades	79	Ah1_00067	Aeromonas phage Ah1	GCA_002957415.1
QAX98649.1	001413	Cluster908_1clades	79	ASfcp2_317	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97955.1	001413	Cluster908_1clades	87	ASswx1_313	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01194.1	001413	Cluster908_1clades	79	ASwh1_129	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39383.1	001413	Cluster908_1clades	87	CC2_219	Aeromonas phage CC2	GCA_000903495.1
ADQ52791.1	001413	Cluster908_1clades	79	PX29p072	Aeromonas phage PX29	GCA_000920195.1
ADM80046.1	001413	Cluster908_1clades	78	phiAS5_ORF0203	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53433.1	001413	Cluster908_1clades	84	65p427	Aeromonas virus 65	GCA_000893255.1
AAQ17734.1	001413	Cluster908_1clades	79	Aeh1ORF074c	Aeromonas virus Aeh1	GCA_000843245.1
QCG76058.1	001414	SIG+TM	81	EST35_0177	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAQ64355.1	001414	SIG+TM	84	KVP40.0285	Vibrio phage KVP40	GCA_000843785.1
QIW90669.1	001414	SIG+TM	84	GCAPEGMB_00322	Vibrio phage V07	GCA_012361095.1
QIW91129.1	001414	SIG+TM	84	COHAPHLL_00293	Vibrio phage V09	GCA_012361135.1
QHJ74464.1	001414	SIG+TM	84	VH12019_00137	Vibrio phage VH1_2019	GCA_009931825.1
AGB06958.1	001414	SIG+TM	84	CF80_gp171	Vibrio phage VH7D	GCA_000914495.1
QBX06187.1	001414	SIG+TM	84	ValB1HC_234	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61204.1	001414	SIG+TM	85	AVU32_gp363	Vibrio phage ValKK3	GCA_001501635.1
AGN30331.1	001414	SIG+TM	84	VPFG_00334	Vibrio phage nt-1	GCA_000910195.2
ALP47252.1	001414	SIG+TM	84	phiGrn1_0018	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47636.1	001414	SIG+TM	84	phiST2_0149	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54812.1	001414	SIG+TM	84	vBValMR10Z_272	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37516.1	001414	SIG+TM	84	pp2_283	Vibriophage phi-pp2	GCA_002630725.1
AIT14385.1	001415	Cluster910_1clades	61	PBI_121Q_495	Escherichia phage 121Q	GCA_000926855.1
QAY00563.1	001415	Cluster910_1clades	61	Ecwhy1_284	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34757.1	001415	Cluster910_1clades	61	ACQ29_gp077	Escherichia phage PBECO4	GCA_001041035.1
BBM62056.1	001415	Cluster910_1clades	61	EO157G_4670	Escherichia phage SP27	GCA_008033345.1
AXC36872.1	001415	Cluster910_1clades	61	-	Escherichia phage UB	GCA_003341455.1
QBO61918.1	001415	Cluster910_1clades	61	G17_00429	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13951.1	001415	Cluster910_1clades	61	vBEcoMphAPEC6_gp327c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80373.1	001415	Cluster910_1clades	61	PSLUR01_00396	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44792.1	001415	Cluster910_1clades	57	RaK2_00519	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
BAG41759.1	001415	Cluster910_1clades	85	RSL1_ORF312	Ralstonia phage phiRSL1	GCA_000879455.1
QCW18845.1	001415	Cluster910_1clades	61	7t3_0324	Salmonella phage 7t3	GCA_006083215.1
AZU98107.1	001415	Cluster910_1clades	61	CPT_Munch_163	Salmonella phage Munch	GCA_004015485.1
QIG62875.1	001415	Cluster910_1clades	61	SEPL_262	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB13763.1	001416	Cluster911_1clades	79	Ccr10_gp233	Caulobacter phage Ccr10	GCA_002619445.1
ARB14108.1	001416	Cluster911_1clades	79	Ccr2_gp232	Caulobacter phage Ccr2	GCA_002619465.1
ARB14802.1	001416	Cluster911_1clades	79	Ccr29_gp246	Caulobacter phage Ccr29	GCA_002619485.1
ARB15142.1	001416	Cluster911_1clades	79	Ccr32_gp224	Caulobacter phage Ccr32	GCA_002619505.1
ARB15476.1	001416	Cluster911_1clades	79	Ccr34_gp234	Caulobacter phage Ccr34	GCA_002619525.1
ARB14450.1	001416	Cluster911_1clades	79	Ccr5_gp230	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68430.1	001416	Cluster911_1clades	84	CcrBL10_gp226	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68954.1	001416	Cluster911_1clades	82	CcrPW_gp415c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87758.1	001416	Cluster911_1clades	79	CcrKarma_gp241	Caulobacter virus Karma	GCA_000901575.1
AFU87405.1	001416	Cluster911_1clades	79	CcrMagneto_gp235	Caulobacter virus Magneto	GCA_000903095.1
AFU86716.1	001416	Cluster911_1clades	84	CcrRogue_gp234	Caulobacter virus Rogue	GCA_000900555.1
AFU88553.1	001416	Cluster911_1clades	79	CcrSwift_gp235	Caulobacter virus Swift	GCA_000899655.1
AFU87061.1	001416	Cluster911_1clades	79	CbK_gp229	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64250.1	001417	SIG+TM	82	KVP40.0181	Vibrio phage KVP40	GCA_000843785.1
QIW90566.1	001417	SIG+TM	82	GCAPEGMB_00219	Vibrio phage V07	GCA_012361095.1
QIW91233.1	001417	SIG+TM	82	COHAPHLL_00397	Vibrio phage V09	GCA_012361135.1
QHJ74364.1	001417	SIG+TM	82	VH12019_00037	Vibrio phage VH1_2019	GCA_009931825.1
AGB06859.1	001417	SIG+TM	84	CF80_gp072	Vibrio phage VH7D	GCA_000914495.1
QBX06286.1	001417	SIG+TM	80	ValB1HC_333	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60915.1	001417	SIG+TM	78	AVU32_gp074	Vibrio phage ValKK3	GCA_001501635.1
AJT60914.1	001417	SIG+TM	80	AVU32_gp073	Vibrio phage ValKK3	GCA_001501635.1
AGN30239.1	001417	SIG+TM	78	VPFG_00240	Vibrio phage nt-1	GCA_000910195.2
ALP47263.1	001417	SIG+TM	80	phiGrn1_0299	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47646.1	001417	SIG+TM	80	phiST2_0055	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54913.1	001417	SIG+TM	80	vBValMR10Z_373	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37411.1	001417	SIG+TM	82	pp2_178	Vibriophage phi-pp2	GCA_002630725.1
AMO43088.1	001418	Cluster913_1clades	72	R1080702_079	Cyanophage S-RIM32	GCA_001754165.1
AMO43317.1	001418	Cluster913_1clades	72	W270710_073	Cyanophage S-RIM44	GCA_002599145.1
AOO11550.1	001418	Cluster913_1clades	72	ES420910_069	Cyanophage S-RIM44	GCA_002599165.1
AOO11789.1	001418	Cluster913_1clades	72	Np050604_073	Cyanophage S-RIM44	GCA_002599185.1
AOO12015.1	001418	Cluster913_1clades	72	Np200711_069	Cyanophage S-RIM44	GCA_002599205.1
AOO12251.1	001418	Cluster913_1clades	72	Np420711_069	Cyanophage S-RIM44	GCA_002599225.1
AOO12490.1	001418	Cluster913_1clades	72	Sn080709_073	Cyanophage S-RIM44	GCA_002599245.1
AOO12716.1	001418	Cluster913_1clades	72	Sn130910_069	Cyanophage S-RIM44	GCA_002599265.1
AOO12955.1	001418	Cluster913_1clades	72	W2100709_073	Cyanophage S-RIM44	GCA_002599285.1
ADO99171.1	001418	Cluster913_1clades	72	Syn1_070	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59521.1	001418	Cluster913_1clades	82	S330809_060	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59283.1	001418	Cluster913_1clades	82	C440309_060	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59759.1	001418	Cluster913_1clades	82	N231010_060	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13582.1	001419	Cluster915_1clades	79	Ccr10_gp054	Caulobacter phage Ccr10	GCA_002619445.1
ARB13928.1	001419	Cluster915_1clades	79	Ccr2_gp053	Caulobacter phage Ccr2	GCA_002619465.1
ARB14617.1	001419	Cluster915_1clades	79	Ccr29_gp060	Caulobacter phage Ccr29	GCA_002619485.1
ARB14973.1	001419	Cluster915_1clades	79	Ccr32_gp054	Caulobacter phage Ccr32	GCA_002619505.1
ARB15304.1	001419	Cluster915_1clades	79	Ccr34_gp055	Caulobacter phage Ccr34	GCA_002619525.1
ARB14271.1	001419	Cluster915_1clades	79	Ccr5_gp053	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68256.1	001419	Cluster915_1clades	80	CcrBL10_gp052	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87923.1	001419	Cluster915_1clades	75	CcrColossus_gp053	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87572.1	001419	Cluster915_1clades	79	CcrKarma_gp055	Caulobacter virus Karma	GCA_000901575.1
AFU87222.1	001419	Cluster915_1clades	79	CcrMagneto_gp052	Caulobacter virus Magneto	GCA_000903095.1
AFU86538.1	001419	Cluster915_1clades	80	CcrRogue_gp056	Caulobacter virus Rogue	GCA_000900555.1
AFU88370.1	001419	Cluster915_1clades	79	CcrSwift_gp052	Caulobacter virus Swift	GCA_000899655.1
AFU86886.1	001419	Cluster915_1clades	79	CbK_gp054	Caulobacter virus phiCbK	GCA_000900535.1
AFC21469.1	001420	Cluster916_1clades	67	GAP32_021	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AHI60380.1	001420	Cluster916_1clades	67	Ea357_227	Erwinia phage Ea35-70	GCA_000914635.1
QBP07337.1	001420	Cluster916_1clades	80	REBECCA_232	Erwinia phage Rebecca	GCA_004521635.1
AUG86018.1	001420	Cluster916_1clades	67	BOSOLAPHORUS_232	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52336.2	001420	Cluster916_1clades	67	DM_236	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86337.1	001420	Cluster916_1clades	67	DESERTFOX_230	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86662.1	001420	Cluster916_1clades	67	MADMEL_234	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86983.1	001420	Cluster916_1clades	67	MORTIMER_235	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52010.1	001420	Cluster916_1clades	67	RAY_230	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51694.1	001420	Cluster916_1clades	67	SIMMY50_235	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65045.2	001420	Cluster916_1clades	67	SPECIALG_234	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMM43590.1	001420	Cluster916_1clades	67	CBB_25	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44141.1	001420	Cluster916_1clades	67	CBB_578	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMO43203.1	001421	Cluster917_1clades	49	R1080702_194	Cyanophage S-RIM32	GCA_001754165.1
AMO43433.1	001421	Cluster917_1clades	49	W270710_189	Cyanophage S-RIM44	GCA_002599145.1
AOO11677.1	001421	Cluster917_1clades	49	ES420910_196	Cyanophage S-RIM44	GCA_002599165.1
AOO11905.1	001421	Cluster917_1clades	49	Np050604_189	Cyanophage S-RIM44	GCA_002599185.1
AOO12143.1	001421	Cluster917_1clades	49	Np200711_197	Cyanophage S-RIM44	GCA_002599205.1
AOO12378.1	001421	Cluster917_1clades	49	Np420711_196	Cyanophage S-RIM44	GCA_002599225.1
AOO12606.1	001421	Cluster917_1clades	49	Sn080709_189	Cyanophage S-RIM44	GCA_002599245.1
AOO12843.1	001421	Cluster917_1clades	49	Sn130910_196	Cyanophage S-RIM44	GCA_002599265.1
AOO13072.1	001421	Cluster917_1clades	49	W2100709_190	Cyanophage S-RIM44	GCA_002599285.1
ADO99292.1	001421	Cluster917_1clades	77	Syn1_192	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59575.1	001421	Cluster917_1clades	51	S330809_114	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59337.1	001421	Cluster917_1clades	51	C440309_114	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59813.1	001421	Cluster917_1clades	51	N231010_114	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43076.1	001422	Cluster918_1clades	47	R1080702_067	Cyanophage S-RIM32	GCA_001754165.1
AMO43303.1	001422	Cluster918_1clades	49	W270710_059	Cyanophage S-RIM44	GCA_002599145.1
AOO11537.1	001422	Cluster918_1clades	49	ES420910_056	Cyanophage S-RIM44	GCA_002599165.1
AOO11775.1	001422	Cluster918_1clades	49	Np050604_059	Cyanophage S-RIM44	GCA_002599185.1
AOO12002.1	001422	Cluster918_1clades	49	Np200711_056	Cyanophage S-RIM44	GCA_002599205.1
AOO12238.1	001422	Cluster918_1clades	49	Np420711_056	Cyanophage S-RIM44	GCA_002599225.1
AOO12476.1	001422	Cluster918_1clades	49	Sn080709_059	Cyanophage S-RIM44	GCA_002599245.1
AOO12703.1	001422	Cluster918_1clades	49	Sn130910_056	Cyanophage S-RIM44	GCA_002599265.1
AOO12941.1	001422	Cluster918_1clades	49	W2100709_059	Cyanophage S-RIM44	GCA_002599285.1
AGG54347.1	001422	Cluster918_1clades	52	CYWG_00063	Cyanophage S-SSM6b	GCA_002710425.1
ADO99157.1	001422	Cluster918_1clades	49	Syn1_056	Prochlorococcus phage Syn1	GCA_000892495.1
AXQ70539.1	001422	Cluster918_1clades	47	HOU04_gp140	Synechococcus phage S-T4	GCA_003443335.1
QJT70053.1	001422	Cluster918_1clades	72	SynMITS9220M01_040	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMO43138.1	001423	Cluster920_1clades	56	R1080702_129	Cyanophage S-RIM32	GCA_001754165.1
AMO43364.1	001423	Cluster920_1clades	56	W270710_120	Cyanophage S-RIM44	GCA_002599145.1
AOO11608.1	001423	Cluster920_1clades	56	ES420910_127	Cyanophage S-RIM44	GCA_002599165.1
AOO11836.1	001423	Cluster920_1clades	56	Np050604_120	Cyanophage S-RIM44	GCA_002599185.1
AOO12073.1	001423	Cluster920_1clades	56	Np200711_127	Cyanophage S-RIM44	GCA_002599205.1
AOO12309.1	001423	Cluster920_1clades	56	Np420711_127	Cyanophage S-RIM44	GCA_002599225.1
AOO12537.1	001423	Cluster920_1clades	56	Sn080709_120	Cyanophage S-RIM44	GCA_002599245.1
AOO12774.1	001423	Cluster920_1clades	56	Sn130910_127	Cyanophage S-RIM44	GCA_002599265.1
AOO13003.1	001423	Cluster920_1clades	56	W2100709_121	Cyanophage S-RIM44	GCA_002599285.1
ADO99222.1	001423	Cluster920_1clades	56	Syn1_121	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59588.1	001423	Cluster920_1clades	61	S330809_127	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59350.1	001423	Cluster920_1clades	70	C440309_127	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59826.1	001423	Cluster920_1clades	70	N231010_127	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43114.1	001424	Cluster921_1clades	55	R1080702_105	Cyanophage S-RIM32	GCA_001754165.1
AMO43341.1	001424	Cluster921_1clades	64	W270710_097	Cyanophage S-RIM44	GCA_002599145.1
AOO11574.1	001424	Cluster921_1clades	60	ES420910_093	Cyanophage S-RIM44	GCA_002599165.1
AOO11813.1	001424	Cluster921_1clades	64	Np050604_097	Cyanophage S-RIM44	GCA_002599185.1
AOO12039.1	001424	Cluster921_1clades	60	Np200711_093	Cyanophage S-RIM44	GCA_002599205.1
AOO12275.1	001424	Cluster921_1clades	60	Np420711_093	Cyanophage S-RIM44	GCA_002599225.1
AOO12514.1	001424	Cluster921_1clades	64	Sn080709_097	Cyanophage S-RIM44	GCA_002599245.1
AOO12740.1	001424	Cluster921_1clades	60	Sn130910_093	Cyanophage S-RIM44	GCA_002599265.1
AOO12980.1	001424	Cluster921_1clades	64	W2100709_098	Cyanophage S-RIM44	GCA_002599285.1
ADO99199.1	001424	Cluster921_1clades	64	Syn1_098	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59553.1	001424	Cluster921_1clades	68	S330809_092	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59315.1	001424	Cluster921_1clades	68	C440309_092	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59791.1	001424	Cluster921_1clades	68	N231010_092	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43123.1	001425	Cluster922_1clades	62	R1080702_114	Cyanophage S-RIM32	GCA_001754165.1
AMO43348.1	001425	Cluster922_1clades	66	W270710_104	Cyanophage S-RIM44	GCA_002599145.1
AOO11592.1	001425	Cluster922_1clades	61	ES420910_111	Cyanophage S-RIM44	GCA_002599165.1
AOO11820.1	001425	Cluster922_1clades	66	Np050604_104	Cyanophage S-RIM44	GCA_002599185.1
AOO12057.1	001425	Cluster922_1clades	61	Np200711_111	Cyanophage S-RIM44	GCA_002599205.1
AOO12293.1	001425	Cluster922_1clades	61	Np420711_111	Cyanophage S-RIM44	GCA_002599225.1
AOO12521.1	001425	Cluster922_1clades	66	Sn080709_104	Cyanophage S-RIM44	GCA_002599245.1
AOO12758.1	001425	Cluster922_1clades	61	Sn130910_111	Cyanophage S-RIM44	GCA_002599265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12987.1	001425	Cluster922_1clades	66	W2100709_105	Cyanophage S-RIM44	GCA_002599285.1
ADO99206.1	001425	Cluster922_1clades	66	Syn1_105	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59568.1	001425	Cluster922_1clades	65	S330809_107	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59330.1	001425	Cluster922_1clades	65	C440309_107	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59806.1	001425	Cluster922_1clades	65	N231010_107	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43426.1	001426	Cluster923_1clades	66	W270710_182	Cyanophage S-RIM44	GCA_002599145.1
AOO11670.1	001426	Cluster923_1clades	66	ES420910_189	Cyanophage S-RIM44	GCA_002599165.1
AOO11898.1	001426	Cluster923_1clades	66	Np050604_182	Cyanophage S-RIM44	GCA_002599185.1
AOO12136.1	001426	Cluster923_1clades	66	Np200711_190	Cyanophage S-RIM44	GCA_002599205.1
AOO12371.1	001426	Cluster923_1clades	66	Np420711_189	Cyanophage S-RIM44	GCA_002599225.1
AOO12599.1	001426	Cluster923_1clades	66	Sn080709_182	Cyanophage S-RIM44	GCA_002599245.1
AOO12836.1	001426	Cluster923_1clades	66	Sn130910_189	Cyanophage S-RIM44	GCA_002599265.1
AOO13065.1	001426	Cluster923_1clades	66	W2100709_183	Cyanophage S-RIM44	GCA_002599285.1
ADO99285.1	001426	Cluster923_1clades	66	Syn1_184	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30624.1	001426	Cluster923_1clades	62	Syn7803US37_147	Synechococcus phage ACG-2014f	GCA_002594065.1
AOV59579.1	001426	Cluster923_1clades	35	S330809_118	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59341.1	001426	Cluster923_1clades	35	C440309_118	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59817.1	001426	Cluster923_1clades	35	N231010_118	Synechococcus phage S-CAM4	GCA_002922155.1
AMO43030.1	001427	Cluster924_1clades	65	R1080702_015	Cyanophage S-RIM32	GCA_001754165.1
AMO43261.1	001427	Cluster924_1clades	65	W270710_016	Cyanophage S-RIM44	GCA_002599145.1
AOO11498.1	001427	Cluster924_1clades	64	ES420910_016	Cyanophage S-RIM44	GCA_002599165.1
AOO11733.1	001427	Cluster924_1clades	65	Np050604_016	Cyanophage S-RIM44	GCA_002599185.1
AOO11963.1	001427	Cluster924_1clades	64	Np200711_016	Cyanophage S-RIM44	GCA_002599205.1
AOO12199.1	001427	Cluster924_1clades	64	Np420711_016	Cyanophage S-RIM44	GCA_002599225.1
AOO12434.1	001427	Cluster924_1clades	65	Sn080709_016	Cyanophage S-RIM44	GCA_002599245.1
AOO12664.1	001427	Cluster924_1clades	64	Sn130910_016	Cyanophage S-RIM44	GCA_002599265.1
AOO12899.1	001427	Cluster924_1clades	65	W2100709_016	Cyanophage S-RIM44	GCA_002599285.1
AGG54477.1	001427	Cluster924_1clades	65	CYWG_00193	Cyanophage S-SSM6b	GCA_002710425.1
ADO99119.1	001427	Cluster924_1clades	65	Syn1_017	Prochlorococcus phage Syn1	GCA_000892495.1
ASR76306.1	001427	Cluster924_1clades	65	PBI_BELLAMY_270	Synechococcus phage Bellamy	GCA_002627525.1
QJT70133.1	001427	Cluster924_1clades	65	SynMITS9220M01_120	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AJK27522.1	001428	Cluster925_1clades	43	PTIM40_95	Cyanophage P-TIM40	GCA_001470935.1
AOO14281.1	001428	Cluster925_1clades	49	Sn110110_087	Cyanophage S-RIM14	GCA_002599065.1
AOO14930.1	001428	Cluster925_1clades	49	W1230910_084	Cyanophage S-RIM14	GCA_002599125.1
AMO43105.1	001428	Cluster925_1clades	47	R1080702_096	Cyanophage S-RIM32	GCA_001754165.1
AGG54302.1	001428	Cluster925_1clades	49	CYWG_00018	Cyanophage S-SSM6b	GCA_002710425.1
AIR93626.1	001428	Cluster925_1clades	38	AVU42_gp082	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76151.1	001428	Cluster925_1clades	44	PBI_BELLAMY_106	Synechococcus phage Bellamy	GCA_002627525.1
QCW22837.1	001428	Cluster925_1clades	48	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50595.1	001428	Cluster925_1clades	48	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50503.1	001428	Cluster925_1clades	48	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59544.1	001428	Cluster925_1clades	48	S330809_083	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59306.1	001428	Cluster925_1clades	48	C440309_083	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59782.1	001428	Cluster925_1clades	48	N231010_083	Synechococcus phage S-CAM4	GCA_002922155.1
AOO14328.1	001429	Cluster926_1clades	43	Sn110110_134	Cyanophage S-RIM14	GCA_002599065.1
AOO14977.1	001429	Cluster926_1clades	43	W1230910_131	Cyanophage S-RIM14	GCA_002599125.1
AMO43264.1	001429	Cluster926_1clades	43	W270710_019	Cyanophage S-RIM44	GCA_002599145.1
AOO11501.1	001429	Cluster926_1clades	43	ES420910_019	Cyanophage S-RIM44	GCA_002599165.1
AOO11736.1	001429	Cluster926_1clades	43	Np050604_019	Cyanophage S-RIM44	GCA_002599185.1
AOO11966.1	001429	Cluster926_1clades	43	Np200711_019	Cyanophage S-RIM44	GCA_002599205.1
AOO12202.1	001429	Cluster926_1clades	43	Np420711_019	Cyanophage S-RIM44	GCA_002599225.1
AOO12437.1	001429	Cluster926_1clades	43	Sn080709_019	Cyanophage S-RIM44	GCA_002599245.1
AOO12667.1	001429	Cluster926_1clades	43	Sn130910_019	Cyanophage S-RIM44	GCA_002599265.1
AOO12902.1	001429	Cluster926_1clades	43	W2100709_019	Cyanophage S-RIM44	GCA_002599285.1
AOV59478.1	001429	Cluster926_1clades	43	S330809_017	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59240.1	001429	Cluster926_1clades	43	C440309_017	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59716.1	001429	Cluster926_1clades	43	N231010_017	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67197.1	001430	Cluster929_1clades	1336	AD1_153	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79949.1	001430	Cluster929_1clades	1027	JA11_144	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66548.1	001430	Cluster929_1clades	1027	JA13_145	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66873.1	001430	Cluster929_1clades	1027	JA29_147	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67518.1	001430	Cluster929_1clades	1027	JA33_144	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08430.1	001430	Cluster929_1clades	1336	Alexandra_158	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58794.1	001430	Cluster929_1clades	1335	Y3_154	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28632.1	001430	Cluster929_1clades	1354	YOLOSWAG_152	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38448.1	001430	Cluster929_1clades	826	BN7874_248	Phage NCTB	GCA_900092385.1
AFH14610.1	001430	Cluster929_1clades	550	Lu11_0078	Pseudomonas phage Lu11	GCA_000897175.1
AFH14611.1	001430	Cluster929_1clades	782	Lu11_0079	Pseudomonas phage Lu11	GCA_000897175.1
AGS82090.1	001430	Cluster929_1clades	1524	PaBG_00215	Pseudomonas phage PaBG	GCA_000912555.1
AHI60154.1	001431	PAT1	823	Ea357_004	Erwinia phage Ea35-70	GCA_000914635.1
QBP07112.1	001431	PAT1	827	REBECCA_4	Erwinia phage Rebecca	GCA_004521635.1
AUG85792.1	001431	PAT1	823	BOSOLAPHORUS_4	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52102.1	001431	PAT1	829	DM_4	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86112.1	001431	PAT1	827	DESERTFOX_4	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86432.1	001431	PAT1	827	MADMEL_4	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86753.1	001431	PAT1	823	MORTIMER_4	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51785.1	001431	PAT1	827	RAY_4	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51466.1	001431	PAT1	823	SIMMY50_4	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64814.1	001431	PAT1	827	SPECIALG_4	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP23997.1	001431	PAT1	892	-	Proteus phage 10	GCA_014071245.1
QKE54317.1	001431	PAT1	874	ACSA002_0030	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60449.1	001432	SecA	780	Ea357_295	Erwinia phage Ea35-70	GCA_000914635.1
QBP07406.1	001432	SecA	780	REBECCA_301	Erwinia phage Rebecca	GCA_004521635.1
AUG86088.1	001432	SecA	780	BOSOLAPHORUS_302	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52404.1	001432	SecA	780	DM_305	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86408.1	001432	SecA	780	DESERTFOX_301	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86729.1	001432	SecA	780	MADMEL_302	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87054.1	001432	SecA	780	MORTIMER_306	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52079.1	001432	SecA	780	RAY_299	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51762.1	001432	SecA	780	SIMMY50_304	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65114.1	001432	SecA	780	SPECIALG_303	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24202.1	001432	SecA	787	-	Proteus phage 10	GCA_014071245.1
QKE54626.1	001432	SecA	761	ACSA002_3090	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60372.1	001433	Cluster933_1clades	711	Ea357_219	Erwinia phage Ea35-70	GCA_000914635.1
QBP07329.1	001433	Cluster933_1clades	711	REBECCA_224	Erwinia phage Rebecca	GCA_004521635.1
AUG86010.1	001433	Cluster933_1clades	711	BOSOLAPHORUS_224	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52327.1	001433	Cluster933_1clades	711	DM_227	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86329.1	001433	Cluster933_1clades	711	DESERTFOX_222	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86652.1	001433	Cluster933_1clades	711	MADMEL_224	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86975.1	001433	Cluster933_1clades	711	MORTIMER_227	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52002.1	001433	Cluster933_1clades	711	RAY_222	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51686.1	001433	Cluster933_1clades	711	SIMMY50_227	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65036.1	001433	Cluster933_1clades	711	SPECIALG_225	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24145.1	001433	Cluster933_1clades	705	-	Proteus phage 10	GCA_014071245.1
QKE54546.1	001433	Cluster933_1clades	690	ACSA002_2300	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13754.1	001434	Cluster934_1clades	707	Ccr10_gp224c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14099.1	001434	Cluster934_1clades	707	Ccr2_gp223c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14788.1	001434	Cluster934_1clades	707	Ccr29_gp232	Caulobacter phage Ccr29	GCA_002619485.1
ARB15132.1	001434	Cluster934_1clades	707	Ccr32_gp214	Caulobacter phage Ccr32	GCA_002619505.1
ARB15466.1	001434	Cluster934_1clades	707	Ccr34_gp224	Caulobacter phage Ccr34	GCA_002619525.1
ARB14441.1	001434	Cluster934_1clades	707	Ccr5_gp221c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68421.1	001434	Cluster934_1clades	590	CcrBL10_gp217c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87748.1	001434	Cluster934_1clades	672	CcrKarma_gp231	Caulobacter virus Karma	GCA_000901575.1
AFU87396.1	001434	Cluster934_1clades	707	CcrMagneto_gp226	Caulobacter virus Magneto	GCA_000903095.1
AFU86707.1	001434	Cluster934_1clades	620	CcrRogue_gp225	Caulobacter virus Rogue	GCA_000900555.1
AFU88544.1	001434	Cluster934_1clades	672	CcrSwift_gp226	Caulobacter virus Swift	GCA_000899655.1
AFU87051.1	001434	Cluster934_1clades	672	CbK_gp219	Caulobacter virus phiCbK	GCA_000900535.1
AUZ94814.1	001435	HslUClpX-AAA	419	FDI40_gp002	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93517.1	001435	HslUClpX-AAA	436	G_258	Bacillus virus G	GCA_000917535.1
AFO71347.1	001435	HslUClpX-AAA	687	CR5_127	Cronobacter phage CR5	GCA_000910235.1
QBP07555.1	001435	HslUClpX-AAA	684	DERBICUS_129	Erwinia phage Derbicus	GCA_004521655.1
ANZ48978.1	001435	HslUClpX-AAA	684	EARLPHILLIPIV_129	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50320.1	001435	HslUClpX-AAA	682	PHOBOS_130	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AXH72840.1	001435	HslUClpX-AAA	401	-	Myoviridae sp.	GCA_003657725.1
QHJ86112.1	001435	HslUClpX-AAA	275	KKIINIFJ_00201	Pseudomonas phage PN05	GCA_009931935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCG76136.1	001435	HslUClpX-AAA	408	EST35_0255	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44209.1	001435	HslUClpX-AAA	404	PBI_SCTP2_194	Salicola phage SCTP-2	GCA_002625545.1
prevph1000000116	001435	HslUClpX-AAA	419	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000083	001435	HslUClpX-AAA	419	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ARB13679.1	001436	Cluster936_1clades	544	Ccr10_gp150c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14024.1	001436	Cluster936_1clades	544	Ccr2_gp149c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14712.1	001436	Cluster936_1clades	544	Ccr29_gp156	Caulobacter phage Ccr29	GCA_002619485.1
ARB15067.1	001436	Cluster936_1clades	552	Ccr32_gp149	Caulobacter phage Ccr32	GCA_002619505.1
ARB15401.1	001436	Cluster936_1clades	552	Ccr34_gp159	Caulobacter phage Ccr34	GCA_002619525.1
ARB14367.1	001436	Cluster936_1clades	544	Ccr5_gp148c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68350.1	001436	Cluster936_1clades	635	CcrBL10_gp146c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87672.1	001436	Cluster936_1clades	544	CcrKarma_gp155	Caulobacter virus Karma	GCA_000901575.1
AFU87321.1	001436	Cluster936_1clades	548	CcrMagneto_gp151	Caulobacter virus Magneto	GCA_000903095.1
AFU86634.1	001436	Cluster936_1clades	637	CcrRogue_gp152	Caulobacter virus Rogue	GCA_000900555.1
AFU88468.1	001436	Cluster936_1clades	547	CcrSwift_gp150	Caulobacter virus Swift	GCA_000899655.1
AFU86985.1	001436	Cluster936_1clades	552	CbK_gp153	Caulobacter virus phiCbK	GCA_000900535.1
ARB13773.1	001437	Cluster938_1clades	586	Ccr10_gp243	Caulobacter phage Ccr10	GCA_002619445.1
ARB14118.1	001437	Cluster938_1clades	586	Ccr2_gp242	Caulobacter phage Ccr2	GCA_002619465.1
ARB14812.1	001437	Cluster938_1clades	586	Ccr29_gp256	Caulobacter phage Ccr29	GCA_002619485.1
ARB15152.1	001437	Cluster938_1clades	586	Ccr32_gp234	Caulobacter phage Ccr32	GCA_002619505.1
ARB15486.1	001437	Cluster938_1clades	586	Ccr34_gp244	Caulobacter phage Ccr34	GCA_002619525.1
ARB14460.1	001437	Cluster938_1clades	589	Ccr5_gp240	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68438.1	001437	Cluster938_1clades	593	CcrBL10_gp234	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87768.1	001437	Cluster938_1clades	586	CcrKarma_gp251	Caulobacter virus Karma	GCA_000901575.1
AFU87415.1	001437	Cluster938_1clades	586	CcrMagneto_gp245	Caulobacter virus Magneto	GCA_000903095.1
AFU86724.1	001437	Cluster938_1clades	582	CcrRogue_gp242	Caulobacter virus Rogue	GCA_000900555.1
AFU88563.1	001437	Cluster938_1clades	586	CcrSwift_gp245	Caulobacter virus Swift	GCA_000899655.1
AFU87071.1	001437	Cluster938_1clades	586	CbK_gp239	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64168.1	001438	START	484	KVP40.0097	Vibrio phage KVP40	GCA_000843785.1
QIW90491.1	001438	START	483	GCAPEGMB_00144	Vibrio phage V07	GCA_012361095.1
QIW90938.1	001438	START	484	COHAPHLL_00075	Vibrio phage V09	GCA_012361135.1
QHJ74279.1	001438	START	484	VH12019_00360	Vibrio phage VH1_2019	GCA_009931825.1
AGB07104.1	001438	START	483	CF80_gp317	Vibrio phage VH7D	GCA_000914495.1
QBX05991.1	001438	START	483	ValB1HC_037	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61004.1	001438	START	483	AVU32_gp163	Vibrio phage ValKK3	GCA_001501635.1
AGN30147.1	001438	START	554	VPFG_00145	Vibrio phage nt-1	GCA_000910195.2
ALP46981.1	001438	START	483	phiGrn1_0211	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47364.1	001438	START	483	phiST2_0344	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54616.1	001438	START	483	vBValMR10Z_75	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37327.1	001438	START	484	pp2_094	Vibriophage phi-pp2	GCA_002630725.1
AHI60445.1	001439	TonB_N	529	Ea357_291	Erwinia phage Ea35-70	GCA_000914635.1
QBP07402.1	001439	TonB_N	529	REBECCA_297	Erwinia phage Rebecca	GCA_004521635.1
AUG86084.1	001439	TonB_N	529	BOSOLAPHORUS_298	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52400.1	001439	TonB_N	529	DM_301	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86404.1	001439	TonB_N	529	DESERTFOX_297	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86725.1	001439	TonB_N	529	MADMEL_298	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87050.1	001439	TonB_N	529	MORTIMER_302	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52075.1	001439	TonB_N	529	RAY_295	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51758.1	001439	TonB_N	529	SIMMY50_300	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65110.1	001439	TonB_N	529	SPECIALG_299	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24198.1	001439	TonB_N	475	-	Proteus phage 10	GCA_014071245.1
QKE54622.1	001439	TonB_N	493	ACSA002_3050	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60317.1	001440	Cluster941_1clades	512	Ea357_166	Erwinia phage Ea35-70	GCA_000914635.1
QBP07276.1	001440	Cluster941_1clades	512	REBECCA_169	Erwinia phage Rebecca	GCA_004521635.1
AUG85956.1	001440	Cluster941_1clades	512	BOSOLAPHORUS_169	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52271.1	001440	Cluster941_1clades	512	DM_173	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86275.1	001440	Cluster941_1clades	512	DESERTFOX_168	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86597.1	001440	Cluster941_1clades	512	MADMEL_169	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86921.1	001440	Cluster941_1clades	512	MORTIMER_172	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51948.1	001440	Cluster941_1clades	512	RAY_167	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51632.1	001440	Cluster941_1clades	512	SIMMY50_170	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64979.1	001440	Cluster941_1clades	512	SPECIALG_169	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24098.1	001440	Cluster941_1clades	513	-	Proteus phage 10	GCA_014071245.1
QKE54474.1	001440	Cluster941_1clades	509	ACSA002_1600	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13712.1	001441	Cluster942_1clades	473	Ccr10_gp182c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14057.1	001441	Cluster942_1clades	473	Ccr2_gp181c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14744.1	001441	Cluster942_1clades	473	Ccr29_gp188	Caulobacter phage Ccr29	GCA_002619485.1
ARB15099.1	001441	Cluster942_1clades	473	Ccr32_gp181	Caulobacter phage Ccr32	GCA_002619505.1
ARB15433.1	001441	Cluster942_1clades	473	Ccr34_gp191	Caulobacter phage Ccr34	GCA_002619525.1
ARB14400.1	001441	Cluster942_1clades	473	Ccr5_gp180c	Caulobacter phage Ccr5	GCA_002619545.1
AFU88103.1	001441	Cluster942_1clades	491	CcrColossus_gp233	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68780.1	001441	Cluster942_1clades	491	CcrPW_gp241	Caulobacter phage CcrPW	GCA_003443275.1
AFU87705.1	001441	Cluster942_1clades	473	CcrKarma_gp188	Caulobacter virus Karma	GCA_000901575.1
AFU87354.1	001441	Cluster942_1clades	473	CcrMagneto_gp184	Caulobacter virus Magneto	GCA_000903095.1
AFU88501.1	001441	Cluster942_1clades	473	CcrSwift_gp183	Caulobacter virus Swift	GCA_000899655.1
AFU87018.1	001441	Cluster942_1clades	473	CbK_gp186	Caulobacter virus phiCbK	GCA_000900535.1
AHI60438.1	001442	Cluster943_1clades	488	Ea357_284	Erwinia phage Ea35-70	GCA_000914635.1
QBP07395.1	001442	Cluster943_1clades	488	REBECCA_290	Erwinia phage Rebecca	GCA_004521635.1
AUG86077.1	001442	Cluster943_1clades	488	BOSOLAPHORUS_291	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52393.1	001442	Cluster943_1clades	488	DM_294	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86397.1	001442	Cluster943_1clades	488	DESERTFOX_290	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86718.1	001442	Cluster943_1clades	488	MADMEL_291	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87043.1	001442	Cluster943_1clades	488	MORTIMER_295	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52068.1	001442	Cluster943_1clades	488	RAY_288	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51751.1	001442	Cluster943_1clades	488	SIMMY50_293	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65103.1	001442	Cluster943_1clades	488	SPECIALG_292	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24191.1	001442	Cluster943_1clades	461	-	Proteus phage 10	GCA_014071245.1
QKE54615.1	001442	Cluster943_1clades	468	ACSA002_2980	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64193.1	001443	QTG	459	KVP40.0122	Vibrio phage KVP40	GCA_000843785.1
QIW90836.1	001443	QTG	458	GCAPEGMB_00521	Vibrio phage V07	GCA_012361095.1
QIW90913.1	001443	QTG	458	COHAPHLL_00050	Vibrio phage V09	GCA_012361135.1
QHJ74305.1	001443	QTG	458	VH12019_00386	Vibrio phage VH1_2019	GCA_009931825.1
AGB06799.1	001443	QTG	458	CF80_gp012	Vibrio phage VH7D	GCA_000914495.1
QBX05967.1	001443	QTG	458	ValB1HC_013	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60979.1	001443	QTG	458	AVU32_gp138	Vibrio phage ValKK3	GCA_001501635.1
AGN30173.2	001443	QTG	464	VPFG_00171	Vibrio phage nt-1	GCA_000910195.2
ALP46987.1	001443	QTG	458	phiGrn1_0234	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47368.1	001443	QTG	458	phiST2_0370	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54592.1	001443	QTG	458	vBValMR10Z_51	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37353.1	001443	QTG	458	pp2_120	Vibriophage phi-pp2	GCA_002630725.1
AHI60446.1	001444	Cluster945_1clades	461	Ea357_292	Erwinia phage Ea35-70	GCA_000914635.1
QBP07403.1	001444	Cluster945_1clades	461	REBECCA_298	Erwinia phage Rebecca	GCA_004521635.1
AUG86085.1	001444	Cluster945_1clades	461	BOSOLAPHORUS_299	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52401.1	001444	Cluster945_1clades	461	DM_302	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86405.1	001444	Cluster945_1clades	461	DESERTFOX_298	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86726.1	001444	Cluster945_1clades	461	MADMEL_299	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87051.1	001444	Cluster945_1clades	461	MORTIMER_303	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52076.1	001444	Cluster945_1clades	461	RAY_296	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51759.1	001444	Cluster945_1clades	461	SIMMY50_301	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65111.1	001444	Cluster945_1clades	461	SPECIALG_300	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24199.1	001444	Cluster945_1clades	442	-	Proteus phage 10	GCA_014071245.1
QKE54623.1	001444	Cluster945_1clades	437	ACSA002_3060	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AMS01115.1	001445	Cluster946_1clades	226	AR9_g030	Bacillus phage AR9	GCA_001743835.1
AMS01116.1	001445	Cluster946_1clades	383	AR9_g031	Bacillus phage AR9	GCA_001743835.1
AMS01119.1	001445	Cluster946_1clades	409	AR9_g034	Bacillus phage AR9	GCA_001743835.1
AMS01120.1	001445	Cluster946_1clades	410	AR9_g035	Bacillus phage AR9	GCA_001743835.1
AMS01121.1	001445	Cluster946_1clades	381	AR9_g036	Bacillus phage AR9	GCA_001743835.1
ALN97767.1	001445	Cluster946_1clades	418	Bp8pS_088	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97770.1	001445	Cluster946_1clades	440	Bp8pS_091	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00037.1	001445	Cluster946_1clades	232	PBI_PBS1_215	Bacillus virus PBS1	GCA_002601325.1
ASU00040.1	001445	Cluster946_1clades	387	PBI_PBS1_218	Bacillus virus PBS1	GCA_002601325.1
ASU00043.1	001445	Cluster946_1clades	410	PBI_PBS1_221	Bacillus virus PBS1	GCA_002601325.1
ASU00044.1	001445	Cluster946_1clades	411	PBI_PBS1_222	Bacillus virus PBS1	GCA_002601325.1
ASU00045.1	001445	Cluster946_1clades	381	PBI_PBS1_223	Bacillus virus PBS1	GCA_002601325.1
ABY62988.1	001446	Cluster947_1clades	367	201phi2-1p158	Pseudomonas phage 201phi2-1	GCA_000875305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANM44881.1	001446	Cluster947_1clades	371	KTN4_123	Pseudomonas phage KTN4	GCA_002607225.1
ARV77265.1	001446	Cluster947_1clades	411	NOXIFER_95	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32258.1	001446	Cluster947_1clades	150	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32257.1	001446	Cluster947_1clades	222	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76773.1	001446	Cluster947_1clades	367	PHABIO_142	Pseudomonas phage Phabio	GCA_002624965.1
AEH03525.1	001446	Cluster947_1clades	376	101	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02636.1	001446	Cluster947_1clades	387	PSA21_108	Pseudomonas phage Psa21	GCA_004340405.1
ATN94832.1	001446	Cluster947_1clades	371	SL2_255	Pseudomonas phage SL2	GCA_002956015.1
QJB22758.1	001446	Cluster947_1clades	371	fnug_115	Pseudomonas phage fnug	GCA_012837215.1
QEM41832.1	001446	Cluster947_1clades	373	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82997.1	001446	Cluster947_1clades	371	PHIKZ096	Pseudomonas virus phiKZ	GCA_000842965.1
AYD79942.1	001447	Cluster948_1clades	307	JA11_137	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD79943.1	001447	Cluster948_1clades	280	JA11_138	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66541.1	001447	Cluster948_1clades	307	JA13_138	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66542.1	001447	Cluster948_1clades	280	JA13_139	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66866.1	001447	Cluster948_1clades	307	JA29_140	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66867.1	001447	Cluster948_1clades	280	JA29_141	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67511.1	001447	Cluster948_1clades	307	JA33_137	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67512.1	001447	Cluster948_1clades	280	JA33_138	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFH14737.1	001447	Cluster948_1clades	304	Lu11_0200	Pseudomonas phage Lu11	GCA_000897175.1
AFH14739.1	001447	Cluster948_1clades	315	Lu11_0202	Pseudomonas phage Lu11	GCA_000897175.1
AFH14743.1	001447	Cluster948_1clades	293	Lu11_0206	Pseudomonas phage Lu11	GCA_000897175.1
ASV44518.1	001447	Cluster948_1clades	384	PBI_SCTP2_503	Salicola phage SCTP-2	GCA_002625545.1
AXG67286.1	001448	Cluster949_1clades	308	AD1_242	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG66463.1	001448	Cluster949_1clades	347	JA13_060	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AWY08614.1	001448	Cluster949_1clades	350	Alexandra_251	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48248.1	001448	Cluster949_1clades	308	ASESINO_235	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48798.1	001448	Cluster949_1clades	295	CHRISDB_236	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AUG86658.1	001448	Cluster949_1clades	342	MADMEL_230	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
ASU03544.1	001448	Cluster949_1clades	333	RISINGSUN_126	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ANJ65042.1	001448	Cluster949_1clades	342	SPECIALG_231	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARW58886.1	001448	Cluster949_1clades	339	Y3_246	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28717.1	001448	Cluster949_1clades	341	YOLOSWAG_240	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QKN86054.1	001448	Cluster949_1clades	307	ACEC001_2110	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKE54392.1	001448	Cluster949_1clades	334	ACSA002_0780	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60419.1	001449	Cluster951_1clades	303	Ea357_265	Erwinia phage Ea35-70	GCA_000914635.1
QBP07376.1	001449	Cluster951_1clades	303	REBECCA_271	Erwinia phage Rebecca	GCA_004521635.1
AUG86058.1	001449	Cluster951_1clades	303	BOSOLAPHORUS_272	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52374.1	001449	Cluster951_1clades	303	DM_275	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86378.1	001449	Cluster951_1clades	303	DESERTFOX_271	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86699.1	001449	Cluster951_1clades	303	MADMEL_272	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87024.1	001449	Cluster951_1clades	303	MORTIMER_276	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52049.1	001449	Cluster951_1clades	303	RAY_269	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51732.1	001449	Cluster951_1clades	303	SIMMY50_274	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65084.1	001449	Cluster951_1clades	303	SPECIALG_273	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24179.1	001449	Cluster951_1clades	277	-	Proteus phage 10	GCA_014071245.1
QKE54599.1	001449	Cluster951_1clades	281	ACSA002_2820	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AGH07712.1	001450	BACTERIALFRINGE	252	CYVG_00269	Cyanophage S-SSM6a	GCA_002710385.1
AAX44484.1	001450	BACTERIALFRINGE	251	PSSM2_106	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12164.1	001450	BACTERIALFRINGE	251	PRTG_00006	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93424.1	001450	BACTERIALFRINGE	299	AVU42_gp081	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30587.1	001450	BACTERIALFRINGE	255	Syn7803US37_110	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54863.1	001450	BACTERIALFRINGE	294	b23_0249	Synechococcus phage B23	GCA_009745195.1
QGT54498.1	001450	BACTERIALFRINGE	294	b3_0256	Synechococcus phage B3	GCA_009745215.1
ASR76150.1	001450	BACTERIALFRINGE	255	PBI_BELLAMY_105	Synechococcus phage Bellamy	GCA_002627525.1
QCW22839.1	001450	BACTERIALFRINGE	259	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50505.1	001450	BACTERIALFRINGE	259	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70601.1	001450	BACTERIALFRINGE	178	HOU04_gp202	Synechococcus phage S-T4	GCA_003443335.1
QJT70089.1	001450	BACTERIALFRINGE	255	SynMITS9220M01_076	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUE22585.1	001451	GxC-R	299	Ah1_00044	Aeromonas phage Ah1	GCA_002957415.1
QAX98620.1	001451	GxC-R	155	ASfcp2_287	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98622.1	001451	GxC-R	144	ASfcp2_289	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52760.1	001451	GxC-R	155	PX29p041	Aeromonas phage PX29	GCA_000920195.1
ADQ52762.1	001451	GxC-R	144	PX29p043	Aeromonas phage PX29	GCA_000920195.1
ADM80016.1	001451	GxC-R	154	phiAS5_ORF0173	Aeromonas phage phiAS5	GCA_000887715.1
ADM80017.1	001451	GxC-R	133	phiAS5_ORF0174	Aeromonas phage phiAS5	GCA_000887715.1
ADM80018.1	001451	GxC-R	137	phiAS5_ORF0175	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17705.1	001451	GxC-R	160	Aeh1ORF046c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17706.1	001451	GxC-R	156	Aeh1ORF047c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17707.1	001451	GxC-R	287	Aeh1ORF048c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17708.1	001451	GxC-R	122	Aeh1ORF049c	Aeromonas virus Aeh1	GCA_000843245.1
ARB13718.1	001452	Cluster954_1clades	294	Ccr10_gp188c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14063.1	001452	Cluster954_1clades	294	Ccr2_gp187c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14750.1	001452	Cluster954_1clades	294	Ccr29_gp194	Caulobacter phage Ccr29	GCA_002619485.1
ARB15105.1	001452	Cluster954_1clades	118	Ccr32_gp187	Caulobacter phage Ccr32	GCA_002619505.1
ARB15439.1	001452	Cluster954_1clades	118	Ccr34_gp197	Caulobacter phage Ccr34	GCA_002619525.1
ARB14406.1	001452	Cluster954_1clades	294	Ccr5_gp186c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68386.1	001452	Cluster954_1clades	298	CcrBL10_gp182c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87711.1	001452	Cluster954_1clades	294	CcrKarma_gp194	Caulobacter virus Karma	GCA_000901575.1
AFU87360.1	001452	Cluster954_1clades	292	CcrMagneto_gp190	Caulobacter virus Magneto	GCA_000903095.1
AFU86672.1	001452	Cluster954_1clades	298	CcrRogue_gp190	Caulobacter virus Rogue	GCA_000900555.1
AFU88507.1	001452	Cluster954_1clades	294	CcrSwift_gp189	Caulobacter virus Swift	GCA_000899655.1
AFU87024.1	001452	Cluster954_1clades	118	CbK_gp192	Caulobacter virus phiCbK	GCA_000900535.1
AHI60338.1	001453	PRODH	285	Ea357_186	Erwinia phage Ea35-70	GCA_000914635.1
QBP07297.1	001453	PRODH	285	REBECCA_190	Erwinia phage Rebecca	GCA_004521635.1
AUG85977.1	001453	PRODH	285	BOSOLAPHORUS_190	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52292.1	001453	PRODH	285	DM_194	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86296.1	001453	PRODH	285	DESERTFOX_189	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86618.1	001453	PRODH	285	MADMEL_190	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86942.1	001453	PRODH	285	MORTIMER_193	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51969.1	001453	PRODH	285	RAY_188	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51653.1	001453	PRODH	285	SIMMY50_191	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65000.1	001453	PRODH	285	SPECIALG_191	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24119.1	001453	PRODH	289	-	Proteus phage 10	GCA_014071245.1
QKE54500.1	001453	PRODH	289	ACSA002_1860	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64268.1	001454	Cluster1379_1clades	197	KVP40.0199	Vibrio phage KVP40	GCA_000843785.1
QIW90585.1	001454	Cluster1379_1clades	197	GCAPEGMB_00238	Vibrio phage V07	GCA_012361095.1
QIW91214.1	001454	Cluster1379_1clades	197	COHAPHLL_00378	Vibrio phage V09	GCA_012361135.1
QHJ74382.1	001454	Cluster1379_1clades	197	VH12019_00055	Vibrio phage VH1_2019	GCA_009931825.1
AGB06885.1	001454	Cluster1379_1clades	197	CF80_gp098	Vibrio phage VH7D	GCA_000914495.1
QBX06261.1	001454	Cluster1379_1clades	197	ValB1HC_308	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60887.1	001454	Cluster1379_1clades	197	AVU32_gp046	Vibrio phage ValKK3	GCA_001501635.1
AGN30258.1	001454	Cluster1379_1clades	197	VPFG_00259	Vibrio phage nt-1	GCA_000910195.2
ALP47073.1	001454	Cluster1379_1clades	197	phiGrn1_0323	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47452.1	001454	Cluster1379_1clades	197	phiST2_0079	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54888.1	001454	Cluster1379_1clades	197	vBValMR10Z_348	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37429.1	001454	Cluster1379_1clades	197	pp2_196	Vibriophage phi-pp2	GCA_002630725.1
AIT14044.1	001455	Cluster956_1clades	262	PBI_121Q_154	Escherichia phage 121Q	GCA_000926855.1
QAY00299.1	001455	Cluster956_1clades	271	Ecwhy1_17	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35049.1	001455	Cluster956_1clades	270	ACQ29_gp369	Escherichia phage PBECO4	GCA_001041035.1
BBM61727.1	001455	Cluster956_1clades	262	EO157G_1380	Escherichia phage SP27	GCA_008033345.1
AXC36626.1	001455	Cluster956_1clades	262	-	Escherichia phage UB	GCA_003341455.1
QBO61655.1	001455	Cluster956_1clades	262	G17_00159	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13708.1	001455	Cluster956_1clades	262	vBEcoMphAPEC6_gp078c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80039.1	001455	Cluster956_1clades	262	PSLUR01_00062	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44506.1	001455	Cluster956_1clades	278	RaK2_00233	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18577.1	001455	Cluster956_1clades	286	7t3_056	Salmonella phage 7t3	GCA_006083215.1
AZU98406.1	001455	Cluster956_1clades	286	CPT_Munch_474	Salmonella phage Munch	GCA_004015485.1
QIG63107.1	001455	Cluster956_1clades	286	SEPL_494	Salmonella phage SE_PL	GCA_011067555.1
AAQ64088.1	001456	Cluster958_1clades	281	KVP40.0017	Vibrio phage KVP40	GCA_000843785.1
QIW90411.1	001456	Cluster958_1clades	281	GCAPEGMB_00064	Vibrio phage V07	GCA_012361095.1
QIW91018.1	001456	Cluster958_1clades	281	COHAPHLL_00155	Vibrio phage V09	GCA_012361135.1
QHJ74200.1	001456	Cluster958_1clades	281	VH12019_00281	Vibrio phage VH1_2019	GCA_009931825.1
AGB07024.1	001456	Cluster958_1clades	281	CF80_gp237	Vibrio phage VH7D	GCA_000914495.1
QBX06072.1	001456	Cluster958_1clades	281	ValB1HC_118	Vibrio phage ValB1 HC	GCA_004771355.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AJT61086.1	001456	Cluster958_1clades	281	AVU32_gp245	Vibrio phage ValKK3	GCA_001501635.1
AGN30069.1	001456	Cluster958_1clades	281	VPFG_00066	Vibrio phage nt-1	GCA_000910195.2
ALP47033.1	001456	Cluster958_1clades	281	phiGrn1_0132	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47412.1	001456	Cluster958_1clades	281	phiST2_0262	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54698.1	001456	Cluster958_1clades	281	vBValMR10Z_157	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37251.1	001456	Cluster958_1clades	251	pp2_017	Vibriophage phi-pp2	GCA_002630725.1
AXG67140.1	001457	Cluster959_1clades	247	AD1_096	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79889.1	001457	Cluster959_1clades	249	JA11_084	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66488.1	001457	Cluster959_1clades	249	JA13_085	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66813.1	001457	Cluster959_1clades	249	JA29_087	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67458.1	001457	Cluster959_1clades	249	JA33_084	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08376.1	001457	Cluster959_1clades	247	Alexandra_101	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58739.1	001457	Cluster959_1clades	247	Y3_099	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28572.1	001457	Cluster959_1clades	249	YOLOSWAG_89	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38291.1	001457	Cluster959_1clades	262	BN7874_122	Phage NCTB	GCA_900092385.1
AFH14785.1	001457	Cluster959_1clades	261	Lu11_0249	Pseudomonas phage Lu11	GCA_000897175.1
AGS82131.1	001457	Cluster959_1clades	263	PaBG_00256	Pseudomonas phage PaBG	GCA_000912555.1
QAU04574.1	001457	Cluster959_1clades	279	ValB1MD_305	Vibrio phage ValB1MD	GCA_004138815.1
AIT13999.1	001458	Cluster960_1clades	276	PBI_121Q_102	Escherichia phage 121Q	GCA_000926855.1
QAY00339.1	001458	Cluster960_1clades	276	Ecwhy1_58	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35085.1	001458	Cluster960_1clades	276	ACQ29_gp405	Escherichia phage PBECO4	GCA_001041035.1
BBM61690.1	001458	Cluster960_1clades	276	EO157G_1010	Escherichia phage SP27	GCA_008033345.1
AXC36662.1	001458	Cluster960_1clades	276	-	Escherichia phage UB	GCA_003341455.1
QBO61694.1	001458	Cluster960_1clades	276	G17_00205	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13743.1	001458	Cluster960_1clades	276	vBEcoMphAPEC6_gp113c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80003.1	001458	Cluster960_1clades	276	PSLUR01_00019	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44480.1	001458	Cluster960_1clades	277	RaK2_00207	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW19127.1	001458	Cluster960_1clades	272	7t3_0612	Salmonella phage 7t3	GCA_006083215.1
AZU98364.1	001458	Cluster960_1clades	272	CPT_Munch_424	Salmonella phage Munch	GCA_004015485.1
QIG62618.1	001458	Cluster960_1clades	272	SEPL_005	Salmonella phage SE_PL	GCA_011067555.1
APU01530.1	001459	ParBC	142	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29038.1	001459	ParBC	138	AP1_0331	Aeromonas phage AP1	GCA_014183365.1
ATI17370.1	001459	ParBC	138	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00224.1	001459	ParBC	138	HWB28_gp328	Aeromonas phage AS-zj	GCA_002627665.1
QAX97811.1	001459	ParBC	138	ASswx1_167	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01340.1	001459	ParBC	142	ASwh1_279	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39436.1	001459	ParBC	138	CC2_369	Aeromonas phage CC2	GCA_000903495.1
ADQ53152.1	001459	ParBC	142	65p144	Aeromonas virus 65	GCA_000893255.1
AFF28146.1	001459	ParBC	221	PAU_148	Sphingomonas phage PAU	GCA_000902455.1
BBI90691.1	001459	ParBC	277	HYO65_gp299	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90998.1	001459	ParBC	277	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39238.1	001459	ParBC	159	BPT24_113	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64089.1	001460	UvsW	274	KVP40.0018	Vibrio phage KVP40	GCA_000843785.1
QIW90412.1	001460	UvsW	274	GCAPEGMB_00065	Vibrio phage V07	GCA_012361095.1
QIW91017.1	001460	UvsW	274	COHAPHLI_00154	Vibrio phage V09	GCA_012361135.1
QHJ74201.1	001460	UvsW	274	VH12019_00282	Vibrio phage VH1_2019	GCA_009931825.1
AGB07025.1	001460	UvsW	274	CF80_gp238	Vibrio phage VH7D	GCA_000914495.1
QBX06071.1	001460	UvsW	274	ValB1HC_117	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61085.1	001460	UvsW	274	AVU32_gp244	Vibrio phage ValKK3	GCA_001501635.1
AIE13791.1	001460	UvsW	274	VPFG_00067	Vibrio phage nt-1	GCA_000910195.2
ALP47037.1	001460	UvsW	274	phiGrn1_0133	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47415.1	001460	UvsW	274	phiST2_0263	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54697.1	001460	UvsW	274	vBValMR10Z_156	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37252.1	001460	UvsW	274	pp2_018	Vibriophage phi-pp2	GCA_002630725.1
AAQ64364.1	001461	Cluster964_1clades	271	KVP40.0294	Vibrio phage KVP40	GCA_000843785.1
QIW90679.1	001461	Cluster964_1clades	243	GCAPEGMB_00332	Vibrio phage V07	GCA_012361095.1
QIW91119.1	001461	Cluster964_1clades	243	COHAPHLI_00283	Vibrio phage V09	GCA_012361135.1
QHJ74474.1	001461	Cluster964_1clades	243	VH12019_00147	Vibrio phage VH1_2019	GCA_009931825.1
AGB06967.1	001461	Cluster964_1clades	243	CF80_gp180	Vibrio phage VH7D	GCA_000914495.1
QBX06177.1	001461	Cluster964_1clades	243	ValB1HC_224	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61194.1	001461	Cluster964_1clades	243	AVU32_gp353	Vibrio phage ValKK3	GCA_001501635.1
AGN30340.1	001461	Cluster964_1clades	243	VPFG_00343	Vibrio phage nt-1	GCA_000910195.2
ALP47045.1	001461	Cluster964_1clades	243	phiGrn1_0027	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47500.1	001461	Cluster964_1clades	157	phiST2_0160	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54803.1	001461	Cluster964_1clades	243	vBValMR10Z_263	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37525.1	001461	Cluster964_1clades	243	pp2_292	Vibriophage phi-pp2	GCA_002630725.1
ARB13813.1	001462	Cluster965_1clades	269	Ccr10_gp283	Caulobacter phage Ccr10	GCA_002619445.1
ARB14158.1	001462	Cluster965_1clades	269	Ccr2_gp282	Caulobacter phage Ccr2	GCA_002619465.1
ARB14852.1	001462	Cluster965_1clades	269	Ccr29_gp296	Caulobacter phage Ccr29	GCA_002619485.1
ARB15191.1	001462	Cluster965_1clades	265	Ccr32_gp273	Caulobacter phage Ccr32	GCA_002619505.1
ARB15525.1	001462	Cluster965_1clades	265	Ccr34_gp283	Caulobacter phage Ccr34	GCA_002619525.1
ARB14500.1	001462	Cluster965_1clades	267	Ccr5_gp280	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68476.1	001462	Cluster965_1clades	154	CcrBL10_gp272	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87810.1	001462	Cluster965_1clades	269	CcrKarma_gp293	Caulobacter virus Karma	GCA_000901575.1
AFU87457.1	001462	Cluster965_1clades	267	CcrMagneto_gp287	Caulobacter virus Magneto	GCA_000903095.1
AFU86761.1	001462	Cluster965_1clades	154	CcrRogue_gp279	Caulobacter virus Rogue	GCA_000900555.1
AFU88602.1	001462	Cluster965_1clades	267	CcrSwift_gp284	Caulobacter virus Swift	GCA_000899655.1
AFU87110.1	001462	Cluster965_1clades	265	CbK_gp278	Caulobacter virus phiCbK	GCA_000900535.1
AHI60430.1	001463	Cluster966_1clades	258	Ea357_276	Erwinia phage Ea35-70	GCA_000914635.1
QBP07387.1	001463	Cluster966_1clades	258	REBECCA_282	Erwinia phage Rebecca	GCA_004521635.1
AUG86069.1	001463	Cluster966_1clades	258	BOSOLAPHORUS_283	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52385.2	001463	Cluster966_1clades	258	DM_286	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86389.1	001463	Cluster966_1clades	258	DESERTFOX_282	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86710.1	001463	Cluster966_1clades	258	MADMEL_283	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87035.1	001463	Cluster966_1clades	258	MORTIMER_287	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52060.1	001463	Cluster966_1clades	258	RAY_280	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51743.1	001463	Cluster966_1clades	258	SIMMY50_285	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65095.2	001463	Cluster966_1clades	258	SPECIALG_284	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24184.1	001463	Cluster966_1clades	267	-	Proteus phage 10	GCA_014071245.1
QKE54608.1	001463	Cluster966_1clades	260	ACSA002_2910	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60299.1	001464	Cluster967_1clades	265	Ea357_148	Erwinia phage Ea35-70	GCA_000914635.1
QBP07257.1	001464	Cluster967_1clades	265	REBECCA_150	Erwinia phage Rebecca	GCA_004521635.1
AUG85937.1	001464	Cluster967_1clades	265	BOSOLAPHORUS_150	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52252.1	001464	Cluster967_1clades	265	DM_154	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86256.1	001464	Cluster967_1clades	265	DESERTFOX_149	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86578.1	001464	Cluster967_1clades	265	MADMEL_150	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86902.1	001464	Cluster967_1clades	265	MORTIMER_153	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51930.1	001464	Cluster967_1clades	265	RAY_149	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51614.1	001464	Cluster967_1clades	265	SIMMY50_152	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64961.1	001464	Cluster967_1clades	265	SPECIALG_151	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24079.1	001464	Cluster967_1clades	260	-	Proteus phage 10	GCA_014071245.1
QKE54453.1	001464	Cluster967_1clades	259	ACSA002_1390	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64322.1	001465	Cluster968_1clades	260	KVP40.0253	Vibrio phage KVP40	GCA_000843785.1
QIW90637.1	001465	Cluster968_1clades	260	GCAPEGMB_00290	Vibrio phage V07	GCA_012361095.1
QIW91162.1	001465	Cluster968_1clades	260	COHAPHLI_00326	Vibrio phage V09	GCA_012361135.1
QHJ74432.1	001465	Cluster968_1clades	260	VH12019_00105	Vibrio phage VH1_2019	GCA_009931825.1
AGB06938.1	001465	Cluster968_1clades	256	CF80_gp151	Vibrio phage VH7D	GCA_000914495.1
QBX06208.1	001465	Cluster968_1clades	261	ValB1HC_255	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61225.1	001465	Cluster968_1clades	256	AVU32_gp384	Vibrio phage ValKK3	GCA_001501635.1
AGN30307.1	001465	Cluster968_1clades	242	VPFG_00308	Vibrio phage nt-1	GCA_000910195.2
ALP47039.1	001465	Cluster968_1clades	256	phiGrn1_0374	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47417.1	001465	Cluster968_1clades	256	phiST2_0129	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54833.1	001465	Cluster968_1clades	261	vBValMR10Z_293	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37481.1	001465	Cluster968_1clades	260	pp2_248	Vibriophage phi-pp2	GCA_002630725.1
AAQ64228.1	001466	Cluster969_1clades	253	KVP40.0159	Vibrio phage KVP40	GCA_000843785.1
QIW90542.1	001466	Cluster969_1clades	253	GCAPEGMB_00195	Vibrio phage V07	GCA_012361095.1
QIW90880.1	001466	Cluster969_1clades	253	COHAPHLI_00017	Vibrio phage V09	GCA_012361135.1
QHJ74340.1	001466	Cluster969_1clades	253	VH12019_00013	Vibrio phage VH1_2019	GCA_009931825.1
AGB06833.1	001466	Cluster969_1clades	253	CF80_gp046	Vibrio phage VH7D	GCA_000914495.1
QBX06313.1	001466	Cluster969_1clades	253	ValB1HC_360	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60944.1	001466	Cluster969_1clades	253	AVU32_gp103	Vibrio phage ValKK3	GCA_001501635.1
AGN30206.1	001466	Cluster969_1clades	253	VPFG_00206	Vibrio phage nt-1	GCA_000910195.2
ALP47042.1	001466	Cluster969_1clades	253	phiGrn1_0270	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47419.1	001466	Cluster969_1clades	253	phiST2_0029	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54556.1	001466	Cluster969_1clades	253	vBValMR10Z_15	Vibrio phage vB_ValM_R10Z	GCA_014337545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN37387.1	001466	Cluster969_1clades	253	pp2_154	Vibriophage phi-pp2	GCA_002630725.1
ARB13552.1	001467	CR-Ubl5	224	Ccr10_gp024	Caulobacter phage Ccr10	GCA_002619445.1
ARB13898.1	001467	CR-Ubl5	224	Ccr2_gp023	Caulobacter phage Ccr2	GCA_002619465.1
ARB14587.1	001467	CR-Ubl5	224	Ccr29_gp030	Caulobacter phage Ccr29	GCA_002619485.1
ARB14942.1	001467	CR-Ubl5	224	Ccr32_gp023	Caulobacter phage Ccr32	GCA_002619505.1
ARB15273.1	001467	CR-Ubl5	224	Ccr34_gp024	Caulobacter phage Ccr34	GCA_002619525.1
ARB14241.1	001467	CR-Ubl5	224	Ccr5_gp023	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68223.1	001467	CR-Ubl5	246	CcrBL10_gp019	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87540.1	001467	CR-Ubl5	228	CcrKarma_gp023	Caulobacter virus Karma	GCA_000901575.1
AFU87192.1	001467	CR-Ubl5	224	CcrMagneto_gp022	Caulobacter virus Magneto	GCA_000903095.1
AFU86503.1	001467	CR-Ubl5	248	CcrRogue_gp021	Caulobacter virus Rogue	GCA_000900555.1
AFU88339.1	001467	CR-Ubl5	224	CcrSwift_gp021	Caulobacter virus Swift	GCA_000899655.1
AFU86855.1	001467	CR-Ubl5	224	CbK_gp023	Caulobacter virus phiCbK	GCA_000900535.1
ARB13550.1	001468	Cluster971_1clades	248	Ccr10_gp022	Caulobacter phage Ccr10	GCA_002619445.1
ARB13896.1	001468	Cluster971_1clades	248	Ccr2_gp021	Caulobacter phage Ccr2	GCA_002619465.1
ARB14585.1	001468	Cluster971_1clades	248	Ccr29_gp028	Caulobacter phage Ccr29	GCA_002619485.1
ARB14940.1	001468	Cluster971_1clades	248	Ccr32_gp021	Caulobacter phage Ccr32	GCA_002619505.1
ARB15271.1	001468	Cluster971_1clades	248	Ccr34_gp022	Caulobacter phage Ccr34	GCA_002619525.1
ARB14239.1	001468	Cluster971_1clades	248	Ccr5_gp021	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68222.1	001468	Cluster971_1clades	242	CcrBL10_gp018	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87538.1	001468	Cluster971_1clades	248	CcrKarma_gp021	Caulobacter virus Karma	GCA_000901575.1
AFU87190.1	001468	Cluster971_1clades	248	CcrMagneto_gp020	Caulobacter virus Magneto	GCA_000903095.1
AFU86502.1	001468	Cluster971_1clades	246	CcrRogue_gp020	Caulobacter virus Rogue	GCA_000900555.1
AFU88337.1	001468	Cluster971_1clades	248	CcrSwift_gp019	Caulobacter virus Swift	GCA_000899655.1
AFU86853.1	001468	Cluster971_1clades	248	CbK_gp021	Caulobacter virus phiCbK	GCA_000900535.1
ARB13708.1	001469	Cluster972_1clades	245	Ccr10_gp178c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14053.1	001469	Cluster972_1clades	245	Ccr2_gp177c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14740.1	001469	Cluster972_1clades	245	Ccr29_gp184	Caulobacter phage Ccr29	GCA_002619485.1
ARB15095.1	001469	Cluster972_1clades	245	Ccr32_gp177	Caulobacter phage Ccr32	GCA_002619505.1
ARB15429.1	001469	Cluster972_1clades	245	Ccr34_gp187	Caulobacter phage Ccr34	GCA_002619525.1
ARB14396.1	001469	Cluster972_1clades	247	Ccr5_gp176c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68378.1	001469	Cluster972_1clades	229	CcrBL10_gp174c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87701.1	001469	Cluster972_1clades	213	CcrKarma_gp184	Caulobacter virus Karma	GCA_000901575.1
AFU87350.1	001469	Cluster972_1clades	245	CcrMagneto_gp180	Caulobacter virus Magneto	GCA_000903095.1
AFU86661.1	001469	Cluster972_1clades	230	CcrRogue_gp179	Caulobacter virus Rogue	GCA_000900555.1
AFU88497.1	001469	Cluster972_1clades	247	CcrSwift_gp179	Caulobacter virus Swift	GCA_000899655.1
AFU87014.1	001469	Cluster972_1clades	245	CbK_gp182	Caulobacter virus phiCbK	GCA_000900535.1
QGZ14570.1	001470	AraC-HTH+AraC-HTH	233	HWC77_gp207	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14569.1	001470	AraC-HTH+AraC-HTH	241	HWC77_gp206	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04163.1	001470	AraC-HTH+AraC-HTH	233	HWC03_gp008	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04164.1	001470	AraC-HTH+AraC-HTH	241	HWC03_gp009	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23194.1	001470	AraC-HTH+AraC-HTH	233	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23193.1	001470	AraC-HTH+AraC-HTH	241	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81017.1	001470	AraC-HTH+AraC-HTH	233	Aphrodite1_0148	Vibrio phage Aphrodite1	GCA_002958015.1
AUR81012.1	001470	AraC-HTH+AraC-HTH	241	Aphrodite1_0149	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47535.1	001470	AraC-HTH+AraC-HTH	233	HWC35_gp141	Vibrio phage USC-1	GCA_006864065.1
QDH47536.1	001470	AraC-HTH+AraC-HTH	241	HWC35_gp142	Vibrio phage USC-1	GCA_006864065.1
BAW98349.1	001470	AraC-HTH+AraC-HTH	197	FDH33_gp140	Vibrio phage pTD1	GCA_002618825.1
BAW98350.1	001470	AraC-HTH+AraC-HTH	235	FDH33_gp141	Vibrio phage pTD1	GCA_002618825.1
AAQ64175.1	001471	Cluster974_1clades	231	KVP40.0104	Vibrio phage KVP40	GCA_000843785.1
QIW90498.1	001471	Cluster974_1clades	231	GCAPEGMB_00151	Vibrio phage V07	GCA_012361095.1
QIW90931.1	001471	Cluster974_1clades	231	COHAPHLL_00068	Vibrio phage V09	GCA_012361135.1
QHJ74286.1	001471	Cluster974_1clades	231	VH12019_00367	Vibrio phage VH1_2019	GCA_009931825.1
AGB07109.1	001471	Cluster974_1clades	231	CF80_gp322	Vibrio phage VH7D	GCA_000914495.1
QBX05985.1	001471	Cluster974_1clades	231	ValB1HC_031	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60998.1	001471	Cluster974_1clades	231	AVU32_gp157	Vibrio phage ValKK3	GCA_001501635.1
AGN30153.1	001471	Cluster974_1clades	221	VPFG_00151	Vibrio phage nt-1	GCA_000910195.2
ALP47052.1	001471	Cluster974_1clades	231	phiGrn1_0217	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47433.1	001471	Cluster974_1clades	231	phiST2_0350	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54610.1	001471	Cluster974_1clades	231	vBValMR10Z_69	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37333.1	001471	Cluster974_1clades	230	pp2_100	Vibriophage phi-pp2	GCA_002630725.1
ARB13685.1	001472	Cluster975_1clades	230	Ccr10_gp155c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14030.1	001472	Cluster975_1clades	230	Ccr2_gp154c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14717.1	001472	Cluster975_1clades	230	Ccr29_gp161	Caulobacter phage Ccr29	GCA_002619485.1
ARB15072.1	001472	Cluster975_1clades	230	Ccr32_gp154	Caulobacter phage Ccr32	GCA_002619505.1
ARB15406.1	001472	Cluster975_1clades	230	Ccr34_gp164	Caulobacter phage Ccr34	GCA_002619525.1
ARB14373.1	001472	Cluster975_1clades	230	Ccr5_gp153c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68354.1	001472	Cluster975_1clades	229	CcrBL10_gp150c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87678.1	001472	Cluster975_1clades	230	CcrKarma_gp161	Caulobacter virus Karma	GCA_000901575.1
AFU87327.1	001472	Cluster975_1clades	230	CcrMagneto_gp157	Caulobacter virus Magneto	GCA_000903095.1
AFU86638.1	001472	Cluster975_1clades	229	CcrRogue_gp156	Caulobacter virus Rogue	GCA_000900555.1
AFU88474.1	001472	Cluster975_1clades	230	CcrSwift_gp156	Caulobacter virus Swift	GCA_000899655.1
AFU86991.1	001472	Cluster975_1clades	230	CbK_gp159	Caulobacter virus phiCbK	GCA_000900535.1
ARB13717.1	001473	Cluster976_1clades	230	Ccr10_gp187c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14062.1	001473	Cluster976_1clades	230	Ccr2_gp186c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14749.1	001473	Cluster976_1clades	230	Ccr29_gp193	Caulobacter phage Ccr29	GCA_002619485.1
ARB15104.1	001473	Cluster976_1clades	230	Ccr32_gp186	Caulobacter phage Ccr32	GCA_002619505.1
ARB15438.1	001473	Cluster976_1clades	230	Ccr34_gp196	Caulobacter phage Ccr34	GCA_002619525.1
ARB14405.1	001473	Cluster976_1clades	230	Ccr5_gp185c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68385.1	001473	Cluster976_1clades	228	CcrBL10_gp181c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87710.1	001473	Cluster976_1clades	230	CcrKarma_gp193	Caulobacter virus Karma	GCA_000901575.1
AFU87359.1	001473	Cluster976_1clades	230	CcrMagneto_gp189	Caulobacter virus Magneto	GCA_000903095.1
AFU86671.1	001473	Cluster976_1clades	228	CcrRogue_gp189	Caulobacter virus Rogue	GCA_000900555.1
AFU88506.1	001473	Cluster976_1clades	230	CcrSwift_gp188	Caulobacter virus Swift	GCA_000899655.1
AFU87023.1	001473	Cluster976_1clades	230	CbK_gp191	Caulobacter virus phiCbK	GCA_000900535.1
ARB13648.1	001474	HIN-HTH	224	Ccr10_gp119c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13993.1	001474	HIN-HTH	224	Ccr2_gp118c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14681.1	001474	HIN-HTH	224	Ccr29_gp125	Caulobacter phage Ccr29	GCA_002619485.1
ARB15036.1	001474	HIN-HTH	224	Ccr32_gp118	Caulobacter phage Ccr32	GCA_002619505.1
ARB15368.1	001474	HIN-HTH	224	Ccr34_gp126	Caulobacter phage Ccr34	GCA_002619525.1
ARB14337.1	001474	HIN-HTH	229	Ccr5_gp119c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68317.1	001474	HIN-HTH	164	CcrBL10_gp113c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87641.1	001474	HIN-HTH	224	CcrKarma_gp124	Caulobacter virus Karma	GCA_000901575.1
AFU87290.1	001474	HIN-HTH	224	CcrMagneto_gp120	Caulobacter virus Magneto	GCA_000903095.1
AFU86601.1	001474	HIN-HTH	220	CcrRogue_gp119	Caulobacter virus Rogue	GCA_000900555.1
AFU88437.1	001474	HIN-HTH	224	CcrSwift_gp119	Caulobacter virus Swift	GCA_000899655.1
AFU86954.1	001474	HIN-HTH	224	CbK_gp122	Caulobacter virus phiCbK	GCA_000900535.1
AGB06886.1	001475	Atrophin-1	133	CF80_gp099	Vibrio phage VH7D	GCA_000914495.1
AGB06887.1	001475	Atrophin-1	217	CF80_gp100	Vibrio phage VH7D	GCA_000914495.1
QBX06259.1	001475	Atrophin-1	217	ValB1HC_306	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06260.1	001475	Atrophin-1	133	ValB1HC_307	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60886.1	001475	Atrophin-1	133	AVU32_gp045	Vibrio phage ValKK3	GCA_001501635.1
AJT60885.1	001475	Atrophin-1	217	AVU32_gp044	Vibrio phage ValKK3	GCA_001501635.1
AGN30259.1	001475	Atrophin-1	224	VPFG_00260	Vibrio phage nt-1	GCA_000910195.2
ALP47149.1	001475	Atrophin-1	133	phiGrn1_0324	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47059.1	001475	Atrophin-1	217	phiGrn1_0325	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47439.1	001475	Atrophin-1	217	phiST2_0080	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54886.1	001475	Atrophin-1	217	vBValMR10Z_346	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QNJ54887.1	001475	Atrophin-1	133	vBValMR10Z_347	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AHI60321.1	001476	Cluster979_1clades	167	Ea357_170	Erwinia phage Ea35-70	GCA_000914635.1
QBP07280.1	001476	Cluster979_1clades	167	REBECCA_173	Erwinia phage Rebecca	GCA_004521635.1
AUG85960.1	001476	Cluster979_1clades	167	BOSOLAPHORUS_173	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52275.1	001476	Cluster979_1clades	167	DM_177	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86279.1	001476	Cluster979_1clades	167	DESERTFOX_172	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86601.1	001476	Cluster979_1clades	167	MADMEL_173	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86925.1	001476	Cluster979_1clades	167	MORTIMER_176	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51952.1	001476	Cluster979_1clades	167	RAY_171	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51636.1	001476	Cluster979_1clades	167	SIMMY50_174	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64983.1	001476	Cluster979_1clades	167	SPECIALG_173	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24102.1	001476	Cluster979_1clades	222	-	Proteus phage 10	GCA_014071245.1
QKE54479.1	001476	Cluster979_1clades	196	ACSA002_1650	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60388.1	001477	Cluster980_1clades	200	Ea357_235	Erwinia phage Ea35-70	GCA_000914635.1
QBP07344.1	001477	Cluster980_1clades	200	REBECCA_239	Erwinia phage Rebecca	GCA_004521635.1
AUG86026.1	001477	Cluster980_1clades	200	BOSOLAPHORUS_240	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52343.1	001477	Cluster980_1clades	200	DM_243	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86345.1	001477	Cluster980_1clades	200	DESERTFOX_238	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86668.1	001477	Cluster980_1clades	200	MADMEL_241	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86991.1	001477	Cluster980_1clades	200	MORTIMER_243	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52017.1	001477	Cluster980_1clades	200	RAY_237	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51701.1	001477	Cluster980_1clades	200	SIMMY50_242	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65052.1	001477	Cluster980_1clades	200	SPECIALG_241	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24157.1	001477	Cluster980_1clades	219	-	Proteus phage 10	GCA_014071245.1
QKE54564.1	001477	Cluster980_1clades	206	ACSA002_2480	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64137.1	001478	Cluster981_1clades	215	KVP40.0066	Vibrio phage KVP40	GCA_000843785.1
QIW90460.1	001478	Cluster981_1clades	215	GCAPEGMB_00113	Vibrio phage V07	GCA_012361095.1
QIW90969.1	001478	Cluster981_1clades	215	COHAPHLL_00106	Vibrio phage V09	GCA_012361135.1
QHJ74249.1	001478	Cluster981_1clades	215	VH12019_00330	Vibrio phage VH1_2019	GCA_009931825.1
AGB07073.1	001478	Cluster981_1clades	215	CF80_gp286	Vibrio phage VH7D	GCA_000914495.1
QBX06022.1	001478	Cluster981_1clades	215	ValB1HC_068	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61036.1	001478	Cluster981_1clades	215	AVU32_gp195	Vibrio phage ValKK3	GCA_001501635.1
AGN30115.1	001478	Cluster981_1clades	215	VPFG_00113	Vibrio phage nt-1	GCA_000910195.2
ALP47060.1	001478	Cluster981_1clades	215	phiGrn1_0181	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47440.1	001478	Cluster981_1clades	215	phiST2_0312	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54647.1	001478	Cluster981_1clades	215	vBValMR10Z_106	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37297.1	001478	Cluster981_1clades	215	pp2_064	Vibriophage phi-pp2	GCA_002630725.1
ARB13742.1	001479	Cluster982_1clades	212	Ccr10_gp212c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14087.1	001479	Cluster982_1clades	212	Ccr2_gp211c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14776.1	001479	Cluster982_1clades	212	Ccr29_gp220	Caulobacter phage Ccr29	GCA_002619485.1
ARB15120.1	001479	Cluster982_1clades	212	Ccr32_gp202	Caulobacter phage Ccr32	GCA_002619505.1
ARB15454.1	001479	Cluster982_1clades	212	Ccr34_gp212	Caulobacter phage Ccr34	GCA_002619525.1
ARB14429.1	001479	Cluster982_1clades	212	Ccr5_gp209c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68408.1	001479	Cluster982_1clades	210	CcrBL10_gp204c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87735.1	001479	Cluster982_1clades	212	CcrKarma_gp218	Caulobacter virus Karma	GCA_000901575.1
AFU87384.1	001479	Cluster982_1clades	212	CcrMagneto_gp214	Caulobacter virus Magneto	GCA_000903095.1
AFU86694.1	001479	Cluster982_1clades	214	CcrRogue_gp212	Caulobacter virus Rogue	GCA_000900555.1
AFU88531.1	001479	Cluster982_1clades	212	CcrSwift_gp213	Caulobacter virus Swift	GCA_000899655.1
AFU87039.1	001479	Cluster982_1clades	212	CbK_gp207	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64266.1	001480	Cluster983_1clades	186	KVP40.0197	Vibrio phage KVP40	GCA_000843785.1
QIW90582.1	001480	Cluster983_1clades	193	GCAPEGMB_00235	Vibrio phage V07	GCA_012361095.1
QIW91216.1	001480	Cluster983_1clades	186	COHAPHLL_00380	Vibrio phage V09	GCA_012361135.1
QHJ74380.1	001480	Cluster983_1clades	193	VH12019_00053	Vibrio phage VH1_2019	GCA_009931825.1
AGB06882.1	001480	Cluster983_1clades	206	CF80_gp095	Vibrio phage VH7D	GCA_000914495.1
QBX06264.1	001480	Cluster983_1clades	211	ValB1HC_311	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60890.1	001480	Cluster983_1clades	211	AVU32_gp049	Vibrio phage ValKK3	GCA_001501635.1
AGN30254.1	001480	Cluster983_1clades	193	VPFG_00255	Vibrio phage nt-1	GCA_000910195.2
ALP47079.1	001480	Cluster983_1clades	190	phiGrn1_0320	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47459.1	001480	Cluster983_1clades	190	phiST2_0076	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54891.1	001480	Cluster983_1clades	206	vBValMR10Z_351	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37427.1	001480	Cluster983_1clades	186	pp2_194	Vibriophage phi-pp2	GCA_002630725.1
AHI60466.1	001481	Cluster984_1clades	209	Ea357_312	Erwinia phage Ea35-70	GCA_000914635.1
QBP07423.1	001481	Cluster984_1clades	209	REBECCA_318	Erwinia phage Rebecca	GCA_004521635.1
AUG86105.1	001481	Cluster984_1clades	209	BOSOLAPHORUS_319	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52421.1	001481	Cluster984_1clades	209	DM_322	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86425.1	001481	Cluster984_1clades	209	DESERTFOX_318	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86746.1	001481	Cluster984_1clades	209	MADMEL_319	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87071.1	001481	Cluster984_1clades	209	MORTIMER_323	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52096.1	001481	Cluster984_1clades	209	RAY_316	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51779.1	001481	Cluster984_1clades	209	SIMMY50_321	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65131.1	001481	Cluster984_1clades	209	SPECIALG_320	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24225.1	001481	Cluster984_1clades	210	-	Proteus phage 10	GCA_014071245.1
QKE54647.1	001481	Cluster984_1clades	208	ACSA002_3300	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60456.1	001482	Cluster985_1clades	209	Ea357_302	Erwinia phage Ea35-70	GCA_000914635.1
QBP07413.1	001482	Cluster985_1clades	209	REBECCA_308	Erwinia phage Rebecca	GCA_004521635.1
AUG86095.1	001482	Cluster985_1clades	209	BOSOLAPHORUS_309	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52411.1	001482	Cluster985_1clades	209	DM_312	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86415.1	001482	Cluster985_1clades	209	DESERTFOX_308	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86736.1	001482	Cluster985_1clades	209	MADMEL_309	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87061.1	001482	Cluster985_1clades	209	MORTIMER_313	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52086.1	001482	Cluster985_1clades	209	RAY_306	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51769.1	001482	Cluster985_1clades	209	SIMMY50_311	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65121.1	001482	Cluster985_1clades	209	SPECIALG_310	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24215.1	001482	Cluster985_1clades	207	-	Proteus phage 10	GCA_014071245.1
QKE54636.1	001482	Cluster985_1clades	208	ACSA002_3190	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64233.1	001483	Cluster986_1clades	208	KVP40.0164	Vibrio phage KVP40	GCA_000843785.1
QIW90547.1	001483	Cluster986_1clades	208	GCAPEGMB_00200	Vibrio phage V07	GCA_012361095.1
QIW90875.1	001483	Cluster986_1clades	208	COHAPHLL_00012	Vibrio phage V09	GCA_012361135.1
QHJ74345.1	001483	Cluster986_1clades	208	VH12019_00018	Vibrio phage VH1_2019	GCA_009931825.1
AGB06839.1	001483	Cluster986_1clades	208	CF80_gp052	Vibrio phage VH7D	GCA_000914495.1
QBX06307.1	001483	Cluster986_1clades	208	ValB1HC_354	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60938.1	001483	Cluster986_1clades	208	AVU32_gp097	Vibrio phage ValKK3	GCA_001501635.1
AGN30213.1	001483	Cluster986_1clades	207	VPFG_00213	Vibrio phage nt-1	GCA_000910195.2
ALP47090.1	001483	Cluster986_1clades	178	phiGrn1_0276	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47470.1	001483	Cluster986_1clades	178	phiST2_0035	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54550.1	001483	Cluster986_1clades	208	vBValMR10Z_9	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37392.1	001483	Cluster986_1clades	208	pp2_159	Vibriophage phi-pp2	GCA_002630725.1
ARB13799.1	001484	Cluster987_1clades	191	Ccr10_gp269	Caulobacter phage Ccr10	GCA_002619445.1
ARB14144.1	001484	Cluster987_1clades	191	Ccr2_gp268	Caulobacter phage Ccr2	GCA_002619465.1
ARB14838.1	001484	Cluster987_1clades	191	Ccr29_gp282	Caulobacter phage Ccr29	GCA_002619485.1
ARB15178.1	001484	Cluster987_1clades	191	Ccr32_gp260	Caulobacter phage Ccr32	GCA_002619505.1
ARB15512.1	001484	Cluster987_1clades	191	Ccr34_gp270	Caulobacter phage Ccr34	GCA_002619525.1
ARB14486.1	001484	Cluster987_1clades	191	Ccr5_gp266	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68464.1	001484	Cluster987_1clades	208	CcrBL10_gp260	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87796.1	001484	Cluster987_1clades	194	CcrKarma_gp279	Caulobacter virus Karma	GCA_000901575.1
AFU87443.1	001484	Cluster987_1clades	194	CcrMagneto_gp273	Caulobacter virus Magneto	GCA_000903095.1
AFU86750.1	001484	Cluster987_1clades	202	CcrRogue_gp268	Caulobacter virus Rogue	GCA_000900555.1
AFU88589.1	001484	Cluster987_1clades	194	CcrSwift_gp271	Caulobacter virus Swift	GCA_000899655.1
AFU87097.1	001484	Cluster987_1clades	191	CbK_gp265	Caulobacter virus phiCbK	GCA_000900535.1
APU01449.1	001485	Cluster988_1clades	200	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28934.1	001485	Cluster988_1clades	206	AP1_0227	Aeromonas phage AP1	GCA_014183365.1
ATI17450.1	001485	Cluster988_1clades	206	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00146.1	001485	Cluster988_1clades	206	HWB28_gp004	Aeromonas phage AS-zj	GCA_002627665.1
AUE22681.1	001485	Cluster988_1clades	101	Ah1_00140	Aeromonas phage Ah1	GCA_002957415.1
QAX98407.1	001485	Cluster988_1clades	101	ASfcp2_63	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97890.1	001485	Cluster988_1clades	206	ASswx1_247	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39410.1	001485	Cluster988_1clades	206	CC2_286	Aeromonas phage CC2	GCA_000903495.1
ADQ52863.1	001485	Cluster988_1clades	131	PX29p144	Aeromonas phage PX29	GCA_000920195.1
ADM80122.1	001485	Cluster988_1clades	130	phiAS5_ORF0279	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53069.1	001485	Cluster988_1clades	200	65p059	Aeromonas virus 65	GCA_000893255.1
AAQ17809.1	001485	Cluster988_1clades	130	Aeh1ORF144c	Aeromonas virus Aeh1	GCA_000843245.1
AMR59707.1	001486	Cluster989_1clades	181	SEGD1_058	Enterobacteria phage SEGD1	GCA_002601865.1
AXF51199.1	001486	Cluster989_1clades	206	WELLINGTON_69	Erwinia phage Wellington	GCA_003344985.1
AFQ96785.1	001486	Cluster989_1clades	186	G173_gp240	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48086.1	001486	Cluster989_1clades	186	ASESINO_73	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48360.1	001486	Cluster989_1clades	186	CAITLIN_65	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48633.1	001486	Cluster989_1clades	181	CHRISDB_71	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49421.1	001486	Cluster989_1clades	206	KWAN_69	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50497.1	001486	Cluster989_1clades	186	STRATTON_72	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85897.1	001486	Cluster989_1clades	181	ACEC001_0590	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20772.1	001486	Cluster989_1clades	157	-	Salmonella phage JN03	GCA_014319805.1
AXF51094.1	001486	Cluster989_1clades	189	MLDJOKPK_00109	Salmonella phage SPAsTU	GCA_003183805.1
AEP83889.1	001486	Cluster989_1clades	181	SPN3US_0056	Salmonella phage SPN3US	GCA_001042275.1
AAQ64196.1	001487	Cluster990_1clades	202	KVP40.0125	Vibrio phage KVP40	GCA_000843785.1
QIW90512.1	001487	Cluster990_1clades	202	GCAPEGMB_00165	Vibrio phage V07	GCA_012361095.1
QIW90910.1	001487	Cluster990_1clades	202	COHAPHLL_00047	Vibrio phage V09	GCA_012361135.1
QHJ74308.1	001487	Cluster990_1clades	202	VH12019_00389	Vibrio phage VH1_2019	GCA_009931825.1
AGB06802.1	001487	Cluster990_1clades	202	CF80_gp015	Vibrio phage VH7D	GCA_000914495.1
QBX05964.1	001487	Cluster990_1clades	202	ValB1HC_010	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60976.1	001487	Cluster990_1clades	202	AVU32_gp135	Vibrio phage ValKK3	GCA_001501635.1
AGN30175.1	001487	Cluster990_1clades	202	VPFG_00173	Vibrio phage nt-1	GCA_000910195.2
ALP47067.1	001487	Cluster990_1clades	202	phiGrn1_0237	Vibrio phage phi-Grn1	GCA_002757115.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALP47447.1	001487	Cluster990_1clades	202	phiST2_0375	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54589.1	001487	Cluster990_1clades	202	vBValMR10Z_48	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37356.1	001487	Cluster990_1clades	202	pp2_123	Vibriophage phi-pp2	GCA_002630725.1
ABY63050.1	001488	Cluster991_1clades	201	201phi2-1p221	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44929.1	001488	Cluster991_1clades	200	KTN4_171	Pseudomonas phage KTN4	GCA_002607225.1
ARV77318.1	001488	Cluster991_1clades	197	NOXIFER_149	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32316.1	001488	Cluster991_1clades	198	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ85927.1	001488	Cluster991_1clades	202	KKIINIFJ_00015	Pseudomonas phage PN05	GCA_009931935.1
ARV76839.1	001488	Cluster991_1clades	194	PHABIO_208	Pseudomonas phage Phabio	GCA_002624965.1
AEH03578.1	001488	Cluster991_1clades	198	155	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02715.1	001488	Cluster991_1clades	188	PSA21_189	Pseudomonas phage Psa21	GCA_004340405.1
ATN94785.1	001488	Cluster991_1clades	200	SL2_208	Pseudomonas phage SL2	GCA_002956015.1
QJB22807.1	001488	Cluster991_1clades	200	fnug_164	Pseudomonas phage fnug	GCA_012837215.1
QEM41889.1	001488	Cluster991_1clades	198	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83037.1	001488	Cluster991_1clades	200	PHIKZ136	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64085.1	001489	Cluster992_1clades	189	KVP40.0014	Vibrio phage KVP40	GCA_000843785.1
QIW90409.1	001489	Cluster992_1clades	189	GCAPEGMB_00062	Vibrio phage V07	GCA_012361095.1
QIW91020.1	001489	Cluster992_1clades	189	COHAPHLL_00157	Vibrio phage V09	GCA_012361135.1
QHJ74197.1	001489	Cluster992_1clades	189	VH12019_00278	Vibrio phage VH1_2019	GCA_009931825.1
AGB07021.1	001489	Cluster992_1clades	201	CF80_gp234	Vibrio phage VH7D	GCA_000914495.1
QBX06075.1	001489	Cluster992_1clades	200	ValB1HC_121	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61089.1	001489	Cluster992_1clades	200	AVU32_gp248	Vibrio phage ValKK3	GCA_001501635.1
AGN30065.2	001489	Cluster992_1clades	179	VPFG_00062	Vibrio phage nt-1	GCA_000910195.2
ALP47141.1	001489	Cluster992_1clades	139	phiGrn1_0129	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47528.1	001489	Cluster992_1clades	139	phiST2_0259	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54701.1	001489	Cluster992_1clades	200	vBValMR10Z_160	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37248.1	001489	Cluster992_1clades	189	pp2_014	Vibriophage phi-pp2	GCA_002630725.1
AAQ64162.1	001490	Cluster993_1clades	181	KVP40.0091	Vibrio phage KVP40	GCA_000843785.1
QIW90486.1	001490	Cluster993_1clades	173	GCAPEGMB_00139	Vibrio phage V07	GCA_012361095.1
QIW90943.1	001490	Cluster993_1clades	181	COHAPHLL_00080	Vibrio phage V09	GCA_012361135.1
QHJ74274.1	001490	Cluster993_1clades	184	VH12019_00355	Vibrio phage VH1_2019	GCA_009931825.1
AGB07099.1	001490	Cluster993_1clades	185	CF80_gp312	Vibrio phage VH7D	GCA_000914495.1
QBX05997.1	001490	Cluster993_1clades	185	ValB1HC_043	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61010.1	001490	Cluster993_1clades	183	AVU32_gp169	Vibrio phage ValKK3	GCA_001501635.1
AGN30141.1	001490	Cluster993_1clades	201	VPFG_00139	Vibrio phage nt-1	GCA_000910195.2
ALP47083.1	001490	Cluster993_1clades	183	phiGrn1_0206	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47465.1	001490	Cluster993_1clades	183	phiST2_0339	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54621.1	001490	Cluster993_1clades	185	vBValMR10Z_80	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37322.1	001490	Cluster993_1clades	184	pp2_089	Vibriophage phi-pp2	GCA_002630725.1
ARB13694.1	001491	TM+TM	200	Ccr10_gp164c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14039.1	001491	TM+TM	200	Ccr2_gp163c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14726.1	001491	TM+TM	200	Ccr29_gp170	Caulobacter phage Ccr29	GCA_002619485.1
ARB15081.1	001491	TM+TM	200	Ccr32_gp163	Caulobacter phage Ccr32	GCA_002619505.1
ARB15415.1	001491	TM+TM	200	Ccr34_gp173	Caulobacter phage Ccr34	GCA_002619525.1
ARB14382.1	001491	TM+TM	200	Ccr5_gp162c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68364.1	001491	TM+TM	194	CcrBL10_gp160c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87687.1	001491	TM+TM	200	CcrKarma_gp170	Caulobacter virus Karma	GCA_000901575.1
AFU87336.1	001491	TM+TM	200	CcrMagneto_gp166	Caulobacter virus Magneto	GCA_000903095.1
AFU86647.1	001491	TM+TM	194	CcrRogue_gp165	Caulobacter virus Rogue	GCA_000900555.1
AFU88483.1	001491	TM+TM	200	CcrSwift_gp165	Caulobacter virus Swift	GCA_000899655.1
AFU87000.1	001491	TM+TM	200	CbK_gp168	Caulobacter virus phiCbK	GCA_000900535.1
ARB13834.1	001492	Cluster996_1clades	118	Ccr10_gp304	Caulobacter phage Ccr10	GCA_002619445.1
ARB14179.1	001492	Cluster996_1clades	118	Ccr2_gp303	Caulobacter phage Ccr2	GCA_002619465.1
ARB14873.1	001492	Cluster996_1clades	118	Ccr29_gp317	Caulobacter phage Ccr29	GCA_002619485.1
ARB15211.1	001492	Cluster996_1clades	118	Ccr32_gp293	Caulobacter phage Ccr32	GCA_002619505.1
ARB15545.1	001492	Cluster996_1clades	118	Ccr34_gp303	Caulobacter phage Ccr34	GCA_002619525.1
ARB14520.1	001492	Cluster996_1clades	132	Ccr5_gp300	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68500.1	001492	Cluster996_1clades	197	CcrBL10_gp296	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87831.1	001492	Cluster996_1clades	118	CcrKarma_gp314	Caulobacter virus Karma	GCA_000901575.1
AFU87478.1	001492	Cluster996_1clades	118	CcrMagneto_gp308	Caulobacter virus Magneto	GCA_000903095.1
AFU86788.1	001492	Cluster996_1clades	196	CcrRogue_gp306	Caulobacter virus Rogue	GCA_000900555.1
AFU88623.1	001492	Cluster996_1clades	118	CcrSwift_gp305	Caulobacter virus Swift	GCA_000899655.1
AFU87130.1	001492	Cluster996_1clades	118	CbK_gp298	Caulobacter virus phiCbK	GCA_000900535.1
QDJ96774.1	001493	HNH	167	PS1_0016	Aeromonas phage PS1	GCA_007051165.2
QFR59407.1	001493	HNH	167	PS2_0016	Aeromonas phage PS2	GCA_009388305.2
AHI60211.1	001493	HNH	196	Ea357_060A	Erwinia phage Ea35-70	GCA_000914635.1
AXF51417.1	001493	HNH	169	WELLINGTON_293	Erwinia phage Wellington	GCA_003344985.1
ANZ49642.1	001493	HNH	169	KWAN_291	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AUG86490.1	001493	HNH	196	MADMEL_62	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86811.1	001493	HNH	196	MORTIMER_62	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51525.1	001493	HNH	196	SIMMY50_63	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64873.1	001493	HNH	196	SPECIALG_63	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGH72117.1	001493	HNH	195	N1M2_257	Klebsiella phage N1M2	GCA_010092605.1
AIX30590.1	001493	HNH	142	Syn7803US37_113	Synechococcus phage ACG-2014f	GCA_002594065.1
CCE26131.1	001493	HNH	175	g107	Yersinia phage phiR1-37	GCA_000895615.1
AHI60305.1	001494	Cluster998_1clades	186	Ea357_154	Erwinia phage Ea35-70	GCA_000914635.1
QBP07263.1	001494	Cluster998_1clades	186	REBECCA_156	Erwinia phage Rebecca	GCA_004521635.1
AUG85943.1	001494	Cluster998_1clades	186	BOSOLAPHORUS_156	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52258.1	001494	Cluster998_1clades	186	DM_160	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86262.1	001494	Cluster998_1clades	186	DESERTFOX_155	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86584.1	001494	Cluster998_1clades	186	MADMEL_156	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86908.1	001494	Cluster998_1clades	186	MORTIMER_159	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51936.1	001494	Cluster998_1clades	186	RAY_155	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51620.1	001494	Cluster998_1clades	186	SIMMY50_158	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64967.1	001494	Cluster998_1clades	186	SPECIALG_157	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24084.1	001494	Cluster998_1clades	182	-	Proteus phage 10	GCA_014071245.1
QKE54459.1	001494	Cluster998_1clades	196	ACSA002_1450	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60364.1	001495	Cluster999_1clades	193	Ea357_211	Erwinia phage Ea35-70	GCA_000914635.1
QBP07321.1	001495	Cluster999_1clades	194	REBECCA_216	Erwinia phage Rebecca	GCA_004521635.1
AUG86002.1	001495	Cluster999_1clades	194	BOSOLAPHORUS_216	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52319.1	001495	Cluster999_1clades	194	DM_219	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86321.1	001495	Cluster999_1clades	194	DESERTFOX_214	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86644.1	001495	Cluster999_1clades	194	MADMEL_216	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86967.1	001495	Cluster999_1clades	194	MORTIMER_219	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51994.1	001495	Cluster999_1clades	194	RAY_214	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51678.1	001495	Cluster999_1clades	194	SIMMY50_219	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65028.1	001495	Cluster999_1clades	190	SPECIALG_217	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24138.1	001495	Cluster999_1clades	146	-	Proteus phage 10	GCA_014071245.1
QKE54538.1	001495	Cluster999_1clades	136	ACSA002_2220	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60222.1	001496	Cluster1001_1clades	186	Ea357_071	Erwinia phage Ea35-70	GCA_000914635.1
QBP07181.1	001496	Cluster1001_1clades	186	REBECCA_73	Erwinia phage Rebecca	GCA_004521635.1
AUG85860.1	001496	Cluster1001_1clades	186	BOSOLAPHORUS_72	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52172.1	001496	Cluster1001_1clades	186	DM_74	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86179.1	001496	Cluster1001_1clades	186	DESERTFOX_71	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86501.1	001496	Cluster1001_1clades	186	MADMEL_73	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86822.1	001496	Cluster1001_1clades	186	MORTIMER_73	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51852.1	001496	Cluster1001_1clades	186	RAY_71	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51536.1	001496	Cluster1001_1clades	186	SIMMY50_74	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64884.1	001496	Cluster1001_1clades	186	SPECIALG_74	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54638.1	001496	Cluster1001_1clades	165	ACSA002_3210	Salmonella phage vB_SalM_SA002	GCA_014131285.1
CCE26106.1	001496	Cluster1001_1clades	192	g082	Yersinia phage phiR1-37	GCA_000895615.1
AHI60283.1	001497	Cluster1002_1clades	191	Ea357_132	Erwinia phage Ea35-70	GCA_000914635.1
QBP07241.1	001497	Cluster1002_1clades	191	REBECCA_134	Erwinia phage Rebecca	GCA_004521635.1
AUG85921.1	001497	Cluster1002_1clades	191	BOSOLAPHORUS_134	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52236.1	001497	Cluster1002_1clades	191	DM_138	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86240.1	001497	Cluster1002_1clades	191	DESERTFOX_133	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86562.1	001497	Cluster1002_1clades	191	MADMEL_134	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86886.1	001497	Cluster1002_1clades	191	MORTIMER_137	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51914.1	001497	Cluster1002_1clades	191	RAY_133	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51598.1	001497	Cluster1002_1clades	191	SIMMY50_136	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64945.1	001497	Cluster1002_1clades	191	SPECIALG_135	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24063.1	001497	Cluster1002_1clades	169	-	Proteus phage 10	GCA_014071245.1
QKE54435.1	001497	Cluster1002_1clades	185	ACSA002_1210	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13777.1	001498	Cluster1003_1clades	190	Ccr10_gp247	Caulobacter phage Ccr10	GCA_002619445.1
ARB14122.1	001498	Cluster1003_1clades	190	Ccr2_gp246	Caulobacter phage Ccr2	GCA_002619465.1

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ARB14816.1	001498	Cluster1003_1clades	190	Ccr29_gp260	Caulobacter phage Ccr29	GCA_002619485.1
ARB15156.1	001498	Cluster1003_1clades	190	Ccr32_gp238	Caulobacter phage Ccr32	GCA_002619505.1
ARB15490.1	001498	Cluster1003_1clades	190	Ccr34_gp248	Caulobacter phage Ccr34	GCA_002619525.1
ARB14464.1	001498	Cluster1003_1clades	190	Ccr5_gp244	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68443.1	001498	Cluster1003_1clades	189	CcrBL10_gp239	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87773.1	001498	Cluster1003_1clades	190	CcrKarma_gp256	Caulobacter virus Karma	GCA_000901575.1
AFU87420.1	001498	Cluster1003_1clades	190	CcrMagneto_gp250	Caulobacter virus Magneto	GCA_000903095.1
AFU86729.1	001498	Cluster1003_1clades	185	CcrRogue_gp247	Caulobacter virus Rogue	GCA_000900555.1
AFU88567.1	001498	Cluster1003_1clades	190	CcrSwift_gp249	Caulobacter virus Swift	GCA_000899655.1
AFU87075.1	001498	Cluster1003_1clades	190	CbK_gp243	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64218.1	001499	Cluster1004_1clades	161	KVP40.0149	Vibrio phage KVP40	GCA_000843785.1
QIW90532.1	001499	Cluster1004_1clades	165	GCAPEGMB_00185	Vibrio phage V07	GCA_012361095.1
QIW90890.1	001499	Cluster1004_1clades	169	COHAPHLL_00027	Vibrio phage V09	GCA_012361135.1
QHJ74330.1	001499	Cluster1004_1clades	169	VH12019_00003	Vibrio phage VH1_2019	GCA_009931825.1
AGB06823.1	001499	Cluster1004_1clades	163	CF80_gp036	Vibrio phage VH7D	GCA_000914495.1
QBX06324.1	001499	Cluster1004_1clades	163	ValB1HC_371	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60954.1	001499	Cluster1004_1clades	163	AVU32_gp113	Vibrio phage ValKK3	GCA_001501635.1
AGN30194.1	001499	Cluster1004_1clades	190	VPFG_00194	Vibrio phage nt-1	GCA_000910195.2
ALP47108.1	001499	Cluster1004_1clades	164	phiGrn1_0259	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47493.1	001499	Cluster1004_1clades	163	phiST2_0017	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54567.1	001499	Cluster1004_1clades	163	vBValMR10Z_26	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37378.1	001499	Cluster1004_1clades	165	pp2_145	Vibriophage phi-pp2	GCA_002630725.1
AAQ64267.1	001500	Cluster1005_1clades	185	KVP40.0198	Vibrio phage KVP40	GCA_000843785.1
QIW90583.1	001500	Cluster1005_1clades	185	GCAPEGMB_00236	Vibrio phage V07	GCA_012361095.1
QIW91215.1	001500	Cluster1005_1clades	185	COHAPHLL_00379	Vibrio phage V09	GCA_012361135.1
QHJ74381.1	001500	Cluster1005_1clades	185	VH12019_00054	Vibrio phage VH1_2019	GCA_009931825.1
AGB06883.1	001500	Cluster1005_1clades	184	CF80_gp096	Vibrio phage VH7D	GCA_000914495.1
QBX06263.1	001500	Cluster1005_1clades	186	ValB1HC_310	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60889.1	001500	Cluster1005_1clades	186	AVU32_gp048	Vibrio phage ValKK3	GCA_001501635.1
AGN30255.2	001500	Cluster1005_1clades	183	VPFG_00256	Vibrio phage nt-1	GCA_000910195.2
ALP47082.1	001500	Cluster1005_1clades	185	phiGrn1_0321	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47463.1	001500	Cluster1005_1clades	185	phiST2_0077	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54890.1	001500	Cluster1005_1clades	184	vBValMR10Z_350	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37428.1	001500	Cluster1005_1clades	185	pp2_195	Vibriophage phi-pp2	GCA_002630725.1
AXH72802.1	001501	Cluster1006_1clades	136	-	Myoviridae sp.	GCA_003657725.1
ABY63294.1	001501	Cluster1006_1clades	122	201phi2-1p143	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44867.1	001501	Cluster1006_1clades	38	KTN4_109	Pseudomonas phage KTN4	GCA_002607225.1
ARV77253.1	001501	Cluster1006_1clades	99	NOXIFER_82	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32237.1	001501	Cluster1006_1clades	95	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76758.1	001501	Cluster1006_1clades	100	PHABIO_127	Pseudomonas phage Phabio	GCA_002624965.1
AEH03508.1	001501	Cluster1006_1clades	122	084	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02619.1	001501	Cluster1006_1clades	97	PSA21_91	Pseudomonas phage Psa21	GCA_004340405.1
ATN94846.1	001501	Cluster1006_1clades	38	SL2_269	Pseudomonas phage SL2	GCA_002956015.1
QEM41816.1	001501	Cluster1006_1clades	95	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26323.1	001501	Cluster1006_1clades	38	PHIKZ082.1	Pseudomonas virus phiKZ	GCA_000842965.1
AFF28027.1	001501	Cluster1006_1clades	183	PAU_29	Sphingomonas phage PAU	GCA_000902455.1
AHI60444.1	001502	Cluster1007_1clades	179	Ea357_290	Erwinia phage Ea35-70	GCA_000914635.1
QBP07401.1	001502	Cluster1007_1clades	179	REBECCA_296	Erwinia phage Rebecca	GCA_004521635.1
AUG86083.1	001502	Cluster1007_1clades	179	BOSOLAPHORUS_297	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52399.2	001502	Cluster1007_1clades	179	DM_300	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86403.1	001502	Cluster1007_1clades	179	DESERTFOX_296	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86724.1	001502	Cluster1007_1clades	179	MADMEL_297	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87049.1	001502	Cluster1007_1clades	179	MORTIMER_301	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52074.1	001502	Cluster1007_1clades	179	RAY_294	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51757.1	001502	Cluster1007_1clades	179	SIMMY50_299	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65109.1	001502	Cluster1007_1clades	179	SPECIALG_298	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24197.1	001502	Cluster1007_1clades	183	-	Proteus phage 10	GCA_014071245.1
QKE54621.1	001502	Cluster1007_1clades	176	ACSA002_3040	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64422.1	001503	Cluster1008_1clades	182	KVP40.0353	Vibrio phage KVP40	GCA_000843785.1
QIW90367.1	001503	Cluster1008_1clades	182	GCAPEGMB_00020	Vibrio phage V07	GCA_012361095.1
QIW91062.1	001503	Cluster1008_1clades	182	COHAPHLL_00199	Vibrio phage V09	GCA_012361135.1
QHJ74536.1	001503	Cluster1008_1clades	182	VH12019_00236	Vibrio phage VH1_2019	GCA_009931825.1
AGB06994.1	001503	Cluster1008_1clades	182	CF80_gp207	Vibrio phage VH7D	GCA_000914495.1
QBX06120.1	001503	Cluster1008_1clades	182	ValB1HC_166	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61132.1	001503	Cluster1008_1clades	182	AVU32_gp291	Vibrio phage ValKK3	GCA_001501635.1
AGN30026.1	001503	Cluster1008_1clades	182	VPFG_00018	Vibrio phage nt-1	GCA_000910195.2
ALP47087.1	001503	Cluster1008_1clades	182	phiGrn1_0087	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47468.1	001503	Cluster1008_1clades	182	phiST2_0219	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54745.1	001503	Cluster1008_1clades	182	vBValMR10Z_205	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37585.1	001503	Cluster1008_1clades	182	pp2_353	Vibriophage phi-pp2	GCA_002630725.1
ARB13757.1	001504	GcrA	182	Ccr10_gp227c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14102.1	001504	GcrA	182	Ccr2_gp226c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14791.1	001504	GcrA	182	Ccr29_gp235	Caulobacter phage Ccr29	GCA_002619485.1
ARB15135.1	001504	GcrA	182	Ccr32_gp217	Caulobacter phage Ccr32	GCA_002619505.1
ARB15469.1	001504	GcrA	182	Ccr34_gp227	Caulobacter phage Ccr34	GCA_002619525.1
ARB14444.1	001504	GcrA	182	Ccr5_gp224c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68424.1	001504	GcrA	181	CcrBL10_gp220c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87751.1	001504	GcrA	182	CcrKarma_gp234	Caulobacter virus Karma	GCA_000901575.1
AFU87399.1	001504	GcrA	182	CcrMagneto_gp229	Caulobacter virus Magneto	GCA_000903095.1
AFU86710.1	001504	GcrA	182	CcrRogue_gp228	Caulobacter virus Rogue	GCA_000900555.1
AFU88547.1	001504	GcrA	182	CcrSwift_gp229	Caulobacter virus Swift	GCA_000899655.1
AFU87054.1	001504	GcrA	182	CbK_gp222	Caulobacter virus phiCbK	GCA_000900535.1
ARB13833.1	001505	MarR-HTH	182	Ccr10_gp303	Caulobacter phage Ccr10	GCA_002619445.1
ARB14178.1	001505	MarR-HTH	182	Ccr2_gp302	Caulobacter phage Ccr2	GCA_002619465.1
ARB14872.1	001505	MarR-HTH	182	Ccr29_gp316	Caulobacter phage Ccr29	GCA_002619485.1
ARB15210.1	001505	MarR-HTH	182	Ccr32_gp292	Caulobacter phage Ccr32	GCA_002619505.1
ARB15544.1	001505	MarR-HTH	182	Ccr34_gp302	Caulobacter phage Ccr34	GCA_002619525.1
ARB14519.1	001505	MarR-HTH	182	Ccr5_gp299	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68498.1	001505	MarR-HTH	182	CcrBL10_gp294	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87830.1	001505	MarR-HTH	182	CcrKarma_gp313	Caulobacter virus Karma	GCA_000901575.1
AFU87477.1	001505	MarR-HTH	182	CcrMagneto_gp307	Caulobacter virus Magneto	GCA_000903095.1
AFU86786.1	001505	MarR-HTH	182	CcrRogue_gp304	Caulobacter virus Rogue	GCA_000900555.1
AFU88622.1	001505	MarR-HTH	182	CcrSwift_gp304	Caulobacter virus Swift	GCA_000899655.1
AFU87129.1	001505	MarR-HTH	182	CbK_gp297	Caulobacter virus phiCbK	GCA_000900535.1
AHI60416.1	001506	Cluster1011_1clades	131	Ea357_262	Erwinia phage Ea35-70	GCA_000914635.1
QBP07373.1	001506	Cluster1011_1clades	86	REBECCA_268	Erwinia phage Rebecca	GCA_004521635.1
AUG86055.1	001506	Cluster1011_1clades	182	BOSOLAPHORUS_269	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52371.2	001506	Cluster1011_1clades	182	DM_272	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86375.1	001506	Cluster1011_1clades	182	DESERTFOX_268	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86696.1	001506	Cluster1011_1clades	182	MADMEL_269	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87021.1	001506	Cluster1011_1clades	86	MORTIMER_273	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52046.2	001506	Cluster1011_1clades	182	RAY_266	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51729.2	001506	Cluster1011_1clades	182	SIMMY50_271	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65081.1	001506	Cluster1011_1clades	86	SPECIALG_270	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24176.1	001506	Cluster1011_1clades	108	-	Proteus phage 10	GCA_014071245.1
QKE54596.1	001506	Cluster1011_1clades	127	ACSA002_2790	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13796.1	001507	Cluster1012_1clades	173	Ccr10_gp266	Caulobacter phage Ccr10	GCA_002619445.1
ARB14141.1	001507	Cluster1012_1clades	173	Ccr2_gp265	Caulobacter phage Ccr2	GCA_002619465.1
ARB14835.1	001507	Cluster1012_1clades	173	Ccr29_gp279	Caulobacter phage Ccr29	GCA_002619485.1
ARB15175.1	001507	Cluster1012_1clades	173	Ccr32_gp257	Caulobacter phage Ccr32	GCA_002619505.1
ARB15509.1	001507	Cluster1012_1clades	173	Ccr34_gp267	Caulobacter phage Ccr34	GCA_002619525.1
ARB14483.1	001507	Cluster1012_1clades	173	Ccr5_gp263	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68461.1	001507	Cluster1012_1clades	180	CcrBL10_gp257	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87793.1	001507	Cluster1012_1clades	137	CcrKarma_gp276	Caulobacter virus Karma	GCA_000901575.1
AFU87440.1	001507	Cluster1012_1clades	173	CcrMagneto_gp270	Caulobacter virus Magneto	GCA_000903095.1
AFU86747.1	001507	Cluster1012_1clades	180	CcrRogue_gp265	Caulobacter virus Rogue	GCA_000900555.1
AFU88586.1	001507	Cluster1012_1clades	137	CcrSwift_gp268	Caulobacter virus Swift	GCA_000899655.1
AFU87094.1	001507	Cluster1012_1clades	137	CbK_gp262	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64238.1	001508	Cluster1013_1clades	109	KVP40.0169	Vibrio phage KVP40	GCA_000843785.1
QIW90553.1	001508	Cluster1013_1clades	109	GCAPEGMB_00206	Vibrio phage V07	GCA_012361095.1
QIW90869.1	001508	Cluster1013_1clades	109	COHAPHLL_00006	Vibrio phage V09	GCA_012361135.1
QHJ74351.1	001508	Cluster1013_1clades	109	VH12019_00024	Vibrio phage VH1_2019	GCA_009931825.1
AGB06844.1	001508	Cluster1013_1clades	119	CF80_gp057	Vibrio phage VH7D	GCA_000914495.1
QBX06302.1	001508	Cluster1013_1clades	119	ValB1HC_349	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60933.1	001508	Cluster1013_1clades	109	AVU32_gp092	Vibrio phage ValKK3	GCA_001501635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN30219.2	001508	Cluster1013_1clades	176	VPFG_00219	Vibrio phage nt-1	GCA_000910195.2
ALP47166.1	001508	Cluster1013_1clades	118	phiGrn1_0281	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47573.1	001508	Cluster1013_1clades	109	phiST2_0040	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54545.1	001508	Cluster1013_1clades	119	vBValMR10Z_4	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37398.1	001508	Cluster1013_1clades	109	pp2_165	Vibriophage phi-pp2	GCA_002630725.1
ARB13741.1	001509	Cluster1014_1clades	162	Ccr10_gp211c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14086.1	001509	Cluster1014_1clades	162	Ccr2_gp210c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14775.1	001509	Cluster1014_1clades	171	Ccr29_gp219	Caulobacter phage Ccr29	GCA_002619485.1
ARB15119.1	001509	Cluster1014_1clades	162	Ccr32_gp201	Caulobacter phage Ccr32	GCA_002619505.1
ARB15453.1	001509	Cluster1014_1clades	162	Ccr34_gp211	Caulobacter phage Ccr34	GCA_002619525.1
ARB14428.1	001509	Cluster1014_1clades	171	Ccr5_gp208c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68407.1	001509	Cluster1014_1clades	174	CcrBL10_gp203c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87734.1	001509	Cluster1014_1clades	171	CcrKarma_gp217	Caulobacter virus Karma	GCA_000901575.1
AFU87383.1	001509	Cluster1014_1clades	173	CcrMagneto_gp213	Caulobacter virus Magneto	GCA_000903095.1
AFU86693.1	001509	Cluster1014_1clades	174	CcrRogue_gp211	Caulobacter virus Rogue	GCA_000900555.1
AFU88530.1	001509	Cluster1014_1clades	173	CcrSwift_gp212	Caulobacter virus Swift	GCA_000899655.1
AFU87038.1	001509	Cluster1014_1clades	173	CbK_gp206	Caulobacter virus phiCbK	GCA_000900535.1
ARB13825.1	001510	SIG+TM+TM+TM	166	Ccr10_gp295	Caulobacter phage Ccr10	GCA_002619445.1
ARB14170.1	001510	SIG+TM+TM+TM	166	Ccr2_gp294	Caulobacter phage Ccr2	GCA_002619465.1
ARB14864.1	001510	SIG+TM+TM+TM	166	Ccr29_gp308	Caulobacter phage Ccr29	GCA_002619485.1
ARB15202.1	001510	SIG+TM+TM+TM	166	Ccr32_gp284	Caulobacter phage Ccr32	GCA_002619505.1
ARB15536.1	001510	SIG+TM+TM+TM	166	Ccr34_gp294	Caulobacter phage Ccr34	GCA_002619525.1
ARB14511.1	001510	SIG+TM+TM+TM	164	Ccr5_gp291	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68492.1	001510	SIG+TM+TM+TM	174	CcrBL10_gp288	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87821.1	001510	SIG+TM+TM+TM	70	CcrKarma_gp304	Caulobacter virus Karma	GCA_000901575.1
AFU87468.1	001510	SIG+TM+TM+TM	174	CcrMagneto_gp298	Caulobacter virus Magneto	GCA_000903095.1
AFU86780.1	001510	SIG+TM+TM+TM	174	CcrRogue_gp298	Caulobacter virus Rogue	GCA_000900555.1
AFU88613.1	001510	SIG+TM+TM+TM	174	CcrSwift_gp295	Caulobacter virus Swift	GCA_000899655.1
AFU87121.1	001510	SIG+TM+TM+TM	166	CbK_gp289	Caulobacter virus phiCbK	GCA_000900535.1
ARB13586.1	001511	Cluster1016_1clades	174	Ccr10_gp058	Caulobacter phage Ccr10	GCA_002619445.1
ARB13932.1	001511	Cluster1016_1clades	174	Ccr2_gp057	Caulobacter phage Ccr2	GCA_002619465.1
ARB14621.1	001511	Cluster1016_1clades	174	Ccr29_gp064	Caulobacter phage Ccr29	GCA_002619485.1
ARB14977.1	001511	Cluster1016_1clades	174	Ccr32_gp058	Caulobacter phage Ccr32	GCA_002619505.1
ARB15308.1	001511	Cluster1016_1clades	174	Ccr34_gp059	Caulobacter phage Ccr34	GCA_002619525.1
ARB14275.1	001511	Cluster1016_1clades	174	Ccr5_gp057	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68259.1	001511	Cluster1016_1clades	110	CcrBL10_gp055	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87576.1	001511	Cluster1016_1clades	174	CcrKarma_gp059	Caulobacter virus Karma	GCA_000901575.1
AFU87226.1	001511	Cluster1016_1clades	174	CcrMagneto_gp056	Caulobacter virus Magneto	GCA_000903095.1
AFU86541.1	001511	Cluster1016_1clades	111	CcrRogue_gp059	Caulobacter virus Rogue	GCA_000900555.1
AFU88374.1	001511	Cluster1016_1clades	174	CcrSwift_gp056	Caulobacter virus Swift	GCA_000899655.1
AFU86890.1	001511	Cluster1016_1clades	174	CbK_gp058	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64125.1	001512	Cluster1017_1clades	170	KVP40.0054	Vibrio phage KVP40	GCA_000843785.1
QIW90447.1	001512	Cluster1017_1clades	170	GCAPEGMB_00100	Vibrio phage V07	GCA_012361095.1
QIW90982.1	001512	Cluster1017_1clades	170	COHAPHLL_00119	Vibrio phage V09	GCA_012361135.1
QHJ74236.1	001512	Cluster1017_1clades	170	VH12019_00317	Vibrio phage VH1_2019	GCA_009931825.1
AGB07060.1	001512	Cluster1017_1clades	169	CF80_gp273	Vibrio phage VH7D	GCA_000914495.1
QBX06036.1	001512	Cluster1017_1clades	169	ValB1HC_082	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61050.1	001512	Cluster1017_1clades	169	AVU32_gp209	Vibrio phage ValKK3	GCA_001501635.1
AGN30103.1	001512	Cluster1017_1clades	170	VPFG_00101	Vibrio phage nt-1	GCA_000910195.2
ALP47099.1	001512	Cluster1017_1clades	169	phiGrn1_0167	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47481.1	001512	Cluster1017_1clades	169	phiST2_0298	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54661.1	001512	Cluster1017_1clades	169	vBValMR10Z_120	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37285.1	001512	Cluster1017_1clades	170	pp2_051	Vibriophage phi-pp2	GCA_002630725.1
AIT14056.1	001513	Proteasome	165	PBI_121Q_166	Escherichia phage 121Q	GCA_000926855.1
QAY00287.1	001513	Proteasome	165	Ecwhy1_5	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35037.1	001513	Proteasome	165	ACQ29_gp357	Escherichia phage PBECO4	GCA_001041035.1
BBM61739.1	001513	Proteasome	165	EO157G_1500	Escherichia phage SP27	GCA_008033345.1
AXC36615.1	001513	Proteasome	165	-	Escherichia phage UB	GCA_003341455.1
QBO61643.1	001513	Proteasome	165	G17_00147	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13697.1	001513	Proteasome	165	vBEcoMphAPEC6_gp067c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80051.1	001513	Proteasome	165	PSLUR01_00074	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44516.1	001513	Proteasome	170	RaK2_00243	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18590.1	001513	Proteasome	167	7t3_069	Salmonella phage 7t3	GCA_006083215.1
AZU98418.1	001513	Proteasome	167	CPT_Munch_486	Salmonella phage Munch	GCA_004015485.1
QIG63095.1	001513	Proteasome	167	SEPL_482	Salmonella phage SE_PL	GCA_011067555.1
ARB13776.1	001514	Cluster1019_1clades	168	Ccr10_gp246	Caulobacter phage Ccr10	GCA_002619445.1
ARB14121.1	001514	Cluster1019_1clades	168	Ccr2_gp245	Caulobacter phage Ccr2	GCA_002619465.1
ARB14815.1	001514	Cluster1019_1clades	168	Ccr29_gp259	Caulobacter phage Ccr29	GCA_002619485.1
ARB15155.1	001514	Cluster1019_1clades	168	Ccr32_gp237	Caulobacter phage Ccr32	GCA_002619505.1
ARB15489.1	001514	Cluster1019_1clades	168	Ccr34_gp247	Caulobacter phage Ccr34	GCA_002619525.1
ARB14463.1	001514	Cluster1019_1clades	168	Ccr5_gp243	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68441.1	001514	Cluster1019_1clades	168	CcrBL10_gp237	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87771.1	001514	Cluster1019_1clades	169	CcrKarma_gp254	Caulobacter virus Karma	GCA_000901575.1
AFU87418.1	001514	Cluster1019_1clades	169	CcrMagneto_gp248	Caulobacter virus Magneto	GCA_000903095.1
AFU86727.1	001514	Cluster1019_1clades	168	CcrRogue_gp245	Caulobacter virus Rogue	GCA_000900555.1
AFU88566.1	001514	Cluster1019_1clades	168	CcrSwift_gp248	Caulobacter virus Swift	GCA_000899655.1
AFU87074.1	001514	Cluster1019_1clades	168	CbK_gp242	Caulobacter virus phiCbK	GCA_000900535.1
ABY63052.1	001515	Cluster1021_1clades	162	201phi2-1p223	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44931.1	001515	Cluster1021_1clades	162	KTN4_173	Pseudomonas phage KTN4	GCA_002607225.1
ARV77316.1	001515	Cluster1021_1clades	166	NOXIFER_147	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32318.1	001515	Cluster1021_1clades	162	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ85925.1	001515	Cluster1021_1clades	168	KKIINIFJ_00013	Pseudomonas phage PN05	GCA_009931935.1
ARV76841.1	001515	Cluster1021_1clades	162	PHABIO_210	Pseudomonas phage Phabio	GCA_002624965.1
AEH03580.1	001515	Cluster1021_1clades	161	157	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02717.1	001515	Cluster1021_1clades	163	PSA21_191	Pseudomonas phage Psa21	GCA_004340405.1
ATN94783.1	001515	Cluster1021_1clades	162	SL2_206	Pseudomonas phage SL2	GCA_002956015.1
QJB22809.1	001515	Cluster1021_1clades	162	fnug_166	Pseudomonas phage fnug	GCA_012837215.1
QEM41891.1	001515	Cluster1021_1clades	162	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83039.1	001515	Cluster1021_1clades	162	PHIKZ138	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64287.1	001516	Cluster1022_1clades	167	KVP40.0218	Vibrio phage KVP40	GCA_000843785.1
QIW90603.1	001516	Cluster1022_1clades	165	GCAPEGMB_00256	Vibrio phage V07	GCA_012361095.1
QIW91196.1	001516	Cluster1022_1clades	165	COHAPHLL_00360	Vibrio phage V09	GCA_012361135.1
QHJ74399.1	001516	Cluster1022_1clades	165	VH12019_00072	Vibrio phage VH1_2019	GCA_009931825.1
AGB06905.1	001516	Cluster1022_1clades	165	CF80_gp118	Vibrio phage VH7D	GCA_000914495.1
QBX06241.1	001516	Cluster1022_1clades	165	ValB1HC_288	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60867.1	001516	Cluster1022_1clades	165	AVU32_gp026	Vibrio phage ValKK3	GCA_001501635.1
AGN30279.2	001516	Cluster1022_1clades	165	VPFG_00280	Vibrio phage nt-1	GCA_000910195.2
ALP47107.1	001516	Cluster1022_1clades	165	phiGrn1_0342	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47490.1	001516	Cluster1022_1clades	165	phiST2_0097	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54867.1	001516	Cluster1022_1clades	165	vBValMR10Z_327	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37448.1	001516	Cluster1022_1clades	165	pp2_215	Vibriophage phi-pp2	GCA_002630725.1
ARB13793.1	001517	Cluster1023_1clades	167	Ccr10_gp263	Caulobacter phage Ccr10	GCA_002619445.1
ARB14138.1	001517	Cluster1023_1clades	167	Ccr2_gp262	Caulobacter phage Ccr2	GCA_002619465.1
ARB14832.1	001517	Cluster1023_1clades	167	Ccr29_gp276	Caulobacter phage Ccr29	GCA_002619485.1
ARB15172.1	001517	Cluster1023_1clades	166	Ccr32_gp254	Caulobacter phage Ccr32	GCA_002619505.1
ARB15506.1	001517	Cluster1023_1clades	166	Ccr34_gp264	Caulobacter phage Ccr34	GCA_002619525.1
ARB14480.1	001517	Cluster1023_1clades	166	Ccr5_gp260	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68458.1	001517	Cluster1023_1clades	166	CcrBL10_gp254	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87790.1	001517	Cluster1023_1clades	167	CcrKarma_gp273	Caulobacter virus Karma	GCA_000901575.1
AFU87437.1	001517	Cluster1023_1clades	167	CcrMagneto_gp267	Caulobacter virus Magneto	GCA_000903095.1
AFU86744.1	001517	Cluster1023_1clades	165	CcrRogue_gp262	Caulobacter virus Rogue	GCA_000900555.1
AFU88583.1	001517	Cluster1023_1clades	167	CcrSwift_gp265	Caulobacter virus Swift	GCA_000899655.1
AFU87091.1	001517	Cluster1023_1clades	166	CbK_gp259	Caulobacter virus phiCbK	GCA_000900535.1
AIT14298.1	001518	Cluster1024_1clades	165	PBI_121Q_408	Escherichia phage 121Q	GCA_000926855.1
QAY00640.1	001518	Cluster1024_1clades	166	Ecwhy1_365	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34836.1	001518	Cluster1024_1clades	165	ACQ29_gp156	Escherichia phage PBECO4	GCA_001041035.1
BBM61972.1	001518	Cluster1024_1clades	165	EO157G_3830	Escherichia phage SP27	GCA_008033345.1
AXC36945.1	001518	Cluster1024_1clades	165	-	Escherichia phage UB	GCA_003341455.1
QBO62006.1	001518	Cluster1024_1clades	165	G17_00517	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14027.1	001518	Cluster1024_1clades	165	vBEcoMphAPEC6_gp404c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80285.1	001518	Cluster1024_1clades	165	PSLUR01_00308	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44712.1	001518	Cluster1024_1clades	163	RaK2_00439	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18755.1	001518	Cluster1024_1clades	161	7t3_0234	Salmonella phage 7t3	GCA_006083215.1
AZU98024.1	001518	Cluster1024_1clades	161	CPT_Munch_080	Salmonella phage Munch	GCA_004015485.1
QIG62956.1	001518	Cluster1024_1clades	161	SEPL_343	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB13772.1	001519	Cluster1025_1clades	165	Ccr10_gp242	Caulobacter phage Ccr10	GCA_002619445.1
ARB14117.1	001519	Cluster1025_1clades	165	Ccr2_gp241	Caulobacter phage Ccr2	GCA_002619465.1
ARB14811.1	001519	Cluster1025_1clades	165	Ccr29_gp255	Caulobacter phage Ccr29	GCA_002619485.1
ARB15151.1	001519	Cluster1025_1clades	164	Ccr32_gp233	Caulobacter phage Ccr32	GCA_002619505.1
ARB15485.1	001519	Cluster1025_1clades	164	Ccr34_gp243	Caulobacter phage Ccr34	GCA_002619525.1
ARB14459.1	001519	Cluster1025_1clades	164	Ccr5_gp239	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68437.1	001519	Cluster1025_1clades	164	CcrBL10_gp233	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87767.1	001519	Cluster1025_1clades	164	CcrKarma_gp250	Caulobacter virus Karma	GCA_000901575.1
AFU87414.1	001519	Cluster1025_1clades	165	CcrMagneto_gp244	Caulobacter virus Magneto	GCA_000903095.1
AFU86723.1	001519	Cluster1025_1clades	164	CcrRogue_gp241	Caulobacter virus Rogue	GCA_000900555.1
AFU88562.1	001519	Cluster1025_1clades	165	CcrSwift_gp244	Caulobacter virus Swift	GCA_000899655.1
AFU87070.1	001519	Cluster1025_1clades	164	CbK_gp238	Caulobacter virus phiCbK	GCA_000900535.1
ARB13822.1	001520	Cluster1026_1clades	164	Ccr10_gp292	Caulobacter phage Ccr10	GCA_002619445.1
ARB14167.1	001520	Cluster1026_1clades	164	Ccr2_gp291	Caulobacter phage Ccr2	GCA_002619465.1
ARB14861.1	001520	Cluster1026_1clades	164	Ccr29_gp305	Caulobacter phage Ccr29	GCA_002619485.1
ARB15200.1	001520	Cluster1026_1clades	164	Ccr32_gp282	Caulobacter phage Ccr32	GCA_002619505.1
ARB15534.1	001520	Cluster1026_1clades	164	Ccr34_gp292	Caulobacter phage Ccr34	GCA_002619525.1
ARB14509.1	001520	Cluster1026_1clades	164	Ccr5_gp289	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68490.1	001520	Cluster1026_1clades	160	CcrBL10_gp286	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87819.1	001520	Cluster1026_1clades	164	CcrKarma_gp302	Caulobacter virus Karma	GCA_000901575.1
AFU87466.1	001520	Cluster1026_1clades	164	CcrMagneto_gp296	Caulobacter virus Magneto	GCA_000903095.1
AFU86778.1	001520	Cluster1026_1clades	160	CcrRogue_gp296	Caulobacter virus Rogue	GCA_000900555.1
AFU88611.1	001520	Cluster1026_1clades	164	CcrSwift_gp293	Caulobacter virus Swift	GCA_000899655.1
AFU87119.1	001520	Cluster1026_1clades	164	CbK_gp287	Caulobacter virus phiCbK	GCA_000900535.1
ARB13795.1	001521	Cluster1027_1clades	164	Ccr10_gp265	Caulobacter phage Ccr10	GCA_002619445.1
ARB14140.1	001521	Cluster1027_1clades	164	Ccr2_gp264	Caulobacter phage Ccr2	GCA_002619465.1
ARB14834.1	001521	Cluster1027_1clades	164	Ccr29_gp278	Caulobacter phage Ccr29	GCA_002619485.1
ARB15174.1	001521	Cluster1027_1clades	164	Ccr32_gp256	Caulobacter phage Ccr32	GCA_002619505.1
ARB15508.1	001521	Cluster1027_1clades	164	Ccr34_gp266	Caulobacter phage Ccr34	GCA_002619525.1
ARB14482.1	001521	Cluster1027_1clades	163	Ccr5_gp262	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68460.1	001521	Cluster1027_1clades	160	CcrBL10_gp256	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87792.1	001521	Cluster1027_1clades	163	CcrKarma_gp275	Caulobacter virus Karma	GCA_000901575.1
AFU87439.1	001521	Cluster1027_1clades	163	CcrMagneto_gp269	Caulobacter virus Magneto	GCA_000903095.1
AFU86746.1	001521	Cluster1027_1clades	160	CcrRogue_gp264	Caulobacter virus Rogue	GCA_000900555.1
AFU88585.1	001521	Cluster1027_1clades	163	CcrSwift_gp267	Caulobacter virus Swift	GCA_000899655.1
AFU87093.1	001521	Cluster1027_1clades	163	CbK_gp261	Caulobacter virus phiCbK	GCA_000900535.1
ARB13821.1	001522	Cluster1028_1clades	161	Ccr10_gp291	Caulobacter phage Ccr10	GCA_002619445.1
ARB14166.1	001522	Cluster1028_1clades	161	Ccr2_gp290	Caulobacter phage Ccr2	GCA_002619465.1
ARB14860.1	001522	Cluster1028_1clades	161	Ccr29_gp304	Caulobacter phage Ccr29	GCA_002619485.1
ARB15199.1	001522	Cluster1028_1clades	161	Ccr32_gp281	Caulobacter phage Ccr32	GCA_002619505.1
ARB15533.1	001522	Cluster1028_1clades	161	Ccr34_gp291	Caulobacter phage Ccr34	GCA_002619525.1
ARB14508.1	001522	Cluster1028_1clades	162	Ccr5_gp288	Caulobacter phage Ccr5	GCA_002619545.1
AFU88198.1	001522	Cluster1028_1clades	139	CcrColossus_gp328	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68875.1	001522	Cluster1028_1clades	139	CcrPW_gp336	Caulobacter phage CcrPW	GCA_003443275.1
AFU87818.1	001522	Cluster1028_1clades	161	CcrKarma_gp301	Caulobacter virus Karma	GCA_000901575.1
AFU87465.1	001522	Cluster1028_1clades	161	CcrMagneto_gp295	Caulobacter virus Magneto	GCA_000903095.1
AFU88610.1	001522	Cluster1028_1clades	161	CcrSwift_gp292	Caulobacter virus Swift	GCA_000899655.1
AFU87118.1	001522	Cluster1028_1clades	161	CbK_gp286	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64306.1	001523	Cluster1030_1clades	160	KVP40.0237	Vibrio phage KVP40	GCA_000843785.1
QIW90622.1	001523	Cluster1030_1clades	160	GCAPEGMB_00275	Vibrio phage V07	GCA_012361095.1
QIW91177.1	001523	Cluster1030_1clades	160	COHAPHLL_00341	Vibrio phage V09	GCA_012361135.1
QHJ74417.1	001523	Cluster1030_1clades	160	VH12019_00090	Vibrio phage VH1_2019	GCA_009931825.1
AGB06925.1	001523	Cluster1030_1clades	160	CF80_gp138	Vibrio phage VH7D	GCA_000914495.1
QBX06221.1	001523	Cluster1030_1clades	160	ValB1HC_268	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60847.1	001523	Cluster1030_1clades	160	AVU32_gp006	Vibrio phage ValKK3	GCA_001501635.1
AGN30294.1	001523	Cluster1030_1clades	160	VPFG_00295	Vibrio phage nt-1	GCA_000910195.2
ALP47113.1	001523	Cluster1030_1clades	160	phiGrn1_0361	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47496.1	001523	Cluster1030_1clades	160	phiST2_0116	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54846.1	001523	Cluster1030_1clades	160	vBValMR10Z_306	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37467.1	001523	Cluster1030_1clades	160	pp2_234	Vibriophage phi-pp2	GCA_002630725.1
ARB13662.1	001524	Cluster1031_1clades	159	Ccr10_gp133c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14007.1	001524	Cluster1031_1clades	159	Ccr2_gp132c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14695.1	001524	Cluster1031_1clades	159	Ccr29_gp139	Caulobacter phage Ccr29	GCA_002619485.1
ARB15049.1	001524	Cluster1031_1clades	159	Ccr32_gp131	Caulobacter phage Ccr32	GCA_002619505.1
ARB15382.1	001524	Cluster1031_1clades	159	Ccr34_gp140	Caulobacter phage Ccr34	GCA_002619525.1
ARB14350.1	001524	Cluster1031_1clades	159	Ccr5_gp131c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68331.1	001524	Cluster1031_1clades	151	CcrBL10_gp127c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87654.1	001524	Cluster1031_1clades	121	CcrKarma_gp137	Caulobacter virus Karma	GCA_000901575.1
AFU87303.1	001524	Cluster1031_1clades	121	CcrMagneto_gp133	Caulobacter virus Magneto	GCA_000903095.1
AFU86615.1	001524	Cluster1031_1clades	122	CcrRogue_gp133	Caulobacter virus Rogue	GCA_000900555.1
AFU88450.1	001524	Cluster1031_1clades	121	CcrSwift_gp132	Caulobacter virus Swift	GCA_000899655.1
AFU86967.1	001524	Cluster1031_1clades	121	CbK_gp135	Caulobacter virus phiCbK	GCA_000900535.1
ARB13590.1	001525	Cluster1032_1clades	158	Ccr10_gp062	Caulobacter phage Ccr10	GCA_002619445.1
ARB13936.1	001525	Cluster1032_1clades	158	Ccr2_gp061	Caulobacter phage Ccr2	GCA_002619465.1
ARB14625.1	001525	Cluster1032_1clades	158	Ccr29_gp068	Caulobacter phage Ccr29	GCA_002619485.1
ARB14981.1	001525	Cluster1032_1clades	158	Ccr32_gp062	Caulobacter phage Ccr32	GCA_002619505.1
ARB15312.1	001525	Cluster1032_1clades	158	Ccr34_gp063	Caulobacter phage Ccr34	GCA_002619525.1
ARB14279.1	001525	Cluster1032_1clades	158	Ccr5_gp061	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68263.1	001525	Cluster1032_1clades	156	CcrBL10_gp059	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87580.1	001525	Cluster1032_1clades	154	CcrKarma_gp063	Caulobacter virus Karma	GCA_000901575.1
AFU87230.1	001525	Cluster1032_1clades	158	CcrMagneto_gp060	Caulobacter virus Magneto	GCA_000903095.1
AFU86546.1	001525	Cluster1032_1clades	154	CcrRogue_gp064	Caulobacter virus Rogue	GCA_000900555.1
AFU88378.1	001525	Cluster1032_1clades	158	CcrSwift_gp060	Caulobacter virus Swift	GCA_000899655.1
AFU86894.1	001525	Cluster1032_1clades	158	CbK_gp062	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64317.1	001526	Cluster1033_1clades	156	KVP40.0248	Vibrio phage KVP40	GCA_000843785.1
QIW90632.1	001526	Cluster1033_1clades	156	GCAPEGMB_00285	Vibrio phage V07	GCA_012361095.1
QIW91167.1	001526	Cluster1033_1clades	156	COHAPHLL_00331	Vibrio phage V09	GCA_012361135.1
QHJ74427.1	001526	Cluster1033_1clades	156	VH12019_00100	Vibrio phage VH1_2019	GCA_009931825.1
AGB06933.1	001526	Cluster1033_1clades	156	CF80_gp146	Vibrio phage VH7D	GCA_000914495.1
QBX06213.1	001526	Cluster1033_1clades	135	ValB1HC_260	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61230.1	001526	Cluster1033_1clades	156	AVU32_gp389	Vibrio phage ValKK3	GCA_001501635.1
AGN30303.1	001526	Cluster1033_1clades	134	VPFG_00304	Vibrio phage nt-1	GCA_000910195.2
ALP47119.1	001526	Cluster1033_1clades	156	phiGrn1_0369	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47501.1	001526	Cluster1033_1clades	156	phiST2_0124	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54838.1	001526	Cluster1033_1clades	135	vBValMR10Z_298	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37476.1	001526	Cluster1033_1clades	156	pp2_243	Vibriophage phi-pp2	GCA_002630725.1
ARB13676.1	001527	YqeY	156	Ccr10_gp147	Caulobacter phage Ccr10	GCA_002619445.1
ARB14021.1	001527	YqeY	156	Ccr2_gp146	Caulobacter phage Ccr2	GCA_002619465.1
ARB14709.1	001527	YqeY	156	Ccr29_gp153	Caulobacter phage Ccr29	GCA_002619485.1
ARB15064.1	001527	YqeY	156	Ccr32_gp146	Caulobacter phage Ccr32	GCA_002619505.1
ARB15398.1	001527	YqeY	156	Ccr34_gp156	Caulobacter phage Ccr34	GCA_002619525.1
ARB14364.1	001527	YqeY	156	Ccr5_gp145	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68346.1	001527	YqeY	153	CcrBL10_gp142	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87669.1	001527	YqeY	156	CcrKarma_gp152	Caulobacter virus Karma	GCA_000901575.1
AFU87318.1	001527	YqeY	156	CcrMagneto_gp148	Caulobacter virus Magneto	GCA_000903095.1
AFU86630.1	001527	YqeY	153	CcrRogue_gp148	Caulobacter virus Rogue	GCA_000900555.1
AFU88465.1	001527	YqeY	156	CcrSwift_gp147	Caulobacter virus Swift	GCA_000899655.1
AFU86982.1	001527	YqeY	156	CbK_gp150	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64229.1	001528	Cluster1035_1clades	155	KVP40.0160	Vibrio phage KVP40	GCA_000843785.1
QIW90543.1	001528	Cluster1035_1clades	155	GCAPEGMB_00196	Vibrio phage V07	GCA_012361095.1
QIW90879.1	001528	Cluster1035_1clades	155	COHAPHLL_00016	Vibrio phage V09	GCA_012361135.1
QHJ74341.1	001528	Cluster1035_1clades	155	VH12019_00014	Vibrio phage VH1_2019	GCA_009931825.1
AGB06834.1	001528	Cluster1035_1clades	143	CF80_gp047	Vibrio phage VH7D	GCA_000914495.1
QBX06312.1	001528	Cluster1035_1clades	153	ValB1HC_359	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60943.1	001528	Cluster1035_1clades	153	AVU32_gp102	Vibrio phage ValKK3	GCA_001501635.1
AGN30207.1	001528	Cluster1035_1clades	156	VPFG_00207	Vibrio phage nt-1	GCA_000910195.2
ALP47125.1	001528	Cluster1035_1clades	153	phiGrn1_0271	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47510.1	001528	Cluster1035_1clades	153	phiST2_0030	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54555.1	001528	Cluster1035_1clades	153	vBValMR10Z_14	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37388.1	001528	Cluster1035_1clades	155	pp2_155	Vibriophage phi-pp2	GCA_002630725.1
ARB13842.1	001529	Cluster1036_1clades	141	Ccr10_gp312	Caulobacter phage Ccr10	GCA_002619445.1
ARB14187.1	001529	Cluster1036_1clades	133	Ccr2_gp311	Caulobacter phage Ccr2	GCA_002619465.1
ARB14881.1	001529	Cluster1036_1clades	133	Ccr29_gp325	Caulobacter phage Ccr29	GCA_002619485.1
ARB15219.1	001529	Cluster1036_1clades	141	Ccr32_gp301	Caulobacter phage Ccr32	GCA_002619505.1
ARB15553.1	001529	Cluster1036_1clades	141	Ccr34_gp311	Caulobacter phage Ccr34	GCA_002619525.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB14528.1	001529	Cluster1036_1clades	141	Ccr5_gp308	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68509.1	001529	Cluster1036_1clades	154	CcrBL10_gp305	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87839.1	001529	Cluster1036_1clades	142	CcrKarma_gp322	Caulobacter virus Karma	GCA_000901575.1
AFU87486.1	001529	Cluster1036_1clades	141	CcrMagneto_gp316	Caulobacter virus Magneto	GCA_000903095.1
AFU86798.1	001529	Cluster1036_1clades	155	CcrRogue_gp316	Caulobacter virus Rogue	GCA_000900555.1
AFU88631.1	001529	Cluster1036_1clades	142	CcrSwift_gp313	Caulobacter virus Swift	GCA_000899655.1
AFU87138.1	001529	Cluster1036_1clades	141	CbK_gp306	Caulobacter virus phiCbK	GCA_000900535.1
ARB13817.1	001530	Cluster1037_1clades	155	Ccr10_gp287	Caulobacter phage Ccr10	GCA_002619445.1
ARB14162.1	001530	Cluster1037_1clades	155	Ccr2_gp286	Caulobacter phage Ccr2	GCA_002619465.1
ARB14856.1	001530	Cluster1037_1clades	155	Ccr29_gp300	Caulobacter phage Ccr29	GCA_002619485.1
ARB15195.1	001530	Cluster1037_1clades	155	Ccr32_gp277	Caulobacter phage Ccr32	GCA_002619505.1
ARB15529.1	001530	Cluster1037_1clades	155	Ccr34_gp287	Caulobacter phage Ccr34	GCA_002619525.1
ARB14504.1	001530	Cluster1037_1clades	155	Ccr5_gp284	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68483.1	001530	Cluster1037_1clades	142	CcrBL10_gp279	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87814.1	001530	Cluster1037_1clades	155	CcrKarma_gp297	Caulobacter virus Karma	GCA_000901575.1
AFU87461.1	001530	Cluster1037_1clades	155	CcrMagneto_gp291	Caulobacter virus Magneto	GCA_000903095.1
AFU86771.1	001530	Cluster1037_1clades	143	CcrRogue_gp289	Caulobacter virus Rogue	GCA_000900555.1
AFU88606.1	001530	Cluster1037_1clades	155	CcrSwift_gp288	Caulobacter virus Swift	GCA_000899655.1
AFU87114.1	001530	Cluster1037_1clades	155	CbK_gp282	Caulobacter virus phiCbK	GCA_000900535.1
AHI60418.1	001531	Cluster1038_1clades	155	Ea357_264	Erwinia phage Ea35-70	GCA_000914635.1
QBP07375.1	001531	Cluster1038_1clades	155	REBECCA_270	Erwinia phage Rebecca	GCA_004521635.1
AUG86057.1	001531	Cluster1038_1clades	155	BOSOLAPHORUS_271	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52373.1	001531	Cluster1038_1clades	155	DM_274	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86377.1	001531	Cluster1038_1clades	155	DESERTFOX_270	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86698.1	001531	Cluster1038_1clades	155	MADMEL_271	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87023.1	001531	Cluster1038_1clades	155	MORTIMER_275	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52048.1	001531	Cluster1038_1clades	155	RAY_268	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51731.1	001531	Cluster1038_1clades	155	SIMMY50_273	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65083.1	001531	Cluster1038_1clades	155	SPECIALG_272	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24178.1	001531	Cluster1038_1clades	147	-	Proteus phage 10	GCA_014071245.1
QKE54598.1	001531	Cluster1038_1clades	151	ACSA002_2810	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64253.1	001532	Cluster1039_1clades	106	KVP40.0184	Vibrio phage KVP40	GCA_000843785.1
QIW90569.1	001532	Cluster1039_1clades	106	GCAPEGMB_00222	Vibrio phage V07	GCA_012361095.1
QIW91230.1	001532	Cluster1039_1clades	106	COHAPHLL_00394	Vibrio phage V09	GCA_012361135.1
QHJ74367.1	001532	Cluster1039_1clades	106	VH12019_00040	Vibrio phage VH1_2019	GCA_009931825.1
AGB06861.1	001532	Cluster1039_1clades	105	CF80_gp074	Vibrio phage VH7D	GCA_000914495.1
QBX06284.1	001532	Cluster1039_1clades	111	ValB1HC_331	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60911.1	001532	Cluster1039_1clades	111	AVU32_gp070	Vibrio phage ValKK3	GCA_001501635.1
AGN30242.2	001532	Cluster1039_1clades	110	VPFG_00243	Vibrio phage nt-1	GCA_000910195.2
ALP47130.1	001532	Cluster1039_1clades	151	phiGrn1_0301	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47502.1	001532	Cluster1039_1clades	155	phiST2_0057	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54911.1	001532	Cluster1039_1clades	111	vBValMR10Z_371	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37414.1	001532	Cluster1039_1clades	87	pp2_181	Vibriophage phi-pp2	GCA_002630725.1
QBO63875.1	001533	Cluster1040_1clades	109	Goslar_00082	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ABY63293.1	001533	Cluster1040_1clades	153	201phi2-1p135	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44860.1	001533	Cluster1040_1clades	80	KTN4_102	Pseudomonas phage KTN4	GCA_002607225.1
ARV77243.1	001533	Cluster1040_1clades	151	NOXIFER_72	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32230.1	001533	Cluster1040_1clades	131	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76751.1	001533	Cluster1040_1clades	110	PHABIO_120	Pseudomonas phage Phabio	GCA_002624965.1
AEH03497.1	001533	Cluster1040_1clades	134	073	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02611.1	001533	Cluster1040_1clades	155	PSA21_83	Pseudomonas phage Psa21	GCA_004340405.1
ATN94853.1	001533	Cluster1040_1clades	45	SL2_276	Pseudomonas phage SL2	GCA_002956015.1
QJB22738.1	001533	Cluster1040_1clades	80	fnug_95	Pseudomonas phage fnug	GCA_012837215.1
QEM41808.1	001533	Cluster1040_1clades	131	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26322.1	001533	Cluster1040_1clades	80	PHIKZ076.4	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64146.1	001534	Cluster1041_1clades	154	KVP40.0075	Vibrio phage KVP40	GCA_000843785.1
QIW90469.1	001534	Cluster1041_1clades	154	GCAPEGMB_00122	Vibrio phage V07	GCA_012361095.1
QIW90960.1	001534	Cluster1041_1clades	154	COHAPHLL_00097	Vibrio phage V09	GCA_012361135.1
QHJ74258.1	001534	Cluster1041_1clades	154	VH12019_00339	Vibrio phage VH1_2019	GCA_009931825.1
AGB07082.1	001534	Cluster1041_1clades	154	CF80_gp295	Vibrio phage VH7D	GCA_000914495.1
QBX06013.1	001534	Cluster1041_1clades	154	ValB1HC_059	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61026.1	001534	Cluster1041_1clades	154	AVU32_gp185	Vibrio phage ValKK3	GCA_001501635.1
AGN30124.1	001534	Cluster1041_1clades	153	VPFG_00122	Vibrio phage nt-1	GCA_000910195.2
ALP47121.1	001534	Cluster1041_1clades	154	phiGrn1_0190	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47505.1	001534	Cluster1041_1clades	154	phiST2_0321	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54638.1	001534	Cluster1041_1clades	154	vBValMR10Z_97	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37306.1	001534	Cluster1041_1clades	138	pp2_073	Vibriophage phi-pp2	GCA_002630725.1
ARB13755.1	001535	Cluster1042_1clades	141	Ccr10_gp225c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14100.1	001535	Cluster1042_1clades	141	Ccr2_gp224c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14789.1	001535	Cluster1042_1clades	141	Ccr29_gp233	Caulobacter phage Ccr29	GCA_002619485.1
ARB15133.1	001535	Cluster1042_1clades	141	Ccr32_gp215	Caulobacter phage Ccr32	GCA_002619505.1
ARB15467.1	001535	Cluster1042_1clades	141	Ccr34_gp225	Caulobacter phage Ccr34	GCA_002619525.1
ARB14442.1	001535	Cluster1042_1clades	141	Ccr5_gp222c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68422.1	001535	Cluster1042_1clades	154	CcrBL10_gp218c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87749.1	001535	Cluster1042_1clades	141	CcrKarma_gp232	Caulobacter virus Karma	GCA_000901575.1
AFU87397.1	001535	Cluster1042_1clades	141	CcrMagneto_gp227	Caulobacter virus Magneto	GCA_000903095.1
AFU86708.1	001535	Cluster1042_1clades	154	CcrRogue_gp226	Caulobacter virus Rogue	GCA_000900555.1
AFU88545.1	001535	Cluster1042_1clades	141	CcrSwift_gp227	Caulobacter virus Swift	GCA_000899655.1
AFU87052.1	001535	Cluster1042_1clades	141	CbK_gp220	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64302.1	001536	Cluster1043_1clades	150	KVP40.0233	Vibrio phage KVP40	GCA_000843785.1
QIW90618.1	001536	Cluster1043_1clades	150	GCAPEGMB_00271	Vibrio phage V07	GCA_012361095.1
QIW91181.1	001536	Cluster1043_1clades	150	COHAPHLL_00345	Vibrio phage V09	GCA_012361135.1
QHJ74413.1	001536	Cluster1043_1clades	150	VH12019_00086	Vibrio phage VH1_2019	GCA_009931825.1
AGB06921.1	001536	Cluster1043_1clades	150	CF80_gp134	Vibrio phage VH7D	GCA_000914495.1
QBX06225.1	001536	Cluster1043_1clades	150	ValB1HC_272	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60851.1	001536	Cluster1043_1clades	150	AVU32_gp010	Vibrio phage ValKK3	GCA_001501635.1
AGN30291.1	001536	Cluster1043_1clades	154	VPFG_00292	Vibrio phage nt-1	GCA_000910195.2
ALP47132.1	001536	Cluster1043_1clades	150	phiGrn1_0357	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47516.1	001536	Cluster1043_1clades	150	phiST2_0112	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54850.1	001536	Cluster1043_1clades	150	vBValMR10Z_310	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37463.1	001536	Cluster1043_1clades	150	pp2_230	Vibriophage phi-pp2	GCA_002630725.1
AHI60309.1	001537	Cluster1044_1clades	154	Ea357_158	Erwinia phage Ea35-70	GCA_000914635.1
QBP07267.1	001537	Cluster1044_1clades	154	REBECCA_160	Erwinia phage Rebecca	GCA_004521635.1
AUG85947.1	001537	Cluster1044_1clades	154	BOSOLAPHORUS_160	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52262.1	001537	Cluster1044_1clades	154	DM_164	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86266.1	001537	Cluster1044_1clades	154	DESERTFOX_159	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86588.1	001537	Cluster1044_1clades	154	MADMEL_160	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86912.1	001537	Cluster1044_1clades	154	MORTIMER_163	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51940.1	001537	Cluster1044_1clades	154	RAY_159	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51624.1	001537	Cluster1044_1clades	154	SIMMY50_162	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64971.1	001537	Cluster1044_1clades	154	SPECIALG_161	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24089.1	001537	Cluster1044_1clades	147	-	Proteus phage 10	GCA_014071245.1
QKE54463.1	001537	Cluster1044_1clades	154	ACSA002_1490	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13687.1	001538	Cluster1045_1clades	142	Ccr10_gp157c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14032.1	001538	Cluster1045_1clades	142	Ccr2_gp156c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14719.1	001538	Cluster1045_1clades	142	Ccr29_gp163	Caulobacter phage Ccr29	GCA_002619485.1
ARB15074.1	001538	Cluster1045_1clades	142	Ccr32_gp156	Caulobacter phage Ccr32	GCA_002619505.1
ARB15408.1	001538	Cluster1045_1clades	142	Ccr34_gp166	Caulobacter phage Ccr34	GCA_002619525.1
ARB14375.1	001538	Cluster1045_1clades	142	Ccr5_gp155c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68356.1	001538	Cluster1045_1clades	153	CcrBL10_gp152c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87680.1	001538	Cluster1045_1clades	142	CcrKarma_gp163	Caulobacter virus Karma	GCA_000901575.1
AFU87329.1	001538	Cluster1045_1clades	142	CcrMagneto_gp159	Caulobacter virus Magneto	GCA_000903095.1
AFU86640.1	001538	Cluster1045_1clades	153	CcrRogue_gp158	Caulobacter virus Rogue	GCA_000900555.1
AFU88476.1	001538	Cluster1045_1clades	142	CcrSwift_gp158	Caulobacter virus Swift	GCA_000899655.1
AFU86993.1	001538	Cluster1045_1clades	142	CbK_gp161	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64139.1	001539	Cluster1046_1clades	152	KVP40.0068	Vibrio phage KVP40	GCA_000843785.1
QIW90462.1	001539	Cluster1046_1clades	152	GCAPEGMB_00115	Vibrio phage V07	GCA_012361095.1
QIW90967.1	001539	Cluster1046_1clades	152	COHAPHLL_00104	Vibrio phage V09	GCA_012361135.1
QHJ74251.1	001539	Cluster1046_1clades	152	VH12019_00332	Vibrio phage VH1_2019	GCA_009931825.1
AGB07075.1	001539	Cluster1046_1clades	153	CF80_gp288	Vibrio phage VH7D	GCA_000914495.1
QBX06020.1	001539	Cluster1046_1clades	153	ValB1HC_066	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61034.1	001539	Cluster1046_1clades	153	AVU32_gp193	Vibrio phage ValKK3	GCA_001501635.1
AGN30117.1	001539	Cluster1046_1clades	153	VPFG_00115	Vibrio phage nt-1	GCA_000910195.2
ALP47124.1	001539	Cluster1046_1clades	153	phiGrn1_0183	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47508.1	001539	Cluster1046_1clades	153	phiST2_0314	Vibrio phage phi-ST2	GCA_002757135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNJ54645.1	001539	Cluster1046_1clades	153	vBValMR10Z_104	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37299.1	001539	Cluster1046_1clades	152	pp2_066	Vibriophage phi-pp2	GCA_002630725.1
AHI60307.1	001540	Cluster1047_1clades	152	Ea357_156	Erwinia phage Ea35-70	GCA_000914635.1
QBP07265.1	001540	Cluster1047_1clades	152	REBECCA_158	Erwinia phage Rebecca	GCA_004521635.1
AUG85945.1	001540	Cluster1047_1clades	152	BOSOLAPHORUS_158	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52260.2	001540	Cluster1047_1clades	152	DM_162	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86264.1	001540	Cluster1047_1clades	152	DESERTFOX_157	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86586.1	001540	Cluster1047_1clades	152	MADMEL_158	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86910.1	001540	Cluster1047_1clades	152	MORTIMER_161	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51938.1	001540	Cluster1047_1clades	152	RAY_157	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51622.1	001540	Cluster1047_1clades	152	SIMMY50_160	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64969.2	001540	Cluster1047_1clades	152	SPECIALG_159	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24086.1	001540	Cluster1047_1clades	140	-	Proteus phage 10	GCA_014071245.1
QKE54461.1	001540	Cluster1047_1clades	146	ACSA002_1470	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13814.1	001541	Cluster1048_1clades	149	Ccr10_gp284	Caulobacter phage Ccr10	GCA_002619445.1
ARB14159.1	001541	Cluster1048_1clades	149	Ccr2_gp283	Caulobacter phage Ccr2	GCA_002619465.1
ARB14853.1	001541	Cluster1048_1clades	149	Ccr29_gp297	Caulobacter phage Ccr29	GCA_002619485.1
ARB15192.1	001541	Cluster1048_1clades	149	Ccr32_gp274	Caulobacter phage Ccr32	GCA_002619505.1
ARB15526.1	001541	Cluster1048_1clades	149	Ccr34_gp284	Caulobacter phage Ccr34	GCA_002619525.1
ARB14501.1	001541	Cluster1048_1clades	149	Ccr5_gp281	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68481.1	001541	Cluster1048_1clades	151	CcrBL10_gp277	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87811.1	001541	Cluster1048_1clades	149	CcrKarma_gp294	Caulobacter virus Karma	GCA_000901575.1
AFU87458.1	001541	Cluster1048_1clades	149	CcrMagneto_gp288	Caulobacter virus Magneto	GCA_000903095.1
AFU86769.1	001541	Cluster1048_1clades	151	CcrRogue_gp287	Caulobacter virus Rogue	GCA_000900555.1
AFU88603.1	001541	Cluster1048_1clades	149	CcrSwift_gp285	Caulobacter virus Swift	GCA_000899655.1
AFU87111.1	001541	Cluster1048_1clades	149	CbK_gp279	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64275.1	001542	TM	143	KVP40.0206	Vibrio phage KVP40	GCA_000843785.1
QIW90591.1	001542	TM	143	GCAPEGMB_00244	Vibrio phage V07	GCA_012361095.1
QIW91208.1	001542	TM	143	COHAPHLL_00372	Vibrio phage V09	GCA_012361135.1
QHJ74387.1	001542	TM	143	VH12019_00060	Vibrio phage VH1_2019	GCA_009931825.1
AGB06892.1	001542	TM	145	CF80_gp105	Vibrio phage VH7D	GCA_000914495.1
QBX06254.1	001542	TM	145	ValB1HC_301	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60880.1	001542	TM	145	AVU32_gp039	Vibrio phage ValKK3	GCA_001501635.1
AGN30265.1	001542	TM	149	VPFG_00266	Vibrio phage nt-1	GCA_000910195.2
ALP47135.1	001542	TM	145	phiGrn1_0330	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47521.1	001542	TM	145	phiST2_0085	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54881.1	001542	TM	145	vBValMR10Z_341	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37435.1	001542	TM	143	pp2_202	Vibriophage phi-pp2	GCA_002630725.1
ARB13734.1	001543	Cluster1050_1clades	148	Ccr10_gp204c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14079.1	001543	Cluster1050_1clades	148	Ccr2_gp203c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14768.1	001543	Cluster1050_1clades	148	Ccr29_gp212	Caulobacter phage Ccr29	GCA_002619485.1
ARB15112.1	001543	Cluster1050_1clades	148	Ccr32_gp194	Caulobacter phage Ccr32	GCA_002619505.1
ARB15446.1	001543	Cluster1050_1clades	148	Ccr34_gp204	Caulobacter phage Ccr34	GCA_002619525.1
ARB14421.1	001543	Cluster1050_1clades	148	Ccr5_gp201c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68401.1	001543	Cluster1050_1clades	146	CcrBL10_gp197c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87727.1	001543	Cluster1050_1clades	148	CcrKarma_gp210	Caulobacter virus Karma	GCA_000901575.1
AFU87376.1	001543	Cluster1050_1clades	148	CcrMagneto_gp206	Caulobacter virus Magneto	GCA_000903095.1
AFU86687.1	001543	Cluster1050_1clades	146	CcrRogue_gp205	Caulobacter virus Rogue	GCA_000900555.1
AFU88523.1	001543	Cluster1050_1clades	148	CcrSwift_gp205	Caulobacter virus Swift	GCA_000899655.1
AFU87031.1	001543	Cluster1050_1clades	148	CbK_gp199	Caulobacter virus phiCbK	GCA_000900535.1
AIT14373.1	001544	Cluster1051_1clades	109	PBI_121Q_483	Escherichia phage 121Q	GCA_000926855.1
QAY00575.1	001544	Cluster1051_1clades	109	Ecwhy1_296	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34768.1	001544	Cluster1051_1clades	109	ACQ29_gp088	Escherichia phage PBECO4	GCA_001041035.1
BBM62044.1	001544	Cluster1051_1clades	109	EO157G_4550	Escherichia phage SP27	GCA_008033345.1
AXC36883.1	001544	Cluster1051_1clades	109	-	Escherichia phage UB	GCA_003341455.1
QBO61931.1	001544	Cluster1051_1clades	109	G17_00442	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13962.1	001544	Cluster1051_1clades	109	vBEcoMphAPEC6_gp338c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80360.1	001544	Cluster1051_1clades	109	PSLUR01_00383	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44782.1	001544	Cluster1051_1clades	117	RaK2_00509	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18833.1	001544	Cluster1051_1clades	148	7t3_0312	Salmonella phage 7t3	GCA_006083215.1
AZU98096.1	001544	Cluster1051_1clades	117	CPT_Munch_152	Salmonella phage Munch	GCA_004015485.1
QIG62886.1	001544	Cluster1051_1clades	117	SEPL_273	Salmonella phage SE_PL	GCA_011067555.1
AHI60286.1	001545	Cluster1052_1clades	145	Ea357_135	Erwinia phage Ea35-70	GCA_000914635.1
QBP07244.1	001545	Cluster1052_1clades	145	REBECCA_137	Erwinia phage Rebecca	GCA_004521635.1
AUG85924.1	001545	Cluster1052_1clades	145	BOSOLAPHORUS_137	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52239.1	001545	Cluster1052_1clades	145	DM_141	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86243.1	001545	Cluster1052_1clades	145	DESERTFOX_136	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86565.1	001545	Cluster1052_1clades	145	MADMEL_137	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86889.1	001545	Cluster1052_1clades	145	MORTIMER_140	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51917.1	001545	Cluster1052_1clades	145	RAY_136	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51601.1	001545	Cluster1052_1clades	145	SIMMY50_139	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64948.1	001545	Cluster1052_1clades	145	SPECIALG_138	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24068.1	001545	Cluster1052_1clades	148	-	Proteus phage 10	GCA_014071245.1
QKE54441.1	001545	Cluster1052_1clades	145	ACSA002_1270	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARB13692.1	001546	Cluster1053_1clades	147	Ccr10_gp162c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14037.1	001546	Cluster1053_1clades	147	Ccr2_gp161c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14724.1	001546	Cluster1053_1clades	147	Ccr29_gp168	Caulobacter phage Ccr29	GCA_002619485.1
ARB15079.1	001546	Cluster1053_1clades	147	Ccr32_gp161	Caulobacter phage Ccr32	GCA_002619505.1
ARB15413.1	001546	Cluster1053_1clades	147	Ccr34_gp171	Caulobacter phage Ccr34	GCA_002619525.1
ARB14380.1	001546	Cluster1053_1clades	147	Ccr5_gp160c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68362.1	001546	Cluster1053_1clades	136	CcrBL10_gp158c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87685.1	001546	Cluster1053_1clades	147	CcrKarma_gp168	Caulobacter virus Karma	GCA_000901575.1
AFU87334.1	001546	Cluster1053_1clades	147	CcrMagneto_gp164	Caulobacter virus Magneto	GCA_000903095.1
AFU86645.1	001546	Cluster1053_1clades	147	CcrRogue_gp163	Caulobacter virus Rogue	GCA_000900555.1
AFU88481.1	001546	Cluster1053_1clades	147	CcrSwift_gp163	Caulobacter virus Swift	GCA_000899655.1
AFU86998.1	001546	Cluster1053_1clades	147	CbK_gp166	Caulobacter virus phiCbK	GCA_000900535.1
AHI60269.1	001547	Cluster1054_1clades	116	Ea357_118	Erwinia phage Ea35-70	GCA_000914635.1
QBP07227.1	001547	Cluster1054_1clades	139	REBECCA_120	Erwinia phage Rebecca	GCA_004521635.1
AUG85907.1	001547	Cluster1054_1clades	116	BOSOLAPHORUS_120	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52222.2	001547	Cluster1054_1clades	116	DM_124	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86226.1	001547	Cluster1054_1clades	116	DESERTFOX_119	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86548.1	001547	Cluster1054_1clades	116	MADMEL_120	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86872.1	001547	Cluster1054_1clades	116	MORTIMER_123	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51900.1	001547	Cluster1054_1clades	116	RAY_119	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51584.1	001547	Cluster1054_1clades	116	SIMMY50_122	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64931.2	001547	Cluster1054_1clades	116	SPECIALG_121	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24056.1	001547	Cluster1054_1clades	147	-	Proteus phage 10	GCA_014071245.1
QKE54428.1	001547	Cluster1054_1clades	123	ACSA002_1140	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64254.1	001548	Cluster1055_1clades	144	KVP40.0185	Vibrio phage KVP40	GCA_000843785.1
QIW90570.1	001548	Cluster1055_1clades	144	GCAPEGMB_00223	Vibrio phage V07	GCA_012361095.1
QIW91229.1	001548	Cluster1055_1clades	144	COHAPHLL_00393	Vibrio phage V09	GCA_012361135.1
QHJ74368.1	001548	Cluster1055_1clades	144	VH12019_00041	Vibrio phage VH1_2019	GCA_009931825.1
AGB06863.1	001548	Cluster1055_1clades	144	CF80_gp076	Vibrio phage VH7D	GCA_000914495.1
QBX06281.1	001548	Cluster1055_1clades	144	ValB1HC_328	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60908.1	001548	Cluster1055_1clades	144	AVU32_gp067	Vibrio phage ValKK3	GCA_001501635.1
AGN30245.1	001548	Cluster1055_1clades	144	VPFG_00246	Vibrio phage nt-1	GCA_000910195.2
ALP47137.1	001548	Cluster1055_1clades	144	phiGrn1_0303	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47523.1	001548	Cluster1055_1clades	144	phiST2_0059	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54908.1	001548	Cluster1055_1clades	144	vBValMR10Z_368	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37415.1	001548	Cluster1055_1clades	144	pp2_182	Vibriophage phi-pp2	GCA_002630725.1
ARB13782.1	001549	Cluster1056_1clades	142	Ccr10_gp252	Caulobacter phage Ccr10	GCA_002619445.1
ARB14127.1	001549	Cluster1056_1clades	142	Ccr2_gp251	Caulobacter phage Ccr2	GCA_002619465.1
ARB14821.1	001549	Cluster1056_1clades	142	Ccr29_gp265	Caulobacter phage Ccr29	GCA_002619485.1
ARB15161.1	001549	Cluster1056_1clades	142	Ccr32_gp243	Caulobacter phage Ccr32	GCA_002619505.1
ARB15495.1	001549	Cluster1056_1clades	142	Ccr34_gp253	Caulobacter phage Ccr34	GCA_002619525.1
ARB14469.1	001549	Cluster1056_1clades	142	Ccr5_gp249	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68448.1	001549	Cluster1056_1clades	140	CcrBL10_gp244	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87778.1	001549	Cluster1056_1clades	142	CcrKarma_gp261	Caulobacter virus Karma	GCA_000901575.1
AFU87425.1	001549	Cluster1056_1clades	142	CcrMagneto_gp255	Caulobacter virus Magneto	GCA_000903095.1
AFU86734.1	001549	Cluster1056_1clades	140	CcrRogue_gp252	Caulobacter virus Rogue	GCA_000900555.1
AFU88572.1	001549	Cluster1056_1clades	142	CcrSwift_gp254	Caulobacter virus Swift	GCA_000899655.1
AFU87080.1	001549	Cluster1056_1clades	142	CbK_gp248	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64320.1	001550	Cluster1057_1clades	139	KVP40.0251	Vibrio phage KVP40	GCA_000843785.1
QIW90635.1	001550	Cluster1057_1clades	139	GCAPEGMB_00288	Vibrio phage V07	GCA_012361095.1
QIW91164.1	001550	Cluster1057_1clades	139	COHAPHLL_00328	Vibrio phage V09	GCA_012361135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QHJ74430.1	001550	Cluster1057_1clades	139	VH12019_00103	Vibrio phage VH1_2019	GCA_009931825.1
AGB06936.1	001550	Cluster1057_1clades	142	CF80_gp149	Vibrio phage VH7D	GCA_000914495.1
QBX06210.1	001550	Cluster1057_1clades	142	ValB1HC_257	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61227.1	001550	Cluster1057_1clades	142	AVU32_gp386	Vibrio phage ValKK3	GCA_001501635.1
AGN30306.1	001550	Cluster1057_1clades	141	VPFG_00307	Vibrio phage nt-1	GCA_000910195.2
ALP47138.1	001550	Cluster1057_1clades	142	phiGrn1_0372	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47525.1	001550	Cluster1057_1clades	142	phiST2_0127	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54835.1	001550	Cluster1057_1clades	142	vBValMR10Z_295	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37479.1	001550	Cluster1057_1clades	139	pp2_246	Vibriophage phi-pp2	GCA_002630725.1
AAQ64291.1	001551	Cluster1058_1clades	141	KVP40.0222	Vibrio phage KVP40	GCA_000843785.1
QIW90607.1	001551	Cluster1058_1clades	120	GCAPEGMB_00260	Vibrio phage V07	GCA_012361095.1
QIW91192.1	001551	Cluster1058_1clades	120	COHAPHLL_00356	Vibrio phage V09	GCA_012361135.1
QHJ74403.1	001551	Cluster1058_1clades	120	VH12019_00076	Vibrio phage VH1_2019	GCA_009931825.1
AGB06909.1	001551	Cluster1058_1clades	120	CF80_gp122	Vibrio phage VH7D	GCA_000914495.1
QBX06237.1	001551	Cluster1058_1clades	120	ValB1HC_284	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60863.1	001551	Cluster1058_1clades	120	AVU32_gp022	Vibrio phage ValKK3	GCA_001501635.1
AGN30282.1	001551	Cluster1058_1clades	118	VPFG_00283	Vibrio phage nt-1	GCA_000910195.2
ALP47163.1	001551	Cluster1058_1clades	120	phiGrn1_0345	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47549.1	001551	Cluster1058_1clades	120	phiST2_0100	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54862.1	001551	Cluster1058_1clades	120	vBValMR10Z_322	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37452.1	001551	Cluster1058_1clades	120	pp2_219	Vibriophage phi-pp2	GCA_002630725.1
ARB13556.1	001552	Cluster1059_1clades	141	Ccr10_gp028	Caulobacter phage Ccr10	GCA_002619445.1
ARB13902.1	001552	Cluster1059_1clades	141	Ccr2_gp027	Caulobacter phage Ccr2	GCA_002619465.1
ARB14591.1	001552	Cluster1059_1clades	141	Ccr29_gp034	Caulobacter phage Ccr29	GCA_002619485.1
ARB14946.1	001552	Cluster1059_1clades	141	Ccr32_gp027	Caulobacter phage Ccr32	GCA_002619505.1
ARB15277.1	001552	Cluster1059_1clades	141	Ccr34_gp028	Caulobacter phage Ccr34	GCA_002619525.1
ARB14245.1	001552	Cluster1059_1clades	141	Ccr5_gp027	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68229.1	001552	Cluster1059_1clades	140	CcrBL10_gp025	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87545.1	001552	Cluster1059_1clades	141	CcrKarma_gp028	Caulobacter virus Karma	GCA_000901575.1
AFU87196.1	001552	Cluster1059_1clades	141	CcrMagneto_gp026	Caulobacter virus Magneto	GCA_000903095.1
AFU86511.1	001552	Cluster1059_1clades	139	CcrRogue_gp029	Caulobacter virus Rogue	GCA_000900555.1
AFU88342.1	001552	Cluster1059_1clades	141	CcrSwift_gp024	Caulobacter virus Swift	GCA_000899655.1
AFU86859.1	001552	Cluster1059_1clades	141	CbK_gp027	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64285.1	001553	Cluster1060_1clades	82	KVP40.0216	Vibrio phage KVP40	GCA_000843785.1
QIW90601.1	001553	Cluster1060_1clades	82	GCAPEGMB_00254	Vibrio phage V07	GCA_012361095.1
QIW91198.1	001553	Cluster1060_1clades	82	COHAPHLL_00362	Vibrio phage V09	GCA_012361135.1
QHJ74397.1	001553	Cluster1060_1clades	82	VH12019_00070	Vibrio phage VH1_2019	GCA_009931825.1
AGB06903.1	001553	Cluster1060_1clades	137	CF80_gp116	Vibrio phage VH7D	GCA_000914495.1
QBX06243.1	001553	Cluster1060_1clades	137	ValB1HC_290	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60869.1	001553	Cluster1060_1clades	137	AVU32_gp028	Vibrio phage ValKK3	GCA_001501635.1
AGN30278.2	001553	Cluster1060_1clades	140	VPFG_00279	Vibrio phage nt-1	GCA_000910195.2
ALP47145.1	001553	Cluster1060_1clades	137	phiGrn1_0340	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47532.1	001553	Cluster1060_1clades	137	phiST2_0095	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54869.1	001553	Cluster1060_1clades	137	vBValMR10Z_329	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37446.1	001553	Cluster1060_1clades	82	pp2_213	Vibriophage phi-pp2	GCA_002630725.1
AHI60354.1	001554	Cluster1061_1clades	140	Ea357_201	Erwinia phage Ea35-70	GCA_000914635.1
QBP07311.1	001554	Cluster1061_1clades	140	REBECCA_206	Erwinia phage Rebecca	GCA_004521635.1
AUG85992.1	001554	Cluster1061_1clades	140	BOSOLAPHORUS_206	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52309.1	001554	Cluster1061_1clades	140	DM_209	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86311.1	001554	Cluster1061_1clades	140	DESERTFOX_204	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86634.1	001554	Cluster1061_1clades	140	MADMEL_206	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86957.1	001554	Cluster1061_1clades	140	MORTIMER_209	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51984.1	001554	Cluster1061_1clades	140	RAY_204	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51668.1	001554	Cluster1061_1clades	140	SIMMY50_209	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65018.1	001554	Cluster1061_1clades	140	SPECIALG_207	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24131.1	001554	Cluster1061_1clades	138	-	Proteus phage 10	GCA_014071245.1
QKE54528.1	001554	Cluster1061_1clades	140	ACSA002_2120	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AIT14101.1	001555	Cluster1062_1clades	131	PBI_121Q_211	Escherichia phage 121Q	GCA_000926855.1
QAY00821.1	001555	Cluster1062_1clades	126	Ecwhy1_548	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34994.1	001555	Cluster1062_1clades	131	ACQ29_gp314	Escherichia phage PBECO4	GCA_001041035.1
BBM61783.1	001555	Cluster1062_1clades	126	EO157G_1940	Escherichia phage SP27	GCA_008033345.1
AXC36574.1	001555	Cluster1062_1clades	126	-	Escherichia phage UB	GCA_003341455.1
QBO61598.1	001555	Cluster1062_1clades	126	G17_00102	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13657.1	001555	Cluster1062_1clades	126	vBEcoMphAPEC6_gp026c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80095.1	001555	Cluster1062_1clades	126	PSLUR01_00118	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44561.1	001555	Cluster1062_1clades	132	RaK2_00288	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18619.1	001555	Cluster1062_1clades	140	7t3_098	Salmonella phage 7t3	GCA_006083215.1
AZU98444.1	001555	Cluster1062_1clades	140	CPT_Munch_512	Salmonella phage Munch	GCA_004015485.1
QIG63069.1	001555	Cluster1062_1clades	140	SEPL_456	Salmonella phage SE_PL	GCA_011067555.1
ABY63068.1	001556	Cluster1063_1clades	134	201phi2-1p239	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44948.1	001556	Cluster1063_1clades	139	KTN4_190	Pseudomonas phage KTN4	GCA_002607225.1
ARV77337.1	001556	Cluster1063_1clades	139	NOXIFER_168	Pseudomonas phage Noxifer	GCA_002625005.1
ARV76858.1	001556	Cluster1063_1clades	103	PHABIO_227	Pseudomonas phage Phabio	GCA_002624965.1
AEH03600.1	001556	Cluster1063_1clades	136	177	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02737.1	001556	Cluster1063_1clades	137	PSA21_211	Pseudomonas phage Psa21	GCA_004340405.1
ATN94766.1	001556	Cluster1063_1clades	139	SL2_189	Pseudomonas phage SL2	GCA_002956015.1
QJB22826.1	001556	Cluster1063_1clades	104	fnug_183	Pseudomonas phage fnug	GCA_012837215.1
QEM41909.1	001556	Cluster1063_1clades	101	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83055.2	001556	Cluster1063_1clades	139	PHIKZ154	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19035.1	001556	Cluster1063_1clades	134	FDH28_gp061	Ralstonia phage RP12	GCA_002617345.1
BAW19320.1	001556	Cluster1063_1clades	116	-	Ralstonia phage RP31	GCA_002617365.1
AUZ94937.1	001557	Cluster1064_1clades	94	FDI40_gp155	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIA65023.1	001557	Cluster1064_1clades	112	S13_226	Cronobacter phage S13	GCA_001503575.1
QHJ78909.1	001557	Cluster1064_1clades	105	-	Myoviridae sp.	GCA_012593985.1
QIG65723.1	001557	Cluster1064_1clades	111	phiOC_p058	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR48121.1	001557	Cluster1064_1clades	100	SmphiM12_489	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13659.1	001557	Cluster1064_1clades	100	PHIN3_396	Sinorhizobium phage phiN3	GCA_001501175.1
BAV39357.1	001557	Cluster1064_1clades	100	BPT24_237	Tenacibaculum phage pT24	GCA_002611925.1
AAQ64244.1	001557	Cluster1064_1clades	139	KVP40.0175	Vibrio phage KVP40	GCA_000843785.1
QIW90560.1	001557	Cluster1064_1clades	118	GCAPEGMB_00213	Vibrio phage V07	GCA_012361095.1
QIW91239.1	001557	Cluster1064_1clades	119	COHAPHLL_00403	Vibrio phage V09	GCA_012361135.1
AIE13773.1	001557	Cluster1064_1clades	118	VPFG_00227	Vibrio phage nt-1	GCA_000910195.2
AFN37405.1	001557	Cluster1064_1clades	118	pp2_172	Vibriophage phi-pp2	GCA_002630725.1
AFC21461.1	001558	Cluster1066_1clades	126	GAP32_014	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14156.1	001558	Cluster1066_1clades	120	PBI_121Q_266	Escherichia phage 121Q	GCA_000926855.1
QAY00779.1	001558	Cluster1066_1clades	139	Ecwhy1_506	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34959.1	001558	Cluster1066_1clades	120	ACQ29_gp279	Escherichia phage PBECO4	GCA_001041035.1
BBM61830.1	001558	Cluster1066_1clades	120	EO157G_2410	Escherichia phage SP27	GCA_008033345.1
AXC37056.1	001558	Cluster1066_1clades	48	-	Escherichia phage UB	GCA_003341455.1
QBO61549.1	001558	Cluster1066_1clades	139	G17_00053	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62155.1	001558	Cluster1066_1clades	139	G17_00666	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14162.1	001558	Cluster1066_1clades	123	vBEcoMphAPEC6_gp539c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80145.1	001558	Cluster1066_1clades	120	PSLUR01_00168	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43583.1	001558	Cluster1066_1clades	123	CBB_18	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44134.1	001558	Cluster1066_1clades	123	CBB_571	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ARB13611.1	001559	TM	138	Ccr10_gp083	Caulobacter phage Ccr10	GCA_002619445.1
ARB13957.1	001559	TM	138	Ccr2_gp082	Caulobacter phage Ccr2	GCA_002619465.1
ARB14647.1	001559	TM	138	Ccr29_gp090	Caulobacter phage Ccr29	GCA_002619485.1
ARB15002.1	001559	TM	138	Ccr32_gp083	Caulobacter phage Ccr32	GCA_002619505.1
ARB15333.1	001559	TM	138	Ccr34_gp090	Caulobacter phage Ccr34	GCA_002619525.1
ARB14300.1	001559	TM	138	Ccr5_gp082	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68283.1	001559	TM	107	CcrBL10_gp079	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87602.1	001559	TM	138	CcrKarma_gp085	Caulobacter virus Karma	GCA_000901575.1
AFU87251.1	001559	TM	138	CcrMagneto_gp081	Caulobacter virus Magneto	GCA_000903095.1
AFU86566.1	001559	TM	107	CcrRogue_gp084	Caulobacter virus Rogue	GCA_000900555.1
AFU88398.1	001559	TM	138	CcrSwift_gp080	Caulobacter virus Swift	GCA_000899655.1
AFU86916.1	001559	TM	138	CbK_gp084	Caulobacter virus phiCbK	GCA_000900535.1
AOO14403.1	001560	TM+TM	123	Sn110110_210	Cyanophage S-RIM14	GCA_002599065.1
AOO15052.1	001560	TM+TM	123	W1230910_207	Cyanophage S-RIM14	GCA_002599125.1
AMO43211.1	001560	TM+TM	118	R1080702_205	Cyanophage S-RIM32	GCA_001754165.1
AMO43440.1	001560	TM+TM	136	W270710_200	Cyanophage S-RIM44	GCA_002599145.1
AOO11683.1	001560	TM+TM	132	ES420910_205	Cyanophage S-RIM44	GCA_002599165.1
AOO11912.1	001560	TM+TM	136	Np050604_200	Cyanophage S-RIM44	GCA_002599185.1
AOO12149.1	001560	TM+TM	132	Np200711_206	Cyanophage S-RIM44	GCA_002599205.1
AOO12384.1	001560	TM+TM	132	Np420711_205	Cyanophage S-RIM44	GCA_002599225.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12613.1	001560	TM+TM	135	Sn080709_200	Cyanophage S-RIM44	GCA_002599245.1
AOO12849.1	001560	TM+TM	132	Sn130910_205	Cyanophage S-RIM44	GCA_002599265.1
AOO13079.1	001560	TM+TM	136	W2100709_201	Cyanophage S-RIM44	GCA_002599285.1
ADO99299.1	001560	TM+TM	137	Syn1_202	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13836.1	001561	Cluster1069_1clades	131	Ccr10_gp306	Caulobacter phage Ccr10	GCA_002619445.1
ARB14181.1	001561	Cluster1069_1clades	131	Ccr2_gp305	Caulobacter phage Ccr2	GCA_002619465.1
ARB14875.1	001561	Cluster1069_1clades	131	Ccr29_gp319	Caulobacter phage Ccr29	GCA_002619485.1
ARB15213.1	001561	Cluster1069_1clades	131	Ccr32_gp295	Caulobacter phage Ccr32	GCA_002619505.1
ARB15547.1	001561	Cluster1069_1clades	131	Ccr34_gp305	Caulobacter phage Ccr34	GCA_002619525.1
ARB14522.1	001561	Cluster1069_1clades	131	Ccr5_gp302	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68502.1	001561	Cluster1069_1clades	128	CcrBL10_gp298	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87833.1	001561	Cluster1069_1clades	131	CcrKarma_gp316	Caulobacter virus Karma	GCA_000901575.1
AFU87480.1	001561	Cluster1069_1clades	131	CcrMagneto_gp310	Caulobacter virus Magneto	GCA_000903095.1
AFU86790.1	001561	Cluster1069_1clades	137	CcrRogue_gp308	Caulobacter virus Rogue	GCA_000900555.1
AFU88625.1	001561	Cluster1069_1clades	131	CcrSwift_gp307	Caulobacter virus Swift	GCA_000899655.1
AFU87132.1	001561	Cluster1069_1clades	131	CbK_gp300	Caulobacter virus phiCbK	GCA_000900535.1
ARB13670.1	001562	Cluster1070_1clades	137	Ccr10_gp141	Caulobacter phage Ccr10	GCA_002619445.1
ARB14015.1	001562	Cluster1070_1clades	137	Ccr2_gp140	Caulobacter phage Ccr2	GCA_002619465.1
ARB14702.1	001562	Cluster1070_1clades	137	Ccr29_gp146	Caulobacter phage Ccr29	GCA_002619485.1
ARB15057.1	001562	Cluster1070_1clades	137	Ccr32_gp139	Caulobacter phage Ccr32	GCA_002619505.1
ARB15391.1	001562	Cluster1070_1clades	137	Ccr34_gp149	Caulobacter phage Ccr34	GCA_002619525.1
ARB14358.1	001562	Cluster1070_1clades	137	Ccr5_gp139	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68338.1	001562	Cluster1070_1clades	135	CcrBL10_gp134	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87663.1	001562	Cluster1070_1clades	137	CcrKarma_gp146	Caulobacter virus Karma	GCA_000901575.1
AFU87312.1	001562	Cluster1070_1clades	137	CcrMagneto_gp142	Caulobacter virus Magneto	GCA_000903095.1
AFU86623.1	001562	Cluster1070_1clades	136	CcrRogue_gp141	Caulobacter virus Rogue	GCA_000900555.1
AFU88459.1	001562	Cluster1070_1clades	137	CcrSwift_gp141	Caulobacter virus Swift	GCA_000899655.1
AFU86976.1	001562	Cluster1070_1clades	137	CbK_gp144	Caulobacter virus phiCbK	GCA_000900535.1
ARB13696.1	001563	Cluster1071_1clades	137	Ccr10_gp166c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14041.1	001563	Cluster1071_1clades	137	Ccr2_gp165c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14728.1	001563	Cluster1071_1clades	137	Ccr29_gp172	Caulobacter phage Ccr29	GCA_002619485.1
ARB15083.1	001563	Cluster1071_1clades	137	Ccr32_gp165	Caulobacter phage Ccr32	GCA_002619505.1
ARB15417.1	001563	Cluster1071_1clades	137	Ccr34_gp175	Caulobacter phage Ccr34	GCA_002619525.1
ARB14384.1	001563	Cluster1071_1clades	137	Ccr5_gp164c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68366.1	001563	Cluster1071_1clades	135	CcrBL10_gp162c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87689.1	001563	Cluster1071_1clades	137	CcrKarma_gp172	Caulobacter virus Karma	GCA_000901575.1
AFU87338.1	001563	Cluster1071_1clades	137	CcrMagneto_gp168	Caulobacter virus Magneto	GCA_000903095.1
AFU86649.1	001563	Cluster1071_1clades	135	CcrRogue_gp167	Caulobacter virus Rogue	GCA_000900555.1
AFU88485.1	001563	Cluster1071_1clades	137	CcrSwift_gp167	Caulobacter virus Swift	GCA_000899655.1
AFU87002.1	001563	Cluster1071_1clades	137	CbK_gp170	Caulobacter virus phiCbK	GCA_000900535.1
ARB13560.1	001564	Cluster1072_1clades	133	Ccr10_gp032	Caulobacter phage Ccr10	GCA_002619445.1
ARB13906.1	001564	Cluster1072_1clades	133	Ccr2_gp031	Caulobacter phage Ccr2	GCA_002619465.1
ARB14595.1	001564	Cluster1072_1clades	133	Ccr29_gp038	Caulobacter phage Ccr29	GCA_002619485.1
ARB14950.1	001564	Cluster1072_1clades	133	Ccr32_gp031	Caulobacter phage Ccr32	GCA_002619505.1
ARB15281.1	001564	Cluster1072_1clades	133	Ccr34_gp032	Caulobacter phage Ccr34	GCA_002619525.1
ARB14249.1	001564	Cluster1072_1clades	133	Ccr5_gp031	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68232.1	001564	Cluster1072_1clades	136	CcrBL10_gp028	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87549.1	001564	Cluster1072_1clades	122	CcrKarma_gp032	Caulobacter virus Karma	GCA_000901575.1
AFU87200.1	001564	Cluster1072_1clades	133	CcrMagneto_gp030	Caulobacter virus Magneto	GCA_000903095.1
AFU86514.1	001564	Cluster1072_1clades	136	CcrRogue_gp032	Caulobacter virus Rogue	GCA_000900555.1
AFU88346.1	001564	Cluster1072_1clades	122	CcrSwift_gp028	Caulobacter virus Swift	GCA_000899655.1
AFU86863.1	001564	Cluster1072_1clades	133	CbK_gp031	Caulobacter virus phiCbK	GCA_000900535.1
AHI60414.1	001565	Cluster1073_1clades	133	Ea357_260	Erwinia phage Ea35-70	GCA_000914635.1
QBP07371.1	001565	Cluster1073_1clades	133	REBECCA_266	Erwinia phage Rebecca	GCA_004521635.1
AUG86053.1	001565	Cluster1073_1clades	133	BOSOLAPHORUS_267	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52369.1	001565	Cluster1073_1clades	133	DM_270	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86373.1	001565	Cluster1073_1clades	133	DESERTFOX_266	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86694.1	001565	Cluster1073_1clades	133	MADMEL_267	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87019.1	001565	Cluster1073_1clades	133	MORTIMER_271	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52044.1	001565	Cluster1073_1clades	133	RAY_264	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51727.1	001565	Cluster1073_1clades	133	SIMMY50_269	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65079.1	001565	Cluster1073_1clades	133	SPECIALG_268	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24174.1	001565	Cluster1073_1clades	130	-	Proteus phage 10	GCA_014071245.1
QKE54594.1	001565	Cluster1073_1clades	136	ACSA002_2770	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60296.1	001566	SIG+CCDC158	114	Ea357_145	Erwinia phage Ea35-70	GCA_000914635.1
QBP07254.1	001566	SIG+CCDC158	135	REBECCA_147	Erwinia phage Rebecca	GCA_004521635.1
AUG85934.1	001566	SIG+CCDC158	114	BOSOLAPHORUS_147	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52249.1	001566	SIG+CCDC158	114	DM_151	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86253.1	001566	SIG+CCDC158	114	DESERTFOX_146	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86575.1	001566	SIG+CCDC158	114	MADMEL_147	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86899.1	001566	SIG+CCDC158	114	MORTIMER_150	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51927.1	001566	SIG+CCDC158	114	RAY_146	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51611.1	001566	SIG+CCDC158	114	SIMMY50_149	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64958.1	001566	SIG+CCDC158	114	SPECIALG_148	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24077.1	001566	SIG+CCDC158	136	-	Proteus phage 10	GCA_014071245.1
QKE54450.1	001566	SIG+CCDC158	128	ACSA002_1360	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64110.1	001567	Cluster1075_1clades	133	KVP40.0039	Vibrio phage KVP40	GCA_000843785.1
QIW90433.1	001567	Cluster1075_1clades	133	GCAPEGMB_00086	Vibrio phage V07	GCA_012361095.1
QIW90996.1	001567	Cluster1075_1clades	133	COHAPHLI_00133	Vibrio phage V09	GCA_012361135.1
QHJ74222.1	001567	Cluster1075_1clades	133	VH12019_00303	Vibrio phage VH1_2019	GCA_009931825.1
AGB07046.1	001567	Cluster1075_1clades	133	CF80_gp259	Vibrio phage VH7D	GCA_000914495.1
QBX06050.1	001567	Cluster1075_1clades	133	ValB1HC_096	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61063.1	001567	Cluster1075_1clades	133	AVU32_gp222	Vibrio phage ValKK3	GCA_001501635.1
AGN30088.1	001567	Cluster1075_1clades	134	VPFG_00086	Vibrio phage nt-1	GCA_000910195.2
ALP47150.1	001567	Cluster1075_1clades	133	phiGrn1_0154	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47536.1	001567	Cluster1075_1clades	133	phiST2_0284	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54676.1	001567	Cluster1075_1clades	133	vBValMR10Z_135	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37272.1	001567	Cluster1075_1clades	133	pp2_038	Vibriophage phi-pp2	GCA_002630725.1
AIT14395.1	001568	Cluster1076_1clades	133	PBI_121Q_505	Escherichia phage 121Q	GCA_000926855.1
QAY00553.1	001568	Cluster1076_1clades	133	Ecwhy1_274	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34747.1	001568	Cluster1076_1clades	133	ACQ29_gp067	Escherichia phage PBECO4	GCA_001041035.1
BBM62066.1	001568	Cluster1076_1clades	133	EO157G_4770	Escherichia phage SP27	GCA_008033345.1
AXC36862.1	001568	Cluster1076_1clades	133	-	Escherichia phage UB	GCA_003341455.1
QBO61907.1	001568	Cluster1076_1clades	133	G17_00418	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13942.1	001568	Cluster1076_1clades	133	vBEcoMphAPEC6_gp318c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80384.1	001568	Cluster1076_1clades	133	PSLUR01_00407	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44276.1	001568	Cluster1076_1clades	132	RaK2_00003	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18859.1	001568	Cluster1076_1clades	129	7t3_0338	Salmonella phage 7t3	GCA_006083215.1
AZU98120.1	001568	Cluster1076_1clades	129	CPT_Munch_176	Salmonella phage Munch	GCA_004015485.1
QIG62862.1	001568	Cluster1076_1clades	129	SEPL_249	Salmonella phage SE_PL	GCA_011067555.1
AAQ64375.1	001569	Cluster1077_1clades	123	KVP40.0305	Vibrio phage KVP40	GCA_000843785.1
QIW90691.1	001569	Cluster1077_1clades	123	GCAPEGMB_00344	Vibrio phage V07	GCA_012361095.1
QIW91107.1	001569	Cluster1077_1clades	123	COHAPHLI_00271	Vibrio phage V09	GCA_012361135.1
QHJ74488.1	001569	Cluster1077_1clades	133	VH12019_00161	Vibrio phage VH1_2019	GCA_009931825.1
AGB06970.1	001569	Cluster1077_1clades	123	CF80_gp183	Vibrio phage VH7D	GCA_000914495.1
QBX06163.1	001569	Cluster1077_1clades	123	ValB1HC_210	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61180.1	001569	Cluster1077_1clades	123	AVU32_gp339	Vibrio phage ValKK3	GCA_001501635.1
AGN30353.1	001569	Cluster1077_1clades	123	VPFG_00356	Vibrio phage nt-1	GCA_000910195.2
ALP47160.1	001569	Cluster1077_1clades	123	phiGrn1_0042	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47547.1	001569	Cluster1077_1clades	123	phiST2_0174	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54789.1	001569	Cluster1077_1clades	123	vBValMR10Z_249	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37537.1	001569	Cluster1077_1clades	123	pp2_304	Vibriophage phi-pp2	GCA_002630725.1
AAQ64097.1	001570	Cluster1078_1clades	132	KVP40.0026	Vibrio phage KVP40	GCA_000843785.1
QIW90420.1	001570	Cluster1078_1clades	132	GCAPEGMB_00073	Vibrio phage V07	GCA_012361095.1
QIW91009.1	001570	Cluster1078_1clades	132	COHAPHLI_00146	Vibrio phage V09	GCA_012361135.1
QHJ74209.1	001570	Cluster1078_1clades	132	VH12019_00290	Vibrio phage VH1_2019	GCA_009931825.1
AGB07033.1	001570	Cluster1078_1clades	126	CF80_gp246	Vibrio phage VH7D	GCA_000914495.1
QBX06063.1	001570	Cluster1078_1clades	132	ValB1HC_109	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61077.1	001570	Cluster1078_1clades	132	AVU32_gp236	Vibrio phage ValKK3	GCA_001501635.1
AGN30077.1	001570	Cluster1078_1clades	129	VPFG_00075	Vibrio phage nt-1	GCA_000910195.2
ALP47157.1	001570	Cluster1078_1clades	126	phiGrn1_0141	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47543.1	001570	Cluster1078_1clades	126	phiST2_0271	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54689.1	001570	Cluster1078_1clades	132	vBValMR10Z_148	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37260.1	001570	Cluster1078_1clades	132	pp2_026	Vibriophage phi-pp2	GCA_002630725.1
AAQ64167.1	001571	Cluster1079_1clades	132	KVP40.0096	Vibrio phage KVP40	GCA_000843785.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW90490.1	001571	Cluster1079_1clades	132	GCAPEGMB_00143	Vibrio phage V07	GCA_012361095.1
QIW90939.1	001571	Cluster1079_1clades	132	COHAPHLL_00076	Vibrio phage V09	GCA_012361135.1
QHJ74278.1	001571	Cluster1079_1clades	132	VH12019_00359	Vibrio phage VH1_2019	GCA_009931825.1
AGB07103.1	001571	Cluster1079_1clades	132	CF80_gp316	Vibrio phage VH7D	GCA_000914495.1
QBX05992.1	001571	Cluster1079_1clades	132	ValB1HC_038	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61005.1	001571	Cluster1079_1clades	132	AVU32_gp164	Vibrio phage ValKK3	GCA_001501635.1
AGN30146.1	001571	Cluster1079_1clades	87	VPFG_00144	Vibrio phage nt-1	GCA_000910195.2
ALP47151.1	001571	Cluster1079_1clades	132	phiGrn1_0210	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47537.1	001571	Cluster1079_1clades	132	phiST2_0343	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54617.1	001571	Cluster1079_1clades	132	vBValMR10Z_76	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37326.1	001571	Cluster1079_1clades	132	pp2_093	Vibriophage phi-pp2	GCA_002630725.1
ARB13764.1	001572	Cluster1080_1clades	131	Ccr10_gp234	Caulobacter phage Ccr10	GCA_002619445.1
ARB14109.1	001572	Cluster1080_1clades	131	Ccr2_gp233	Caulobacter phage Ccr2	GCA_002619465.1
ARB14803.1	001572	Cluster1080_1clades	131	Ccr29_gp247	Caulobacter phage Ccr29	GCA_002619485.1
ARB15143.1	001572	Cluster1080_1clades	131	Ccr32_gp225	Caulobacter phage Ccr32	GCA_002619505.1
ARB15477.1	001572	Cluster1080_1clades	131	Ccr34_gp235	Caulobacter phage Ccr34	GCA_002619525.1
ARB14451.1	001572	Cluster1080_1clades	131	Ccr5_gp231	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68431.1	001572	Cluster1080_1clades	132	CcrBL10_gp227	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87759.1	001572	Cluster1080_1clades	131	CcrKarma_gp242	Caulobacter virus Karma	GCA_000901575.1
AFU87406.1	001572	Cluster1080_1clades	131	CcrMagneto_gp236	Caulobacter virus Magneto	GCA_000903095.1
AFU86717.1	001572	Cluster1080_1clades	132	CcrRogue_gp235	Caulobacter virus Rogue	GCA_000900555.1
AFU88554.1	001572	Cluster1080_1clades	131	CcrSwift_gp236	Caulobacter virus Swift	GCA_000899655.1
AFU87062.1	001572	Cluster1080_1clades	131	CbK_gp230	Caulobacter virus phiCbK	GCA_000900535.1
ARB13657.1	001573	Cluster1081_1clades	128	Ccr10_gp128c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14002.1	001573	Cluster1081_1clades	128	Ccr2_gp127c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14690.1	001573	Cluster1081_1clades	128	Ccr29_gp134	Caulobacter phage Ccr29	GCA_002619485.1
ARB15044.1	001573	Cluster1081_1clades	128	Ccr32_gp126	Caulobacter phage Ccr32	GCA_002619505.1
ARB15377.1	001573	Cluster1081_1clades	128	Ccr34_gp135	Caulobacter phage Ccr34	GCA_002619525.1
ARB14345.1	001573	Cluster1081_1clades	130	Ccr5_gp126c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68325.1	001573	Cluster1081_1clades	131	CcrBL10_gp121c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87649.1	001573	Cluster1081_1clades	130	CcrKarma_gp132	Caulobacter virus Karma	GCA_000901575.1
AFU87298.1	001573	Cluster1081_1clades	130	CcrMagneto_gp128	Caulobacter virus Magneto	GCA_000903095.1
AFU86610.1	001573	Cluster1081_1clades	131	CcrRogue_gp128	Caulobacter virus Rogue	GCA_000900555.1
AFU88445.1	001573	Cluster1081_1clades	130	CcrSwift_gp127	Caulobacter virus Swift	GCA_000899655.1
AFU86962.1	001573	Cluster1081_1clades	128	CbK_gp130	Caulobacter virus phiCbK	GCA_000900535.1
ARB13804.1	001574	Cluster1082_1clades	126	Ccr10_gp274	Caulobacter phage Ccr10	GCA_002619445.1
ARB14149.1	001574	Cluster1082_1clades	126	Ccr2_gp273	Caulobacter phage Ccr2	GCA_002619465.1
ARB14843.1	001574	Cluster1082_1clades	126	Ccr29_gp287	Caulobacter phage Ccr29	GCA_002619485.1
ARB15183.1	001574	Cluster1082_1clades	126	Ccr32_gp265	Caulobacter phage Ccr32	GCA_002619505.1
ARB15517.1	001574	Cluster1082_1clades	126	Ccr34_gp275	Caulobacter phage Ccr34	GCA_002619525.1
ARB14492.1	001574	Cluster1082_1clades	122	Ccr5_gp272	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68470.1	001574	Cluster1082_1clades	131	CcrBL10_gp266	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87802.1	001574	Cluster1082_1clades	92	CcrKarma_gp285	Caulobacter virus Karma	GCA_000901575.1
AFU87449.1	001574	Cluster1082_1clades	122	CcrMagneto_gp279	Caulobacter virus Magneto	GCA_000903095.1
AFU86755.1	001574	Cluster1082_1clades	131	CcrRogue_gp273	Caulobacter virus Rogue	GCA_000900555.1
AFU88594.1	001574	Cluster1082_1clades	122	CcrSwift_gp276	Caulobacter virus Swift	GCA_000899655.1
AFU87102.1	001574	Cluster1082_1clades	126	CbK_gp270	Caulobacter virus phiCbK	GCA_000900535.1
APU01595.1	001575	Cluster1083_1clades	127	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29044.1	001575	Cluster1083_1clades	127	AP1_0337	Aeromonas phage AP1	GCA_014183365.1
ATI17316.1	001575	Cluster1083_1clades	127	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00278.1	001575	Cluster1083_1clades	127	HWB28_gp274	Aeromonas phage AS-zj	GCA_002627665.1
AUE22665.1	001575	Cluster1083_1clades	131	Ah1_00124	Aeromonas phage Ah1	GCA_002957415.1
QAX98391.1	001575	Cluster1083_1clades	117	ASfcp2_46	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97759.1	001575	Cluster1083_1clades	127	ASswx1_114	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39464.1	001575	Cluster1083_1clades	127	CC2_423	Aeromonas phage CC2	GCA_000903495.1
ADQ52846.1	001575	Cluster1083_1clades	117	PX29p127	Aeromonas phage PX29	GCA_000920195.1
ADM80105.1	001575	Cluster1083_1clades	120	phiAS5_ORF0262	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53219.1	001575	Cluster1083_1clades	128	65p211	Aeromonas virus 65	GCA_000893255.1
AAQ17793.1	001575	Cluster1083_1clades	117	Aeh1ORF128c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64120.1	001576	Cluster1084_1clades	130	KVP40.0049	Vibrio phage KVP40	GCA_000843785.1
QIW90442.1	001576	Cluster1084_1clades	130	GCAPEGMB_00095	Vibrio phage V07	GCA_012361095.1
QIW90987.1	001576	Cluster1084_1clades	130	COHAPHLL_00124	Vibrio phage V09	GCA_012361135.1
QHJ74231.1	001576	Cluster1084_1clades	130	VH12019_00312	Vibrio phage VH1_2019	GCA_009931825.1
AGB07055.1	001576	Cluster1084_1clades	130	CF80_gp268	Vibrio phage VH7D	GCA_000914495.1
QBX06041.1	001576	Cluster1084_1clades	130	ValB1HC_087	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61055.1	001576	Cluster1084_1clades	130	AVU32_gp214	Vibrio phage ValKK3	GCA_001501635.1
AGN30098.1	001576	Cluster1084_1clades	128	VPFG_00096	Vibrio phage nt-1	GCA_000910195.2
ALP47153.1	001576	Cluster1084_1clades	130	phiGrn1_0162	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47539.1	001576	Cluster1084_1clades	130	phiST2_0293	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54666.1	001576	Cluster1084_1clades	130	vBValMR10Z_125	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37281.1	001576	Cluster1084_1clades	110	pp2_047	Vibriophage phi-pp2	GCA_002630725.1
AAQ64176.1	001577	Cluster1085_1clades	130	KVP40.0105	Vibrio phage KVP40	GCA_000843785.1
QIW90499.1	001577	Cluster1085_1clades	130	GCAPEGMB_00152	Vibrio phage V07	GCA_012361095.1
QIW90930.1	001577	Cluster1085_1clades	130	COHAPHLL_00067	Vibrio phage V09	GCA_012361135.1
QHJ74287.1	001577	Cluster1085_1clades	130	VH12019_00368	Vibrio phage VH1_2019	GCA_009931825.1
AGB07110.1	001577	Cluster1085_1clades	130	CF80_gp323	Vibrio phage VH7D	GCA_000914495.1
QBX05984.1	001577	Cluster1085_1clades	130	ValB1HC_030	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60997.1	001577	Cluster1085_1clades	130	AVU32_gp156	Vibrio phage ValKK3	GCA_001501635.1
AGN30154.1	001577	Cluster1085_1clades	130	VPFG_00152	Vibrio phage nt-1	GCA_000910195.2
ALP47154.1	001577	Cluster1085_1clades	130	phiGrn1_0218	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47538.1	001577	Cluster1085_1clades	130	phiST2_0351	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54609.1	001577	Cluster1085_1clades	130	vBValMR10Z_68	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37334.1	001577	Cluster1085_1clades	130	pp2_101	Vibriophage phi-pp2	GCA_002630725.1
APU01455.1	001578	SIG+AAA_13	54	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29097.1	001578	SIG+AAA_13	73	AP1_0390	Aeromonas phage AP1	GCA_014183365.1
ATI17442.1	001578	SIG+AAA_13	120	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00153.1	001578	SIG+AAA_13	120	HWB28_gp399	Aeromonas phage AS-zj	GCA_002627665.1
AUE22776.1	001578	SIG+AAA_13	128	Ah1_00258	Aeromonas phage Ah1	GCA_002957415.1
QAX97882.1	001578	SIG+AAA_13	120	ASswx1_239	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01266.1	001578	SIG+AAA_13	122	ASwh1_203	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39414.1	001578	SIG+AAA_13	120	CC2_295	Aeromonas phage CC2	GCA_000903495.1
ADQ52954.1	001578	SIG+AAA_13	130	PX29p235	Aeromonas phage PX29	GCA_000920195.1
ADM79879.1	001578	SIG+AAA_13	129	phiAS5_ORF0036	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53075.1	001578	SIG+AAA_13	121	65p065	Aeromonas virus 65	GCA_000893255.1
AAQ17901.1	001578	SIG+AAA_13	129	Aeh1ORF239c	Aeromonas virus Aeh1	GCA_000843245.1
ARB13735.1	001579	Cluster1087_1clades	127	Ccr10_gp205c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14080.1	001579	Cluster1087_1clades	127	Ccr2_gp204c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14769.1	001579	Cluster1087_1clades	127	Ccr29_gp213	Caulobacter phage Ccr29	GCA_002619485.1
ARB15113.1	001579	Cluster1087_1clades	127	Ccr32_gp195	Caulobacter phage Ccr32	GCA_002619505.1
ARB15447.1	001579	Cluster1087_1clades	127	Ccr34_gp205	Caulobacter phage Ccr34	GCA_002619525.1
ARB14422.1	001579	Cluster1087_1clades	127	Ccr5_gp202c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68402.1	001579	Cluster1087_1clades	130	CcrBL10_gp198c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87728.1	001579	Cluster1087_1clades	100	CcrKarma_gp211	Caulobacter virus Karma	GCA_000901575.1
AFU87377.1	001579	Cluster1087_1clades	127	CcrMagneto_gp207	Caulobacter virus Magneto	GCA_000903095.1
AFU86688.1	001579	Cluster1087_1clades	130	CcrRogue_gp206	Caulobacter virus Rogue	GCA_000900555.1
AFU88524.1	001579	Cluster1087_1clades	127	CcrSwift_gp206	Caulobacter virus Swift	GCA_000899655.1
AFU87032.1	001579	Cluster1087_1clades	127	CbK_gp200	Caulobacter virus phiCbK	GCA_000900535.1
ARB13819.1	001580	Cluster1088_1clades	130	Ccr10_gp289	Caulobacter phage Ccr10	GCA_002619445.1
ARB14164.1	001580	Cluster1088_1clades	130	Ccr2_gp288	Caulobacter phage Ccr2	GCA_002619465.1
ARB14858.1	001580	Cluster1088_1clades	130	Ccr29_gp302	Caulobacter phage Ccr29	GCA_002619485.1
ARB15197.1	001580	Cluster1088_1clades	130	Ccr32_gp279	Caulobacter phage Ccr32	GCA_002619505.1
ARB15531.1	001580	Cluster1088_1clades	130	Ccr34_gp289	Caulobacter phage Ccr34	GCA_002619525.1
ARB14506.1	001580	Cluster1088_1clades	130	Ccr5_gp286	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68485.1	001580	Cluster1088_1clades	124	CcrBL10_gp281	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87816.1	001580	Cluster1088_1clades	130	CcrKarma_gp299	Caulobacter virus Karma	GCA_000901575.1
AFU87463.1	001580	Cluster1088_1clades	130	CcrMagneto_gp293	Caulobacter virus Magneto	GCA_000903095.1
AFU86773.1	001580	Cluster1088_1clades	130	CcrRogue_gp291	Caulobacter virus Rogue	GCA_000900555.1
AFU88608.1	001580	Cluster1088_1clades	130	CcrSwift_gp290	Caulobacter virus Swift	GCA_000899655.1
AFU87116.1	001580	Cluster1088_1clades	130	CbK_gp284	Caulobacter virus phiCbK	GCA_000900535.1
ABY62836.1	001581	Cluster1089_1clades	110	201phi2-1p001	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44759.1	001581	Cluster1089_1clades	129	KTN4_001	Pseudomonas phage KTN4	GCA_002607225.1
QBX32148.1	001581	Cluster1089_1clades	49	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32149.1	001581	Cluster1089_1clades	68	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ86179.1	001581	Cluster1089_1clades	123	KKIINIFJ_00269	Pseudomonas phage PN05	GCA_009931935.1
ARV77099.1	001581	Cluster1089_1clades	130	PHABIO_471	Pseudomonas phage Phabio	GCA_002624965.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEH03427.1	001581	Cluster1089_1clades	117	001	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02531.1	001581	Cluster1089_1clades	123	PSA21_1	Pseudomonas phage Psa21	GCA_004340405.1
ATN94584.1	001581	Cluster1089_1clades	129	SL2_007	Pseudomonas phage SL2	GCA_002956015.1
QJB22644.1	001581	Cluster1089_1clades	129	fnug_1	Pseudomonas phage fnug	GCA_012837215.1
QEM41730.1	001581	Cluster1089_1clades	117	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82902.1	001581	Cluster1089_1clades	129	PHIKZ001	Pseudomonas virus phiKZ	GCA_000842965.1
ARB13789.1	001582	DUF1937	129	Ccr10_gp259	Caulobacter phage Ccr10	GCA_002619445.1
ARB14134.1	001582	DUF1937	129	Ccr2_gp258	Caulobacter phage Ccr2	GCA_002619465.1
ARB14828.1	001582	DUF1937	129	Ccr29_gp272	Caulobacter phage Ccr29	GCA_002619485.1
ARB15168.1	001582	DUF1937	129	Ccr32_gp250	Caulobacter phage Ccr32	GCA_002619505.1
ARB15502.1	001582	DUF1937	129	Ccr34_gp260	Caulobacter phage Ccr34	GCA_002619525.1
ARB14476.1	001582	DUF1937	129	Ccr5_gp256	Caulobacter phage Ccr5	GCA_002619545.1
AXQ69369.1	001582	DUF1937	130	CcrBL9_gp345	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69929.1	001582	DUF1937	129	CcrSC_gp347	Caulobacter phage CcrSC	GCA_003443315.1
AFU87786.1	001582	DUF1937	129	CcrKarma_gp269	Caulobacter virus Karma	GCA_000901575.1
AFU87433.1	001582	DUF1937	129	CcrMagneto_gp263	Caulobacter virus Magneto	GCA_000903095.1
AFU88579.1	001582	DUF1937	129	CcrSwift_gp261	Caulobacter virus Swift	GCA_000899655.1
AFU87087.1	001582	DUF1937	129	CbK_gp255	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64203.1	001583	Cluster1091_1clades	129	KVP40.0132	Vibrio phage KVP40	GCA_000843785.1
QIW90518.1	001583	Cluster1091_1clades	84	GCAPEGMB_00171	Vibrio phage V07	GCA_012361095.1
QIW90904.1	001583	Cluster1091_1clades	84	COHAPHLL_00041	Vibrio phage V09	GCA_012361135.1
QHJ74314.1	001583	Cluster1091_1clades	84	VH12019_00395	Vibrio phage VH1_2019	GCA_009931825.1
AGB06808.1	001583	Cluster1091_1clades	86	CF80_gp021	Vibrio phage VH7D	GCA_000914495.1
QBX05957.1	001583	Cluster1091_1clades	86	ValB1HC_003	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60969.1	001583	Cluster1091_1clades	82	AVU32_gp128	Vibrio phage ValKK3	GCA_001501635.1
AIE13794.1	001583	Cluster1091_1clades	84	VPFG_00180	Vibrio phage nt-1	GCA_000910195.2
ALP47254.1	001583	Cluster1091_1clades	84	phiGrn1_0244	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47634.1	001583	Cluster1091_1clades	84	phiST2_0382	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54582.1	001583	Cluster1091_1clades	84	vBValMR10Z_41	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37363.1	001583	Cluster1091_1clades	84	pp2_130	Vibriophage phi-pp2	GCA_002630725.1
AIT14166.1	001584	Cluster1092_1clades	99	PBI_121Q_276	Escherichia phage 121Q	GCA_000926855.1
QAY00769.1	001584	Cluster1092_1clades	99	Ecwhy1_495	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34948.1	001584	Cluster1092_1clades	99	ACQ29_gp268	Escherichia phage PBECO4	GCA_001041035.1
BBM61841.1	001584	Cluster1092_1clades	99	EO157G_2520	Escherichia phage SP27	GCA_008033345.1
AXC37050.1	001584	Cluster1092_1clades	65	-	Escherichia phage UB	GCA_003341455.1
QBO61539.1	001584	Cluster1092_1clades	99	G17_00043	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62145.1	001584	Cluster1092_1clades	99	G17_00656	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14153.1	001584	Cluster1092_1clades	99	vBEcoMphAPEC6_gp530c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80153.1	001584	Cluster1092_1clades	99	PSLUR01_00176	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18710.1	001584	Cluster1092_1clades	129	7t3_0189	Salmonella phage 7t3	GCA_006083215.1
AZU97982.1	001584	Cluster1092_1clades	129	CPT_Munch_038	Salmonella phage Munch	GCA_004015485.1
QIG62996.1	001584	Cluster1092_1clades	129	SEPL_383	Salmonella phage SE_PL	GCA_011067555.1
AAQ64313.1	001585	Cluster1093_1clades	128	KVP40.0244	Vibrio phage KVP40	GCA_000843785.1
QIW90628.1	001585	Cluster1093_1clades	109	GCAPEGMB_00281	Vibrio phage V07	GCA_012361095.1
QIW91171.1	001585	Cluster1093_1clades	109	COHAPHLL_00335	Vibrio phage V09	GCA_012361135.1
QHJ74423.1	001585	Cluster1093_1clades	109	VH12019_00096	Vibrio phage VH1_2019	GCA_009931825.1
AGB06929.1	001585	Cluster1093_1clades	128	CF80_gp142	Vibrio phage VH7D	GCA_000914495.1
QBX06217.1	001585	Cluster1093_1clades	109	ValB1HC_264	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60843.1	001585	Cluster1093_1clades	109	AVU32_gp002	Vibrio phage ValKK3	GCA_001501635.1
AGN30299.2	001585	Cluster1093_1clades	109	VPFG_00300	Vibrio phage nt-1	GCA_000910195.2
ALP47183.1	001585	Cluster1093_1clades	109	phiGrn1_0365	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47583.1	001585	Cluster1093_1clades	104	phiST2_0120	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54842.1	001585	Cluster1093_1clades	109	vBValMR10Z_302	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37472.1	001585	Cluster1093_1clades	109	pp2_239	Vibriophage phi-pp2	GCA_002630725.1
ARB13816.1	001586	Cluster1094_1clades	127	Ccr10_gp286	Caulobacter phage Ccr10	GCA_002619445.1
ARB14161.1	001586	Cluster1094_1clades	127	Ccr2_gp285	Caulobacter phage Ccr2	GCA_002619465.1
ARB14855.1	001586	Cluster1094_1clades	127	Ccr29_gp299	Caulobacter phage Ccr29	GCA_002619485.1
ARB15194.1	001586	Cluster1094_1clades	127	Ccr32_gp276	Caulobacter phage Ccr32	GCA_002619505.1
ARB15528.1	001586	Cluster1094_1clades	127	Ccr34_gp286	Caulobacter phage Ccr34	GCA_002619525.1
ARB14503.1	001586	Cluster1094_1clades	127	Ccr5_gp283	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68477.1	001586	Cluster1094_1clades	128	CcrBL10_gp273	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87813.1	001586	Cluster1094_1clades	127	CcrKarma_gp296	Caulobacter virus Karma	GCA_000901575.1
AFU87460.1	001586	Cluster1094_1clades	127	CcrMagneto_gp290	Caulobacter virus Magneto	GCA_000903095.1
AFU86762.1	001586	Cluster1094_1clades	128	CcrRogue_gp280	Caulobacter virus Rogue	GCA_000900555.1
AFU88605.1	001586	Cluster1094_1clades	127	CcrSwift_gp287	Caulobacter virus Swift	GCA_000899655.1
AFU87113.1	001586	Cluster1094_1clades	127	CbK_gp281	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64157.1	001587	Cluster1095_1clades	127	KVP40.0086	Vibrio phage KVP40	GCA_000843785.1
QIW90481.1	001587	Cluster1095_1clades	127	GCAPEGMB_00134	Vibrio phage V07	GCA_012361095.1
QIW90948.1	001587	Cluster1095_1clades	127	COHAPHLL_00085	Vibrio phage V09	GCA_012361135.1
QHJ74269.1	001587	Cluster1095_1clades	127	VH12019_00350	Vibrio phage VH1_2019	GCA_009931825.1
AGB07094.1	001587	Cluster1095_1clades	117	CF80_gp307	Vibrio phage VH7D	GCA_000914495.1
QBX06001.1	001587	Cluster1095_1clades	127	ValB1HC_047	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61015.1	001587	Cluster1095_1clades	117	AVU32_gp174	Vibrio phage ValKK3	GCA_001501635.1
AGN30136.1	001587	Cluster1095_1clades	127	VPFG_00134	Vibrio phage nt-1	GCA_000910195.2
ALP47167.1	001587	Cluster1095_1clades	117	phiGrn1_0201	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47553.1	001587	Cluster1095_1clades	117	phiST2_0334	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54625.1	001587	Cluster1095_1clades	127	vBValMR10Z_84	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37318.1	001587	Cluster1095_1clades	127	pp2_085	Vibriophage phi-pp2	GCA_002630725.1
ARB13843.1	001588	Cluster1096_1clades	118	Ccr10_gp313	Caulobacter phage Ccr10	GCA_002619445.1
ARB14188.1	001588	Cluster1096_1clades	118	Ccr2_gp312	Caulobacter phage Ccr2	GCA_002619465.1
ARB14882.1	001588	Cluster1096_1clades	118	Ccr29_gp326	Caulobacter phage Ccr29	GCA_002619485.1
ARB15220.1	001588	Cluster1096_1clades	118	Ccr32_gp302	Caulobacter phage Ccr32	GCA_002619505.1
ARB15554.1	001588	Cluster1096_1clades	118	Ccr34_gp312	Caulobacter phage Ccr34	GCA_002619525.1
ARB14529.1	001588	Cluster1096_1clades	118	Ccr5_gp309	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68510.1	001588	Cluster1096_1clades	126	CcrBL10_gp306	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87840.1	001588	Cluster1096_1clades	118	CcrKarma_gp323	Caulobacter virus Karma	GCA_000901575.1
AFU87487.1	001588	Cluster1096_1clades	118	CcrMagneto_gp317	Caulobacter virus Magneto	GCA_000903095.1
AFU86799.1	001588	Cluster1096_1clades	127	CcrRogue_gp317	Caulobacter virus Rogue	GCA_000900555.1
AFU88632.1	001588	Cluster1096_1clades	118	CcrSwift_gp314	Caulobacter virus Swift	GCA_000899655.1
AFU87139.1	001588	Cluster1096_1clades	118	CbK_gp307	Caulobacter virus phiCbK	GCA_000900535.1
ARB13731.1	001589	Cluster1097_1clades	127	Ccr10_gp201c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14076.1	001589	Cluster1097_1clades	127	Ccr2_gp200c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14765.1	001589	Cluster1097_1clades	127	Ccr29_gp209	Caulobacter phage Ccr29	GCA_002619485.1
ARB15109.1	001589	Cluster1097_1clades	127	Ccr32_gp191	Caulobacter phage Ccr32	GCA_002619505.1
ARB15443.1	001589	Cluster1097_1clades	127	Ccr34_gp201	Caulobacter phage Ccr34	GCA_002619525.1
ARB14418.1	001589	Cluster1097_1clades	127	Ccr5_gp198c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68398.1	001589	Cluster1097_1clades	126	CcrBL10_gp194c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87724.1	001589	Cluster1097_1clades	127	CcrKarma_gp207	Caulobacter virus Karma	GCA_000901575.1
AFU87373.1	001589	Cluster1097_1clades	127	CcrMagneto_gp203	Caulobacter virus Magneto	GCA_000903095.1
AFU86684.1	001589	Cluster1097_1clades	121	CcrRogue_gp202	Caulobacter virus Rogue	GCA_000900555.1
AFU88520.1	001589	Cluster1097_1clades	127	CcrSwift_gp202	Caulobacter virus Swift	GCA_000899655.1
AFU87028.1	001589	Cluster1097_1clades	127	CbK_gp196	Caulobacter virus phiCbK	GCA_000900535.1
ARB13779.1	001590	Cluster1098_1clades	127	Ccr10_gp249	Caulobacter phage Ccr10	GCA_002619445.1
ARB14124.1	001590	Cluster1098_1clades	127	Ccr2_gp248	Caulobacter phage Ccr2	GCA_002619465.1
ARB14818.1	001590	Cluster1098_1clades	127	Ccr29_gp262	Caulobacter phage Ccr29	GCA_002619485.1
ARB15158.1	001590	Cluster1098_1clades	127	Ccr32_gp240	Caulobacter phage Ccr32	GCA_002619505.1
ARB15492.1	001590	Cluster1098_1clades	127	Ccr34_gp250	Caulobacter phage Ccr34	GCA_002619525.1
ARB14466.1	001590	Cluster1098_1clades	127	Ccr5_gp246	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68445.1	001590	Cluster1098_1clades	123	CcrBL10_gp241	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87775.1	001590	Cluster1098_1clades	127	CcrKarma_gp258	Caulobacter virus Karma	GCA_000901575.1
AFU87422.1	001590	Cluster1098_1clades	127	CcrMagneto_gp252	Caulobacter virus Magneto	GCA_000903095.1
AFU86731.1	001590	Cluster1098_1clades	123	CcrRogue_gp249	Caulobacter virus Rogue	GCA_000900555.1
AFU88569.1	001590	Cluster1098_1clades	127	CcrSwift_gp251	Caulobacter virus Swift	GCA_000899655.1
AFU87077.1	001590	Cluster1098_1clades	127	CbK_gp245	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64314.1	001591	Cluster1099_1clades	115	KVP40.0245	Vibrio phage KVP40	GCA_000843785.1
QIW90629.1	001591	Cluster1099_1clades	115	GCAPEGMB_00282	Vibrio phage V07	GCA_012361095.1
QIW91170.1	001591	Cluster1099_1clades	115	COHAPHLL_00334	Vibrio phage V09	GCA_012361135.1
QHJ74424.1	001591	Cluster1099_1clades	115	VH12019_00097	Vibrio phage VH1_2019	GCA_009931825.1
AGB06930.1	001591	Cluster1099_1clades	115	CF80_gp143	Vibrio phage VH7D	GCA_000914495.1
QBX06216.1	001591	Cluster1099_1clades	115	ValB1HC_263	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60842.1	001591	Cluster1099_1clades	115	AVU32_gp001	Vibrio phage ValKK3	GCA_001501635.1
AGN30300.1	001591	Cluster1099_1clades	125	VPFG_00301	Vibrio phage nt-1	GCA_000910195.2
ALP47175.1	001591	Cluster1099_1clades	115	phiGrn1_0366	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47560.1	001591	Cluster1099_1clades	115	phiST2_0121	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54841.1	001591	Cluster1099_1clades	115	vBValMR10Z_301	Vibrio phage vB_ValM_R10Z	GCA_014337545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN37473.1	001591	Cluster1099_1clades	115	pp2_240	Vibriophage phi-pp2	GCA_002630725.1
AAQ64373.1	001592	Cluster1100_1clades	124	KVP40.0303	Vibrio phage KVP40	GCA_000843785.1
QIW90689.1	001592	Cluster1100_1clades	124	GCAPEGMB_00342	Vibrio phage V07	GCA_012361095.1
QIW91109.1	001592	Cluster1100_1clades	124	COHAPHLL_00273	Vibrio phage V09	GCA_012361135.1
QHJ74485.1	001592	Cluster1100_1clades	124	VH12019_00158	Vibrio phage VH1_2019	GCA_009931825.1
QBX06165.1	001592	Cluster1100_1clades	121	ValB1HC_212	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61182.1	001592	Cluster1100_1clades	121	AVU32_gp341	Vibrio phage ValKK3	GCA_001501635.1
AGN30351.1	001592	Cluster1100_1clades	123	VPFG_00354	Vibrio phage nt-1	GCA_000910195.2
ALP47250.1	001592	Cluster1100_1clades	85	phiGrn1_0040	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47548.1	001592	Cluster1100_1clades	122	phiST2_0172	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54791.1	001592	Cluster1100_1clades	121	vBValMR10Z_251	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07210.1	001592	Cluster1100_1clades	122	VmeM32_00224	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFN37535.1	001592	Cluster1100_1clades	124	pp2_302	Vibriophage phi-pp2	GCA_002630725.1
AAQ64113.1	001593	Cluster1101_1clades	122	KVP40.0042	Vibrio phage KVP40	GCA_000843785.1
QIW90436.1	001593	Cluster1101_1clades	122	GCAPEGMB_00089	Vibrio phage V07	GCA_012361095.1
QIW90993.1	001593	Cluster1101_1clades	122	COHAPHLL_00130	Vibrio phage V09	GCA_012361135.1
QHJ74225.1	001593	Cluster1101_1clades	122	VH12019_00306	Vibrio phage VH1_2019	GCA_009931825.1
AGB07049.1	001593	Cluster1101_1clades	124	CF80_gp262	Vibrio phage VH7D	GCA_000914495.1
QBX06047.1	001593	Cluster1101_1clades	122	ValB1HC_093	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61061.1	001593	Cluster1101_1clades	122	AVU32_gp220	Vibrio phage ValKK3	GCA_001501635.1
AGN30092.1	001593	Cluster1101_1clades	122	VPFG_00090	Vibrio phage nt-1	GCA_000910195.2
ALP47162.1	001593	Cluster1101_1clades	122	phiGrn1_0156	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47554.1	001593	Cluster1101_1clades	117	phiST2_0287	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54673.1	001593	Cluster1101_1clades	122	vBValMR10Z_132	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37275.1	001593	Cluster1101_1clades	122	pp2_041	Vibriophage phi-pp2	GCA_002630725.1
AAQ64158.1	001594	Cluster1103_1clades	118	KVP40.0087	Vibrio phage KVP40	GCA_000843785.1
QIW90482.1	001594	Cluster1103_1clades	109	GCAPEGMB_00135	Vibrio phage V07	GCA_012361095.1
QIW90947.1	001594	Cluster1103_1clades	109	COHAPHLL_00084	Vibrio phage V09	GCA_012361135.1
QHJ74270.1	001594	Cluster1103_1clades	109	VH12019_00351	Vibrio phage VH1_2019	GCA_009931825.1
AGB07095.1	001594	Cluster1103_1clades	97	CF80_gp308	Vibrio phage VH7D	GCA_000914495.1
QBX06000.1	001594	Cluster1103_1clades	109	ValB1HC_046	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61014.1	001594	Cluster1103_1clades	109	AVU32_gp173	Vibrio phage ValKK3	GCA_001501635.1
AGN30137.1	001594	Cluster1103_1clades	122	VPFG_00135	Vibrio phage nt-1	GCA_000910195.2
ALP47182.1	001594	Cluster1103_1clades	109	phiGrn1_0202	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47691.1	001594	Cluster1103_1clades	60	phiST2_0335	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54624.1	001594	Cluster1103_1clades	109	vBValMR10Z_83	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37319.1	001594	Cluster1103_1clades	109	pp2_086	Vibriophage phi-pp2	GCA_002630725.1
QAY00542.1	001595	Cluster1104_1clades	117	Ecwhy1_263	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34733.1	001595	Cluster1104_1clades	117	ACQ29_gp053	Escherichia phage PBECO4	GCA_001041035.1
BBM62081.1	001595	Cluster1104_1clades	117	EO157G_4920	Escherichia phage SP27	GCA_008033345.1
AXC36849.1	001595	Cluster1104_1clades	117	-	Escherichia phage UB	GCA_003341455.1
QBO61892.1	001595	Cluster1104_1clades	117	G17_00403	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13929.1	001595	Cluster1104_1clades	117	vBEcoMphAPEC6_gp304c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80395.1	001595	Cluster1104_1clades	117	PSLUR01_00418	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXH72437.1	001595	Cluster1104_1clades	122	-	Myoviridae sp.	GCA_003657725.1
QIG65960.1	001595	Cluster1104_1clades	117	phiOC_p318	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QCW18878.1	001595	Cluster1104_1clades	113	7t3_0357	Salmonella phage 7t3	GCA_006083215.1
AZU98136.1	001595	Cluster1104_1clades	113	CPT_Munch_192	Salmonella phage Munch	GCA_004015485.1
QIG62846.1	001595	Cluster1104_1clades	113	SEPL_233	Salmonella phage SE_PL	GCA_011067555.1
ARB13838.1	001596	Cluster1105_1clades	120	Ccr10_gp308	Caulobacter phage Ccr10	GCA_002619445.1
ARB14183.1	001596	Cluster1105_1clades	120	Ccr2_gp307	Caulobacter phage Ccr2	GCA_002619465.1
ARB14877.1	001596	Cluster1105_1clades	120	Ccr29_gp321	Caulobacter phage Ccr29	GCA_002619485.1
ARB15215.1	001596	Cluster1105_1clades	120	Ccr32_gp297	Caulobacter phage Ccr32	GCA_002619505.1
ARB15549.1	001596	Cluster1105_1clades	120	Ccr34_gp307	Caulobacter phage Ccr34	GCA_002619525.1
ARB14524.1	001596	Cluster1105_1clades	120	Ccr5_gp304	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68504.1	001596	Cluster1105_1clades	121	CcrBL10_gp300	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87835.1	001596	Cluster1105_1clades	120	CcrKarma_gp318	Caulobacter virus Karma	GCA_000901575.1
AFU87482.1	001596	Cluster1105_1clades	120	CcrMagneto_gp312	Caulobacter virus Magneto	GCA_000903095.1
AFU86792.1	001596	Cluster1105_1clades	121	CcrRogue_gp310	Caulobacter virus Rogue	GCA_000900555.1
AFU88627.1	001596	Cluster1105_1clades	120	CcrSwift_gp309	Caulobacter virus Swift	GCA_000899655.1
AFU87134.1	001596	Cluster1105_1clades	120	CbK_gp302	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64276.1	001597	Cluster1106_1clades	117	KVP40.0207	Vibrio phage KVP40	GCA_000843785.1
QIW90592.1	001597	Cluster1106_1clades	117	GCAPEGMB_00245	Vibrio phage V07	GCA_012361095.1
QIW91207.1	001597	Cluster1106_1clades	117	COHAPHLL_00371	Vibrio phage V09	GCA_012361135.1
QHJ74388.1	001597	Cluster1106_1clades	118	VH12019_00061	Vibrio phage VH1_2019	GCA_009931825.1
AGB06893.1	001597	Cluster1106_1clades	89	CF80_gp106	Vibrio phage VH7D	GCA_000914495.1
QBX06253.1	001597	Cluster1106_1clades	118	ValB1HC_300	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60879.1	001597	Cluster1106_1clades	117	AVU32_gp038	Vibrio phage ValKK3	GCA_001501635.1
AGN30266.2	001597	Cluster1106_1clades	121	VPFG_00267	Vibrio phage nt-1	GCA_000910195.2
ALP47239.1	001597	Cluster1106_1clades	89	phiGrn1_0331	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47614.1	001597	Cluster1106_1clades	93	phiST2_0086	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54880.1	001597	Cluster1106_1clades	118	vBValMR10Z_340	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37436.1	001597	Cluster1106_1clades	117	pp2_203	Vibriophage phi-pp2	GCA_002630725.1
ARB13584.1	001598	Cluster1107_1clades	121	Ccr10_gp056	Caulobacter phage Ccr10	GCA_002619445.1
ARB13930.1	001598	Cluster1107_1clades	116	Ccr2_gp055	Caulobacter phage Ccr2	GCA_002619465.1
ARB14619.1	001598	Cluster1107_1clades	116	Ccr29_gp062	Caulobacter phage Ccr29	GCA_002619485.1
ARB14975.1	001598	Cluster1107_1clades	121	Ccr32_gp056	Caulobacter phage Ccr32	GCA_002619505.1
ARB15306.1	001598	Cluster1107_1clades	121	Ccr34_gp057	Caulobacter phage Ccr34	GCA_002619525.1
ARB14273.1	001598	Cluster1107_1clades	116	Ccr5_gp055	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68257.1	001598	Cluster1107_1clades	113	CcrBL10_gp053	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87574.1	001598	Cluster1107_1clades	115	CcrKarma_gp057	Caulobacter virus Karma	GCA_000901575.1
AFU87224.1	001598	Cluster1107_1clades	115	CcrMagneto_gp054	Caulobacter virus Magneto	GCA_000903095.1
AFU86539.1	001598	Cluster1107_1clades	113	CcrRogue_gp057	Caulobacter virus Rogue	GCA_000900555.1
AFU88372.1	001598	Cluster1107_1clades	115	CcrSwift_gp054	Caulobacter virus Swift	GCA_000899655.1
AFU86888.1	001598	Cluster1107_1clades	116	CbK_gp056	Caulobacter virus phiCbK	GCA_000900535.1
ARB13736.1	001599	Cluster1108_1clades	121	Ccr10_gp206c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14081.1	001599	Cluster1108_1clades	119	Ccr2_gp205c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14770.1	001599	Cluster1108_1clades	119	Ccr29_gp214	Caulobacter phage Ccr29	GCA_002619485.1
ARB15114.1	001599	Cluster1108_1clades	121	Ccr32_gp196	Caulobacter phage Ccr32	GCA_002619505.1
ARB15448.1	001599	Cluster1108_1clades	119	Ccr34_gp206	Caulobacter phage Ccr34	GCA_002619525.1
ARB14423.1	001599	Cluster1108_1clades	119	Ccr5_gp203c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68403.1	001599	Cluster1108_1clades	121	CcrBL10_gp199c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87729.1	001599	Cluster1108_1clades	119	CcrKarma_gp212	Caulobacter virus Karma	GCA_000901575.1
AFU87378.1	001599	Cluster1108_1clades	119	CcrMagneto_gp208	Caulobacter virus Magneto	GCA_000903095.1
AFU86689.1	001599	Cluster1108_1clades	119	CcrRogue_gp207	Caulobacter virus Rogue	GCA_000900555.1
AFU88525.1	001599	Cluster1108_1clades	119	CcrSwift_gp207	Caulobacter virus Swift	GCA_000899655.1
AFU87033.1	001599	Cluster1108_1clades	119	CbK_gp201	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64297.1	001600	Cluster1109_1clades	111	KVP40.0228	Vibrio phage KVP40	GCA_000843785.1
QIW90613.1	001600	Cluster1109_1clades	105	GCAPEGMB_00266	Vibrio phage V07	GCA_012361095.1
QIW91186.1	001600	Cluster1109_1clades	105	COHAPHLL_00350	Vibrio phage V09	GCA_012361135.1
QHJ74408.1	001600	Cluster1109_1clades	105	VH12019_00081	Vibrio phage VH1_2019	GCA_009931825.1
AGB06915.1	001600	Cluster1109_1clades	105	CF80_gp128	Vibrio phage VH7D	GCA_000914495.1
QBX06231.1	001600	Cluster1109_1clades	105	ValB1HC_278	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60857.1	001600	Cluster1109_1clades	120	AVU32_gp016	Vibrio phage ValKK3	GCA_001501635.1
AGN30288.1	001600	Cluster1109_1clades	97	VPFG_00289	Vibrio phage nt-1	GCA_000910195.2
ALP47193.1	001600	Cluster1109_1clades	105	phiGrn1_0351	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47581.1	001600	Cluster1109_1clades	105	phiST2_0106	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54856.1	001600	Cluster1109_1clades	105	vBValMR10Z_316	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37458.1	001600	Cluster1109_1clades	105	pp2_225	Vibriophage phi-pp2	GCA_002630725.1
AAQ64262.1	001601	Cluster1110_1clades	118	KVP40.0193	Vibrio phage KVP40	GCA_000843785.1
QIW90578.1	001601	Cluster1110_1clades	107	GCAPEGMB_00231	Vibrio phage V07	GCA_012361095.1
QIW91220.1	001601	Cluster1110_1clades	107	COHAPHLL_00384	Vibrio phage V09	GCA_012361135.1
QHJ74376.1	001601	Cluster1110_1clades	107	VH12019_00049	Vibrio phage VH1_2019	GCA_009931825.1
AGB06873.1	001601	Cluster1110_1clades	107	CF80_gp086	Vibrio phage VH7D	GCA_000914495.1
QBX06273.1	001601	Cluster1110_1clades	107	ValB1HC_320	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60899.1	001601	Cluster1110_1clades	107	AVU32_gp058	Vibrio phage ValKK3	GCA_001501635.1
AGN30251.2	001601	Cluster1110_1clades	107	VPFG_00252	Vibrio phage nt-1	GCA_000910195.2
ALP47188.1	001601	Cluster1110_1clades	107	phiGrn1_0312	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47576.1	001601	Cluster1110_1clades	107	phiST2_0068	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54900.1	001601	Cluster1110_1clades	107	vBValMR10Z_360	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37424.1	001601	Cluster1110_1clades	107	pp2_191	Vibriophage phi-pp2	GCA_002630725.1
ARB13783.1	001602	Cluster1111_1clades	118	Ccr10_gp253	Caulobacter phage Ccr10	GCA_002619445.1
ARB14128.1	001602	Cluster1111_1clades	118	Ccr2_gp252	Caulobacter phage Ccr2	GCA_002619465.1
ARB14822.1	001602	Cluster1111_1clades	118	Ccr29_gp266	Caulobacter phage Ccr29	GCA_002619485.1
ARB15162.1	001602	Cluster1111_1clades	118	Ccr32_gp244	Caulobacter phage Ccr32	GCA_002619505.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB15496.1	001602	Cluster1111_1clades	118	Ccr34_gp254	Caulobacter phage Ccr34	GCA_002619525.1
ARB14470.1	001602	Cluster1111_1clades	118	Ccr5_gp250	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68449.1	001602	Cluster1111_1clades	118	CcrBL10_gp245	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87779.1	001602	Cluster1111_1clades	118	CcrKarma_gp262	Caulobacter virus Karma	GCA_000901575.1
AFU87426.1	001602	Cluster1111_1clades	118	CcrMagneto_gp256	Caulobacter virus Magneto	GCA_000903095.1
AFU86736.1	001602	Cluster1111_1clades	118	CcrRogue_gp254	Caulobacter virus Rogue	GCA_000900555.1
AFU88573.1	001602	Cluster1111_1clades	118	CcrSwift_gp255	Caulobacter virus Swift	GCA_000899655.1
AFU87081.1	001602	Cluster1111_1clades	118	CbK_gp249	Caulobacter virus phiCbK	GCA_000900535.1
AHI60362.1	001603	Cluster1112_1clades	118	Ea357_209	Erwinia phage Ea35-70	GCA_000914635.1
QBP07319.1	001603	Cluster1112_1clades	118	REBECCA_214	Erwinia phage Rebecca	GCA_004521635.1
AUG86000.1	001603	Cluster1112_1clades	118	BOSOLAPHORUS_214	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52317.1	001603	Cluster1112_1clades	118	DM_217	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86319.1	001603	Cluster1112_1clades	118	DESERTFOX_212	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86642.1	001603	Cluster1112_1clades	118	MADMEL_214	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86965.1	001603	Cluster1112_1clades	118	MORTIMER_217	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51992.1	001603	Cluster1112_1clades	118	RAY_212	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51676.1	001603	Cluster1112_1clades	118	SIMMY50_217	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65026.1	001603	Cluster1112_1clades	118	SPECIALG_215	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24136.1	001603	Cluster1112_1clades	116	-	Proteus phage 10	GCA_014071245.1
QKE54536.1	001603	Cluster1112_1clades	115	ACSA002_2200	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64312.1	001604	Cluster1113_1clades	117	KVP40.0243	Vibrio phage KVP40	GCA_000843785.1
QIW90627.1	001604	Cluster1113_1clades	116	GCAPEGMB_00280	Vibrio phage V07	GCA_012361095.1
QIW91172.1	001604	Cluster1113_1clades	116	COHAPHLL_00336	Vibrio phage V09	GCA_012361135.1
QHJ74422.1	001604	Cluster1113_1clades	116	VH12019_00095	Vibrio phage VH1_2019	GCA_009931825.1
AGB06928.1	001604	Cluster1113_1clades	116	CF80_gp141	Vibrio phage VH7D	GCA_000914495.1
QBX06218.1	001604	Cluster1113_1clades	116	ValB1HC_265	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60844.1	001604	Cluster1113_1clades	116	AVU32_gp003	Vibrio phage ValKK3	GCA_001501635.1
AGN30298.1	001604	Cluster1113_1clades	116	VPFG_00299	Vibrio phage nt-1	GCA_000910195.2
ALP47171.1	001604	Cluster1113_1clades	116	phiGrn1_0364	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47557.1	001604	Cluster1113_1clades	116	phiST2_0119	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54843.1	001604	Cluster1113_1clades	116	vBValMR10Z_303	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37471.1	001604	Cluster1113_1clades	116	pp2_238	Vibriophage phi-pp2	GCA_002630725.1
AAQ64433.1	001605	Cluster1114_1clades	117	KVP40.0365	Vibrio phage KVP40	GCA_000843785.1
QIW90379.1	001605	Cluster1114_1clades	113	GCAPEGMB_00032	Vibrio phage V07	GCA_012361095.1
QIW91050.1	001605	Cluster1114_1clades	113	COHAPHLL_00187	Vibrio phage V09	GCA_012361135.1
QHJ74492.1	001605	Cluster1114_1clades	112	VH12019_00165	Vibrio phage VH1_2019	GCA_009931825.1
AGB06972.1	001605	Cluster1114_1clades	112	CF80_gp185	Vibrio phage VH7D	GCA_000914495.1
QBX06108.1	001605	Cluster1114_1clades	113	ValB1HC_154	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61175.1	001605	Cluster1114_1clades	112	AVU32_gp334	Vibrio phage ValKK3	GCA_001501635.1
AGN30035.1	001605	Cluster1114_1clades	113	VPFG_00030	Vibrio phage nt-1	GCA_000910195.2
ALP47178.1	001605	Cluster1114_1clades	112	phiGrn1_0045	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47565.1	001605	Cluster1114_1clades	112	phiST2_0178	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54733.1	001605	Cluster1114_1clades	113	vBValMR10Z_193	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37597.1	001605	Cluster1114_1clades	113	pp2_365	Vibriophage phi-pp2	GCA_002630725.1
AFC21917.1	001606	Cluster1115_1clades	117	GAP32_460	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21918.1	001606	Cluster1115_1clades	104	GAP32_461	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21919.1	001606	Cluster1115_1clades	98	GAP32_462	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44043.1	001606	Cluster1115_1clades	112	CBB_480	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44044.1	001606	Cluster1115_1clades	105	CBB_481	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44045.1	001606	Cluster1115_1clades	99	CBB_482	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88999.1	001606	Cluster1115_1clades	107	BF_0474	Serratia phage BF	GCA_002619745.1
AQW89000.1	001606	Cluster1115_1clades	103	BF_0475	Serratia phage BF	GCA_002619745.1
SOK59282.1	001606	Cluster1115_1clades	104	g474	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59283.1	001606	Cluster1115_1clades	103	g475	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58747.1	001606	Cluster1115_1clades	104	g470	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58748.1	001606	Cluster1115_1clades	103	g471	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13840.1	001607	Cluster1116_1clades	102	Ccr10_gp310	Caulobacter phage Ccr10	GCA_002619445.1
ARB14185.1	001607	Cluster1116_1clades	102	Ccr2_gp309	Caulobacter phage Ccr2	GCA_002619465.1
ARB14879.1	001607	Cluster1116_1clades	102	Ccr29_gp323	Caulobacter phage Ccr29	GCA_002619485.1
ARB15217.1	001607	Cluster1116_1clades	102	Ccr32_gp299	Caulobacter phage Ccr32	GCA_002619505.1
ARB15551.1	001607	Cluster1116_1clades	102	Ccr34_gp309	Caulobacter phage Ccr34	GCA_002619525.1
ARB14526.1	001607	Cluster1116_1clades	102	Ccr5_gp306	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68506.1	001607	Cluster1116_1clades	115	CcrBL10_gp302	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87837.1	001607	Cluster1116_1clades	102	CcrKarma_gp320	Caulobacter virus Karma	GCA_000901575.1
AFU87484.1	001607	Cluster1116_1clades	102	CcrMagneto_gp314	Caulobacter virus Magneto	GCA_000903095.1
AFU86794.1	001607	Cluster1116_1clades	117	CcrRogue_gp312	Caulobacter virus Rogue	GCA_000900555.1
AFU88629.1	001607	Cluster1116_1clades	102	CcrSwift_gp311	Caulobacter virus Swift	GCA_000899655.1
AFU87136.1	001607	Cluster1116_1clades	102	CbK_gp304	Caulobacter virus phiCbK	GCA_000900535.1
ARB13656.1	001608	Cluster1117_1clades	117	Ccr10_gp127c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14001.1	001608	Cluster1117_1clades	117	Ccr2_gp126c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14689.1	001608	Cluster1117_1clades	117	Ccr29_gp133	Caulobacter phage Ccr29	GCA_002619485.1
ARB15043.1	001608	Cluster1117_1clades	117	Ccr32_gp125	Caulobacter phage Ccr32	GCA_002619505.1
ARB15376.1	001608	Cluster1117_1clades	117	Ccr34_gp134	Caulobacter phage Ccr34	GCA_002619525.1
ARB14344.1	001608	Cluster1117_1clades	117	Ccr5_gp125c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68324.1	001608	Cluster1117_1clades	117	CcrBL10_gp120c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87648.1	001608	Cluster1117_1clades	117	CcrKarma_gp131	Caulobacter virus Karma	GCA_000901575.1
AFU87297.1	001608	Cluster1117_1clades	117	CcrMagneto_gp127	Caulobacter virus Magneto	GCA_000903095.1
AFU86609.1	001608	Cluster1117_1clades	116	CcrRogue_gp127	Caulobacter virus Rogue	GCA_000900555.1
AFU88444.1	001608	Cluster1117_1clades	117	CcrSwift_gp126	Caulobacter virus Swift	GCA_000899655.1
AFU86961.1	001608	Cluster1117_1clades	117	CbK_gp129	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64261.1	001609	Cluster1118_1clades	116	KVP40.0192	Vibrio phage KVP40	GCA_000843785.1
QIW90577.1	001609	Cluster1118_1clades	116	GCAPEGMB_00230	Vibrio phage V07	GCA_012361095.1
QIW91221.1	001609	Cluster1118_1clades	116	COHAPHLL_00385	Vibrio phage V09	GCA_012361135.1
QHJ74375.1	001609	Cluster1118_1clades	66	VH12019_00048	Vibrio phage VH1_2019	GCA_009931825.1
AGB06872.1	001609	Cluster1118_1clades	115	CF80_gp085	Vibrio phage VH7D	GCA_000914495.1
QBX06274.1	001609	Cluster1118_1clades	115	ValB1HC_321	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60900.1	001609	Cluster1118_1clades	115	AVU32_gp059	Vibrio phage ValKK3	GCA_001501635.1
AGN30250.1	001609	Cluster1118_1clades	111	VPFG_00251	Vibrio phage nt-1	GCA_000910195.2
ALP47174.1	001609	Cluster1118_1clades	115	phiGrn1_0311	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47561.1	001609	Cluster1118_1clades	115	phiST2_0067	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54901.1	001609	Cluster1118_1clades	115	vBValMR10Z_361	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37423.1	001609	Cluster1118_1clades	116	pp2_190	Vibriophage phi-pp2	GCA_002630725.1
ARB13640.1	001610	Cluster1119_1clades	115	Ccr10_gp111c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13985.1	001610	Cluster1119_1clades	115	Ccr2_gp110c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14673.1	001610	Cluster1119_1clades	115	Ccr29_gp117	Caulobacter phage Ccr29	GCA_002619485.1
ARB15028.1	001610	Cluster1119_1clades	115	Ccr32_gp110	Caulobacter phage Ccr32	GCA_002619505.1
ARB15360.1	001610	Cluster1119_1clades	115	Ccr34_gp118	Caulobacter phage Ccr34	GCA_002619525.1
ARB14329.1	001610	Cluster1119_1clades	115	Ccr5_gp111c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68309.1	001610	Cluster1119_1clades	116	CcrBL10_gp105c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87632.1	001610	Cluster1119_1clades	115	CcrKarma_gp115	Caulobacter virus Karma	GCA_000901575.1
AFU87281.1	001610	Cluster1119_1clades	115	CcrMagneto_gp111	Caulobacter virus Magneto	GCA_000903095.1
AFU86593.1	001610	Cluster1119_1clades	116	CcrRogue_gp111	Caulobacter virus Rogue	GCA_000900555.1
AFU88428.1	001610	Cluster1119_1clades	115	CcrSwift_gp110	Caulobacter virus Swift	GCA_000899655.1
AFU86946.1	001610	Cluster1119_1clades	115	CbK_gp114	Caulobacter virus phiCbK	GCA_000900535.1
ARB13707.1	001611	SIG+TM	116	Ccr10_gp177c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14052.1	001611	SIG+TM	116	Ccr2_gp176c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14739.1	001611	SIG+TM	116	Ccr29_gp183	Caulobacter phage Ccr29	GCA_002619485.1
ARB15094.1	001611	SIG+TM	116	Ccr32_gp176	Caulobacter phage Ccr32	GCA_002619505.1
ARB15428.1	001611	SIG+TM	116	Ccr34_gp186	Caulobacter phage Ccr34	GCA_002619525.1
ARB14395.1	001611	SIG+TM	116	Ccr5_gp175c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68377.1	001611	SIG+TM	116	CcrBL10_gp173c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87700.1	001611	SIG+TM	116	CcrKarma_gp183	Caulobacter virus Karma	GCA_000901575.1
AFU87349.1	001611	SIG+TM	116	CcrMagneto_gp179	Caulobacter virus Magneto	GCA_000903095.1
AFU86660.1	001611	SIG+TM	111	CcrRogue_gp178	Caulobacter virus Rogue	GCA_000900555.1
AFU88496.1	001611	SIG+TM	116	CcrSwift_gp178	Caulobacter virus Swift	GCA_000899655.1
AFU87013.1	001611	SIG+TM	116	CbK_gp181	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64217.1	001612	Cluster1121_1clades	104	KVP40.0147	Vibrio phage KVP40	GCA_000843785.1
QIW90530.1	001612	Cluster1121_1clades	104	GCAPEGMB_00183	Vibrio phage V07	GCA_012361095.1
QIW90892.1	001612	Cluster1121_1clades	104	COHAPHLL_00029	Vibrio phage V09	GCA_012361135.1
QHJ74328.1	001612	Cluster1121_1clades	104	VH12019_00001	Vibrio phage VH1_2019	GCA_009931825.1
AGB06821.1	001612	Cluster1121_1clades	114	CF80_gp034	Vibrio phage VH7D	GCA_000914495.1
QBX06326.1	001612	Cluster1121_1clades	114	ValB1HC_373	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60956.1	001612	Cluster1121_1clades	114	AVU32_gp115	Vibrio phage ValKK3	GCA_001501635.1
AGN30192.1	001612	Cluster1121_1clades	116	VPFG_00192	Vibrio phage nt-1	GCA_000910195.2
ALP47176.1	001612	Cluster1121_1clades	114	phiGrn1_0257	Vibrio phage phi-Grn1	GCA_002757115.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALP47562.1	001612	Cluster1121_1clades	114	phiST2_0014	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54569.1	001612	Cluster1121_1clades	114	vBValMR10Z_28	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37376.1	001612	Cluster1121_1clades	104	pp2_143	Vibriophage phi-pp2	GCA_002630725.1
ARB13829.1	001613	Cluster1122_1clades	114	Ccr10_gp299	Caulobacter phage Ccr10	GCA_002619445.1
ARB14174.1	001613	Cluster1122_1clades	114	Ccr2_gp298	Caulobacter phage Ccr2	GCA_002619465.1
ARB14868.1	001613	Cluster1122_1clades	114	Ccr29_gp312	Caulobacter phage Ccr29	GCA_002619485.1
ARB15206.1	001613	Cluster1122_1clades	114	Ccr32_gp288	Caulobacter phage Ccr32	GCA_002619505.1
ARB15540.1	001613	Cluster1122_1clades	114	Ccr34_gp298	Caulobacter phage Ccr34	GCA_002619525.1
ARB14515.1	001613	Cluster1122_1clades	91	Ccr5_gp295	Caulobacter phage Ccr5	GCA_002619545.1
AXQ69593.1	001613	Cluster1122_1clades	107	CcrSC_gp011	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70093.1	001613	Cluster1122_1clades	107	CcrSC_gp511	Caulobacter phage CcrSC	GCA_003443315.1
AFU87825.1	001613	Cluster1122_1clades	115	CcrKarma_gp308	Caulobacter virus Karma	GCA_000901575.1
AFU87472.1	001613	Cluster1122_1clades	114	CcrMagneto_gp302	Caulobacter virus Magneto	GCA_000903095.1
AFU88617.1	001613	Cluster1122_1clades	114	CcrSwift_gp299	Caulobacter virus Swift	GCA_000899655.1
AFU87125.1	001613	Cluster1122_1clades	114	CbK_gp293	Caulobacter virus phiCbK	GCA_000900535.1
AIT14043.1	001614	Cluster1123_1clades	113	PBI_121Q_153	Escherichia phage 121Q	GCA_000926855.1
QAY00300.1	001614	Cluster1123_1clades	113	Ecwhy1_18	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35050.1	001614	Cluster1123_1clades	113	ACQ29_gp370	Escherichia phage PBECO4	GCA_001041035.1
BBM61726.1	001614	Cluster1123_1clades	113	EO157G_1370	Escherichia phage SP27	GCA_008033345.1
AXC36627.1	001614	Cluster1123_1clades	113	-	Escherichia phage UB	GCA_003341455.1
QBO61656.1	001614	Cluster1123_1clades	113	G17_00160	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13709.1	001614	Cluster1123_1clades	113	vBEcoMphAPEC6_gp079c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80038.1	001614	Cluster1123_1clades	113	PSLUR01_00061	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44505.1	001614	Cluster1123_1clades	112	RaK2_00232	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18576.1	001614	Cluster1123_1clades	109	7t3_055	Salmonella phage 7t3	GCA_006083215.1
AZU98405.1	001614	Cluster1123_1clades	109	CPT_Munch_473	Salmonella phage Munch	GCA_004015485.1
QIG63108.1	001614	Cluster1123_1clades	76	SEPL_495	Salmonella phage SE_PL	GCA_011067555.1
APU01535.1	001615	Cluster1124_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29073.1	001615	Cluster1124_1clades	112	AP1_0366	Aeromonas phage AP1	GCA_014183365.1
ATI17356.1	001615	Cluster1124_1clades	112	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00238.1	001615	Cluster1124_1clades	112	HWB28_gp314	Aeromonas phage AS-zj	GCA_002627665.1
QAX97800.1	001615	Cluster1124_1clades	112	ASswx1_155	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01345.1	001615	Cluster1124_1clades	112	ASwh1_284	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39444.1	001615	Cluster1124_1clades	112	CC2_382	Aeromonas phage CC2	GCA_000903495.1
ADQ53157.1	001615	Cluster1124_1clades	112	65p149	Aeromonas virus 65	GCA_000893255.1
ANS06092.1	001615	Cluster1124_1clades	105	ABCD_0230	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97247.1	001615	Cluster1124_1clades	105	E_239	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70857.1	001615	Cluster1124_1clades	105	phiC120_c151	Escherichia phage phiC120	GCA_002621185.1
AAX78765.1	001615	Cluster1124_1clades	95	RB43ORF243w	Escherichia virus RB43	GCA_000863505.1
AAQ64436.1	001616	Cluster1125_1clades	110	KVP40.0368	Vibrio phage KVP40	GCA_000843785.1
QIW90382.1	001616	Cluster1125_1clades	110	GCAPEGMB_00035	Vibrio phage V07	GCA_012361095.1
QIW91047.1	001616	Cluster1125_1clades	110	COHAPHLL_00184	Vibrio phage V09	GCA_012361135.1
QHJ74549.1	001616	Cluster1125_1clades	110	VH12019_00249	Vibrio phage VH1_2019	GCA_009931825.1
AGB07006.1	001616	Cluster1125_1clades	112	CF80_gp219	Vibrio phage VH7D	GCA_000914495.1
QBX06105.1	001616	Cluster1125_1clades	111	ValB1HC_151	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61119.1	001616	Cluster1125_1clades	111	AVU32_gp278	Vibrio phage ValKK3	GCA_001501635.1
AGN30038.1	001616	Cluster1125_1clades	111	VPFG_00033	Vibrio phage nt-1	GCA_000910195.2
ALP47180.1	001616	Cluster1125_1clades	111	phiGrn1_0101	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47564.1	001616	Cluster1125_1clades	112	phiST2_0232	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54730.1	001616	Cluster1125_1clades	111	vBValMR10Z_190	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37600.1	001616	Cluster1125_1clades	110	pp2_368	Vibriophage phi-pp2	GCA_002630725.1
AGH56824.1	001617	Cluster1126_1clades	112	CPXG_00021	Cyanophage P-RSM6	GCA_000906155.1
AJK27615.1	001617	Cluster1126_1clades	110	PTIM40_201	Cyanophage P-TIM40	GCA_001470935.1
AMO43190.1	001617	Cluster1126_1clades	76	R1080702_181	Cyanophage S-RIM32	GCA_001754165.1
AMO43416.1	001617	Cluster1126_1clades	91	W270710_172	Cyanophage S-RIM44	GCA_002599145.1
AOO11660.1	001617	Cluster1126_1clades	91	ES420910_179	Cyanophage S-RIM44	GCA_002599165.1
AOO11888.1	001617	Cluster1126_1clades	91	Np050604_172	Cyanophage S-RIM44	GCA_002599185.1
AOO12126.1	001617	Cluster1126_1clades	91	Np200711_180	Cyanophage S-RIM44	GCA_002599205.1
AOO12361.1	001617	Cluster1126_1clades	91	Np420711_179	Cyanophage S-RIM44	GCA_002599225.1
AOO12589.1	001617	Cluster1126_1clades	91	Sn080709_172	Cyanophage S-RIM44	GCA_002599245.1
AOO12826.1	001617	Cluster1126_1clades	91	Sn130910_179	Cyanophage S-RIM44	GCA_002599265.1
AOO13055.1	001617	Cluster1126_1clades	91	W2100709_173	Cyanophage S-RIM44	GCA_002599285.1
ADO99275.1	001617	Cluster1126_1clades	110	Syn1_174	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13815.1	001618	Cluster1127_1clades	100	Ccr10_gp285	Caulobacter phage Ccr10	GCA_002619445.1
ARB14160.1	001618	Cluster1127_1clades	100	Ccr2_gp284	Caulobacter phage Ccr2	GCA_002619465.1
ARB14854.1	001618	Cluster1127_1clades	100	Ccr29_gp298	Caulobacter phage Ccr29	GCA_002619485.1
ARB15193.1	001618	Cluster1127_1clades	79	Ccr32_gp275	Caulobacter phage Ccr32	GCA_002619505.1
ARB15527.1	001618	Cluster1127_1clades	78	Ccr34_gp285	Caulobacter phage Ccr34	GCA_002619525.1
ARB14502.1	001618	Cluster1127_1clades	100	Ccr5_gp282	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68482.1	001618	Cluster1127_1clades	111	CcrBL10_gp278	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87812.1	001618	Cluster1127_1clades	100	CcrKarma_gp295	Caulobacter virus Karma	GCA_000901575.1
AFU87459.1	001618	Cluster1127_1clades	100	CcrMagneto_gp289	Caulobacter virus Magneto	GCA_000903095.1
AFU86770.1	001618	Cluster1127_1clades	111	CcrRogue_gp288	Caulobacter virus Rogue	GCA_000900555.1
AFU88604.1	001618	Cluster1127_1clades	100	CcrSwift_gp286	Caulobacter virus Swift	GCA_000899655.1
AFU87112.1	001618	Cluster1127_1clades	100	CbK_gp280	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64169.1	001619	Cluster1128_1clades	110	KVP40.0098	Vibrio phage KVP40	GCA_000843785.1
QIW90492.1	001619	Cluster1128_1clades	87	GCAPEGMB_00145	Vibrio phage V07	GCA_012361095.1
QIW90937.1	001619	Cluster1128_1clades	87	COHAPHLL_00074	Vibrio phage V09	GCA_012361135.1
QHJ74280.1	001619	Cluster1128_1clades	87	VH12019_00361	Vibrio phage VH1_2019	GCA_009931825.1
AGB07105.1	001619	Cluster1128_1clades	90	CF80_gp318	Vibrio phage VH7D	GCA_000914495.1
QBX05990.1	001619	Cluster1128_1clades	90	ValB1HC_036	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61003.1	001619	Cluster1128_1clades	90	AVU32_gp162	Vibrio phage ValKK3	GCA_001501635.1
AGN30148.1	001619	Cluster1128_1clades	87	VPFG_00146	Vibrio phage nt-1	GCA_000910195.2
ALP47232.1	001619	Cluster1128_1clades	90	phiGrn1_0212	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47617.1	001619	Cluster1128_1clades	90	phiST2_0345	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54615.1	001619	Cluster1128_1clades	90	vBValMR10Z_74	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37328.1	001619	Cluster1128_1clades	87	pp2_095	Vibriophage phi-pp2	GCA_002630725.1
ARB13845.1	001620	Cluster1129_1clades	110	Ccr10_gp315	Caulobacter phage Ccr10	GCA_002619445.1
ARB14190.1	001620	Cluster1129_1clades	110	Ccr2_gp314	Caulobacter phage Ccr2	GCA_002619465.1
ARB14884.1	001620	Cluster1129_1clades	110	Ccr29_gp328	Caulobacter phage Ccr29	GCA_002619485.1
ARB15222.1	001620	Cluster1129_1clades	110	Ccr32_gp304	Caulobacter phage Ccr32	GCA_002619505.1
ARB15556.1	001620	Cluster1129_1clades	110	Ccr34_gp314	Caulobacter phage Ccr34	GCA_002619525.1
ARB14531.1	001620	Cluster1129_1clades	110	Ccr5_gp311	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68512.1	001620	Cluster1129_1clades	110	CcrBL10_gp308	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87842.1	001620	Cluster1129_1clades	110	CcrKarma_gp325	Caulobacter virus Karma	GCA_000901575.1
AFU87489.1	001620	Cluster1129_1clades	110	CcrMagneto_gp319	Caulobacter virus Magneto	GCA_000903095.1
AFU86801.1	001620	Cluster1129_1clades	110	CcrRogue_gp319	Caulobacter virus Rogue	GCA_000900555.1
AFU88634.1	001620	Cluster1129_1clades	110	CcrSwift_gp316	Caulobacter virus Swift	GCA_000899655.1
AFU87141.1	001620	Cluster1129_1clades	110	CbK_gp309	Caulobacter virus phiCbK	GCA_000900535.1
AHI60334.1	001621	Cluster1130_1clades	101	Ea357_182	Erwinia phage Ea35-70	GCA_000914635.1
QBP07293.1	001621	Cluster1130_1clades	110	REBECCA_186	Erwinia phage Rebecca	GCA_004521635.1
AUG85973.1	001621	Cluster1130_1clades	110	BOSOLAPHORUS_186	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52288.1	001621	Cluster1130_1clades	110	DM_190	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86292.1	001621	Cluster1130_1clades	110	DESERTFOX_185	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86614.1	001621	Cluster1130_1clades	110	MADMEL_186	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86938.1	001621	Cluster1130_1clades	110	MORTIMER_189	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51965.1	001621	Cluster1130_1clades	110	RAY_184	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51649.1	001621	Cluster1130_1clades	110	SIMMY50_187	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64996.1	001621	Cluster1130_1clades	110	SPECIALG_186	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24116.1	001621	Cluster1130_1clades	100	-	Proteus phage 10	GCA_014071245.1
QKE54494.1	001621	Cluster1130_1clades	97	ACSA002_1800	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AMR59844.1	001622	GTP_EFTU	69	SEGD1_197	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49841.1	001622	GTP_EFTU	110	MACHINA_203	Erwinia phage Machina	GCA_002758035.1
AFQ96660.1	001622	GTP_EFTU	109	G173_gp115	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48226.1	001622	GTP_EFTU	109	ASESINO_213	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48497.1	001622	GTP_EFTU	109	CAITLIN_202	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48777.1	001622	GTP_EFTU	109	CHRISDB_215	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49285.1	001622	GTP_EFTU	110	HUXLEY_203	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50113.1	001622	GTP_EFTU	110	PARSHIK_204	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50639.1	001622	GTP_EFTU	109	STRATTON_214	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86034.1	001622	GTP_EFTU	69	ACEC001_1910	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09146.1	001622	GTP_EFTU	71	MLDJOKPK_00247	Salmonella phage SPAsTU	GCA_003183805.1
AEP84025.1	001622	GTP_EFTU	69	SPN3US_0192	Salmonella phage SPN3US	GCA_001042275.1
AIT14077.1	001623	SIG+TM+TM	108	PBI_121Q_187	Escherichia phage 121Q	GCA_000926855.1
QAY00846.1	001623	SIG+TM+TM	108	Ecwhy1_574	Escherichia phage Ecwhy_1	GCA_004146585.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGC35017.1	001623	SIG+TM+TM	108	ACQ29_gp337	Escherichia phage PBECO4	GCA_001041035.1
BBM61760.1	001623	SIG+TM+TM	108	EO157G_1710	Escherichia phage SP27	GCA_008033345.1
AXC36594.1	001623	SIG+TM+TM	108	-	Escherichia phage UB	GCA_003341455.1
QBO61622.1	001623	SIG+TM+TM	108	G17_00126	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13679.1	001623	SIG+TM+TM	108	vBEcoMphAPEC6_gp049c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80071.1	001623	SIG+TM+TM	108	PSLUR01_00094	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44537.1	001623	SIG+TM+TM	107	RaK2_00264	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18618.1	001623	SIG+TM+TM	110	7t3_097	Salmonella phage 7t3	GCA_006083215.1
AZU98443.1	001623	SIG+TM+TM	110	CPT_Munch_511	Salmonella phage Munch	GCA_004015485.1
QIG63070.1	001623	SIG+TM+TM	110	SEPL_457	Salmonella phage SE_PL	GCA_011067555.1
AAQ64109.1	001624	Cluster1133_1clades	109	KVP40.0038	Vibrio phage KVP40	GCA_000843785.1
QIW90432.1	001624	Cluster1133_1clades	109	GCAPEGMB_00085	Vibrio phage V07	GCA_012361095.1
QIW90997.1	001624	Cluster1133_1clades	109	COHAPHLL_00134	Vibrio phage V09	GCA_012361135.1
QHJ74221.1	001624	Cluster1133_1clades	109	VH12019_00302	Vibrio phage VH1_2019	GCA_009931825.1
AGB07045.1	001624	Cluster1133_1clades	109	CF80_gp258	Vibrio phage VH7D	GCA_000914495.1
QBX06051.1	001624	Cluster1133_1clades	109	ValB1HC_097	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61064.1	001624	Cluster1133_1clades	109	AVU32_gp223	Vibrio phage ValKK3	GCA_001501635.1
AGN30087.1	001624	Cluster1133_1clades	109	VPFG_00085	Vibrio phage nt-1	GCA_000910195.2
ALP47181.1	001624	Cluster1133_1clades	109	phiGrn1_0153	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47570.1	001624	Cluster1133_1clades	109	phiST2_0283	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54677.1	001624	Cluster1133_1clades	109	vBValMR10Z_136	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37271.1	001624	Cluster1133_1clades	109	pp2_037	Vibriophage phi-pp2	GCA_002630725.1
AAQ64226.1	001625	Cluster1134_1clades	109	KVP40.0157	Vibrio phage KVP40	GCA_000843785.1
QIW90540.1	001625	Cluster1134_1clades	109	GCAPEGMB_00193	Vibrio phage V07	GCA_012361095.1
QIW90882.1	001625	Cluster1134_1clades	109	COHAPHLL_00019	Vibrio phage V09	GCA_012361135.1
QHJ74338.1	001625	Cluster1134_1clades	109	VH12019_00011	Vibrio phage VH1_2019	GCA_009931825.1
AGB06831.1	001625	Cluster1134_1clades	104	CF80_gp044	Vibrio phage VH7D	GCA_000914495.1
QBX06315.1	001625	Cluster1134_1clades	107	ValB1HC_362	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60946.1	001625	Cluster1134_1clades	107	AVU32_gp105	Vibrio phage ValKK3	GCA_001501635.1
AGN30204.1	001625	Cluster1134_1clades	102	VPFG_00204	Vibrio phage nt-1	GCA_000910195.2
ALP47187.1	001625	Cluster1134_1clades	107	phiGrn1_0268	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47577.1	001625	Cluster1134_1clades	107	phiST2_0027	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54558.1	001625	Cluster1134_1clades	107	vBValMR10Z_17	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37385.1	001625	Cluster1134_1clades	109	pp2_152	Vibriophage phi-pp2	GCA_002630725.1
AAQ64334.1	001626	Cluster1135_1clades	108	KVP40.0265	Vibrio phage KVP40	GCA_000843785.1
QIW90649.1	001626	Cluster1135_1clades	109	GCAPEGMB_00302	Vibrio phage V07	GCA_012361095.1
QIW91150.1	001626	Cluster1135_1clades	108	COHAPHLL_00314	Vibrio phage V09	GCA_012361135.1
QHJ74444.1	001626	Cluster1135_1clades	108	VH12019_00117	Vibrio phage VH1_2019	GCA_009931825.1
AGB06942.1	001626	Cluster1135_1clades	108	CF80_gp155	Vibrio phage VH7D	GCA_000914495.1
QBX06204.1	001626	Cluster1135_1clades	108	ValB1HC_251	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61221.1	001626	Cluster1135_1clades	108	AVU32_gp380	Vibrio phage ValKK3	GCA_001501635.1
AIE13778.1	001626	Cluster1135_1clades	71	VPFG_00312	Vibrio phage nt-1	GCA_000910195.2
ALP47185.1	001626	Cluster1135_1clades	108	phiGrn1_0001	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47574.1	001626	Cluster1135_1clades	108	phiST2_0133	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54829.1	001626	Cluster1135_1clades	108	vBValMR10Z_289	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37494.1	001626	Cluster1135_1clades	108	pp2_261	Vibriophage phi-pp2	GCA_002630725.1
AAQ64257.1	001627	Cluster1136_1clades	108	KVP40.0188	Vibrio phage KVP40	GCA_000843785.1
QIW90573.1	001627	Cluster1136_1clades	108	GCAPEGMB_00226	Vibrio phage V07	GCA_012361095.1
QIW91225.1	001627	Cluster1136_1clades	108	COHAPHLL_00389	Vibrio phage V09	GCA_012361135.1
QHJ74371.1	001627	Cluster1136_1clades	108	VH12019_00044	Vibrio phage VH1_2019	GCA_009931825.1
AGB06867.1	001627	Cluster1136_1clades	103	CF80_gp080	Vibrio phage VH7D	GCA_000914495.1
QBX06279.1	001627	Cluster1136_1clades	103	ValB1HC_326	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60905.1	001627	Cluster1136_1clades	106	AVU32_gp064	Vibrio phage ValKK3	GCA_001501635.1
AGN30247.1	001627	Cluster1136_1clades	107	VPFG_00248	Vibrio phage nt-1	GCA_000910195.2
ALP47190.1	001627	Cluster1136_1clades	106	phiGrn1_0305	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47584.1	001627	Cluster1136_1clades	103	phiST2_0062	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54906.1	001627	Cluster1136_1clades	103	vBValMR10Z_366	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37419.1	001627	Cluster1136_1clades	108	pp2_186	Vibriophage phi-pp2	GCA_002630725.1
ARB13730.1	001628	Cluster1137_1clades	106	Ccr10_gp200c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14075.1	001628	Cluster1137_1clades	106	Ccr2_gp199c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14764.1	001628	Cluster1137_1clades	106	Ccr29_gp208	Caulobacter phage Ccr29	GCA_002619485.1
ARB15108.1	001628	Cluster1137_1clades	106	Ccr32_gp190	Caulobacter phage Ccr32	GCA_002619505.1
ARB15442.1	001628	Cluster1137_1clades	106	Ccr34_gp200	Caulobacter phage Ccr34	GCA_002619525.1
ARB14417.1	001628	Cluster1137_1clades	106	Ccr5_gp197c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68397.1	001628	Cluster1137_1clades	107	CcrBL10_gp193c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87723.1	001628	Cluster1137_1clades	105	CcrKarma_gp206	Caulobacter virus Karma	GCA_000901575.1
AFU87372.1	001628	Cluster1137_1clades	106	CcrMagneto_gp202	Caulobacter virus Magneto	GCA_000903095.1
AFU86683.1	001628	Cluster1137_1clades	108	CcrRogue_gp201	Caulobacter virus Rogue	GCA_000900555.1
AFU88519.1	001628	Cluster1137_1clades	106	CcrSwift_gp201	Caulobacter virus Swift	GCA_000899655.1
AFU87027.1	001628	Cluster1137_1clades	106	CbK_gp195	Caulobacter virus phiCbK	GCA_000900535.1
ARB13835.1	001629	Cluster1138_1clades	108	Ccr10_gp305	Caulobacter phage Ccr10	GCA_002619445.1
ARB14180.1	001629	Cluster1138_1clades	108	Ccr2_gp304	Caulobacter phage Ccr2	GCA_002619465.1
ARB14874.1	001629	Cluster1138_1clades	108	Ccr29_gp318	Caulobacter phage Ccr29	GCA_002619485.1
ARB15212.1	001629	Cluster1138_1clades	108	Ccr32_gp294	Caulobacter phage Ccr32	GCA_002619505.1
ARB15546.1	001629	Cluster1138_1clades	108	Ccr34_gp304	Caulobacter phage Ccr34	GCA_002619525.1
ARB14521.1	001629	Cluster1138_1clades	108	Ccr5_gp301	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68501.1	001629	Cluster1138_1clades	108	CcrBL10_gp297	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87832.1	001629	Cluster1138_1clades	108	CcrKarma_gp315	Caulobacter virus Karma	GCA_000901575.1
AFU87479.1	001629	Cluster1138_1clades	108	CcrMagneto_gp309	Caulobacter virus Magneto	GCA_000903095.1
AFU86789.1	001629	Cluster1138_1clades	108	CcrRogue_gp307	Caulobacter virus Rogue	GCA_000900555.1
AFU88624.1	001629	Cluster1138_1clades	108	CcrSwift_gp306	Caulobacter virus Swift	GCA_000899655.1
AFU87131.1	001629	Cluster1138_1clades	108	CbK_gp299	Caulobacter virus phiCbK	GCA_000900535.1
AIT14302.1	001630	Cluster1139_1clades	98	PBI_121Q_412	Escherichia phage 121Q	GCA_000926855.1
QAY00636.1	001630	Cluster1139_1clades	97	Ecwhy1_361	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34833.1	001630	Cluster1139_1clades	97	ACQ29_gp153	Escherichia phage PBECO4	GCA_001041035.1
BBM61976.1	001630	Cluster1139_1clades	97	EO157G_3870	Escherichia phage SP27	GCA_008033345.1
AXC36941.1	001630	Cluster1139_1clades	97	-	Escherichia phage UB	GCA_003341455.1
QBO62002.1	001630	Cluster1139_1clades	97	G17_00513	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14023.1	001630	Cluster1139_1clades	97	vBEcoMphAPEC6_gp399c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80289.1	001630	Cluster1139_1clades	97	PSLUR01_00312	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44715.1	001630	Cluster1139_1clades	102	RaK2_00442	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18759.1	001630	Cluster1139_1clades	108	7t3_0238	Salmonella phage 7t3	GCA_006083215.1
AZU98028.1	001630	Cluster1139_1clades	108	CPT_Munch_084	Salmonella phage Munch	GCA_004015485.1
QIG62952.1	001630	Cluster1139_1clades	108	SEPL_339	Salmonella phage SE_PL	GCA_011067555.1
ARB13713.1	001631	Cluster1140_1clades	106	Ccr10_gp183c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14058.1	001631	Cluster1140_1clades	106	Ccr2_gp182c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14745.1	001631	Cluster1140_1clades	106	Ccr29_gp189	Caulobacter phage Ccr29	GCA_002619485.1
ARB15100.1	001631	Cluster1140_1clades	106	Ccr32_gp182	Caulobacter phage Ccr32	GCA_002619505.1
ARB15434.1	001631	Cluster1140_1clades	106	Ccr34_gp192	Caulobacter phage Ccr34	GCA_002619525.1
ARB14401.1	001631	Cluster1140_1clades	106	Ccr5_gp181c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68382.1	001631	Cluster1140_1clades	107	CcrBL10_gp178c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87706.1	001631	Cluster1140_1clades	106	CcrKarma_gp189	Caulobacter virus Karma	GCA_000901575.1
AFU87355.1	001631	Cluster1140_1clades	106	CcrMagneto_gp185	Caulobacter virus Magneto	GCA_000903095.1
AFU86667.1	001631	Cluster1140_1clades	104	CcrRogue_gp185	Caulobacter virus Rogue	GCA_000900555.1
AFU88502.1	001631	Cluster1140_1clades	106	CcrSwift_gp184	Caulobacter virus Swift	GCA_000899655.1
AFU87019.1	001631	Cluster1140_1clades	106	CbK_gp187	Caulobacter virus phiCbK	GCA_000900535.1
AUE22710.1	001632	Cluster1141_1clades	95	Ah1_00190	Aeromonas phage Ah1	GCA_002957415.1
QAX98437.1	001632	Cluster1141_1clades	49	ASfcp2_93	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52891.1	001632	Cluster1141_1clades	49	PX29p172	Aeromonas phage PX29	GCA_000920195.1
ADM80158.1	001632	Cluster1141_1clades	95	phiAS5_ORF0315	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17844.1	001632	Cluster1141_1clades	95	Aeh1ORF178c	Aeromonas virus Aeh1	GCA_000843245.1
QBZ70719.1	001632	Cluster1141_1clades	101	pETSU_138	Edwardsiella virus pEt-SU	GCA_004800915.1
AFA44546.1	001632	Cluster1141_1clades	100	RaK2_00273	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AEV89651.1	001632	Cluster1141_1clades	99	OBP_214	Pseudomonas phage OBP	GCA_000896635.1
QCW18625.1	001632	Cluster1141_1clades	107	7t3_0104	Salmonella phage 7t3	GCA_006083215.1
AZU98450.1	001632	Cluster1141_1clades	107	CPT_Munch_518	Salmonella phage Munch	GCA_004015485.1
QIG63063.1	001632	Cluster1141_1clades	107	SEPL_450	Salmonella phage SE_PL	GCA_011067555.1
AQW88883.1	001632	Cluster1141_1clades	104	BF_0358	Serratia phage BF	GCA_002619745.1
AAQ64189.1	001633	Cluster1142_1clades	104	KVP40.0118	Vibrio phage KVP40	GCA_000843785.1
QIW90832.1	001633	Cluster1142_1clades	104	GCAPEGMB_00517	Vibrio phage V07	GCA_012361095.1
QIW90917.1	001633	Cluster1142_1clades	104	COHAPHLL_00054	Vibrio phage V09	GCA_012361135.1
QHJ74301.1	001633	Cluster1142_1clades	104	VH12019_00382	Vibrio phage VH1_2019	GCA_009931825.1
AGB06795.1	001633	Cluster1142_1clades	105	CF80_gp008	Vibrio phage VH7D	GCA_000914495.1
QBX05971.1	001633	Cluster1142_1clades	105	ValB1HC_017	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60983.1	001633	Cluster1142_1clades	105	AVU32_gp142	Vibrio phage ValKK3	GCA_001501635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN30169.1	001633	Cluster1142_1clades	106	VPFG_00167	Vibrio phage nt-1	GCA_000910195.2
ALP47192.1	001633	Cluster1142_1clades	105	phiGrn1_0230	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47579.1	001633	Cluster1142_1clades	105	phiST2_0365	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54596.1	001633	Cluster1142_1clades	105	vBValMR10Z_55	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37348.1	001633	Cluster1142_1clades	104	pp2_115	Vibriophage phi-pp2	GCA_002630725.1
AAQ64105.1	001634	Cluster1143_1clades	104	KVP40.0034	Vibrio phage KVP40	GCA_000843785.1
QIW90428.1	001634	Cluster1143_1clades	96	GCAPEGMB_00081	Vibrio phage V07	GCA_012361095.1
QIW91001.1	001634	Cluster1143_1clades	96	COHAPHLL_00138	Vibrio phage V09	GCA_012361135.1
QHJ74217.1	001634	Cluster1143_1clades	96	VH12019_00298	Vibrio phage VH1_2019	GCA_009931825.1
AGB07041.1	001634	Cluster1143_1clades	96	CF80_gp254	Vibrio phage VH7D	GCA_000914495.1
QBX06055.1	001634	Cluster1143_1clades	96	ValB1HC_101	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61068.1	001634	Cluster1143_1clades	96	AVU32_gp227	Vibrio phage ValKK3	GCA_001501635.1
AGN30083.1	001634	Cluster1143_1clades	96	VPFG_00081	Vibrio phage nt-1	GCA_000910195.2
ALP47215.1	001634	Cluster1143_1clades	96	phiGrn1_0149	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47605.1	001634	Cluster1143_1clades	96	phiST2_0279	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54681.1	001634	Cluster1143_1clades	96	vBValMR10Z_140	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37267.1	001634	Cluster1143_1clades	96	pp2_033	Vibriophage phi-pp2	GCA_002630725.1
AAQ64211.1	001635	Cluster1144_1clades	104	KVP40.0141	Vibrio phage KVP40	GCA_000843785.1
QIW90526.1	001635	Cluster1144_1clades	100	GCAPEGMB_00179	Vibrio phage V07	GCA_012361095.1
QIW90896.1	001635	Cluster1144_1clades	100	COHAPHLL_00033	Vibrio phage V09	GCA_012361135.1
QHJ74322.1	001635	Cluster1144_1clades	100	VH12019_00403	Vibrio phage VH1_2019	GCA_009931825.1
AGB06816.1	001635	Cluster1144_1clades	98	CF80_gp029	Vibrio phage VH7D	GCA_000914495.1
QBX06331.1	001635	Cluster1144_1clades	98	ValB1HC_378	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60961.1	001635	Cluster1144_1clades	98	AVU32_gp120	Vibrio phage ValKK3	GCA_001501635.1
AGN30189.1	001635	Cluster1144_1clades	97	VPFG_00189	Vibrio phage nt-1	GCA_000910195.2
ALP47212.1	001635	Cluster1144_1clades	98	phiGrn1_0252	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47602.1	001635	Cluster1144_1clades	98	phiST2_0007	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54574.1	001635	Cluster1144_1clades	98	vBValMR10Z_33	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37372.1	001635	Cluster1144_1clades	100	pp2_139	Vibriophage phi-pp2	GCA_002630725.1
AAQ64127.1	001636	Cluster1145_1clades	103	KVP40.0056	Vibrio phage KVP40	GCA_000843785.1
QIW90449.1	001636	Cluster1145_1clades	99	GCAPEGMB_00102	Vibrio phage V07	GCA_012361095.1
QIW90980.1	001636	Cluster1145_1clades	99	COHAPHLL_00117	Vibrio phage V09	GCA_012361135.1
QHJ74238.1	001636	Cluster1145_1clades	99	VH12019_00319	Vibrio phage VH1_2019	GCA_009931825.1
AGB07063.1	001636	Cluster1145_1clades	99	CF80_gp276	Vibrio phage VH7D	GCA_000914495.1
QBX06033.1	001636	Cluster1145_1clades	99	ValB1HC_079	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61047.1	001636	Cluster1145_1clades	99	AVU32_gp206	Vibrio phage ValKK3	GCA_001501635.1
AGN30105.1	001636	Cluster1145_1clades	100	VPFG_00103	Vibrio phage nt-1	GCA_000910195.2
ALP47205.1	001636	Cluster1145_1clades	99	phiGrn1_0170	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47597.1	001636	Cluster1145_1clades	99	phiST2_0301	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54658.1	001636	Cluster1145_1clades	99	vBValMR10Z_117	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37287.1	001636	Cluster1145_1clades	99	pp2_053	Vibriophage phi-pp2	GCA_002630725.1
AAQ64154.1	001637	Cluster1146_1clades	102	KVP40.0083	Vibrio phage KVP40	GCA_000843785.1
QIW90478.1	001637	Cluster1146_1clades	89	GCAPEGMB_00131	Vibrio phage V07	GCA_012361095.1
QIW90951.1	001637	Cluster1146_1clades	89	COHAPHLL_00088	Vibrio phage V09	GCA_012361135.1
QHJ74266.1	001637	Cluster1146_1clades	102	VH12019_00347	Vibrio phage VH1_2019	GCA_009931825.1
AGB07091.1	001637	Cluster1146_1clades	88	CF80_gp304	Vibrio phage VH7D	GCA_000914495.1
QBX06004.1	001637	Cluster1146_1clades	88	ValB1HC_050	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61018.1	001637	Cluster1146_1clades	88	AVU32_gp177	Vibrio phage ValKK3	GCA_001501635.1
AGN30133.1	001637	Cluster1146_1clades	100	VPFG_00131	Vibrio phage nt-1	GCA_000910195.2
ALP47244.1	001637	Cluster1146_1clades	88	phiGrn1_0198	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47625.1	001637	Cluster1146_1clades	88	phiST2_0331	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54628.1	001637	Cluster1146_1clades	88	vBValMR10Z_87	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37315.1	001637	Cluster1146_1clades	102	pp2_082	Vibriophage phi-pp2	GCA_002630725.1
AAQ64363.1	001638	Cluster1147_1clades	102	KVP40.0293	Vibrio phage KVP40	GCA_000843785.1
QIW90677.1	001638	Cluster1147_1clades	102	GCAPEGMB_00330	Vibrio phage V07	GCA_012361095.1
QIW91121.1	001638	Cluster1147_1clades	102	COHAPHLL_00285	Vibrio phage V09	GCA_012361135.1
QHJ74472.1	001638	Cluster1147_1clades	102	VH12019_00145	Vibrio phage VH1_2019	GCA_009931825.1
AGB06966.1	001638	Cluster1147_1clades	102	CF80_gp179	Vibrio phage VH7D	GCA_000914495.1
QBX06179.1	001638	Cluster1147_1clades	102	ValB1HC_226	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61196.1	001638	Cluster1147_1clades	102	AVU32_gp355	Vibrio phage ValKK3	GCA_001501635.1
AGN30339.1	001638	Cluster1147_1clades	102	VPFG_00342	Vibrio phage nt-1	GCA_000910195.2
ALP47195.1	001638	Cluster1147_1clades	102	phiGrn1_0026	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47585.1	001638	Cluster1147_1clades	102	phiST2_0157	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54804.1	001638	Cluster1147_1clades	102	vBValMR10Z_264	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37524.1	001638	Cluster1147_1clades	102	pp2_291	Vibriophage phi-pp2	GCA_002630725.1
ARB13852.1	001639	Cluster1148_1clades	101	Ccr10_gp322	Caulobacter phage Ccr10	GCA_002619445.1
ARB14197.1	001639	Cluster1148_1clades	101	Ccr2_gp321	Caulobacter phage Ccr2	GCA_002619465.1
ARB14891.1	001639	Cluster1148_1clades	101	Ccr29_gp335	Caulobacter phage Ccr29	GCA_002619485.1
ARB15229.1	001639	Cluster1148_1clades	101	Ccr32_gp311	Caulobacter phage Ccr32	GCA_002619505.1
ARB15563.1	001639	Cluster1148_1clades	101	Ccr34_gp321	Caulobacter phage Ccr34	GCA_002619525.1
ARB14537.1	001639	Cluster1148_1clades	101	Ccr5_gp317	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68521.1	001639	Cluster1148_1clades	97	CcrBL10_gp317	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87848.1	001639	Cluster1148_1clades	101	CcrKarma_gp331	Caulobacter virus Karma	GCA_000901575.1
AFU87496.1	001639	Cluster1148_1clades	101	CcrMagneto_gp326	Caulobacter virus Magneto	GCA_000903095.1
AFU86811.1	001639	Cluster1148_1clades	98	CcrRogue_gp329	Caulobacter virus Rogue	GCA_000900555.1
AFU88641.1	001639	Cluster1148_1clades	101	CcrSwift_gp323	Caulobacter virus Swift	GCA_000899655.1
AFU87148.1	001639	Cluster1148_1clades	101	CbK_gp316	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64183.1	001640	Cluster1149_1clades	100	KVP40.0112	Vibrio phage KVP40	GCA_000843785.1
QIW90506.1	001640	Cluster1149_1clades	100	GCAPEGMB_00159	Vibrio phage V07	GCA_012361095.1
QIW90923.1	001640	Cluster1149_1clades	100	COHAPHLL_00060	Vibrio phage V09	GCA_012361135.1
QHJ74295.1	001640	Cluster1149_1clades	100	VH12019_00376	Vibrio phage VH1_2019	GCA_009931825.1
AGB06788.1	001640	Cluster1149_1clades	101	CF80_gp001	Vibrio phage VH7D	GCA_000914495.1
QBX05978.1	001640	Cluster1149_1clades	101	ValB1HC_024	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60991.1	001640	Cluster1149_1clades	101	AVU32_gp150	Vibrio phage ValKK3	GCA_001501635.1
AGN30163.1	001640	Cluster1149_1clades	101	VPFG_00161	Vibrio phage nt-1	GCA_000910195.2
ALP47221.1	001640	Cluster1149_1clades	94	phiGrn1_0222	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47587.1	001640	Cluster1149_1clades	101	phiST2_0357	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54603.1	001640	Cluster1149_1clades	94	vBValMR10Z_62	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37341.1	001640	Cluster1149_1clades	100	pp2_108	Vibriophage phi-pp2	GCA_002630725.1
AAQ64289.1	001641	Cluster1150_1clades	100	KVP40.0220	Vibrio phage KVP40	GCA_000843785.1
QIW90605.1	001641	Cluster1150_1clades	89	GCAPEGMB_00258	Vibrio phage V07	GCA_012361095.1
QIW91194.1	001641	Cluster1150_1clades	89	COHAPHLL_00358	Vibrio phage V09	GCA_012361135.1
QHJ74401.1	001641	Cluster1150_1clades	89	VH12019_00074	Vibrio phage VH1_2019	GCA_009931825.1
AGB06907.1	001641	Cluster1150_1clades	89	CF80_gp120	Vibrio phage VH7D	GCA_000914495.1
QBX06239.1	001641	Cluster1150_1clades	89	ValB1HC_286	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60865.1	001641	Cluster1150_1clades	89	AVU32_gp024	Vibrio phage ValKK3	GCA_001501635.1
AGN30280.1	001641	Cluster1150_1clades	91	VPFG_00281	Vibrio phage nt-1	GCA_000910195.2
ALP47240.1	001641	Cluster1150_1clades	89	phiGrn1_0343	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47623.1	001641	Cluster1150_1clades	89	phiST2_0098	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54864.1	001641	Cluster1150_1clades	89	vBValMR10Z_324	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37450.1	001641	Cluster1150_1clades	89	pp2_217	Vibriophage phi-pp2	GCA_002630725.1
ARB13700.1	001642	Cluster1151_1clades	100	Ccr10_gp170c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14045.1	001642	Cluster1151_1clades	100	Ccr2_gp169c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14732.1	001642	Cluster1151_1clades	100	Ccr29_gp176	Caulobacter phage Ccr29	GCA_002619485.1
ARB15087.1	001642	Cluster1151_1clades	100	Ccr32_gp169	Caulobacter phage Ccr32	GCA_002619505.1
ARB15421.1	001642	Cluster1151_1clades	100	Ccr34_gp179	Caulobacter phage Ccr34	GCA_002619525.1
ARB14388.1	001642	Cluster1151_1clades	100	Ccr5_gp168c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68370.1	001642	Cluster1151_1clades	100	CcrBL10_gp166c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87693.1	001642	Cluster1151_1clades	100	CcrKarma_gp176	Caulobacter virus Karma	GCA_000901575.1
AFU87342.1	001642	Cluster1151_1clades	100	CcrMagneto_gp172	Caulobacter virus Magneto	GCA_000903095.1
AFU86653.1	001642	Cluster1151_1clades	100	CcrRogue_gp171	Caulobacter virus Rogue	GCA_000900555.1
AFU88489.1	001642	Cluster1151_1clades	100	CcrSwift_gp171	Caulobacter virus Swift	GCA_000899655.1
AFU87006.1	001642	Cluster1151_1clades	100	CbK_gp174	Caulobacter virus phiCbK	GCA_000900535.1
AGH07458.1	001643	Cluster1152_1clades	100	CYVG_00014	Cyanophage S-SSM6a	GCA_002710385.1
AAX44510.1	001643	Cluster1152_1clades	61	PSSM2_132	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12456.1	001643	Cluster1152_1clades	61	PRTG_00309	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93629.1	001643	Cluster1152_1clades	81	AVU42_gp105	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30613.1	001643	Cluster1152_1clades	75	Syn7803US37_136	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54885.1	001643	Cluster1152_1clades	50	b23_0271	Synechococcus phage B23	GCA_009745195.1
QGT54520.1	001643	Cluster1152_1clades	50	b3_0278	Synechococcus phage B3	GCA_009745215.1
ASR76174.1	001643	Cluster1152_1clades	66	PBI_BELLAMY_129	Synechococcus phage Bellamy	GCA_002627525.1
QCW22884.1	001643	Cluster1152_1clades	68	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50473.1	001643	Cluster1152_1clades	72	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70578.1	001643	Cluster1152_1clades	58	HOU04_gp179	Synechococcus phage S-T4	GCA_003443335.1
QJT70116.1	001643	Cluster1152_1clades	71	SynMITS9220M01_103	Synechococcus phage SynMITS9220M01	GCA_013187275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAQ64188.1	001644	Cluster1153_1clades	99	KVP40.0117	Vibrio phage KVP40	GCA_000843785.1
QIW90831.1	001644	Cluster1153_1clades	99	GCAPEGMB_00516	Vibrio phage V07	GCA_012361095.1
QIW90918.1	001644	Cluster1153_1clades	99	COHAPHLL_00055	Vibrio phage V09	GCA_012361135.1
QHJ74300.1	001644	Cluster1153_1clades	99	VH12019_00381	Vibrio phage VH1_2019	GCA_009931825.1
AGB06794.1	001644	Cluster1153_1clades	99	CF80_gp007	Vibrio phage VH7D	GCA_000914495.1
QBX05972.1	001644	Cluster1153_1clades	99	ValB1HC_018	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60984.1	001644	Cluster1153_1clades	99	AVU32_gp143	Vibrio phage ValKK3	GCA_001501635.1
AGN30168.1	001644	Cluster1153_1clades	99	VPFG_00166	Vibrio phage nt-1	GCA_000910195.2
ALP47207.1	001644	Cluster1153_1clades	99	phiGrn1_0229	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47595.1	001644	Cluster1153_1clades	99	phiST2_0364	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54597.1	001644	Cluster1153_1clades	99	vBValMR10Z_56	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37347.1	001644	Cluster1153_1clades	99	pp2_114	Vibriophage phi-pp2	GCA_002630725.1
AAQ64357.1	001645	Cluster1154_1clades	99	KVP40.0287	Vibrio phage KVP40	GCA_000843785.1
QIW90671.1	001645	Cluster1154_1clades	99	GCAPEGMB_00324	Vibrio phage V07	GCA_012361095.1
QIW91127.1	001645	Cluster1154_1clades	99	COHAPHLL_00291	Vibrio phage V09	GCA_012361135.1
QHJ74466.1	001645	Cluster1154_1clades	99	VH12019_00139	Vibrio phage VH1_2019	GCA_009931825.1
AGB06960.1	001645	Cluster1154_1clades	89	CF80_gp173	Vibrio phage VH7D	GCA_000914495.1
QBX06185.1	001645	Cluster1154_1clades	99	ValB1HC_232	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61202.1	001645	Cluster1154_1clades	99	AVU32_gp361	Vibrio phage ValKK3	GCA_001501635.1
AGN30333.1	001645	Cluster1154_1clades	99	VPFG_00336	Vibrio phage nt-1	GCA_000910195.2
ALP47332.1	001645	Cluster1154_1clades	43	phiGrn1_0020	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47715.1	001645	Cluster1154_1clades	43	phiST2_0151	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54810.1	001645	Cluster1154_1clades	99	vBValMR10Z_270	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37518.1	001645	Cluster1154_1clades	99	pp2_285	Vibriophage phi-pp2	GCA_002630725.1
ARB13753.1	001646	Cluster1155_1clades	93	Ccr10_gp223c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14098.1	001646	Cluster1155_1clades	93	Ccr2_gp222c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14787.1	001646	Cluster1155_1clades	93	Ccr29_gp231	Caulobacter phage Ccr29	GCA_002619485.1
ARB15131.1	001646	Cluster1155_1clades	93	Ccr32_gp213	Caulobacter phage Ccr32	GCA_002619505.1
ARB15465.1	001646	Cluster1155_1clades	93	Ccr34_gp223	Caulobacter phage Ccr34	GCA_002619525.1
ARB14440.1	001646	Cluster1155_1clades	93	Ccr5_gp220c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68420.1	001646	Cluster1155_1clades	99	CcrBL10_gp216c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87747.1	001646	Cluster1155_1clades	93	CcrKarma_gp230	Caulobacter virus Karma	GCA_000901575.1
AFU87395.1	001646	Cluster1155_1clades	93	CcrMagneto_gp225	Caulobacter virus Magneto	GCA_000903095.1
AFU86706.1	001646	Cluster1155_1clades	99	CcrRogue_gp224	Caulobacter virus Rogue	GCA_000900555.1
AFU88543.1	001646	Cluster1155_1clades	93	CcrSwift_gp225	Caulobacter virus Swift	GCA_000899655.1
AFU87050.1	001646	Cluster1155_1clades	93	CbK_gp218	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64107.1	001647	Cluster1156_1clades	98	KVP40.0036	Vibrio phage KVP40	GCA_000843785.1
QIW90430.1	001647	Cluster1156_1clades	98	GCAPEGMB_00083	Vibrio phage V07	GCA_012361095.1
QIW90999.1	001647	Cluster1156_1clades	98	COHAPHLL_00136	Vibrio phage V09	GCA_012361135.1
QHJ74219.1	001647	Cluster1156_1clades	98	VH12019_00300	Vibrio phage VH1_2019	GCA_009931825.1
AGB07043.1	001647	Cluster1156_1clades	98	CF80_gp256	Vibrio phage VH7D	GCA_000914495.1
QBX06053.1	001647	Cluster1156_1clades	98	ValB1HC_099	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61066.1	001647	Cluster1156_1clades	97	AVU32_gp225	Vibrio phage ValKK3	GCA_001501635.1
AGN30085.1	001647	Cluster1156_1clades	98	VPFG_00083	Vibrio phage nt-1	GCA_000910195.2
ALP47211.1	001647	Cluster1156_1clades	98	phiGrn1_0151	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47600.1	001647	Cluster1156_1clades	98	phiST2_0281	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54679.1	001647	Cluster1156_1clades	98	vBValMR10Z_138	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37269.1	001647	Cluster1156_1clades	98	pp2_035	Vibriophage phi-pp2	GCA_002630725.1
ARB13774.1	001648	Cluster1157_1clades	98	Ccr10_gp244	Caulobacter phage Ccr10	GCA_002619445.1
ARB14119.1	001648	Cluster1157_1clades	98	Ccr2_gp243	Caulobacter phage Ccr2	GCA_002619465.1
ARB14813.1	001648	Cluster1157_1clades	98	Ccr29_gp257	Caulobacter phage Ccr29	GCA_002619485.1
ARB15153.1	001648	Cluster1157_1clades	98	Ccr32_gp235	Caulobacter phage Ccr32	GCA_002619505.1
ARB15487.1	001648	Cluster1157_1clades	98	Ccr34_gp245	Caulobacter phage Ccr34	GCA_002619525.1
ARB14461.1	001648	Cluster1157_1clades	98	Ccr5_gp241	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68439.1	001648	Cluster1157_1clades	97	CcrBL10_gp235	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87769.1	001648	Cluster1157_1clades	98	CcrKarma_gp252	Caulobacter virus Karma	GCA_000901575.1
AFU87416.1	001648	Cluster1157_1clades	98	CcrMagneto_gp246	Caulobacter virus Magneto	GCA_000903095.1
AFU86725.1	001648	Cluster1157_1clades	98	CcrRogue_gp243	Caulobacter virus Rogue	GCA_000900555.1
AFU88564.1	001648	Cluster1157_1clades	98	CcrSwift_gp246	Caulobacter virus Swift	GCA_000899655.1
AFU87072.1	001648	Cluster1157_1clades	98	CbK_gp240	Caulobacter virus phiCbK	GCA_000900535.1
ARB13553.1	001649	Cluster1158_1clades	90	Ccr10_gp025	Caulobacter phage Ccr10	GCA_002619445.1
ARB13899.1	001649	Cluster1158_1clades	90	Ccr2_gp024	Caulobacter phage Ccr2	GCA_002619465.1
ARB14588.1	001649	Cluster1158_1clades	90	Ccr29_gp031	Caulobacter phage Ccr29	GCA_002619485.1
ARB14943.1	001649	Cluster1158_1clades	90	Ccr32_gp024	Caulobacter phage Ccr32	GCA_002619505.1
ARB15274.1	001649	Cluster1158_1clades	90	Ccr34_gp025	Caulobacter phage Ccr34	GCA_002619525.1
ARB14242.1	001649	Cluster1158_1clades	92	Ccr5_gp024	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68224.1	001649	Cluster1158_1clades	93	CcrBL10_gp020	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87541.1	001649	Cluster1158_1clades	98	CcrKarma_gp024	Caulobacter virus Karma	GCA_000901575.1
AFU87193.1	001649	Cluster1158_1clades	90	CcrMagneto_gp023	Caulobacter virus Magneto	GCA_000903095.1
AFU86506.1	001649	Cluster1158_1clades	92	CcrRogue_gp024	Caulobacter virus Rogue	GCA_000900555.1
AFU88340.1	001649	Cluster1158_1clades	90	CcrSwift_gp022	Caulobacter virus Swift	GCA_000899655.1
AFU86856.1	001649	Cluster1158_1clades	90	CbK_gp024	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64185.1	001650	Cluster1159_1clades	97	KVP40.0114	Vibrio phage KVP40	GCA_000843785.1
QIW90508.1	001650	Cluster1159_1clades	97	GCAPEGMB_00161	Vibrio phage V07	GCA_012361095.1
QIW90921.1	001650	Cluster1159_1clades	97	COHAPHLL_00058	Vibrio phage V09	GCA_012361135.1
QHJ74297.1	001650	Cluster1159_1clades	97	VH12019_00378	Vibrio phage VH1_2019	GCA_009931825.1
AGB06790.1	001650	Cluster1159_1clades	97	CF80_gp003	Vibrio phage VH7D	GCA_000914495.1
QBX05976.1	001650	Cluster1159_1clades	97	ValB1HC_022	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60989.1	001650	Cluster1159_1clades	97	AVU32_gp148	Vibrio phage ValKK3	GCA_001501635.1
AGN30165.1	001650	Cluster1159_1clades	97	VPFG_00163	Vibrio phage nt-1	GCA_000910195.2
ALP47214.1	001650	Cluster1159_1clades	97	phiGrn1_0224	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47603.1	001650	Cluster1159_1clades	97	phiST2_0359	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54601.1	001650	Cluster1159_1clades	85	vBValMR10Z_60	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37343.1	001650	Cluster1159_1clades	97	pp2_110	Vibriophage phi-pp2	GCA_002630725.1
AAQ64338.1	001651	Cluster1160_1clades	86	KVP40.0269	Vibrio phage KVP40	GCA_000843785.1
QIW90653.1	001651	Cluster1160_1clades	86	GCAPEGMB_00306	Vibrio phage V07	GCA_012361095.1
QIW91146.1	001651	Cluster1160_1clades	86	COHAPHLL_00310	Vibrio phage V09	GCA_012361135.1
QHJ74448.1	001651	Cluster1160_1clades	86	VH12019_00121	Vibrio phage VH1_2019	GCA_009931825.1
AGB06944.1	001651	Cluster1160_1clades	86	CF80_gp157	Vibrio phage VH7D	GCA_000914495.1
QBX06202.1	001651	Cluster1160_1clades	86	ValB1HC_249	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61219.1	001651	Cluster1160_1clades	86	AVU32_gp378	Vibrio phage ValKK3	GCA_001501635.1
AGN30313.2	001651	Cluster1160_1clades	97	VPFG_00315	Vibrio phage nt-1	GCA_000910195.2
ALP47247.1	001651	Cluster1160_1clades	86	phiGrn1_0003	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47630.1	001651	Cluster1160_1clades	86	phiST2_0135	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54827.1	001651	Cluster1160_1clades	86	vBValMR10Z_287	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37498.1	001651	Cluster1160_1clades	86	pp2_265	Vibriophage phi-pp2	GCA_002630725.1
AAQ64270.1	001652	LPD20	96	KVP40.0201	Vibrio phage KVP40	GCA_000843785.1
QIW90587.1	001652	LPD20	96	GCAPEGMB_00240	Vibrio phage V07	GCA_012361095.1
QIW91212.1	001652	LPD20	96	COHAPHLL_00376	Vibrio phage V09	GCA_012361135.1
QHJ74384.1	001652	LPD20	96	VH12019_00057	Vibrio phage VH1_2019	GCA_009931825.1
AGB06888.1	001652	LPD20	96	CF80_gp101	Vibrio phage VH7D	GCA_000914495.1
QBX06258.1	001652	LPD20	96	ValB1HC_305	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60884.1	001652	LPD20	96	AVU32_gp043	Vibrio phage ValKK3	GCA_001501635.1
AGN30261.1	001652	LPD20	96	VPFG_00262	Vibrio phage nt-1	GCA_000910195.2
ALP47216.1	001652	LPD20	96	phiGrn1_0326	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47607.1	001652	LPD20	96	phiST2_0081	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54885.1	001652	LPD20	96	vBValMR10Z_345	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37431.1	001652	LPD20	96	pp2_198	Vibriophage phi-pp2	GCA_002630725.1
AAQ64232.1	001653	Cluster1162_1clades	95	KVP40.0163	Vibrio phage KVP40	GCA_000843785.1
QIW90546.1	001653	Cluster1162_1clades	91	GCAPEGMB_00199	Vibrio phage V07	GCA_012361095.1
QIW90876.1	001653	Cluster1162_1clades	91	COHAPHLL_00013	Vibrio phage V09	GCA_012361135.1
QHJ74344.1	001653	Cluster1162_1clades	91	VH12019_00017	Vibrio phage VH1_2019	GCA_009931825.1
AGB06837.1	001653	Cluster1162_1clades	90	CF80_gp050	Vibrio phage VH7D	GCA_000914495.1
QBX06309.1	001653	Cluster1162_1clades	91	ValB1HC_356	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60940.1	001653	Cluster1162_1clades	90	AVU32_gp099	Vibrio phage ValKK3	GCA_001501635.1
AGN30210.1	001653	Cluster1162_1clades	90	VPFG_00210	Vibrio phage nt-1	GCA_000910195.2
ALP47234.1	001653	Cluster1162_1clades	90	phiGrn1_0274	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47619.1	001653	Cluster1162_1clades	90	phiST2_0033	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54552.1	001653	Cluster1162_1clades	91	vBValMR10Z_11	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37391.1	001653	Cluster1162_1clades	91	pp2_158	Vibriophage phi-pp2	GCA_002630725.1
ARB13709.1	001654	Cluster1163_1clades	95	Ccr10_gp179c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14054.1	001654	Cluster1163_1clades	95	Ccr2_gp178c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14741.1	001654	Cluster1163_1clades	95	Ccr29_gp185	Caulobacter phage Ccr29	GCA_002619485.1
ARB15096.1	001654	Cluster1163_1clades	95	Ccr32_gp178	Caulobacter phage Ccr32	GCA_002619505.1
ARB15430.1	001654	Cluster1163_1clades	95	Ccr34_gp188	Caulobacter phage Ccr34	GCA_002619525.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB14397.1	001654	Cluster1163_1clades	95	Ccr5_gp177c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68379.1	001654	Cluster1163_1clades	94	CcrBL10_gp175c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87702.1	001654	Cluster1163_1clades	95	CcrKarma_gp185	Caulobacter virus Karma	GCA_000901575.1
AFU87351.1	001654	Cluster1163_1clades	95	CcrMagneto_gp181	Caulobacter virus Magneto	GCA_000903095.1
AFU86662.1	001654	Cluster1163_1clades	94	CcrRogue_gp180	Caulobacter virus Rogue	GCA_000900555.1
AFU88498.1	001654	Cluster1163_1clades	95	CcrSwift_gp180	Caulobacter virus Swift	GCA_000899655.1
AFU87015.1	001654	Cluster1163_1clades	95	CbK_gp183	Caulobacter virus phiCbK	GCA_000900535.1
ARB13558.1	001655	Cluster1164_1clades	89	Ccr10_gp030	Caulobacter phage Ccr10	GCA_002619445.1
ARB13904.1	001655	Cluster1164_1clades	89	Ccr2_gp029	Caulobacter phage Ccr2	GCA_002619465.1
ARB14593.1	001655	Cluster1164_1clades	89	Ccr29_gp036	Caulobacter phage Ccr29	GCA_002619485.1
ARB14948.1	001655	Cluster1164_1clades	89	Ccr32_gp029	Caulobacter phage Ccr32	GCA_002619505.1
ARB15279.1	001655	Cluster1164_1clades	89	Ccr34_gp030	Caulobacter phage Ccr34	GCA_002619525.1
ARB14247.1	001655	Cluster1164_1clades	89	Ccr5_gp029	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68231.1	001655	Cluster1164_1clades	84	CcrBL10_gp027	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87547.1	001655	Cluster1164_1clades	89	CcrKarma_gp030	Caulobacter virus Karma	GCA_000901575.1
AFU87198.1	001655	Cluster1164_1clades	89	CcrMagneto_gp028	Caulobacter virus Magneto	GCA_000903095.1
AFU86513.1	001655	Cluster1164_1clades	94	CcrRogue_gp031	Caulobacter virus Rogue	GCA_000900555.1
AFU88344.1	001655	Cluster1164_1clades	89	CcrSwift_gp026	Caulobacter virus Swift	GCA_000899655.1
AFU86861.1	001655	Cluster1164_1clades	89	CbK_gp029	Caulobacter virus phiCbK	GCA_000900535.1
ARB13580.1	001656	Cluster1165_1clades	94	Ccr10_gp052	Caulobacter phage Ccr10	GCA_002619445.1
ARB13926.1	001656	Cluster1165_1clades	94	Ccr2_gp051	Caulobacter phage Ccr2	GCA_002619465.1
ARB14615.1	001656	Cluster1165_1clades	94	Ccr29_gp058	Caulobacter phage Ccr29	GCA_002619485.1
ARB14971.1	001656	Cluster1165_1clades	94	Ccr32_gp052	Caulobacter phage Ccr32	GCA_002619505.1
ARB15302.1	001656	Cluster1165_1clades	94	Ccr34_gp053	Caulobacter phage Ccr34	GCA_002619525.1
ARB14269.1	001656	Cluster1165_1clades	94	Ccr5_gp051	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68254.1	001656	Cluster1165_1clades	94	CcrBL10_gp050	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87570.1	001656	Cluster1165_1clades	94	CcrKarma_gp053	Caulobacter virus Karma	GCA_000901575.1
AFU87220.1	001656	Cluster1165_1clades	94	CcrMagneto_gp050	Caulobacter virus Magneto	GCA_000903095.1
AFU86536.1	001656	Cluster1165_1clades	94	CcrRogue_gp054	Caulobacter virus Rogue	GCA_000900555.1
AFU88368.1	001656	Cluster1165_1clades	94	CcrSwift_gp050	Caulobacter virus Swift	GCA_000899655.1
AFU86884.1	001656	Cluster1165_1clades	94	CbK_gp052	Caulobacter virus phiCbK	GCA_000900535.1
ARB13837.1	001657	Cluster1166_1clades	88	Ccr10_gp307	Caulobacter phage Ccr10	GCA_002619445.1
ARB14182.1	001657	Cluster1166_1clades	92	Ccr2_gp306	Caulobacter phage Ccr2	GCA_002619465.1
ARB14876.1	001657	Cluster1166_1clades	88	Ccr29_gp320	Caulobacter phage Ccr29	GCA_002619485.1
ARB15214.1	001657	Cluster1166_1clades	88	Ccr32_gp296	Caulobacter phage Ccr32	GCA_002619505.1
ARB15548.1	001657	Cluster1166_1clades	88	Ccr34_gp306	Caulobacter phage Ccr34	GCA_002619525.1
ARB14523.1	001657	Cluster1166_1clades	92	Ccr5_gp303	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68503.1	001657	Cluster1166_1clades	94	CcrBL10_gp299	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87834.1	001657	Cluster1166_1clades	92	CcrKarma_gp317	Caulobacter virus Karma	GCA_000901575.1
AFU87481.1	001657	Cluster1166_1clades	92	CcrMagneto_gp311	Caulobacter virus Magneto	GCA_000903095.1
AFU86791.1	001657	Cluster1166_1clades	94	CcrRogue_gp309	Caulobacter virus Rogue	GCA_000900555.1
AFU88626.1	001657	Cluster1166_1clades	92	CcrSwift_gp308	Caulobacter virus Swift	GCA_000899655.1
AFU87133.1	001657	Cluster1166_1clades	92	CbK_gp301	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64121.1	001658	Cluster1167_1clades	72	KVP40.0050	Vibrio phage KVP40	GCA_000843785.1
QIW90443.1	001658	Cluster1167_1clades	87	GCAPEGMB_00096	Vibrio phage V07	GCA_012361095.1
QIW90986.1	001658	Cluster1167_1clades	87	COHAPHLL_00123	Vibrio phage V09	GCA_012361135.1
QHJ74232.1	001658	Cluster1167_1clades	87	VH12019_00313	Vibrio phage VH1_2019	GCA_009931825.1
AGB07056.1	001658	Cluster1167_1clades	94	CF80_gp269	Vibrio phage VH7D	GCA_000914495.1
QBX06040.1	001658	Cluster1167_1clades	89	ValB1HC_086	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61054.1	001658	Cluster1167_1clades	89	AVU32_gp213	Vibrio phage ValKK3	GCA_001501635.1
AGN30099.2	001658	Cluster1167_1clades	86	VPFG_00097	Vibrio phage nt-1	GCA_000910195.2
ALP47237.1	001658	Cluster1167_1clades	89	phiGrn1_0163	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47629.1	001658	Cluster1167_1clades	87	phiST2_0294	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54665.1	001658	Cluster1167_1clades	89	vBValMR10Z_124	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37282.1	001658	Cluster1167_1clades	87	pp2_048	Vibriophage phi-pp2	GCA_002630725.1
AAQ64272.1	001659	Cluster1168_1clades	93	KVP40.0203	Vibrio phage KVP40	GCA_000843785.1
QIW90588.1	001659	Cluster1168_1clades	93	GCAPEGMB_00241	Vibrio phage V07	GCA_012361095.1
QIW91211.1	001659	Cluster1168_1clades	93	COHAPHLL_00375	Vibrio phage V09	GCA_012361135.1
QHJ74385.1	001659	Cluster1168_1clades	94	VH12019_00058	Vibrio phage VH1_2019	GCA_009931825.1
AGB06889.1	001659	Cluster1168_1clades	93	CF80_gp102	Vibrio phage VH7D	GCA_000914495.1
QBX06257.1	001659	Cluster1168_1clades	93	ValB1HC_304	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60883.1	001659	Cluster1168_1clades	93	AVU32_gp042	Vibrio phage ValKK3	GCA_001501635.1
AGN30262.1	001659	Cluster1168_1clades	93	VPFG_00263	Vibrio phage nt-1	GCA_000910195.2
ALP47225.1	001659	Cluster1168_1clades	93	phiGrn1_0327	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47613.1	001659	Cluster1168_1clades	93	phiST2_0082	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54884.1	001659	Cluster1168_1clades	93	vBValMR10Z_344	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37432.1	001659	Cluster1168_1clades	93	pp2_199	Vibriophage phi-pp2	GCA_002630725.1
AAQ64179.1	001660	Cluster1169_1clades	93	KVP40.0108	Vibrio phage KVP40	GCA_000843785.1
QIW90502.1	001660	Cluster1169_1clades	93	GCAPEGMB_00155	Vibrio phage V07	GCA_012361095.1
QIW90927.1	001660	Cluster1169_1clades	93	COHAPHLL_00064	Vibrio phage V09	GCA_012361135.1
QHJ74290.1	001660	Cluster1169_1clades	93	VH12019_00371	Vibrio phage VH1_2019	GCA_009931825.1
AGB07113.1	001660	Cluster1169_1clades	93	CF80_gp326	Vibrio phage VH7D	GCA_000914495.1
QBX05981.1	001660	Cluster1169_1clades	93	ValB1HC_027	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60994.1	001660	Cluster1169_1clades	93	AVU32_gp153	Vibrio phage ValKK3	GCA_001501635.1
AGN30157.1	001660	Cluster1169_1clades	92	VPFG_00155	Vibrio phage nt-1	GCA_000910195.2
ALP47224.1	001660	Cluster1169_1clades	93	phiGrn1_0219	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47612.1	001660	Cluster1169_1clades	93	phiST2_0354	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54606.1	001660	Cluster1169_1clades	93	vBValMR10Z_65	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37337.1	001660	Cluster1169_1clades	93	pp2_104	Vibriophage phi-pp2	GCA_002630725.1
ARB13839.1	001661	Cluster1170_1clades	88	Ccr10_gp309	Caulobacter phage Ccr10	GCA_002619445.1
ARB14184.1	001661	Cluster1170_1clades	88	Ccr2_gp308	Caulobacter phage Ccr2	GCA_002619465.1
ARB14878.1	001661	Cluster1170_1clades	88	Ccr29_gp322	Caulobacter phage Ccr29	GCA_002619485.1
ARB15216.1	001661	Cluster1170_1clades	88	Ccr32_gp298	Caulobacter phage Ccr32	GCA_002619505.1
ARB15550.1	001661	Cluster1170_1clades	88	Ccr34_gp308	Caulobacter phage Ccr34	GCA_002619525.1
ARB14525.1	001661	Cluster1170_1clades	88	Ccr5_gp305	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68505.1	001661	Cluster1170_1clades	47	CcrBL10_gp301	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87836.1	001661	Cluster1170_1clades	88	CcrKarma_gp319	Caulobacter virus Karma	GCA_000901575.1
AFU87483.1	001661	Cluster1170_1clades	88	CcrMagneto_gp313	Caulobacter virus Magneto	GCA_000903095.1
AFU86793.1	001661	Cluster1170_1clades	93	CcrRogue_gp311	Caulobacter virus Rogue	GCA_000900555.1
AFU88628.1	001661	Cluster1170_1clades	88	CcrSwift_gp310	Caulobacter virus Swift	GCA_000899655.1
AFU87135.1	001661	Cluster1170_1clades	88	CbK_gp303	Caulobacter virus phiCbK	GCA_000900535.1
ARB13683.1	001662	Cluster1171_1clades	87	Ccr10_gp153c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14028.1	001662	Cluster1171_1clades	70	Ccr2_gp152c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14715.1	001662	Cluster1171_1clades	87	Ccr29_gp159	Caulobacter phage Ccr29	GCA_002619485.1
ARB15070.1	001662	Cluster1171_1clades	87	Ccr32_gp152	Caulobacter phage Ccr32	GCA_002619505.1
ARB15404.1	001662	Cluster1171_1clades	87	Ccr34_gp162	Caulobacter phage Ccr34	GCA_002619525.1
ARB14371.1	001662	Cluster1171_1clades	87	Ccr5_gp151c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68352.1	001662	Cluster1171_1clades	85	CcrBL10_gp148c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87676.1	001662	Cluster1171_1clades	87	CcrKarma_gp159	Caulobacter virus Karma	GCA_000901575.1
AFU87325.1	001662	Cluster1171_1clades	87	CcrMagneto_gp155	Caulobacter virus Magneto	GCA_000903095.1
AFU86636.1	001662	Cluster1171_1clades	92	CcrRogue_gp154	Caulobacter virus Rogue	GCA_000900555.1
AFU88472.1	001662	Cluster1171_1clades	87	CcrSwift_gp154	Caulobacter virus Swift	GCA_000899655.1
AFU86989.1	001662	Cluster1171_1clades	87	CbK_gp157	Caulobacter virus phiCbK	GCA_000900535.1
ARB13607.1	001663	Cluster1172_1clades	88	Ccr10_gp079	Caulobacter phage Ccr10	GCA_002619445.1
ARB13953.1	001663	Cluster1172_1clades	88	Ccr2_gp078	Caulobacter phage Ccr2	GCA_002619465.1
ARB14644.1	001663	Cluster1172_1clades	88	Ccr29_gp087	Caulobacter phage Ccr29	GCA_002619485.1
ARB14999.1	001663	Cluster1172_1clades	92	Ccr32_gp080	Caulobacter phage Ccr32	GCA_002619505.1
ARB15330.1	001663	Cluster1172_1clades	92	Ccr34_gp086	Caulobacter phage Ccr34	GCA_002619525.1
ARB14296.1	001663	Cluster1172_1clades	88	Ccr5_gp078	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68281.1	001663	Cluster1172_1clades	89	CcrBL10_gp077	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87597.1	001663	Cluster1172_1clades	88	CcrKarma_gp080	Caulobacter virus Karma	GCA_000901575.1
AFU87247.1	001663	Cluster1172_1clades	88	CcrMagneto_gp077	Caulobacter virus Magneto	GCA_000903095.1
AFU86563.1	001663	Cluster1172_1clades	87	CcrRogue_gp081	Caulobacter virus Rogue	GCA_000900555.1
AFU88395.1	001663	Cluster1172_1clades	88	CcrSwift_gp077	Caulobacter virus Swift	GCA_000899655.1
AFU86911.1	001663	Cluster1172_1clades	92	CbK_gp079	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64197.1	001664	WYL	91	KVP40.0126	Vibrio phage KVP40	GCA_000843785.1
QIW90513.1	001664	WYL	91	GCAPEGMB_00166	Vibrio phage V07	GCA_012361095.1
QIW90909.1	001664	WYL	91	COHAPHLL_00046	Vibrio phage V09	GCA_012361135.1
QHJ74309.1	001664	WYL	91	VH12019_00390	Vibrio phage VH1_2019	GCA_009931825.1
AGB06803.1	001664	WYL	91	CF80_gp016	Vibrio phage VH7D	GCA_000914495.1
QBX05963.1	001664	WYL	91	ValB1HC_009	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60975.1	001664	WYL	91	AVU32_gp134	Vibrio phage ValKK3	GCA_001501635.1
AGN30176.1	001664	WYL	91	VPFG_00174	Vibrio phage nt-1	GCA_000910195.2
ALP47230.1	001664	WYL	91	phiGrn1_0238	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47616.1	001664	WYL	91	phiST2_0376	Vibrio phage phi-ST2	GCA_002757135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNJ54588.1	001664	WYL	91	vBValMR10Z_47	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37357.1	001664	WYL	91	pp2_124	Vibriophage phi-pp2	GCA_002630725.1
ARB13699.1	001665	SIG+TM	88	Ccr10_gp169c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14044.1	001665	SIG+TM	88	Ccr2_gp168c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14731.1	001665	SIG+TM	88	Ccr29_gp175	Caulobacter phage Ccr29	GCA_002619485.1
ARB15086.1	001665	SIG+TM	88	Ccr32_gp168	Caulobacter phage Ccr32	GCA_002619505.1
ARB15420.1	001665	SIG+TM	88	Ccr34_gp178	Caulobacter phage Ccr34	GCA_002619525.1
ARB14387.1	001665	SIG+TM	88	Ccr5_gp167c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68369.1	001665	SIG+TM	91	CcrBL10_gp165c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87692.1	001665	SIG+TM	88	CcrKarma_gp175	Caulobacter virus Karma	GCA_000901575.1
AFU87341.1	001665	SIG+TM	88	CcrMagneto_gp171	Caulobacter virus Magneto	GCA_000903095.1
AFU86652.1	001665	SIG+TM	91	CcrRogue_gp170	Caulobacter virus Rogue	GCA_000900555.1
AFU88488.1	001665	SIG+TM	88	CcrSwift_gp170	Caulobacter virus Swift	GCA_000899655.1
AFU87005.1	001665	SIG+TM	88	CbK_gp173	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64112.1	001666	Cluster1175_1clades	90	KVP40.0041	Vibrio phage KVP40	GCA_000843785.1
QIW90435.1	001666	Cluster1175_1clades	86	GCAPEGMB_00088	Vibrio phage V07	GCA_012361095.1
QIW90994.1	001666	Cluster1175_1clades	86	COHAPHLL_00131	Vibrio phage V09	GCA_012361135.1
QHJ74224.1	001666	Cluster1175_1clades	86	VH12019_00305	Vibrio phage VH1_2019	GCA_009931825.1
AGB07048.1	001666	Cluster1175_1clades	80	CF80_gp261	Vibrio phage VH7D	GCA_000914495.1
QBX06048.1	001666	Cluster1175_1clades	86	ValB1HC_094	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61062.1	001666	Cluster1175_1clades	86	AVU32_gp221	Vibrio phage ValKK3	GCA_001501635.1
AGN30091.2	001666	Cluster1175_1clades	80	VPFG_00089	Vibrio phage nt-1	GCA_000910195.2
ALP47248.1	001666	Cluster1175_1clades	86	phiGrn1_0155	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47643.1	001666	Cluster1175_1clades	80	phiST2_0286	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54674.1	001666	Cluster1175_1clades	86	vBValMR10Z_133	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37274.1	001666	Cluster1175_1clades	80	pp2_040	Vibriophage phi-pp2	GCA_002630725.1
AAQ64156.1	001667	Cluster1176_1clades	90	KVP40.0085	Vibrio phage KVP40	GCA_000843785.1
QIW90480.1	001667	Cluster1176_1clades	90	GCAPEGMB_00133	Vibrio phage V07	GCA_012361095.1
QIW90949.1	001667	Cluster1176_1clades	90	COHAPHLL_00086	Vibrio phage V09	GCA_012361135.1
QHJ74268.1	001667	Cluster1176_1clades	90	VH12019_00349	Vibrio phage VH1_2019	GCA_009931825.1
AGB07093.1	001667	Cluster1176_1clades	89	CF80_gp306	Vibrio phage VH7D	GCA_000914495.1
QBX06002.1	001667	Cluster1176_1clades	89	ValB1HC_048	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61016.1	001667	Cluster1176_1clades	89	AVU32_gp175	Vibrio phage ValKK3	GCA_001501635.1
AGN30135.1	001667	Cluster1176_1clades	88	VPFG_00133	Vibrio phage nt-1	GCA_000910195.2
ALP47269.1	001667	Cluster1176_1clades	79	phiGrn1_0200	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47648.1	001667	Cluster1176_1clades	79	phiST2_0333	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54626.1	001667	Cluster1176_1clades	89	vBValMR10Z_85	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37317.1	001667	Cluster1176_1clades	79	pp2_084	Vibriophage phi-pp2	GCA_002630725.1
AAQ64359.1	001668	Cluster1177_1clades	90	KVP40.0289	Vibrio phage KVP40	GCA_000843785.1
QIW90673.1	001668	Cluster1177_1clades	90	GCAPEGMB_00326	Vibrio phage V07	GCA_012361095.1
QIW91125.1	001668	Cluster1177_1clades	90	COHAPHLL_00289	Vibrio phage V09	GCA_012361135.1
QHJ74468.1	001668	Cluster1177_1clades	90	VH12019_00141	Vibrio phage VH1_2019	GCA_009931825.1
AGB06962.1	001668	Cluster1177_1clades	90	CF80_gp175	Vibrio phage VH7D	GCA_000914495.1
QBX06183.1	001668	Cluster1177_1clades	90	ValB1HC_230	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61200.1	001668	Cluster1177_1clades	90	AVU32_gp359	Vibrio phage ValKK3	GCA_001501635.1
AGN30335.1	001668	Cluster1177_1clades	90	VPFG_00338	Vibrio phage nt-1	GCA_000910195.2
ALP47231.1	001668	Cluster1177_1clades	90	phiGrn1_0022	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47618.1	001668	Cluster1177_1clades	90	phiST2_0153	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54808.1	001668	Cluster1177_1clades	90	vBValMR10Z_268	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37520.1	001668	Cluster1177_1clades	90	pp2_287	Vibriophage phi-pp2	GCA_002630725.1
AFC21456.1	001669	Cluster1178_1clades	90	GAP32_009	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14200.1	001669	Cluster1178_1clades	90	PBI_121Q_310	Escherichia phage 121Q	GCA_000926855.1
QAY00738.1	001669	Cluster1178_1clades	90	Ecwhy1_463	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34919.1	001669	Cluster1178_1clades	83	ACQ29_gp239	Escherichia phage PBECO4	GCA_001041035.1
BBM61873.1	001669	Cluster1178_1clades	90	EO157G_2840	Escherichia phage SP27	GCA_008033345.1
AXC37022.1	001669	Cluster1178_1clades	90	-	Escherichia phage UB	GCA_003341455.1
QBO61505.1	001669	Cluster1178_1clades	90	G17_00009	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62111.1	001669	Cluster1178_1clades	90	G17_00622	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14121.1	001669	Cluster1178_1clades	83	vBEcoMphAPEC6_gp498c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80183.1	001669	Cluster1178_1clades	90	PSLUR01_00206	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43574.1	001669	Cluster1178_1clades	90	CBB_562	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44125.1	001669	Cluster1178_1clades	90	CBB_9	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ARB13732.1	001670	PP-binding	85	Ccr10_gp202c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14077.1	001670	PP-binding	85	Ccr2_gp201c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14766.1	001670	PP-binding	85	Ccr29_gp210	Caulobacter phage Ccr29	GCA_002619485.1
ARB15110.1	001670	PP-binding	85	Ccr32_gp192	Caulobacter phage Ccr32	GCA_002619505.1
ARB15444.1	001670	PP-binding	85	Ccr34_gp202	Caulobacter phage Ccr34	GCA_002619525.1
ARB14419.1	001670	PP-binding	41	Ccr5_gp199c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68399.1	001670	PP-binding	90	CcrBL10_gp195c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87725.1	001670	PP-binding	85	CcrKarma_gp208	Caulobacter virus Karma	GCA_000901575.1
AFU87374.1	001670	PP-binding	85	CcrMagneto_gp204	Caulobacter virus Magneto	GCA_000903095.1
AFU86685.1	001670	PP-binding	77	CcrRogue_gp203	Caulobacter virus Rogue	GCA_000900555.1
AFU88521.1	001670	PP-binding	85	CcrSwift_gp203	Caulobacter virus Swift	GCA_000899655.1
AFU87029.1	001670	PP-binding	85	CbK_gp197	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64358.1	001671	Cluster1180_1clades	89	KVP40.0288	Vibrio phage KVP40	GCA_000843785.1
QIW90672.1	001671	Cluster1180_1clades	89	GCAPEGMB_00325	Vibrio phage V07	GCA_012361095.1
QIW91126.1	001671	Cluster1180_1clades	89	COHAPHLL_00290	Vibrio phage V09	GCA_012361135.1
QHJ74467.1	001671	Cluster1180_1clades	89	VH12019_00140	Vibrio phage VH1_2019	GCA_009931825.1
AGB06961.1	001671	Cluster1180_1clades	89	CF80_gp174	Vibrio phage VH7D	GCA_000914495.1
QBX06184.1	001671	Cluster1180_1clades	89	ValB1HC_231	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61201.1	001671	Cluster1180_1clades	89	AVU32_gp360	Vibrio phage ValKK3	GCA_001501635.1
AGN30334.1	001671	Cluster1180_1clades	89	VPFG_00337	Vibrio phage nt-1	GCA_000910195.2
ALP47236.1	001671	Cluster1180_1clades	89	phiGrn1_0021	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47622.1	001671	Cluster1180_1clades	89	phiST2_0152	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54809.1	001671	Cluster1180_1clades	89	vBValMR10Z_269	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37519.1	001671	Cluster1180_1clades	89	pp2_286	Vibriophage phi-pp2	GCA_002630725.1
ARB13737.1	001672	Cluster1181_1clades	89	Ccr10_gp207c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14082.1	001672	Cluster1181_1clades	89	Ccr2_gp206c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14771.1	001672	Cluster1181_1clades	89	Ccr29_gp215	Caulobacter phage Ccr29	GCA_002619485.1
ARB15115.1	001672	Cluster1181_1clades	89	Ccr32_gp197	Caulobacter phage Ccr32	GCA_002619505.1
ARB15449.1	001672	Cluster1181_1clades	89	Ccr34_gp207	Caulobacter phage Ccr34	GCA_002619525.1
ARB14424.1	001672	Cluster1181_1clades	89	Ccr5_gp204c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68404.1	001672	Cluster1181_1clades	89	CcrBL10_gp200c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87730.1	001672	Cluster1181_1clades	89	CcrKarma_gp213	Caulobacter virus Karma	GCA_000901575.1
AFU87379.1	001672	Cluster1181_1clades	89	CcrMagneto_gp209	Caulobacter virus Magneto	GCA_000903095.1
AFU86690.1	001672	Cluster1181_1clades	89	CcrRogue_gp208	Caulobacter virus Rogue	GCA_000900555.1
AFU88526.1	001672	Cluster1181_1clades	89	CcrSwift_gp208	Caulobacter virus Swift	GCA_000899655.1
AFU87034.1	001672	Cluster1181_1clades	89	CbK_gp202	Caulobacter virus phiCbK	GCA_000900535.1
ARB13750.1	001673	Cluster1182_1clades	89	Ccr10_gp220c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14095.1	001673	Cluster1182_1clades	89	Ccr2_gp219c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14784.1	001673	Cluster1182_1clades	89	Ccr29_gp228	Caulobacter phage Ccr29	GCA_002619485.1
ARB15128.1	001673	Cluster1182_1clades	89	Ccr32_gp210	Caulobacter phage Ccr32	GCA_002619505.1
ARB15462.1	001673	Cluster1182_1clades	89	Ccr34_gp220	Caulobacter phage Ccr34	GCA_002619525.1
ARB14437.1	001673	Cluster1182_1clades	89	Ccr5_gp217c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68417.1	001673	Cluster1182_1clades	85	CcrBL10_gp213c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87744.1	001673	Cluster1182_1clades	77	CcrKarma_gp227	Caulobacter virus Karma	GCA_000901575.1
AFU87392.1	001673	Cluster1182_1clades	89	CcrMagneto_gp222	Caulobacter virus Magneto	GCA_000903095.1
AFU86703.1	001673	Cluster1182_1clades	85	CcrRogue_gp221	Caulobacter virus Rogue	GCA_000900555.1
AFU88540.1	001673	Cluster1182_1clades	89	CcrSwift_gp222	Caulobacter virus Swift	GCA_000899655.1
AFU87047.1	001673	Cluster1182_1clades	89	CbK_gp215	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64119.1	001674	Cluster1183_1clades	88	KVP40.0048	Vibrio phage KVP40	GCA_000843785.1
QIW90441.1	001674	Cluster1183_1clades	88	GCAPEGMB_00094	Vibrio phage V07	GCA_012361095.1
QIW90988.1	001674	Cluster1183_1clades	88	COHAPHLL_00125	Vibrio phage V09	GCA_012361135.1
QHJ74230.1	001674	Cluster1183_1clades	88	VH12019_00311	Vibrio phage VH1_2019	GCA_009931825.1
AGB07054.1	001674	Cluster1183_1clades	76	CF80_gp267	Vibrio phage VH7D	GCA_000914495.1
QBX06042.1	001674	Cluster1183_1clades	88	ValB1HC_088	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61056.1	001674	Cluster1183_1clades	88	AVU32_gp215	Vibrio phage ValKK3	GCA_001501635.1
AGN30097.2	001674	Cluster1183_1clades	86	VPFG_00095	Vibrio phage nt-1	GCA_000910195.2
ALP47278.1	001674	Cluster1183_1clades	76	phiGrn1_0161	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47658.1	001674	Cluster1183_1clades	76	phiST2_0292	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54667.1	001674	Cluster1183_1clades	88	vBValMR10Z_126	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37280.1	001674	Cluster1183_1clades	88	pp2_046	Vibriophage phi-pp2	GCA_002630725.1
AAQ64283.1	001675	Cluster1184_1clades	88	KVP40.0214	Vibrio phage KVP40	GCA_000843785.1
QIW90599.1	001675	Cluster1184_1clades	88	GCAPEGMB_00252	Vibrio phage V07	GCA_012361095.1
QIW91200.1	001675	Cluster1184_1clades	88	COHAPHLL_00364	Vibrio phage V09	GCA_012361135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QHJ74395.1	001675	Cluster1184_1clades	88	VH12019_00068	Vibrio phage VH1_2019	GCA_009931825.1
AGB06901.1	001675	Cluster1184_1clades	88	CF80_gp114	Vibrio phage VH7D	GCA_000914495.1
QBX06245.1	001675	Cluster1184_1clades	88	ValB1HC_292	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60871.1	001675	Cluster1184_1clades	88	AVU32_gp030	Vibrio phage ValKK3	GCA_001501635.1
AGN30276.1	001675	Cluster1184_1clades	88	VPFG_00277	Vibrio phage nt-1	GCA_000910195.2
ALP47245.1	001675	Cluster1184_1clades	88	phiGrn1_0338	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47628.1	001675	Cluster1184_1clades	88	phiST2_0093	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54871.1	001675	Cluster1184_1clades	88	vBValMR10Z_331	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37444.1	001675	Cluster1184_1clades	88	pp2_211	Vibriophage phi-pp2	GCA_002630725.1
ARB13784.1	001676	Cluster1185_1clades	88	Ccr10_gp254	Caulobacter phage Ccr10	GCA_002619445.1
ARB14129.1	001676	Cluster1185_1clades	88	Ccr2_gp253	Caulobacter phage Ccr2	GCA_002619465.1
ARB14823.1	001676	Cluster1185_1clades	88	Ccr29_gp267	Caulobacter phage Ccr29	GCA_002619485.1
ARB15163.1	001676	Cluster1185_1clades	88	Ccr32_gp245	Caulobacter phage Ccr32	GCA_002619505.1
ARB15497.1	001676	Cluster1185_1clades	88	Ccr34_gp255	Caulobacter phage Ccr34	GCA_002619525.1
ARB14471.1	001676	Cluster1185_1clades	88	Ccr5_gp251	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68450.1	001676	Cluster1185_1clades	86	CcrBL10_gp246	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87780.1	001676	Cluster1185_1clades	88	CcrKarma_gp263	Caulobacter virus Karma	GCA_000901575.1
AFU87427.1	001676	Cluster1185_1clades	88	CcrMagneto_gp257	Caulobacter virus Magneto	GCA_000903095.1
AFU86737.1	001676	Cluster1185_1clades	86	CcrRogue_gp255	Caulobacter virus Rogue	GCA_000900555.1
AFU88574.1	001676	Cluster1185_1clades	88	CcrSwift_gp256	Caulobacter virus Swift	GCA_000899655.1
AFU87082.1	001676	Cluster1185_1clades	88	CbK_gp250	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64138.1	001677	Cluster1186_1clades	85	KVP40.0067	Vibrio phage KVP40	GCA_000843785.1
QIW90461.1	001677	Cluster1186_1clades	85	GCAPEGMB_00114	Vibrio phage V07	GCA_012361095.1
QIW90968.1	001677	Cluster1186_1clades	85	COHAPHLL_00105	Vibrio phage V09	GCA_012361135.1
QHJ74250.1	001677	Cluster1186_1clades	86	VH12019_00331	Vibrio phage VH1_2019	GCA_009931825.1
AGB07074.1	001677	Cluster1186_1clades	88	CF80_gp287	Vibrio phage VH7D	GCA_000914495.1
QBX06021.1	001677	Cluster1186_1clades	88	ValB1HC_067	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61035.1	001677	Cluster1186_1clades	88	AVU32_gp194	Vibrio phage ValKK3	GCA_001501635.1
AGN30116.1	001677	Cluster1186_1clades	87	VPFG_00114	Vibrio phage nt-1	GCA_000910195.2
ALP47243.1	001677	Cluster1186_1clades	88	phiGrn1_0182	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47632.1	001677	Cluster1186_1clades	85	phiST2_0313	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54646.1	001677	Cluster1186_1clades	88	vBValMR10Z_105	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37298.1	001677	Cluster1186_1clades	86	pp2_065	Vibriophage phi-pp2	GCA_002630725.1
ARB13530.1	001678	SIG+TM	78	Ccr10_gp345	Caulobacter phage Ccr10	GCA_002619445.1
ARB15585.1	001678	SIG+TM	87	Ccr34_gp003	Caulobacter phage Ccr34	GCA_002619525.1
AFU87519.1	001678	SIG+TM	82	CcrKarma_gp002	Caulobacter virus Karma	GCA_000901575.1
AFU87852.1	001678	SIG+TM	82	CcrKarma_gp335	Caulobacter virus Karma	GCA_000901575.1
AFU87172.1	001678	SIG+TM	82	CcrMagneto_gp002	Caulobacter virus Magneto	GCA_000903095.1
AFU87500.1	001678	SIG+TM	82	CcrMagneto_gp330	Caulobacter virus Magneto	GCA_000903095.1
AFU86484.1	001678	SIG+TM	82	CcrRogue_gp002	Caulobacter virus Rogue	GCA_000900555.1
AFU86815.1	001678	SIG+TM	82	CcrRogue_gp333	Caulobacter virus Rogue	GCA_000900555.1
AFU88320.1	001678	SIG+TM	82	CcrSwift_gp002	Caulobacter virus Swift	GCA_000899655.1
AFU88645.1	001678	SIG+TM	82	CcrSwift_gp327	Caulobacter virus Swift	GCA_000899655.1
AFU86834.1	001678	SIG+TM	87	CbK_gp002	Caulobacter virus phiCbK	GCA_000900535.1
AFU87152.1	001678	SIG+TM	87	CbK_gp320	Caulobacter virus phiCbK	GCA_000900535.1
ARB13575.1	001679	Cluster1188_1clades	85	Ccr10_gp047	Caulobacter phage Ccr10	GCA_002619445.1
ARB13921.1	001679	Cluster1188_1clades	85	Ccr2_gp046	Caulobacter phage Ccr2	GCA_002619465.1
ARB14610.1	001679	Cluster1188_1clades	85	Ccr29_gp053	Caulobacter phage Ccr29	GCA_002619485.1
ARB14966.1	001679	Cluster1188_1clades	85	Ccr32_gp047	Caulobacter phage Ccr32	GCA_002619505.1
ARB15297.1	001679	Cluster1188_1clades	85	Ccr34_gp048	Caulobacter phage Ccr34	GCA_002619525.1
ARB14264.1	001679	Cluster1188_1clades	85	Ccr5_gp046	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68249.1	001679	Cluster1188_1clades	86	CcrBL10_gp045	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87565.1	001679	Cluster1188_1clades	85	CcrKarma_gp048	Caulobacter virus Karma	GCA_000901575.1
AFU87215.1	001679	Cluster1188_1clades	85	CcrMagneto_gp045	Caulobacter virus Magneto	GCA_000903095.1
AFU86531.1	001679	Cluster1188_1clades	86	CcrRogue_gp049	Caulobacter virus Rogue	GCA_000900555.1
AFU88363.1	001679	Cluster1188_1clades	85	CcrSwift_gp045	Caulobacter virus Swift	GCA_000899655.1
AFU86879.1	001679	Cluster1188_1clades	85	CbK_gp047	Caulobacter virus phiCbK	GCA_000900535.1
ARB13824.1	001680	Cluster1189_1clades	86	Ccr10_gp294	Caulobacter phage Ccr10	GCA_002619445.1
ARB14169.1	001680	Cluster1189_1clades	86	Ccr2_gp293	Caulobacter phage Ccr2	GCA_002619465.1
ARB14863.1	001680	Cluster1189_1clades	86	Ccr29_gp307	Caulobacter phage Ccr29	GCA_002619485.1
ARB15201.1	001680	Cluster1189_1clades	86	Ccr32_gp283	Caulobacter phage Ccr32	GCA_002619505.1
ARB15535.1	001680	Cluster1189_1clades	86	Ccr34_gp293	Caulobacter phage Ccr34	GCA_002619525.1
ARB14510.1	001680	Cluster1189_1clades	86	Ccr5_gp290	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68491.1	001680	Cluster1189_1clades	86	CcrBL10_gp287	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87820.1	001680	Cluster1189_1clades	86	CcrKarma_gp303	Caulobacter virus Karma	GCA_000901575.1
AFU87467.1	001680	Cluster1189_1clades	86	CcrMagneto_gp297	Caulobacter virus Magneto	GCA_000903095.1
AFU86779.1	001680	Cluster1189_1clades	86	CcrRogue_gp297	Caulobacter virus Rogue	GCA_000900555.1
AFU88612.1	001680	Cluster1189_1clades	86	CcrSwift_gp294	Caulobacter virus Swift	GCA_000899655.1
AFU87120.1	001680	Cluster1189_1clades	86	CbK_gp288	Caulobacter virus phiCbK	GCA_000900535.1
ARB13671.1	001681	Cluster1190_1clades	84	Ccr10_gp142	Caulobacter phage Ccr10	GCA_002619445.1
ARB14016.1	001681	Cluster1190_1clades	84	Ccr2_gp141	Caulobacter phage Ccr2	GCA_002619465.1
ARB14703.1	001681	Cluster1190_1clades	84	Ccr29_gp147	Caulobacter phage Ccr29	GCA_002619485.1
ARB15058.1	001681	Cluster1190_1clades	84	Ccr32_gp140	Caulobacter phage Ccr32	GCA_002619505.1
ARB15392.1	001681	Cluster1190_1clades	84	Ccr34_gp150	Caulobacter phage Ccr34	GCA_002619525.1
ARB14359.1	001681	Cluster1190_1clades	84	Ccr5_gp140	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68339.1	001681	Cluster1190_1clades	84	CcrBL10_gp135	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87664.1	001681	Cluster1190_1clades	84	CcrKarma_gp147	Caulobacter virus Karma	GCA_000901575.1
AFU87313.1	001681	Cluster1190_1clades	84	CcrMagneto_gp143	Caulobacter virus Magneto	GCA_000903095.1
AFU86624.1	001681	Cluster1190_1clades	84	CcrRogue_gp142	Caulobacter virus Rogue	GCA_000900555.1
AFU88460.1	001681	Cluster1190_1clades	84	CcrSwift_gp142	Caulobacter virus Swift	GCA_000899655.1
AFU86977.1	001681	Cluster1190_1clades	84	CbK_gp145	Caulobacter virus phiCbK	GCA_000900535.1
ANZ49911.1	001682	SIG+TM	75	MACHINA_273	Erwinia phage Machina	GCA_002758035.1
AXF51412.1	001682	SIG+TM	84	WELLINGTON_286	Erwinia phage Wellington	GCA_003344985.1
ANZ48295.1	001682	SIG+TM	78	ASESINO_282	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48566.1	001682	SIG+TM	75	CAITLIN_271	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48844.1	001682	SIG+TM	75	CHRISDB_282	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49354.1	001682	SIG+TM	75	HUXLEY_272	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49637.1	001682	SIG+TM	84	KWAN_285	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50182.1	001682	SIG+TM	75	PARSHIK_273	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50706.1	001682	SIG+TM	78	STRATTON_281	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86102.1	001682	SIG+TM	79	ACEC001_2590	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51109.1	001682	SIG+TM	78	MLDJOKPK_00179	Salmonella phage SPAsTU	GCA_003183805.1
AEP84094.1	001682	SIG+TM	79	SPN3US_0261	Salmonella phage SPN3US	GCA_001042275.1
AMR59670.1	001683	Cluster1192_1clades	55	SEGD1_019	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49673.1	001683	Cluster1192_1clades	58	MACHINA_35	Erwinia phage Machina	GCA_002758035.1
AFQ96746.1	001683	Cluster1192_1clades	63	G173_gp201	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48049.1	001683	Cluster1192_1clades	62	ASESINO_36	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48325.1	001683	Cluster1192_1clades	61	CAITLIN_30	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48597.1	001683	Cluster1192_1clades	61	CHRISDB_35	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49118.1	001683	Cluster1192_1clades	58	HUXLEY_36	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49946.1	001683	Cluster1192_1clades	58	PARSHIK_37	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50459.1	001683	Cluster1192_1clades	84	STRATTON_34	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85859.1	001683	Cluster1192_1clades	65	ACEC001_0210	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51101.1	001683	Cluster1192_1clades	65	MLDJOKPK_00147	Salmonella phage SPAsTU	GCA_003183805.1
AEP83853.1	001683	Cluster1192_1clades	55	SPN3US_0020	Salmonella phage SPN3US	GCA_001042275.1
AAQ64223.1	001684	Cluster1193_1clades	83	KVP40.0154	Vibrio phage KVP40	GCA_000843785.1
QIW90537.1	001684	Cluster1193_1clades	83	GCAPEGMB_00190	Vibrio phage V07	GCA_012361095.1
QIW90885.1	001684	Cluster1193_1clades	83	COHAPHLL_00022	Vibrio phage V09	GCA_012361135.1
QHJ74335.1	001684	Cluster1193_1clades	83	VH12019_00008	Vibrio phage VH1_2019	GCA_009931825.1
AGB06827.1	001684	Cluster1193_1clades	83	CF80_gp040	Vibrio phage VH7D	GCA_000914495.1
QBX06319.1	001684	Cluster1193_1clades	83	ValB1HC_366	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60950.1	001684	Cluster1193_1clades	83	AVU32_gp109	Vibrio phage ValKK3	GCA_001501635.1
AGN30200.1	001684	Cluster1193_1clades	83	VPFG_00200	Vibrio phage nt-1	GCA_000910195.2
ALP47257.1	001684	Cluster1193_1clades	83	phiGrn1_0264	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47639.1	001684	Cluster1193_1clades	83	phiST2_0023	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54562.1	001684	Cluster1193_1clades	83	vBValMR10Z_21	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37382.1	001684	Cluster1193_1clades	83	pp2_149	Vibriophage phi-pp2	GCA_002630725.1
AMO43324.1	001685	Cluster1194_1clades	62	W270710_080	Cyanophage S-RIM44	GCA_002599145.1
AOO11558.1	001685	Cluster1194_1clades	64	ES420910_077	Cyanophage S-RIM44	GCA_002599165.1
AOO11796.1	001685	Cluster1194_1clades	62	Np050604_080	Cyanophage S-RIM44	GCA_002599185.1
AOO12023.1	001685	Cluster1194_1clades	64	Np200711_077	Cyanophage S-RIM44	GCA_002599205.1
AOO12259.1	001685	Cluster1194_1clades	64	Np420711_077	Cyanophage S-RIM44	GCA_002599225.1
AOO12497.1	001685	Cluster1194_1clades	62	Sn080709_080	Cyanophage S-RIM44	GCA_002599245.1
AOO12724.1	001685	Cluster1194_1clades	64	Sn130910_077	Cyanophage S-RIM44	GCA_002599265.1
AOO12962.1	001685	Cluster1194_1clades	62	W2100709_080	Cyanophage S-RIM44	GCA_002599285.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADO99180.1	001685	Cluster1194_1clades	83	Syn1_079	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59535.1	001685	Cluster1194_1clades	61	S330809_074	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59297.1	001685	Cluster1194_1clades	61	C440309_074	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59773.1	001685	Cluster1194_1clades	61	N231010_074	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13701.1	001686	SIG+TM	83	Ccr10_gp171c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14046.1	001686	SIG+TM	83	Ccr2_gp170c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14733.1	001686	SIG+TM	83	Ccr29_gp177	Caulobacter phage Ccr29	GCA_002619485.1
ARB15088.1	001686	SIG+TM	83	Ccr32_gp170	Caulobacter phage Ccr32	GCA_002619505.1
ARB15422.1	001686	SIG+TM	83	Ccr34_gp180	Caulobacter phage Ccr34	GCA_002619525.1
ARB14389.1	001686	SIG+TM	83	Ccr5_gp169c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68371.1	001686	SIG+TM	82	CcrBL10_gp167c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87694.1	001686	SIG+TM	83	CcrKarma_gp177	Caulobacter virus Karma	GCA_000901575.1
AFU87343.1	001686	SIG+TM	83	CcrMagneto_gp173	Caulobacter virus Magneto	GCA_000903095.1
AFU86654.1	001686	SIG+TM	82	CcrRogue_gp172	Caulobacter virus Rogue	GCA_000900555.1
AFU88490.1	001686	SIG+TM	83	CcrSwift_gp172	Caulobacter virus Swift	GCA_000899655.1
AFU87007.1	001686	SIG+TM	83	CbK_gp175	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64311.1	001687	Cluster1197_1clades	48	KVP40.0242	Vibrio phage KVP40	GCA_000843785.1
QIW90626.1	001687	Cluster1197_1clades	82	GCAPEGMB_00279	Vibrio phage V07	GCA_012361095.1
QIW91173.1	001687	Cluster1197_1clades	82	COHAPHLL_00337	Vibrio phage V09	GCA_012361135.1
QHJ74421.1	001687	Cluster1197_1clades	82	VH12019_00094	Vibrio phage VH1_2019	GCA_009931825.1
AGB06927.1	001687	Cluster1197_1clades	83	CF80_gp140	Vibrio phage VH7D	GCA_000914495.1
QBX06219.1	001687	Cluster1197_1clades	79	ValB1HC_266	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60845.1	001687	Cluster1197_1clades	78	AVU32_gp004	Vibrio phage ValKK3	GCA_001501635.1
AGN30297.2	001687	Cluster1197_1clades	78	VPFG_00298	Vibrio phage nt-1	GCA_000910195.2
ALP47256.1	001687	Cluster1197_1clades	83	phiGrn1_0363	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47645.1	001687	Cluster1197_1clades	80	phiST2_0118	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54844.1	001687	Cluster1197_1clades	78	vBValMR10Z_304	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37470.1	001687	Cluster1197_1clades	48	pp2_237	Vibriophage phi-pp2	GCA_002630725.1
AAQ64319.1	001688	Cluster1198_1clades	82	KVP40.0250	Vibrio phage KVP40	GCA_000843785.1
QIW90634.1	001688	Cluster1198_1clades	82	GCAPEGMB_00287	Vibrio phage V07	GCA_012361095.1
QIW91165.1	001688	Cluster1198_1clades	82	COHAPHLL_00329	Vibrio phage V09	GCA_012361135.1
QHJ74429.1	001688	Cluster1198_1clades	82	VH12019_00102	Vibrio phage VH1_2019	GCA_009931825.1
AGB06935.1	001688	Cluster1198_1clades	82	CF80_gp148	Vibrio phage VH7D	GCA_000914495.1
QBX06211.1	001688	Cluster1198_1clades	82	ValB1HC_258	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61228.1	001688	Cluster1198_1clades	82	AVU32_gp387	Vibrio phage ValKK3	GCA_001501635.1
AGN30305.1	001688	Cluster1198_1clades	82	VPFG_00306	Vibrio phage nt-1	GCA_000910195.2
ALP47259.1	001688	Cluster1198_1clades	82	phiGrn1_0371	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47640.1	001688	Cluster1198_1clades	82	phiST2_0126	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54836.1	001688	Cluster1198_1clades	82	vBValMR10Z_296	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37478.1	001688	Cluster1198_1clades	82	pp2_245	Vibriophage phi-pp2	GCA_002630725.1
ARB13579.1	001689	Cluster1199_1clades	81	Ccr10_gp051	Caulobacter phage Ccr10	GCA_002619445.1
ARB13925.1	001689	Cluster1199_1clades	81	Ccr2_gp050	Caulobacter phage Ccr2	GCA_002619465.1
ARB14614.1	001689	Cluster1199_1clades	81	Ccr29_gp057	Caulobacter phage Ccr29	GCA_002619485.1
ARB14970.1	001689	Cluster1199_1clades	81	Ccr32_gp051	Caulobacter phage Ccr32	GCA_002619505.1
ARB15301.1	001689	Cluster1199_1clades	81	Ccr34_gp052	Caulobacter phage Ccr34	GCA_002619525.1
ARB14268.1	001689	Cluster1199_1clades	81	Ccr5_gp050	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68253.1	001689	Cluster1199_1clades	82	CcrBL10_gp049	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87569.1	001689	Cluster1199_1clades	50	CcrKarma_gp052	Caulobacter virus Karma	GCA_000901575.1
AFU87219.1	001689	Cluster1199_1clades	80	CcrMagneto_gp049	Caulobacter virus Magneto	GCA_000903095.1
AFU86535.1	001689	Cluster1199_1clades	82	CcrRogue_gp053	Caulobacter virus Rogue	GCA_000900555.1
AFU88367.1	001689	Cluster1199_1clades	80	CcrSwift_gp049	Caulobacter virus Swift	GCA_000899655.1
AFU86883.1	001689	Cluster1199_1clades	81	CbK_gp051	Caulobacter virus phiCbK	GCA_000900535.1
ARB13812.1	001690	Cluster1200_1clades	82	Ccr10_gp282	Caulobacter phage Ccr10	GCA_002619445.1
ARB14157.1	001690	Cluster1200_1clades	82	Ccr2_gp281	Caulobacter phage Ccr2	GCA_002619465.1
ARB14851.1	001690	Cluster1200_1clades	82	Ccr29_gp295	Caulobacter phage Ccr29	GCA_002619485.1
ARB15190.1	001690	Cluster1200_1clades	81	Ccr32_gp272	Caulobacter phage Ccr32	GCA_002619505.1
ARB15524.1	001690	Cluster1200_1clades	81	Ccr34_gp282	Caulobacter phage Ccr34	GCA_002619525.1
ARB14499.1	001690	Cluster1200_1clades	82	Ccr5_gp279	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68479.1	001690	Cluster1200_1clades	66	CcrBL10_gp275	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87809.1	001690	Cluster1200_1clades	82	CcrKarma_gp292	Caulobacter virus Karma	GCA_000901575.1
AFU87456.1	001690	Cluster1200_1clades	81	CcrMagneto_gp286	Caulobacter virus Magneto	GCA_000903095.1
AFU86765.1	001690	Cluster1200_1clades	80	CcrRogue_gp283	Caulobacter virus Rogue	GCA_000900555.1
AFU88601.1	001690	Cluster1200_1clades	82	CcrSwift_gp283	Caulobacter virus Swift	GCA_000899655.1
AFU87109.1	001690	Cluster1200_1clades	81	CbK_gp277	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64124.1	001691	Cluster1201_1clades	81	KVP40.0053	Vibrio phage KVP40	GCA_000843785.1
QIW90446.1	001691	Cluster1201_1clades	81	GCAPEGMB_00099	Vibrio phage V07	GCA_012361095.1
QIW90983.1	001691	Cluster1201_1clades	81	COHAPHLL_00120	Vibrio phage V09	GCA_012361135.1
QHJ74235.1	001691	Cluster1201_1clades	81	VH12019_00316	Vibrio phage VH1_2019	GCA_009931825.1
AGB07059.1	001691	Cluster1201_1clades	81	CF80_gp272	Vibrio phage VH7D	GCA_000914495.1
QBX06037.1	001691	Cluster1201_1clades	81	ValB1HC_083	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61051.1	001691	Cluster1201_1clades	81	AVU32_gp210	Vibrio phage ValKK3	GCA_001501635.1
AGN30102.1	001691	Cluster1201_1clades	81	VPFG_00100	Vibrio phage nt-1	GCA_000910195.2
ALP47262.1	001691	Cluster1201_1clades	81	phiGrn1_0166	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47641.1	001691	Cluster1201_1clades	81	phiST2_0297	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54662.1	001691	Cluster1201_1clades	81	vBValMR10Z_121	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37284.1	001691	Cluster1201_1clades	81	pp2_050	Vibriophage phi-pp2	GCA_002630725.1
ARB13771.1	001692	Cluster1202_1clades	81	Ccr10_gp241	Caulobacter phage Ccr10	GCA_002619445.1
ARB14116.1	001692	Cluster1202_1clades	81	Ccr2_gp240	Caulobacter phage Ccr2	GCA_002619465.1
ARB14810.1	001692	Cluster1202_1clades	81	Ccr29_gp254	Caulobacter phage Ccr29	GCA_002619485.1
ARB15150.1	001692	Cluster1202_1clades	81	Ccr32_gp232	Caulobacter phage Ccr32	GCA_002619505.1
ARB15484.1	001692	Cluster1202_1clades	81	Ccr34_gp242	Caulobacter phage Ccr34	GCA_002619525.1
ARB14458.1	001692	Cluster1202_1clades	81	Ccr5_gp238	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68436.1	001692	Cluster1202_1clades	80	CcrBL10_gp232	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87766.1	001692	Cluster1202_1clades	81	CcrKarma_gp249	Caulobacter virus Karma	GCA_000901575.1
AFU87413.1	001692	Cluster1202_1clades	81	CcrMagneto_gp243	Caulobacter virus Magneto	GCA_000903095.1
AFU86722.1	001692	Cluster1202_1clades	80	CcrRogue_gp240	Caulobacter virus Rogue	GCA_000900555.1
AFU88561.1	001692	Cluster1202_1clades	81	CcrSwift_gp243	Caulobacter virus Swift	GCA_000899655.1
AFU87069.1	001692	Cluster1202_1clades	81	CbK_gp237	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64117.1	001693	Cluster1203_1clades	80	KVP40.0046	Vibrio phage KVP40	GCA_000843785.1
QIW90439.1	001693	Cluster1203_1clades	76	GCAPEGMB_00092	Vibrio phage V07	GCA_012361095.1
QIW90990.1	001693	Cluster1203_1clades	76	COHAPHLL_00127	Vibrio phage V09	GCA_012361135.1
QHJ74228.1	001693	Cluster1203_1clades	76	VH12019_00309	Vibrio phage VH1_2019	GCA_009931825.1
AGB07052.1	001693	Cluster1203_1clades	80	CF80_gp265	Vibrio phage VH7D	GCA_000914495.1
QBX06044.1	001693	Cluster1203_1clades	76	ValB1HC_090	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61058.1	001693	Cluster1203_1clades	76	AVU32_gp217	Vibrio phage ValKK3	GCA_001501635.1
AGN30095.2	001693	Cluster1203_1clades	76	VPFG_00093	Vibrio phage nt-1	GCA_000910195.2
ALP47277.1	001693	Cluster1203_1clades	76	phiGrn1_0159	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47657.1	001693	Cluster1203_1clades	76	phiST2_0290	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54669.1	001693	Cluster1203_1clades	76	vBValMR10Z_128	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37278.1	001693	Cluster1203_1clades	76	pp2_044	Vibriophage phi-pp2	GCA_002630725.1
AGB06956.1	001694	Cluster1204_2clades	80	CF80_gp169	Vibrio phage VH7D	GCA_000914495.1
AAQ64353.1	001694	Cluster1204_2clades	80	KVP40.0283	Vibrio phage KVP40	GCA_000843785.1
QIW90667.1	001694	Cluster1204_2clades	80	GCAPEGMB_00320	Vibrio phage V07	GCA_012361095.1
QIW91131.1	001694	Cluster1204_2clades	80	COHAPHLL_00295	Vibrio phage V09	GCA_012361135.1
QHJ74462.1	001694	Cluster1204_2clades	80	VH12019_00135	Vibrio phage VH1_2019	GCA_009931825.1
QBX06189.1	001694	Cluster1204_2clades	80	ValB1HC_236	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61206.1	001694	Cluster1204_2clades	80	AVU32_gp365	Vibrio phage ValKK3	GCA_001501635.1
AGN30329.1	001694	Cluster1204_2clades	80	VPFG_00332	Vibrio phage nt-1	GCA_000910195.2
ALP47264.1	001694	Cluster1204_2clades	80	phiGrn1_0016	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47644.1	001694	Cluster1204_2clades	80	phiST2_0147	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54814.1	001694	Cluster1204_2clades	80	vBValMR10Z_274	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37514.1	001694	Cluster1204_2clades	80	pp2_281	Vibriophage phi-pp2	GCA_002630725.1
AAQ64093.1	001695	Cluster1205_1clades	78	KVP40.0022	Vibrio phage KVP40	GCA_000843785.1
QIW90416.1	001695	Cluster1205_1clades	78	GCAPEGMB_00069	Vibrio phage V07	GCA_012361095.1
QIW91013.1	001695	Cluster1205_1clades	78	COHAPHLL_00150	Vibrio phage V09	GCA_012361135.1
QHJ74205.1	001695	Cluster1205_1clades	78	VH12019_00286	Vibrio phage VH1_2019	GCA_009931825.1
AGB07029.1	001695	Cluster1205_1clades	78	CF80_gp242	Vibrio phage VH7D	GCA_000914495.1
QBX06067.1	001695	Cluster1205_1clades	78	ValB1HC_113	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61081.1	001695	Cluster1205_1clades	80	AVU32_gp240	Vibrio phage ValKK3	GCA_001501635.1
AGN30073.1	001695	Cluster1205_1clades	75	VPFG_00071	Vibrio phage nt-1	GCA_000910195.2
ALP47265.1	001695	Cluster1205_1clades	80	phiGrn1_0137	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47651.1	001695	Cluster1205_1clades	78	phiST2_0267	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54693.1	001695	Cluster1205_1clades	78	vBValMR10Z_152	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37256.1	001695	Cluster1205_1clades	64	pp2_022	Vibriophage phi-pp2	GCA_002630725.1
AAQ64133.1	001696	ArsC	79	KVP40.0062	Vibrio phage KVP40	GCA_000843785.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW90456.1	001696	ArsC	79	GCAPEGMB_00109	Vibrio phage V07	GCA_012361095.1
QIW90973.1	001696	ArsC	79	COHAPHLL_00110	Vibrio phage V09	GCA_012361135.1
QHJ74245.1	001696	ArsC	79	VH12019_00326	Vibrio phage VH1_2019	GCA_009931825.1
AGB07069.1	001696	ArsC	39	CF80_gp282	Vibrio phage VH7D	GCA_000914495.1
QBX06026.1	001696	ArsC	79	ValB1HC_072	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61040.1	001696	ArsC	79	AVU32_gp199	Vibrio phage ValKK3	GCA_001501635.1
AGN30111.1	001696	ArsC	79	VPFG_00109	Vibrio phage nt-1	GCA_000910195.2
ALP47267.1	001696	ArsC	79	phiGrn1_0177	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47647.1	001696	ArsC	79	phiST2_0308	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54651.1	001696	ArsC	79	vBValMR10Z_110	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37293.1	001696	ArsC	79	pp2_060	Vibriophage phi-pp2	GCA_002630725.1
AAQ64293.1	001697	Cluster1207_1clades	79	KVP40.0224	Vibrio phage KVP40	GCA_000843785.1
QIW90609.1	001697	Cluster1207_1clades	79	GCAPEGMB_00262	Vibrio phage V07	GCA_012361095.1
QIW91190.1	001697	Cluster1207_1clades	79	COHAPHLL_00354	Vibrio phage V09	GCA_012361135.1
QHJ74405.1	001697	Cluster1207_1clades	79	VH12019_00078	Vibrio phage VH1_2019	GCA_009931825.1
AGB06911.1	001697	Cluster1207_1clades	79	CF80_gp124	Vibrio phage VH7D	GCA_000914495.1
QBX06235.1	001697	Cluster1207_1clades	79	ValB1HC_282	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60861.1	001697	Cluster1207_1clades	79	AVU32_gp020	Vibrio phage ValKK3	GCA_001501635.1
AGN30285.1	001697	Cluster1207_1clades	79	VPFG_00286	Vibrio phage nt-1	GCA_000910195.2
ALP47270.1	001697	Cluster1207_1clades	79	phiGrn1_0347	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47650.1	001697	Cluster1207_1clades	79	phiST2_0102	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54860.1	001697	Cluster1207_1clades	79	vBValMR10Z_320	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37454.1	001697	Cluster1207_1clades	79	pp2_221	Vibriophage phi-pp2	GCA_002630725.1
ARB13581.1	001698	Cluster1208_1clades	73	Ccr10_gp053	Caulobacter phage Ccr10	GCA_002619445.1
ARB13927.1	001698	Cluster1208_1clades	73	Ccr2_gp052	Caulobacter phage Ccr2	GCA_002619465.1
ARB14616.1	001698	Cluster1208_1clades	73	Ccr29_gp059	Caulobacter phage Ccr29	GCA_002619485.1
ARB14972.1	001698	Cluster1208_1clades	73	Ccr32_gp053	Caulobacter phage Ccr32	GCA_002619505.1
ARB15303.1	001698	Cluster1208_1clades	73	Ccr34_gp054	Caulobacter phage Ccr34	GCA_002619525.1
ARB14270.1	001698	Cluster1208_1clades	79	Ccr5_gp052	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68255.1	001698	Cluster1208_1clades	79	CcrBL10_gp051	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87571.1	001698	Cluster1208_1clades	79	CcrKarma_gp054	Caulobacter virus Karma	GCA_000901575.1
AFU87221.1	001698	Cluster1208_1clades	73	CcrMagneto_gp051	Caulobacter virus Magneto	GCA_000903095.1
AFU86537.1	001698	Cluster1208_1clades	79	CcrRogue_gp055	Caulobacter virus Rogue	GCA_000900555.1
AFU88369.1	001698	Cluster1208_1clades	73	CcrSwift_gp051	Caulobacter virus Swift	GCA_000899655.1
AFU86885.1	001698	Cluster1208_1clades	79	CbK_gp053	Caulobacter virus phiCbK	GCA_000900535.1
ARB13698.1	001699	SIG+TM	79	Ccr10_gp168c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14043.1	001699	SIG+TM	79	Ccr2_gp167c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14730.1	001699	SIG+TM	79	Ccr29_gp174	Caulobacter phage Ccr29	GCA_002619485.1
ARB15085.1	001699	SIG+TM	79	Ccr32_gp167	Caulobacter phage Ccr32	GCA_002619505.1
ARB15419.1	001699	SIG+TM	79	Ccr34_gp177	Caulobacter phage Ccr34	GCA_002619525.1
ARB14386.1	001699	SIG+TM	79	Ccr5_gp166c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68368.1	001699	SIG+TM	79	CcrBL10_gp164c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87691.1	001699	SIG+TM	79	CcrKarma_gp174	Caulobacter virus Karma	GCA_000901575.1
AFU87340.1	001699	SIG+TM	79	CcrMagneto_gp170	Caulobacter virus Magneto	GCA_000903095.1
AFU86651.1	001699	SIG+TM	79	CcrRogue_gp169	Caulobacter virus Rogue	GCA_000900555.1
AFU88487.1	001699	SIG+TM	79	CcrSwift_gp169	Caulobacter virus Swift	GCA_000899655.1
AFU87004.1	001699	SIG+TM	79	CbK_gp172	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64147.1	001700	Gp45_2	78	KVP40.0076	Vibrio phage KVP40	GCA_000843785.1
QIW90470.1	001700	Gp45_2	69	GCAPEGMB_00123	Vibrio phage V07	GCA_012361095.1
QIW90959.1	001700	Gp45_2	69	COHAPHLL_00096	Vibrio phage V09	GCA_012361135.1
QHJ74259.1	001700	Gp45_2	69	VH12019_00340	Vibrio phage VH1_2019	GCA_009931825.1
AGB07083.1	001700	Gp45_2	71	CF80_gp296	Vibrio phage VH7D	GCA_000914495.1
QBX06012.1	001700	Gp45_2	69	ValB1HC_058	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61025.1	001700	Gp45_2	69	AVU32_gp184	Vibrio phage ValKK3	GCA_001501635.1
AGN30125.2	001700	Gp45_2	69	VPFG_00123	Vibrio phage nt-1	GCA_000910195.2
ALP47294.1	001700	Gp45_2	69	phiGrn1_0191	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47674.1	001700	Gp45_2	69	phiST2_0322	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54637.1	001700	Gp45_2	69	vBValMR10Z_96	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37307.1	001700	Gp45_2	69	pp2_074	Vibriophage phi-pp2	GCA_002630725.1
AMO43326.1	001701	Cluster1211_1clades	37	W270710_082	Cyanophage S-RIM44	GCA_002599145.1
AOO11560.1	001701	Cluster1211_1clades	37	ES420910_079	Cyanophage S-RIM44	GCA_002599165.1
AOO11798.1	001701	Cluster1211_1clades	37	Np050604_082	Cyanophage S-RIM44	GCA_002599185.1
AOO12025.1	001701	Cluster1211_1clades	37	Np200711_079	Cyanophage S-RIM44	GCA_002599205.1
AOO12261.1	001701	Cluster1211_1clades	37	Np420711_079	Cyanophage S-RIM44	GCA_002599225.1
AOO12499.1	001701	Cluster1211_1clades	37	Sn080709_082	Cyanophage S-RIM44	GCA_002599245.1
AOO12726.1	001701	Cluster1211_1clades	37	Sn130910_079	Cyanophage S-RIM44	GCA_002599265.1
AOO12965.1	001701	Cluster1211_1clades	37	W2100709_083	Cyanophage S-RIM44	GCA_002599285.1
ADO99182.1	001701	Cluster1211_1clades	78	Syn1_081	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59537.1	001701	Cluster1211_1clades	77	S330809_076	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59299.1	001701	Cluster1211_1clades	77	C440309_076	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59775.1	001701	Cluster1211_1clades	77	N231010_076	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13660.1	001702	Cluster1212_1clades	75	Ccr10_gp131c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14005.1	001702	Cluster1212_1clades	75	Ccr2_gp130c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14693.1	001702	Cluster1212_1clades	75	Ccr29_gp137	Caulobacter phage Ccr29	GCA_002619485.1
ARB15047.1	001702	Cluster1212_1clades	70	Ccr32_gp129	Caulobacter phage Ccr32	GCA_002619505.1
ARB15380.1	001702	Cluster1212_1clades	70	Ccr34_gp138	Caulobacter phage Ccr34	GCA_002619525.1
ARB14348.1	001702	Cluster1212_1clades	78	Ccr5_gp129c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68328.1	001702	Cluster1212_1clades	70	CcrBL10_gp124c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87652.1	001702	Cluster1212_1clades	78	CcrKarma_gp135	Caulobacter virus Karma	GCA_000901575.1
AFU87301.1	001702	Cluster1212_1clades	75	CcrMagneto_gp131	Caulobacter virus Magneto	GCA_000903095.1
AFU86613.1	001702	Cluster1212_1clades	78	CcrRogue_gp131	Caulobacter virus Rogue	GCA_000900555.1
AFU88448.1	001702	Cluster1212_1clades	78	CcrSwift_gp130	Caulobacter virus Swift	GCA_000899655.1
AFU86965.1	001702	Cluster1212_1clades	78	CbK_gp133	Caulobacter virus phiCbK	GCA_000900535.1
AMR59787.1	001703	Cluster1213_1clades	72	SEGD1_140	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49784.1	001703	Cluster1213_1clades	73	MACHINA_146	Erwinia phage Machina	GCA_002758035.1
AFQ96602.1	001703	Cluster1213_1clades	77	G173_gp057	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48166.1	001703	Cluster1213_1clades	77	ASESINO_153	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48440.1	001703	Cluster1213_1clades	73	CAITLIN_145	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48716.1	001703	Cluster1213_1clades	75	CHRISDB_154	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49228.1	001703	Cluster1213_1clades	73	HUXLEY_146	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50056.1	001703	Cluster1213_1clades	73	PARSHIK_147	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50579.1	001703	Cluster1213_1clades	77	STRATTON_154	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85977.1	001703	Cluster1213_1clades	72	ACEC001_1390	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN08983.1	001703	Cluster1213_1clades	73	MLDJOKPK_00013	Salmonella phage SPAsTU	GCA_003183805.1
AEP83969.1	001703	Cluster1213_1clades	72	SPN3US_0136	Salmonella phage SPN3US	GCA_001042275.1
ARB13778.1	001704	Cluster1214_1clades	76	Ccr10_gp248	Caulobacter phage Ccr10	GCA_002619445.1
ARB14123.1	001704	Cluster1214_1clades	76	Ccr2_gp247	Caulobacter phage Ccr2	GCA_002619465.1
ARB14817.1	001704	Cluster1214_1clades	76	Ccr29_gp261	Caulobacter phage Ccr29	GCA_002619485.1
ARB15157.1	001704	Cluster1214_1clades	77	Ccr32_gp239	Caulobacter phage Ccr32	GCA_002619505.1
ARB15491.1	001704	Cluster1214_1clades	77	Ccr34_gp249	Caulobacter phage Ccr34	GCA_002619525.1
ARB14465.1	001704	Cluster1214_1clades	77	Ccr5_gp245	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68444.1	001704	Cluster1214_1clades	75	CcrBL10_gp240	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87774.1	001704	Cluster1214_1clades	77	CcrKarma_gp257	Caulobacter virus Karma	GCA_000901575.1
AFU87421.1	001704	Cluster1214_1clades	76	CcrMagneto_gp251	Caulobacter virus Magneto	GCA_000903095.1
AFU86730.1	001704	Cluster1214_1clades	75	CcrRogue_gp248	Caulobacter virus Rogue	GCA_000900555.1
AFU88568.1	001704	Cluster1214_1clades	76	CcrSwift_gp250	Caulobacter virus Swift	GCA_000899655.1
AFU87076.1	001704	Cluster1214_1clades	77	CbK_gp244	Caulobacter virus phiCbK	GCA_000900535.1
AIT14148.1	001705	Cluster1215_1clades	60	PBI_121Q_258	Escherichia phage 121Q	GCA_000926855.1
AIT14149.1	001705	Cluster1215_1clades	63	PBI_121Q_259	Escherichia phage 121Q	GCA_000926855.1
AIT14151.1	001705	Cluster1215_1clades	62	PBI_121Q_261	Escherichia phage 121Q	GCA_000926855.1
AGC34962.1	001705	Cluster1215_1clades	62	ACQ29_gp282	Escherichia phage PBECO4	GCA_001041035.1
AGC34963.1	001705	Cluster1215_1clades	66	ACQ29_gp283	Escherichia phage PBECO4	GCA_001041035.1
BBM61826.1	001705	Cluster1215_1clades	77	EO157G_2370	Escherichia phage SP27	GCA_008033345.1
QBO61552.1	001705	Cluster1215_1clades	62	G17_00056	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61554.1	001705	Cluster1215_1clades	63	G17_00058	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61555.1	001705	Cluster1215_1clades	60	G17_00059	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14165.1	001705	Cluster1215_1clades	61	vBEcoMphAPEC6_gp542c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14166.1	001705	Cluster1215_1clades	66	vBEcoMphAPEC6_gp543c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80140.1	001705	Cluster1215_1clades	62	PSLUR01_00163	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64100.1	001706	Cluster1216_1clades	76	KVP40.0029	Vibrio phage KVP40	GCA_000843785.1
QIW90423.1	001706	Cluster1216_1clades	76	GCAPEGMB_00076	Vibrio phage V07	GCA_012361095.1
QIW91006.1	001706	Cluster1216_1clades	76	COHAPHLL_00143	Vibrio phage V09	GCA_012361135.1
QHJ74212.1	001706	Cluster1216_1clades	76	VH12019_00293	Vibrio phage VH1_2019	GCA_009931825.1
AGB07036.1	001706	Cluster1216_1clades	76	CF80_gp249	Vibrio phage VH7D	GCA_000914495.1
QBX06060.1	001706	Cluster1216_1clades	76	ValB1HC_106	Vibrio phage ValB1 HC	GCA_004771355.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AJT61073.1	001706	Cluster1216_1clades	76	AVU32_gp232	Vibrio phage ValKK3	GCA_001501635.1
AGN30079.1	001706	Cluster1216_1clades	74	VPFG_00077	Vibrio phage nt-1	GCA_000910195.2
ALP47276.1	001706	Cluster1216_1clades	76	phiGrn1_0144	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47659.1	001706	Cluster1216_1clades	76	phiST2_0274	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54686.1	001706	Cluster1216_1clades	76	vBValMR10Z_145	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37263.1	001706	Cluster1216_1clades	76	pp2_029	Vibriophage phi-pp2	GCA_002630725.1
AAQ64165.1	001707	SIG+TM	76	KVP40.0094	Vibrio phage KVP40	GCA_000843785.1
QIW90488.1	001707	SIG+TM	76	GCAPEGMB_00141	Vibrio phage V07	GCA_012361095.1
QIW90941.1	001707	SIG+TM	76	COHAPHLL_00078	Vibrio phage V09	GCA_012361135.1
QHJ74276.1	001707	SIG+TM	76	VH12019_00357	Vibrio phage VH1_2019	GCA_009931825.1
AGB07101.1	001707	SIG+TM	76	CF80_gp314	Vibrio phage VH7D	GCA_000914495.1
QBX05994.1	001707	SIG+TM	76	ValB1HC_040	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61007.1	001707	SIG+TM	76	AVU32_gp166	Vibrio phage ValKK3	GCA_001501635.1
AGN30144.1	001707	SIG+TM	76	VPFG_00142	Vibrio phage nt-1	GCA_000910195.2
ALP47279.1	001707	SIG+TM	76	phiGrn1_0208	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47656.1	001707	SIG+TM	76	phiST2_0341	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54619.1	001707	SIG+TM	76	vBValMR10Z_78	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37324.1	001707	SIG+TM	76	pp2_091	Vibriophage phi-pp2	GCA_002630725.1
AAQ64292.1	001708	Kelch_4	76	KVP40.0223	Vibrio phage KVP40	GCA_000843785.1
QIW90608.1	001708	Kelch_4	76	GCAPEGMB_00261	Vibrio phage V07	GCA_012361095.1
QIW91191.1	001708	Kelch_4	76	COHAPHLL_00355	Vibrio phage V09	GCA_012361135.1
QHJ74404.1	001708	Kelch_4	76	VH12019_00077	Vibrio phage VH1_2019	GCA_009931825.1
AGB06910.1	001708	Kelch_4	76	CF80_gp123	Vibrio phage VH7D	GCA_000914495.1
QBX06236.1	001708	Kelch_4	76	ValB1HC_283	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60862.1	001708	Kelch_4	76	AVU32_gp021	Vibrio phage ValKK3	GCA_001501635.1
AGN30284.1	001708	Kelch_4	76	VPFG_00285	Vibrio phage nt-1	GCA_000910195.2
ALP47280.1	001708	Kelch_4	76	phiGrn1_0346	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47662.1	001708	Kelch_4	76	phiST2_0101	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54861.1	001708	Kelch_4	76	vBValMR10Z_321	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37453.1	001708	Kelch_4	76	pp2_220	Vibriophage phi-pp2	GCA_002630725.1
AAQ64144.1	001709	Cluster1219_1clades	75	KVP40.0073	Vibrio phage KVP40	GCA_000843785.1
QIW90467.1	001709	Cluster1219_1clades	74	GCAPEGMB_00120	Vibrio phage V07	GCA_012361095.1
QIW90962.1	001709	Cluster1219_1clades	74	COHAPHLL_00099	Vibrio phage V09	GCA_012361135.1
QHJ74256.1	001709	Cluster1219_1clades	74	VH12019_00337	Vibrio phage VH1_2019	GCA_009931825.1
AGB07080.1	001709	Cluster1219_1clades	51	CF80_gp293	Vibrio phage VH7D	GCA_000914495.1
QBX06015.1	001709	Cluster1219_1clades	74	ValB1HC_061	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61029.1	001709	Cluster1219_1clades	75	AVU32_gp188	Vibrio phage ValKK3	GCA_001501635.1
AGN30122.1	001709	Cluster1219_1clades	75	VPFG_00120	Vibrio phage nt-1	GCA_000910195.2
ALP47326.1	001709	Cluster1219_1clades	51	phiGrn1_0188	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47708.1	001709	Cluster1219_1clades	51	phiST2_0319	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54640.1	001709	Cluster1219_1clades	74	vBValMR10Z_99	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37304.1	001709	Cluster1219_1clades	74	pp2_071	Vibriophage phi-pp2	GCA_002630725.1
APU01664.1	001710	Cluster1220_1clades	75	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53296.1	001710	Cluster1220_1clades	75	65p288	Aeromonas virus 65	GCA_000893255.1
QIW90698.1	001710	Cluster1220_1clades	69	GCAPEGMB_00360	Vibrio phage V07	GCA_012361095.1
QIW91100.1	001710	Cluster1220_1clades	69	COHAPHLL_00255	Vibrio phage V09	GCA_012361135.1
QHJ74497.1	001710	Cluster1220_1clades	69	VH12019_00179	Vibrio phage VH1_2019	GCA_009931825.1
QBX06158.1	001710	Cluster1220_1clades	69	ValB1HC_205	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61172.1	001710	Cluster1220_1clades	53	AVU32_gp331	Vibrio phage ValKK3	GCA_001501635.1
AGN30364.1	001710	Cluster1220_1clades	69	VPFG_00367	Vibrio phage nt-1	GCA_000910195.2
ALP47292.1	001710	Cluster1220_1clades	69	phiGrn1_0049	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47675.1	001710	Cluster1220_1clades	69	phiST2_0181	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54784.1	001710	Cluster1220_1clades	69	vBValMR10Z_244	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37545.1	001710	Cluster1220_1clades	69	pp2_312	Vibriophage phi-pp2	GCA_002630725.1
AAQ64290.1	001711	SIG+TM	72	KVP40.0221	Vibrio phage KVP40	GCA_000843785.1
QIW90606.1	001711	SIG+TM	71	GCAPEGMB_00259	Vibrio phage V07	GCA_012361095.1
QIW91193.1	001711	SIG+TM	72	COHAPHLL_00357	Vibrio phage V09	GCA_012361135.1
QHJ74402.1	001711	SIG+TM	72	VH12019_00075	Vibrio phage VH1_2019	GCA_009931825.1
AGB06908.1	001711	SIG+TM	71	CF80_gp121	Vibrio phage VH7D	GCA_000914495.1
QBX06238.1	001711	SIG+TM	71	ValB1HC_285	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60864.1	001711	SIG+TM	71	AVU32_gp023	Vibrio phage ValKK3	GCA_001501635.1
AGN30281.1	001711	SIG+TM	75	VPFG_00282	Vibrio phage nt-1	GCA_000910195.2
ALP47289.1	001711	SIG+TM	71	phiGrn1_0344	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47667.1	001711	SIG+TM	71	phiST2_0099	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54863.1	001711	SIG+TM	71	vBValMR10Z_323	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37451.1	001711	SIG+TM	71	pp2_218	Vibriophage phi-pp2	GCA_002630725.1
AMO43311.1	001712	Cluster1222_1clades	61	W270710_067	Cyanophage S-RIM44	GCA_002599145.1
AOO11545.1	001712	Cluster1222_1clades	61	ES420910_064	Cyanophage S-RIM44	GCA_002599165.1
AOO11783.1	001712	Cluster1222_1clades	61	Np050604_067	Cyanophage S-RIM44	GCA_002599185.1
AOO12010.1	001712	Cluster1222_1clades	61	Np200711_064	Cyanophage S-RIM44	GCA_002599205.1
AOO12246.1	001712	Cluster1222_1clades	61	Np420711_064	Cyanophage S-RIM44	GCA_002599225.1
AOO12484.1	001712	Cluster1222_1clades	61	Sn080709_067	Cyanophage S-RIM44	GCA_002599245.1
AOO12711.1	001712	Cluster1222_1clades	61	Sn130910_064	Cyanophage S-RIM44	GCA_002599265.1
AOO12949.1	001712	Cluster1222_1clades	61	W2100709_067	Cyanophage S-RIM44	GCA_002599285.1
ADO99165.1	001712	Cluster1222_1clades	61	Syn1_064	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59529.1	001712	Cluster1222_1clades	75	S330809_068	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59291.1	001712	Cluster1222_1clades	75	C440309_068	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59767.1	001712	Cluster1222_1clades	75	N231010_068	Synechococcus phage S-CAM4	GCA_002922155.1
AAQ64278.1	001713	Cluster1223_1clades	74	KVP40.0209	Vibrio phage KVP40	GCA_000843785.1
QIW90594.1	001713	Cluster1223_1clades	74	GCAPEGMB_00247	Vibrio phage V07	GCA_012361095.1
QIW91204.1	001713	Cluster1223_1clades	74	COHAPHLL_00368	Vibrio phage V09	GCA_012361135.1
QHJ74390.1	001713	Cluster1223_1clades	74	VH12019_00063	Vibrio phage VH1_2019	GCA_009931825.1
AGB06896.1	001713	Cluster1223_1clades	74	CF80_gp109	Vibrio phage VH7D	GCA_000914495.1
QBX06250.1	001713	Cluster1223_1clades	74	ValB1HC_297	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60876.1	001713	Cluster1223_1clades	74	AVU32_gp035	Vibrio phage ValKK3	GCA_001501635.1
AGN30271.1	001713	Cluster1223_1clades	73	VPFG_00272	Vibrio phage nt-1	GCA_000910195.2
ALP47283.1	001713	Cluster1223_1clades	74	phiGrn1_0334	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47663.1	001713	Cluster1223_1clades	74	phiST2_0089	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54876.1	001713	Cluster1223_1clades	74	vBValMR10Z_336	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37439.1	001713	Cluster1223_1clades	74	pp2_206	Vibriophage phi-pp2	GCA_002630725.1
AAQ64118.1	001714	TM	73	KVP40.0047	Vibrio phage KVP40	GCA_000843785.1
QIW90440.1	001714	TM	71	GCAPEGMB_00093	Vibrio phage V07	GCA_012361095.1
QIW90989.1	001714	TM	71	COHAPHLL_00126	Vibrio phage V09	GCA_012361135.1
QHJ74229.1	001714	TM	71	VH12019_00310	Vibrio phage VH1_2019	GCA_009931825.1
AGB07053.1	001714	TM	73	CF80_gp266	Vibrio phage VH7D	GCA_000914495.1
QBX06043.1	001714	TM	71	ValB1HC_089	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61057.1	001714	TM	71	AVU32_gp216	Vibrio phage ValKK3	GCA_001501635.1
AGN30096.2	001714	TM	71	VPFG_00094	Vibrio phage nt-1	GCA_000910195.2
ALP47285.1	001714	TM	71	phiGrn1_0160	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47666.1	001714	TM	71	phiST2_0291	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54668.1	001714	TM	71	vBValMR10Z_127	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37279.1	001714	TM	71	pp2_045	Vibriophage phi-pp2	GCA_002630725.1
ARB13794.1	001715	Cluster1226_1clades	72	Ccr10_gp264	Caulobacter phage Ccr10	GCA_002619445.1
ARB14139.1	001715	Cluster1226_1clades	72	Ccr2_gp263	Caulobacter phage Ccr2	GCA_002619465.1
ARB14833.1	001715	Cluster1226_1clades	72	Ccr29_gp277	Caulobacter phage Ccr29	GCA_002619485.1
ARB15173.1	001715	Cluster1226_1clades	72	Ccr32_gp255	Caulobacter phage Ccr32	GCA_002619505.1
ARB15507.1	001715	Cluster1226_1clades	72	Ccr34_gp265	Caulobacter phage Ccr34	GCA_002619525.1
ARB14481.1	001715	Cluster1226_1clades	72	Ccr5_gp261	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68459.1	001715	Cluster1226_1clades	73	CcrBL10_gp255	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87791.1	001715	Cluster1226_1clades	72	CcrKarma_gp274	Caulobacter virus Karma	GCA_000901575.1
AFU87438.1	001715	Cluster1226_1clades	72	CcrMagneto_gp268	Caulobacter virus Magneto	GCA_000903095.1
AFU86745.1	001715	Cluster1226_1clades	73	CcrRogue_gp263	Caulobacter virus Rogue	GCA_000900555.1
AFU88584.1	001715	Cluster1226_1clades	72	CcrSwift_gp266	Caulobacter virus Swift	GCA_000899655.1
AFU87092.1	001715	Cluster1226_1clades	72	CbK_gp260	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64236.1	001716	Cluster1227_1clades	72	KVP40.0167	Vibrio phage KVP40	GCA_000843785.1
QIW90550.1	001716	Cluster1227_1clades	68	GCAPEGMB_00203	Vibrio phage V07	GCA_012361095.1
QIW90872.1	001716	Cluster1227_1clades	68	COHAPHLL_00009	Vibrio phage V09	GCA_012361135.1
QHJ74348.1	001716	Cluster1227_1clades	68	VH12019_00021	Vibrio phage VH1_2019	GCA_009931825.1
AGB06842.1	001716	Cluster1227_1clades	70	CF80_gp055	Vibrio phage VH7D	GCA_000914495.1
QBX06304.1	001716	Cluster1227_1clades	70	ValB1HC_351	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60935.1	001716	Cluster1227_1clades	70	AVU32_gp094	Vibrio phage ValKK3	GCA_001501635.1
AGN30217.1	001716	Cluster1227_1clades	73	VPFG_00217	Vibrio phage nt-1	GCA_000910195.2
ALP47290.1	001716	Cluster1227_1clades	70	phiGrn1_0279	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47672.1	001716	Cluster1227_1clades	70	phiST2_0038	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54547.1	001716	Cluster1227_1clades	70	vBValMR10Z_6	Vibrio phage vB_ValM_R10Z	GCA_014337545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN37395.1	001716	Cluster1227_1clades	72	pp2_162	Vibriophage phi-pp2	GCA_002630725.1
AAQ64235.1	001717	Cluster1228_1clades	69	KVP40.0166	Vibrio phage KVP40	GCA_000843785.1
QIW90549.1	001717	Cluster1228_1clades	69	GCAPEGMB_00202	Vibrio phage V07	GCA_012361095.1
QIW90873.1	001717	Cluster1228_1clades	69	COHAPHLL_00010	Vibrio phage V09	GCA_012361135.1
QHJ74347.1	001717	Cluster1228_1clades	69	VH12019_00020	Vibrio phage VH1_2019	GCA_009931825.1
AGB06841.1	001717	Cluster1228_1clades	71	CF80_gp054	Vibrio phage VH7D	GCA_000914495.1
QBX06305.1	001717	Cluster1228_1clades	71	ValB1HC_352	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60936.1	001717	Cluster1228_1clades	71	AVU32_gp095	Vibrio phage ValKK3	GCA_001501635.1
AGN30215.1	001717	Cluster1228_1clades	71	VPFG_00215	Vibrio phage nt-1	GCA_000910195.2
ALP47287.1	001717	Cluster1228_1clades	71	phiGrn1_0278	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47669.1	001717	Cluster1228_1clades	71	phiST2_0037	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54548.1	001717	Cluster1228_1clades	72	vBValMR10Z_7	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37394.1	001717	Cluster1228_1clades	69	pp2_161	Vibriophage phi-pp2	GCA_002630725.1
AAQ64208.1	001718	Cluster1229_1clades	69	KVP40.0138	Vibrio phage KVP40	GCA_000843785.1
QIW90523.1	001718	Cluster1229_1clades	69	GCAPEGMB_00176	Vibrio phage V07	GCA_012361095.1
QIW90899.1	001718	Cluster1229_1clades	69	COHAPHLL_00036	Vibrio phage V09	GCA_012361135.1
QHJ74319.1	001718	Cluster1229_1clades	69	VH12019_00400	Vibrio phage VH1_2019	GCA_009931825.1
AGB06813.1	001718	Cluster1229_1clades	71	CF80_gp026	Vibrio phage VH7D	GCA_000914495.1
QBX06334.1	001718	Cluster1229_1clades	71	ValB1HC_381	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60964.1	001718	Cluster1229_1clades	71	AVU32_gp123	Vibrio phage ValKK3	GCA_001501635.1
AGN30187.1	001718	Cluster1229_1clades	70	VPFG_00187	Vibrio phage nt-1	GCA_000910195.2
ALP47286.1	001718	Cluster1229_1clades	71	phiGrn1_0249	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47670.1	001718	Cluster1229_1clades	71	phiST2_0004	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54577.1	001718	Cluster1229_1clades	71	vBValMR10Z_36	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37369.1	001718	Cluster1229_1clades	69	pp2_136	Vibriophage phi-pp2	GCA_002630725.1
AAQ64376.1	001719	Cluster1230_1clades	70	KVP40.0306	Vibrio phage KVP40	GCA_000843785.1
QIW90692.1	001719	Cluster1230_1clades	70	GCAPEGMB_00345	Vibrio phage V07	GCA_012361095.1
QIW91106.1	001719	Cluster1230_1clades	70	COHAPHLL_00270	Vibrio phage V09	GCA_012361135.1
QHJ74489.1	001719	Cluster1230_1clades	70	VH12019_00162	Vibrio phage VH1_2019	GCA_009931825.1
AGB06971.1	001719	Cluster1230_1clades	70	CF80_gp184	Vibrio phage VH7D	GCA_000914495.1
QBX06162.1	001719	Cluster1230_1clades	70	ValB1HC_209	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61179.1	001719	Cluster1230_1clades	70	AVU32_gp338	Vibrio phage ValKK3	GCA_001501635.1
AGN30354.1	001719	Cluster1230_1clades	70	VPFG_00357	Vibrio phage nt-1	GCA_000910195.2
ALP47291.1	001719	Cluster1230_1clades	70	phiGrn1_0043	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47671.1	001719	Cluster1230_1clades	70	phiST2_0175	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54788.1	001719	Cluster1230_1clades	70	vBValMR10Z_248	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37538.1	001719	Cluster1230_1clades	70	pp2_305	Vibriophage phi-pp2	GCA_002630725.1
AAQ64199.1	001720	Cluster1231_1clades	68	KVP40.0128	Vibrio phage KVP40	GCA_000843785.1
QIW90514.1	001720	Cluster1231_1clades	68	GCAPEGMB_00167	Vibrio phage V07	GCA_012361095.1
QIW90908.1	001720	Cluster1231_1clades	68	COHAPHLL_00045	Vibrio phage V09	GCA_012361135.1
QHJ74310.1	001720	Cluster1231_1clades	68	VH12019_00391	Vibrio phage VH1_2019	GCA_009931825.1
AGB06805.1	001720	Cluster1231_1clades	68	CF80_gp018	Vibrio phage VH7D	GCA_000914495.1
QBX05961.1	001720	Cluster1231_1clades	68	ValB1HC_007	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60973.1	001720	Cluster1231_1clades	68	AVU32_gp132	Vibrio phage ValKK3	GCA_001501635.1
AGN30178.1	001720	Cluster1231_1clades	68	VPFG_00176	Vibrio phage nt-1	GCA_000910195.2
ALP47298.1	001720	Cluster1231_1clades	68	phiGrn1_0240	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47676.1	001720	Cluster1231_1clades	68	phiST2_0378	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54586.1	001720	Cluster1231_1clades	68	vBValMR10Z_45	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37359.1	001720	Cluster1231_1clades	68	pp2_126	Vibriophage phi-pp2	GCA_002630725.1
AAQ64344.1	001721	Cluster1232_1clades	68	KVP40.0275	Vibrio phage KVP40	GCA_000843785.1
QIW90658.1	001721	Cluster1232_1clades	68	GCAPEGMB_00311	Vibrio phage V07	GCA_012361095.1
QIW91140.1	001721	Cluster1232_1clades	68	COHAPHLL_00304	Vibrio phage V09	GCA_012361135.1
QHJ74453.1	001721	Cluster1232_1clades	68	VH12019_00126	Vibrio phage VH1_2019	GCA_009931825.1
AGB06947.1	001721	Cluster1232_1clades	67	CF80_gp160	Vibrio phage VH7D	GCA_000914495.1
QBX06198.1	001721	Cluster1232_1clades	67	ValB1HC_245	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61215.1	001721	Cluster1232_1clades	67	AVU32_gp374	Vibrio phage ValKK3	GCA_001501635.1
AGN30321.1	001721	Cluster1232_1clades	67	VPFG_00323	Vibrio phage nt-1	GCA_000910195.2
ALP47299.1	001721	Cluster1232_1clades	67	phiGrn1_0007	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47680.1	001721	Cluster1232_1clades	67	phiST2_0139	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54823.1	001721	Cluster1232_1clades	67	vBValMR10Z_283	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37504.1	001721	Cluster1232_1clades	68	pp2_271	Vibriophage phi-pp2	GCA_002630725.1
ARB13568.1	001722	Cluster1233_1clades	67	Ccr10_gp040c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13914.1	001722	Cluster1233_1clades	67	Ccr2_gp039c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14603.1	001722	Cluster1233_1clades	67	Ccr29_gp046	Caulobacter phage Ccr29	GCA_002619485.1
ARB14959.1	001722	Cluster1233_1clades	67	Ccr32_gp040	Caulobacter phage Ccr32	GCA_002619505.1
ARB15290.1	001722	Cluster1233_1clades	67	Ccr34_gp041	Caulobacter phage Ccr34	GCA_002619525.1
ARB14257.1	001722	Cluster1233_1clades	67	Ccr5_gp039c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68244.1	001722	Cluster1233_1clades	68	CcrBL10_gp040c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87558.1	001722	Cluster1233_1clades	67	CcrKarma_gp041	Caulobacter virus Karma	GCA_000901575.1
AFU87208.1	001722	Cluster1233_1clades	67	CcrMagneto_gp038	Caulobacter virus Magneto	GCA_000903095.1
AFU86525.1	001722	Cluster1233_1clades	68	CcrRogue_gp043	Caulobacter virus Rogue	GCA_000900555.1
AFU88356.1	001722	Cluster1233_1clades	67	CcrSwift_gp038	Caulobacter virus Swift	GCA_000899655.1
AFU86872.1	001722	Cluster1233_1clades	67	CbK_gp040	Caulobacter virus phiCbK	GCA_000900535.1
ARB13567.1	001723	Cluster1234_1clades	68	Ccr10_gp039	Caulobacter phage Ccr10	GCA_002619445.1
ARB13913.1	001723	Cluster1234_1clades	68	Ccr2_gp038	Caulobacter phage Ccr2	GCA_002619465.1
ARB14602.1	001723	Cluster1234_1clades	68	Ccr29_gp045	Caulobacter phage Ccr29	GCA_002619485.1
ARB14958.1	001723	Cluster1234_1clades	68	Ccr32_gp039	Caulobacter phage Ccr32	GCA_002619505.1
ARB15289.1	001723	Cluster1234_1clades	68	Ccr34_gp040	Caulobacter phage Ccr34	GCA_002619525.1
ARB14256.1	001723	Cluster1234_1clades	68	Ccr5_gp038	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68243.1	001723	Cluster1234_1clades	65	CcrBL10_gp039	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87557.1	001723	Cluster1234_1clades	68	CcrKarma_gp040	Caulobacter virus Karma	GCA_000901575.1
AFU87207.1	001723	Cluster1234_1clades	68	CcrMagneto_gp037	Caulobacter virus Magneto	GCA_000903095.1
AFU86524.1	001723	Cluster1234_1clades	65	CcrRogue_gp042	Caulobacter virus Rogue	GCA_000900555.1
AFU88355.1	001723	Cluster1234_1clades	68	CcrSwift_gp037	Caulobacter virus Swift	GCA_000899655.1
AFU86871.1	001723	Cluster1234_1clades	68	CbK_gp039	Caulobacter virus phiCbK	GCA_000900535.1
ARB13587.1	001724	Cluster1235_1clades	67	Ccr10_gp059	Caulobacter phage Ccr10	GCA_002619445.1
ARB13933.1	001724	Cluster1235_1clades	67	Ccr2_gp058	Caulobacter phage Ccr2	GCA_002619465.1
ARB14622.1	001724	Cluster1235_1clades	67	Ccr29_gp065	Caulobacter phage Ccr29	GCA_002619485.1
ARB14978.1	001724	Cluster1235_1clades	67	Ccr32_gp059	Caulobacter phage Ccr32	GCA_002619505.1
ARB15309.1	001724	Cluster1235_1clades	67	Ccr34_gp060	Caulobacter phage Ccr34	GCA_002619525.1
ARB14276.1	001724	Cluster1235_1clades	67	Ccr5_gp058	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68260.1	001724	Cluster1235_1clades	67	CcrBL10_gp056	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87577.1	001724	Cluster1235_1clades	67	CcrKarma_gp060	Caulobacter virus Karma	GCA_000901575.1
AFU87227.1	001724	Cluster1235_1clades	67	CcrMagneto_gp057	Caulobacter virus Magneto	GCA_000903095.1
AFU86542.1	001724	Cluster1235_1clades	67	CcrRogue_gp060	Caulobacter virus Rogue	GCA_000900555.1
AFU88375.1	001724	Cluster1235_1clades	67	CcrSwift_gp057	Caulobacter virus Swift	GCA_000899655.1
AFU86891.1	001724	Cluster1235_1clades	67	CbK_gp059	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64101.1	001725	N_methyl	66	KVP40.0030	Vibrio phage KVP40	GCA_000843785.1
QIW90424.1	001725	N_methyl	66	GCAPEGMB_00077	Vibrio phage V07	GCA_012361095.1
QIW91005.1	001725	N_methyl	66	COHAPHLL_00142	Vibrio phage V09	GCA_012361135.1
QHJ74213.1	001725	N_methyl	66	VH12019_00294	Vibrio phage VH1_2019	GCA_009931825.1
AGB07037.1	001725	N_methyl	67	CF80_gp250	Vibrio phage VH7D	GCA_000914495.1
QBX06059.1	001725	N_methyl	67	ValB1HC_105	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61072.1	001725	N_methyl	67	AVU32_gp231	Vibrio phage ValKK3	GCA_001501635.1
AGN30080.1	001725	N_methyl	61	VPFG_00078	Vibrio phage nt-1	GCA_000910195.2
ALP47300.1	001725	N_methyl	67	phiGrn1_0145	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47679.1	001725	N_methyl	67	phiST2_0275	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54685.1	001725	N_methyl	67	vBValMR10Z_144	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37264.1	001725	N_methyl	66	pp2_030	Vibriophage phi-pp2	GCA_002630725.1
AHI60316.1	001726	Cluster1237_1clades	66	Ea357_165	Erwinia phage Ea35-70	GCA_000914635.1
QBP07275.1	001726	Cluster1237_1clades	66	REBECCA_168	Erwinia phage Rebecca	GCA_004521635.1
AUG85955.1	001726	Cluster1237_1clades	66	BOSOLAPHORUS_168	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52270.1	001726	Cluster1237_1clades	66	DM_172	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86274.1	001726	Cluster1237_1clades	66	DESERTFOX_167	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86596.1	001726	Cluster1237_1clades	66	MADMEL_168	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86920.1	001726	Cluster1237_1clades	66	MORTIMER_171	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51947.1	001726	Cluster1237_1clades	66	RAY_166	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51631.1	001726	Cluster1237_1clades	66	SIMMY50_169	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64978.1	001726	Cluster1237_1clades	66	SPECIALG_168	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24097.1	001726	Cluster1237_1clades	65	-	Proteus phage 10	GCA_014071245.1
QKE54473.1	001726	Cluster1237_1clades	66	ACSA002_1590	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64234.1	001727	Cluster1238_1clades	65	KVP40.0165	Vibrio phage KVP40	GCA_000843785.1
QIW90548.1	001727	Cluster1238_1clades	61	GCAPEGMB_00201	Vibrio phage V07	GCA_012361095.1
QIW90874.1	001727	Cluster1238_1clades	61	COHAPHLL_00011	Vibrio phage V09	GCA_012361135.1
QHJ74346.1	001727	Cluster1238_1clades	61	VH12019_00019	Vibrio phage VH1_2019	GCA_009931825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGB06840.1	001727	Cluster1238_1clades	46	CF80_gp053	Vibrio phage VH7D	GCA_000914495.1
QBX06306.1	001727	Cluster1238_1clades	61	ValB1HC_353	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60937.1	001727	Cluster1238_1clades	65	AVU32_gp096	Vibrio phage ValKK3	GCA_001501635.1
AGN30216.1	001727	Cluster1238_1clades	63	VPFG_00216	Vibrio phage nt-1	GCA_000910195.2
ALP47304.1	001727	Cluster1238_1clades	65	phiGrn1_0277	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47711.1	001727	Cluster1238_1clades	46	phiST2_0036	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54549.1	001727	Cluster1238_1clades	61	vBValMR10Z_8	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37393.1	001727	Cluster1238_1clades	61	pp2_160	Vibriophage phi-pp2	GCA_002630725.1
AAQ64103.1	001728	Cluster1239_1clades	64	KVP40.0032	Vibrio phage KVP40	GCA_000843785.1
QIW90426.1	001728	Cluster1239_1clades	64	GCAPEGMB_00079	Vibrio phage V07	GCA_012361095.1
QIW91003.1	001728	Cluster1239_1clades	64	COHAPHLL_00140	Vibrio phage V09	GCA_012361135.1
QHJ74215.1	001728	Cluster1239_1clades	64	VH12019_00296	Vibrio phage VH1_2019	GCA_009931825.1
AGB07039.1	001728	Cluster1239_1clades	64	CF80_gp252	Vibrio phage VH7D	GCA_000914495.1
QBX06057.1	001728	Cluster1239_1clades	64	ValB1HC_103	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61070.1	001728	Cluster1239_1clades	64	AVU32_gp229	Vibrio phage ValKK3	GCA_001501635.1
AGN30082.1	001728	Cluster1239_1clades	65	VPFG_00080	Vibrio phage nt-1	GCA_000910195.2
ALP47307.1	001728	Cluster1239_1clades	64	phiGrn1_0147	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47686.1	001728	Cluster1239_1clades	64	phiST2_0277	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54683.1	001728	Cluster1239_1clades	64	vBValMR10Z_142	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37266.1	001728	Cluster1239_1clades	64	pp2_032	Vibriophage phi-pp2	GCA_002630725.1
AAQ64166.1	001729	Cluster1240_1clades	63	KVP40.0095	Vibrio phage KVP40	GCA_000843785.1
QIW90489.1	001729	Cluster1240_1clades	63	GCAPEGMB_00142	Vibrio phage V07	GCA_012361095.1
QIW90940.1	001729	Cluster1240_1clades	63	COHAPHLL_00077	Vibrio phage V09	GCA_012361135.1
QHJ74277.1	001729	Cluster1240_1clades	63	VH12019_00358	Vibrio phage VH1_2019	GCA_009931825.1
AGB07102.1	001729	Cluster1240_1clades	63	CF80_gp315	Vibrio phage VH7D	GCA_000914495.1
QBX05993.1	001729	Cluster1240_1clades	63	ValB1HC_039	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61006.1	001729	Cluster1240_1clades	63	AVU32_gp165	Vibrio phage ValKK3	GCA_001501635.1
AGN30145.1	001729	Cluster1240_1clades	63	VPFG_00143	Vibrio phage nt-1	GCA_000910195.2
ALP47308.1	001729	Cluster1240_1clades	63	phiGrn1_0209	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47688.1	001729	Cluster1240_1clades	63	phiST2_0342	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54618.1	001729	Cluster1240_1clades	63	vBValMR10Z_77	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37325.1	001729	Cluster1240_1clades	63	pp2_092	Vibriophage phi-pp2	GCA_002630725.1
AAQ64096.1	001730	Cluster1241_1clades	61	KVP40.0025	Vibrio phage KVP40	GCA_000843785.1
QIW90419.1	001730	Cluster1241_1clades	45	GCAPEGMB_00072	Vibrio phage V07	GCA_012361095.1
QIW91010.1	001730	Cluster1241_1clades	45	COHAPHLL_00147	Vibrio phage V09	GCA_012361135.1
QHJ74208.1	001730	Cluster1241_1clades	45	VH12019_00289	Vibrio phage VH1_2019	GCA_009931825.1
AGB07032.1	001730	Cluster1241_1clades	45	CF80_gp245	Vibrio phage VH7D	GCA_000914495.1
QBX06064.1	001730	Cluster1241_1clades	45	ValB1HC_110	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61078.1	001730	Cluster1241_1clades	45	AVU32_gp237	Vibrio phage ValKK3	GCA_001501635.1
AGN30268.2	001730	Cluster1241_1clades	56	VPFG_00269	Vibrio phage nt-1	GCA_000910195.2
ALP47331.1	001730	Cluster1241_1clades	45	phiGrn1_0140	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47712.1	001730	Cluster1241_1clades	45	phiST2_0270	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54690.1	001730	Cluster1241_1clades	45	vBValMR10Z_149	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37259.1	001730	Cluster1241_1clades	45	pp2_025	Vibriophage phi-pp2	GCA_002630725.1
ARB13758.1	001731	Cluster1242_1clades	59	Ccr10_gp228c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14103.1	001731	Cluster1242_1clades	59	Ccr2_gp227c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14792.1	001731	Cluster1242_1clades	59	Ccr29_gp236	Caulobacter phage Ccr29	GCA_002619485.1
ARB15136.1	001731	Cluster1242_1clades	59	Ccr32_gp218	Caulobacter phage Ccr32	GCA_002619505.1
ARB15470.1	001731	Cluster1242_1clades	59	Ccr34_gp228	Caulobacter phage Ccr34	GCA_002619525.1
ARB14445.1	001731	Cluster1242_1clades	59	Ccr5_gp225c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68425.1	001731	Cluster1242_1clades	61	CcrBL10_gp221c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87752.1	001731	Cluster1242_1clades	59	CcrKarma_gp235	Caulobacter virus Karma	GCA_000901575.1
AFU87400.1	001731	Cluster1242_1clades	59	CcrMagneto_gp230	Caulobacter virus Magneto	GCA_000903095.1
AFU86711.1	001731	Cluster1242_1clades	61	CcrRogue_gp229	Caulobacter virus Rogue	GCA_000900555.1
AFU88548.1	001731	Cluster1242_1clades	59	CcrSwift_gp230	Caulobacter virus Swift	GCA_000899655.1
AFU87055.1	001731	Cluster1242_1clades	59	CbK_gp223	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64227.1	001732	Cluster1243_1clades	59	KVP40.0158	Vibrio phage KVP40	GCA_000843785.1
QIW90541.1	001732	Cluster1243_1clades	59	GCAPEGMB_00194	Vibrio phage V07	GCA_012361095.1
QIW90881.1	001732	Cluster1243_1clades	59	COHAPHLL_00018	Vibrio phage V09	GCA_012361135.1
QHJ74339.1	001732	Cluster1243_1clades	59	VH12019_00012	Vibrio phage VH1_2019	GCA_009931825.1
AGB06832.1	001732	Cluster1243_1clades	59	CF80_gp045	Vibrio phage VH7D	GCA_000914495.1
QBX06314.1	001732	Cluster1243_1clades	59	ValB1HC_361	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60945.1	001732	Cluster1243_1clades	59	AVU32_gp104	Vibrio phage ValKK3	GCA_001501635.1
AGN30205.1	001732	Cluster1243_1clades	57	VPFG_00205	Vibrio phage nt-1	GCA_000910195.2
ALP47314.1	001732	Cluster1243_1clades	59	phiGrn1_0269	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47693.1	001732	Cluster1243_1clades	59	phiST2_0028	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54557.1	001732	Cluster1243_1clades	59	vBValMR10Z_16	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37386.1	001732	Cluster1243_1clades	59	pp2_153	Vibriophage phi-pp2	GCA_002630725.1
AUE22700.1	001733	Cluster1244_1clades	53	Ah1_00159	Aeromonas phage Ah1	GCA_002957415.1
QAY01329.1	001733	Cluster1244_1clades	54	ASwh1_267	Aeromonas phage Aswh_1	GCA_004146945.1
ADM80143.1	001733	Cluster1244_1clades	54	phiAS5_ORF0300	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17831.1	001733	Cluster1244_1clades	53	Aeh1ORF165c	Aeromonas virus Aeh1	GCA_000843245.1
AFA44795.1	001733	Cluster1244_1clades	53	RaK2_00524	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AAQ64381.1	001733	Cluster1244_1clades	59	KVP40.0311	Vibrio phage KVP40	GCA_000843785.1
QIW90696.1	001733	Cluster1244_1clades	59	GCAPEGMB_00350	Vibrio phage V07	GCA_012361095.1
QIW91102.1	001733	Cluster1244_1clades	59	COHAPHLL_00265	Vibrio phage V09	GCA_012361135.1
QHJ74494.1	001733	Cluster1244_1clades	59	VH12019_00168	Vibrio phage VH1_2019	GCA_009931825.1
AGN30356.1	001733	Cluster1244_1clades	59	VPFG_00359	Vibrio phage nt-1	GCA_000910195.2
ALP47313.1	001733	Cluster1244_1clades	59	phiGrn1_0047	Vibrio phage phi-Grn1	GCA_002757115.1
AFN37542.1	001733	Cluster1244_1clades	59	pp2_309	Vibriophage phi-pp2	GCA_002630725.1
AMO43381.1	001734	Cluster1245_1clades	57	W270710_137	Cyanophage S-RIM44	GCA_002599145.1
AOO11626.1	001734	Cluster1245_1clades	57	ES420910_145	Cyanophage S-RIM44	GCA_002599165.1
AOO11853.1	001734	Cluster1245_1clades	57	Np050604_137	Cyanophage S-RIM44	GCA_002599185.1
AOO12091.1	001734	Cluster1245_1clades	57	Np200711_145	Cyanophage S-RIM44	GCA_002599205.1
AOO12327.1	001734	Cluster1245_1clades	57	Np420711_145	Cyanophage S-RIM44	GCA_002599225.1
AOO12554.1	001734	Cluster1245_1clades	57	Sn080709_137	Cyanophage S-RIM44	GCA_002599245.1
AOO12792.1	001734	Cluster1245_1clades	57	Sn130910_145	Cyanophage S-RIM44	GCA_002599265.1
AOO13020.1	001734	Cluster1245_1clades	57	W2100709_138	Cyanophage S-RIM44	GCA_002599285.1
ADO99239.1	001734	Cluster1245_1clades	57	Syn1_138	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59605.1	001734	Cluster1245_1clades	59	S330809_144	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59367.1	001734	Cluster1245_1clades	59	C440309_144	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59843.1	001734	Cluster1245_1clades	59	N231010_144	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13849.1	001735	Cluster1246_1clades	57	Ccr10_gp319	Caulobacter phage Ccr10	GCA_002619445.1
ARB14194.1	001735	Cluster1246_1clades	57	Ccr2_gp318	Caulobacter phage Ccr2	GCA_002619465.1
ARB14888.1	001735	Cluster1246_1clades	57	Ccr29_gp332	Caulobacter phage Ccr29	GCA_002619485.1
ARB15226.1	001735	Cluster1246_1clades	57	Ccr32_gp308	Caulobacter phage Ccr32	GCA_002619505.1
ARB15560.1	001735	Cluster1246_1clades	57	Ccr34_gp318	Caulobacter phage Ccr34	GCA_002619525.1
ARB14534.1	001735	Cluster1246_1clades	57	Ccr5_gp314	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68517.1	001735	Cluster1246_1clades	58	CcrBL10_gp313	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87845.1	001735	Cluster1246_1clades	57	CcrKarma_gp328	Caulobacter virus Karma	GCA_000901575.1
AFU87493.1	001735	Cluster1246_1clades	57	CcrMagneto_gp323	Caulobacter virus Magneto	GCA_000903095.1
AFU86807.1	001735	Cluster1246_1clades	58	CcrRogue_gp325	Caulobacter virus Rogue	GCA_000900555.1
AFU88638.1	001735	Cluster1246_1clades	57	CcrSwift_gp320	Caulobacter virus Swift	GCA_000899655.1
AFU87145.1	001735	Cluster1246_1clades	57	CbK_gp313	Caulobacter virus phiCbK	GCA_000900535.1
ARB13634.1	001736	Cluster1247_1clades	57	Ccr10_gp105	Caulobacter phage Ccr10	GCA_002619445.1
ARB13979.1	001736	Cluster1247_1clades	57	Ccr2_gp104	Caulobacter phage Ccr2	GCA_002619465.1
ARB14667.1	001736	Cluster1247_1clades	57	Ccr29_gp111	Caulobacter phage Ccr29	GCA_002619485.1
ARB15022.1	001736	Cluster1247_1clades	57	Ccr32_gp104	Caulobacter phage Ccr32	GCA_002619505.1
ARB15354.1	001736	Cluster1247_1clades	57	Ccr34_gp112	Caulobacter phage Ccr34	GCA_002619525.1
ARB14323.1	001736	Cluster1247_1clades	57	Ccr5_gp105	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68303.1	001736	Cluster1247_1clades	54	CcrBL10_gp099	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87626.1	001736	Cluster1247_1clades	57	CcrKarma_gp109	Caulobacter virus Karma	GCA_000901575.1
AFU87275.1	001736	Cluster1247_1clades	57	CcrMagneto_gp105	Caulobacter virus Magneto	GCA_000903095.1
AFU86587.1	001736	Cluster1247_1clades	48	CcrRogue_gp105	Caulobacter virus Rogue	GCA_000900555.1
AFU88422.1	001736	Cluster1247_1clades	57	CcrSwift_gp104	Caulobacter virus Swift	GCA_000899655.1
AFU86940.1	001736	Cluster1247_1clades	57	CbK_gp108	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64428.1	001737	Cluster1248_1clades	55	KVP40.0359	Vibrio phage KVP40	GCA_000843785.1
QIW90373.1	001737	Cluster1248_1clades	55	GCAPEGMB_00026	Vibrio phage V07	GCA_012361095.1
QIW91056.1	001737	Cluster1248_1clades	55	COHAPHLL_00193	Vibrio phage V09	GCA_012361135.1
QHJ74542.1	001737	Cluster1248_1clades	55	VH12019_00242	Vibrio phage VH1_2019	GCA_009931825.1
AGB07000.1	001737	Cluster1248_1clades	55	CF80_gp213	Vibrio phage VH7D	GCA_000914495.1
QBX06114.1	001737	Cluster1248_1clades	55	ValB1HC_160	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61126.1	001737	Cluster1248_1clades	55	AVU32_gp285	Vibrio phage ValKK3	GCA_001501635.1
AGN30032.1	001737	Cluster1248_1clades	55	VPFG_00024	Vibrio phage nt-1	GCA_000910195.2
ALP47323.1	001737	Cluster1248_1clades	55	phiGrn1_0093	Vibrio phage phi-Grn1	GCA_002757115.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALP47702.1	001737	Cluster1248_1clades	55	phiST2_0225	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54739.1	001737	Cluster1248_1clades	55	vBValMR10Z_199	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37591.1	001737	Cluster1248_1clades	55	pp2_359	Vibriophage phi-pp2	GCA_002630725.1
AAQ64356.1	001738	Cluster1249_1clades	52	KVP40.0286	Vibrio phage KVP40	GCA_000843785.1
QIW90670.1	001738	Cluster1249_1clades	52	GCAPEGMB_00323	Vibrio phage V07	GCA_012361095.1
QIW91128.1	001738	Cluster1249_1clades	52	COHAPHLL_00292	Vibrio phage V09	GCA_012361135.1
QHJ74465.1	001738	Cluster1249_1clades	52	VH12019_00138	Vibrio phage VH1_2019	GCA_009931825.1
AGB06959.1	001738	Cluster1249_1clades	55	CF80_gp172	Vibrio phage VH7D	GCA_000914495.1
QBX06186.1	001738	Cluster1249_1clades	51	ValB1HC_233	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61203.1	001738	Cluster1249_1clades	51	AVU32_gp362	Vibrio phage ValKK3	GCA_001501635.1
AGN30332.1	001738	Cluster1249_1clades	51	VPFG_00335	Vibrio phage nt-1	GCA_000910195.2
ALP47324.1	001738	Cluster1249_1clades	55	phiGrn1_0019	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47705.1	001738	Cluster1249_1clades	55	phiST2_0150	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54811.1	001738	Cluster1249_1clades	51	vBValMR10Z_271	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37517.1	001738	Cluster1249_1clades	52	pp2_284	Vibriophage phi-pp2	GCA_002630725.1
AMO43248.1	001739	Cluster1250_1clades	54	W270710_003	Cyanophage S-RIM44	GCA_002599145.1
AOO11485.1	001739	Cluster1250_1clades	54	ES420910_003	Cyanophage S-RIM44	GCA_002599165.1
AOO11720.1	001739	Cluster1250_1clades	54	Np050604_003	Cyanophage S-RIM44	GCA_002599185.1
AOO11950.1	001739	Cluster1250_1clades	54	Np200711_003	Cyanophage S-RIM44	GCA_002599205.1
AOO12186.1	001739	Cluster1250_1clades	54	Np420711_003	Cyanophage S-RIM44	GCA_002599225.1
AOO12421.1	001739	Cluster1250_1clades	54	Sn080709_003	Cyanophage S-RIM44	GCA_002599245.1
AOO12651.1	001739	Cluster1250_1clades	54	Sn130910_003	Cyanophage S-RIM44	GCA_002599265.1
AOO12886.1	001739	Cluster1250_1clades	54	W2100709_003	Cyanophage S-RIM44	GCA_002599285.1
ADO99106.1	001739	Cluster1250_1clades	54	Syn1_004	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59463.1	001739	Cluster1250_1clades	44	S330809_002	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59225.1	001739	Cluster1250_1clades	44	C440309_002	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59701.1	001739	Cluster1250_1clades	44	N231010_002	Synechococcus phage S-CAM4	GCA_002922155.1
ARB13591.1	001740	Cluster1251_1clades	54	Ccr10_gp063	Caulobacter phage Ccr10	GCA_002619445.1
ARB13937.1	001740	Cluster1251_1clades	54	Ccr2_gp062	Caulobacter phage Ccr2	GCA_002619465.1
ARB14626.1	001740	Cluster1251_1clades	54	Ccr29_gp069	Caulobacter phage Ccr29	GCA_002619485.1
ARB14982.1	001740	Cluster1251_1clades	54	Ccr32_gp063	Caulobacter phage Ccr32	GCA_002619505.1
ARB15313.1	001740	Cluster1251_1clades	54	Ccr34_gp064	Caulobacter phage Ccr34	GCA_002619525.1
ARB14280.1	001740	Cluster1251_1clades	54	Ccr5_gp062	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68264.1	001740	Cluster1251_1clades	53	CcrBL10_gp060	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87581.1	001740	Cluster1251_1clades	54	CcrKarma_gp064	Caulobacter virus Karma	GCA_000901575.1
AFU87231.1	001740	Cluster1251_1clades	54	CcrMagneto_gp061	Caulobacter virus Magneto	GCA_000903095.1
AFU86547.1	001740	Cluster1251_1clades	53	CcrRogue_gp065	Caulobacter virus Rogue	GCA_000900555.1
AFU88379.1	001740	Cluster1251_1clades	54	CcrSwift_gp061	Caulobacter virus Swift	GCA_000899655.1
AFU86895.1	001740	Cluster1251_1clades	54	CbK_gp063	Caulobacter virus phiCbK	GCA_000900535.1
AIT14019.1	001741	Cluster1252_1clades	54	PBI_121Q_125	Escherichia phage 121Q	GCA_000926855.1
AIT14020.1	001741	Cluster1252_1clades	54	PBI_121Q_126	Escherichia phage 121Q	GCA_000926855.1
QAY00319.1	001741	Cluster1252_1clades	54	Ecwhy1_37	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00320.1	001741	Cluster1252_1clades	54	Ecwhy1_38	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35067.1	001741	Cluster1252_1clades	54	ACQ29_gp387	Escherichia phage PBECO4	GCA_001041035.1
BBM61708.1	001741	Cluster1252_1clades	48	EO157G_1190	Escherichia phage SP27	GCA_008033345.1
AXC36644.1	001741	Cluster1252_1clades	54	-	Escherichia phage UB	GCA_003341455.1
QBO61676.1	001741	Cluster1252_1clades	54	G17_00184	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61677.1	001741	Cluster1252_1clades	54	G17_00185	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13725.1	001741	Cluster1252_1clades	54	vBEcoMphAPEC6_gp095c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13726.1	001741	Cluster1252_1clades	54	vBEcoMphAPEC6_gp096c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80020.1	001741	Cluster1252_1clades	54	PSLUR01_00039	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64095.1	001742	Cluster1253_1clades	53	KVP40.0024	Vibrio phage KVP40	GCA_000843785.1
QIW90418.1	001742	Cluster1253_1clades	53	GCAPEGMB_00071	Vibrio phage V07	GCA_012361095.1
QIW91011.1	001742	Cluster1253_1clades	53	COHAPHLL_00148	Vibrio phage V09	GCA_012361135.1
QHJ74207.1	001742	Cluster1253_1clades	53	VH12019_00288	Vibrio phage VH1_2019	GCA_009931825.1
AGB07031.1	001742	Cluster1253_1clades	53	CF80_gp244	Vibrio phage VH7D	GCA_000914495.1
QBX06065.1	001742	Cluster1253_1clades	53	ValB1HC_111	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61079.1	001742	Cluster1253_1clades	53	AVU32_gp238	Vibrio phage ValKK3	GCA_001501635.1
AGN30075.1	001742	Cluster1253_1clades	53	VPFG_00073	Vibrio phage nt-1	GCA_000910195.2
ALP47325.1	001742	Cluster1253_1clades	53	phiGrn1_0139	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47706.1	001742	Cluster1253_1clades	53	phiST2_0269	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54691.1	001742	Cluster1253_1clades	52	vBValMR10Z_150	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37258.1	001742	Cluster1253_1clades	53	pp2_024	Vibriophage phi-pp2	GCA_002630725.1
ARB13739.1	001743	Cluster1254_1clades	52	Ccr10_gp209c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14084.1	001743	Cluster1254_1clades	52	Ccr2_gp208c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14773.1	001743	Cluster1254_1clades	52	Ccr29_gp217	Caulobacter phage Ccr29	GCA_002619485.1
ARB15117.1	001743	Cluster1254_1clades	52	Ccr32_gp199	Caulobacter phage Ccr32	GCA_002619505.1
ARB15451.1	001743	Cluster1254_1clades	52	Ccr34_gp209	Caulobacter phage Ccr34	GCA_002619525.1
ARB14426.1	001743	Cluster1254_1clades	52	Ccr5_gp206c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68405.1	001743	Cluster1254_1clades	51	CcrBL10_gp201c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87732.1	001743	Cluster1254_1clades	52	CcrKarma_gp215	Caulobacter virus Karma	GCA_000901575.1
AFU87381.1	001743	Cluster1254_1clades	52	CcrMagneto_gp211	Caulobacter virus Magneto	GCA_000903095.1
AFU86691.1	001743	Cluster1254_1clades	51	CcrRogue_gp209	Caulobacter virus Rogue	GCA_000900555.1
AFU88528.1	001743	Cluster1254_1clades	52	CcrSwift_gp210	Caulobacter virus Swift	GCA_000899655.1
AFU87036.1	001743	Cluster1254_1clades	52	CbK_gp204	Caulobacter virus phiCbK	GCA_000900535.1
ARB13703.1	001744	Cluster1255_1clades	49	Ccr10_gp173c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14048.1	001744	Cluster1255_1clades	49	Ccr2_gp172c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14735.1	001744	Cluster1255_1clades	49	Ccr29_gp179	Caulobacter phage Ccr29	GCA_002619485.1
ARB15090.1	001744	Cluster1255_1clades	48	Ccr32_gp172	Caulobacter phage Ccr32	GCA_002619505.1
ARB15424.1	001744	Cluster1255_1clades	48	Ccr34_gp182	Caulobacter phage Ccr34	GCA_002619525.1
ARB14391.1	001744	Cluster1255_1clades	48	Ccr5_gp171c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68373.1	001744	Cluster1255_1clades	47	CcrBL10_gp169c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87696.1	001744	Cluster1255_1clades	48	CcrKarma_gp179	Caulobacter virus Karma	GCA_000901575.1
AFU87345.1	001744	Cluster1255_1clades	48	CcrMagneto_gp175	Caulobacter virus Magneto	GCA_000903095.1
AFU86656.1	001744	Cluster1255_1clades	49	CcrRogue_gp174	Caulobacter virus Rogue	GCA_000900555.1
AFU88492.1	001744	Cluster1255_1clades	48	CcrSwift_gp174	Caulobacter virus Swift	GCA_000899655.1
AFU87009.1	001744	Cluster1255_1clades	48	CbK_gp177	Caulobacter virus phiCbK	GCA_000900535.1
ARB13610.1	001745	Cluster1256_1clades	48	Ccr10_gp082	Caulobacter phage Ccr10	GCA_002619445.1
ARB13956.1	001745	Cluster1256_1clades	48	Ccr2_gp081	Caulobacter phage Ccr2	GCA_002619465.1
ARB14646.1	001745	Cluster1256_1clades	48	Ccr29_gp089	Caulobacter phage Ccr29	GCA_002619485.1
ARB15001.1	001745	Cluster1256_1clades	45	Ccr32_gp082	Caulobacter phage Ccr32	GCA_002619505.1
ARB15332.1	001745	Cluster1256_1clades	45	Ccr34_gp089	Caulobacter phage Ccr34	GCA_002619525.1
ARB14299.1	001745	Cluster1256_1clades	45	Ccr5_gp081	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68282.1	001745	Cluster1256_1clades	45	CcrBL10_gp078	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87600.1	001745	Cluster1256_1clades	45	CcrKarma_gp083	Caulobacter virus Karma	GCA_000901575.1
AFU87250.1	001745	Cluster1256_1clades	45	CcrMagneto_gp080	Caulobacter virus Magneto	GCA_000903095.1
AFU86565.1	001745	Cluster1256_1clades	45	CcrRogue_gp083	Caulobacter virus Rogue	GCA_000900555.1
AFU88397.1	001745	Cluster1256_1clades	45	CcrSwift_gp079	Caulobacter virus Swift	GCA_000899655.1
AFU86915.1	001745	Cluster1256_1clades	45	CbK_gp083	Caulobacter virus phiCbK	GCA_000900535.1
AIT14181.1	001746	Cluster1257_1clades	47	PBI_121Q_291	Escherichia phage 121Q	GCA_000926855.1
QAY00756.1	001746	Cluster1257_1clades	47	Ecwhy1_482	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34935.1	001746	Cluster1257_1clades	47	ACQ29_gp255	Escherichia phage PBECO4	GCA_001041035.1
BBM61856.1	001746	Cluster1257_1clades	47	EO157G_2670	Escherichia phage SP27	GCA_008033345.1
AXC37038.1	001746	Cluster1257_1clades	47	-	Escherichia phage UB	GCA_003341455.1
QBO61524.1	001746	Cluster1257_1clades	47	G17_00028	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62130.1	001746	Cluster1257_1clades	47	G17_00641	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14138.1	001746	Cluster1257_1clades	47	vBEcoMphAPEC6_gp515c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80166.1	001746	Cluster1257_1clades	47	PSLUR01_00189	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18705.1	001746	Cluster1257_1clades	45	7t3_0184	Salmonella phage 7t3	GCA_006083215.1
AZU97977.1	001746	Cluster1257_1clades	45	CPT_Munch_033	Salmonella phage Munch	GCA_004015485.1
QIG63001.1	001746	Cluster1257_1clades	45	SEPL_388	Salmonella phage SE_PL	GCA_011067555.1
AAQ64212.1	001747	Cluster1258_1clades	45	KVP40.0142	Vibrio phage KVP40	GCA_000843785.1
QIW90527.1	001747	Cluster1258_1clades	45	GCAPEGMB_00180	Vibrio phage V07	GCA_012361095.1
QIW90895.1	001747	Cluster1258_1clades	45	COHAPHLL_00032	Vibrio phage V09	GCA_012361135.1
QHJ74323.1	001747	Cluster1258_1clades	45	VH12019_00404	Vibrio phage VH1_2019	GCA_009931825.1
AGB06817.1	001747	Cluster1258_1clades	45	CF80_gp030	Vibrio phage VH7D	GCA_000914495.1
QBX06330.1	001747	Cluster1258_1clades	45	ValB1HC_377	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60960.1	001747	Cluster1258_1clades	45	AVU32_gp119	Vibrio phage ValKK3	GCA_001501635.1
AIE13796.1	001747	Cluster1258_1clades	45	VPFG_p17	Vibrio phage nt-1	GCA_000910195.2
ALP47330.1	001747	Cluster1258_1clades	45	phiGrn1_0253	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47713.1	001747	Cluster1258_1clades	45	phiST2_0008	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54573.1	001747	Cluster1258_1clades	45	vBValMR10Z_32	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37373.1	001747	Cluster1258_1clades	45	pp2_140	Vibriophage phi-pp2	GCA_002630725.1
ABY62989.1	001748	Cluster1260_1clades	922	201phi2-1p159	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44882.1	001748	Cluster1260_1clades	816	KTN4_124	Pseudomonas phage KTN4	GCA_002607225.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARV77266.1	001748	Cluster1260_1clades	465	NOXIFER_96	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32259.1	001748	Cluster1260_1clades	844	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76774.1	001748	Cluster1260_1clades	905	PHABIO_143	Pseudomonas phage Phabio	GCA_002624965.1
AEH03526.1	001748	Cluster1260_1clades	853	102	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02637.1	001748	Cluster1260_1clades	704	PSA21_109	Pseudomonas phage Psa21	GCA_004340405.1
ATN94831.1	001748	Cluster1260_1clades	816	SL2_254	Pseudomonas phage SL2	GCA_002956015.1
QJB22759.1	001748	Cluster1260_1clades	816	fnug_116	Pseudomonas phage fnug	GCA_012837215.1
QEM41833.1	001748	Cluster1260_1clades	844	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82998.1	001748	Cluster1260_1clades	816	PHIKZ097	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64451.1	001749	Cluster1261_1clades	894	KVP40.0383	Vibrio phage KVP40	GCA_000843785.1
QIW90396.1	001749	Cluster1261_1clades	894	GCAPEGMB_00049	Vibrio phage V07	GCA_012361095.1
QIW91033.1	001749	Cluster1261_1clades	894	COHAPHLL_00170	Vibrio phage V09	GCA_012361135.1
QHJ74563.1	001749	Cluster1261_1clades	894	VH12019_00263	Vibrio phage VH1_2019	GCA_009931825.1
QBX06090.1	001749	Cluster1261_1clades	897	ValB1HC_136	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61104.1	001749	Cluster1261_1clades	897	AVU32_gp263	Vibrio phage ValKK3	GCA_001501635.1
AGN30051.1	001749	Cluster1261_1clades	900	VPFG_00046	Vibrio phage nt-1	GCA_000910195.2
ALP46961.1	001749	Cluster1261_1clades	897	phiGrn1_0114	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47341.1	001749	Cluster1261_1clades	897	phiST2_0245	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54716.1	001749	Cluster1261_1clades	897	vBValMR10Z_175	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37614.1	001749	Cluster1261_1clades	894	pp2_382	Vibriophage phi-pp2	GCA_002630725.1
AXG67153.1	001750	DUF3751	779	AD1_109	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79902.1	001750	DUF3751	773	JA11_097	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66501.1	001750	DUF3751	773	JA13_098	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66826.1	001750	DUF3751	773	JA29_100	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67471.1	001750	DUF3751	773	JA33_097	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08387.1	001750	DUF3751	780	Alexandra_115	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58751.1	001750	DUF3751	775	Y3_111	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28585.1	001750	DUF3751	775	YOLOSWAG_103	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38306.1	001750	DUF3751	810	BN7874_137	Phage NCTB	GCA_900092385.1
AFH14767.1	001750	DUF3751	769	Lu11_0230	Pseudomonas phage Lu11	GCA_000897175.1
AGS82117.1	001750	DUF3751	772	PaBG_00243	Pseudomonas phage PaBG	GCA_000912555.1
ABY63033.1	001751	Med15	696	201phi2-1p204	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44917.1	001751	Med15	721	KTN4_159	Pseudomonas phage KTN4	GCA_002607225.1
ARV77295.1	001751	Med15	701	NOXIFER_126	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32301.1	001751	Med15	687	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76822.1	001751	Med15	697	PHABIO_191	Pseudomonas phage Phabio	GCA_002624965.1
AEH03563.1	001751	Med15	261	140	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02950.1	001751	Med15	722	PSA21_174	Pseudomonas phage Psa21	GCA_004340405.1
ATN94797.1	001751	Med15	721	SL2_220	Pseudomonas phage SL2	GCA_002956015.1
QJB22795.1	001751	Med15	721	fnug_152	Pseudomonas phage fnug	GCA_012837215.1
QEM41874.1	001751	Med15	687	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83025.1	001751	Med15	721	PHIKZ124	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64396.1	001752	TM+TM	656	KVP40.0326	Vibrio phage KVP40	GCA_000843785.1
QIW90708.1	001752	TM+TM	656	GCAPEGMB_00389	Vibrio phage V07	GCA_012361095.1
QIW91089.1	001752	TM+TM	656	COHAPHLL_00226	Vibrio phage V09	GCA_012361135.1
QHJ74508.1	001752	TM+TM	656	VH12019_00208	Vibrio phage VH1_2019	GCA_009931825.1
QBX06147.1	001752	TM+TM	657	ValB1HC_193	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61159.1	001752	TM+TM	657	AVU32_gp318	Vibrio phage ValKK3	GCA_001501635.1
AGN30377.2	001752	TM+TM	623	VPFG_00380	Vibrio phage nt-1	GCA_000910195.2
ALP46968.1	001752	TM+TM	657	phiGrn1_0060	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47348.1	001752	TM+TM	657	phiST2_0192	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54772.1	001752	TM+TM	657	vBValMR10Z_232	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37558.1	001752	TM+TM	656	pp2_326	Vibriophage phi-pp2	GCA_002630725.1
ABY62937.1	001753	Cluster1267_1clades	631	201phi2-1p105	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44831.1	001753	Cluster1267_1clades	626	KTN4_073	Pseudomonas phage KTN4	GCA_002607225.1
ARV77221.1	001753	Cluster1267_1clades	625	NOXIFER_50	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32206.1	001753	Cluster1267_1clades	621	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76713.1	001753	Cluster1267_1clades	628	PHABIO_82	Pseudomonas phage Phabio	GCA_002624965.1
AEH03480.1	001753	Cluster1267_1clades	602	053	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02586.1	001753	Cluster1267_1clades	634	PSA21_56	Pseudomonas phage Psa21	GCA_004340405.1
ATN94881.1	001753	Cluster1267_1clades	626	SL2_304	Pseudomonas phage SL2	GCA_002956015.1
QJB22709.1	001753	Cluster1267_1clades	626	fnug_66	Pseudomonas phage fnug	GCA_012837215.1
QEM41783.1	001753	Cluster1267_1clades	621	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82955.1	001753	Cluster1267_1clades	626	PHIKZ054	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63099.1	001754	Cluster1268_1clades	629	201phi2-1p271	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44975.1	001754	Cluster1268_1clades	519	KTN4_217	Pseudomonas phage KTN4	GCA_002607225.1
ARV77362.1	001754	Cluster1268_1clades	612	NOXIFER_193	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32365.1	001754	Cluster1268_1clades	568	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76892.1	001754	Cluster1268_1clades	613	PHABIO_261	Pseudomonas phage Phabio	GCA_002624965.1
AEH03631.1	001754	Cluster1268_1clades	595	208	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02768.1	001754	Cluster1268_1clades	538	PSA21_242	Pseudomonas phage Psa21	GCA_004340405.1
ATN94739.1	001754	Cluster1268_1clades	519	SL2_162	Pseudomonas phage SL2	GCA_002956015.1
QJB22853.1	001754	Cluster1268_1clades	519	fnug_210	Pseudomonas phage fnug	GCA_012837215.1
QEM41939.1	001754	Cluster1268_1clades	568	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83078.1	001754	Cluster1268_1clades	519	PHIKZ177	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62971.1	001755	Cluster1269_1clades	467	201phi2-1p140	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44865.1	001755	Cluster1269_1clades	473	KTN4_107	Pseudomonas phage KTN4	GCA_002607225.1
ARV77248.1	001755	Cluster1269_1clades	437	NOXIFER_77	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32235.1	001755	Cluster1269_1clades	474	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76756.1	001755	Cluster1269_1clades	499	PHABIO_125	Pseudomonas phage Phabio	GCA_002624965.1
AEH03503.1	001755	Cluster1269_1clades	431	079	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02616.1	001755	Cluster1269_1clades	570	PSA21_88	Pseudomonas phage Psa21	GCA_004340405.1
ATN94848.1	001755	Cluster1269_1clades	473	SL2_271	Pseudomonas phage SL2	GCA_002956015.1
QJB22743.1	001755	Cluster1269_1clades	473	fnug_100	Pseudomonas phage fnug	GCA_012837215.1
QEM41814.1	001755	Cluster1269_1clades	476	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82982.1	001755	Cluster1269_1clades	473	PHIKZ081	Pseudomonas virus phiKZ	GCA_000842965.1
ARB13720.1	001756	Cluster1271_1clades	377	Ccr10_gp190c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14065.1	001756	Cluster1271_1clades	377	Ccr2_gp189c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14754.1	001756	Cluster1271_1clades	383	Ccr29_gp198	Caulobacter phage Ccr29	GCA_002619485.1
ARB14408.1	001756	Cluster1271_1clades	379	Ccr5_gp188c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68388.1	001756	Cluster1271_1clades	453	CcrBL10_gp184c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88167.1	001756	Cluster1271_1clades	454	CcrColossus_gp297	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68844.1	001756	Cluster1271_1clades	170	CcrPW_gp305	Caulobacter phage CcrPW	GCA_003443275.1
AFU87713.1	001756	Cluster1271_1clades	362	CcrKarma_gp196	Caulobacter virus Karma	GCA_000901575.1
AFU87362.1	001756	Cluster1271_1clades	362	CcrMagneto_gp192	Caulobacter virus Magneto	GCA_000903095.1
AFU86674.1	001756	Cluster1271_1clades	470	CcrRogue_gp192	Caulobacter virus Rogue	GCA_000900555.1
AFU88509.1	001756	Cluster1271_1clades	362	CcrSwift_gp191	Caulobacter virus Swift	GCA_000899655.1
AHI60361.1	001757	Cluster1272_1clades	429	Ea357_208	Erwinia phage Ea35-70	GCA_000914635.1
QBP07318.1	001757	Cluster1272_1clades	429	REBECCA_213	Erwinia phage Rebecca	GCA_004521635.1
AUG85999.1	001757	Cluster1272_1clades	429	BOSOLAPHORUS_213	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52316.1	001757	Cluster1272_1clades	429	DM_216	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86318.1	001757	Cluster1272_1clades	429	DESERTFOX_211	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86641.1	001757	Cluster1272_1clades	429	MADMEL_213	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86964.1	001757	Cluster1272_1clades	429	MORTIMER_216	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51991.1	001757	Cluster1272_1clades	429	RAY_211	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51675.1	001757	Cluster1272_1clades	429	SIMMY50_216	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65025.1	001757	Cluster1272_1clades	429	SPECIALG_214	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54535.1	001757	Cluster1272_1clades	443	ACSA002_2190	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AXG67214.1	001758	Cluster1273_1clades	392	AD1_170	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79964.1	001758	Cluster1273_1clades	391	JA11_159	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66562.1	001758	Cluster1273_1clades	391	JA13_159	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66887.1	001758	Cluster1273_1clades	391	JA29_161	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67533.1	001758	Cluster1273_1clades	391	JA33_159	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08444.1	001758	Cluster1273_1clades	392	Alexandra_175	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58811.1	001758	Cluster1273_1clades	392	Y3_171	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28645.1	001758	Cluster1273_1clades	392	YOLOSWAG_166	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38474.1	001758	Cluster1273_1clades	440	BN7874_267	Phage NCTB	GCA_900092385.1
AFH14626.1	001758	Cluster1273_1clades	380	Lu11_0094	Pseudomonas phage Lu11	GCA_000897175.1
AGS82082.1	001758	Cluster1273_1clades	381	PaBG_00207	Pseudomonas phage PaBG	GCA_000912555.1
AHI60285.1	001759	Cluster1274_1clades	438	Ea357_134	Erwinia phage Ea35-70	GCA_000914635.1
QBP07243.1	001759	Cluster1274_1clades	438	REBECCA_136	Erwinia phage Rebecca	GCA_004521635.1
AUG85923.1	001759	Cluster1274_1clades	438	BOSOLAPHORUS_136	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52238.1	001759	Cluster1274_1clades	438	DM_140	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86242.1	001759	Cluster1274_1clades	438	DESERTFOX_135	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86564.1	001759	Cluster1274_1clades	438	MADMEL_136	Erwinia phage vB_EamM_MadMel	GCA_002957755.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86888.1	001759	Cluster1274_1clades	438	MORTIMER_139	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51916.1	001759	Cluster1274_1clades	438	RAY_135	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51600.1	001759	Cluster1274_1clades	438	SIMMY50_138	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64947.1	001759	Cluster1274_1clades	438	SPECIALG_137	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24065.1	001759	Cluster1274_1clades	414	-	Proteus phage 10	GCA_014071245.1
ABY62978.1	001760	Cluster1275_1clades	414	201phi2-1p148	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44871.1	001760	Cluster1275_1clades	422	KTN4_113	Pseudomonas phage KTN4	GCA_002607225.1
ARV77257.1	001760	Cluster1275_1clades	413	NOXIFER_87	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32243.1	001760	Cluster1275_1clades	412	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76763.1	001760	Cluster1275_1clades	422	PHABIO_132	Pseudomonas phage Phabio	GCA_002624965.1
AEH03513.1	001760	Cluster1275_1clades	413	089	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02624.1	001760	Cluster1275_1clades	429	PSA21_96	Pseudomonas phage Psa21	GCA_004340405.1
ATN94842.1	001760	Cluster1275_1clades	428	SL2_265	Pseudomonas phage SL2	GCA_002956015.1
QJB22748.1	001760	Cluster1275_1clades	422	fnug_105	Pseudomonas phage fnug	GCA_012837215.1
QEM41821.1	001760	Cluster1275_1clades	412	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82987.2	001760	Cluster1275_1clades	422	PHIKZ086	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67189.1	001761	Glycos_transf_2	402	AD1_145	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79939.1	001761	Glycos_transf_2	366	JA11_134	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66538.1	001761	Glycos_transf_2	366	JA13_135	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66863.1	001761	Glycos_transf_2	366	JA29_137	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67508.1	001761	Glycos_transf_2	366	JA33_134	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08422.1	001761	Glycos_transf_2	414	Alexandra_150	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58786.1	001761	Glycos_transf_2	390	Y3_146	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28624.1	001761	Glycos_transf_2	394	YOLOSWAG_144	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38424.1	001761	Glycos_transf_2	385	BN7874_234	Phage NCTB	GCA_900092385.1
AFH14606.1	001761	Glycos_transf_2	366	Lu11_0074	Pseudomonas phage Lu11	GCA_000897175.1
AGS82098.1	001761	Glycos_transf_2	424	PaBG_00223	Pseudomonas phage PaBG	GCA_000912555.1
AGH56992.1	001762	NEC	419	CPXG_00189	Cyanophage P-RSM6	GCA_000906155.1
AOO14224.1	001762	NEC	308	Sn110110_030	Cyanophage S-RIM14	GCA_002599065.1
AOO14226.1	001762	NEC	358	Sn110110_032	Cyanophage S-RIM14	GCA_002599065.1
AOO14876.1	001762	NEC	308	W1230910_030	Cyanophage S-RIM14	GCA_002599125.1
AOO14878.1	001762	NEC	358	W1230910_032	Cyanophage S-RIM14	GCA_002599125.1
AOV59557.1	001762	NEC	284	S330809_096	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59566.1	001762	NEC	300	S330809_105	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59319.1	001762	NEC	284	C440309_096	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59328.1	001762	NEC	300	C440309_105	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59795.1	001762	NEC	284	N231010_096	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59804.1	001762	NEC	300	N231010_105	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67373.1	001763	Cluster1278_1clades	379	AD1_329	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80125.1	001763	Cluster1278_1clades	377	JA11_320	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66725.1	001763	Cluster1278_1clades	377	JA13_322	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67043.1	001763	Cluster1278_1clades	377	JA29_317	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67694.1	001763	Cluster1278_1clades	377	JA33_320	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08596.1	001763	Cluster1278_1clades	380	Alexandra_348	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58972.1	001763	Cluster1278_1clades	376	Y3_332	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28800.1	001763	Cluster1278_1clades	379	YOLOSWAG_332	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38259.1	001763	Cluster1278_1clades	388	BN7874_090	Phage NCTB	GCA_900092385.1
AFH14715.1	001763	Cluster1278_1clades	369	Lu11_0178	Pseudomonas phage Lu11	GCA_000897175.1
AGS81997.1	001763	Cluster1278_1clades	377	PaBG_00112	Pseudomonas phage PaBG	GCA_000912555.1
AXG67260.1	001764	Cluster1279_1clades	373	AD1_216	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80007.1	001764	Cluster1279_1clades	372	JA11_202	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66605.1	001764	Cluster1279_1clades	372	JA13_202	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66930.1	001764	Cluster1279_1clades	372	JA29_204	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67577.1	001764	Cluster1279_1clades	345	JA33_203	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08489.1	001764	Cluster1279_1clades	368	Alexandra_226	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58861.1	001764	Cluster1279_1clades	369	Y3_221	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28693.1	001764	Cluster1279_1clades	368	YOLOSWAG_215	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38172.1	001764	Cluster1279_1clades	387	BN7874_003	Phage NCTB	GCA_900092385.1
AFH14666.1	001764	Cluster1279_1clades	361	Lu11_0132	Pseudomonas phage Lu11	GCA_000897175.1
AGS82040.1	001764	Cluster1279_1clades	373	PaBG_00157	Pseudomonas phage PaBG	GCA_000912555.1
AXG67226.1	001765	Cluster1280_1clades	343	AD1_182	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79976.1	001765	Cluster1280_1clades	365	JA11_171	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66574.1	001765	Cluster1280_1clades	365	JA13_171	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66899.1	001765	Cluster1280_1clades	365	JA29_173	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67545.1	001765	Cluster1280_1clades	365	JA33_171	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08455.1	001765	Cluster1280_1clades	368	Alexandra_187	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58823.1	001765	Cluster1280_1clades	368	Y3_183	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28657.1	001765	Cluster1280_1clades	367	YOLOSWAG_178	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38498.1	001765	Cluster1280_1clades	379	BN7874_279	Phage NCTB	GCA_900092385.1
AFH14639.1	001765	Cluster1280_1clades	299	Lu11_0107	Pseudomonas phage Lu11	GCA_000897175.1
AGS82070.1	001765	Cluster1280_1clades	309	PaBG_00194	Pseudomonas phage PaBG	GCA_000912555.1
AXG67123.1	001766	Phagetail-L+SUN	349	AD1_079	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67125.1	001766	Phagetail-L+SUN	358	AD1_081	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79880.1	001766	Phagetail-L+SUN	360	JA11_075	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66479.1	001766	Phagetail-L+SUN	360	JA13_076	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66804.1	001766	Phagetail-L+SUN	360	JA29_078	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67449.1	001766	Phagetail-L+SUN	360	JA33_075	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08359.1	001766	Phagetail-L+SUN	353	Alexandra_82	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08361.1	001766	Phagetail-L+SUN	363	Alexandra_84	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58722.1	001766	Phagetail-L+SUN	330	Y3_082	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58724.1	001766	Phagetail-L+SUN	364	Y3_084	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28556.1	001766	Phagetail-L+SUN	353	YOLOSWAG_73	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ARB13629.1	001767	Cluster1282_1clades	362	Ccr10_gp100	Caulobacter phage Ccr10	GCA_002619445.1
ARB13974.1	001767	Cluster1282_1clades	362	Ccr2_gp099	Caulobacter phage Ccr2	GCA_002619465.1
ARB14663.1	001767	Cluster1282_1clades	362	Ccr29_gp107	Caulobacter phage Ccr29	GCA_002619485.1
ARB15018.1	001767	Cluster1282_1clades	293	Ccr32_gp100	Caulobacter phage Ccr32	GCA_002619505.1
ARB15350.1	001767	Cluster1282_1clades	293	Ccr34_gp108	Caulobacter phage Ccr34	GCA_002619525.1
ARB14318.1	001767	Cluster1282_1clades	362	Ccr5_gp100	Caulobacter phage Ccr5	GCA_002619545.1
AFU87621.1	001767	Cluster1282_1clades	362	CcrKarma_gp104	Caulobacter virus Karma	GCA_000901575.1
AFU87270.1	001767	Cluster1282_1clades	362	CcrMagneto_gp100	Caulobacter virus Magneto	GCA_000903095.1
AFU88417.1	001767	Cluster1282_1clades	362	CcrSwift_gp099	Caulobacter virus Swift	GCA_000899655.1
AFU86935.1	001767	Cluster1282_1clades	362	CbK_gp103	Caulobacter virus phiCbK	GCA_000900535.1
QHJ85981.1	001767	Cluster1282_1clades	319	KKIINIFJ_00069	Pseudomonas phage PN05	GCA_009931935.1
AXG67281.1	001768	Cluster1284_1clades	345	AD1_237	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80025.1	001768	Cluster1284_1clades	345	JA11_220	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66624.1	001768	Cluster1284_1clades	345	JA13_221	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66948.1	001768	Cluster1284_1clades	345	JA29_222	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67595.1	001768	Cluster1284_1clades	345	JA33_221	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08505.1	001768	Cluster1284_1clades	345	Alexandra_246	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58881.1	001768	Cluster1284_1clades	345	Y3_241	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28806.1	001768	Cluster1284_1clades	344	YOLOSWAG_236	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38188.1	001768	Cluster1284_1clades	351	BN7874_019	Phage NCTB	GCA_900092385.1
AFH14705.1	001768	Cluster1284_1clades	336	Lu11_0170	Pseudomonas phage Lu11	GCA_000897175.1
AGS82002.1	001768	Cluster1284_1clades	338	PaBG_00118	Pseudomonas phage PaBG	GCA_000912555.1
AXG67372.1	001769	Cluster1285_1clades	290	AD1_328	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80124.1	001769	Cluster1285_1clades	279	JA11_319	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66724.1	001769	Cluster1285_1clades	274	JA13_321	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67042.1	001769	Cluster1285_1clades	279	JA29_316	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67693.1	001769	Cluster1285_1clades	279	JA33_319	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08595.1	001769	Cluster1285_1clades	288	Alexandra_347	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58971.1	001769	Cluster1285_1clades	281	Y3_331	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28799.1	001769	Cluster1285_1clades	287	YOLOSWAG_331	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38258.1	001769	Cluster1285_1clades	256	BN7874_089	Phage NCTB	GCA_900092385.1
AFH14714.1	001769	Cluster1285_1clades	346	Lu11_0177	Pseudomonas phage Lu11	GCA_000897175.1
QKE11209.1	001769	Cluster1285_1clades	210	PaBG_00113	Pseudomonas phage PaBG	GCA_000912555.1
QDB70276.1	001770	Cluster1286_1clades	328	CF8_0108	Aeromonas phage CF8	GCA_006384595.2
QDJ97254.1	001770	Cluster1286_1clades	307	D6_0094	Aeromonas phage D6	GCA_007051205.2
QDH47088.1	001770	Cluster1286_1clades	308	LAh10_26	Aeromonas phage LAh10	GCA_006863975.1
QDJ96867.1	001770	Cluster1286_1clades	333	PS1_0108	Aeromonas phage PS1	GCA_007051165.2
QFR59499.1	001770	Cluster1286_1clades	333	PS2_0108	Aeromonas phage PS2	GCA_009388305.2
QBZ70636.1	001770	Cluster1286_1clades	312	pETSU_055	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03841.1	001770	Cluster1286_1clades	241	JOAD_74	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03596.1	001770	Cluster1286_1clades	241	RISINGSUN_74	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71953.1	001770	Cluster1286_1clades	235	N1M2_90	Klebsiella phage N1M2	GCA_010092605.1
CAG27161.1	001770	Cluster1286_1clades	251	PPEV_gp067	Pseudomonas phage EL	GCA_000866825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEV89554.1	001770	Cluster1286_1clades	306	OBP_117	Pseudomonas phage OBP	GCA_000896635.1
QDB70333.1	001771	Cluster1287_1clades	146	CF8_0163	Aeromonas phage CF8	GCA_006384595.2
QDJ97333.1	001771	Cluster1287_1clades	165	D6_0174	Aeromonas phage D6	GCA_007051205.2
QDH47168.1	001771	Cluster1287_1clades	165	LAh10_93	Aeromonas phage LAh10	GCA_006863975.1
QDJ96682.1	001771	Cluster1287_1clades	147	PS1_0171	Aeromonas phage PS1	GCA_007051165.2
QBZ70721.1	001771	Cluster1287_1clades	133	pETSU_140	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03740.1	001771	Cluster1287_1clades	175	JOAD_175	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03496.1	001771	Cluster1287_1clades	175	RISINGSUN_174	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72035.1	001771	Cluster1287_1clades	133	N1M2_172	Klebsiella phage N1M2	GCA_010092605.1
QMP24035.1	001771	Cluster1287_1clades	141	-	Proteus phage 10	GCA_014071245.1
AFH14901.1	001771	Cluster1287_1clades	330	Lu11_0363	Pseudomonas phage Lu11	GCA_000897175.1
AEV89655.1	001771	Cluster1287_1clades	133	OBP_218	Pseudomonas phage OBP	GCA_000896635.1
ABY63067.1	001772	Cluster1288_1clades	316	201phi2-1p238	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44947.1	001772	Cluster1288_1clades	304	KTN4_189	Pseudomonas phage KTN4	GCA_002607225.1
ARV77333.1	001772	Cluster1288_1clades	301	NOXIFER_164	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32335.1	001772	Cluster1288_1clades	322	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76857.1	001772	Cluster1288_1clades	325	PHABIO_226	Pseudomonas phage Phabio	GCA_002624965.1
AEH03599.1	001772	Cluster1288_1clades	320	176	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02736.1	001772	Cluster1288_1clades	308	PSA21_210	Pseudomonas phage Psa21	GCA_004340405.1
ATN94767.1	001772	Cluster1288_1clades	304	SL2_190	Pseudomonas phage SL2	GCA_002956015.1
QJB22825.1	001772	Cluster1288_1clades	304	fnug_182	Pseudomonas phage fnug	GCA_012837215.1
QEM41908.1	001772	Cluster1288_1clades	322	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83054.1	001772	Cluster1288_1clades	304	PHIKZ153	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64194.1	001773	QueF_N+QueF	302	KVP40.0123	Vibrio phage KVP40	GCA_000843785.1
QIW90510.1	001773	QueF_N+QueF	224	GCAPEGMB_00163	Vibrio phage V07	GCA_012361095.1
QIW90912.1	001773	QueF_N+QueF	302	COHAPHLL_00049	Vibrio phage V09	GCA_012361135.1
QHJ74306.1	001773	QueF_N+QueF	302	VH12019_00387	Vibrio phage VH1_2019	GCA_009931825.1
AGB06800.1	001773	QueF_N+QueF	302	CF80_gp013	Vibrio phage VH7D	GCA_000914495.1
QBX05966.1	001773	QueF_N+QueF	302	ValB1HC_012	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60978.1	001773	QueF_N+QueF	302	AVU32_gp137	Vibrio phage ValKK3	GCA_001501635.1
ALP47024.1	001773	QueF_N+QueF	302	phiGrn1_0235	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47403.1	001773	QueF_N+QueF	303	phiST2_0373	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54591.1	001773	QueF_N+QueF	302	vBValMR10Z_50	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37354.1	001773	QueF_N+QueF	302	pp2_121	Vibriophage phi-pp2	GCA_002630725.1
ABY63041.1	001774	Cluster1290_1clades	290	201phi2-1p212	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44920.1	001774	Cluster1290_1clades	290	KTN4_162	Pseudomonas phage KTN4	GCA_002607225.1
ARV77299.1	001774	Cluster1290_1clades	290	NOXIFER_130	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32307.1	001774	Cluster1290_1clades	292	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76830.1	001774	Cluster1290_1clades	292	PHABIO_199	Pseudomonas phage Phabio	GCA_002624965.1
AEH03569.1	001774	Cluster1290_1clades	273	146	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02706.1	001774	Cluster1290_1clades	291	PSA21_180	Pseudomonas phage Psa21	GCA_004340405.1
ATN94794.1	001774	Cluster1290_1clades	290	SL2_217	Pseudomonas phage SL2	GCA_002956015.1
QJB22798.1	001774	Cluster1290_1clades	290	fnug_155	Pseudomonas phage fnug	GCA_012837215.1
QEM41880.1	001774	Cluster1290_1clades	292	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83028.1	001774	Cluster1290_1clades	290	PHIKZ127	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62969.1	001775	Cluster1291_1clades	283	201phi2-1p138	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44863.1	001775	Cluster1291_1clades	285	KTN4_105	Pseudomonas phage KTN4	GCA_002607225.1
ARV77246.1	001775	Cluster1291_1clades	283	NOXIFER_75	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32233.1	001775	Cluster1291_1clades	283	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76754.1	001775	Cluster1291_1clades	278	PHABIO_123	Pseudomonas phage Phabio	GCA_002624965.1
AEH03500.1	001775	Cluster1291_1clades	282	076	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02614.1	001775	Cluster1291_1clades	286	PSA21_86	Pseudomonas phage Psa21	GCA_004340405.1
ATN94850.1	001775	Cluster1291_1clades	285	SL2_273	Pseudomonas phage SL2	GCA_002956015.1
QJB22741.1	001775	Cluster1291_1clades	285	fnug_98	Pseudomonas phage fnug	GCA_012837215.1
QEM41812.1	001775	Cluster1291_1clades	283	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82980.2	001775	Cluster1291_1clades	285	PHIKZ079	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67171.1	001776	Cluster1292_1clades	268	AD1_127	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79921.1	001776	Cluster1292_1clades	267	JA11_116	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66520.1	001776	Cluster1292_1clades	267	JA13_117	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66845.1	001776	Cluster1292_1clades	267	JA29_119	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67490.1	001776	Cluster1292_1clades	267	JA33_116	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08404.1	001776	Cluster1292_1clades	271	Alexandra_132	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58768.1	001776	Cluster1292_1clades	270	Y3_128	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28607.1	001776	Cluster1292_1clades	279	YOLOSWAG_126	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38382.1	001776	Cluster1292_1clades	264	BN7874_208	Phage NCTB	GCA_900092385.1
AFH14586.1	001776	Cluster1292_1clades	237	Lu11_0055	Pseudomonas phage Lu11	GCA_000897175.1
AGS81954.2	001776	Cluster1292_1clades	248	PaBG_00070	Pseudomonas phage PaBG	GCA_000912555.1
QDB70337.1	001777	Cluster1293_1clades	148	CF8_0168	Aeromonas phage CF8	GCA_006384595.2
QDJ96684.1	001777	Cluster1293_1clades	266	PS1_0173	Aeromonas phage PS1	GCA_007051165.2
QHE95177.1	001777	Cluster1293_1clades	266	PS2_0175	Aeromonas phage PS2	GCA_009388305.2
QBZ70709.1	001777	Cluster1293_1clades	252	pETSU_128	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70728.1	001777	Cluster1293_1clades	251	pETSU_147	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03748.1	001777	Cluster1293_1clades	279	JOAD_167	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03504.1	001777	Cluster1293_1clades	279	RISINGSUN_166	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH72039.1	001777	Cluster1293_1clades	256	N1M2_176	Klebsiella phage N1M2	GCA_010092605.1
CAG27237.1	001777	Cluster1293_1clades	182	PPEV_gp143	Pseudomonas phage EL	GCA_000866825.1
AEV89636.1	001777	Cluster1293_1clades	246	OBP_199	Pseudomonas phage OBP	GCA_000896635.1
AEV89660.1	001777	Cluster1293_1clades	266	OBP_223	Pseudomonas phage OBP	GCA_000896635.1
QIG63341.1	001778	Tox-ParB	193	DAC16_108	Bacteroides phage DAC16	GCA_013387695.1
QIG63607.1	001778	Tox-ParB	193	DAC19_116	Bacteroides phage DAC19	GCA_013387715.1
QIG63868.1	001778	Tox-ParB	193	DAC20_115	Bacteroides phage DAC20	GCA_013387725.1
QIG64131.1	001778	Tox-ParB	193	DAC22_117	Bacteroides phage DAC22	GCA_013387735.1
QIG64388.1	001778	Tox-ParB	193	DAC23_110	Bacteroides phage DAC23	GCA_013387745.1
ANS06028.1	001778	Tox-ParB	176	ABCD_0174	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97187.1	001778	Tox-ParB	177	E_179	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78704.1	001778	Tox-ParB	178	RB43ORF182c	Escherichia virus RB43	GCA_000863505.1
AFF28115.1	001778	Tox-ParB	185	PAU_117	Sphingomonas phage PAU	GCA_000902455.1
AFF28116.1	001778	Tox-ParB	210	PAU_118	Sphingomonas phage PAU	GCA_000902455.1
BAV39154.1	001778	Tox-ParB	278	BPT24_032	Tenacibaculum phage pT24	GCA_002611925.1
AXG67223.1	001779	Cluster1295_1clades	272	AD1_179	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79973.1	001779	Cluster1295_1clades	252	JA11_168	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66571.1	001779	Cluster1295_1clades	252	JA13_168	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66896.1	001779	Cluster1295_1clades	254	JA29_170	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67542.1	001779	Cluster1295_1clades	252	JA33_168	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08452.1	001779	Cluster1295_1clades	271	Alexandra_184	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58820.1	001779	Cluster1295_1clades	276	Y3_180	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28654.1	001779	Cluster1295_1clades	272	YOLOSWAG_175	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38491.1	001779	Cluster1295_1clades	254	BN7874_276	Phage NCTB	GCA_900092385.1
AFH14635.1	001779	Cluster1295_1clades	255	Lu11_0103	Pseudomonas phage Lu11	GCA_000897175.1
QKE11216.1	001779	Cluster1295_1clades	270	PaBG_00198	Pseudomonas phage PaBG	GCA_000912555.1
ABY62968.1	001780	Cluster1296_1clades	157	201phi2-1p137	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44862.1	001780	Cluster1296_1clades	164	KTN4_104	Pseudomonas phage KTN4	GCA_002607225.1
ARV77245.1	001780	Cluster1296_1clades	180	NOXIFER_74	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32232.1	001780	Cluster1296_1clades	198	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76753.1	001780	Cluster1296_1clades	204	PHABIO_122	Pseudomonas phage Phabio	GCA_002624965.1
AEH03499.1	001780	Cluster1296_1clades	206	075	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02613.1	001780	Cluster1296_1clades	261	PSA21_85	Pseudomonas phage Psa21	GCA_004340405.1
ATN94851.1	001780	Cluster1296_1clades	164	SL2_274	Pseudomonas phage SL2	GCA_002956015.1
QJB22740.1	001780	Cluster1296_1clades	164	fnug_97	Pseudomonas phage fnug	GCA_012837215.1
QEM41810.1	001780	Cluster1296_1clades	152	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82979.1	001780	Cluster1296_1clades	164	PHIKZ078	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67263.1	001781	Cluster1297_1clades	230	AD1_219	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80010.1	001781	Cluster1297_1clades	212	JA11_205	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66608.1	001781	Cluster1297_1clades	205	JA13_205	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66933.1	001781	Cluster1297_1clades	212	JA29_207	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67580.1	001781	Cluster1297_1clades	212	JA33_206	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08492.1	001781	Cluster1297_1clades	226	Alexandra_229	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58864.1	001781	Cluster1297_1clades	223	Y3_224	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28696.1	001781	Cluster1297_1clades	208	YOLOSWAG_218	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38175.1	001781	Cluster1297_1clades	251	BN7874_006	Phage NCTB	GCA_900092385.1
AFH14669.1	001781	Cluster1297_1clades	171	Lu11_0135	Pseudomonas phage Lu11	GCA_000897175.1
AGS82038.1	001781	Cluster1297_1clades	185	PaBG_00155	Pseudomonas phage PaBG	GCA_000912555.1
APU01461.1	001782	SIG+LprI	220	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29003.1	001782	SIG+LprI	239	AP1_0296	Aeromonas phage AP1	GCA_014183365.1
ATI17436.1	001782	SIG+LprI	239	-	Aeromonas phage AS-szw	GCA_002743635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU00159.1	001782	SIG+LprI	239	HWB28_gp393	Aeromonas phage AS-zj	GCA_002627665.1
QAX97876.1	001782	SIG+LprI	239	ASswx1_233	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01303.1	001782	SIG+LprI	200	ASwh1_240	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39273.1	001782	SIG+LprI	239	CC2_301	Aeromonas phage CC2	GCA_000903495.1
QDJ97342.1	001782	SIG+LprI	246	D6_0183	Aeromonas phage D6	GCA_007051205.2
QDH47113.1	001782	SIG+LprI	246	LAh10_102	Aeromonas phage LAh10	GCA_006863975.1
ADQ53082.1	001782	SIG+LprI	91	65p072	Aeromonas virus 65	GCA_000893255.1
ADQ53083.1	001782	SIG+LprI	117	65p073	Aeromonas virus 65	GCA_000893255.1
ABY63118.1	001783	Cluster1299_1clades	230	201phi2-1p292	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44991.1	001783	Cluster1299_1clades	241	KTN4_233	Pseudomonas phage KTN4	GCA_002607225.1
ARV77449.1	001783	Cluster1299_1clades	223	NOXIFER_284	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32379.1	001783	Cluster1299_1clades	239	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76919.1	001783	Cluster1299_1clades	220	PHABIO_288	Pseudomonas phage Phabio	GCA_002624965.1
AEH03649.1	001783	Cluster1299_1clades	233	226	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02787.1	001783	Cluster1299_1clades	224	PSA21_261	Pseudomonas phage Psa21	GCA_004340405.1
ATN94723.1	001783	Cluster1299_1clades	241	SL2_146	Pseudomonas phage SL2	GCA_002956015.1
QJB22869.1	001783	Cluster1299_1clades	241	fnug_226	Pseudomonas phage fnug	GCA_012837215.1
QEM41952.1	001783	Cluster1299_1clades	239	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83093.2	001783	Cluster1299_1clades	245	PHIKZ192	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63123.1	001784	Cluster1300_1clades	223	201phi2-1p297	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44999.1	001784	Cluster1300_1clades	219	KTN4_241	Pseudomonas phage KTN4	GCA_002607225.1
ARV77393.1	001784	Cluster1300_1clades	243	NOXIFER_228	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32384.1	001784	Cluster1300_1clades	223	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76924.1	001784	Cluster1300_1clades	217	PHABIO_293	Pseudomonas phage Phabio	GCA_002624965.1
AEH03655.1	001784	Cluster1300_1clades	223	232	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02791.1	001784	Cluster1300_1clades	217	PSA21_265	Pseudomonas phage Psa21	GCA_004340405.1
ATN94715.1	001784	Cluster1300_1clades	219	SL2_138	Pseudomonas phage SL2	GCA_002956015.1
QJB22877.1	001784	Cluster1300_1clades	219	fnug_234	Pseudomonas phage fnug	GCA_012837215.1
QEM41957.1	001784	Cluster1300_1clades	223	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83101.1	001784	Cluster1300_1clades	219	PHIKZ200	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67241.1	001785	Cluster1301_1clades	237	AD1_197	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79989.1	001785	Cluster1301_1clades	237	JA11_184	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66587.1	001785	Cluster1301_1clades	237	JA13_184	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66912.1	001785	Cluster1301_1clades	237	JA29_186	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67558.1	001785	Cluster1301_1clades	237	JA33_184	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08471.1	001785	Cluster1301_1clades	237	Alexandra_207	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58839.1	001785	Cluster1301_1clades	237	Y3_199	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28670.1	001785	Cluster1301_1clades	238	YOLOSWAG_191	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38514.1	001785	Cluster1301_1clades	216	BN7874_286	Phage NCTB	GCA_900092385.1
AFH14647.1	001785	Cluster1301_1clades	242	Lu11_0115	Pseudomonas phage Lu11	GCA_000897175.1
AGS82063.2	001785	Cluster1301_1clades	212	PaBG_00187	Pseudomonas phage PaBG	GCA_000912555.1
AXG67180.1	001786	Cluster1302_1clades	229	AD1_136	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79930.1	001786	Cluster1302_1clades	220	JA11_125	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66529.1	001786	Cluster1302_1clades	220	JA13_126	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66854.1	001786	Cluster1302_1clades	220	JA29_128	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67499.1	001786	Cluster1302_1clades	220	JA33_125	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08413.1	001786	Cluster1302_1clades	231	Alexandra_141	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58777.1	001786	Cluster1302_1clades	224	Y3_137	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28615.1	001786	Cluster1302_1clades	227	YOLOSWAG_135	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38401.1	001786	Cluster1302_1clades	216	BN7874_218	Phage NCTB	GCA_900092385.1
AFH14594.1	001786	Cluster1302_1clades	240	Lu11_0063	Pseudomonas phage Lu11	GCA_000897175.1
AGS81962.1	001786	Cluster1302_1clades	219	PaBG_00078	Pseudomonas phage PaBG	GCA_000912555.1
AHI60252.1	001787	Cluster1303_1clades	234	Ea357_101	Erwinia phage Ea35-70	GCA_000914635.1
QBP07210.1	001787	Cluster1303_1clades	234	REBECCA_103	Erwinia phage Rebecca	GCA_004521635.1
AUG85889.1	001787	Cluster1303_1clades	234	BOSOLAPHORUS_102	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52204.1	001787	Cluster1303_1clades	234	DM_106	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86208.1	001787	Cluster1303_1clades	234	DESERTFOX_101	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86531.1	001787	Cluster1303_1clades	234	MADMEL_103	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86854.1	001787	Cluster1303_1clades	234	MORTIMER_105	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51882.1	001787	Cluster1303_1clades	234	RAY_101	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51566.1	001787	Cluster1303_1clades	234	SIMMY50_104	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64914.1	001787	Cluster1303_1clades	234	SPECIALG_104	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54390.1	001787	Cluster1303_1clades	224	ACSA002_0760	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AIT14326.1	001788	Cluster1304_1clades	229	PBI_121Q_436	Escherichia phage 121Q	GCA_000926855.1
QAY00615.1	001788	Cluster1304_1clades	229	Ecwhy1_339	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34811.1	001788	Cluster1304_1clades	229	ACQ29_gp131	Escherichia phage PBECO4	GCA_001041035.1
BBM61999.1	001788	Cluster1304_1clades	229	EO157G_4100	Escherichia phage SP27	GCA_008033345.1
AXC36922.1	001788	Cluster1304_1clades	229	-	Escherichia phage UB	GCA_003341455.1
QBO61978.1	001788	Cluster1304_1clades	229	G17_00489	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14002.1	001788	Cluster1304_1clades	130	vBEcoMphAPEC6_gp378c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80313.1	001788	Cluster1304_1clades	229	PSLUR01_00336	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18782.1	001788	Cluster1304_1clades	212	7t3_0261	Salmonella phage 7t3	GCA_006083215.1
AZU98047.1	001788	Cluster1304_1clades	212	CPT_Munch_103	Salmonella phage Munch	GCA_004015485.1
QIG62933.1	001788	Cluster1304_1clades	212	SEPL_320	Salmonella phage SE_PL	GCA_011067555.1
QIW90531.1	001789	IONCHANNEL	228	GCAPEGMB_00184	Vibrio phage V07	GCA_012361095.1
QIW90891.1	001789	IONCHANNEL	228	COHAPHLL_00028	Vibrio phage V09	GCA_012361135.1
QHJ74329.1	001789	IONCHANNEL	228	VH12019_00002	Vibrio phage VH1_2019	GCA_009931825.1
AGB06822.1	001789	IONCHANNEL	207	CF80_gp035	Vibrio phage VH7D	GCA_000914495.1
QBX06325.1	001789	IONCHANNEL	227	ValB1HC_372	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60955.1	001789	IONCHANNEL	227	AVU32_gp114	Vibrio phage ValKK3	GCA_001501635.1
AGN30193.1	001789	IONCHANNEL	228	VPFG_00193	Vibrio phage nt-1	GCA_000910195.2
ALP47069.1	001789	IONCHANNEL	200	phiGrn1_0258	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47495.1	001789	IONCHANNEL	161	phiST2_0016	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54568.1	001789	IONCHANNEL	227	vBValMR10Z_27	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37377.1	001789	IONCHANNEL	228	pp2_144	Vibriophage phi-pp2	GCA_002630725.1
APU01679.1	001790	Cluster1306_1clades	228	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28814.1	001790	Cluster1306_1clades	228	AP1_0107	Aeromonas phage AP1	GCA_014183665.1
ATI17612.1	001790	Cluster1306_1clades	228	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00384.1	001790	Cluster1306_1clades	228	HWB28_gp168	Aeromonas phage AS-zj	GCA_002627665.1
QAX98054.1	001790	Cluster1306_1clades	228	ASswx1_414	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01092.1	001790	Cluster1306_1clades	228	ASwh1_24	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39348.1	001790	Cluster1306_1clades	228	CC2_115	Aeromonas phage CC2	GCA_000903495.1
ADQ53313.1	001790	Cluster1306_1clades	143	65p305	Aeromonas virus 65	GCA_000893255.1
ADQ53314.1	001790	Cluster1306_1clades	86	65p306	Aeromonas virus 65	GCA_000893255.1
AEO93533.1	001790	Cluster1306_1clades	226	G_274	Bacillus virus G	GCA_000917535.1
ARM70949.1	001790	Cluster1306_1clades	228	phiC120_c244	Escherichia phage phiC120	GCA_002621185.1
ABY63110.1	001791	Cluster1307_1clades	136	201phi2-1p283	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44985.1	001791	Cluster1307_1clades	134	KTN4_227	Pseudomonas phage KTN4	GCA_002607225.1
ARV77370.1	001791	Cluster1307_1clades	228	NOXIFER_201	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32376.1	001791	Cluster1307_1clades	139	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76906.1	001791	Cluster1307_1clades	136	PHABIO_275	Pseudomonas phage Phabio	GCA_002624965.1
AEH03645.1	001791	Cluster1307_1clades	136	222	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02777.1	001791	Cluster1307_1clades	140	PSA21_251	Pseudomonas phage Psa21	GCA_004340405.1
ATN94729.1	001791	Cluster1307_1clades	134	SL2_152	Pseudomonas phage SL2	GCA_002956015.1
QJB22863.1	001791	Cluster1307_1clades	134	fnug_220	Pseudomonas phage fnug	GCA_012837215.1
QEM41949.1	001791	Cluster1307_1clades	139	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83087.1	001791	Cluster1307_1clades	134	PHIKZ186	Pseudomonas virus phiKZ	GCA_000842965.1
QDB70293.1	001792	Cluster1308_1clades	208	CF8_0125	Aeromonas phage CF8	GCA_006384595.2
QDJ97270.1	001792	Cluster1308_1clades	206	D6_0110	Aeromonas phage D6	GCA_007051205.2
QDH47137.1	001792	Cluster1308_1clades	206	LAh10_42	Aeromonas phage LAh10	GCA_006863975.1
QDJ96885.1	001792	Cluster1308_1clades	164	PS1_0126	Aeromonas phage PS1	GCA_007051165.2
QFR59517.1	001792	Cluster1308_1clades	164	PS2_0126	Aeromonas phage PS2	GCA_009388305.2
QBZ70656.1	001792	Cluster1308_1clades	206	pETSU_075	Edwardsiella virus pEt-SU	GCA_004800915.1
ASU03823.1	001792	Cluster1308_1clades	220	JOAD_92	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03578.1	001792	Cluster1308_1clades	220	RISINGSUN_92	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGH71972.1	001792	Cluster1308_1clades	205	N1M2_109	Klebsiella phage N1M2	GCA_010092605.1
CAG27201.1	001792	Cluster1308_1clades	210	PPEV_gp107	Pseudomonas phage EL	GCA_000866825.1
AEV89573.1	001792	Cluster1308_1clades	206	OBP_136	Pseudomonas phage OBP	GCA_000896635.1
ABY63259.1	001793	Cluster1309_1clades	167	201phi2-1p436	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27189.1	001793	Cluster1309_1clades	153	PPEV_gp095	Pseudomonas phage EL	GCA_000866825.1
ANM45116.1	001793	Cluster1309_1clades	174	KTN4_358	Pseudomonas phage KTN4	GCA_002607225.1
QBX32531.1	001793	Cluster1309_1clades	166	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77078.1	001793	Cluster1309_1clades	215	PHABIO_447	Pseudomonas phage Phabio	GCA_002624965.1
ARV77082.1	001793	Cluster1309_1clades	153	PHABIO_453	Pseudomonas phage Phabio	GCA_002624965.1
AEH03790.1	001793	Cluster1309_1clades	168	367	Pseudomonas phage PhiPA3	GCA_001502095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBJ02927.1	001793	Cluster1309_1clades	170	PSA21_401	Pseudomonas phage Psa21	GCA_004340405.1
ATN94591.1	001793	Cluster1309_1clades	170	SL2_014	Pseudomonas phage SL2	GCA_002956015.1
QJB22993.1	001793	Cluster1309_1clades	174	fnug_350	Pseudomonas phage fnug	GCA_012837215.1
AAL83198.1	001793	Cluster1309_1clades	170	PHIKZ297	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62952.1	001794	Cluster1310_1clades	201	201phi2-1p120	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44844.1	001794	Cluster1310_1clades	187	KTN4_086	Pseudomonas phage KTN4	GCA_002607225.1
ARV77228.1	001794	Cluster1310_1clades	200	NOXIFER_57	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32212.1	001794	Cluster1310_1clades	203	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76731.1	001794	Cluster1310_1clades	207	PHABIO_100	Pseudomonas phage Phabio	GCA_002624965.1
AEH03485.1	001794	Cluster1310_1clades	212	058	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02595.1	001794	Cluster1310_1clades	192	PSA21_66	Pseudomonas phage Psa21	GCA_004340405.1
ATN94869.1	001794	Cluster1310_1clades	202	SL2_292	Pseudomonas phage SL2	GCA_002956015.1
QJB22722.1	001794	Cluster1310_1clades	202	fnug_79	Pseudomonas phage fnug	GCA_012837215.1
QEM41790.1	001794	Cluster1310_1clades	203	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82965.1	001794	Cluster1310_1clades	182	PHIKZ064	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60273.1	001795	Cluster1311_1clades	210	Ea357_122	Erwinia phage Ea35-70	GCA_000914635.1
QBP07231.1	001795	Cluster1311_1clades	210	REBECCA_124	Erwinia phage Rebecca	GCA_004521635.1
AUG85911.1	001795	Cluster1311_1clades	210	BOSOLAPHORUS_124	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52226.2	001795	Cluster1311_1clades	210	DM_128	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86230.1	001795	Cluster1311_1clades	210	DESERTFOX_123	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86552.1	001795	Cluster1311_1clades	210	MADMEL_124	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86876.1	001795	Cluster1311_1clades	210	MORTIMER_127	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51904.1	001795	Cluster1311_1clades	210	RAY_123	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51588.1	001795	Cluster1311_1clades	210	SIMMY50_126	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64935.2	001795	Cluster1311_1clades	210	SPECIALG_125	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54431.1	001795	Cluster1311_1clades	205	ACSA002_1170	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64173.1	001796	Cluster1312_1clades	206	KVP40.0102	Vibrio phage KVP40	GCA_000843785.1
QIW90496.1	001796	Cluster1312_1clades	206	GCAPEGMB_00149	Vibrio phage V07	GCA_012361095.1
QIW90933.1	001796	Cluster1312_1clades	206	COHAPHLL_00070	Vibrio phage V09	GCA_012361135.1
QHJ74284.1	001796	Cluster1312_1clades	206	VH12019_00365	Vibrio phage VH1_2019	GCA_009931825.1
AGB07108.1	001796	Cluster1312_1clades	206	CF80_gp321	Vibrio phage VH7D	GCA_000914495.1
QBX05987.1	001796	Cluster1312_1clades	206	ValB1HC_033	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61000.1	001796	Cluster1312_1clades	206	AVU32_gp159	Vibrio phage ValKK3	GCA_001501635.1
AGN30151.1	001796	Cluster1312_1clades	205	VPFG_00149	Vibrio phage nt-1	GCA_000910195.2
ALP47065.1	001796	Cluster1312_1clades	206	phiGrn1_0215	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47445.1	001796	Cluster1312_1clades	206	phiST2_0348	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54612.1	001796	Cluster1312_1clades	206	vBValMR10Z_71	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ABY63057.1	001797	Cluster1313_1clades	206	201phi2-1p228	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44937.1	001797	Cluster1313_1clades	177	KTN4_179	Pseudomonas phage KTN4	GCA_002607225.1
ARV77310.1	001797	Cluster1313_1clades	183	NOXIFER_141	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32323.1	001797	Cluster1313_1clades	177	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76847.1	001797	Cluster1313_1clades	177	PHABIO_216	Pseudomonas phage Phabio	GCA_002624965.1
AEH03585.1	001797	Cluster1313_1clades	175	162	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02723.1	001797	Cluster1313_1clades	179	PSA21_197	Pseudomonas phage Psa21	GCA_004340405.1
ATN94777.1	001797	Cluster1313_1clades	177	SL2_200	Pseudomonas phage SL2	GCA_002956015.1
QJB22815.1	001797	Cluster1313_1clades	177	fnug_172	Pseudomonas phage fnug	GCA_012837215.1
QEM41896.1	001797	Cluster1313_1clades	177	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83044.1	001797	Cluster1313_1clades	177	PHIKZ143	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67218.1	001798	Cluster1314_1clades	183	AD1_174	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79968.1	001798	Cluster1314_1clades	184	JA11_163	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66566.1	001798	Cluster1314_1clades	184	JA13_163	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66891.1	001798	Cluster1314_1clades	184	JA29_165	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67537.1	001798	Cluster1314_1clades	184	JA33_163	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08448.1	001798	Cluster1314_1clades	181	Alexandra_179	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58815.1	001798	Cluster1314_1clades	182	Y3_175	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28649.1	001798	Cluster1314_1clades	205	YOLOSWAG_170	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38482.1	001798	Cluster1314_1clades	157	BN7874_271	Phage NCTB	GCA_900092385.1
AFH14630.1	001798	Cluster1314_1clades	125	Lu11_0098	Pseudomonas phage Lu11	GCA_000897175.1
AGS82078.2	001798	Cluster1314_1clades	170	PaBG_00203	Pseudomonas phage PaBG	GCA_000912555.1
AAQ64243.1	001799	Cluster1315_1clades	201	KVP40.0174	Vibrio phage KVP40	GCA_000843785.1
QIW90559.1	001799	Cluster1315_1clades	201	GCAPEGMB_00212	Vibrio phage V07	GCA_012361095.1
QHJ74357.1	001799	Cluster1315_1clades	201	VH12019_00030	Vibrio phage VH1_2019	GCA_009931825.1
AGB06849.1	001799	Cluster1315_1clades	202	CF80_gp062	Vibrio phage VH7D	GCA_000914495.1
QBX06297.1	001799	Cluster1315_1clades	203	ValB1HC_344	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60925.1	001799	Cluster1315_1clades	202	AVU32_gp084	Vibrio phage ValKK3	GCA_001501635.1
AGN30226.1	001799	Cluster1315_1clades	204	VPFG_00226	Vibrio phage nt-1	GCA_000910195.2
ALP47068.1	001799	Cluster1315_1clades	202	phiGrn1_0288	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47461.1	001799	Cluster1315_1clades	187	phiST2_0045	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54923.1	001799	Cluster1315_1clades	203	vBValMR10Z_383	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37404.1	001799	Cluster1315_1clades	201	pp2_171	Vibriophage phi-pp2	GCA_002630725.1
APU01761.1	001800	Cluster1316_1clades	196	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28813.1	001800	Cluster1316_1clades	197	AP1_0106	Aeromonas phage AP1	GCA_014183365.1
ATI17613.1	001800	Cluster1316_1clades	197	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00383.1	001800	Cluster1316_1clades	197	HWB28_gp169	Aeromonas phage AS-zj	GCA_002627665.1
QAY01474.1	001800	Cluster1316_1clades	196	ASwh1_415	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39471.1	001800	Cluster1316_1clades	197	CC2_113	Aeromonas phage CC2	GCA_000903495.1
ADQ53404.1	001800	Cluster1316_1clades	196	65p397	Aeromonas virus 65	GCA_000893255.1
ANS06009.1	001800	Cluster1316_1clades	197	ABCD_0249	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97267.1	001800	Cluster1316_1clades	198	E_259	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70958.1	001800	Cluster1316_1clades	197	phiC120_c253	Escherichia phage phiC120	GCA_002621185.1
AAX78788.1	001800	Cluster1316_1clades	97	RB43ORF266w	Escherichia virus RB43	GCA_000863505.1
AAQ64440.1	001801	Cluster1317_1clades	197	KVP40.0372	Vibrio phage KVP40	GCA_000843785.1
QIW90385.1	001801	Cluster1317_1clades	197	GCAPEGMB_00038	Vibrio phage V07	GCA_012361095.1
QIW91044.1	001801	Cluster1317_1clades	197	COHAPHLL_00181	Vibrio phage V09	GCA_012361135.1
QHJ74552.1	001801	Cluster1317_1clades	197	VH12019_00252	Vibrio phage VH1_2019	GCA_009931825.1
QBX06102.1	001801	Cluster1317_1clades	197	ValB1HC_148	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61116.1	001801	Cluster1317_1clades	197	AVU32_gp275	Vibrio phage ValKK3	GCA_001501635.1
AGN30041.1	001801	Cluster1317_1clades	196	VPFG_00036	Vibrio phage nt-1	GCA_000910195.2
ALP47072.1	001801	Cluster1317_1clades	197	phiGrn1_0104	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47451.1	001801	Cluster1317_1clades	197	phiST2_0235	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54727.1	001801	Cluster1317_1clades	197	vBValMR10Z_187	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37603.1	001801	Cluster1317_1clades	197	pp2_371	Vibriophage phi-pp2	GCA_002630725.1
AXG67363.1	001802	Cluster1318_1clades	181	AD1_319	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80115.1	001802	Cluster1318_1clades	192	JA11_310	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66716.1	001802	Cluster1318_1clades	192	JA13_313	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67034.1	001802	Cluster1318_1clades	191	JA29_308	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67685.1	001802	Cluster1318_1clades	192	JA33_311	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08585.1	001802	Cluster1318_1clades	180	Alexandra_336	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58962.1	001802	Cluster1318_1clades	186	Y3_322	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28789.1	001802	Cluster1318_1clades	189	YOLOSWAG_320	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38246.1	001802	Cluster1318_1clades	171	BN7874_077	Phage NCTB	GCA_900092385.1
AFH14694.1	001802	Cluster1318_1clades	183	Lu11_0160	Pseudomonas phage Lu11	GCA_000897175.1
AGS82010.1	001802	Cluster1318_1clades	194	PaBG_00126	Pseudomonas phage PaBG	GCA_000912555.1
AAQ64367.1	001803	Cluster1320_1clades	191	KVP40.0297	Vibrio phage KVP40	GCA_000843785.1
QIW90682.1	001803	Cluster1320_1clades	191	GCAPEGMB_00335	Vibrio phage V07	GCA_012361095.1
QIW91116.1	001803	Cluster1320_1clades	191	COHAPHLL_00280	Vibrio phage V09	GCA_012361135.1
QHJ74477.1	001803	Cluster1320_1clades	191	VH12019_00150	Vibrio phage VH1_2019	GCA_009931825.1
QBX06174.1	001803	Cluster1320_1clades	191	ValB1HC_221	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61191.1	001803	Cluster1320_1clades	191	AVU32_gp350	Vibrio phage ValKK3	GCA_001501635.1
AGN30343.1	001803	Cluster1320_1clades	190	VPFG_00346	Vibrio phage nt-1	GCA_000910195.2
ALP47077.1	001803	Cluster1320_1clades	191	phiGrn1_0030	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47457.1	001803	Cluster1320_1clades	191	phiST2_0163	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54800.1	001803	Cluster1320_1clades	191	vBValMR10Z_260	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37528.1	001803	Cluster1320_1clades	191	pp2_295	Vibriophage phi-pp2	GCA_002630725.1
AAQ64219.1	001804	TM+TM	183	KVP40.0150	Vibrio phage KVP40	GCA_000843785.1
QIW90533.1	001804	TM+TM	180	GCAPEGMB_00186	Vibrio phage V07	GCA_012361095.1
QIW90889.1	001804	TM+TM	180	COHAPHLL_00026	Vibrio phage V09	GCA_012361135.1
QHJ74331.1	001804	TM+TM	180	VH12019_00004	Vibrio phage VH1_2019	GCA_009931825.1
QBX06323.1	001804	TM+TM	185	ValB1HC_370	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60953.1	001804	TM+TM	185	AVU32_gp112	Vibrio phage ValKK3	GCA_001501635.1
AGN30195.1	001804	TM+TM	158	VPFG_00195	Vibrio phage nt-1	GCA_000910195.2
ALP47085.1	001804	TM+TM	183	phiGrn1_0260	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47464.1	001804	TM+TM	185	phiST2_0018	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54566.1	001804	TM+TM	185	vBValMR10Z_25	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37379.1	001804	TM+TM	180	pp2_146	Vibriophage phi-pp2	GCA_002630725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AHI60191.1	001805	Cluster1322_1clades	183	Ea357_041	Erwinia phage Ea35-70	GCA_000914635.1
QBP07149.1	001805	Cluster1322_1clades	183	REBECCA_41	Erwinia phage Rebecca	GCA_004521635.1
AUG85829.1	001805	Cluster1322_1clades	183	BOSOLAPHORUS_41	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52140.1	001805	Cluster1322_1clades	183	DM_42	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86149.1	001805	Cluster1322_1clades	183	DESERTFOX_41	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86469.1	001805	Cluster1322_1clades	183	MADMEL_41	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86790.1	001805	Cluster1322_1clades	183	MORTIMER_41	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51822.1	001805	Cluster1322_1clades	183	RAY_41	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51504.1	001805	Cluster1322_1clades	183	SIMMY50_42	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64851.1	001805	Cluster1322_1clades	183	SPECIALG_41	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54353.1	001805	Cluster1322_1clades	181	ACSA002_0390	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ABY63028.1	001806	Cluster1323_1clades	180	201phi2-1p198	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44912.1	001806	Cluster1323_1clades	177	KTN4_154	Pseudomonas phage KTN4	GCA_002607225.1
ARV77290.1	001806	Cluster1323_1clades	169	NOXIFER_121	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32296.1	001806	Cluster1323_1clades	178	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76817.1	001806	Cluster1323_1clades	178	PHABIO_186	Pseudomonas phage Phabio	GCA_002624965.1
AEH03558.1	001806	Cluster1323_1clades	180	135	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02696.1	001806	Cluster1323_1clades	181	PSA21_169	Pseudomonas phage Psa21	GCA_004340405.1
ATN94802.1	001806	Cluster1323_1clades	177	SL2_225	Pseudomonas phage SL2	GCA_002956015.1
QJB22790.1	001806	Cluster1323_1clades	177	fnug_147	Pseudomonas phage fnug	GCA_012837215.1
QEM41870.1	001806	Cluster1323_1clades	178	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83020.1	001806	Cluster1323_1clades	177	PHIKZ119	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63055.1	001807	Cluster1324_1clades	152	201phi2-1p226	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44934.1	001807	Cluster1324_1clades	168	KTN4_176	Pseudomonas phage KTN4	GCA_002607225.1
ARV77313.1	001807	Cluster1324_1clades	180	NOXIFER_144	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32321.1	001807	Cluster1324_1clades	164	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76844.1	001807	Cluster1324_1clades	145	PHABIO_213	Pseudomonas phage Phabio	GCA_002624965.1
AEH03583.1	001807	Cluster1324_1clades	167	160	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02720.1	001807	Cluster1324_1clades	171	PSA21_194	Pseudomonas phage Psa21	GCA_004340405.1
ATN94780.1	001807	Cluster1324_1clades	168	SL2_203	Pseudomonas phage SL2	GCA_002956015.1
QJB22812.1	001807	Cluster1324_1clades	168	fnug_169	Pseudomonas phage fnug	GCA_012837215.1
QEM41894.1	001807	Cluster1324_1clades	164	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83042.1	001807	Cluster1324_1clades	168	PHIKZ141	Pseudomonas virus phiKZ	GCA_000842965.1
AMR59773.1	001808	Cluster1325_1clades	156	SEGD1_126	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ48153.1	001808	Cluster1325_1clades	154	ASESINO_140	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
AIT14398.1	001808	Cluster1325_1clades	173	PBI_121Q_508	Escherichia phage 121Q	GCA_000926855.1
AGC34744.1	001808	Cluster1325_1clades	177	ACQ29_gp064	Escherichia phage PBECO4	GCA_001041035.1
BBM62069.1	001808	Cluster1325_1clades	178	EO157G_4800	Escherichia phage SP27	GCA_008033345.1
AXC36859.1	001808	Cluster1325_1clades	177	-	Escherichia phage UB	GCA_003341455.1
QKN85963.1	001808	Cluster1325_1clades	161	ACEC001_1250	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61904.1	001808	Cluster1325_1clades	178	G17_00415	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QNI20827.1	001808	Cluster1325_1clades	161	-	Salmonella phage JN03	GCA_014319805.1
AWN08991.1	001808	Cluster1325_1clades	157	MLDJOKPK_00030	Salmonella phage SPAsTU	GCA_003183805.1
AEP83956.1	001808	Cluster1325_1clades	156	SPN3US_0123	Salmonella phage SPN3US	GCA_001042275.1
QIW90521.1	001809	Cluster1326_1clades	175	GCAPEGMB_00174	Vibrio phage V07	GCA_012361095.1
QIW90901.1	001809	Cluster1326_1clades	175	COHAPHLL_00038	Vibrio phage V09	GCA_012361135.1
QHJ74317.1	001809	Cluster1326_1clades	175	VH12019_00398	Vibrio phage VH1_2019	GCA_009931825.1
AGB06811.1	001809	Cluster1326_1clades	177	CF80_gp024	Vibrio phage VH7D	GCA_000914495.1
QBX06336.1	001809	Cluster1326_1clades	174	ValB1HC_383	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60966.1	001809	Cluster1326_1clades	175	AVU32_gp125	Vibrio phage ValKK3	GCA_001501635.1
AGN30185.1	001809	Cluster1326_1clades	174	VPFG_00185	Vibrio phage nt-1	GCA_000910195.2
ALP47092.1	001809	Cluster1326_1clades	175	phiGrn1_0247	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47475.1	001809	Cluster1326_1clades	174	phiST2_0002	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54579.1	001809	Cluster1326_1clades	174	vBValMR10Z_38	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37367.1	001809	Cluster1326_1clades	175	pp2_134	Vibriophage phi-pp2	GCA_002630725.1
AHI60308.1	001810	Cluster1327_1clades	176	Ea357_157	Erwinia phage Ea35-70	GCA_000914635.1
QBP07266.1	001810	Cluster1327_1clades	176	REBECCA_159	Erwinia phage Rebecca	GCA_004521635.1
AUG85946.1	001810	Cluster1327_1clades	176	BOSOLAPHORUS_159	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52261.1	001810	Cluster1327_1clades	176	DM_163	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86265.1	001810	Cluster1327_1clades	176	DESERTFOX_158	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86587.1	001810	Cluster1327_1clades	176	MADMEL_159	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86911.1	001810	Cluster1327_1clades	176	MORTIMER_162	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51939.1	001810	Cluster1327_1clades	176	RAY_158	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51623.1	001810	Cluster1327_1clades	176	SIMMY50_161	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64970.1	001810	Cluster1327_1clades	176	SPECIALG_160	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54462.1	001810	Cluster1327_1clades	174	ACSA002_1480	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AXF51216.1	001811	Cluster1328_1clades	154	WELLINGTON_86	Erwinia phage Wellington	GCA_003344985.1
ABY63230.1	001811	Cluster1328_1clades	171	201phi2-1p406	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45097.1	001811	Cluster1328_1clades	171	KTN4_339	Pseudomonas phage KTN4	GCA_002607225.1
ARV77479.1	001811	Cluster1328_1clades	176	NOXIFER_314	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32510.1	001811	Cluster1328_1clades	171	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77033.1	001811	Cluster1328_1clades	171	PHABIO_402	Pseudomonas phage Phabio	GCA_002624965.1
AEH03764.1	001811	Cluster1328_1clades	171	341	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94616.1	001811	Cluster1328_1clades	171	SL2_039	Pseudomonas phage SL2	GCA_002956015.1
QJB22973.1	001811	Cluster1328_1clades	171	fnug_330	Pseudomonas phage fnug	GCA_012837215.1
QEM42083.1	001811	Cluster1328_1clades	153	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83183.2	001811	Cluster1328_1clades	153	PHIKZ282	Pseudomonas virus phiKZ	GCA_000842965.1
ARB13716.1	001812	Cluster1329_1clades	173	Ccr10_gp186c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14061.1	001812	Cluster1329_1clades	173	Ccr2_gp185c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14748.1	001812	Cluster1329_1clades	173	Ccr29_gp192	Caulobacter phage Ccr29	GCA_002619485.1
ARB15103.1	001812	Cluster1329_1clades	173	Ccr32_gp185	Caulobacter phage Ccr32	GCA_002619505.1
ARB15437.1	001812	Cluster1329_1clades	173	Ccr34_gp195	Caulobacter phage Ccr34	GCA_002619525.1
ARB14404.1	001812	Cluster1329_1clades	173	Ccr5_gp184c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87709.1	001812	Cluster1329_1clades	173	CcrKarma_gp192	Caulobacter virus Karma	GCA_000901575.1
AFU87358.1	001812	Cluster1329_1clades	173	CcrMagneto_gp188	Caulobacter virus Magneto	GCA_000903095.1
AFU86670.1	001812	Cluster1329_1clades	175	CcrRogue_gp188	Caulobacter virus Rogue	GCA_000900555.1
AFU88505.1	001812	Cluster1329_1clades	173	CcrSwift_gp187	Caulobacter virus Swift	GCA_000899655.1
AFU87022.1	001812	Cluster1329_1clades	173	CbK_gp190	Caulobacter virus phiCbK	GCA_000900535.1
AHI60437.1	001813	Cluster1330_1clades	168	Ea357_283	Erwinia phage Ea35-70	GCA_000914635.1
QBP07394.1	001813	Cluster1330_1clades	168	REBECCA_289	Erwinia phage Rebecca	GCA_004521635.1
AUG86076.1	001813	Cluster1330_1clades	168	BOSOLAPHORUS_290	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52392.1	001813	Cluster1330_1clades	168	DM_293	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86396.1	001813	Cluster1330_1clades	168	DESERTFOX_289	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86717.1	001813	Cluster1330_1clades	168	MADMEL_290	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87042.1	001813	Cluster1330_1clades	168	MORTIMER_294	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52067.1	001813	Cluster1330_1clades	168	RAY_287	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51750.1	001813	Cluster1330_1clades	168	SIMMY50_292	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65102.1	001813	Cluster1330_1clades	168	SPECIALG_291	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54614.1	001813	Cluster1330_1clades	166	ACSA002_2970	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60284.1	001814	Cluster1331_1clades	166	Ea357_133	Erwinia phage Ea35-70	GCA_000914635.1
QBP07242.1	001814	Cluster1331_1clades	166	REBECCA_135	Erwinia phage Rebecca	GCA_004521635.1
AUG85922.1	001814	Cluster1331_1clades	166	BOSOLAPHORUS_135	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52237.1	001814	Cluster1331_1clades	166	DM_139	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86241.1	001814	Cluster1331_1clades	166	DESERTFOX_134	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86563.1	001814	Cluster1331_1clades	166	MADMEL_135	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86887.1	001814	Cluster1331_1clades	166	MORTIMER_138	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51915.1	001814	Cluster1331_1clades	166	RAY_134	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51599.1	001814	Cluster1331_1clades	166	SIMMY50_137	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64946.1	001814	Cluster1331_1clades	166	SPECIALG_136	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54436.1	001814	Cluster1331_1clades	162	ACSA002_1220	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ABY62899.1	001815	Cluster1332_1clades	157	201phi2-1p066	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44812.1	001815	Cluster1332_1clades	157	KTN4_054	Pseudomonas phage KTN4	GCA_002607225.1
ARV77203.1	001815	Cluster1332_1clades	163	NOXIFER_32	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32182.1	001815	Cluster1332_1clades	164	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76680.1	001815	Cluster1332_1clades	149	PHABIO_49	Pseudomonas phage Phabio	GCA_002624965.1
AEH03457.1	001815	Cluster1332_1clades	164	030	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02561.1	001815	Cluster1332_1clades	162	PSA21_31	Pseudomonas phage Psa21	GCA_004340405.1
ATN94899.1	001815	Cluster1332_1clades	157	SL2_322	Pseudomonas phage SL2	GCA_002956015.1
QJB22691.1	001815	Cluster1332_1clades	157	fnug_48	Pseudomonas phage fnug	GCA_012837215.1
QEM41760.1	001815	Cluster1332_1clades	164	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82942.1	001815	Cluster1332_1clades	157	PHIKZ041	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64443.1	001816	Cluster1333_1clades	162	KVP40.0375	Vibrio phage KVP40	GCA_000843785.1
QIW90388.1	001816	Cluster1333_1clades	162	GCAPEGMB_00041	Vibrio phage V07	GCA_012361095.1
QIW91041.1	001816	Cluster1333_1clades	162	COHAPHLL_00178	Vibrio phage V09	GCA_012361135.1
QHJ74555.1	001816	Cluster1333_1clades	162	VH12019_00255	Vibrio phage VH1_2019	GCA_009931825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06099.1	001816	Cluster1333_1clades	162	ValB1HC_145	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61113.1	001816	Cluster1333_1clades	162	AVU32_gp272	Vibrio phage ValKK3	GCA_001501635.1
AGN30043.1	001816	Cluster1333_1clades	162	VPFG_00038	Vibrio phage nt-1	GCA_000910195.2
ALP47111.1	001816	Cluster1333_1clades	162	phiGrn1_0107	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47494.1	001816	Cluster1333_1clades	162	phiST2_0238	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54724.1	001816	Cluster1333_1clades	162	vBValMR10Z_184	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37606.1	001816	Cluster1333_1clades	162	pp2_374	Vibriophage phi-pp2	GCA_002630725.1
AHI60176.1	001817	Cluster1334_1clades	128	Ea357_026	Erwinia phage Ea35-70	GCA_000914635.1
QBP07134.1	001817	Cluster1334_1clades	162	REBECCA_26	Erwinia phage Rebecca	GCA_004521635.1
AUG85814.1	001817	Cluster1334_1clades	128	BOSOLAPHORUS_26	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52124.3	001817	Cluster1334_1clades	162	DM_26	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86134.1	001817	Cluster1334_1clades	162	DESERTFOX_26	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86454.1	001817	Cluster1334_1clades	162	MADMEL_26	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86775.1	001817	Cluster1334_1clades	128	MORTIMER_26	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51807.2	001817	Cluster1334_1clades	162	RAY_26	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51489.2	001817	Cluster1334_1clades	128	SIMMY50_27	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64836.3	001817	Cluster1334_1clades	162	SPECIALG_26	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54340.1	001817	Cluster1334_1clades	132	ACSA002_0260	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60287.1	001818	Cluster1335_1clades	161	Ea357_136	Erwinia phage Ea35-70	GCA_000914635.1
QBP07245.1	001818	Cluster1335_1clades	161	REBECCA_138	Erwinia phage Rebecca	GCA_004521635.1
AUG85925.1	001818	Cluster1335_1clades	161	BOSOLAPHORUS_138	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52240.1	001818	Cluster1335_1clades	161	DM_142	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86244.1	001818	Cluster1335_1clades	161	DESERTFOX_137	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86566.1	001818	Cluster1335_1clades	161	MADMEL_138	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86890.1	001818	Cluster1335_1clades	161	MORTIMER_141	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51918.1	001818	Cluster1335_1clades	161	RAY_137	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51602.1	001818	Cluster1335_1clades	161	SIMMY50_140	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64949.1	001818	Cluster1335_1clades	161	SPECIALG_139	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54442.1	001818	Cluster1335_1clades	159	ACSA002_1280	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64315.1	001819	Cluster1337_1clades	144	KVP40.0246	Vibrio phage KVP40	GCA_000843785.1
QIW90630.1	001819	Cluster1337_1clades	144	GCAPEGMB_00283	Vibrio phage V07	GCA_012361095.1
QIW91169.1	001819	Cluster1337_1clades	144	COHAPHLL_00333	Vibrio phage V09	GCA_012361135.1
QHJ74425.1	001819	Cluster1337_1clades	144	VH12019_00098	Vibrio phage VH1_2019	GCA_009931825.1
AGB06931.1	001819	Cluster1337_1clades	155	CF80_gp144	Vibrio phage VH7D	GCA_000914495.1
QBX06215.1	001819	Cluster1337_1clades	155	ValB1HC_262	Vibrio phage ValB1 HC	GCA_004771355.1
AGN30301.1	001819	Cluster1337_1clades	148	VPFG_00302	Vibrio phage nt-1	GCA_000910195.2
ALP47114.1	001819	Cluster1337_1clades	160	phiGrn1_0367	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47509.1	001819	Cluster1337_1clades	153	phiST2_0122	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54840.1	001819	Cluster1337_1clades	155	vBValMR10Z_300	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37474.1	001819	Cluster1337_1clades	144	pp2_241	Vibriophage phi-pp2	GCA_002630725.1
AAQ64220.1	001820	NACHT	138	KVP40.0151	Vibrio phage KVP40	GCA_000843785.1
QIW90534.1	001820	NACHT	138	GCAPEGMB_00187	Vibrio phage V07	GCA_012361095.1
QIW90888.1	001820	NACHT	138	COHAPHLL_00025	Vibrio phage V09	GCA_012361135.1
QHJ74332.1	001820	NACHT	138	VH12019_00005	Vibrio phage VH1_2019	GCA_009931825.1
AGB06824.1	001820	NACHT	154	CF80_gp037	Vibrio phage VH7D	GCA_000914495.1
QBX06322.1	001820	NACHT	154	ValB1HC_369	Vibrio phage ValB1 HC	GCA_004771355.1
AGN30196.1	001820	NACHT	138	VPFG_00196	Vibrio phage nt-1	GCA_000910195.2
ALP47122.1	001820	NACHT	154	phiGrn1_0261	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47507.1	001820	NACHT	154	phiST2_0019	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54565.1	001820	NACHT	154	vBValMR10Z_24	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37380.1	001820	NACHT	155	pp2_147	Vibriophage phi-pp2	GCA_002630725.1
AHI60165.1	001821	Cluster1339_1clades	154	Ea357_015	Erwinia phage Ea35-70	GCA_000914635.1
QBP07123.1	001821	Cluster1339_1clades	154	REBECCA_15	Erwinia phage Rebecca	GCA_004521635.1
AUG85803.1	001821	Cluster1339_1clades	154	BOSOLAPHORUS_15	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52113.1	001821	Cluster1339_1clades	154	DM_15	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86123.1	001821	Cluster1339_1clades	154	DESERTFOX_15	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86443.1	001821	Cluster1339_1clades	154	MADMEL_15	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86764.1	001821	Cluster1339_1clades	154	MORTIMER_15	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51796.1	001821	Cluster1339_1clades	154	RAY_15	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51478.1	001821	Cluster1339_1clades	154	SIMMY50_16	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64825.1	001821	Cluster1339_1clades	154	SPECIALG_15	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54329.1	001821	Cluster1339_1clades	136	ACSA002_0150	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60386.1	001822	Cluster1340_1clades	153	Ea357_233	Erwinia phage Ea35-70	GCA_000914635.1
QBP07342.1	001822	Cluster1340_1clades	153	REBECCA_237	Erwinia phage Rebecca	GCA_004521635.1
AUG86024.1	001822	Cluster1340_1clades	153	BOSOLAPHORUS_238	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52341.1	001822	Cluster1340_1clades	153	DM_241	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86343.1	001822	Cluster1340_1clades	153	DESERTFOX_236	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86667.1	001822	Cluster1340_1clades	153	MADMEL_239	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86989.1	001822	Cluster1340_1clades	153	MORTIMER_241	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52015.1	001822	Cluster1340_1clades	153	RAY_235	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51699.1	001822	Cluster1340_1clades	153	SIMMY50_240	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65050.1	001822	Cluster1340_1clades	153	SPECIALG_239	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54562.1	001822	Cluster1340_1clades	152	ACSA002_2460	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AXQ69051.1	001823	Cluster1341_1clades	152	CcrBL9_gp027	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69567.1	001823	Cluster1341_1clades	152	CcrBL9_gp543	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87871.1	001823	Cluster1341_1clades	84	CcrColossus_gp001	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68540.1	001823	Cluster1341_1clades	84	CcrPW_gp001c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68990.1	001823	Cluster1341_1clades	84	CcrPW_gp451c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69611.1	001823	Cluster1341_1clades	83	CcrSC_gp029	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70111.1	001823	Cluster1341_1clades	83	CcrSC_gp529	Caulobacter phage CcrSC	GCA_003443315.1
AFU86486.1	001823	Cluster1341_1clades	85	CcrRogue_gp004	Caulobacter virus Rogue	GCA_000900555.1
AFU86817.1	001823	Cluster1341_1clades	85	CcrRogue_gp335	Caulobacter virus Rogue	GCA_000900555.1
AFU88322.1	001823	Cluster1341_1clades	85	CcrSwift_gp004	Caulobacter virus Swift	GCA_000899655.1
AFU88647.1	001823	Cluster1341_1clades	85	CcrSwift_gp329	Caulobacter virus Swift	GCA_000899655.1
AMR59764.1	001824	Cluster1342_1clades	150	SEGD1_117	Enterobacteria phage SEGD1	GCA_002601865.1
AXF51272.1	001824	Cluster1342_1clades	150	WELLINGTON_142	Erwinia phage Wellington	GCA_003344985.1
AFQ96581.1	001824	Cluster1342_1clades	149	G173_gp036	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48141.1	001824	Cluster1342_1clades	150	ASESINO_128	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48418.1	001824	Cluster1342_1clades	150	CAITLIN_123	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48691.1	001824	Cluster1342_1clades	150	CHRISDB_129	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49493.1	001824	Cluster1342_1clades	150	KWAN_141	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50556.1	001824	Cluster1342_1clades	149	STRATTON_131	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85954.1	001824	Cluster1342_1clades	150	ACEC001_1160	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN08996.1	001824	Cluster1342_1clades	150	MLDJOKPK_00044	Salmonella phage SPAsTU	GCA_003183805.1
AEP83946.1	001824	Cluster1342_1clades	150	SPN3US_0113	Salmonella phage SPN3US	GCA_001042275.1
ABY62976.1	001825	Cluster1343_1clades	145	201phi2-1p146	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44870.1	001825	Cluster1343_1clades	149	KTN4_112	Pseudomonas phage KTN4	GCA_002607225.1
ARV77255.1	001825	Cluster1343_1clades	147	NOXIFER_85	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32241.1	001825	Cluster1343_1clades	146	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76761.1	001825	Cluster1343_1clades	146	PHABIO_130	Pseudomonas phage Phabio	GCA_002624965.1
AEH03511.1	001825	Cluster1343_1clades	147	087	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02622.1	001825	Cluster1343_1clades	146	PSA21_94	Pseudomonas phage Psa21	GCA_004340405.1
ATN94843.1	001825	Cluster1343_1clades	149	SL2_266	Pseudomonas phage SL2	GCA_002956015.1
QJB22747.1	001825	Cluster1343_1clades	149	fnug_104	Pseudomonas phage fnug	GCA_012837215.1
QEM41819.1	001825	Cluster1343_1clades	146	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82986.1	001825	Cluster1343_1clades	149	PHIKZ085	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62995.1	001826	Cluster1344_1clades	123	201phi2-1p165	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44887.1	001826	Cluster1344_1clades	140	KTN4_129	Pseudomonas phage KTN4	GCA_002607225.1
ARV77270.1	001826	Cluster1344_1clades	136	NOXIFER_101	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32264.1	001826	Cluster1344_1clades	143	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76779.1	001826	Cluster1344_1clades	124	PHABIO_148	Pseudomonas phage Phabio	GCA_002624965.1
AEH03531.1	001826	Cluster1344_1clades	143	107	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02642.1	001826	Cluster1344_1clades	127	PSA21_114	Pseudomonas phage Psa21	GCA_004340405.1
ATN94826.1	001826	Cluster1344_1clades	140	SL2_249	Pseudomonas phage SL2	GCA_002956015.1
QJB22764.1	001826	Cluster1344_1clades	140	fnug_121	Pseudomonas phage fnug	GCA_012837215.1
QEM41838.1	001826	Cluster1344_1clades	143	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83003.2	001826	Cluster1344_1clades	148	PHIKZ102	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63149.1	001827	Cluster1345_1clades	119	201phi2-1p324	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45087.1	001827	Cluster1345_1clades	111	KTN4_329	Pseudomonas phage KTN4	GCA_002607225.1
ARV77477.1	001827	Cluster1345_1clades	113	NOXIFER_312	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32493.1	001827	Cluster1345_1clades	119	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76953.1	001827	Cluster1345_1clades	148	PHABIO_322	Pseudomonas phage Phabio	GCA_002624965.1
AEH03751.1	001827	Cluster1345_1clades	113	328	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02895.1	001827	Cluster1345_1clades	111	PSA21_369	Pseudomonas phage Psa21	GCA_004340405.1
ATN94628.1	001827	Cluster1345_1clades	111	SL2_051	Pseudomonas phage SL2	GCA_002956015.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QJB22963.1	001827	Cluster1345_1clades	111	fnug_320	Pseudomonas phage fnug	GCA_012837215.1
QEM42066.1	001827	Cluster1345_1clades	119	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83173.1	001827	Cluster1345_1clades	111	PHIKZ272	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14088.1	001828	Cluster1346_1clades	147	PBI_121Q_198	Escherichia phage 121Q	GCA_000926855.1
QAY00834.1	001828	Cluster1346_1clades	147	Ecwhy1_562	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35006.1	001828	Cluster1346_1clades	147	ACQ29_gp326	Escherichia phage PBECO4	GCA_001041035.1
BBM61771.1	001828	Cluster1346_1clades	147	EO157G_1820	Escherichia phage SP27	GCA_008033345.1
AXC36583.1	001828	Cluster1346_1clades	147	-	Escherichia phage UB	GCA_003341455.1
QBO61611.1	001828	Cluster1346_1clades	147	G17_00115	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13669.1	001828	Cluster1346_1clades	147	vBEcoMphAPEC6_gp038c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80082.1	001828	Cluster1346_1clades	147	PSLUR01_00105	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18586.1	001828	Cluster1346_1clades	140	7t3_065	Salmonella phage 7t3	GCA_006083215.1
AZU98414.1	001828	Cluster1346_1clades	140	CPT_Munch_482	Salmonella phage Munch	GCA_004015485.1
QIG63099.1	001828	Cluster1346_1clades	140	SEPL_486	Salmonella phage SE_PL	GCA_011067555.1
AHI60327.1	001829	TM	146	Ea357_175	Erwinia phage Ea35-70	GCA_000914635.1
QBP07286.1	001829	TM	146	REBECCA_179	Erwinia phage Rebecca	GCA_004521635.1
AUG85966.1	001829	TM	146	BOSOLAPHORUS_179	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52281.1	001829	TM	146	DM_183	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86285.1	001829	TM	146	DESERTFOX_178	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86607.1	001829	TM	146	MADMEL_179	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86931.1	001829	TM	146	MORTIMER_182	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51958.1	001829	TM	146	RAY_177	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51642.1	001829	TM	146	SIMMY50_180	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64989.1	001829	TM	146	SPECIALG_179	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54487.1	001829	TM	138	ACSA002_1730	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60274.1	001830	Cluster1348_1clades	64	Ea357_123	Erwinia phage Ea35-70	GCA_000914635.1
QBP07232.1	001830	Cluster1348_1clades	64	REBECCA_125	Erwinia phage Rebecca	GCA_004521635.1
AUG85912.1	001830	Cluster1348_1clades	64	BOSOLAPHORUS_125	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52227.1	001830	Cluster1348_1clades	64	DM_129	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86231.1	001830	Cluster1348_1clades	64	DESERTFOX_124	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86553.1	001830	Cluster1348_1clades	63	MADMEL_125	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86877.1	001830	Cluster1348_1clades	64	MORTIMER_128	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51905.1	001830	Cluster1348_1clades	64	RAY_124	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51589.1	001830	Cluster1348_1clades	63	SIMMY50_127	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64936.1	001830	Cluster1348_1clades	64	SPECIALG_126	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54362.1	001830	Cluster1348_1clades	146	ACSA002_0480	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ABY63056.1	001831	TM	137	201phi2-1p227	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44936.1	001831	TM	131	KTN4_178	Pseudomonas phage KTN4	GCA_002607225.1
ARV77311.1	001831	TM	143	NOXIFER_142	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32322.1	001831	TM	134	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76846.1	001831	TM	134	PHABIO_215	Pseudomonas phage Phabio	GCA_002624965.1
AEH03584.1	001831	TM	135	161	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02722.1	001831	TM	111	PSA21_196	Pseudomonas phage Psa21	GCA_004340405.1
ATN94778.1	001831	TM	131	SL2_201	Pseudomonas phage SL2	GCA_002956015.1
QJB22814.1	001831	TM	131	fnug_171	Pseudomonas phage fnug	GCA_012837215.1
QEM41895.1	001831	TM	134	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83043.1	001831	TM	131	PHIKZ142	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60366.1	001832	Cluster1350_1clades	142	Ea357_213	Erwinia phage Ea35-70	GCA_000914635.1
QBP07323.1	001832	Cluster1350_1clades	142	REBECCA_218	Erwinia phage Rebecca	GCA_004521635.1
AUG86004.1	001832	Cluster1350_1clades	142	BOSOLAPHORUS_218	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52321.1	001832	Cluster1350_1clades	142	DM_221	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86323.1	001832	Cluster1350_1clades	142	DESERTFOX_216	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86646.1	001832	Cluster1350_1clades	142	MADMEL_218	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86969.1	001832	Cluster1350_1clades	142	MORTIMER_221	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51996.1	001832	Cluster1350_1clades	142	RAY_216	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51680.1	001832	Cluster1350_1clades	142	SIMMY50_221	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65030.1	001832	Cluster1350_1clades	142	SPECIALG_219	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54540.1	001832	Cluster1350_1clades	142	ACSA002_2240	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64160.1	001833	Cluster1351_1clades	77	KVP40.0089	Vibrio phage KVP40	GCA_000843785.1
QIW90484.1	001833	Cluster1351_1clades	77	GCAPEGMB_00137	Vibrio phage V07	GCA_012361095.1
QIW90945.1	001833	Cluster1351_1clades	77	COHAPHLL_00082	Vibrio phage V09	GCA_012361135.1
QHJ74272.1	001833	Cluster1351_1clades	77	VH12019_00353	Vibrio phage VH1_2019	GCA_009931825.1
AGB07097.1	001833	Cluster1351_1clades	77	CF80_gp310	Vibrio phage VH7D	GCA_000914495.1
QBX05999.1	001833	Cluster1351_1clades	141	ValB1HC_045	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61012.1	001833	Cluster1351_1clades	77	AVU32_gp171	Vibrio phage ValKK3	GCA_001501635.1
AGN30139.1	001833	Cluster1351_1clades	75	VPFG_00137	Vibrio phage nt-1	GCA_000910195.2
ALP47273.1	001833	Cluster1351_1clades	77	phiGrn1_0204	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47653.1	001833	Cluster1351_1clades	77	phiST2_0337	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54623.1	001833	Cluster1351_1clades	141	vBValMR10Z_82	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AHI60180.1	001834	Cluster1352_1clades	137	Ea357_030	Erwinia phage Ea35-70	GCA_000914635.1
QBP07138.1	001834	Cluster1352_1clades	139	REBECCA_30	Erwinia phage Rebecca	GCA_004521635.1
AUG85818.1	001834	Cluster1352_1clades	137	BOSOLAPHORUS_30	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52128.1	001834	Cluster1352_1clades	76	DM_30	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH52129.1	001834	Cluster1352_1clades	43	DM_31	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86138.1	001834	Cluster1352_1clades	137	DESERTFOX_30	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86458.1	001834	Cluster1352_1clades	137	MADMEL_30	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86779.1	001834	Cluster1352_1clades	137	MORTIMER_30	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51811.1	001834	Cluster1352_1clades	137	RAY_30	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51493.1	001834	Cluster1352_1clades	137	SIMMY50_31	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64840.1	001834	Cluster1352_1clades	137	SPECIALG_30	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60256.1	001835	Cluster1353_1clades	138	Ea357_105	Erwinia phage Ea35-70	GCA_000914635.1
QBP07213.1	001835	Cluster1353_1clades	138	REBECCA_106	Erwinia phage Rebecca	GCA_004521635.1
AUG85893.1	001835	Cluster1353_1clades	138	BOSOLAPHORUS_106	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52208.2	001835	Cluster1353_1clades	138	DM_110	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86212.1	001835	Cluster1353_1clades	138	DESERTFOX_105	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86534.1	001835	Cluster1353_1clades	138	MADMEL_106	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86858.1	001835	Cluster1353_1clades	138	MORTIMER_109	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51886.1	001835	Cluster1353_1clades	138	RAY_105	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51570.1	001835	Cluster1353_1clades	138	SIMMY50_108	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64918.1	001835	Cluster1353_1clades	138	SPECIALG_108	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54401.1	001835	Cluster1353_1clades	139	ACSA002_0870	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60463.1	001836	Cluster1354_1clades	136	Ea357_309	Erwinia phage Ea35-70	GCA_000914635.1
QBP07420.1	001836	Cluster1354_1clades	136	REBECCA_315	Erwinia phage Rebecca	GCA_004521635.1
AUG86102.1	001836	Cluster1354_1clades	136	BOSOLAPHORUS_316	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52418.1	001836	Cluster1354_1clades	136	DM_319	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86422.1	001836	Cluster1354_1clades	136	DESERTFOX_315	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86743.1	001836	Cluster1354_1clades	136	MADMEL_316	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87068.1	001836	Cluster1354_1clades	136	MORTIMER_320	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52093.1	001836	Cluster1354_1clades	136	RAY_313	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51776.1	001836	Cluster1354_1clades	136	SIMMY50_318	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65128.1	001836	Cluster1354_1clades	136	SPECIALG_317	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54643.1	001836	Cluster1354_1clades	136	ACSA002_3260	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60459.1	001837	Cluster1356_1clades	131	Ea357_305	Erwinia phage Ea35-70	GCA_000914635.1
QBP07416.1	001837	Cluster1356_1clades	131	REBECCA_311	Erwinia phage Rebecca	GCA_004521635.1
AUG86098.1	001837	Cluster1356_1clades	131	BOSOLAPHORUS_312	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ASB43083.1	001837	Cluster1356_1clades	131	DM_315	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86418.1	001837	Cluster1356_1clades	131	DESERTFOX_311	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86739.1	001837	Cluster1356_1clades	131	MADMEL_312	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87064.1	001837	Cluster1356_1clades	131	MORTIMER_316	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52089.1	001837	Cluster1356_1clades	131	RAY_309	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51772.1	001837	Cluster1356_1clades	131	SIMMY50_314	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65124.1	001837	Cluster1356_1clades	131	SPECIALG_313	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24218.1	001837	Cluster1356_1clades	127	-	Proteus phage 10	GCA_014071245.1
AAQ64279.1	001838	Cluster1358_1clades	113	KVP40.0210	Vibrio phage KVP40	GCA_000843785.1
QIW90595.1	001838	Cluster1358_1clades	127	GCAPEGMB_00248	Vibrio phage V07	GCA_012361095.1
QIW91203.1	001838	Cluster1358_1clades	127	COHAPHLL_00367	Vibrio phage V09	GCA_012361135.1
QHJ74391.1	001838	Cluster1358_1clades	127	VH12019_00064	Vibrio phage VH1_2019	GCA_009931825.1
AGB06897.1	001838	Cluster1358_1clades	127	CF80_gp110	Vibrio phage VH7D	GCA_000914495.1
QBX06249.1	001838	Cluster1358_1clades	127	ValB1HC_296	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60875.1	001838	Cluster1358_1clades	61	AVU32_gp034	Vibrio phage ValKK3	GCA_001501635.1
ALP47310.1	001838	Cluster1358_1clades	61	phiGrn1_0335	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47541.1	001838	Cluster1358_1clades	127	phiST2_0090	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54875.1	001838	Cluster1358_1clades	127	vBValMR10Z_335	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37440.1	001838	Cluster1358_1clades	127	pp2_207	Vibriophage phi-pp2	GCA_002630725.1
AHI60345.1	001839	Cluster1359_1clades	90	Ea357_193	Erwinia phage Ea35-70	GCA_000914635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBP07303.1	001839	Cluster1359_1clades	124	REBECCA_197	Erwinia phage Rebecca	GCA_004521635.1
AUG85984.1	001839	Cluster1359_1clades	90	BOSOLAPHORUS_197	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52299.1	001839	Cluster1359_1clades	90	DM_201	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86303.1	001839	Cluster1359_1clades	90	DESERTFOX_196	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86625.1	001839	Cluster1359_1clades	90	MADMEL_197	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86949.1	001839	Cluster1359_1clades	90	MORTIMER_200	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51976.1	001839	Cluster1359_1clades	90	RAY_195	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51660.1	001839	Cluster1359_1clades	90	SIMMY50_198	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65007.1	001839	Cluster1359_1clades	90	SPECIALG_198	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24127.1	001839	Cluster1359_1clades	91	-	Proteus phage 10	GCA_014071245.1
AHI60403.1	001840	Cluster1360_1clades	120	Ea357_249	Erwinia phage Ea35-70	GCA_000914635.1
QBP07359.1	001840	Cluster1360_1clades	120	REBECCA_254	Erwinia phage Rebecca	GCA_004521635.1
AUG86041.1	001840	Cluster1360_1clades	120	BOSOLAPHORUS_255	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52358.1	001840	Cluster1360_1clades	120	DM_259	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86361.1	001840	Cluster1360_1clades	120	DESERTFOX_254	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86683.1	001840	Cluster1360_1clades	120	MADMEL_256	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87007.1	001840	Cluster1360_1clades	120	MORTIMER_259	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52033.1	001840	Cluster1360_1clades	120	RAY_253	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51716.1	001840	Cluster1360_1clades	120	SIMMY50_258	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65068.1	001840	Cluster1360_1clades	120	SPECIALG_257	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54588.1	001840	Cluster1360_1clades	121	ACSA002_2720	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64299.1	001841	Cluster1361_1clades	120	KVP40.0230	Vibrio phage KVP40	GCA_000843785.1
QIW90615.1	001841	Cluster1361_1clades	120	GCAPEGMB_00268	Vibrio phage V07	GCA_012361095.1
QIW91184.1	001841	Cluster1361_1clades	120	COHAPHLL_00348	Vibrio phage V09	GCA_012361135.1
QHJ74410.1	001841	Cluster1361_1clades	120	VH12019_00083	Vibrio phage VH1_2019	GCA_009931825.1
AGB06917.1	001841	Cluster1361_1clades	119	CF80_gp130	Vibrio phage VH7D	GCA_000914495.1
QBX06229.1	001841	Cluster1361_1clades	119	ValB1HC_276	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60855.1	001841	Cluster1361_1clades	119	AVU32_gp014	Vibrio phage ValKK3	GCA_001501635.1
ALP47164.1	001841	Cluster1361_1clades	119	phiGrn1_0353	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47551.1	001841	Cluster1361_1clades	119	phiST2_0108	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54854.1	001841	Cluster1361_1clades	119	vBValMR10Z_314	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37460.1	001841	Cluster1361_1clades	120	pp2_227	Vibriophage phi-pp2	GCA_002630725.1
AAQ64407.1	001842	SIG+TM	119	KVP40.0338	Vibrio phage KVP40	GCA_000843785.1
QIW90352.1	001842	SIG+TM	119	GCAPEGMB_00005	Vibrio phage V07	GCA_012361095.1
QIW91077.1	001842	SIG+TM	119	COHAPHLL_00214	Vibrio phage V09	GCA_012361135.1
QHJ74520.1	001842	SIG+TM	119	VH12019_00220	Vibrio phage VH1_2019	GCA_009931825.1
QBX06135.1	001842	SIG+TM	119	ValB1HC_181	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61147.1	001842	SIG+TM	119	AVU32_gp306	Vibrio phage ValKK3	GCA_001501635.1
AGN30011.1	001842	SIG+TM	119	VPFG_00003	Vibrio phage nt-1	GCA_000910195.2
ALP47227.1	001842	SIG+TM	92	phiGrn1_0072	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47550.1	001842	SIG+TM	119	phiST2_0204	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54760.1	001842	SIG+TM	119	vBValMR10Z_220	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37570.1	001842	SIG+TM	119	pp2_338	Vibriophage phi-pp2	GCA_002630725.1
AAQ64281.1	001843	SIG+TM+TM	112	KVP40.0212	Vibrio phage KVP40	GCA_000843785.1
QIW90597.1	001843	SIG+TM+TM	112	GCAPEGMB_00250	Vibrio phage V07	GCA_012361095.1
QHJ74393.1	001843	SIG+TM+TM	112	VH12019_00066	Vibrio phage VH1_2019	GCA_009931825.1
AGB06899.1	001843	SIG+TM+TM	111	CF80_gp112	Vibrio phage VH7D	GCA_000914495.1
QBX06247.1	001843	SIG+TM+TM	111	ValB1HC_294	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60873.1	001843	SIG+TM+TM	111	AVU32_gp032	Vibrio phage ValKK3	GCA_001501635.1
AGN30273.1	001843	SIG+TM+TM	119	VPFG_00274	Vibrio phage nt-1	GCA_000910195.2
ALP47251.1	001843	SIG+TM+TM	85	phiGrn1_0337	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47567.1	001843	SIG+TM+TM	111	phiST2_0092	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54873.1	001843	SIG+TM+TM	111	vBValMR10Z_333	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37442.1	001843	SIG+TM+TM	112	pp2_209	Vibriophage phi-pp2	GCA_002630725.1
ABY63063.1	001844	Cluster1365_1clades	108	201phi2-1p234	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44944.1	001844	Cluster1365_1clades	106	KTN4_186	Pseudomonas phage KTN4	GCA_002607225.1
ARV77328.1	001844	Cluster1365_1clades	119	NOXIFER_159	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32331.1	001844	Cluster1365_1clades	106	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76853.1	001844	Cluster1365_1clades	103	PHABIO_222	Pseudomonas phage Phabio	GCA_002624965.1
AEH03596.1	001844	Cluster1365_1clades	106	173	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02732.1	001844	Cluster1365_1clades	101	PSA21_206	Pseudomonas phage Psa21	GCA_004340405.1
ATN94770.1	001844	Cluster1365_1clades	106	SL2_193	Pseudomonas phage SL2	GCA_002956015.1
QJB22822.1	001844	Cluster1365_1clades	106	fnug_179	Pseudomonas phage fnug	GCA_012837215.1
QEM41904.1	001844	Cluster1365_1clades	106	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83051.1	001844	Cluster1365_1clades	106	PHIKZ150	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60298.1	001845	Cluster1366_1clades	118	Ea357_147	Erwinia phage Ea35-70	GCA_000914635.1
QBP07256.1	001845	Cluster1366_1clades	118	REBECCA_149	Erwinia phage Rebecca	GCA_004521635.1
AUG85936.1	001845	Cluster1366_1clades	118	BOSOLAPHORUS_149	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52251.1	001845	Cluster1366_1clades	118	DM_153	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86255.1	001845	Cluster1366_1clades	118	DESERTFOX_148	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86577.1	001845	Cluster1366_1clades	118	MADMEL_149	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86901.1	001845	Cluster1366_1clades	118	MORTIMER_152	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51929.1	001845	Cluster1366_1clades	118	RAY_148	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51613.1	001845	Cluster1366_1clades	118	SIMMY50_151	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64960.1	001845	Cluster1366_1clades	118	SPECIALG_150	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54452.1	001845	Cluster1366_1clades	116	ACSA002_1380	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AHI60197.1	001846	Cluster1367_1clades	114	Ea357_047	Erwinia phage Ea35-70	GCA_000914635.1
QBP07155.1	001846	Cluster1367_1clades	118	REBECCA_47	Erwinia phage Rebecca	GCA_004521635.1
AUG85835.1	001846	Cluster1367_1clades	118	BOSOLAPHORUS_47	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52146.1	001846	Cluster1367_1clades	118	DM_48	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86155.1	001846	Cluster1367_1clades	118	DESERTFOX_47	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86475.1	001846	Cluster1367_1clades	118	MADMEL_47	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86796.1	001846	Cluster1367_1clades	118	MORTIMER_47	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51828.2	001846	Cluster1367_1clades	118	RAY_47	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASB43073.1	001846	Cluster1367_1clades	118	SIMMY50_48	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64857.1	001846	Cluster1367_1clades	118	SPECIALG_47	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54389.1	001846	Cluster1367_1clades	116	ACSA002_0750	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64301.1	001847	Cluster1368_1clades	96	KVP40.0232	Vibrio phage KVP40	GCA_000843785.1
QIW90617.1	001847	Cluster1368_1clades	96	GCAPEGMB_00270	Vibrio phage V07	GCA_012361095.1
QIW91182.1	001847	Cluster1368_1clades	96	COHAPHLL_00346	Vibrio phage V09	GCA_012361135.1
QHJ74412.1	001847	Cluster1368_1clades	96	VH12019_00085	Vibrio phage VH1_2019	GCA_009931825.1
AGB06920.1	001847	Cluster1368_1clades	117	CF80_gp133	Vibrio phage VH7D	GCA_000914495.1
QBX06226.1	001847	Cluster1368_1clades	102	ValB1HC_273	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60852.1	001847	Cluster1368_1clades	102	AVU32_gp011	Vibrio phage ValKK3	GCA_001501635.1
ALP47197.1	001847	Cluster1368_1clades	102	phiGrn1_0356	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47586.1	001847	Cluster1368_1clades	102	phiST2_0111	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54851.1	001847	Cluster1368_1clades	102	vBValMR10Z_311	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37462.1	001847	Cluster1368_1clades	96	pp2_229	Vibriophage phi-pp2	GCA_002630725.1
AAQ64282.1	001848	SIG+TM+TM	114	KVP40.0213	Vibrio phage KVP40	GCA_000843785.1
QIW90598.1	001848	SIG+TM+TM	114	GCAPEGMB_00251	Vibrio phage V07	GCA_012361095.1
QIW91201.1	001848	SIG+TM+TM	114	COHAPHLL_00365	Vibrio phage V09	GCA_012361135.1
QHJ74394.1	001848	SIG+TM+TM	114	VH12019_00067	Vibrio phage VH1_2019	GCA_009931825.1
AGB06900.1	001848	SIG+TM+TM	89	CF80_gp113	Vibrio phage VH7D	GCA_000914495.1
QBX06246.1	001848	SIG+TM+TM	114	ValB1HC_293	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60872.1	001848	SIG+TM+TM	114	AVU32_gp031	Vibrio phage ValKK3	GCA_001501635.1
AGN30274.1	001848	SIG+TM+TM	114	VPFG_00275	Vibrio phage nt-1	GCA_000910195.2
AGN30275.1	001848	SIG+TM+TM	114	VPFG_00276	Vibrio phage nt-1	GCA_000910195.2
QNJ54872.1	001848	SIG+TM+TM	114	vBValMR10Z_332	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37443.1	001848	SIG+TM+TM	114	pp2_210	Vibriophage phi-pp2	GCA_002630725.1
AHI60164.1	001849	Cluster1370_1clades	109	Ea357_014	Erwinia phage Ea35-70	GCA_000914635.1
QBP07122.1	001849	Cluster1370_1clades	109	REBECCA_14	Erwinia phage Rebecca	GCA_004521635.1
AUG85802.1	001849	Cluster1370_1clades	109	BOSOLAPHORUS_14	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52112.2	001849	Cluster1370_1clades	109	DM_14	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86122.1	001849	Cluster1370_1clades	109	DESERTFOX_14	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86442.1	001849	Cluster1370_1clades	109	MADMEL_14	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86763.1	001849	Cluster1370_1clades	109	MORTIMER_14	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51795.1	001849	Cluster1370_1clades	109	RAY_14	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51477.2	001849	Cluster1370_1clades	109	SIMMY50_15	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64824.2	001849	Cluster1370_1clades	109	SPECIALG_14	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54328.1	001849	Cluster1370_1clades	114	ACSA002_0140	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64178.1	001850	Cluster1371_1clades	110	KVP40.0107	Vibrio phage KVP40	GCA_000843785.1
QIW90501.1	001850	Cluster1371_1clades	110	GCAPEGMB_00154	Vibrio phage V07	GCA_012361095.1
QIW90928.1	001850	Cluster1371_1clades	110	COHAPHLL_00065	Vibrio phage V09	GCA_012361135.1
QHJ74289.1	001850	Cluster1371_1clades	110	VH12019_00370	Vibrio phage VH1_2019	GCA_009931825.1
AGB07112.1	001850	Cluster1371_1clades	111	CF80_gp325	Vibrio phage VH7D	GCA_000914495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX05982.1	001850	Cluster1371_1clades	111	ValB1HC_028	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60995.1	001850	Cluster1371_1clades	111	AVU32_gp154	Vibrio phage ValKK3	GCA_001501635.1
AGN30156.1	001850	Cluster1371_1clades	113	VPFG_00154	Vibrio phage nt-1	GCA_000910195.2
ALP47566.1	001850	Cluster1371_1clades	111	phiST2_0353	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54607.1	001850	Cluster1371_1clades	111	vBValMR10Z_66	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37336.1	001850	Cluster1371_1clades	110	pp2_103	Vibriophage phi-pp2	GCA_002630725.1
AAQ64372.1	001851	Cluster1372_1clades	112	KVP40.0302	Vibrio phage KVP40	GCA_000843785.1
QIW90688.1	001851	Cluster1372_1clades	111	GCAPEGMB_00341	Vibrio phage V07	GCA_012361095.1
QIW91110.1	001851	Cluster1372_1clades	111	COHAPHLI_00274	Vibrio phage V09	GCA_012361135.1
QHJ74484.1	001851	Cluster1372_1clades	111	VH12019_00157	Vibrio phage VH1_2019	GCA_009931825.1
QBX06166.1	001851	Cluster1372_1clades	111	ValB1HC_213	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61183.1	001851	Cluster1372_1clades	111	AVU32_gp342	Vibrio phage ValKK3	GCA_001501635.1
AGN30350.1	001851	Cluster1372_1clades	110	VPFG_00353	Vibrio phage nt-1	GCA_000910195.2
ALP47179.1	001851	Cluster1372_1clades	111	phiGrn1_0039	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47568.1	001851	Cluster1372_1clades	110	phiST2_0171	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54792.1	001851	Cluster1372_1clades	111	vBValMR10Z_252	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37534.1	001851	Cluster1372_1clades	111	pp2_301	Vibriophage phi-pp2	GCA_002630725.1
AHI60342.1	001852	Cluster1373_1clades	112	Ea357_190	Erwinia phage Ea35-70	GCA_000914635.1
QBP07301.1	001852	Cluster1373_1clades	112	REBECCA_194	Erwinia phage Rebecca	GCA_004521635.1
AUG85981.1	001852	Cluster1373_1clades	112	BOSOLAPHORUS_194	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52296.1	001852	Cluster1373_1clades	112	DM_198	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86300.1	001852	Cluster1373_1clades	112	DESERTFOX_193	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86622.1	001852	Cluster1373_1clades	112	MADMEL_194	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86946.1	001852	Cluster1373_1clades	112	MORTIMER_197	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51973.1	001852	Cluster1373_1clades	112	RAY_192	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51657.1	001852	Cluster1373_1clades	112	SIMMY50_195	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65004.1	001852	Cluster1373_1clades	112	SPECIALG_195	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QMP24122.1	001852	Cluster1373_1clades	111	-	Proteus phage 10	GCA_014071245.1
AAQ64240.1	001853	Cluster1374_1clades	111	KVP40.0171	Vibrio phage KVP40	GCA_000843785.1
QIW90556.1	001853	Cluster1374_1clades	105	GCAPEGMB_00209	Vibrio phage V07	GCA_012361095.1
QIW90866.1	001853	Cluster1374_1clades	106	COHAPHLI_00003	Vibrio phage V09	GCA_012361135.1
QHJ74354.1	001853	Cluster1374_1clades	111	VH12019_00027	Vibrio phage VH1_2019	GCA_009931825.1
AGB06845.1	001853	Cluster1374_1clades	71	CF80_gp058	Vibrio phage VH7D	GCA_000914495.1
QBX06300.1	001853	Cluster1374_1clades	71	ValB1HC_347	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60929.1	001853	Cluster1374_1clades	71	AVU32_gp088	Vibrio phage ValKK3	GCA_001501635.1
ALP47288.1	001853	Cluster1374_1clades	71	phiGrn1_0283	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47668.1	001853	Cluster1374_1clades	71	phiST2_0042	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54542.1	001853	Cluster1374_1clades	71	vBValMR10Z_1	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37400.1	001853	Cluster1374_1clades	74	pp2_167	Vibriophage phi-pp2	GCA_002630725.1
AHI60368.1	001854	Cluster1375_1clades	100	Ea357_215	Erwinia phage Ea35-70	GCA_000914635.1
QBP07325.1	001854	Cluster1375_1clades	100	REBECCA_220	Erwinia phage Rebecca	GCA_004521635.1
AUG86006.1	001854	Cluster1375_1clades	100	BOSOLAPHORUS_220	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52323.1	001854	Cluster1375_1clades	100	DM_223	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86325.1	001854	Cluster1375_1clades	100	DESERTFOX_218	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86648.1	001854	Cluster1375_1clades	100	MADMEL_220	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86971.1	001854	Cluster1375_1clades	100	MORTIMER_223	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51998.1	001854	Cluster1375_1clades	100	RAY_218	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51682.1	001854	Cluster1375_1clades	100	SIMMY50_223	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65032.1	001854	Cluster1375_1clades	100	SPECIALG_221	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54542.1	001854	Cluster1375_1clades	111	ACSA002_2260	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ABY63046.1	001855	Cluster1376_1clades	107	201phi2-1p217	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44925.1	001855	Cluster1376_1clades	110	KTN4_167	Pseudomonas phage KTN4	GCA_002607225.1
ARV77322.1	001855	Cluster1376_1clades	106	NOXIFER_153	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32312.1	001855	Cluster1376_1clades	107	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76835.1	001855	Cluster1376_1clades	107	PHABIO_204	Pseudomonas phage Phabio	GCA_002624965.1
AEH03574.1	001855	Cluster1376_1clades	107	151	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02711.1	001855	Cluster1376_1clades	105	PSA21_185	Pseudomonas phage Psa21	GCA_004340405.1
ATN94789.1	001855	Cluster1376_1clades	110	SL2_212	Pseudomonas phage SL2	GCA_002956015.1
QJB22803.1	001855	Cluster1376_1clades	110	fnug_160	Pseudomonas phage fnug	GCA_012837215.1
QEM41885.1	001855	Cluster1376_1clades	107	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83033.1	001855	Cluster1376_1clades	110	PHIKZ132	Pseudomonas virus phiKZ	GCA_000842965.1
AMO43101.1	001856	Cluster1377_1clades	66	R1080702_092	Cyanophage S-RIM32	GCA_001754165.1
AMO43330.1	001856	Cluster1377_1clades	66	W270710_086	Cyanophage S-RIM44	GCA_002599145.1
AOO11563.1	001856	Cluster1377_1clades	66	ES420910_082	Cyanophage S-RIM44	GCA_002599165.1
AOO11802.1	001856	Cluster1377_1clades	66	Np050604_086	Cyanophage S-RIM44	GCA_002599185.1
AOO12028.1	001856	Cluster1377_1clades	66	Np200711_082	Cyanophage S-RIM44	GCA_002599205.1
AOO12264.1	001856	Cluster1377_1clades	66	Np420711_082	Cyanophage S-RIM44	GCA_002599225.1
AOO12503.1	001856	Cluster1377_1clades	66	Sn080709_086	Cyanophage S-RIM44	GCA_002599245.1
AOO12729.1	001856	Cluster1377_1clades	66	Sn130910_082	Cyanophage S-RIM44	GCA_002599265.1
AOO12969.1	001856	Cluster1377_1clades	66	W2100709_087	Cyanophage S-RIM44	GCA_002599285.1
AGG54331.1	001856	Cluster1377_1clades	64	CYWG_00047	Cyanophage S-SSM6b	GCA_002710425.1
ADO99186.1	001856	Cluster1377_1clades	110	Syn1_085	Prochlorococcus phage Syn1	GCA_000892495.1
AIT14423.1	001857	Ribosomal_S30AE	110	PBI_121Q_533	Escherichia phage 121Q	GCA_000926855.1
QAY00527.1	001857	Ribosomal_S30AE	110	Ecwhy1_248	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34719.1	001857	Ribosomal_S30AE	110	ACQ29_gp039	Escherichia phage PBECO4	GCA_001041035.1
BBM62095.1	001857	Ribosomal_S30AE	110	EO157G_5060	Escherichia phage SP27	GCA_008033345.1
AXC36837.1	001857	Ribosomal_S30AE	110	-	Escherichia phage UB	GCA_003341455.1
QBO61878.1	001857	Ribosomal_S30AE	110	G17_00389	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13917.1	001857	Ribosomal_S30AE	110	vBEcoMphAPEC6_gp292c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80409.1	001857	Ribosomal_S30AE	110	PSLUR01_00432	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18903.1	001857	Ribosomal_S30AE	106	7t3_0382	Salmonella phage 7t3	GCA_006083215.1
AZU98160.1	001857	Ribosomal_S30AE	106	CPT_Munch_216	Salmonella phage Munch	GCA_004015485.1
QIG62824.1	001857	Ribosomal_S30AE	106	SEPL_211	Salmonella phage SE_PL	GCA_011067555.1
AAQ64247.1	001858	Cluster1379_1clades	107	KVP40.0178	Vibrio phage KVP40	GCA_000843785.1
QIW90563.1	001858	Cluster1379_1clades	82	GCAPEGMB_00216	Vibrio phage V07	GCA_012361095.1
QIW91236.1	001858	Cluster1379_1clades	82	COHAPHLI_00400	Vibrio phage V09	GCA_012361135.1
QHJ74361.1	001858	Cluster1379_1clades	82	VH12019_00034	Vibrio phage VH1_2019	GCA_009931825.1
AGB06854.1	001858	Cluster1379_1clades	83	CF80_gp067	Vibrio phage VH7D	GCA_000914495.1
QBX06291.1	001858	Cluster1379_1clades	83	ValB1HC_338	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60921.1	001858	Cluster1379_1clades	83	AVU32_gp080	Vibrio phage ValKK3	GCA_001501635.1
ALP47258.1	001858	Cluster1379_1clades	83	phiGrn1_0293	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47638.1	001858	Cluster1379_1clades	83	phiST2_0050	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54918.1	001858	Cluster1379_1clades	83	vBValMR10Z_378	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37408.1	001858	Cluster1379_1clades	82	pp2_175	Vibriophage phi-pp2	GCA_002630725.1
AAQ64371.1	001859	Cluster1380_1clades	104	KVP40.0301	Vibrio phage KVP40	GCA_000843785.1
QIW90687.1	001859	Cluster1380_1clades	104	GCAPEGMB_00340	Vibrio phage V07	GCA_012361095.1
QIW91111.1	001859	Cluster1380_1clades	104	COHAPHLI_00275	Vibrio phage V09	GCA_012361135.1
QHJ74483.1	001859	Cluster1380_1clades	104	VH12019_00156	Vibrio phage VH1_2019	GCA_009931825.1
QBX06167.1	001859	Cluster1380_1clades	104	ValB1HC_214	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61184.1	001859	Cluster1380_1clades	104	AVU32_gp343	Vibrio phage ValKK3	GCA_001501635.1
AGN30349.1	001859	Cluster1380_1clades	105	VPFG_00352	Vibrio phage nt-1	GCA_000910195.2
ALP47194.1	001859	Cluster1380_1clades	104	phiGrn1_0038	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47578.1	001859	Cluster1380_1clades	106	phiST2_0170	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54793.1	001859	Cluster1380_1clades	104	vBValMR10Z_253	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37533.1	001859	Cluster1380_1clades	104	pp2_300	Vibriophage phi-pp2	GCA_002630725.1
ARB13801.1	001860	Cluster1381_1clades	104	Ccr10_gp271	Caulobacter phage Ccr10	GCA_002619445.1
ARB14146.1	001860	Cluster1381_1clades	104	Ccr2_gp270	Caulobacter phage Ccr2	GCA_002619465.1
ARB14840.1	001860	Cluster1381_1clades	104	Ccr29_gp284	Caulobacter phage Ccr29	GCA_002619485.1
ARB15180.1	001860	Cluster1381_1clades	104	Ccr32_gp262	Caulobacter phage Ccr32	GCA_002619505.1
ARB15514.1	001860	Cluster1381_1clades	104	Ccr34_gp272	Caulobacter phage Ccr34	GCA_002619525.1
ARB14488.1	001860	Cluster1381_1clades	104	Ccr5_gp268	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68468.1	001860	Cluster1381_1clades	101	CcrBL10_gp264	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87798.1	001860	Cluster1381_1clades	104	CcrKarma_gp281	Caulobacter virus Karma	GCA_000901575.1
AFU87445.1	001860	Cluster1381_1clades	104	CcrMagneto_gp275	Caulobacter virus Magneto	GCA_000903095.1
AFU88591.1	001860	Cluster1381_1clades	104	CcrSwift_gp273	Caulobacter virus Swift	GCA_000899655.1
AFU87099.1	001860	Cluster1381_1clades	104	CbK_gp267	Caulobacter virus phiCbK	GCA_000900535.1
AJK27485.1	001861	Cluster1382_1clades	52	PTIM40_58	Cyanophage P-TIM40	GCA_001470935.1
AOO14240.1	001861	Cluster1382_1clades	54	Sn110110_046	Cyanophage S-RIM14	GCA_002599065.1
AOO14892.1	001861	Cluster1382_1clades	54	W1230910_046	Cyanophage S-RIM14	GCA_002599125.1
AGH07487.1	001861	Cluster1382_1clades	104	CYVG_00043	Cyanophage S-SSM6a	GCA_002710385.1
AGG54465.1	001861	Cluster1382_1clades	65	CYWG_00181	Cyanophage S-SSM6b	GCA_002710425.1
AGH26300.1	001861	Cluster1382_1clades	89	CPMG_00200	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44540.1	001861	Cluster1382_1clades	65	PSSM2_162	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12431.1	001861	Cluster1382_1clades	65	PRTG_00281	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93475.1	001861	Cluster1382_1clades	79	AVU42_gp138	Prochlorococcus phage P-TIM68	GCA_001503075.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASR76199.1	001861	Cluster1382_1clades	64	PBI_BELLAMY_154	Synechococcus phage Bellamy	GCA_002627525.1
QJT70147.1	001861	Cluster1382_1clades	62	SynMITS9220M01_134	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14214.1	001862	Cluster1383_1clades	78	PBI_121Q_324	Escherichia phage 121Q	GCA_000926855.1
AIT14215.1	001862	Cluster1383_1clades	85	PBI_121Q_325	Escherichia phage 121Q	GCA_000926855.1
QAY00723.1	001862	Cluster1383_1clades	87	Ecwhy1_448	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34906.1	001862	Cluster1383_1clades	74	ACQ29_gp226	Escherichia phage PBECO4	GCA_001041035.1
BBM61888.1	001862	Cluster1383_1clades	85	EO157G_2990	Escherichia phage SP27	GCA_008033345.1
AXC37011.1	001862	Cluster1383_1clades	39	-	Escherichia phage UB	GCA_003341455.1
QBO62094.1	001862	Cluster1383_1clades	85	G17_00605	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62096.1	001862	Cluster1383_1clades	74	G17_00607	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14106.1	001862	Cluster1383_1clades	104	vBEcoMphAPEC6_gp483c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80198.1	001862	Cluster1383_1clades	74	PSLUR01_00221	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80200.1	001862	Cluster1383_1clades	85	PSLUR01_00223	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64442.1	001863	Cluster1384_1clades	102	KVP40.0374	Vibrio phage KVP40	GCA_000843785.1
QIW90387.1	001863	Cluster1384_1clades	91	GCAPEGMB_00040	Vibrio phage V07	GCA_012361095.1
QIW91042.1	001863	Cluster1384_1clades	91	COHAPHLL_00179	Vibrio phage V09	GCA_012361135.1
QHJ74554.1	001863	Cluster1384_1clades	91	VH12019_00254	Vibrio phage VH1_2019	GCA_009931825.1
QBX06100.1	001863	Cluster1384_1clades	88	ValB1HC_146	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61114.1	001863	Cluster1384_1clades	88	AVU32_gp273	Vibrio phage ValKK3	GCA_001501635.1
AGN30042.1	001863	Cluster1384_1clades	91	VPFG_00037	Vibrio phage nt-1	GCA_000910195.2
ALP47242.1	001863	Cluster1384_1clades	88	phiGrn1_0106	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47626.1	001863	Cluster1384_1clades	88	phiST2_0237	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54725.1	001863	Cluster1384_1clades	88	vBValMR10Z_185	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37605.1	001863	Cluster1384_1clades	91	pp2_373	Vibriophage phi-pp2	GCA_002630725.1
AIT14005.1	001864	Cluster1385_1clades	96	PBI_121Q_108	Escherichia phage 121Q	GCA_000926855.1
QAY00333.1	001864	Cluster1385_1clades	101	Ecwhy1_52	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35079.1	001864	Cluster1385_1clades	96	ACQ29_gp399	Escherichia phage PBECO4	GCA_001041035.1
BBM61696.1	001864	Cluster1385_1clades	96	EO157G_1070	Escherichia phage SP27	GCA_008033345.1
AXC36656.1	001864	Cluster1385_1clades	96	-	Escherichia phage UB	GCA_003341455.1
QBO61688.1	001864	Cluster1385_1clades	96	G17_00199	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13737.1	001864	Cluster1385_1clades	96	vBEcoMphAPEC6_gp107c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80009.1	001864	Cluster1385_1clades	96	PSLUR01_00025	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18544.1	001864	Cluster1385_1clades	98	7t3_014	Salmonella phage 7t3	GCA_006083215.1
AZU98376.1	001864	Cluster1385_1clades	98	CPT_Munch_437	Salmonella phage Munch	GCA_004015485.1
QIG63137.1	001864	Cluster1385_1clades	98	SEPL_524	Salmonella phage SE_PL	GCA_011067555.1
ABY63295.1	001865	SIG+TM	95	201phi2-1p242	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44951.1	001865	SIG+TM	96	KTN4_193	Pseudomonas phage KTN4	GCA_002607225.1
ARV77340.1	001865	SIG+TM	99	NOXIFER_171	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32337.1	001865	SIG+TM	95	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76861.1	001865	SIG+TM	93	PHABIO_230	Pseudomonas phage Phabio	GCA_002624965.1
AEH03603.1	001865	SIG+TM	96	180	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02740.1	001865	SIG+TM	95	PSA21_214	Pseudomonas phage Psa21	GCA_004340405.1
ATN94763.1	001865	SIG+TM	96	SL2_186	Pseudomonas phage SL2	GCA_002956015.1
QJB22829.1	001865	SIG+TM	96	fnug_186	Pseudomonas phage fnug	GCA_012837215.1
QEM41912.1	001865	SIG+TM	95	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26337.1	001865	SIG+TM	96	PHIKZ156.1	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64286.1	001866	Cluster1388_1clades	97	KVP40.0217	Vibrio phage KVP40	GCA_000843785.1
QIW90602.1	001866	Cluster1388_1clades	95	GCAPEGMB_00255	Vibrio phage V07	GCA_012361095.1
QIW91197.1	001866	Cluster1388_1clades	95	COHAPHLL_00361	Vibrio phage V09	GCA_012361135.1
QHJ74398.1	001866	Cluster1388_1clades	95	VH12019_00071	Vibrio phage VH1_2019	GCA_009931825.1
AGB06904.1	001866	Cluster1388_1clades	96	CF80_gp117	Vibrio phage VH7D	GCA_000914495.1
QBX06242.1	001866	Cluster1388_1clades	96	ValB1HC_289	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60868.1	001866	Cluster1388_1clades	95	AVU32_gp027	Vibrio phage ValKK3	GCA_001501635.1
ALP47217.1	001866	Cluster1388_1clades	96	phiGrn1_0341	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47606.1	001866	Cluster1388_1clades	96	phiST2_0096	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54868.1	001866	Cluster1388_1clades	96	vBValMR10Z_328	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37447.1	001866	Cluster1388_1clades	95	pp2_214	Vibriophage phi-pp2	GCA_002630725.1
AAQ64342.1	001867	Cluster1389_1clades	97	KVP40.0273	Vibrio phage KVP40	GCA_000843785.1
QIW90656.1	001867	Cluster1389_1clades	90	GCAPEGMB_00309	Vibrio phage V07	GCA_012361095.1
QIW91142.1	001867	Cluster1389_1clades	90	COHAPHLL_00306	Vibrio phage V09	GCA_012361135.1
QHJ74451.1	001867	Cluster1389_1clades	90	VH12019_00124	Vibrio phage VH1_2019	GCA_009931825.1
QBX06199.1	001867	Cluster1389_1clades	76	ValB1HC_246	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61216.1	001867	Cluster1389_1clades	76	AVU32_gp375	Vibrio phage ValKK3	GCA_001501635.1
AGN30319.1	001867	Cluster1389_1clades	89	VPFG_00321	Vibrio phage nt-1	GCA_000910195.2
ALP47274.1	001867	Cluster1389_1clades	76	phiGrn1_0006	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47661.1	001867	Cluster1389_1clades	76	phiST2_0138	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54824.1	001867	Cluster1389_1clades	77	vBValMR10Z_284	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37502.1	001867	Cluster1389_1clades	90	pp2_269	Vibriophage phi-pp2	GCA_002630725.1
AMO43217.1	001868	Ferredoxin-betagrasp	96	R1080702_212	Cyanophage S-RIM32	GCA_001754165.1
AAX44658.1	001868	Ferredoxin-betagrasp	97	PSSM2_281	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12317.1	001868	Ferredoxin-betagrasp	97	PRTG_00164	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIX30714.1	001868	Ferredoxin-betagrasp	97	Syn7803US37_237	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76113.1	001868	Ferredoxin-betagrasp	96	PBI_BELLAMY_68	Synechococcus phage Bellamy	GCA_002627525.1
QCW22954.1	001868	Ferredoxin-betagrasp	97	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50669.1	001868	Ferredoxin-betagrasp	97	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59667.1	001868	Ferredoxin-betagrasp	97	S330809_206	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59429.1	001868	Ferredoxin-betagrasp	97	C440309_206	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59904.1	001868	Ferredoxin-betagrasp	97	N231010_205	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70501.1	001868	Ferredoxin-betagrasp	97	HOU04_gp102	Synechococcus phage S-T4	GCA_003443335.1
AAQ64304.1	001869	Cluster1391_1clades	92	KVP40.0235	Vibrio phage KVP40	GCA_000843785.1
QIW90620.1	001869	Cluster1391_1clades	92	GCAPEGMB_00273	Vibrio phage V07	GCA_012361095.1
QIW91179.1	001869	Cluster1391_1clades	92	COHAPHLL_00343	Vibrio phage V09	GCA_012361135.1
QHJ74415.1	001869	Cluster1391_1clades	92	VH12019_00088	Vibrio phage VH1_2019	GCA_009931825.1
AGB06923.1	001869	Cluster1391_1clades	95	CF80_gp136	Vibrio phage VH7D	GCA_000914495.1
QBX06223.1	001869	Cluster1391_1clades	95	ValB1HC_270	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60849.1	001869	Cluster1391_1clades	95	AVU32_gp008	Vibrio phage ValKK3	GCA_001501635.1
ALP47220.1	001869	Cluster1391_1clades	95	phiGrn1_0359	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47608.1	001869	Cluster1391_1clades	95	phiST2_0114	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54848.1	001869	Cluster1391_1clades	95	vBValMR10Z_308	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37465.1	001869	Cluster1391_1clades	92	pp2_232	Vibriophage phi-pp2	GCA_002630725.1
AAQ64445.1	001870	Cluster1392_1clades	68	KVP40.0377	Vibrio phage KVP40	GCA_000843785.1
QIW90390.1	001870	Cluster1392_1clades	68	GCAPEGMB_00043	Vibrio phage V07	GCA_012361095.1
QIW91039.1	001870	Cluster1392_1clades	68	COHAPHLL_00176	Vibrio phage V09	GCA_012361135.1
QHJ74557.1	001870	Cluster1392_1clades	68	VH12019_00257	Vibrio phage VH1_2019	GCA_009931825.1
QBX06097.1	001870	Cluster1392_1clades	69	ValB1HC_143	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61111.1	001870	Cluster1392_1clades	69	AVU32_gp270	Vibrio phage ValKK3	GCA_001501635.1
AGN30045.2	001870	Cluster1392_1clades	95	VPFG_00040	Vibrio phage nt-1	GCA_000910195.2
ALP47293.1	001870	Cluster1392_1clades	69	phiGrn1_0109	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47687.1	001870	Cluster1392_1clades	64	phiST2_0240	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54722.1	001870	Cluster1392_1clades	64	vBValMR10Z_182	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37608.1	001870	Cluster1392_1clades	68	pp2_376	Vibriophage phi-pp2	GCA_002630725.1
AAQ64273.1	001871	Cluster1393_1clades	89	KVP40.0204	Vibrio phage KVP40	GCA_000843785.1
QIW90589.1	001871	Cluster1393_1clades	95	GCAPEGMB_00242	Vibrio phage V07	GCA_012361095.1
QIW91210.1	001871	Cluster1393_1clades	94	COHAPHLL_00374	Vibrio phage V09	GCA_012361135.1
AGB06890.1	001871	Cluster1393_1clades	89	CF80_gp103	Vibrio phage VH7D	GCA_000914495.1
QBX06256.1	001871	Cluster1393_1clades	89	ValB1HC_303	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60882.1	001871	Cluster1393_1clades	89	AVU32_gp041	Vibrio phage ValKK3	GCA_001501635.1
AGN30263.1	001871	Cluster1393_1clades	94	VPFG_00264	Vibrio phage nt-1	GCA_000910195.2
ALP47238.1	001871	Cluster1393_1clades	89	phiGrn1_0328	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47624.1	001871	Cluster1393_1clades	89	phiST2_0083	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54883.1	001871	Cluster1393_1clades	89	vBValMR10Z_343	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37433.1	001871	Cluster1393_1clades	94	pp2_200	Vibriophage phi-pp2	GCA_002630725.1
AAQ64221.1	001872	Cluster1394_1clades	93	KVP40.0152	Vibrio phage KVP40	GCA_000843785.1
QIW90535.1	001872	Cluster1394_1clades	91	GCAPEGMB_00188	Vibrio phage V07	GCA_012361095.1
QIW90887.1	001872	Cluster1394_1clades	91	COHAPHLL_00024	Vibrio phage V09	GCA_012361135.1
QHJ74333.1	001872	Cluster1394_1clades	91	VH12019_00006	Vibrio phage VH1_2019	GCA_009931825.1
AGB06825.1	001872	Cluster1394_1clades	84	CF80_gp038	Vibrio phage VH7D	GCA_000914495.1
QBX06321.1	001872	Cluster1394_1clades	91	ValB1HC_368	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60952.1	001872	Cluster1394_1clades	91	AVU32_gp111	Vibrio phage ValKK3	GCA_001501635.1
AGN30197.1	001872	Cluster1394_1clades	75	VPFG_00197	Vibrio phage nt-1	GCA_000910195.2
ALP47255.1	001872	Cluster1394_1clades	84	phiGrn1_0262	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47637.1	001872	Cluster1394_1clades	84	phiST2_0020	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54564.1	001872	Cluster1394_1clades	91	vBValMR10Z_23	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AAQ64294.1	001873	SIG+TM	88	KVP40.0225	Vibrio phage KVP40	GCA_000843785.1
QIW90610.1	001873	SIG+TM	88	GCAPEGMB_00263	Vibrio phage V07	GCA_012361095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW91189.1	001873	SIG+TM	88	COHAPHLL_00353	Vibrio phage V09	GCA_012361135.1
QHJ74406.1	001873	SIG+TM	89	VH12019_00079	Vibrio phage VH1_2019	GCA_009931825.1
AGB06912.1	001873	SIG+TM	92	CF80_gp125	Vibrio phage VH7D	GCA_000914495.1
QBX06234.1	001873	SIG+TM	92	ValB1HC_281	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60860.1	001873	SIG+TM	92	AVU32_gp019	Vibrio phage ValKK3	GCA_001501635.1
AGN30286.1	001873	SIG+TM	88	VPFG_00287	Vibrio phage nt-1	GCA_000910195.2
ALP47329.1	001873	SIG+TM	45	phiGrn1_0349	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54859.1	001873	SIG+TM	92	vBValMR10Z_319	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37455.1	001873	SIG+TM	88	pp2_222	Vibriophage phi-pp2	GCA_002630725.1
AIT14157.1	001874	Cluster1396_1clades	79	PBI_121Q_267	Escherichia phage 121Q	GCA_000926855.1
QAY00778.1	001874	Cluster1396_1clades	79	Ecwhy1_505	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34953.1	001874	Cluster1396_1clades	79	ACQ29_gp273	Escherichia phage PBECO4	GCA_001041035.1
AGC34957.1	001874	Cluster1396_1clades	92	ACQ29_gp277	Escherichia phage PBECO4	GCA_001041035.1
BBM61831.1	001874	Cluster1396_1clades	79	EO157G_2420	Escherichia phage SP27	GCA_008033345.1
BBM61835.1	001874	Cluster1396_1clades	79	EO157G_2460	Escherichia phage SP27	GCA_008033345.1
QBO61548.1	001874	Cluster1396_1clades	79	G17_00052	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62154.1	001874	Cluster1396_1clades	79	G17_00665	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14157.1	001874	Cluster1396_1clades	79	vBEcoMphAPEC6_gp534c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14161.1	001874	Cluster1396_1clades	79	vBEcoMphAPEC6_gp538c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80146.1	001874	Cluster1396_1clades	79	PSLUR01_00169	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64210.1	001875	Cluster1397_1clades	90	KVP40.0140	Vibrio phage KVP40	GCA_000843785.1
QIW90525.1	001875	Cluster1397_1clades	90	GCAPEGMB_00178	Vibrio phage V07	GCA_012361095.1
QIW90897.1	001875	Cluster1397_1clades	90	COHAPHLL_00034	Vibrio phage V09	GCA_012361135.1
QHJ74321.1	001875	Cluster1397_1clades	90	VH12019_00402	Vibrio phage VH1_2019	GCA_009931825.1
AGB06815.1	001875	Cluster1397_1clades	90	CF80_gp028	Vibrio phage VH7D	GCA_000914495.1
QBX06332.1	001875	Cluster1397_1clades	90	ValB1HC_379	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60962.1	001875	Cluster1397_1clades	90	AVU32_gp121	Vibrio phage ValKK3	GCA_001501635.1
ALP47233.1	001875	Cluster1397_1clades	90	phiGrn1_0251	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47620.1	001875	Cluster1397_1clades	90	phiST2_0006	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54575.1	001875	Cluster1397_1clades	90	vBValMR10Z_34	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37371.1	001875	Cluster1397_1clades	90	pp2_138	Vibriophage phi-pp2	GCA_002630725.1
APU01670.1	001876	Cluster1398_1clades	90	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29026.1	001876	Cluster1398_1clades	90	AP1_0319	Aeromonas phage AP1	GCA_014183365.1
QMV29119.1	001876	Cluster1398_1clades	59	AP1_0416	Aeromonas phage AP1	GCA_014183365.1
ATI17310.1	001876	Cluster1398_1clades	59	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00284.1	001876	Cluster1398_1clades	68	HWB28_gp268	Aeromonas phage AS-zj	GCA_002627665.1
ASU00370.1	001876	Cluster1398_1clades	90	HWB28_gp182	Aeromonas phage AS-zj	GCA_002627665.1
QAX97753.1	001876	Cluster1398_1clades	59	ASswx1_108	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97660.1	001876	Cluster1398_1clades	90	ASswx1_14	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01402.1	001876	Cluster1398_1clades	59	ASwh1_343	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39299.1	001876	Cluster1398_1clades	59	CC2_001	Aeromonas phage CC2	GCA_000903495.1
ADQ53301.1	001876	Cluster1398_1clades	90	65p293	Aeromonas virus 65	GCA_000893255.1
AAQ64391.1	001877	Cluster1400_1clades	87	KVP40.0321	Vibrio phage KVP40	GCA_000843785.1
QIW90703.1	001877	Cluster1400_1clades	84	GCAPEGMB_00384	Vibrio phage V07	GCA_012361095.1
QIW91094.1	001877	Cluster1400_1clades	84	COHAPHLL_00231	Vibrio phage V09	GCA_012361135.1
QHJ74503.1	001877	Cluster1400_1clades	84	VH12019_00203	Vibrio phage VH1_2019	GCA_009931825.1
QBX06152.1	001877	Cluster1400_1clades	84	ValB1HC_198	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61164.1	001877	Cluster1400_1clades	84	AVU32_gp323	Vibrio phage ValKK3	GCA_001501635.1
AGN30372.2	001877	Cluster1400_1clades	84	VPFG_00375	Vibrio phage nt-1	GCA_000910195.2
ALP47253.1	001877	Cluster1400_1clades	84	phiGrn1_0055	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47635.1	001877	Cluster1400_1clades	84	phiST2_0187	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54777.1	001877	Cluster1400_1clades	84	vBValMR10Z_237	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37553.1	001877	Cluster1400_1clades	84	pp2_321	Vibriophage phi-pp2	GCA_002630725.1
AAQ64098.1	001878	Cluster1401_1clades	81	KVP40.0027	Vibrio phage KVP40	GCA_000843785.1
QIW90421.1	001878	Cluster1401_1clades	81	GCAPEGMB_00074	Vibrio phage V07	GCA_012361095.1
QIW91008.1	001878	Cluster1401_1clades	81	COHAPHLL_00145	Vibrio phage V09	GCA_012361135.1
QHJ74210.1	001878	Cluster1401_1clades	81	VH12019_00291	Vibrio phage VH1_2019	GCA_009931825.1
AGB07034.1	001878	Cluster1401_1clades	81	CF80_gp247	Vibrio phage VH7D	GCA_000914495.1
QBX06062.1	001878	Cluster1401_1clades	81	ValB1HC_108	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61076.1	001878	Cluster1401_1clades	84	AVU32_gp235	Vibrio phage ValKK3	GCA_001501635.1
ALP47319.1	001878	Cluster1401_1clades	57	phiGrn1_0142	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47695.1	001878	Cluster1401_1clades	57	phiST2_0272	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54688.1	001878	Cluster1401_1clades	81	vBValMR10Z_147	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37261.1	001878	Cluster1401_1clades	81	pp2_027	Vibriophage phi-pp2	GCA_002630725.1
AIT14227.1	001879	Cluster1402_1clades	73	PBI_121Q_337	Escherichia phage 121Q	GCA_000926855.1
QAY00708.1	001879	Cluster1402_1clades	83	Ecwhy1_433	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00709.1	001879	Cluster1402_1clades	78	Ecwhy1_434	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34896.1	001879	Cluster1402_1clades	50	ACQ29_gp216	Escherichia phage PBECO4	GCA_001041035.1
BBM61903.1	001879	Cluster1402_1clades	73	EO157G_3140	Escherichia phage SP27	GCA_008033345.1
AXC37001.1	001879	Cluster1402_1clades	77	-	Escherichia phage UB	GCA_003341455.1
AXC37002.1	001879	Cluster1402_1clades	82	-	Escherichia phage UB	GCA_003341455.1
QBO62078.1	001879	Cluster1402_1clades	75	G17_00589	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14093.1	001879	Cluster1402_1clades	80	vBEcoMphAPEC6_gp470c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80216.1	001879	Cluster1402_1clades	77	PSLUR01_00239	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
SCA80217.1	001879	Cluster1402_1clades	80	PSLUR01_00240	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64252.1	001880	Cluster1403_1clades	82	KVP40.0183	Vibrio phage KVP40	GCA_000843785.1
QIW90568.1	001880	Cluster1403_1clades	82	GCAPEGMB_00221	Vibrio phage V07	GCA_012361095.1
QIW91231.1	001880	Cluster1403_1clades	82	COHAPHLL_00395	Vibrio phage V09	GCA_012361135.1
QHJ74366.1	001880	Cluster1403_1clades	82	VH12019_00039	Vibrio phage VH1_2019	GCA_009931825.1
AGB06860.1	001880	Cluster1403_1clades	40	CF80_gp073	Vibrio phage VH7D	GCA_000914495.1
QBX06285.1	001880	Cluster1403_1clades	73	ValB1HC_332	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60912.1	001880	Cluster1403_1clades	73	AVU32_gp071	Vibrio phage ValKK3	GCA_001501635.1
ALP47334.1	001880	Cluster1403_1clades	40	phiGrn1_0300	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47665.1	001880	Cluster1403_1clades	73	phiST2_0056	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54912.1	001880	Cluster1403_1clades	73	vBValMR10Z_372	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37413.1	001880	Cluster1403_1clades	76	pp2_180	Vibriophage phi-pp2	GCA_002630725.1
AAX44626.1	001881	Cluster1404_1clades	57	PSSM2_249	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12344.1	001881	Cluster1404_1clades	57	PRTG_00191	Prochlorococcus phage P-SSM5	GCA_002991095.1
QGT54942.1	001881	Cluster1404_1clades	79	b23_0331	Synechococcus phage B23	GCA_009745195.1
QGT54577.1	001881	Cluster1404_1clades	79	b3_0337	Synechococcus phage B3	GCA_009745215.1
ASR76228.1	001881	Cluster1404_1clades	82	PBI_BELLAMY_189	Synechococcus phage Bellamy	GCA_002627525.1
QCW23019.1	001881	Cluster1404_1clades	56	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50524.1	001881	Cluster1404_1clades	56	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59642.1	001881	Cluster1404_1clades	82	S330809_181	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59404.1	001881	Cluster1404_1clades	82	C440309_181	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59880.1	001881	Cluster1404_1clades	82	N231010_181	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70524.1	001881	Cluster1404_1clades	56	HOU04_gp125	Synechococcus phage S-T4	GCA_003443335.1
AAQ64386.1	001882	Cluster1405_1clades	81	KVP40.0316	Vibrio phage KVP40	GCA_000843785.1
QIW90700.1	001882	Cluster1405_1clades	77	GCAPEGMB_00380	Vibrio phage V07	GCA_012361095.1
QIW91098.1	001882	Cluster1405_1clades	77	COHAPHLL_00236	Vibrio phage V09	GCA_012361135.1
QHJ74499.1	001882	Cluster1405_1clades	77	VH12019_00198	Vibrio phage VH1_2019	GCA_009931825.1
QBX06156.1	001882	Cluster1405_1clades	78	ValB1HC_202	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61169.1	001882	Cluster1405_1clades	78	AVU32_gp328	Vibrio phage ValKK3	GCA_001501635.1
AGN30367.1	001882	Cluster1405_1clades	77	VPFG_00370	Vibrio phage nt-1	GCA_000910195.2
ALP47272.1	001882	Cluster1405_1clades	78	phiGrn1_0378	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47652.1	001882	Cluster1405_1clades	78	phiST2_0183	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54781.1	001882	Cluster1405_1clades	78	vBValMR10Z_241	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37549.1	001882	Cluster1405_1clades	77	pp2_317	Vibriophage phi-pp2	GCA_002630725.1
AAQ64177.1	001883	SIG+TM	79	KVP40.0106	Vibrio phage KVP40	GCA_000843785.1
QIW90500.1	001883	SIG+TM	79	GCAPEGMB_00153	Vibrio phage V07	GCA_012361095.1
QIW90929.1	001883	SIG+TM	79	COHAPHLL_00066	Vibrio phage V09	GCA_012361135.1
QHJ74288.1	001883	SIG+TM	79	VH12019_00369	Vibrio phage VH1_2019	GCA_009931825.1
AGB07111.1	001883	SIG+TM	41	CF80_gp324	Vibrio phage VH7D	GCA_000914495.1
QBX05983.1	001883	SIG+TM	79	ValB1HC_029	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60996.1	001883	SIG+TM	79	AVU32_gp155	Vibrio phage ValKK3	GCA_001501635.1
AGN30155.1	001883	SIG+TM	79	VPFG_00153	Vibrio phage nt-1	GCA_000910195.2
ALP47714.1	001883	SIG+TM	43	phiST2_0352	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54608.1	001883	SIG+TM	79	vBValMR10Z_67	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37335.1	001883	SIG+TM	79	pp2_102	Vibriophage phi-pp2	GCA_002630725.1
AIT14347.1	001884	Anti-TRAP	75	PBI_121Q_457	Escherichia phage 121Q	GCA_000926855.1
QAY00597.1	001884	Anti-TRAP	75	Ecwhy1_320	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34792.1	001884	Anti-TRAP	75	ACQ29_gp112	Escherichia phage PBECO4	GCA_001041035.1
BBM62018.1	001884	Anti-TRAP	75	EO157G_4290	Escherichia phage SP27	GCA_008033345.1
AXC36908.1	001884	Anti-TRAP	75	-	Escherichia phage UB	GCA_003341455.1
QBO61957.1	001884	Anti-TRAP	75	G17_00468	Escherichia phage vB_EcoM_G17	GCA_004521135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDF13984.1	001884	Anti-TRAP	75	vBEcoMphAPEC6_gp360c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80334.1	001884	Anti-TRAP	75	PSLUR01_00357	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18799.1	001884	Anti-TRAP	77	7t3_0278	Salmonella phage 7t3	GCA_006083215.1
AZU98064.1	001884	Anti-TRAP	77	CPT_Munch_120	Salmonella phage Munch	GCA_004015485.1
QIG62918.1	001884	Anti-TRAP	77	SEPL_305	Salmonella phage SE_PL	GCA_011067555.1
QIW90450.1	001885	Cluster1408_1clades	72	GCAPEGMB_00103	Vibrio phage V07	GCA_012361095.1
QIW90979.1	001885	Cluster1408_1clades	72	COHAPHLL_00116	Vibrio phage V09	GCA_012361135.1
QHJ74239.1	001885	Cluster1408_1clades	72	VH12019_00320	Vibrio phage VH1_2019	GCA_009931825.1
AGB07064.1	001885	Cluster1408_1clades	67	CF80_gp277	Vibrio phage VH7D	GCA_000914495.1
QBX06032.1	001885	Cluster1408_1clades	61	ValB1HC_078	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61046.1	001885	Cluster1408_1clades	67	AVU32_gp205	Vibrio phage ValKK3	GCA_001501635.1
AIE13793.1	001885	Cluster1408_1clades	76	-	Vibrio phage nt-1	GCA_000910195.2
ALP47301.1	001885	Cluster1408_1clades	66	phiGrn1_0171	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47681.1	001885	Cluster1408_1clades	66	phiST2_0302	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54657.1	001885	Cluster1408_1clades	61	vBValMR10Z_116	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37288.1	001885	Cluster1408_1clades	72	pp2_054	Vibriophage phi-pp2	GCA_002630725.1
AMO43328.1	001886	Cluster1409_1clades	75	W270710_084	Cyanophage S-RIM44	GCA_002599145.1
AOO11561.1	001886	Cluster1409_1clades	76	ES420910_080	Cyanophage S-RIM44	GCA_002599165.1
AOO11800.1	001886	Cluster1409_1clades	75	Np050604_084	Cyanophage S-RIM44	GCA_002599185.1
AOO12026.1	001886	Cluster1409_1clades	76	Np200711_080	Cyanophage S-RIM44	GCA_002599205.1
AOO12262.1	001886	Cluster1409_1clades	76	Np420711_080	Cyanophage S-RIM44	GCA_002599225.1
AOO12501.1	001886	Cluster1409_1clades	75	Sn080709_084	Cyanophage S-RIM44	GCA_002599245.1
AOO12727.1	001886	Cluster1409_1clades	76	Sn130910_080	Cyanophage S-RIM44	GCA_002599265.1
AOO12967.1	001886	Cluster1409_1clades	75	W2100709_085	Cyanophage S-RIM44	GCA_002599285.1
AOV59538.1	001886	Cluster1409_1clades	75	S330809_077	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59300.1	001886	Cluster1409_1clades	75	C440309_077	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59776.1	001886	Cluster1409_1clades	75	N231010_077	Synechococcus phage S-CAM4	GCA_002922155.1
QIW90593.1	001887	Cluster1410_1clades	74	GCAPEGMB_00246	Vibrio phage V07	GCA_012361095.1
QIW91206.1	001887	Cluster1410_1clades	74	COHAPHLL_00370	Vibrio phage V09	GCA_012361135.1
QHJ74389.1	001887	Cluster1410_1clades	74	VH12019_00062	Vibrio phage VH1_2019	GCA_009931825.1
AGB06894.1	001887	Cluster1410_1clades	74	CF80_gp107	Vibrio phage VH7D	GCA_000914495.1
QBX06252.1	001887	Cluster1410_1clades	74	ValB1HC_299	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60878.1	001887	Cluster1410_1clades	74	AVU32_gp037	Vibrio phage ValKK3	GCA_001501635.1
AGN30267.1	001887	Cluster1410_1clades	74	VPFG_00268	Vibrio phage nt-1	GCA_000910195.2
ALP47282.1	001887	Cluster1410_1clades	74	phiGrn1_0332	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47664.1	001887	Cluster1410_1clades	74	phiST2_0087	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54879.1	001887	Cluster1410_1clades	74	vBValMR10Z_339	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37437.1	001887	Cluster1410_1clades	74	pp2_204	Vibriophage phi-pp2	GCA_002630725.1
AIT14029.1	001888	Cluster1411_1clades	71	PBI_121Q_138	Escherichia phage 121Q	GCA_000926855.1
QAY00313.1	001888	Cluster1411_1clades	71	Ecwhy1_31	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35062.1	001888	Cluster1411_1clades	71	ACQ29_gp382	Escherichia phage PBECO4	GCA_001041035.1
BBM61713.1	001888	Cluster1411_1clades	71	EO157G_1240	Escherichia phage SP27	GCA_008033345.1
AXC36638.1	001888	Cluster1411_1clades	71	-	Escherichia phage UB	GCA_003341455.1
QBO61670.1	001888	Cluster1411_1clades	71	G17_00175	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13719.1	001888	Cluster1411_1clades	71	vBEcoMphAPEC6_gp089c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80025.1	001888	Cluster1411_1clades	71	PSLUR01_00047	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18554.1	001888	Cluster1411_1clades	71	7t3_029	Salmonella phage 7t3	GCA_006083215.1
AZU98383.1	001888	Cluster1411_1clades	71	CPT_Munch_449	Salmonella phage Munch	GCA_004015485.1
QIG63129.1	001888	Cluster1411_1clades	71	SEPL_516	Salmonella phage SE_PL	GCA_011067555.1
AAQ64255.1	001889	Cluster1412_1clades	70	KVP40.0186	Vibrio phage KVP40	GCA_000843785.1
QIW90571.1	001889	Cluster1412_1clades	61	GCAPEGMB_00224	Vibrio phage V07	GCA_012361095.1
QIW91228.1	001889	Cluster1412_1clades	61	COHAPHLL_00392	Vibrio phage V09	GCA_012361135.1
QHJ74369.1	001889	Cluster1412_1clades	61	VH12019_00042	Vibrio phage VH1_2019	GCA_009931825.1
AGB06864.1	001889	Cluster1412_1clades	61	CF80_gp077	Vibrio phage VH7D	GCA_000914495.1
QBX06280.1	001889	Cluster1412_1clades	61	ValB1HC_327	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60907.1	001889	Cluster1412_1clades	61	AVU32_gp066	Vibrio phage ValKK3	GCA_001501635.1
ALP47312.1	001889	Cluster1412_1clades	61	phiGrn1_0304	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47690.1	001889	Cluster1412_1clades	61	phiST2_0060	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54907.1	001889	Cluster1412_1clades	61	vBValMR10Z_367	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37416.1	001889	Cluster1412_1clades	61	pp2_183	Vibriophage phi-pp2	GCA_002630725.1
AMO43273.1	001890	Cluster1413_1clades	63	W270710_028	Cyanophage S-RIM44	GCA_002599145.1
AOO11507.1	001890	Cluster1413_1clades	63	ES420910_025	Cyanophage S-RIM44	GCA_002599165.1
AOO11745.1	001890	Cluster1413_1clades	63	Np050604_028	Cyanophage S-RIM44	GCA_002599185.1
AOO11972.1	001890	Cluster1413_1clades	63	Np200711_025	Cyanophage S-RIM44	GCA_002599205.1
AOO12208.1	001890	Cluster1413_1clades	63	Np420711_025	Cyanophage S-RIM44	GCA_002599225.1
AOO12446.1	001890	Cluster1413_1clades	63	Sn080709_028	Cyanophage S-RIM44	GCA_002599245.1
AOO12673.1	001890	Cluster1413_1clades	63	Sn130910_025	Cyanophage S-RIM44	GCA_002599265.1
AOO12911.1	001890	Cluster1413_1clades	63	W2100709_028	Cyanophage S-RIM44	GCA_002599285.1
AOV59483.1	001890	Cluster1413_1clades	67	S330809_022	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59245.1	001890	Cluster1413_1clades	67	C440309_022	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59721.1	001890	Cluster1413_1clades	67	N231010_022	Synechococcus phage S-CAM4	GCA_002922155.1
AIT14103.1	001891	Cluster1414_1clades	58	PBI_121Q_213	Escherichia phage 121Q	GCA_000926855.1
QAY00819.1	001891	Cluster1414_1clades	58	Ecwhy1_546	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34992.1	001891	Cluster1414_1clades	58	ACQ29_gp312	Escherichia phage PBECO4	GCA_001041035.1
BBM61785.1	001891	Cluster1414_1clades	58	EO157G_1960	Escherichia phage SP27	GCA_008033345.1
AXC36572.1	001891	Cluster1414_1clades	58	-	Escherichia phage UB	GCA_003341455.1
QBO61596.1	001891	Cluster1414_1clades	58	G17_00100	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13655.1	001891	Cluster1414_1clades	58	vBEcoMphAPEC6_gp024c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80097.1	001891	Cluster1414_1clades	58	PSLUR01_00120	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18633.1	001891	Cluster1414_1clades	64	7t3_0112	Salmonella phage 7t3	GCA_006083215.1
AZU98458.1	001891	Cluster1414_1clades	63	CPT_Munch_526	Salmonella phage Munch	GCA_004015485.1
QIG63056.1	001891	Cluster1414_1clades	64	SEPL_443	Salmonella phage SE_PL	GCA_011067555.1
AHI60172.1	001892	S4	63	Ea357_022	Erwinia phage Ea35-70	GCA_000914635.1
QBP07130.1	001892	S4	63	REBECCA_22	Erwinia phage Rebecca	GCA_004521635.1
AUG85810.1	001892	S4	63	BOSOLAPHORUS_22	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52120.1	001892	S4	63	DM_22	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86130.1	001892	S4	63	DESERTFOX_22	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86450.1	001892	S4	63	MADMEL_22	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86771.1	001892	S4	63	MORTIMER_22	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51803.1	001892	S4	63	RAY_22	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51485.1	001892	S4	63	SIMMY50_23	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64832.1	001892	S4	63	SPECIALG_22	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QKE54336.1	001892	S4	63	ACSA002_0220	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AAQ64182.1	001893	Cluster1416_1clades	62	KVP40.0111	Vibrio phage KVP40	GCA_000843785.1
QIW90505.1	001893	Cluster1416_1clades	62	GCAPEGMB_00158	Vibrio phage V07	GCA_012361095.1
QIW90924.1	001893	Cluster1416_1clades	62	COHAPHLL_00061	Vibrio phage V09	GCA_012361135.1
QHJ74294.1	001893	Cluster1416_1clades	62	VH12019_00375	Vibrio phage VH1_2019	GCA_009931825.1
QBX05979.1	001893	Cluster1416_1clades	59	ValB1HC_025	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60992.1	001893	Cluster1416_1clades	59	AVU32_gp151	Vibrio phage ValKK3	GCA_001501635.1
AGN30162.1	001893	Cluster1416_1clades	61	VPFG_00160	Vibrio phage nt-1	GCA_000910195.2
ALP47327.1	001893	Cluster1416_1clades	51	phiGrn1_0221	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47707.1	001893	Cluster1416_1clades	51	phiST2_0356	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54604.1	001893	Cluster1416_1clades	51	vBValMR10Z_63	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37340.1	001893	Cluster1416_1clades	62	pp2_107	Vibriophage phi-pp2	GCA_002630725.1
AAQ64350.1	001894	Cluster1417_1clades	61	KVP40.0280	Vibrio phage KVP40	GCA_000843785.1
QIW90664.1	001894	Cluster1417_1clades	61	GCAPEGMB_00317	Vibrio phage V07	GCA_012361095.1
QIW91134.1	001894	Cluster1417_1clades	61	COHAPHLL_00298	Vibrio phage V09	GCA_012361135.1
QHJ74459.1	001894	Cluster1417_1clades	61	VH12019_00132	Vibrio phage VH1_2019	GCA_009931825.1
AGB06953.1	001894	Cluster1417_1clades	61	CF80_gp166	Vibrio phage VH7D	GCA_000914495.1
QBX06192.1	001894	Cluster1417_1clades	61	ValB1HC_239	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61209.1	001894	Cluster1417_1clades	61	AVU32_gp368	Vibrio phage ValKK3	GCA_001501635.1
AGN30327.1	001894	Cluster1417_1clades	61	VPFG_00329	Vibrio phage nt-1	GCA_000910195.2
ALP47311.1	001894	Cluster1417_1clades	61	phiGrn1_0013	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54817.1	001894	Cluster1417_1clades	61	vBValMR10Z_277	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37511.1	001894	Cluster1417_1clades	61	pp2_278	Vibriophage phi-pp2	GCA_002630725.1
AAQ64300.1	001895	Cluster1418_1clades	59	KVP40.0231	Vibrio phage KVP40	GCA_000843785.1
QIW90616.1	001895	Cluster1418_1clades	59	GCAPEGMB_00269	Vibrio phage V07	GCA_012361095.1
QIW91183.1	001895	Cluster1418_1clades	59	COHAPHLL_00347	Vibrio phage V09	GCA_012361135.1
QHJ74411.1	001895	Cluster1418_1clades	59	VH12019_00084	Vibrio phage VH1_2019	GCA_009931825.1
AGB06919.1	001895	Cluster1418_1clades	59	CF80_gp132	Vibrio phage VH7D	GCA_000914495.1
QBX06227.1	001895	Cluster1418_1clades	59	ValB1HC_274	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60853.1	001895	Cluster1418_1clades	59	AVU32_gp012	Vibrio phage ValKK3	GCA_001501635.1
ALP47315.1	001895	Cluster1418_1clades	59	phiGrn1_0355	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47692.1	001895	Cluster1418_1clades	59	phiST2_0110	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54852.1	001895	Cluster1418_1clades	59	vBValMR10Z_312	Vibrio phage vB_ValM_R10Z	GCA_014337545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN37461.1	001895	Cluster1418_1clades	59	pp2_228	Vibriophage phi-pp2	GCA_002630725.1
QIW90552.1	001896	Cluster1419_1clades	57	GCAPEGMB_00205	Vibrio phage V07	GCA_012361095.1
QIW90870.1	001896	Cluster1419_1clades	57	COHAPHLL_00007	Vibrio phage V09	GCA_012361135.1
QHJ74350.1	001896	Cluster1419_1clades	57	VH12019_00023	Vibrio phage VH1_2019	GCA_009931825.1
AGB06843.1	001896	Cluster1419_1clades	56	CF80_gp056	Vibrio phage VH7D	GCA_000914495.1
QBX06303.1	001896	Cluster1419_1clades	56	ValB1HC_350	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60934.1	001896	Cluster1419_1clades	56	AVU32_gp093	Vibrio phage ValKK3	GCA_001501635.1
AGN30218.1	001896	Cluster1419_1clades	56	VPFG_00218	Vibrio phage nt-1	GCA_000910195.2
ALP47320.1	001896	Cluster1419_1clades	56	phiGrn1_0280	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47701.1	001896	Cluster1419_1clades	56	phiST2_0039	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54546.1	001896	Cluster1419_1clades	56	vBValMR10Z_5	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37397.1	001896	Cluster1419_1clades	57	pp2_164	Vibriophage phi-pp2	GCA_002630725.1
AAQ64265.1	001897	Cluster1420_1clades	56	KVP40.0196	Vibrio phage KVP40	GCA_000843785.1
QIW90581.1	001897	Cluster1420_1clades	56	GCAPEGMB_00234	Vibrio phage V07	GCA_012361095.1
QIW91217.1	001897	Cluster1420_1clades	56	COHAPHLL_00381	Vibrio phage V09	GCA_012361135.1
QHJ74379.1	001897	Cluster1420_1clades	56	VH12019_00052	Vibrio phage VH1_2019	GCA_009931825.1
AGB06881.1	001897	Cluster1420_1clades	56	CF80_gp094	Vibrio phage VH7D	GCA_000914495.1
QBX06265.1	001897	Cluster1420_1clades	56	ValB1HC_312	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60891.1	001897	Cluster1420_1clades	56	AVU32_gp050	Vibrio phage ValKK3	GCA_001501635.1
ALP47322.1	001897	Cluster1420_1clades	56	phiGrn1_0319	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47700.1	001897	Cluster1420_1clades	56	phiST2_0075	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54892.1	001897	Cluster1420_1clades	56	vBValMR10Z_352	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37426.1	001897	Cluster1420_1clades	56	pp2_193	Vibriophage phi-pp2	GCA_002630725.1
AAQ64447.1	001898	DUF2685	56	KVP40.0379	Vibrio phage KVP40	GCA_000843785.1
QIW90392.1	001898	DUF2685	56	GCAPEGMB_00045	Vibrio phage V07	GCA_012361095.1
QIW91037.1	001898	DUF2685	56	COHAPHLL_00174	Vibrio phage V09	GCA_012361135.1
QHJ74559.1	001898	DUF2685	56	VH12019_00259	Vibrio phage VH1_2019	GCA_009931825.1
QBX06094.1	001898	DUF2685	56	ValB1HC_140	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61108.1	001898	DUF2685	56	AVU32_gp267	Vibrio phage ValKK3	GCA_001501635.1
AGN30047.1	001898	DUF2685	56	VPFG_00042	Vibrio phage nt-1	GCA_000910195.2
ALP47321.1	001898	DUF2685	56	phiGrn1_0111	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47698.1	001898	DUF2685	56	phiST2_0242	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54720.1	001898	DUF2685	56	vBValMR10Z_179	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37610.1	001898	DUF2685	56	pp2_378	Vibriophage phi-pp2	GCA_002630725.1
ARB13608.1	001899	Cluster1422_1clades	52	Ccr10_gp080	Caulobacter phage Ccr10	GCA_002619445.1
ARB13954.1	001899	Cluster1422_1clades	52	Ccr2_gp079	Caulobacter phage Ccr2	GCA_002619465.1
ARB14645.1	001899	Cluster1422_1clades	52	Ccr29_gp088	Caulobacter phage Ccr29	GCA_002619485.1
ARB15000.1	001899	Cluster1422_1clades	52	Ccr32_gp081	Caulobacter phage Ccr32	GCA_002619505.1
ARB15331.1	001899	Cluster1422_1clades	52	Ccr34_gp087	Caulobacter phage Ccr34	GCA_002619525.1
ARB14297.1	001899	Cluster1422_1clades	52	Ccr5_gp079	Caulobacter phage Ccr5	GCA_002619545.1
AFU87966.1	001899	Cluster1422_1clades	48	CcrColossus_gp096	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87598.1	001899	Cluster1422_1clades	52	CcrKarma_gp081	Caulobacter virus Karma	GCA_000901575.1
AFU87248.1	001899	Cluster1422_1clades	52	CcrMagneto_gp078	Caulobacter virus Magneto	GCA_000903095.1
AFU88396.1	001899	Cluster1422_1clades	52	CcrSwift_gp078	Caulobacter virus Swift	GCA_000899655.1
AFU86912.1	001899	Cluster1422_1clades	52	CbK_gp080	Caulobacter virus phiCbK	GCA_000900535.1
AOO14327.1	001900	Cluster1423_1clades	34	Sn110110_133	Cyanophage S-RIM14	GCA_002599065.1
AOO14976.1	001900	Cluster1423_1clades	34	W1230910_130	Cyanophage S-RIM14	GCA_002599125.1
AMO43263.1	001900	Cluster1423_1clades	39	W270710_018	Cyanophage S-RIM44	GCA_002599145.1
AOO11500.1	001900	Cluster1423_1clades	39	ES420910_018	Cyanophage S-RIM44	GCA_002599165.1
AOO11735.1	001900	Cluster1423_1clades	39	Np050604_018	Cyanophage S-RIM44	GCA_002599185.1
AOO11965.1	001900	Cluster1423_1clades	39	Np200711_018	Cyanophage S-RIM44	GCA_002599205.1
AOO12201.1	001900	Cluster1423_1clades	39	Np420711_018	Cyanophage S-RIM44	GCA_002599225.1
AOO12436.1	001900	Cluster1423_1clades	39	Sn080709_018	Cyanophage S-RIM44	GCA_002599245.1
AOO12666.1	001900	Cluster1423_1clades	39	Sn130910_018	Cyanophage S-RIM44	GCA_002599265.1
AOO12901.1	001900	Cluster1423_1clades	39	W2100709_018	Cyanophage S-RIM44	GCA_002599285.1
ADO99121.1	001900	Cluster1423_1clades	39	Syn1_019	Prochlorococcus phage Syn1	GCA_000892495.1
AMO43219.1	001901	Cluster1426_1clades	1108	R1080702_214	Cyanophage S-RIM32	GCA_001754165.1
AMO43452.1	001901	Cluster1426_1clades	1108	W270710_213	Cyanophage S-RIM44	GCA_002599145.1
AOO11693.1	001901	Cluster1426_1clades	1104	ES420910_216	Cyanophage S-RIM44	GCA_002599165.1
AOO11924.1	001901	Cluster1426_1clades	1108	Np050604_213	Cyanophage S-RIM44	GCA_002599185.1
AOO12159.1	001901	Cluster1426_1clades	1104	Np200711_217	Cyanophage S-RIM44	GCA_002599205.1
AOO12394.1	001901	Cluster1426_1clades	1104	Np420711_216	Cyanophage S-RIM44	GCA_002599225.1
AOO12625.1	001901	Cluster1426_1clades	1108	Sn080709_213	Cyanophage S-RIM44	GCA_002599245.1
AOO12859.1	001901	Cluster1426_1clades	1104	Sn130910_216	Cyanophage S-RIM44	GCA_002599265.1
AOO13091.1	001901	Cluster1426_1clades	1108	W2100709_214	Cyanophage S-RIM44	GCA_002599285.1
ADO99312.1	001901	Cluster1426_1clades	1108	Syn1_216	Prochlorococcus phage Syn1	GCA_000892495.1
ABY63072.1	001902	CR-ATPase9+PTX	161	201phi2-1p244	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44953.1	001902	CR-ATPase9+PTX	316	KTN4_195	Pseudomonas phage KTN4	GCA_002607225.1
ARV77342.1	001902	CR-ATPase9+PTX	162	NOXIFER_173	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32340.1	001902	CR-ATPase9+PTX	524	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76863.1	001902	CR-ATPase9+PTX	161	PHABIO_232	Pseudomonas phage Phabio	GCA_002624965.1
AEH03605.1	001902	CR-ATPase9+PTX	319	182	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94761.1	001902	CR-ATPase9+PTX	316	SL2_184	Pseudomonas phage SL2	GCA_002956015.1
QJB22831.1	001902	CR-ATPase9+PTX	316	fnug_188	Pseudomonas phage fnug	GCA_012837215.1
QEM41914.1	001902	CR-ATPase9+PTX	524	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83059.1	001902	CR-ATPase9+PTX	316	PHIKZ158	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60458.1	001903	Cluster1428_1clades	492	Ea357_304	Erwinia phage Ea35-70	GCA_000914635.1
QBP07415.1	001903	Cluster1428_1clades	512	REBECCA_310	Erwinia phage Rebecca	GCA_004521635.1
AUG86097.1	001903	Cluster1428_1clades	492	BOSOLAPHORUS_311	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ASB43082.1	001903	Cluster1428_1clades	492	DM_314	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86417.1	001903	Cluster1428_1clades	492	DESERTFOX_310	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86738.1	001903	Cluster1428_1clades	492	MADMEL_311	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87063.1	001903	Cluster1428_1clades	492	MORTIMER_315	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52088.1	001903	Cluster1428_1clades	492	RAY_308	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51771.1	001903	Cluster1428_1clades	492	SIMMY50_313	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65123.1	001903	Cluster1428_1clades	492	SPECIALG_312	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60174.1	001904	Cluster1430_1clades	466	Ea357_024	Erwinia phage Ea35-70	GCA_000914635.1
QBP07132.1	001904	Cluster1430_1clades	466	REBECCA_24	Erwinia phage Rebecca	GCA_004521635.1
AUG85812.1	001904	Cluster1430_1clades	466	BOSOLAPHORUS_24	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52122.1	001904	Cluster1430_1clades	466	DM_24	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86132.1	001904	Cluster1430_1clades	466	DESERTFOX_24	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86452.1	001904	Cluster1430_1clades	466	MADMEL_24	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86773.1	001904	Cluster1430_1clades	466	MORTIMER_24	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51805.1	001904	Cluster1430_1clades	466	RAY_24	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51487.1	001904	Cluster1430_1clades	466	SIMMY50_25	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64834.1	001904	Cluster1430_1clades	466	SPECIALG_24	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMR59785.1	001905	Cluster1431_1clades	104	SEGD1_138	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96598.1	001905	Cluster1431_1clades	416	G173_gp053	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48162.1	001905	Cluster1431_1clades	459	ASESINO_149	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48437.1	001905	Cluster1431_1clades	348	CAITLIN_142	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48712.1	001905	Cluster1431_1clades	316	CHRISDB_150	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50574.1	001905	Cluster1431_1clades	417	STRATTON_149	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85974.1	001905	Cluster1431_1clades	267	ACEC001_1360	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20836.1	001905	Cluster1431_1clades	267	-	Salmonella phage JN03	GCA_014319805.1
AXF51056.1	001905	Cluster1431_1clades	244	MLDJOKPK_00017	Salmonella phage SPAsTU	GCA_003183805.1
AEP83967.1	001905	Cluster1431_1clades	146	SPN3US_0134	Salmonella phage SPN3US	GCA_001042275.1
AHI60447.1	001906	Cluster1432_1clades	456	Ea357_293	Erwinia phage Ea35-70	GCA_000914635.1
QBP07404.1	001906	Cluster1432_1clades	456	REBECCA_299	Erwinia phage Rebecca	GCA_004521635.1
AUG86086.1	001906	Cluster1432_1clades	456	BOSOLAPHORUS_300	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52402.1	001906	Cluster1432_1clades	456	DM_303	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86406.1	001906	Cluster1432_1clades	456	DESERTFOX_299	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86727.1	001906	Cluster1432_1clades	456	MADMEL_300	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87052.1	001906	Cluster1432_1clades	456	MORTIMER_304	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52077.1	001906	Cluster1432_1clades	456	RAY_297	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51760.1	001906	Cluster1432_1clades	456	SIMMY50_302	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65112.1	001906	Cluster1432_1clades	456	SPECIALG_301	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY62984.1	001907	phiKZ_IP	426	201phi2-1p154	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44877.1	001907	phiKZ_IP	440	KTN4_119	Pseudomonas phage KTN4	GCA_002607225.1
QBX32250.1	001907	phiKZ_IP	432	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76769.1	001907	phiKZ_IP	428	PHABIO_138	Pseudomonas phage Phabio	GCA_002624965.1
AEH03519.1	001907	phiKZ_IP	438	095	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02630.1	001907	phiKZ_IP	440	PSA21_102	Pseudomonas phage Psa21	GCA_004340405.1
ATN94836.1	001907	phiKZ_IP	440	SL2_259	Pseudomonas phage SL2	GCA_002956015.1
QJB22754.1	001907	phiKZ_IP	440	fnug_111	Pseudomonas phage fnug	GCA_012837215.1
QEM41827.1	001907	phiKZ_IP	432	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAL82993.1	001907	phiKZ_IP	440	PHIKZ092	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60340.1	001908	DUF1926	419	Ea357_188	Erwinia phage Ea35-70	GCA_000914635.1
QBP07299.1	001908	DUF1926	419	REBECCA_192	Erwinia phage Rebecca	GCA_004521635.1
AUG85979.1	001908	DUF1926	419	BOSOLAPHORUS_192	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52294.1	001908	DUF1926	419	DM_196	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86298.1	001908	DUF1926	419	DESERTFOX_191	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86620.1	001908	DUF1926	419	MADMEL_192	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86944.1	001908	DUF1926	419	MORTIMER_195	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51971.1	001908	DUF1926	419	RAY_190	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51655.1	001908	DUF1926	419	SIMMY50_193	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65002.1	001908	DUF1926	419	SPECIALG_193	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AEO93382.1	001909	IMPDH	327	G_120	Bacillus virus G	GCA_000917535.1
QIG63471.1	001909	IMPDH	324	DAC16_242	Bacteroides phage DAC16	GCA_013387695.1
QIG63734.1	001909	IMPDH	324	DAC19_247	Bacteroides phage DAC19	GCA_013387715.1
QIG63995.1	001909	IMPDH	324	DAC20_246	Bacteroides phage DAC20	GCA_013387725.1
QIG64259.1	001909	IMPDH	324	DAC22_249	Bacteroides phage DAC22	GCA_013387735.1
QIG64515.1	001909	IMPDH	324	DAC23_241	Bacteroides phage DAC23	GCA_013387745.1
BBA65551.1	001909	IMPDH	344	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96546.1	001909	IMPDH	350	Xoosp13_360	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000296	001909	IMPDH	420	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000228	001909	IMPDH	420	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AHI60324.1	001910	Cluster1436_1clades	394	Ea357_173	Erwinia phage Ea35-70	GCA_000914635.1
QBP07283.1	001910	Cluster1436_1clades	394	REBECCA_176	Erwinia phage Rebecca	GCA_004521635.1
AUG85963.1	001910	Cluster1436_1clades	394	BOSOLAPHORUS_176	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52278.2	001910	Cluster1436_1clades	394	DM_180	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86282.1	001910	Cluster1436_1clades	396	DESERTFOX_175	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86604.1	001910	Cluster1436_1clades	394	MADMEL_176	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86928.1	001910	Cluster1436_1clades	394	MORTIMER_179	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51955.1	001910	Cluster1436_1clades	394	RAY_174	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51639.1	001910	Cluster1436_1clades	394	SIMMY50_177	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64986.1	001910	Cluster1436_1clades	388	SPECIALG_176	Erwinia phage vB_EamM_Special G	GCA_002624385.1
CAG27193.1	001911	Cluster1438_1clades	252	PPEV_gp099	Pseudomonas phage EL	GCA_000866825.1
ANM44774.1	001911	Cluster1438_1clades	370	KTN4_016	Pseudomonas phage KTN4	GCA_002607225.1
QBX32281.1	001911	Cluster1438_1clades	157	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32282.1	001911	Cluster1438_1clades	186	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76806.1	001911	Cluster1438_1clades	248	PHABIO_175	Pseudomonas phage Phabio	GCA_002624965.1
AEH03546.1	001911	Cluster1438_1clades	271	122	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94932.1	001911	Cluster1438_1clades	370	SL2_355	Pseudomonas phage SL2	GCA_002956015.1
QJB22659.1	001911	Cluster1438_1clades	385	fnug_16	Pseudomonas phage fnug	GCA_012837215.1
QEM41855.1	001911	Cluster1438_1clades	385	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82915.1	001911	Cluster1438_1clades	370	PHIKZ014	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60348.1	001912	Cluster1439_1clades	379	Ea357_196	Erwinia phage Ea35-70	GCA_000914635.1
QBP07306.1	001912	Cluster1439_1clades	379	REBECCA_200	Erwinia phage Rebecca	GCA_004521635.1
AUG85987.1	001912	Cluster1439_1clades	379	BOSOLAPHORUS_200	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52302.1	001912	Cluster1439_1clades	379	DM_204	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86306.1	001912	Cluster1439_1clades	379	DESERTFOX_199	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86628.1	001912	Cluster1439_1clades	378	MADMEL_200	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86952.1	001912	Cluster1439_1clades	378	MORTIMER_203	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51979.1	001912	Cluster1439_1clades	379	RAY_198	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51663.1	001912	Cluster1439_1clades	379	SIMMY50_201	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65010.1	001912	Cluster1439_1clades	379	SPECIALG_201	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60406.1	001913	Cluster1440_1clades	379	Ea357_252	Erwinia phage Ea35-70	GCA_000914635.1
QBP07363.1	001913	Cluster1440_1clades	300	REBECCA_258	Erwinia phage Rebecca	GCA_004521635.1
AUG86045.1	001913	Cluster1440_1clades	300	BOSOLAPHORUS_259	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52361.1	001913	Cluster1440_1clades	379	DM_262	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86365.1	001913	Cluster1440_1clades	300	DESERTFOX_258	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86686.1	001913	Cluster1440_1clades	379	MADMEL_259	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87011.1	001913	Cluster1440_1clades	300	MORTIMER_263	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52036.1	001913	Cluster1440_1clades	379	RAY_256	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51719.1	001913	Cluster1440_1clades	379	SIMMY50_261	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65071.1	001913	Cluster1440_1clades	369	SPECIALG_260	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY62908.1	001914	TCAD10	347	201phi2-1p075	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44818.1	001914	TCAD10	357	KTN4_060	Pseudomonas phage KTN4	GCA_002607225.1
QBX32192.1	001914	TCAD10	271	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76690.1	001914	TCAD10	375	PHABIO_59	Pseudomonas phage Phabio	GCA_002624965.1
AEH03466.1	001914	TCAD10	337	039	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02569.1	001914	TCAD10	305	PSA21_39	Pseudomonas phage Psa21	GCA_004340405.1
ATN94893.1	001914	TCAD10	357	SL2_316	Pseudomonas phage SL2	GCA_002956015.1
QJB22697.1	001914	TCAD10	357	fnug_54	Pseudomonas phage fnug	GCA_012837215.1
QEM41770.1	001914	TCAD10	339	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82944.1	001914	TCAD10	357	PHIKZ043	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60276.1	001915	Cluster1443_1clades	362	Ea357_125	Erwinia phage Ea35-70	GCA_000914635.1
QBP07234.1	001915	Cluster1443_1clades	362	REBECCA_127	Erwinia phage Rebecca	GCA_004521635.1
AUG85914.1	001915	Cluster1443_1clades	362	BOSOLAPHORUS_127	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52229.1	001915	Cluster1443_1clades	362	DM_131	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86233.1	001915	Cluster1443_1clades	362	DESERTFOX_126	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86555.1	001915	Cluster1443_1clades	362	MADMEL_127	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86879.1	001915	Cluster1443_1clades	362	MORTIMER_130	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51907.1	001915	Cluster1443_1clades	362	RAY_126	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51591.1	001915	Cluster1443_1clades	362	SIMMY50_129	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64938.1	001915	Cluster1443_1clades	362	SPECIALG_128	Erwinia phage vB_EamM_Special G	GCA_002624385.1
prevph1000000396	001916	Cluster1444_1clades	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000519	001916	Cluster1444_1clades	118	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000520	001916	Cluster1444_1clades	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000549	001916	Cluster1444_1clades	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000810	001916	Cluster1444_1clades	92	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000274	001916	Cluster1444_1clades	348	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000315	001916	Cluster1444_1clades	231	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000394	001916	Cluster1444_1clades	299	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000407	001916	Cluster1444_1clades	294	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000556	001916	Cluster1444_1clades	220	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AHI60250.1	001917	Cluster1447_1clades	301	Ea357_099	Erwinia phage Ea35-70	GCA_000914635.1
QBP07208.1	001917	Cluster1447_1clades	336	REBECCA_101	Erwinia phage Rebecca	GCA_004521635.1
AUG85887.1	001917	Cluster1447_1clades	301	BOSOLAPHORUS_100	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52202.2	001917	Cluster1447_1clades	301	DM_104	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86206.1	001917	Cluster1447_1clades	301	DESERTFOX_99	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86529.1	001917	Cluster1447_1clades	301	MADMEL_101	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86852.1	001917	Cluster1447_1clades	301	MORTIMER_103	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51880.1	001917	Cluster1447_1clades	301	RAY_99	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51564.1	001917	Cluster1447_1clades	301	SIMMY50_102	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64912.2	001917	Cluster1447_1clades	301	SPECIALG_102	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60200.1	001918	Cluster1448_1clades	329	Ea357_050	Erwinia phage Ea35-70	GCA_000914635.1
QBP07159.1	001918	Cluster1448_1clades	329	REBECCA_51	Erwinia phage Rebecca	GCA_004521635.1
AUG85839.1	001918	Cluster1448_1clades	329	BOSOLAPHORUS_51	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52151.1	001918	Cluster1448_1clades	329	DM_53	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86158.1	001918	Cluster1448_1clades	329	DESERTFOX_50	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86479.1	001918	Cluster1448_1clades	312	MADMEL_51	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86800.1	001918	Cluster1448_1clades	329	MORTIMER_51	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51831.1	001918	Cluster1448_1clades	329	RAY_50	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51514.1	001918	Cluster1448_1clades	329	SIMMY50_52	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64862.1	001918	Cluster1448_1clades	329	SPECIALG_52	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AUE22668.1	001919	ADP	300	Ah1_00127	Aeromonas phage Ah1	GCA_002957415.1
ADQ52850.1	001919	ADP	304	PX29p131	Aeromonas phage PX29	GCA_000920195.1
ADM80109.1	001919	ADP	299	phiAS5_ORF0266	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17797.1	001919	ADP	293	Aeh1ORF132c	Aeromonas virus Aeh1	GCA_000843245.1
AEO93493.1	001919	ADP	290	G_234	Bacillus virus G	GCA_000917535.1
AIA64848.1	001919	ADP	301	S13_049	Cronobacter phage S13	GCA_001503575.1
QCW19073.1	001919	ADP	321	7t3_0553	Salmonella phage 7t3	GCA_006083215.1
AZU98316.1	001919	ADP	321	CPT_Munch_372	Salmonella phage Munch	GCA_004015485.1
QIG62668.1	001919	ADP	321	SEPL_055	Salmonella phage SE_PL	GCA_011067555.1
AQW88874.1	001919	ADP	309	BF_0349	Serratia phage BF	GCA_002619745.1
AXG67196.1	001920	Cluster1450_1clades	261	AD1_152	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79948.1	001920	Cluster1450_1clades	254	JA11_143	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66547.1	001920	Cluster1450_1clades	254	JA13_144	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66872.1	001920	Cluster1450_1clades	254	JA29_146	Dickeya phage vB_DsoM_JA29	GCA_003568475.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG67517.1	001920	Cluster1450_1clades	254	JA33_143	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08429.1	001920	Cluster1450_1clades	261	Alexandra_157	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58793.1	001920	Cluster1450_1clades	261	Y3_153	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28631.1	001920	Cluster1450_1clades	257	YOLOSWAG_151	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38446.1	001920	Cluster1450_1clades	267	BN7874_247	Phage NCTB	GCA_900092385.1
AGS82091.1	001920	Cluster1450_1clades	318	PaBG_00216	Pseudomonas phage PaBG	GCA_000912555.1
AHI60405.1	001921	Cluster1451_1clades	302	Ea357_251	Erwinia phage Ea35-70	GCA_000914635.1
QBP07362.1	001921	Cluster1451_1clades	264	REBECCA_257	Erwinia phage Rebecca	GCA_004521635.1
AUG86044.1	001921	Cluster1451_1clades	264	BOSOLAPHORUS_258	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52360.1	001921	Cluster1451_1clades	302	DM_261	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86364.1	001921	Cluster1451_1clades	264	DESERTFOX_257	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86685.1	001921	Cluster1451_1clades	302	MADMEL_258	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87010.1	001921	Cluster1451_1clades	264	MORTIMER_262	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52035.1	001921	Cluster1451_1clades	285	RAY_255	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51718.1	001921	Cluster1451_1clades	302	SIMMY50_260	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65070.1	001921	Cluster1451_1clades	302	SPECIALG_259	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43051.1	001922	Cluster1452_1clades	231	R1080702_042	Cyanophage S-RIM32	GCA_001754165.1
AMO43291.1	001922	Cluster1452_1clades	290	W270710_047	Cyanophage S-RIM44	GCA_002599145.1
AOO11525.1	001922	Cluster1452_1clades	290	ES420910_044	Cyanophage S-RIM44	GCA_002599165.1
AOO11763.1	001922	Cluster1452_1clades	290	Np050604_047	Cyanophage S-RIM44	GCA_002599185.1
AOO11990.1	001922	Cluster1452_1clades	290	Np200711_044	Cyanophage S-RIM44	GCA_002599205.1
AOO12226.1	001922	Cluster1452_1clades	290	Np420711_044	Cyanophage S-RIM44	GCA_002599225.1
AOO12464.1	001922	Cluster1452_1clades	290	Sn080709_047	Cyanophage S-RIM44	GCA_002599245.1
AOO12691.1	001922	Cluster1452_1clades	290	Sn130910_044	Cyanophage S-RIM44	GCA_002599265.1
AOO12929.1	001922	Cluster1452_1clades	290	W2100709_047	Cyanophage S-RIM44	GCA_002599285.1
ADO99145.1	001922	Cluster1452_1clades	290	Syn1_044	Prochlorococcus phage Syn1	GCA_000892495.1
ABY62912.1	001923	Cluster1454_1clades	276	201phi2-1p079	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44823.1	001923	Cluster1454_1clades	178	KTN4_065	Pseudomonas phage KTN4	GCA_002607225.1
QBX32197.1	001923	Cluster1454_1clades	264	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76695.1	001923	Cluster1454_1clades	287	PHABIO_64	Pseudomonas phage Phabio	GCA_002624965.1
AEH03471.1	001923	Cluster1454_1clades	170	044	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02572.1	001923	Cluster1454_1clades	183	PSA21_42	Pseudomonas phage Psa21	GCA_004340405.1
ATN94889.1	001923	Cluster1454_1clades	178	SL2_312	Pseudomonas phage SL2	GCA_002956015.1
QJB22701.1	001923	Cluster1454_1clades	178	fnug_58	Pseudomonas phage fnug	GCA_012837215.1
QEM41774.1	001923	Cluster1454_1clades	264	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82948.1	001923	Cluster1454_1clades	178	PHIKZ047	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ49860.1	001924	Cluster1455_1clades	245	MACHINA_222	Erwinia phage Machina	GCA_002758035.1
AXF51363.1	001924	Cluster1455_1clades	205	WELLINGTON_237	Erwinia phage Wellington	GCA_003344985.1
AFQ96677.1	001924	Cluster1455_1clades	268	G173_gp132	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48243.1	001924	Cluster1455_1clades	263	ASESINO_230	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48517.1	001924	Cluster1455_1clades	278	CAITLIN_222	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48794.1	001924	Cluster1455_1clades	277	CHRISDB_232	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49304.1	001924	Cluster1455_1clades	245	HUXLEY_222	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49589.1	001924	Cluster1455_1clades	205	KWAN_237	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50132.1	001924	Cluster1455_1clades	245	PARSHIK_223	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50657.1	001924	Cluster1455_1clades	268	STRATTON_232	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ABY62881.1	001925	Cluster1456_1clades	273	201phi2-1p048	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44805.1	001925	Cluster1456_1clades	256	KTN4_047	Pseudomonas phage KTN4	GCA_002607225.1
QBX32171.1	001925	Cluster1456_1clades	253	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76666.1	001925	Cluster1456_1clades	269	PHABIO_35	Pseudomonas phage Phabio	GCA_002624965.1
AEH03446.1	001925	Cluster1456_1clades	252	020	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02549.1	001925	Cluster1456_1clades	255	PSA21_19	Pseudomonas phage Psa21	GCA_004340405.1
ATN94906.1	001925	Cluster1456_1clades	256	SL2_329	Pseudomonas phage SL2	GCA_002956015.1
QJB22684.1	001925	Cluster1456_1clades	256	fnug_41	Pseudomonas phage fnug	GCA_012837215.1
QEM41751.1	001925	Cluster1456_1clades	253	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82935.1	001925	Cluster1456_1clades	256	PHIKZ034	Pseudomonas virus phiKZ	GCA_000842965.1
AMR59758.1	001926	Cluster1457_1clades	270	SEGD1_111	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96575.1	001926	Cluster1457_1clades	256	G173_gp030	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48136.1	001926	Cluster1457_1clades	272	ASESINO_123	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48413.1	001926	Cluster1457_1clades	265	CAITLIN_118	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48685.1	001926	Cluster1457_1clades	266	CHRISDB_123	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50550.1	001926	Cluster1457_1clades	272	STRATTON_125	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85948.1	001926	Cluster1457_1clades	270	ACEC001_1100	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20816.1	001926	Cluster1457_1clades	270	-	Salmonella phage JN03	GCA_014319805.1
AWN09002.1	001926	Cluster1457_1clades	273	MLDJOKPK_00050	Salmonella phage SPAsTU	GCA_003183805.1
AEP83940.1	001926	Cluster1457_1clades	270	SPN3US_0107	Salmonella phage SPN3US	GCA_001042275.1
ABY63036.1	001927	Cluster1458_1clades	224	201phi2-1p207	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44918.1	001927	Cluster1458_1clades	210	KTN4_160	Pseudomonas phage KTN4	GCA_002607225.1
QBX32304.1	001927	Cluster1458_1clades	234	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76825.1	001927	Cluster1458_1clades	242	PHABIO_194	Pseudomonas phage Phabio	GCA_002624965.1
AEH03567.1	001927	Cluster1458_1clades	223	144	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02703.1	001927	Cluster1458_1clades	266	PSA21_177	Pseudomonas phage Psa21	GCA_004340405.1
ATN94796.1	001927	Cluster1458_1clades	210	SL2_219	Pseudomonas phage SL2	GCA_002956015.1
QJB22796.1	001927	Cluster1458_1clades	210	fnug_153	Pseudomonas phage fnug	GCA_012837215.1
QEM41877.1	001927	Cluster1458_1clades	234	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83026.1	001927	Cluster1458_1clades	210	PHIKZ125	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60407.1	001928	Cluster1459_1clades	257	Ea357_253	Erwinia phage Ea35-70	GCA_000914635.1
QBP07364.1	001928	Cluster1459_1clades	260	REBECCA_259	Erwinia phage Rebecca	GCA_004521635.1
AUG86046.1	001928	Cluster1459_1clades	260	BOSOLAPHORUS_260	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52362.1	001928	Cluster1459_1clades	257	DM_263	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86366.1	001928	Cluster1459_1clades	260	DESERTFOX_259	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86687.1	001928	Cluster1459_1clades	257	MADMEL_260	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87012.1	001928	Cluster1459_1clades	260	MORTIMER_264	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52037.1	001928	Cluster1459_1clades	257	RAY_257	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51720.1	001928	Cluster1459_1clades	257	SIMMY50_262	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65072.1	001928	Cluster1459_1clades	257	SPECIALG_261	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60210.1	001929	Cluster1460_1clades	255	Ea357_060	Erwinia phage Ea35-70	GCA_000914635.1
QBP07169.1	001929	Cluster1460_1clades	255	REBECCA_61	Erwinia phage Rebecca	GCA_004521635.1
AUG85849.1	001929	Cluster1460_1clades	255	BOSOLAPHORUS_61	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52161.1	001929	Cluster1460_1clades	255	DM_63	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86168.1	001929	Cluster1460_1clades	255	DESERTFOX_60	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86489.1	001929	Cluster1460_1clades	255	MADMEL_61	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86810.1	001929	Cluster1460_1clades	255	MORTIMER_61	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51841.1	001929	Cluster1460_1clades	255	RAY_60	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51524.1	001929	Cluster1460_1clades	255	SIMMY50_62	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64872.1	001929	Cluster1460_1clades	255	SPECIALG_62	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60217.1	001930	Cluster1461_1clades	254	Ea357_066	Erwinia phage Ea35-70	GCA_000914635.1
QBP07175.1	001930	Cluster1461_1clades	254	REBECCA_67	Erwinia phage Rebecca	GCA_004521635.1
AUG85855.1	001930	Cluster1461_1clades	254	BOSOLAPHORUS_67	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52167.1	001930	Cluster1461_1clades	254	DM_69	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86174.1	001930	Cluster1461_1clades	254	DESERTFOX_66	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86496.1	001930	Cluster1461_1clades	254	MADMEL_68	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86817.1	001930	Cluster1461_1clades	254	MORTIMER_68	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51847.1	001930	Cluster1461_1clades	254	RAY_66	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51531.1	001930	Cluster1461_1clades	254	SIMMY50_69	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64879.1	001930	Cluster1461_1clades	254	SPECIALG_69	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QGZ14534.1	001931	Cluster1462_1clades	235	HWC77_gp171	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14536.1	001931	Cluster1462_1clades	238	HWC77_gp173	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04200.1	001931	Cluster1462_1clades	235	HWC03_gp045	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04198.1	001931	Cluster1462_1clades	238	HWC03_gp043	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23160.1	001931	Cluster1462_1clades	235	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23162.1	001931	Cluster1462_1clades	238	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81015.1	001931	Cluster1462_1clades	238	Aphrodite1_0179	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47568.1	001931	Cluster1462_1clades	235	HWC35_gp174	Vibrio phage USC-1	GCA_006864065.1
QDH47566.1	001931	Cluster1462_1clades	238	HWC35_gp172	Vibrio phage USC-1	GCA_006864065.1
BAW98382.1	001931	Cluster1462_1clades	251	FDH33_gp173	Vibrio phage pTD1	GCA_002618825.1
AHI60216.1	001932	Cluster1463_1clades	240	Ea357_065	Erwinia phage Ea35-70	GCA_000914635.1
QBP07174.1	001932	Cluster1463_1clades	240	REBECCA_66	Erwinia phage Rebecca	GCA_004521635.1
AUG85854.1	001932	Cluster1463_1clades	240	BOSOLAPHORUS_66	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52166.1	001932	Cluster1463_1clades	240	DM_68	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86173.1	001932	Cluster1463_1clades	240	DESERTFOX_65	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86495.1	001932	Cluster1463_1clades	240	MADMEL_67	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86816.1	001932	Cluster1463_1clades	240	MORTIMER_67	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51846.1	001932	Cluster1463_1clades	240	RAY_65	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51530.1	001932	Cluster1463_1clades	240	SIMMY50_68	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANJ64878.1	001932	Cluster1463_1clades	240	SPECIALG_68	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60421.1	001933	Cluster1464_1clades	238	Ea357_267	Erwinia phage Ea35-70	GCA_000914635.1
QBP07378.1	001933	Cluster1464_1clades	238	REBECCA_273	Erwinia phage Rebecca	GCA_004521635.1
AUG86060.1	001933	Cluster1464_1clades	238	BOSOLAPHORUS_274	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52376.1	001933	Cluster1464_1clades	238	DM_277	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86380.1	001933	Cluster1464_1clades	238	DESERTFOX_273	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86701.1	001933	Cluster1464_1clades	238	MADMEL_274	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87026.1	001933	Cluster1464_1clades	235	MORTIMER_278	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52051.1	001933	Cluster1464_1clades	238	RAY_271	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51734.1	001933	Cluster1464_1clades	238	SIMMY50_276	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65086.1	001933	Cluster1464_1clades	238	SPECIALG_275	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60428.1	001934	Cluster1465_1clades	236	Ea357_274	Erwinia phage Ea35-70	GCA_000914635.1
QBP07385.1	001934	Cluster1465_1clades	236	REBECCA_280	Erwinia phage Rebecca	GCA_004521635.1
AUG86067.1	001934	Cluster1465_1clades	236	BOSOLAPHORUS_281	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52383.1	001934	Cluster1465_1clades	236	DM_284	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86387.1	001934	Cluster1465_1clades	236	DESERTFOX_280	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86708.1	001934	Cluster1465_1clades	236	MADMEL_281	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87033.1	001934	Cluster1465_1clades	236	MORTIMER_285	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52058.1	001934	Cluster1465_1clades	236	RAY_278	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51741.1	001934	Cluster1465_1clades	236	SIMMY50_283	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65093.1	001934	Cluster1465_1clades	236	SPECIALG_282	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QDH83535.1	001935	Cluster1466_1clades	206	H1O15_gp253	Achromobacter phage Motura	GCA_006964305.1
AFU88118.1	001935	Cluster1466_1clades	216	CcrColossus_gp248	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68796.1	001935	Cluster1466_1clades	218	CcrPW_gp257	Caulobacter phage CcrPW	GCA_003443275.1
AFC21951.1	001935	Cluster1466_1clades	235	GAP32_492	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44077.1	001935	Cluster1466_1clades	236	CBB_514	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89034.1	001935	Cluster1466_1clades	228	BF_0509	Serratia phage BF	GCA_002619745.1
AGR47833.2	001935	Cluster1466_1clades	233	SmphiM12_201	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13042.1	001935	Cluster1466_1clades	233	PHIM19_137	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12683.1	001935	Cluster1466_1clades	233	PHIM7_137	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13415.1	001935	Cluster1466_1clades	235	PHIN3_152	Sinorhizobium phage phiN3	GCA_001501175.1
AHI60412.1	001936	Cluster1467_1clades	232	Ea357_258	Erwinia phage Ea35-70	GCA_000914635.1
QBP07369.1	001936	Cluster1467_1clades	232	REBECCA_264	Erwinia phage Rebecca	GCA_004521635.1
AUG86051.1	001936	Cluster1467_1clades	232	BOSOLAPHORUS_265	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52367.1	001936	Cluster1467_1clades	232	DM_268	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86371.1	001936	Cluster1467_1clades	232	DESERTFOX_264	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86692.1	001936	Cluster1467_1clades	232	MADMEL_265	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87017.1	001936	Cluster1467_1clades	232	MORTIMER_269	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52042.1	001936	Cluster1467_1clades	232	RAY_262	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51725.1	001936	Cluster1467_1clades	235	SIMMY50_267	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65077.1	001936	Cluster1467_1clades	232	SPECIALG_266	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60228.1	001937	Cluster1469_1clades	233	Ea357_077	Erwinia phage Ea35-70	GCA_000914635.1
QBP07187.1	001937	Cluster1469_1clades	233	REBECCA_79	Erwinia phage Rebecca	GCA_004521635.1
AUG85866.1	001937	Cluster1469_1clades	233	BOSOLAPHORUS_78	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52178.1	001937	Cluster1469_1clades	233	DM_80	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86185.1	001937	Cluster1469_1clades	233	DESERTFOX_77	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86507.1	001937	Cluster1469_1clades	233	MADMEL_79	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86828.1	001937	Cluster1469_1clades	233	MORTIMER_79	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51858.1	001937	Cluster1469_1clades	233	RAY_77	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51542.1	001937	Cluster1469_1clades	233	SIMMY50_80	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64890.1	001937	Cluster1469_1clades	233	SPECIALG_80	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60378.1	001938	Cluster1470_1clades	233	Ea357_225	Erwinia phage Ea35-70	GCA_000914635.1
QBP07335.1	001938	Cluster1470_1clades	233	REBECCA_230	Erwinia phage Rebecca	GCA_004521635.1
AUG86016.1	001938	Cluster1470_1clades	233	BOSOLAPHORUS_230	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52333.1	001938	Cluster1470_1clades	233	DM_233	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86335.1	001938	Cluster1470_1clades	233	DESERTFOX_228	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86659.1	001938	Cluster1470_1clades	233	MADMEL_231	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86981.1	001938	Cluster1470_1clades	233	MORTIMER_233	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52008.1	001938	Cluster1470_1clades	233	RAY_228	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51692.1	001938	Cluster1470_1clades	233	SIMMY50_233	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65043.1	001938	Cluster1470_1clades	233	SPECIALG_232	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63246.1	001939	Cluster1471_1clades	226	201phi2-1p423	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45104.1	001939	Cluster1471_1clades	217	KTN4_346	Pseudomonas phage KTN4	GCA_002607225.1
QBX32520.1	001939	Cluster1471_1clades	233	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77054.1	001939	Cluster1471_1clades	225	PHABIO_423	Pseudomonas phage Phabio	GCA_002624965.1
AEH03774.1	001939	Cluster1471_1clades	220	351	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02910.1	001939	Cluster1471_1clades	216	PSA21_384	Pseudomonas phage Psa21	GCA_004340405.1
ATN94610.1	001939	Cluster1471_1clades	217	SL2_033	Pseudomonas phage SL2	GCA_002956015.1
QJB22980.1	001939	Cluster1471_1clades	217	fnug_337	Pseudomonas phage fnug	GCA_012837215.1
QEM42093.1	001939	Cluster1471_1clades	233	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83188.1	001939	Cluster1471_1clades	217	PHIKZ287	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62837.1	001940	Cluster1472_1clades	179	201phi2-1p002	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44760.1	001940	Cluster1472_1clades	194	KTN4_002	Pseudomonas phage KTN4	GCA_002607225.1
QBX32150.1	001940	Cluster1472_1clades	193	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76632.1	001940	Cluster1472_1clades	197	PHABIO_1	Pseudomonas phage Phabio	GCA_002624965.1
AEH03428.1	001940	Cluster1472_1clades	197	002	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02532.1	001940	Cluster1472_1clades	229	PSA21_2	Pseudomonas phage Psa21	GCA_004340405.1
ATN94583.1	001940	Cluster1472_1clades	194	SL2_006	Pseudomonas phage SL2	GCA_002956015.1
QJB22645.1	001940	Cluster1472_1clades	194	fnug_2	Pseudomonas phage fnug	GCA_012837215.1
QEM41731.1	001940	Cluster1472_1clades	193	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82903.1	001940	Cluster1472_1clades	194	PHIKZ002	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63212.1	001941	Cluster1473_1clades	70	201phi2-1p387	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44764.1	001941	Cluster1473_1clades	171	KTN4_006	Pseudomonas phage KTN4	GCA_002607225.1
QBX32481.1	001941	Cluster1473_1clades	176	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76888.1	001941	Cluster1473_1clades	207	PHABIO_257	Pseudomonas phage Phabio	GCA_002624965.1
ARV77013.1	001941	Cluster1473_1clades	150	PHABIO_382	Pseudomonas phage Phabio	GCA_002624965.1
AEH03743.1	001941	Cluster1473_1clades	168	320	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02883.1	001941	Cluster1473_1clades	227	PSA21_357	Pseudomonas phage Psa21	GCA_004340405.1
QJB22649.1	001941	Cluster1473_1clades	171	fnug_6	Pseudomonas phage fnug	GCA_012837215.1
QEM42053.1	001941	Cluster1473_1clades	176	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82907.1	001941	Cluster1473_1clades	171	PHIKZ006	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60375.1	001942	Cluster1474_1clades	223	Ea357_222	Erwinia phage Ea35-70	GCA_000914635.1
QBP07332.1	001942	Cluster1474_1clades	223	REBECCA_227	Erwinia phage Rebecca	GCA_004521635.1
AUG86013.1	001942	Cluster1474_1clades	223	BOSOLAPHORUS_227	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52330.1	001942	Cluster1474_1clades	223	DM_230	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86332.1	001942	Cluster1474_1clades	225	DESERTFOX_225	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86655.1	001942	Cluster1474_1clades	223	MADMEL_227	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86978.1	001942	Cluster1474_1clades	225	MORTIMER_230	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52005.1	001942	Cluster1474_1clades	223	RAY_225	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51689.1	001942	Cluster1474_1clades	225	SIMMY50_230	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65039.1	001942	Cluster1474_1clades	225	SPECIALG_228	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT14095.1	001943	STYKIN	224	PBI_121Q_205	Escherichia phage 121Q	GCA_000926855.1
AGC34999.1	001943	STYKIN	224	ACQ29_gp319	Escherichia phage PBECO4	GCA_001041035.1
BBM61777.1	001943	STYKIN	213	EO157G_1880	Escherichia phage SP27	GCA_008033345.1
AXC36578.1	001943	STYKIN	213	-	Escherichia phage UB	GCA_003341455.1
QBO61604.1	001943	STYKIN	213	G17_00108	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13662.1	001943	STYKIN	213	vBEcoMphAPEC6_gp031c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80089.1	001943	STYKIN	213	PSLUR01_00112	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18628.1	001943	STYKIN	213	7t3_0107	Salmonella phage 7t3	GCA_006083215.1
AZU98453.1	001943	STYKIN	213	CPT_Munch_521	Salmonella phage Munch	GCA_004015485.1
QIG63061.1	001943	STYKIN	213	SEPL_448	Salmonella phage SE_PL	GCA_011067555.1
AHI60271.1	001944	Cluster1476_1clades	209	Ea357_120	Erwinia phage Ea35-70	GCA_000914635.1
QBP07229.1	001944	Cluster1476_1clades	223	REBECCA_122	Erwinia phage Rebecca	GCA_004521635.1
AUG85909.1	001944	Cluster1476_1clades	209	BOSOLAPHORUS_122	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52224.2	001944	Cluster1476_1clades	209	DM_126	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86228.1	001944	Cluster1476_1clades	209	DESERTFOX_121	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86550.1	001944	Cluster1476_1clades	209	MADMEL_122	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86874.1	001944	Cluster1476_1clades	209	MORTIMER_125	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51902.1	001944	Cluster1476_1clades	209	RAY_121	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51586.1	001944	Cluster1476_1clades	209	SIMMY50_124	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64933.2	001944	Cluster1476_1clades	209	SPECIALG_123	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AXH70955.1	001945	CheB-Methylesterase	214	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70952.1	001945	CheB-Methylesterase	221	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96714.1	001945	CheB-Methylesterase	200	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96715.1	001945	CheB-Methylesterase	216	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX97033.1	001945	CheB-Methylesterase	200	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX97034.1	001945	CheB-Methylesterase	216	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96079.1	001945	CheB-Methylesterase	200	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96080.1	001945	CheB-Methylesterase	216	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96397.1	001945	CheB-Methylesterase	200	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96398.1	001945	CheB-Methylesterase	216	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QMV28812.1	001946	Cluster1478_1clades	85	AP1_0105	Aeromonas phage AP1	GCA_014183365.1
QMV29060.1	001946	Cluster1478_1clades	208	AP1_0353	Aeromonas phage AP1	GCA_014183365.1
ATI17615.1	001946	Cluster1478_1clades	206	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17614.1	001946	Cluster1478_1clades	214	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00381.1	001946	Cluster1478_1clades	208	HWB28_gp171	Aeromonas phage AS-zj	GCA_002627665.1
ASU00382.1	001946	Cluster1478_1clades	217	HWB28_gp170	Aeromonas phage AS-zj	GCA_002627665.1
QAX97648.1	001946	Cluster1478_1clades	214	ASswx1_2	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97649.1	001946	Cluster1478_1clades	206	ASswx1_3	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39222.1	001946	Cluster1478_1clades	206	CC2_111	Aeromonas phage CC2	GCA_000903495.1
AFN39223.1	001946	Cluster1478_1clades	217	CC2_112	Aeromonas phage CC2	GCA_000903495.1
QDH83495.1	001947	SIG+SpoIID	193	H1O15_gp311	Achromobacter phage Motura	GCA_006964305.1
AND75274.1	001947	SIG+SpoIID	151	ME3_113	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AMS01105.1	001947	SIG+SpoIID	214	AR9_g020	Bacillus phage AR9	GCA_001743835.1
ALN97746.1	001947	SIG+SpoIID	217	Bp8pS_067	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00027.1	001947	SIG+SpoIID	214	PBI_PBS1_205	Bacillus virus PBS1	GCA_002601325.1
QBO63891.1	001947	SIG+SpoIID	165	Goslar_00098	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QCG76248.1	001947	SIG+SpoIID	188	EST35_0368	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBA65719.1	001947	SIG+SpoIID	199	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65260.1	001947	SIG+SpoIID	199	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96300.1	001947	SIG+SpoIID	199	Xoosp13_113	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AHI60374.1	001948	Cluster1480_1clades	215	Ea357_221	Erwinia phage Ea35-70	GCA_000914635.1
QBP07331.1	001948	Cluster1480_1clades	215	REBECCA_226	Erwinia phage Rebecca	GCA_004521635.1
AUG86012.1	001948	Cluster1480_1clades	215	BOSOLAPHORUS_226	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52329.1	001948	Cluster1480_1clades	215	DM_229	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86331.1	001948	Cluster1480_1clades	215	DESERTFOX_224	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86654.1	001948	Cluster1480_1clades	215	MADMEL_226	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86977.1	001948	Cluster1480_1clades	215	MORTIMER_229	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52004.1	001948	Cluster1480_1clades	215	RAY_224	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51688.2	001948	Cluster1480_1clades	215	SIMMY50_229	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65038.1	001948	Cluster1480_1clades	215	SPECIALG_227	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60223.1	001949	Cluster1481_1clades	214	Ea357_072	Erwinia phage Ea35-70	GCA_000914635.1
QBP07182.1	001949	Cluster1481_1clades	214	REBECCA_74	Erwinia phage Rebecca	GCA_004521635.1
AUG85861.1	001949	Cluster1481_1clades	214	BOSOLAPHORUS_73	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52173.1	001949	Cluster1481_1clades	214	DM_75	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86180.1	001949	Cluster1481_1clades	214	DESERTFOX_72	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86502.1	001949	Cluster1481_1clades	214	MADMEL_74	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86823.1	001949	Cluster1481_1clades	214	MORTIMER_74	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51853.1	001949	Cluster1481_1clades	214	RAY_72	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51537.1	001949	Cluster1481_1clades	214	SIMMY50_75	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64885.1	001949	Cluster1481_1clades	214	SPECIALG_75	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60194.1	001950	Cluster1482_1clades	209	Ea357_044	Erwinia phage Ea35-70	GCA_000914635.1
QBP07152.1	001950	Cluster1482_1clades	209	REBECCA_44	Erwinia phage Rebecca	GCA_004521635.1
AUG85832.1	001950	Cluster1482_1clades	209	BOSOLAPHORUS_44	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52143.1	001950	Cluster1482_1clades	209	DM_45	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86152.1	001950	Cluster1482_1clades	209	DESERTFOX_44	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86472.1	001950	Cluster1482_1clades	209	MADMEL_44	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86793.1	001950	Cluster1482_1clades	209	MORTIMER_44	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51825.1	001950	Cluster1482_1clades	209	RAY_44	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51507.1	001950	Cluster1482_1clades	209	SIMMY50_45	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64854.1	001950	Cluster1482_1clades	209	SPECIALG_44	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60289.1	001951	TM+TM+TM	209	Ea357_138	Erwinia phage Ea35-70	GCA_000914635.1
QBP07247.1	001951	TM+TM+TM	209	REBECCA_140	Erwinia phage Rebecca	GCA_004521635.1
AUG85927.1	001951	TM+TM+TM	209	BOSOLAPHORUS_140	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52242.1	001951	TM+TM+TM	209	DM_144	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86246.1	001951	TM+TM+TM	209	DESERTFOX_139	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86568.1	001951	TM+TM+TM	209	MADMEL_140	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86892.1	001951	TM+TM+TM	209	MORTIMER_143	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51920.1	001951	TM+TM+TM	209	RAY_139	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51604.1	001951	TM+TM+TM	209	SIMMY50_142	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64951.1	001951	TM+TM+TM	209	SPECIALG_141	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AAQ64441.1	001952	Cluster1484_1clades	208	KVP40.0373	Vibrio phage KVP40	GCA_000843785.1
QIW90386.1	001952	Cluster1484_1clades	208	GCAPEGMB_00039	Vibrio phage V07	GCA_012361095.1
QIW91043.1	001952	Cluster1484_1clades	208	COHAPHLL_00180	Vibrio phage V09	GCA_012361135.1
QHJ74553.1	001952	Cluster1484_1clades	208	VH12019_00253	Vibrio phage VH1_2019	GCA_009931825.1
QBX06101.1	001952	Cluster1484_1clades	208	ValB1HC_147	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61115.1	001952	Cluster1484_1clades	208	AVU32_gp274	Vibrio phage ValKK3	GCA_001501635.1
ALP47063.1	001952	Cluster1484_1clades	208	phiGrn1_0105	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47443.1	001952	Cluster1484_1clades	208	phiST2_0236	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54726.1	001952	Cluster1484_1clades	208	vBValMR10Z_186	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37604.1	001952	Cluster1484_1clades	208	pp2_372	Vibriophage phi-pp2	GCA_002630725.1
AHI60376.1	001953	Cluster1485_1clades	208	Ea357_223	Erwinia phage Ea35-70	GCA_000914635.1
QBP07333.1	001953	Cluster1485_1clades	208	REBECCA_228	Erwinia phage Rebecca	GCA_004521635.1
AUG86014.1	001953	Cluster1485_1clades	208	BOSOLAPHORUS_228	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52331.1	001953	Cluster1485_1clades	208	DM_231	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86333.1	001953	Cluster1485_1clades	208	DESERTFOX_226	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86656.1	001953	Cluster1485_1clades	208	MADMEL_228	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86979.1	001953	Cluster1485_1clades	208	MORTIMER_231	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52006.1	001953	Cluster1485_1clades	208	RAY_226	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51690.1	001953	Cluster1485_1clades	208	SIMMY50_231	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65040.1	001953	Cluster1485_1clades	208	SPECIALG_229	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AXG67301.1	001954	Cluster1486_1clades	134	AD1_257	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80053.1	001954	Cluster1486_1clades	142	JA11_248	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66652.1	001954	Cluster1486_1clades	142	JA13_249	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66976.1	001954	Cluster1486_1clades	137	JA29_250	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66978.1	001954	Cluster1486_1clades	137	JA29_252	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67623.1	001954	Cluster1486_1clades	142	JA33_249	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08527.1	001954	Cluster1486_1clades	136	Alexandra_270	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58906.1	001954	Cluster1486_1clades	139	Y3_266	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AGS81920.1	001954	Cluster1486_1clades	207	PaBG_00036	Pseudomonas phage PaBG	GCA_000912555.1
BAG41508.1	001954	Cluster1486_1clades	116	RSL1_ORF062	Ralstonia phage phiRSL1	GCA_000879455.1
AMO43312.1	001955	Cluster1487_1clades	203	W270710_068	Cyanophage S-RIM44	GCA_002599145.1
AOO11546.1	001955	Cluster1487_1clades	203	ES420910_065	Cyanophage S-RIM44	GCA_002599165.1
AOO11784.1	001955	Cluster1487_1clades	203	Np050604_068	Cyanophage S-RIM44	GCA_002599185.1
AOO12011.1	001955	Cluster1487_1clades	203	Np200711_065	Cyanophage S-RIM44	GCA_002599205.1
AOO12247.1	001955	Cluster1487_1clades	203	Np420711_065	Cyanophage S-RIM44	GCA_002599225.1
AOO12485.1	001955	Cluster1487_1clades	203	Sn080709_068	Cyanophage S-RIM44	GCA_002599245.1
AOO12712.1	001955	Cluster1487_1clades	203	Sn130910_065	Cyanophage S-RIM44	GCA_002599265.1
AOO12950.1	001955	Cluster1487_1clades	203	W2100709_068	Cyanophage S-RIM44	GCA_002599285.1
AGH26149.1	001955	Cluster1487_1clades	202	CPMG_00048	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99166.1	001955	Cluster1487_1clades	203	Syn1_065	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60260.1	001956	Cluster1488_1clades	203	Ea357_109	Erwinia phage Ea35-70	GCA_000914635.1
QBP07217.1	001956	Cluster1488_1clades	203	REBECCA_110	Erwinia phage Rebecca	GCA_004521635.1
AUG85897.1	001956	Cluster1488_1clades	203	BOSOLAPHORUS_110	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52212.1	001956	Cluster1488_1clades	203	DM_114	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86216.1	001956	Cluster1488_1clades	203	DESERTFOX_109	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86538.1	001956	Cluster1488_1clades	203	MADMEL_110	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86863.1	001956	Cluster1488_1clades	203	MORTIMER_114	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51891.1	001956	Cluster1488_1clades	203	RAY_110	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51575.1	001956	Cluster1488_1clades	203	SIMMY50_113	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64922.1	001956	Cluster1488_1clades	203	SPECIALG_112	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60230.1	001957	Cluster1489_1clades	201	Ea357_079	Erwinia phage Ea35-70	GCA_000914635.1
QBP07189.1	001957	Cluster1489_1clades	201	REBECCA_81	Erwinia phage Rebecca	GCA_004521635.1
AUG85868.1	001957	Cluster1489_1clades	201	BOSOLAPHORUS_80	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52180.1	001957	Cluster1489_1clades	201	DM_82	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86187.1	001957	Cluster1489_1clades	201	DESERTFOX_79	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86509.1	001957	Cluster1489_1clades	201	MADMEL_81	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86830.1	001957	Cluster1489_1clades	201	MORTIMER_81	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51860.1	001957	Cluster1489_1clades	201	RAY_79	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51544.1	001957	Cluster1489_1clades	201	SIMMY50_82	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANJ64892.1	001957	Cluster1489_1clades	201	SPECIALG_82	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60241.1	001958	Cluster1490_1clades	198	Ea357_090	Erwinia phage Ea35-70	GCA_000914635.1
QBP07199.1	001958	Cluster1490_1clades	198	REBECCA_92	Erwinia phage Rebecca	GCA_004521635.1
AUG85878.1	001958	Cluster1490_1clades	198	BOSOLAPHORUS_91	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52193.2	001958	Cluster1490_1clades	198	DM_95	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86197.1	001958	Cluster1490_1clades	198	DESERTFOX_90	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86520.1	001958	Cluster1490_1clades	198	MADMEL_92	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86843.1	001958	Cluster1490_1clades	198	MORTIMER_94	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51871.1	001958	Cluster1490_1clades	198	RAY_90	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51555.1	001958	Cluster1490_1clades	198	SIMMY50_93	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64903.2	001958	Cluster1490_1clades	198	SPECIALG_93	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13655.1	001959	Cluster1491_1clades	196	Ccr10_gp126c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14000.1	001959	Cluster1491_1clades	196	Ccr2_gp125c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14688.1	001959	Cluster1491_1clades	183	Ccr29_gp132	Caulobacter phage Ccr29	GCA_002619485.1
ARB15042.1	001959	Cluster1491_1clades	190	Ccr32_gp124	Caulobacter phage Ccr32	GCA_002619505.1
ARB15375.1	001959	Cluster1491_1clades	190	Ccr34_gp133	Caulobacter phage Ccr34	GCA_002619525.1
ARB14343.1	001959	Cluster1491_1clades	194	Ccr5_gp340	Caulobacter phage Ccr5	GCA_002619545.1
AFU87647.1	001959	Cluster1491_1clades	193	CcrKarma_gp130	Caulobacter virus Karma	GCA_000901575.1
AFU87296.1	001959	Cluster1491_1clades	170	CcrMagneto_gp126	Caulobacter virus Magneto	GCA_000903095.1
AFU88443.1	001959	Cluster1491_1clades	170	CcrSwift_gp125	Caulobacter virus Swift	GCA_000899655.1
AFU86960.1	001959	Cluster1491_1clades	190	CbK_gp128	Caulobacter virus phiCbK	GCA_000900535.1
ABY62951.1	001960	Cluster1492_1clades	168	201phi2-1p119	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44843.1	001960	Cluster1492_1clades	185	KTN4_085	Pseudomonas phage KTN4	GCA_002607225.1
QBX32211.1	001960	Cluster1492_1clades	196	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76730.1	001960	Cluster1492_1clades	168	PHABIO_99	Pseudomonas phage Phabio	GCA_002624965.1
AEH03484.1	001960	Cluster1492_1clades	179	057	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02594.1	001960	Cluster1492_1clades	164	PSA21_65	Pseudomonas phage Psa21	GCA_004340405.1
ATN94870.1	001960	Cluster1492_1clades	185	SL2_293	Pseudomonas phage SL2	GCA_002956015.1
QJB22721.1	001960	Cluster1492_1clades	185	fnug_78	Pseudomonas phage fnug	GCA_012837215.1
QEM41789.1	001960	Cluster1492_1clades	196	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82964.1	001960	Cluster1492_1clades	185	PHIKZ063	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60188.1	001961	Cluster1493_1clades	194	Ea357_038	Erwinia phage Ea35-70	GCA_000914635.1
QBP07146.1	001961	Cluster1493_1clades	194	REBECCA_38	Erwinia phage Rebecca	GCA_004521635.1
AUG85826.1	001961	Cluster1493_1clades	194	BOSOLAPHORUS_38	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52137.1	001961	Cluster1493_1clades	194	DM_39	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86146.1	001961	Cluster1493_1clades	194	DESERTFOX_38	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86466.1	001961	Cluster1493_1clades	194	MADMEL_38	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86787.1	001961	Cluster1493_1clades	194	MORTIMER_38	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51819.1	001961	Cluster1493_1clades	194	RAY_38	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51501.1	001961	Cluster1493_1clades	194	SIMMY50_39	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64848.1	001961	Cluster1493_1clades	194	SPECIALG_38	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60367.1	001962	Cluster1494_1clades	193	Ea357_214	Erwinia phage Ea35-70	GCA_000914635.1
QBP07324.1	001962	Cluster1494_1clades	193	REBECCA_219	Erwinia phage Rebecca	GCA_004521635.1
AUG86005.1	001962	Cluster1494_1clades	193	BOSOLAPHORUS_219	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52322.1	001962	Cluster1494_1clades	193	DM_222	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86324.1	001962	Cluster1494_1clades	193	DESERTFOX_217	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86647.1	001962	Cluster1494_1clades	193	MADMEL_219	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86970.1	001962	Cluster1494_1clades	193	MORTIMER_222	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51997.1	001962	Cluster1494_1clades	193	RAY_217	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51681.1	001962	Cluster1494_1clades	193	SIMMY50_222	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65031.1	001962	Cluster1494_1clades	193	SPECIALG_220	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60358.1	001963	Cluster1495_1clades	190	Ea357_205	Erwinia phage Ea35-70	GCA_000914635.1
QBP07315.1	001963	Cluster1495_1clades	190	REBECCA_210	Erwinia phage Rebecca	GCA_004521635.1
AUG85996.1	001963	Cluster1495_1clades	190	BOSOLAPHORUS_210	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52313.1	001963	Cluster1495_1clades	190	DM_213	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86315.1	001963	Cluster1495_1clades	190	DESERTFOX_208	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86638.1	001963	Cluster1495_1clades	190	MADMEL_210	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86961.1	001963	Cluster1495_1clades	190	MORTIMER_213	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51988.1	001963	Cluster1495_1clades	190	RAY_208	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51672.1	001963	Cluster1495_1clades	190	SIMMY50_213	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65022.1	001963	Cluster1495_1clades	190	SPECIALG_211	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13563.1	001964	Cluster1496_1clades	189	Ccr10_gp035	Caulobacter phage Ccr10	GCA_002619445.1
ARB13909.1	001964	Cluster1496_1clades	189	Ccr2_gp034	Caulobacter phage Ccr2	GCA_002619465.1
ARB14598.1	001964	Cluster1496_1clades	189	Ccr29_gp041	Caulobacter phage Ccr29	GCA_002619485.1
ARB14953.1	001964	Cluster1496_1clades	189	Ccr32_gp034	Caulobacter phage Ccr32	GCA_002619505.1
ARB15284.1	001964	Cluster1496_1clades	189	Ccr34_gp035	Caulobacter phage Ccr34	GCA_002619525.1
ARB14252.1	001964	Cluster1496_1clades	189	Ccr5_gp034	Caulobacter phage Ccr5	GCA_002619545.1
AFU87552.1	001964	Cluster1496_1clades	186	CcrKarma_gp035	Caulobacter virus Karma	GCA_000901575.1
AFU87203.1	001964	Cluster1496_1clades	186	CcrMagneto_gp033	Caulobacter virus Magneto	GCA_000903095.1
AFU88349.1	001964	Cluster1496_1clades	186	CcrSwift_gp031	Caulobacter virus Swift	GCA_000899655.1
AFU86866.1	001964	Cluster1496_1clades	189	CbK_gp034	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64152.1	001965	Cluster1497_1clades	186	KVP40.0081	Vibrio phage KVP40	GCA_000843785.1
QIW90476.1	001965	Cluster1497_1clades	172	GCAPEGMB_00129	Vibrio phage V07	GCA_012361095.1
QIW90953.1	001965	Cluster1497_1clades	172	COHAPHLI_00090	Vibrio phage V09	GCA_012361135.1
QHJ74264.1	001965	Cluster1497_1clades	172	VH12019_00345	Vibrio phage VH1_2019	GCA_009931825.1
AGB07089.1	001965	Cluster1497_1clades	172	CF80_gp302	Vibrio phage VH7D	GCA_000914495.1
QBX06006.1	001965	Cluster1497_1clades	172	ValB1HC_052	Vibrio phage ValB1 HC	GCA_004771355.1
AGN30130.2	001965	Cluster1497_1clades	172	VPFG_00128	Vibrio phage nt-1	GCA_000910195.2
ALP47477.1	001965	Cluster1497_1clades	172	phiST2_0329	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54630.1	001965	Cluster1497_1clades	172	vBValMR10Z_89	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37313.1	001965	Cluster1497_1clades	172	pp2_080	Vibriophage phi-pp2	GCA_002630725.1
AHI60413.1	001966	Cluster1498_1clades	185	Ea357_259	Erwinia phage Ea35-70	GCA_000914635.1
QBP07370.1	001966	Cluster1498_1clades	185	REBECCA_265	Erwinia phage Rebecca	GCA_004521635.1
AUG86052.1	001966	Cluster1498_1clades	185	BOSOLAPHORUS_266	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52368.1	001966	Cluster1498_1clades	185	DM_269	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86372.1	001966	Cluster1498_1clades	185	DESERTFOX_265	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86693.1	001966	Cluster1498_1clades	185	MADMEL_266	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87018.1	001966	Cluster1498_1clades	185	MORTIMER_270	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52043.1	001966	Cluster1498_1clades	185	RAY_263	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51726.1	001966	Cluster1498_1clades	185	SIMMY50_268	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65078.1	001966	Cluster1498_1clades	185	SPECIALG_267	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60186.1	001967	Cluster1499_1clades	184	Ea357_036	Erwinia phage Ea35-70	GCA_000914635.1
QBP07144.1	001967	Cluster1499_1clades	184	REBECCA_36	Erwinia phage Rebecca	GCA_004521635.1
AUG85824.1	001967	Cluster1499_1clades	184	BOSOLAPHORUS_36	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52135.1	001967	Cluster1499_1clades	184	DM_37	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86144.1	001967	Cluster1499_1clades	184	DESERTFOX_36	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86464.1	001967	Cluster1499_1clades	184	MADMEL_36	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86785.1	001967	Cluster1499_1clades	184	MORTIMER_36	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51817.1	001967	Cluster1499_1clades	184	RAY_36	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51499.1	001967	Cluster1499_1clades	184	SIMMY50_37	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64846.1	001967	Cluster1499_1clades	184	SPECIALG_36	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60214.1	001968	Cluster1500_1clades	184	Ea357_063	Erwinia phage Ea35-70	GCA_000914635.1
QBP07172.1	001968	Cluster1500_1clades	184	REBECCA_64	Erwinia phage Rebecca	GCA_004521635.1
AUG85852.1	001968	Cluster1500_1clades	183	BOSOLAPHORUS_64	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52164.1	001968	Cluster1500_1clades	183	DM_66	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86171.1	001968	Cluster1500_1clades	184	DESERTFOX_63	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86493.1	001968	Cluster1500_1clades	183	MADMEL_65	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86814.1	001968	Cluster1500_1clades	184	MORTIMER_65	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51844.1	001968	Cluster1500_1clades	183	RAY_63	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51528.1	001968	Cluster1500_1clades	183	SIMMY50_66	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64876.1	001968	Cluster1500_1clades	184	SPECIALG_66	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63084.1	001969	Cluster1501_1clades	178	201phi2-1p256	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44968.1	001969	Cluster1501_1clades	174	KTN4_210	Pseudomonas phage KTN4	GCA_002607225.1
QBX32358.1	001969	Cluster1501_1clades	180	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76876.1	001969	Cluster1501_1clades	176	PHABIO_245	Pseudomonas phage Phabio	GCA_002624965.1
AEH03622.1	001969	Cluster1501_1clades	180	199	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02758.1	001969	Cluster1501_1clades	183	PSA21_232	Pseudomonas phage Psa21	GCA_004340405.1
ATN94746.1	001969	Cluster1501_1clades	174	SL2_169	Pseudomonas phage SL2	GCA_002956015.1
QJB22846.1	001969	Cluster1501_1clades	174	fnug_203	Pseudomonas phage fnug	GCA_012837215.1
QEM41932.1	001969	Cluster1501_1clades	180	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83071.1	001969	Cluster1501_1clades	174	PHIKZ170	Pseudomonas virus phiKZ	GCA_000842965.1
AMR59762.1	001970	Cluster1502_1clades	110	SEGD1_115	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49761.1	001970	Cluster1502_1clades	108	MACHINA_123	Erwinia phage Machina	GCA_002758035.1
AXF51269.1	001970	Cluster1502_1clades	108	WELLINGTON_139	Erwinia phage Wellington	GCA_003344985.1
ANZ49205.1	001970	Cluster1502_1clades	108	HUXLEY_123	Erwinia phage vB_EamM_Huxley	GCA_001745635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ49490.1	001970	Cluster1502_1clades	108	KWAN_138	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50033.1	001970	Cluster1502_1clades	108	PARSHIK_124	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QKN85952.1	001970	Cluster1502_1clades	104	ACEC001_1140	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20819.1	001970	Cluster1502_1clades	183	-	Salmonella phage JN03	GCA_014319805.1
AWN08998.1	001970	Cluster1502_1clades	110	MLDJOKPK_00046	Salmonella phage SPAsTU	GCA_003183805.1
AEP83944.1	001970	Cluster1502_1clades	104	SPN3US_0111	Salmonella phage SPN3US	GCA_001042275.1
AHI60206.1	001971	Cluster1503_1clades	182	Ea357_056	Erwinia phage Ea35-70	GCA_000914635.1
QBP07165.1	001971	Cluster1503_1clades	182	REBECCA_57	Erwinia phage Rebecca	GCA_004521635.1
AUG85845.1	001971	Cluster1503_1clades	182	BOSOLAPHORUS_57	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52157.1	001971	Cluster1503_1clades	182	DM_59	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86164.1	001971	Cluster1503_1clades	182	DESERTFOX_56	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86485.1	001971	Cluster1503_1clades	176	MADMEL_57	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86806.1	001971	Cluster1503_1clades	182	MORTIMER_57	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51837.1	001971	Cluster1503_1clades	182	RAY_56	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51520.1	001971	Cluster1503_1clades	182	SIMMY50_58	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64868.1	001971	Cluster1503_1clades	182	SPECIALG_58	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60343.1	001972	Cluster1504_1clades	181	Ea357_191	Erwinia phage Ea35-70	GCA_000914635.1
QBP07302.1	001972	Cluster1504_1clades	181	REBECCA_195	Erwinia phage Rebecca	GCA_004521635.1
AUG85982.1	001972	Cluster1504_1clades	181	BOSOLAPHORUS_195	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52297.2	001972	Cluster1504_1clades	181	DM_199	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86301.1	001972	Cluster1504_1clades	181	DESERTFOX_194	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86623.1	001972	Cluster1504_1clades	181	MADMEL_195	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86947.1	001972	Cluster1504_1clades	181	MORTIMER_198	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51974.1	001972	Cluster1504_1clades	181	RAY_193	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51658.1	001972	Cluster1504_1clades	181	SIMMY50_196	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65005.1	001972	Cluster1504_1clades	181	SPECIALG_196	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60357.1	001973	Cluster1505_1clades	181	Ea357_204	Erwinia phage Ea35-70	GCA_000914635.1
QBP07314.1	001973	Cluster1505_1clades	181	REBECCA_209	Erwinia phage Rebecca	GCA_004521635.1
AUG85995.1	001973	Cluster1505_1clades	181	BOSOLAPHORUS_209	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52312.1	001973	Cluster1505_1clades	181	DM_212	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86314.1	001973	Cluster1505_1clades	181	DESERTFOX_207	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86637.1	001973	Cluster1505_1clades	181	MADMEL_209	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86960.1	001973	Cluster1505_1clades	181	MORTIMER_212	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51987.1	001973	Cluster1505_1clades	181	RAY_207	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51671.1	001973	Cluster1505_1clades	181	SIMMY50_212	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65021.1	001973	Cluster1505_1clades	181	SPECIALG_210	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43106.1	001974	Cluster1506_1clades	72	R1080702_097	Cyanophage S-RIM32	GCA_001754165.1
AMO43333.1	001974	Cluster1506_1clades	179	W270710_089	Cyanophage S-RIM44	GCA_002599145.1
AOO11566.1	001974	Cluster1506_1clades	179	ES420910_085	Cyanophage S-RIM44	GCA_002599165.1
AOO11805.1	001974	Cluster1506_1clades	179	Np050604_089	Cyanophage S-RIM44	GCA_002599185.1
AOO12031.1	001974	Cluster1506_1clades	179	Np200711_085	Cyanophage S-RIM44	GCA_002599205.1
AOO12267.1	001974	Cluster1506_1clades	179	Np420711_085	Cyanophage S-RIM44	GCA_002599225.1
AOO12506.1	001974	Cluster1506_1clades	179	Sn080709_089	Cyanophage S-RIM44	GCA_002599245.1
AOO12732.1	001974	Cluster1506_1clades	179	Sn130910_085	Cyanophage S-RIM44	GCA_002599265.1
AOO12972.1	001974	Cluster1506_1clades	179	W2100709_090	Cyanophage S-RIM44	GCA_002599285.1
ADO99191.1	001974	Cluster1506_1clades	179	Syn1_090	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60268.1	001975	Cluster1507_1clades	179	Ea357_117	Erwinia phage Ea35-70	GCA_000914635.1
QBP07226.1	001975	Cluster1507_1clades	179	REBECCA_119	Erwinia phage Rebecca	GCA_004521635.1
AUG85906.1	001975	Cluster1507_1clades	179	BOSOLAPHORUS_119	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52221.1	001975	Cluster1507_1clades	179	DM_123	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86225.1	001975	Cluster1507_1clades	179	DESERTFOX_118	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86547.1	001975	Cluster1507_1clades	179	MADMEL_119	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86871.1	001975	Cluster1507_1clades	179	MORTIMER_122	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51899.1	001975	Cluster1507_1clades	179	RAY_118	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51583.1	001975	Cluster1507_1clades	179	SIMMY50_121	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64930.1	001975	Cluster1507_1clades	179	SPECIALG_120	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AUE22815.1	001976	Cluster1508_1clades	172	Ah1_00297	Aeromonas phage Ah1	GCA_002957415.1
QAX98528.1	001976	Cluster1508_1clades	169	ASfcp2_192	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98529.1	001976	Cluster1508_1clades	169	ASfcp2_193	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98530.1	001976	Cluster1508_1clades	175	ASfcp2_194	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52991.1	001976	Cluster1508_1clades	169	PX29p272	Aeromonas phage PX29	GCA_000920195.1
ADQ52992.1	001976	Cluster1508_1clades	171	PX29p273	Aeromonas phage PX29	GCA_000920195.1
ADQ52993.1	001976	Cluster1508_1clades	175	PX29p274	Aeromonas phage PX29	GCA_000920195.1
ADM79916.1	001976	Cluster1508_1clades	164	phiAS5_ORF0073	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17943.1	001976	Cluster1508_1clades	178	Aeh1ORF278c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17944.1	001976	Cluster1508_1clades	169	Aeh1ORF279c	Aeromonas virus Aeh1	GCA_000843245.1
AMR59829.1	001977	HDGYP	176	SEGD1_182	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96645.1	001977	HDGYP	176	G173_gp100	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48211.1	001977	HDGYP	176	ASESINO_198	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48482.1	001977	HDGYP	178	CAITLIN_187	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48761.1	001977	HDGYP	178	CHRISDB_199	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50622.1	001977	HDGYP	176	STRATTON_197	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86019.1	001977	HDGYP	94	ACEC001_1780	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20874.1	001977	HDGYP	176	-	Salmonella phage JN03	GCA_014319805.1
AWN09159.1	001977	HDGYP	175	MLDJOKPK_00263	Salmonella phage SPAsTU	GCA_003183805.1
AEP84011.1	001977	HDGYP	175	SPN3US_0178	Salmonella phage SPN3US	GCA_001042275.1
ARB13830.1	001978	Cluster1510_1clades	177	Ccr10_gp300	Caulobacter phage Ccr10	GCA_002619445.1
ARB14175.1	001978	Cluster1510_1clades	177	Ccr2_gp299	Caulobacter phage Ccr2	GCA_002619465.1
ARB14869.1	001978	Cluster1510_1clades	177	Ccr29_gp313	Caulobacter phage Ccr29	GCA_002619485.1
ARB15207.1	001978	Cluster1510_1clades	177	Ccr32_gp289	Caulobacter phage Ccr32	GCA_002619505.1
ARB15541.1	001978	Cluster1510_1clades	177	Ccr34_gp299	Caulobacter phage Ccr34	GCA_002619525.1
ARB14516.1	001978	Cluster1510_1clades	177	Ccr5_gp296	Caulobacter phage Ccr5	GCA_002619545.1
AFU87827.1	001978	Cluster1510_1clades	177	CcrKarma_gp310	Caulobacter virus Karma	GCA_000901575.1
AFU87474.1	001978	Cluster1510_1clades	177	CcrMagneto_gp304	Caulobacter virus Magneto	GCA_000903095.1
AFU88619.1	001978	Cluster1510_1clades	177	CcrSwift_gp301	Caulobacter virus Swift	GCA_000899655.1
AFU87126.1	001978	Cluster1510_1clades	177	CbK_gp294	Caulobacter virus phiCbK	GCA_000900535.1
AMO43111.1	001979	Cluster1511_1clades	176	R1080702_102	Cyanophage S-RIM32	GCA_001754165.1
AMO43338.1	001979	Cluster1511_1clades	176	W270710_094	Cyanophage S-RIM44	GCA_002599145.1
AOO11571.1	001979	Cluster1511_1clades	176	ES420910_090	Cyanophage S-RIM44	GCA_002599165.1
AOO11810.1	001979	Cluster1511_1clades	176	Np050604_094	Cyanophage S-RIM44	GCA_002599185.1
AOO12036.1	001979	Cluster1511_1clades	176	Np200711_090	Cyanophage S-RIM44	GCA_002599205.1
AOO12272.1	001979	Cluster1511_1clades	176	Np420711_090	Cyanophage S-RIM44	GCA_002599225.1
AOO12511.1	001979	Cluster1511_1clades	176	Sn080709_094	Cyanophage S-RIM44	GCA_002599245.1
AOO12737.1	001979	Cluster1511_1clades	176	Sn130910_090	Cyanophage S-RIM44	GCA_002599265.1
AOO12977.1	001979	Cluster1511_1clades	176	W2100709_095	Cyanophage S-RIM44	GCA_002599285.1
ADO99196.1	001979	Cluster1511_1clades	176	Syn1_095	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60225.1	001980	Cluster1512_1clades	176	Ea357_074	Erwinia phage Ea35-70	GCA_000914635.1
QBP07184.1	001980	Cluster1512_1clades	176	REBECCA_76	Erwinia phage Rebecca	GCA_004521635.1
AUG85863.1	001980	Cluster1512_1clades	176	BOSOLAPHORUS_75	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52175.1	001980	Cluster1512_1clades	176	DM_77	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86182.1	001980	Cluster1512_1clades	176	DESERTFOX_74	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86504.1	001980	Cluster1512_1clades	176	MADMEL_76	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86825.1	001980	Cluster1512_1clades	176	MORTIMER_76	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51855.1	001980	Cluster1512_1clades	176	RAY_74	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51539.1	001980	Cluster1512_1clades	176	SIMMY50_77	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64887.1	001980	Cluster1512_1clades	176	SPECIALG_77	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60226.1	001981	Cluster1513_1clades	176	Ea357_075	Erwinia phage Ea35-70	GCA_000914635.1
QBP07185.1	001981	Cluster1513_1clades	176	REBECCA_77	Erwinia phage Rebecca	GCA_004521635.1
AUG85864.1	001981	Cluster1513_1clades	176	BOSOLAPHORUS_76	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52176.1	001981	Cluster1513_1clades	176	DM_78	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86183.1	001981	Cluster1513_1clades	176	DESERTFOX_75	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86505.1	001981	Cluster1513_1clades	176	MADMEL_77	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86826.1	001981	Cluster1513_1clades	176	MORTIMER_77	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51856.1	001981	Cluster1513_1clades	176	RAY_75	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51540.1	001981	Cluster1513_1clades	176	SIMMY50_78	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64888.1	001981	Cluster1513_1clades	176	SPECIALG_78	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60382.1	001982	Cluster1514_1clades	176	Ea357_229	Erwinia phage Ea35-70	GCA_000914635.1
QBP07339.1	001982	Cluster1514_1clades	176	REBECCA_234	Erwinia phage Rebecca	GCA_004521635.1
AUG86021.1	001982	Cluster1514_1clades	176	BOSOLAPHORUS_235	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52338.1	001982	Cluster1514_1clades	176	DM_238	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86340.1	001982	Cluster1514_1clades	176	DESERTFOX_233	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86664.1	001982	Cluster1514_1clades	176	MADMEL_236	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86985.1	001982	Cluster1514_1clades	176	MORTIMER_237	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52012.1	001982	Cluster1514_1clades	176	RAY_232	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51696.1	001982	Cluster1514_1clades	176	SIMMY50_237	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANJ65047.1	001982	Cluster1514_1clades	176	SPECIALG_236	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63121.1	001983	Cluster1515_1clades	165	201phi2-1p295	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44997.1	001983	Cluster1515_1clades	162	KTN4_239	Pseudomonas phage KTN4	GCA_002607225.1
QBX32382.1	001983	Cluster1515_1clades	162	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76922.1	001983	Cluster1515_1clades	165	PHABIO_291	Pseudomonas phage Phabio	GCA_002624965.1
AEH03653.1	001983	Cluster1515_1clades	173	230	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02789.1	001983	Cluster1515_1clades	160	PSA21_263	Pseudomonas phage Psa21	GCA_004340405.1
ATN94717.1	001983	Cluster1515_1clades	162	SL2_140	Pseudomonas phage SL2	GCA_002956015.1
QJB22875.1	001983	Cluster1515_1clades	162	fnug_232	Pseudomonas phage fnug	GCA_012837215.1
QEM41955.1	001983	Cluster1515_1clades	162	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83099.1	001983	Cluster1515_1clades	162	PHIKZ198	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60243.1	001984	Cluster1516_1clades	173	Ea357_092	Erwinia phage Ea35-70	GCA_000914635.1
QBP07201.1	001984	Cluster1516_1clades	173	REBECCA_94	Erwinia phage Rebecca	GCA_004521635.1
AUG85880.1	001984	Cluster1516_1clades	173	BOSOLAPHORUS_93	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52195.1	001984	Cluster1516_1clades	173	DM_97	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86199.1	001984	Cluster1516_1clades	173	DESERTFOX_92	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86522.1	001984	Cluster1516_1clades	173	MADMEL_94	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86845.1	001984	Cluster1516_1clades	173	MORTIMER_96	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51873.1	001984	Cluster1516_1clades	173	RAY_92	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51557.1	001984	Cluster1516_1clades	173	SIMMY50_95	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64905.1	001984	Cluster1516_1clades	173	SPECIALG_95	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AFC21705.1	001985	Caudo_TAP	137	GAP32_255	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT14498.1	001985	Caudo_TAP	171	PBI_121Q_608	Escherichia phage 121Q	GCA_000926855.1
QAY00451.1	001985	Caudo_TAP	172	Ecwhy1_171	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35194.1	001985	Caudo_TAP	171	ACQ29_gp514	Escherichia phage PBECO4	GCA_001041035.1
BBM62170.1	001985	Caudo_TAP	171	EO157G_5810	Escherichia phage SP27	GCA_008033345.1
AXC36765.1	001985	Caudo_TAP	171	-	Escherichia phage UB	GCA_003341455.1
QBO61805.1	001985	Caudo_TAP	171	G17_00316	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13849.1	001985	Caudo_TAP	171	vBEcoMphAPEC6_gp220c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80482.1	001985	Caudo_TAP	171	PSLUR01_00505	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43825.1	001985	Caudo_TAP	137	CBB_261	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AHI60404.1	001986	Cluster1518_1clades	169	Ea357_250	Erwinia phage Ea35-70	GCA_000914635.1
QBP07360.1	001986	Cluster1518_1clades	169	REBECCA_255	Erwinia phage Rebecca	GCA_004521635.1
AUG86042.1	001986	Cluster1518_1clades	169	BOSOLAPHORUS_256	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52359.1	001986	Cluster1518_1clades	169	DM_260	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86362.1	001986	Cluster1518_1clades	169	DESERTFOX_255	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86684.1	001986	Cluster1518_1clades	169	MADMEL_257	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87008.1	001986	Cluster1518_1clades	169	MORTIMER_260	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52034.1	001986	Cluster1518_1clades	169	RAY_254	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51717.1	001986	Cluster1518_1clades	169	SIMMY50_259	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65069.1	001986	Cluster1518_1clades	169	SPECIALG_258	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63061.1	001987	Cluster1519_1clades	160	201phi2-1p232	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44942.1	001987	Cluster1519_1clades	168	KTN4_184	Pseudomonas phage KTN4	GCA_002607225.1
QBX32329.1	001987	Cluster1519_1clades	158	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76851.1	001987	Cluster1519_1clades	155	PHABIO_220	Pseudomonas phage Phabio	GCA_002624965.1
AEH03594.1	001987	Cluster1519_1clades	160	171	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02730.1	001987	Cluster1519_1clades	160	PSA21_204	Pseudomonas phage Psa21	GCA_004340405.1
ATN94772.1	001987	Cluster1519_1clades	168	SL2_195	Pseudomonas phage SL2	GCA_002956015.1
QJB22820.1	001987	Cluster1519_1clades	168	fnug_177	Pseudomonas phage fnug	GCA_012837215.1
QEM41902.1	001987	Cluster1519_1clades	158	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83049.1	001987	Cluster1519_1clades	168	PHIKZ148	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14082.1	001988	Cluster1520_1clades	146	PBI_121Q_192	Escherichia phage 121Q	GCA_000926855.1
QAY00841.1	001988	Cluster1520_1clades	146	Ecwhy1_569	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35012.1	001988	Cluster1520_1clades	146	ACQ29_gp332	Escherichia phage PBECO4	GCA_001041035.1
BBM61765.1	001988	Cluster1520_1clades	146	EO157G_1760	Escherichia phage SP27	GCA_008033345.1
AXC36590.1	001988	Cluster1520_1clades	146	-	Escherichia phage UB	GCA_003341455.1
QBO61617.1	001988	Cluster1520_1clades	146	G17_00121	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13675.1	001988	Cluster1520_1clades	146	vBEcoMphAPEC6_gp045c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80076.1	001988	Cluster1520_1clades	146	PSLUR01_00099	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44543.1	001988	Cluster1520_1clades	135	RaK2_00270	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
CCE26247.1	001988	Cluster1520_1clades	166	g224	Yersinia phage phiR1-37	GCA_000895615.1
AHI60187.1	001989	Cluster1521_1clades	165	Ea357_037	Erwinia phage Ea35-70	GCA_000914635.1
QBP07145.1	001989	Cluster1521_1clades	165	REBECCA_37	Erwinia phage Rebecca	GCA_004521635.1
AUG85825.1	001989	Cluster1521_1clades	165	BOSOLAPHORUS_37	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52136.1	001989	Cluster1521_1clades	165	DM_38	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86145.1	001989	Cluster1521_1clades	165	DESERTFOX_37	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86465.1	001989	Cluster1521_1clades	165	MADMEL_37	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86786.1	001989	Cluster1521_1clades	165	MORTIMER_37	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51818.1	001989	Cluster1521_1clades	165	RAY_37	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51500.1	001989	Cluster1521_1clades	165	SIMMY50_38	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64847.1	001989	Cluster1521_1clades	165	SPECIALG_37	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60464.1	001990	Cluster1522_1clades	165	Ea357_310	Erwinia phage Ea35-70	GCA_000914635.1
QBP07421.1	001990	Cluster1522_1clades	165	REBECCA_316	Erwinia phage Rebecca	GCA_004521635.1
AUG86103.1	001990	Cluster1522_1clades	165	BOSOLAPHORUS_317	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52419.2	001990	Cluster1522_1clades	165	DM_320	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86423.1	001990	Cluster1522_1clades	165	DESERTFOX_316	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86744.1	001990	Cluster1522_1clades	165	MADMEL_317	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87069.1	001990	Cluster1522_1clades	165	MORTIMER_321	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52094.1	001990	Cluster1522_1clades	165	RAY_314	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51777.1	001990	Cluster1522_1clades	165	SIMMY50_319	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65129.2	001990	Cluster1522_1clades	165	SPECIALG_318	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60251.1	001991	Cluster1523_1clades	132	Ea357_100	Erwinia phage Ea35-70	GCA_000914635.1
QBP07209.1	001991	Cluster1523_1clades	160	REBECCA_102	Erwinia phage Rebecca	GCA_004521635.1
AUG85888.1	001991	Cluster1523_1clades	160	BOSOLAPHORUS_101	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52203.1	001991	Cluster1523_1clades	160	DM_105	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86207.1	001991	Cluster1523_1clades	160	DESERTFOX_100	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86530.1	001991	Cluster1523_1clades	132	MADMEL_102	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86853.1	001991	Cluster1523_1clades	160	MORTIMER_104	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51881.2	001991	Cluster1523_1clades	160	RAY_100	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51565.2	001991	Cluster1523_1clades	160	SIMMY50_103	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64913.1	001991	Cluster1523_1clades	160	SPECIALG_103	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60183.1	001992	Cluster1524_1clades	159	Ea357_033	Erwinia phage Ea35-70	GCA_000914635.1
QBP07141.1	001992	Cluster1524_1clades	159	REBECCA_33	Erwinia phage Rebecca	GCA_004521635.1
AUG85821.1	001992	Cluster1524_1clades	159	BOSOLAPHORUS_33	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52132.1	001992	Cluster1524_1clades	159	DM_34	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86141.1	001992	Cluster1524_1clades	159	DESERTFOX_33	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86461.1	001992	Cluster1524_1clades	159	MADMEL_33	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86782.1	001992	Cluster1524_1clades	159	MORTIMER_33	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51814.1	001992	Cluster1524_1clades	159	RAY_33	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51496.1	001992	Cluster1524_1clades	159	SIMMY50_34	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64843.1	001992	Cluster1524_1clades	159	SPECIALG_33	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QDB70347.1	001993	Cluster1525_1clades	152	CF8_0178	Aeromonas phage CF8	GCA_006384595.2
QDJ97344.1	001993	Cluster1525_1clades	159	D6_0185	Aeromonas phage D6	GCA_007051205.2
QDH47173.1	001993	Cluster1525_1clades	159	LAh10_104	Aeromonas phage LAh10	GCA_006863975.1
QDJ96696.1	001993	Cluster1525_1clades	149	PS1_0185	Aeromonas phage PS1	GCA_007051165.2
QDJ96697.1	001993	Cluster1525_1clades	139	PS1_0186	Aeromonas phage PS1	GCA_007051165.2
QFR59329.1	001993	Cluster1525_1clades	149	PS2_0187	Aeromonas phage PS2	GCA_009388305.2
QFR59330.1	001993	Cluster1525_1clades	139	PS2_0188	Aeromonas phage PS2	GCA_009388305.2
QBZ70730.1	001993	Cluster1525_1clades	155	pETSU_149	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72041.1	001993	Cluster1525_1clades	152	N1M2_178	Klebsiella phage N1M2	GCA_010092605.1
AEV89662.1	001993	Cluster1525_1clades	152	OBP_225	Pseudomonas phage OBP	GCA_000896635.1
AHI60339.1	001994	Cluster1526_1clades	157	Ea357_187	Erwinia phage Ea35-70	GCA_000914635.1
QBP07298.1	001994	Cluster1526_1clades	157	REBECCA_191	Erwinia phage Rebecca	GCA_004521635.1
AUG85978.1	001994	Cluster1526_1clades	157	BOSOLAPHORUS_191	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52293.1	001994	Cluster1526_1clades	157	DM_195	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86297.1	001994	Cluster1526_1clades	157	DESERTFOX_190	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86619.1	001994	Cluster1526_1clades	157	MADMEL_191	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86943.1	001994	Cluster1526_1clades	157	MORTIMER_194	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51970.1	001994	Cluster1526_1clades	157	RAY_189	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51654.1	001994	Cluster1526_1clades	157	SIMMY50_192	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65001.1	001994	Cluster1526_1clades	157	SPECIALG_192	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT14267.1	001995	Cluster1527_1clades	149	PBI_121Q_377	Escherichia phage 121Q	GCA_000926855.1
QAY00670.1	001995	Cluster1527_1clades	148	Ecwhy1_395	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00671.1	001995	Cluster1527_1clades	149	Ecwhy1_396	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34865.1	001995	Cluster1527_1clades	149	ACQ29_gp185	Escherichia phage PBECO4	GCA_001041035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBM61941.1	001995	Cluster1527_1clades	157	EO157G_3520	Escherichia phage SP27	GCA_008033345.1
BBM61942.1	001995	Cluster1527_1clades	148	EO157G_3530	Escherichia phage SP27	GCA_008033345.1
AXC36974.1	001995	Cluster1527_1clades	149	-	Escherichia phage UB	GCA_003341455.1
QBO62037.1	001995	Cluster1527_1clades	149	G17_00548	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14058.1	001995	Cluster1527_1clades	149	vBEcoMphAPEC6_gp435c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80256.1	001995	Cluster1527_1clades	149	PSLUR01_00279	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AHI60229.1	001996	Cluster1528_1clades	156	Ea357_078	Erwinia phage Ea35-70	GCA_000914635.1
QBP07188.1	001996	Cluster1528_1clades	156	REBECCA_80	Erwinia phage Rebecca	GCA_004521635.1
AUG85867.1	001996	Cluster1528_1clades	156	BOSOLAPHORUS_79	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52179.1	001996	Cluster1528_1clades	156	DM_81	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86186.1	001996	Cluster1528_1clades	156	DESERTFOX_78	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86508.1	001996	Cluster1528_1clades	156	MADMEL_80	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86829.1	001996	Cluster1528_1clades	156	MORTIMER_80	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51859.1	001996	Cluster1528_1clades	156	RAY_78	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51543.1	001996	Cluster1528_1clades	156	SIMMY50_81	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64891.1	001996	Cluster1528_1clades	156	SPECIALG_81	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60293.1	001997	Cluster1529_1clades	156	Ea357_142	Erwinia phage Ea35-70	GCA_000914635.1
QBP07251.1	001997	Cluster1529_1clades	156	REBECCA_144	Erwinia phage Rebecca	GCA_004521635.1
AUG85931.1	001997	Cluster1529_1clades	156	BOSOLAPHORUS_144	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52246.1	001997	Cluster1529_1clades	156	DM_148	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86250.1	001997	Cluster1529_1clades	156	DESERTFOX_143	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86572.1	001997	Cluster1529_1clades	156	MADMEL_144	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86896.1	001997	Cluster1529_1clades	156	MORTIMER_147	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51924.1	001997	Cluster1529_1clades	156	RAY_143	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51608.1	001997	Cluster1529_1clades	156	SIMMY50_146	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64955.1	001997	Cluster1529_1clades	156	SPECIALG_145	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AXQ69230.1	001998	Cluster1530_1clades	155	CcrBL9_gp206	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69784.1	001998	Cluster1530_1clades	154	CcrSC_gp202	Caulobacter phage CcrSC	GCA_003443315.1
AIF27784.1	001998	Cluster1530_1clades	127	SmphiM12_500	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13112.1	001998	Cluster1530_1clades	127	PHIM19_207	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12752.1	001998	Cluster1530_1clades	127	PHIM7_207	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13482.1	001998	Cluster1530_1clades	127	PHIN3_219	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81318.1	001998	Cluster1530_1clades	112	SEA_JUSTBECAUSE_153	Streptomyces phage JustBecause	GCA_003613775.1
QJD53721.1	001998	Cluster1530_1clades	112	SEA_KELA_151	Streptomyces phage Kela	GCA_012934305.1
QBZ72049.1	001998	Cluster1530_1clades	115	SEA_KRADAL_153	Streptomyces phage Kradal	GCA_004799925.1
AXH66312.1	001998	Cluster1530_1clades	115	SEA_SATIS_153	Streptomyces phage Satis	GCA_003366315.1
AHI60355.1	001999	Cluster1531_1clades	153	Ea357_202	Erwinia phage Ea35-70	GCA_000914635.1
QBP07312.1	001999	Cluster1531_1clades	153	REBECCA_207	Erwinia phage Rebecca	GCA_004521635.1
AUG85993.1	001999	Cluster1531_1clades	153	BOSOLAPHORUS_207	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52310.1	001999	Cluster1531_1clades	153	DM_210	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86312.1	001999	Cluster1531_1clades	153	DESERTFOX_205	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86635.1	001999	Cluster1531_1clades	153	MADMEL_207	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86958.1	001999	Cluster1531_1clades	153	MORTIMER_210	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51985.1	001999	Cluster1531_1clades	153	RAY_205	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51669.1	001999	Cluster1531_1clades	153	SIMMY50_210	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65019.1	001999	Cluster1531_1clades	153	SPECIALG_208	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60410.1	002000	Cluster1534_1clades	151	Ea357_256	Erwinia phage Ea35-70	GCA_000914635.1
QBP07367.1	002000	Cluster1534_1clades	151	REBECCA_262	Erwinia phage Rebecca	GCA_004521635.1
AUG86049.1	002000	Cluster1534_1clades	151	BOSOLAPHORUS_263	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52365.1	002000	Cluster1534_1clades	151	DM_266	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86369.1	002000	Cluster1534_1clades	151	DESERTFOX_262	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86690.1	002000	Cluster1534_1clades	151	MADMEL_263	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87015.1	002000	Cluster1534_1clades	151	MORTIMER_267	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52040.1	002000	Cluster1534_1clades	151	RAY_260	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51723.1	002000	Cluster1534_1clades	151	SIMMY50_265	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65075.1	002000	Cluster1534_1clades	151	SPECIALG_264	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13811.1	002001	Cluster1535_1clades	150	Ccr10_gp281	Caulobacter phage Ccr10	GCA_002619445.1
ARB14156.1	002001	Cluster1535_1clades	150	Ccr2_gp280	Caulobacter phage Ccr2	GCA_002619465.1
ARB14850.1	002001	Cluster1535_1clades	150	Ccr29_gp294	Caulobacter phage Ccr29	GCA_002619485.1
ARB15188.1	002001	Cluster1535_1clades	150	Ccr32_gp270	Caulobacter phage Ccr32	GCA_002619505.1
ARB15522.1	002001	Cluster1535_1clades	150	Ccr34_gp280	Caulobacter phage Ccr34	GCA_002619525.1
ARB14498.1	002001	Cluster1535_1clades	150	Ccr5_gp278	Caulobacter phage Ccr5	GCA_002619545.1
AFU87808.1	002001	Cluster1535_1clades	127	CcrKarma_gp291	Caulobacter virus Karma	GCA_000901575.1
AFU87454.1	002001	Cluster1535_1clades	150	CcrMagneto_gp284	Caulobacter virus Magneto	GCA_000903095.1
AFU88600.1	002001	Cluster1535_1clades	150	CcrSwift_gp282	Caulobacter virus Swift	GCA_000899655.1
AFU87107.1	002001	Cluster1535_1clades	150	CbK_gp275	Caulobacter virus phiCbK	GCA_000900535.1
AHI60189.1	002002	SspB	150	Ea357_039	Erwinia phage Ea35-70	GCA_000914635.1
QBP07147.1	002002	SspB	150	REBECCA_39	Erwinia phage Rebecca	GCA_004521635.1
AUG85827.1	002002	SspB	150	BOSOLAPHORUS_39	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52138.1	002002	SspB	150	DM_40	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86147.1	002002	SspB	150	DESERTFOX_39	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86467.1	002002	SspB	150	MADMEL_39	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86788.1	002002	SspB	150	MORTIMER_39	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51820.1	002002	SspB	150	RAY_39	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51502.1	002002	SspB	150	SIMMY50_40	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64849.1	002002	SspB	150	SPECIALG_39	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60423.1	002003	DUF2829	150	Ea357_269	Erwinia phage Ea35-70	GCA_000914635.1
QBP07380.1	002003	DUF2829	150	REBECCA_275	Erwinia phage Rebecca	GCA_004521635.1
AUG86062.1	002003	DUF2829	150	BOSOLAPHORUS_276	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52378.1	002003	DUF2829	150	DM_279	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86382.1	002003	DUF2829	150	DESERTFOX_275	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86703.1	002003	DUF2829	150	MADMEL_276	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87028.1	002003	DUF2829	150	MORTIMER_280	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52053.1	002003	DUF2829	150	RAY_273	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51736.1	002003	DUF2829	150	SIMMY50_278	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65088.1	002003	DUF2829	150	SPECIALG_277	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60181.1	002004	Cluster1538_1clades	148	Ea357_031	Erwinia phage Ea35-70	GCA_000914635.1
QBP07139.1	002004	Cluster1538_1clades	148	REBECCA_31	Erwinia phage Rebecca	GCA_004521635.1
AUG85819.1	002004	Cluster1538_1clades	148	BOSOLAPHORUS_31	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52130.1	002004	Cluster1538_1clades	148	DM_32	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86139.1	002004	Cluster1538_1clades	148	DESERTFOX_31	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86459.1	002004	Cluster1538_1clades	148	MADMEL_31	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86780.1	002004	Cluster1538_1clades	148	MORTIMER_31	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51812.1	002004	Cluster1538_1clades	148	RAY_31	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51494.1	002004	Cluster1538_1clades	148	SIMMY50_32	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64841.1	002004	Cluster1538_1clades	148	SPECIALG_31	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60208.1	002005	Cluster1539_1clades	148	Ea357_058	Erwinia phage Ea35-70	GCA_000914635.1
QBP07167.1	002005	Cluster1539_1clades	148	REBECCA_59	Erwinia phage Rebecca	GCA_004521635.1
AUG85847.1	002005	Cluster1539_1clades	148	BOSOLAPHORUS_59	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52159.1	002005	Cluster1539_1clades	148	DM_61	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86166.1	002005	Cluster1539_1clades	148	DESERTFOX_58	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86487.1	002005	Cluster1539_1clades	148	MADMEL_59	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86808.1	002005	Cluster1539_1clades	148	MORTIMER_59	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51839.1	002005	Cluster1539_1clades	148	RAY_58	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51522.1	002005	Cluster1539_1clades	148	SIMMY50_60	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64870.1	002005	Cluster1539_1clades	148	SPECIALG_60	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60415.1	002006	Cluster1540_1clades	125	Ea357_261	Erwinia phage Ea35-70	GCA_000914635.1
QBP07372.1	002006	Cluster1540_1clades	148	REBECCA_267	Erwinia phage Rebecca	GCA_004521635.1
AUG86054.1	002006	Cluster1540_1clades	125	BOSOLAPHORUS_268	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52370.2	002006	Cluster1540_1clades	125	DM_271	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86374.1	002006	Cluster1540_1clades	125	DESERTFOX_267	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86695.1	002006	Cluster1540_1clades	125	MADMEL_268	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87020.1	002006	Cluster1540_1clades	125	MORTIMER_272	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52045.1	002006	Cluster1540_1clades	125	RAY_265	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51728.1	002006	Cluster1540_1clades	125	SIMMY50_270	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65080.2	002006	Cluster1540_1clades	125	SPECIALG_269	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63040.1	002007	Cluster1541_1clades	143	201phi2-1p211	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44919.1	002007	Cluster1541_1clades	147	KTN4_161	Pseudomonas phage KTN4	GCA_002607225.1
ARV77298.1	002007	Cluster1541_1clades	143	NOXIFER_129	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32306.1	002007	Cluster1541_1clades	142	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76829.1	002007	Cluster1541_1clades	144	PHABIO_198	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02705.1	002007	Cluster1541_1clades	145	PSA21_179	Pseudomonas phage Psa21	GCA_004340405.1
ATN94795.1	002007	Cluster1541_1clades	147	SL2_218	Pseudomonas phage SL2	GCA_002956015.1
QJB22797.1	002007	Cluster1541_1clades	147	fnug_154	Pseudomonas phage fnug	GCA_012837215.1
QEM41879.1	002007	Cluster1541_1clades	142	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAL83027.1	002007	Cluster1541_1clades	147	PHIKZ126	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63087.1	002008	Cluster1542_1clades	125	201phi2-1p259	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44970.1	002008	Cluster1542_1clades	146	KTN4_212	Pseudomonas phage KTN4	GCA_002607225.1
QBX32360.1	002008	Cluster1542_1clades	125	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76878.1	002008	Cluster1542_1clades	131	PHABIO_247	Pseudomonas phage Phabio	GCA_002624965.1
AEH03624.1	002008	Cluster1542_1clades	125	201	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02760.1	002008	Cluster1542_1clades	127	PSA21_234	Pseudomonas phage Psa21	GCA_004340405.1
ATN94744.1	002008	Cluster1542_1clades	146	SL2_167	Pseudomonas phage SL2	GCA_002956015.1
QJB22848.1	002008	Cluster1542_1clades	146	fnug_205	Pseudomonas phage fnug	GCA_012837215.1
QEM41934.1	002008	Cluster1542_1clades	125	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83073.1	002008	Cluster1542_1clades	146	PHIKZ172	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60335.1	002009	Cluster1543_1clades	146	Ea357_183	Erwinia phage Ea35-70	GCA_000914635.1
QBP07294.1	002009	Cluster1543_1clades	146	REBECCA_187	Erwinia phage Rebecca	GCA_004521635.1
AUG85974.1	002009	Cluster1543_1clades	146	BOSOLAPHORUS_187	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52289.1	002009	Cluster1543_1clades	146	DM_191	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86293.1	002009	Cluster1543_1clades	146	DESERTFOX_186	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86615.1	002009	Cluster1543_1clades	146	MADMEL_187	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86939.1	002009	Cluster1543_1clades	146	MORTIMER_190	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51966.1	002009	Cluster1543_1clades	146	RAY_185	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51650.1	002009	Cluster1543_1clades	146	SIMMY50_188	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64997.1	002009	Cluster1543_1clades	146	SPECIALG_188	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60155.1	002010	Cluster1544_1clades	144	Ea357_005	Erwinia phage Ea35-70	GCA_000914635.1
QBP07113.1	002010	Cluster1544_1clades	146	REBECCA_5	Erwinia phage Rebecca	GCA_004521635.1
AUG85793.1	002010	Cluster1544_1clades	146	BOSOLAPHORUS_5	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52103.1	002010	Cluster1544_1clades	146	DM_5	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86113.1	002010	Cluster1544_1clades	146	DESERTFOX_5	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86433.1	002010	Cluster1544_1clades	146	MADMEL_5	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86754.1	002010	Cluster1544_1clades	146	MORTIMER_5	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51786.2	002010	Cluster1544_1clades	146	RAY_5	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51467.2	002010	Cluster1544_1clades	146	SIMMY50_5	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64815.1	002010	Cluster1544_1clades	146	SPECIALG_5	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63163.1	002011	Cluster1545_1clades	142	201phi2-1p338	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45027.1	002011	Cluster1545_1clades	137	KTN4_269	Pseudomonas phage KTN4	GCA_002607225.1
QBX32419.1	002011	Cluster1545_1clades	141	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76967.1	002011	Cluster1545_1clades	143	PHABIO_336	Pseudomonas phage Phabio	GCA_002624965.1
AEH03688.1	002011	Cluster1545_1clades	139	265	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02820.1	002011	Cluster1545_1clades	138	PSA21_294	Pseudomonas phage Psa21	GCA_004340405.1
ATN94687.1	002011	Cluster1545_1clades	137	SL2_110	Pseudomonas phage SL2	GCA_002956015.1
QJB22904.1	002011	Cluster1545_1clades	137	fnug_261	Pseudomonas phage fnug	GCA_012837215.1
QEM41990.1	002011	Cluster1545_1clades	141	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83125.1	002011	Cluster1545_1clades	144	PHIKZ224	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60202.1	002012	Cluster1546_1clades	143	Ea357_052	Erwinia phage Ea35-70	GCA_000914635.1
QBP07161.1	002012	Cluster1546_1clades	143	REBECCA_53	Erwinia phage Rebecca	GCA_004521635.1
AUG85841.1	002012	Cluster1546_1clades	143	BOSOLAPHORUS_53	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52153.1	002012	Cluster1546_1clades	143	DM_55	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86160.1	002012	Cluster1546_1clades	143	DESERTFOX_52	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86481.1	002012	Cluster1546_1clades	143	MADMEL_53	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86802.1	002012	Cluster1546_1clades	143	MORTIMER_53	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51833.1	002012	Cluster1546_1clades	143	RAY_52	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51516.1	002012	Cluster1546_1clades	143	SIMMY50_54	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64864.1	002012	Cluster1546_1clades	143	SPECIALG_54	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60341.1	002013	Cluster1547_1clades	141	Ea357_189	Erwinia phage Ea35-70	GCA_000914635.1
QBP07300.1	002013	Cluster1547_1clades	141	REBECCA_193	Erwinia phage Rebecca	GCA_004521635.1
AUG85980.1	002013	Cluster1547_1clades	141	BOSOLAPHORUS_193	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52295.1	002013	Cluster1547_1clades	141	DM_197	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86299.1	002013	Cluster1547_1clades	141	DESERTFOX_192	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86621.1	002013	Cluster1547_1clades	141	MADMEL_193	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86945.1	002013	Cluster1547_1clades	141	MORTIMER_196	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51972.1	002013	Cluster1547_1clades	141	RAY_191	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51656.1	002013	Cluster1547_1clades	141	SIMMY50_194	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65003.1	002013	Cluster1547_1clades	141	SPECIALG_194	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60209.1	002014	Cluster1548_1clades	139	Ea357_059	Erwinia phage Ea35-70	GCA_000914635.1
QBP07168.1	002014	Cluster1548_1clades	139	REBECCA_60	Erwinia phage Rebecca	GCA_004521635.1
AUG85848.1	002014	Cluster1548_1clades	139	BOSOLAPHORUS_60	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52160.1	002014	Cluster1548_1clades	139	DM_62	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86167.1	002014	Cluster1548_1clades	139	DESERTFOX_59	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86488.1	002014	Cluster1548_1clades	139	MADMEL_60	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86809.1	002014	Cluster1548_1clades	139	MORTIMER_60	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51840.1	002014	Cluster1548_1clades	139	RAY_59	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51523.1	002014	Cluster1548_1clades	139	SIMMY50_61	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64871.1	002014	Cluster1548_1clades	139	SPECIALG_61	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60282.1	002015	Cluster1549_1clades	137	Ea357_131	Erwinia phage Ea35-70	GCA_000914635.1
QBP07240.1	002015	Cluster1549_1clades	137	REBECCA_133	Erwinia phage Rebecca	GCA_004521635.1
AUG85920.1	002015	Cluster1549_1clades	137	BOSOLAPHORUS_133	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52235.1	002015	Cluster1549_1clades	137	DM_137	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86239.1	002015	Cluster1549_1clades	137	DESERTFOX_132	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86561.1	002015	Cluster1549_1clades	137	MADMEL_133	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86885.1	002015	Cluster1549_1clades	137	MORTIMER_136	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51913.1	002015	Cluster1549_1clades	137	RAY_132	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51597.1	002015	Cluster1549_1clades	137	SIMMY50_135	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64944.1	002015	Cluster1549_1clades	137	SPECIALG_134	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60178.1	002016	Cluster1550_1clades	136	Ea357_028	Erwinia phage Ea35-70	GCA_000914635.1
QBP07136.1	002016	Cluster1550_1clades	136	REBECCA_28	Erwinia phage Rebecca	GCA_004521635.1
AUG85816.1	002016	Cluster1550_1clades	136	BOSOLAPHORUS_28	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52126.1	002016	Cluster1550_1clades	136	DM_28	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86136.1	002016	Cluster1550_1clades	136	DESERTFOX_28	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86456.1	002016	Cluster1550_1clades	136	MADMEL_28	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86777.1	002016	Cluster1550_1clades	136	MORTIMER_28	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51809.1	002016	Cluster1550_1clades	136	RAY_28	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51491.1	002016	Cluster1550_1clades	136	SIMMY50_29	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64838.1	002016	Cluster1550_1clades	136	SPECIALG_28	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60201.1	002017	Cluster1551_1clades	136	Ea357_051	Erwinia phage Ea35-70	GCA_000914635.1
QBP07160.1	002017	Cluster1551_1clades	136	REBECCA_52	Erwinia phage Rebecca	GCA_004521635.1
AUG85840.1	002017	Cluster1551_1clades	136	BOSOLAPHORUS_52	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52152.1	002017	Cluster1551_1clades	136	DM_54	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86159.1	002017	Cluster1551_1clades	136	DESERTFOX_51	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86480.1	002017	Cluster1551_1clades	136	MADMEL_52	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86801.1	002017	Cluster1551_1clades	136	MORTIMER_52	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51832.1	002017	Cluster1551_1clades	136	RAY_51	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51515.1	002017	Cluster1551_1clades	136	SIMMY50_53	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64863.1	002017	Cluster1551_1clades	136	SPECIALG_53	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43073.1	002018	Cluster1552_1clades	136	R1080702_064	Cyanophage S-RIM32	GCA_001754165.1
AMO43301.1	002018	Cluster1552_1clades	76	W270710_057	Cyanophage S-RIM44	GCA_002599145.1
AOO11535.1	002018	Cluster1552_1clades	76	ES420910_054	Cyanophage S-RIM44	GCA_002599165.1
AOO11773.1	002018	Cluster1552_1clades	76	Np050604_057	Cyanophage S-RIM44	GCA_002599185.1
AOO12000.1	002018	Cluster1552_1clades	76	Np200711_054	Cyanophage S-RIM44	GCA_002599205.1
AOO12236.1	002018	Cluster1552_1clades	76	Np420711_054	Cyanophage S-RIM44	GCA_002599225.1
AOO12474.1	002018	Cluster1552_1clades	76	Sn080709_057	Cyanophage S-RIM44	GCA_002599245.1
AOO12701.1	002018	Cluster1552_1clades	76	Sn130910_054	Cyanophage S-RIM44	GCA_002599265.1
AOO12939.1	002018	Cluster1552_1clades	76	W2100709_057	Cyanophage S-RIM44	GCA_002599285.1
ADO99155.1	002018	Cluster1552_1clades	76	Syn1_054	Prochlorococcus phage Syn1	GCA_000892495.1
QGT54699.1	002019	Cluster1553_1clades	135	b23_0084	Synechococcus phage B23	GCA_009745195.1
QGT54700.1	002019	Cluster1553_1clades	126	b23_0085	Synechococcus phage B23	GCA_009745195.1
QGT54701.1	002019	Cluster1553_1clades	118	b23_0086	Synechococcus phage B23	GCA_009745195.1
QGT54703.1	002019	Cluster1553_1clades	136	b23_0088	Synechococcus phage B23	GCA_009745195.1
QGT54726.1	002019	Cluster1553_1clades	119	b23_0111	Synechococcus phage B23	GCA_009745195.1
QGT54329.1	002019	Cluster1553_1clades	135	b3_0085	Synechococcus phage B3	GCA_009745215.1
QGT54330.1	002019	Cluster1553_1clades	126	b3_0086	Synechococcus phage B3	GCA_009745215.1
QGT54331.1	002019	Cluster1553_1clades	118	b3_0087	Synechococcus phage B3	GCA_009745215.1
QGT54333.1	002019	Cluster1553_1clades	136	b3_0089	Synechococcus phage B3	GCA_009745215.1
QGT54356.1	002019	Cluster1553_1clades	119	b3_0112	Synechococcus phage B3	GCA_009745215.1
ABY63162.1	002020	Cluster1554_1clades	135	201phi2-1p337	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45026.1	002020	Cluster1554_1clades	132	KTN4_268	Pseudomonas phage KTN4	GCA_002607225.1
QBX32418.1	002020	Cluster1554_1clades	131	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76966.1	002020	Cluster1554_1clades	130	PHABIO_335	Pseudomonas phage Phabio	GCA_002624965.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEH03687.1	002020	Cluster1554_1clades	131	264	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02819.1	002020	Cluster1554_1clades	88	PSA21_293	Pseudomonas phage Psa21	GCA_004340405.1
ATN94688.1	002020	Cluster1554_1clades	132	SL2_111	Pseudomonas phage SL2	GCA_002956015.1
QJB22903.1	002020	Cluster1554_1clades	132	fnug_260	Pseudomonas phage fnug	GCA_012837215.1
QEM41989.1	002020	Cluster1554_1clades	131	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83124.1	002020	Cluster1554_1clades	132	PHIKZ223	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60344.1	002021	Cluster1555_1clades	133	Ea357_192	Erwinia phage Ea35-70	GCA_000914635.1
QBP07426.1	002021	Cluster1555_1clades	135	REBECCA_196	Erwinia phage Rebecca	GCA_004521635.1
AUG85983.1	002021	Cluster1555_1clades	133	BOSOLAPHORUS_196	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52298.1	002021	Cluster1555_1clades	133	DM_200	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86302.1	002021	Cluster1555_1clades	133	DESERTFOX_195	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86624.1	002021	Cluster1555_1clades	133	MADMEL_196	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86948.1	002021	Cluster1555_1clades	133	MORTIMER_199	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51975.1	002021	Cluster1555_1clades	133	RAY_194	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51659.1	002021	Cluster1555_1clades	133	SIMMY50_197	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65006.2	002021	Cluster1555_1clades	133	SPECIALG_197	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13788.1	002022	Cluster1556_1clades	133	Ccr10_gp258	Caulobacter phage Ccr10	GCA_002619445.1
ARB14133.1	002022	Cluster1556_1clades	133	Ccr2_gp257	Caulobacter phage Ccr2	GCA_002619465.1
ARB14827.1	002022	Cluster1556_1clades	133	Ccr29_gp271	Caulobacter phage Ccr29	GCA_002619485.1
ARB15167.1	002022	Cluster1556_1clades	132	Ccr32_gp249	Caulobacter phage Ccr32	GCA_002619505.1
ARB15501.1	002022	Cluster1556_1clades	132	Ccr34_gp259	Caulobacter phage Ccr34	GCA_002619525.1
ARB14475.1	002022	Cluster1556_1clades	132	Ccr5_gp255	Caulobacter phage Ccr5	GCA_002619545.1
AFU87785.1	002022	Cluster1556_1clades	132	CcrKarma_gp268	Caulobacter virus Karma	GCA_000901575.1
AFU87432.1	002022	Cluster1556_1clades	132	CcrMagneto_gp262	Caulobacter virus Magneto	GCA_000903095.1
AFU88578.1	002022	Cluster1556_1clades	133	CcrSwift_gp260	Caulobacter virus Swift	GCA_000899655.1
AFU87086.1	002022	Cluster1556_1clades	132	CbK_gp254	Caulobacter virus phiCbK	GCA_000900535.1
AHI60249.1	002023	Cluster1557_1clades	133	Ea357_098	Erwinia phage Ea35-70	GCA_000914635.1
QBP07207.1	002023	Cluster1557_1clades	133	REBECCA_100	Erwinia phage Rebecca	GCA_004521635.1
AUG85886.1	002023	Cluster1557_1clades	133	BOSOLAPHORUS_99	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52201.1	002023	Cluster1557_1clades	133	DM_103	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86205.1	002023	Cluster1557_1clades	133	DESERTFOX_98	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86528.1	002023	Cluster1557_1clades	133	MADMEL_100	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86851.1	002023	Cluster1557_1clades	133	MORTIMER_102	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51879.1	002023	Cluster1557_1clades	133	RAY_98	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51563.1	002023	Cluster1557_1clades	133	SIMMY50_101	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64911.1	002023	Cluster1557_1clades	133	SPECIALG_101	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60393.1	002024	Cluster1558_1clades	130	Ea357_240	Erwinia phage Ea35-70	GCA_000914635.1
QBP07349.1	002024	Cluster1558_1clades	130	REBECCA_244	Erwinia phage Rebecca	GCA_004521635.1
AUG86031.1	002024	Cluster1558_1clades	130	BOSOLAPHORUS_245	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52348.1	002024	Cluster1558_1clades	130	DM_248	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86350.1	002024	Cluster1558_1clades	130	DESERTFOX_243	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86673.1	002024	Cluster1558_1clades	130	MADMEL_246	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86996.1	002024	Cluster1558_1clades	130	MORTIMER_248	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52022.1	002024	Cluster1558_1clades	130	RAY_242	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51706.1	002024	Cluster1558_1clades	130	SIMMY50_247	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65057.1	002024	Cluster1558_1clades	130	SPECIALG_246	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60426.1	002025	Cluster1559_1clades	130	Ea357_272	Erwinia phage Ea35-70	GCA_000914635.1
QBP07383.1	002025	Cluster1559_1clades	129	REBECCA_278	Erwinia phage Rebecca	GCA_004521635.1
AUG86065.1	002025	Cluster1559_1clades	129	BOSOLAPHORUS_279	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52381.1	002025	Cluster1559_1clades	130	DM_282	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86385.1	002025	Cluster1559_1clades	130	DESERTFOX_278	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86706.1	002025	Cluster1559_1clades	130	MADMEL_279	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87031.1	002025	Cluster1559_1clades	130	MORTIMER_283	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52056.1	002025	Cluster1559_1clades	130	RAY_276	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51739.1	002025	Cluster1559_1clades	129	SIMMY50_281	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65091.1	002025	Cluster1559_1clades	130	SPECIALG_280	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13632.1	002026	Cluster1560_1clades	129	Ccr10_gp103	Caulobacter phage Ccr10	GCA_002619445.1
ARB13977.1	002026	Cluster1560_1clades	129	Ccr2_gp102	Caulobacter phage Ccr2	GCA_002619465.1
ARB14321.1	002026	Cluster1560_1clades	129	Ccr5_gp103	Caulobacter phage Ccr5	GCA_002619545.1
AFU88007.1	002026	Cluster1560_1clades	126	CcrColossus_gp137	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68683.1	002026	Cluster1560_1clades	52	CcrPW_gp144	Caulobacter phage CcrPW	GCA_003443275.1
AFU87624.1	002026	Cluster1560_1clades	129	CcrKarma_gp107	Caulobacter virus Karma	GCA_000901575.1
AFU87273.1	002026	Cluster1560_1clades	129	CcrMagneto_gp103	Caulobacter virus Magneto	GCA_000903095.1
AFU86585.1	002026	Cluster1560_1clades	128	CcrRogue_gp103	Caulobacter virus Rogue	GCA_000900555.1
AFU88420.1	002026	Cluster1560_1clades	129	CcrSwift_gp102	Caulobacter virus Swift	GCA_000899655.1
AFU86938.1	002026	Cluster1560_1clades	129	CbK_gp106	Caulobacter virus phiCbK	GCA_000900535.1
AHI60326.1	002027	Cluster1561_1clades	128	Ea357_174	Erwinia phage Ea35-70	GCA_000914635.1
QBP07285.1	002027	Cluster1561_1clades	128	REBECCA_178	Erwinia phage Rebecca	GCA_004521635.1
AUG85965.1	002027	Cluster1561_1clades	128	BOSOLAPHORUS_178	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52280.1	002027	Cluster1561_1clades	128	DM_182	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86284.1	002027	Cluster1561_1clades	128	DESERTFOX_177	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86606.1	002027	Cluster1561_1clades	128	MADMEL_178	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86930.1	002027	Cluster1561_1clades	128	MORTIMER_181	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51957.1	002027	Cluster1561_1clades	128	RAY_176	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51641.1	002027	Cluster1561_1clades	128	SIMMY50_179	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64988.1	002027	Cluster1561_1clades	128	SPECIALG_178	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60365.1	002028	Cluster1562_1clades	127	Ea357_212	Erwinia phage Ea35-70	GCA_000914635.1
QBP07322.1	002028	Cluster1562_1clades	127	REBECCA_217	Erwinia phage Rebecca	GCA_004521635.1
AUG86003.1	002028	Cluster1562_1clades	127	BOSOLAPHORUS_217	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52320.1	002028	Cluster1562_1clades	127	DM_220	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86322.1	002028	Cluster1562_1clades	127	DESERTFOX_215	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86645.1	002028	Cluster1562_1clades	127	MADMEL_217	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86968.1	002028	Cluster1562_1clades	127	MORTIMER_220	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51995.1	002028	Cluster1562_1clades	127	RAY_215	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51679.1	002028	Cluster1562_1clades	127	SIMMY50_220	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65029.1	002028	Cluster1562_1clades	127	SPECIALG_218	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60290.1	002029	TM+TM	126	Ea357_139	Erwinia phage Ea35-70	GCA_000914635.1
QBP07248.1	002029	TM+TM	126	REBECCA_141	Erwinia phage Rebecca	GCA_004521635.1
AUG85928.1	002029	TM+TM	126	BOSOLAPHORUS_141	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52243.1	002029	TM+TM	126	DM_145	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86247.1	002029	TM+TM	126	DESERTFOX_140	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86569.1	002029	TM+TM	126	MADMEL_141	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86893.1	002029	TM+TM	126	MORTIMER_144	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51921.1	002029	TM+TM	126	RAY_140	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51605.1	002029	TM+TM	126	SIMMY50_143	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64952.1	002029	TM+TM	126	SPECIALG_142	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60401.1	002030	Cluster1564_1clades	108	Ea357_248	Erwinia phage Ea35-70	GCA_000914635.1
QBP07357.1	002030	Cluster1564_1clades	125	REBECCA_252	Erwinia phage Rebecca	GCA_004521635.1
AUG86039.1	002030	Cluster1564_1clades	108	BOSOLAPHORUS_253	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52356.1	002030	Cluster1564_1clades	108	DM_257	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86359.1	002030	Cluster1564_1clades	108	DESERTFOX_252	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86681.1	002030	Cluster1564_1clades	108	MADMEL_254	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87005.1	002030	Cluster1564_1clades	108	MORTIMER_257	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52031.1	002030	Cluster1564_1clades	108	RAY_251	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51714.1	002030	Cluster1564_1clades	108	SIMMY50_256	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65066.2	002030	Cluster1564_1clades	108	SPECIALG_255	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13555.1	002031	Cluster1565_1clades	123	Ccr10_gp027	Caulobacter phage Ccr10	GCA_002619445.1
ARB13901.1	002031	Cluster1565_1clades	123	Ccr2_gp026	Caulobacter phage Ccr2	GCA_002619465.1
ARB14590.1	002031	Cluster1565_1clades	123	Ccr29_gp033	Caulobacter phage Ccr29	GCA_002619485.1
ARB14945.1	002031	Cluster1565_1clades	123	Ccr32_gp026	Caulobacter phage Ccr32	GCA_002619505.1
ARB15276.1	002031	Cluster1565_1clades	123	Ccr34_gp027	Caulobacter phage Ccr34	GCA_002619525.1
ARB14244.1	002031	Cluster1565_1clades	124	Ccr5_gp026	Caulobacter phage Ccr5	GCA_002619545.1
AFU87544.1	002031	Cluster1565_1clades	123	CcrKarma_gp027	Caulobacter virus Karma	GCA_000901575.1
AFU87195.1	002031	Cluster1565_1clades	124	CcrMagneto_gp025	Caulobacter virus Magneto	GCA_000903095.1
AFU88341.1	002031	Cluster1565_1clades	123	CcrSwift_gp023	Caulobacter virus Swift	GCA_000899655.1
AFU86858.1	002031	Cluster1565_1clades	123	CbK_gp026	Caulobacter virus phiCbK	GCA_000900535.1
ARB13583.1	002032	Cluster1566_1clades	123	Ccr10_gp055	Caulobacter phage Ccr10	GCA_002619445.1
ARB13929.1	002032	Cluster1566_1clades	123	Ccr2_gp054	Caulobacter phage Ccr2	GCA_002619465.1
ARB14618.1	002032	Cluster1566_1clades	110	Ccr29_gp061	Caulobacter phage Ccr29	GCA_002619485.1
ARB14974.1	002032	Cluster1566_1clades	123	Ccr32_gp055	Caulobacter phage Ccr32	GCA_002619505.1
ARB15305.1	002032	Cluster1566_1clades	123	Ccr34_gp056	Caulobacter phage Ccr34	GCA_002619525.1
ARB14272.1	002032	Cluster1566_1clades	123	Ccr5_gp054	Caulobacter phage Ccr5	GCA_002619545.1
AFU87573.1	002032	Cluster1566_1clades	110	CcrKarma_gp056	Caulobacter virus Karma	GCA_000901575.1
AFU87223.1	002032	Cluster1566_1clades	110	CcrMagneto_gp053	Caulobacter virus Magneto	GCA_000903095.1
AFU88371.1	002032	Cluster1566_1clades	123	CcrSwift_gp053	Caulobacter virus Swift	GCA_000899655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU86887.1	002032	Cluster1566_1clades	123	CbK_gp055	Caulobacter virus phiCbK	GCA_000900535.1
AHI60255.1	002033	Cluster1567_1clades	116	Ea357_104	Erwinia phage Ea35-70	GCA_000914635.1
QBP07212.1	002033	Cluster1567_1clades	123	REBECCA_105	Erwinia phage Rebecca	GCA_004521635.1
AUG85892.1	002033	Cluster1567_1clades	116	BOSOLAPHORUS_105	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52207.1	002033	Cluster1567_1clades	116	DM_109	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86211.1	002033	Cluster1567_1clades	116	DESERTFOX_104	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86533.1	002033	Cluster1567_1clades	123	MADMEL_105	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86857.1	002033	Cluster1567_1clades	116	MORTIMER_108	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51885.1	002033	Cluster1567_1clades	116	RAY_104	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51569.1	002033	Cluster1567_1clades	116	SIMMY50_107	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64917.1	002033	Cluster1567_1clades	116	SPECIALG_107	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60219.1	002034	Cluster1568_1clades	121	Ea357_068	Erwinia phage Ea35-70	GCA_000914635.1
QBP07177.1	002034	Cluster1568_1clades	121	REBECCA_69	Erwinia phage Rebecca	GCA_004521635.1
AUG85857.1	002034	Cluster1568_1clades	121	BOSOLAPHORUS_69	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52169.1	002034	Cluster1568_1clades	121	DM_71	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86176.1	002034	Cluster1568_1clades	121	DESERTFOX_68	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86498.1	002034	Cluster1568_1clades	121	MADMEL_70	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86819.1	002034	Cluster1568_1clades	121	MORTIMER_70	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51849.1	002034	Cluster1568_1clades	121	RAY_68	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51533.1	002034	Cluster1568_1clades	121	SIMMY50_71	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64881.1	002034	Cluster1568_1clades	121	SPECIALG_71	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60236.1	002035	Cluster1569_1clades	121	Ea357_085	Erwinia phage Ea35-70	GCA_000914635.1
QBP07195.1	002035	Cluster1569_1clades	121	REBECCA_88	Erwinia phage Rebecca	GCA_004521635.1
AUG85874.1	002035	Cluster1569_1clades	121	BOSOLAPHORUS_87	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52187.1	002035	Cluster1569_1clades	121	DM_89	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86193.1	002035	Cluster1569_1clades	121	DESERTFOX_86	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86516.1	002035	Cluster1569_1clades	121	MADMEL_88	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86837.1	002035	Cluster1569_1clades	121	MORTIMER_88	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51867.1	002035	Cluster1569_1clades	121	RAY_86	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51551.1	002035	Cluster1569_1clades	121	SIMMY50_89	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64899.1	002035	Cluster1569_1clades	121	SPECIALG_89	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60363.1	002036	Cluster1570_1clades	120	Ea357_210	Erwinia phage Ea35-70	GCA_000914635.1
QBP07320.1	002036	Cluster1570_1clades	120	REBECCA_215	Erwinia phage Rebecca	GCA_004521635.1
AUG86001.1	002036	Cluster1570_1clades	120	BOSOLAPHORUS_215	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52318.1	002036	Cluster1570_1clades	120	DM_218	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86320.1	002036	Cluster1570_1clades	120	DESERTFOX_213	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86643.1	002036	Cluster1570_1clades	120	MADMEL_215	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86966.1	002036	Cluster1570_1clades	120	MORTIMER_218	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51993.1	002036	Cluster1570_1clades	120	RAY_213	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51677.1	002036	Cluster1570_1clades	120	SIMMY50_218	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65027.1	002036	Cluster1570_1clades	120	SPECIALG_216	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13682.1	002037	Cluster1571_1clades	120	Ccr10_gp152c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14027.1	002037	Cluster1571_1clades	120	Ccr2_gp151c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14714.1	002037	Cluster1571_1clades	77	Ccr29_gp158	Caulobacter phage Ccr29	GCA_002619485.1
ARB15069.1	002037	Cluster1571_1clades	77	Ccr32_gp151	Caulobacter phage Ccr32	GCA_002619505.1
ARB15403.1	002037	Cluster1571_1clades	77	Ccr34_gp161	Caulobacter phage Ccr34	GCA_002619525.1
ARB14370.1	002037	Cluster1571_1clades	77	Ccr5_gp150c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87675.1	002037	Cluster1571_1clades	77	CcrKarma_gp158	Caulobacter virus Karma	GCA_000901575.1
AFU87324.1	002037	Cluster1571_1clades	77	CcrMagneto_gp154	Caulobacter virus Magneto	GCA_000903095.1
AFU88471.1	002037	Cluster1571_1clades	77	CcrSwift_gp153	Caulobacter virus Swift	GCA_000899655.1
AFU86988.1	002037	Cluster1571_1clades	77	CbK_gp156	Caulobacter virus phiCbK	GCA_000900535.1
ARB13666.1	002038	Cluster1572_1clades	79	Ccr10_gp137	Caulobacter phage Ccr10	GCA_002619445.1
ARB14011.1	002038	Cluster1572_1clades	79	Ccr2_gp136	Caulobacter phage Ccr2	GCA_002619465.1
ARB15387.1	002038	Cluster1572_1clades	47	Ccr34_gp145	Caulobacter phage Ccr34	GCA_002619525.1
ARB14354.1	002038	Cluster1572_1clades	79	Ccr5_gp135	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68728.1	002038	Cluster1572_1clades	88	CcrPW_gp189	Caulobacter phage CcrPW	GCA_003443275.1
AFU87659.1	002038	Cluster1572_1clades	79	CcrKarma_gp142	Caulobacter virus Karma	GCA_000901575.1
AFU87308.1	002038	Cluster1572_1clades	79	CcrMagneto_gp138	Caulobacter virus Magneto	GCA_000903095.1
AFU86619.1	002038	Cluster1572_1clades	119	CcrRogue_gp137	Caulobacter virus Rogue	GCA_000900555.1
AFU88455.1	002038	Cluster1572_1clades	79	CcrSwift_gp137	Caulobacter virus Swift	GCA_000899655.1
AFU86972.1	002038	Cluster1572_1clades	79	CbK_gp140	Caulobacter virus phiCbK	GCA_000900535.1
ARB13780.1	002039	Cluster1573_1clades	119	Ccr10_gp250	Caulobacter phage Ccr10	GCA_002619445.1
ARB14125.1	002039	Cluster1573_1clades	119	Ccr2_gp249	Caulobacter phage Ccr2	GCA_002619465.1
ARB14819.1	002039	Cluster1573_1clades	119	Ccr29_gp263	Caulobacter phage Ccr29	GCA_002619485.1
ARB15159.1	002039	Cluster1573_1clades	119	Ccr32_gp241	Caulobacter phage Ccr32	GCA_002619505.1
ARB15493.1	002039	Cluster1573_1clades	119	Ccr34_gp251	Caulobacter phage Ccr34	GCA_002619525.1
ARB14467.1	002039	Cluster1573_1clades	119	Ccr5_gp247	Caulobacter phage Ccr5	GCA_002619545.1
AFU87776.1	002039	Cluster1573_1clades	119	CcrKarma_gp259	Caulobacter virus Karma	GCA_000901575.1
AFU87423.1	002039	Cluster1573_1clades	119	CcrMagneto_gp253	Caulobacter virus Magneto	GCA_000903095.1
AFU88570.1	002039	Cluster1573_1clades	119	CcrSwift_gp252	Caulobacter virus Swift	GCA_000899655.1
AFU87078.1	002039	Cluster1573_1clades	119	CbK_gp246	Caulobacter virus phiCbK	GCA_000900535.1
AHI60212.1	002040	SIG+TM	110	Ea357_061	Erwinia phage Ea35-70	GCA_000914635.1
QBP07170.1	002040	SIG+TM	117	REBECCA_62	Erwinia phage Rebecca	GCA_004521635.1
AUG85850.1	002040	SIG+TM	117	BOSOLAPHORUS_62	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52162.1	002040	SIG+TM	117	DM_64	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86169.1	002040	SIG+TM	117	DESERTFOX_61	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86491.1	002040	SIG+TM	117	MADMEL_63	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86812.1	002040	SIG+TM	117	MORTIMER_63	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51842.2	002040	SIG+TM	117	RAY_61	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51526.2	002040	SIG+TM	117	SIMMY50_64	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64874.1	002040	SIG+TM	117	SPECIALG_64	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43075.1	002041	Cluster1575_1clades	57	R1080702_066	Cyanophage S-RIM32	GCA_001754165.1
AMO43302.1	002041	Cluster1575_1clades	64	W270710_058	Cyanophage S-RIM44	GCA_002599145.1
AOO11536.1	002041	Cluster1575_1clades	64	ES420910_055	Cyanophage S-RIM44	GCA_002599165.1
AOO11774.1	002041	Cluster1575_1clades	64	Np050604_058	Cyanophage S-RIM44	GCA_002599185.1
AOO12001.1	002041	Cluster1575_1clades	64	Np200711_055	Cyanophage S-RIM44	GCA_002599205.1
AOO12237.1	002041	Cluster1575_1clades	64	Np420711_055	Cyanophage S-RIM44	GCA_002599225.1
AOO12475.1	002041	Cluster1575_1clades	64	Sn080709_058	Cyanophage S-RIM44	GCA_002599245.1
AOO12702.1	002041	Cluster1575_1clades	64	Sn130910_055	Cyanophage S-RIM44	GCA_002599265.1
AOO12940.1	002041	Cluster1575_1clades	64	W2100709_058	Cyanophage S-RIM44	GCA_002599285.1
ADO99156.1	002041	Cluster1575_1clades	115	Syn1_055	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60175.1	002042	Cluster1576_1clades	114	Ea357_025	Erwinia phage Ea35-70	GCA_000914635.1
QBP07133.1	002042	Cluster1576_1clades	114	REBECCA_25	Erwinia phage Rebecca	GCA_004521635.1
AUG85813.1	002042	Cluster1576_1clades	114	BOSOLAPHORUS_25	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52123.1	002042	Cluster1576_1clades	114	DM_25	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86133.1	002042	Cluster1576_1clades	114	DESERTFOX_25	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86453.1	002042	Cluster1576_1clades	114	MADMEL_25	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86774.1	002042	Cluster1576_1clades	114	MORTIMER_25	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51806.1	002042	Cluster1576_1clades	114	RAY_25	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51488.1	002042	Cluster1576_1clades	114	SIMMY50_26	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64835.1	002042	Cluster1576_1clades	114	SPECIALG_25	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60427.1	002043	Cluster1577_1clades	114	Ea357_273	Erwinia phage Ea35-70	GCA_000914635.1
QBP07384.1	002043	Cluster1577_1clades	114	REBECCA_279	Erwinia phage Rebecca	GCA_004521635.1
AUG86066.1	002043	Cluster1577_1clades	114	BOSOLAPHORUS_280	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52382.1	002043	Cluster1577_1clades	114	DM_283	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86386.1	002043	Cluster1577_1clades	114	DESERTFOX_279	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86707.1	002043	Cluster1577_1clades	114	MADMEL_280	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87032.1	002043	Cluster1577_1clades	114	MORTIMER_284	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52057.1	002043	Cluster1577_1clades	114	RAY_277	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51740.1	002043	Cluster1577_1clades	114	SIMMY50_282	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65092.1	002043	Cluster1577_1clades	114	SPECIALG_281	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13844.1	002044	Cluster1579_1clades	109	Ccr10_gp314	Caulobacter phage Ccr10	GCA_002619445.1
ARB14189.1	002044	Cluster1579_1clades	109	Ccr2_gp313	Caulobacter phage Ccr2	GCA_002619465.1
ARB14883.1	002044	Cluster1579_1clades	109	Ccr29_gp327	Caulobacter phage Ccr29	GCA_002619485.1
ARB15221.1	002044	Cluster1579_1clades	109	Ccr32_gp303	Caulobacter phage Ccr32	GCA_002619505.1
ARB15555.1	002044	Cluster1579_1clades	109	Ccr34_gp313	Caulobacter phage Ccr34	GCA_002619525.1
ARB14530.1	002044	Cluster1579_1clades	109	Ccr5_gp310	Caulobacter phage Ccr5	GCA_002619545.1
AFU87841.1	002044	Cluster1579_1clades	109	CcrKarma_gp324	Caulobacter virus Karma	GCA_000901575.1
AFU87488.1	002044	Cluster1579_1clades	109	CcrMagneto_gp318	Caulobacter virus Magneto	GCA_000903095.1
AFU88633.1	002044	Cluster1579_1clades	109	CcrSwift_gp315	Caulobacter virus Swift	GCA_000899655.1
AFU87140.1	002044	Cluster1579_1clades	109	CbK_gp308	Caulobacter virus phiCbK	GCA_000900535.1
AHI60177.1	002045	Cluster1580_1clades	109	Ea357_027	Erwinia phage Ea35-70	GCA_000914635.1
QBP07135.1	002045	Cluster1580_1clades	109	REBECCA_27	Erwinia phage Rebecca	GCA_004521635.1
AUG85815.1	002045	Cluster1580_1clades	109	BOSOLAPHORUS_27	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52125.1	002045	Cluster1580_1clades	109	DM_27	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86135.1	002045	Cluster1580_1clades	109	DESERTFOX_27	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86455.1	002045	Cluster1580_1clades	109	MADMEL_27	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86776.1	002045	Cluster1580_1clades	109	MORTIMER_27	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51808.1	002045	Cluster1580_1clades	109	RAY_27	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51490.1	002045	Cluster1580_1clades	109	SIMMY50_28	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64837.1	002045	Cluster1580_1clades	109	SPECIALG_27	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AUE22652.1	002046	Cluster1581_1clades	90	Ah1_00111	Aeromonas phage Ah1	GCA_002957415.1
QAX98378.1	002046	Cluster1581_1clades	90	ASfcp2_32	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52831.1	002046	Cluster1581_1clades	90	PX29p112	Aeromonas phage PX29	GCA_000920195.1
ADM80091.1	002046	Cluster1581_1clades	93	phiAS5_ORF0248	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17778.1	002046	Cluster1581_1clades	90	Aeh1ORF116c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21907.1	002046	Cluster1581_1clades	104	GAP32_451	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44033.1	002046	Cluster1581_1clades	105	CBB_470	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88992.1	002046	Cluster1581_1clades	109	BF_0467	Serratia phage BF	GCA_002619745.1
SOK59272.1	002046	Cluster1581_1clades	105	g464	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58736.1	002046	Cluster1581_1clades	105	g459	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13571.1	002047	Cluster1582_1clades	108	Ccr10_gp043	Caulobacter phage Ccr10	GCA_002619445.1
ARB13917.1	002047	Cluster1582_1clades	108	Ccr2_gp042	Caulobacter phage Ccr2	GCA_002619465.1
ARB14606.1	002047	Cluster1582_1clades	108	Ccr29_gp049	Caulobacter phage Ccr29	GCA_002619485.1
ARB14962.1	002047	Cluster1582_1clades	108	Ccr32_gp043	Caulobacter phage Ccr32	GCA_002619505.1
ARB15293.1	002047	Cluster1582_1clades	108	Ccr34_gp044	Caulobacter phage Ccr34	GCA_002619525.1
ARB14260.1	002047	Cluster1582_1clades	108	Ccr5_gp042	Caulobacter phage Ccr5	GCA_002619545.1
AFU87561.1	002047	Cluster1582_1clades	108	CcrKarma_gp044	Caulobacter virus Karma	GCA_000901575.1
AFU87211.1	002047	Cluster1582_1clades	108	CcrMagneto_gp041	Caulobacter virus Magneto	GCA_000903095.1
AFU88359.1	002047	Cluster1582_1clades	108	CcrSwift_gp041	Caulobacter virus Swift	GCA_000899655.1
AFU86875.1	002047	Cluster1582_1clades	108	CbK_gp043	Caulobacter virus phiCbK	GCA_000900535.1
AHI60259.1	002048	Cluster1583_1clades	99	Ea357_108	Erwinia phage Ea35-70	GCA_000914635.1
QBP07216.1	002048	Cluster1583_1clades	108	REBECCA_109	Erwinia phage Rebecca	GCA_004521635.1
AUG85896.1	002048	Cluster1583_1clades	108	BOSOLAPHORUS_109	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52211.1	002048	Cluster1583_1clades	108	DM_113	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86215.1	002048	Cluster1583_1clades	108	DESERTFOX_108	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86537.1	002048	Cluster1583_1clades	108	MADMEL_109	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86862.1	002048	Cluster1583_1clades	108	MORTIMER_113	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51890.1	002048	Cluster1583_1clades	108	RAY_109	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51574.2	002048	Cluster1583_1clades	108	SIMMY50_112	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64921.1	002048	Cluster1583_1clades	108	SPECIALG_111	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43059.1	002049	Cluster1584_1clades	89	R1080702_050	Cyanophage S-RIM32	GCA_001754165.1
AMO43297.1	002049	Cluster1584_1clades	99	W270710_053	Cyanophage S-RIM44	GCA_002599145.1
AOO11531.1	002049	Cluster1584_1clades	99	ES420910_050	Cyanophage S-RIM44	GCA_002599165.1
AOO11769.1	002049	Cluster1584_1clades	99	Np050604_053	Cyanophage S-RIM44	GCA_002599185.1
AOO11996.1	002049	Cluster1584_1clades	104	Np200711_050	Cyanophage S-RIM44	GCA_002599205.1
AOO12232.1	002049	Cluster1584_1clades	104	Np420711_050	Cyanophage S-RIM44	GCA_002599225.1
AOO12470.1	002049	Cluster1584_1clades	99	Sn080709_053	Cyanophage S-RIM44	GCA_002599245.1
AOO12697.1	002049	Cluster1584_1clades	104	Sn130910_050	Cyanophage S-RIM44	GCA_002599265.1
AOO12935.1	002049	Cluster1584_1clades	104	W2100709_053	Cyanophage S-RIM44	GCA_002599285.1
ADO99151.1	002049	Cluster1584_1clades	107	Syn1_050	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60392.1	002050	Cluster1585_1clades	107	Ea357_239	Erwinia phage Ea35-70	GCA_000914635.1
QBP07348.1	002050	Cluster1585_1clades	107	REBECCA_243	Erwinia phage Rebecca	GCA_004521635.1
AUG86030.1	002050	Cluster1585_1clades	65	BOSOLAPHORUS_244	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52347.1	002050	Cluster1585_1clades	65	DM_247	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86349.1	002050	Cluster1585_1clades	65	DESERTFOX_242	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86672.1	002050	Cluster1585_1clades	65	MADMEL_245	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86995.1	002050	Cluster1585_1clades	65	MORTIMER_247	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52021.1	002050	Cluster1585_1clades	65	RAY_241	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51705.1	002050	Cluster1585_1clades	65	SIMMY50_246	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65056.1	002050	Cluster1585_1clades	65	SPECIALG_245	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60402.1	002051	Cluster1586_1clades	107	Ea357_248A	Erwinia phage Ea35-70	GCA_000914635.1
QBP07358.1	002051	Cluster1586_1clades	107	REBECCA_253	Erwinia phage Rebecca	GCA_004521635.1
AUG86040.1	002051	Cluster1586_1clades	107	BOSOLAPHORUS_254	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52357.1	002051	Cluster1586_1clades	107	DM_258	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86360.1	002051	Cluster1586_1clades	107	DESERTFOX_253	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86682.1	002051	Cluster1586_1clades	107	MADMEL_255	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87006.1	002051	Cluster1586_1clades	107	MORTIMER_258	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52032.1	002051	Cluster1586_1clades	107	RAY_252	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51715.1	002051	Cluster1586_1clades	107	SIMMY50_257	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65067.1	002051	Cluster1586_1clades	107	SPECIALG_256	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60199.1	002052	Cluster1587_1clades	106	Ea357_049	Erwinia phage Ea35-70	GCA_000914635.1
QBP07158.1	002052	Cluster1587_1clades	106	REBECCA_50	Erwinia phage Rebecca	GCA_004521635.1
AUG85838.1	002052	Cluster1587_1clades	106	BOSOLAPHORUS_50	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52150.1	002052	Cluster1587_1clades	106	DM_52	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86157.1	002052	Cluster1587_1clades	106	DESERTFOX_49	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86478.1	002052	Cluster1587_1clades	106	MADMEL_50	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86799.1	002052	Cluster1587_1clades	106	MORTIMER_50	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51830.1	002052	Cluster1587_1clades	106	RAY_49	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51513.1	002052	Cluster1587_1clades	106	SIMMY50_51	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64861.1	002052	Cluster1587_1clades	106	SPECIALG_51	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60278.1	002053	Cluster1588_1clades	106	Ea357_127	Erwinia phage Ea35-70	GCA_000914635.1
QBP07236.1	002053	Cluster1588_1clades	106	REBECCA_129	Erwinia phage Rebecca	GCA_004521635.1
AUG85916.1	002053	Cluster1588_1clades	106	BOSOLAPHORUS_129	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52231.1	002053	Cluster1588_1clades	106	DM_133	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86235.1	002053	Cluster1588_1clades	106	DESERTFOX_128	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86557.1	002053	Cluster1588_1clades	106	MADMEL_129	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86881.1	002053	Cluster1588_1clades	106	MORTIMER_132	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51909.1	002053	Cluster1588_1clades	106	RAY_128	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51593.1	002053	Cluster1588_1clades	106	SIMMY50_131	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64940.1	002053	Cluster1588_1clades	106	SPECIALG_130	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60346.1	002054	Cluster1589_1clades	106	Ea357_194	Erwinia phage Ea35-70	GCA_000914635.1
QBP07304.1	002054	Cluster1589_1clades	106	REBECCA_198	Erwinia phage Rebecca	GCA_004521635.1
AUG85985.1	002054	Cluster1589_1clades	106	BOSOLAPHORUS_198	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52300.1	002054	Cluster1589_1clades	106	DM_202	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86304.1	002054	Cluster1589_1clades	106	DESERTFOX_197	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86626.1	002054	Cluster1589_1clades	106	MADMEL_198	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86950.1	002054	Cluster1589_1clades	106	MORTIMER_201	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51977.1	002054	Cluster1589_1clades	106	RAY_196	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51661.1	002054	Cluster1589_1clades	106	SIMMY50_199	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65008.1	002054	Cluster1589_1clades	106	SPECIALG_199	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60182.1	002055	Cluster1590_1clades	90	Ea357_032	Erwinia phage Ea35-70	GCA_000914635.1
QBP07140.1	002055	Cluster1590_1clades	106	REBECCA_32	Erwinia phage Rebecca	GCA_004521635.1
AUG85820.1	002055	Cluster1590_1clades	106	BOSOLAPHORUS_32	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52131.1	002055	Cluster1590_1clades	106	DM_33	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86140.1	002055	Cluster1590_1clades	106	DESERTFOX_32	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86460.1	002055	Cluster1590_1clades	106	MADMEL_32	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86781.1	002055	Cluster1590_1clades	106	MORTIMER_32	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51813.2	002055	Cluster1590_1clades	106	RAY_32	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51495.2	002055	Cluster1590_1clades	106	SIMMY50_33	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64842.3	002055	Cluster1590_1clades	106	SPECIALG_32	Erwinia phage vB_EamM_Special G	GCA_002624385.1
APU01777.1	002056	Cluster1591_1clades	98	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17523.1	002056	Cluster1591_1clades	100	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00473.1	002056	Cluster1591_1clades	100	HWB28_gp079	Aeromonas phage AS-zj	GCA_002627665.1
AUE22613.1	002056	Cluster1591_1clades	106	Ah1_00072	Aeromonas phage Ah1	GCA_002957415.1
QAX97965.1	002056	Cluster1591_1clades	100	ASswx1_323	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01176.1	002056	Cluster1591_1clades	97	ASwh1_110	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ52797.1	002056	Cluster1591_1clades	94	PX29p078	Aeromonas phage PX29	GCA_000920195.1
ADM80053.1	002056	Cluster1591_1clades	93	phiAS5_ORF0210	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53420.1	002056	Cluster1591_1clades	100	65p413	Aeromonas virus 65	GCA_000893255.1
AAQ17740.1	002056	Cluster1591_1clades	94	Aeh1ORF079c	Aeromonas virus Aeh1	GCA_000843245.1
ARB13806.1	002057	SIG+TM	105	Ccr10_gp276	Caulobacter phage Ccr10	GCA_002619445.1
ARB14151.1	002057	SIG+TM	105	Ccr2_gp275	Caulobacter phage Ccr2	GCA_002619465.1
ARB14845.1	002057	SIG+TM	105	Ccr29_gp289	Caulobacter phage Ccr29	GCA_002619485.1
ARB15185.1	002057	SIG+TM	105	Ccr32_gp267	Caulobacter phage Ccr32	GCA_002619505.1
ARB15519.1	002057	SIG+TM	105	Ccr34_gp277	Caulobacter phage Ccr34	GCA_002619525.1
ARB14494.1	002057	SIG+TM	105	Ccr5_gp274	Caulobacter phage Ccr5	GCA_002619545.1
AFU87804.1	002057	SIG+TM	105	CcrKarma_gp287	Caulobacter virus Karma	GCA_000901575.1
AFU87451.1	002057	SIG+TM	101	CcrMagneto_gp281	Caulobacter virus Magneto	GCA_000903095.1
AFU88596.1	002057	SIG+TM	105	CcrSwift_gp278	Caulobacter virus Swift	GCA_000899655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU87104.1	002057	SIG+TM	105	CbK_gp272	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64159.1	002058	Cluster1593_1clades	99	KVP40.0088	Vibrio phage KVP40	GCA_000843785.1
QIW90483.1	002058	Cluster1593_1clades	99	GCAPEGMB_00136	Vibrio phage V07	GCA_012361095.1
QIW90946.1	002058	Cluster1593_1clades	99	COHAPHLL_00083	Vibrio phage V09	GCA_012361135.1
QHJ74271.1	002058	Cluster1593_1clades	99	VH12019_00352	Vibrio phage VH1_2019	GCA_009931825.1
AGB07096.1	002058	Cluster1593_1clades	99	CF80_gp309	Vibrio phage VH7D	GCA_000914495.1
AJT61013.1	002058	Cluster1593_1clades	98	AVU32_gp172	Vibrio phage ValKK3	GCA_001501635.1
AGN30138.1	002058	Cluster1593_1clades	105	VPFG_00136	Vibrio phage nt-1	GCA_000910195.2
ALP47206.1	002058	Cluster1593_1clades	99	phiGrn1_0203	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47596.1	002058	Cluster1593_1clades	99	phiST2_0336	Vibrio phage phi-ST2	GCA_002757135.1
AFN37320.1	002058	Cluster1593_1clades	99	pp2_087	Vibriophage phi-pp2	GCA_002630725.1
AHI60192.1	002059	Cluster1594_1clades	105	Ea357_042	Erwinia phage Ea35-70	GCA_000914635.1
QBP07150.1	002059	Cluster1594_1clades	105	REBECCA_42	Erwinia phage Rebecca	GCA_004521635.1
AUG85830.1	002059	Cluster1594_1clades	105	BOSOLAPHORUS_42	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52141.1	002059	Cluster1594_1clades	105	DM_43	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86150.1	002059	Cluster1594_1clades	105	DESERTFOX_42	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86470.1	002059	Cluster1594_1clades	105	MADMEL_42	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86791.1	002059	Cluster1594_1clades	105	MORTIMER_42	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51823.1	002059	Cluster1594_1clades	105	RAY_42	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51505.1	002059	Cluster1594_1clades	105	SIMMY50_43	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64852.1	002059	Cluster1594_1clades	105	SPECIALG_42	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60277.1	002060	Cluster1595_1clades	105	Ea357_126	Erwinia phage Ea35-70	GCA_000914635.1
QBP07235.1	002060	Cluster1595_1clades	105	REBECCA_128	Erwinia phage Rebecca	GCA_004521635.1
AUG85915.1	002060	Cluster1595_1clades	105	BOSOLAPHORUS_128	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52230.1	002060	Cluster1595_1clades	105	DM_132	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86234.1	002060	Cluster1595_1clades	105	DESERTFOX_127	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86556.1	002060	Cluster1595_1clades	105	MADMEL_128	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86880.1	002060	Cluster1595_1clades	105	MORTIMER_131	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51908.1	002060	Cluster1595_1clades	105	RAY_127	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51592.1	002060	Cluster1595_1clades	105	SIMMY50_130	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64939.1	002060	Cluster1595_1clades	105	SPECIALG_129	Erwinia phage vB_EamM_Special G	GCA_002624385.1
QIG63300.1	002061	Cluster1596_1clades	99	DAC16_67	Bacteroides phage DAC16	GCA_013387695.1
QIG63305.1	002061	Cluster1596_1clades	105	DAC16_72	Bacteroides phage DAC16	GCA_013387695.1
QIG63559.1	002061	Cluster1596_1clades	99	DAC19_68	Bacteroides phage DAC19	GCA_013387715.1
QIG63564.1	002061	Cluster1596_1clades	105	DAC19_73	Bacteroides phage DAC19	GCA_013387715.1
QIG63820.1	002061	Cluster1596_1clades	99	DAC20_67	Bacteroides phage DAC20	GCA_013387725.1
QIG63825.1	002061	Cluster1596_1clades	105	DAC20_72	Bacteroides phage DAC20	GCA_013387725.1
QIG64082.1	002061	Cluster1596_1clades	99	DAC22_68	Bacteroides phage DAC22	GCA_013387735.1
QIG64087.1	002061	Cluster1596_1clades	105	DAC22_73	Bacteroides phage DAC22	GCA_013387735.1
QIG64345.1	002061	Cluster1596_1clades	99	DAC23_67	Bacteroides phage DAC23	GCA_013387745.1
QIG64350.1	002061	Cluster1596_1clades	105	DAC23_72	Bacteroides phage DAC23	GCA_013387745.1
AHI60193.1	002062	Cluster1597_1clades	104	Ea357_043	Erwinia phage Ea35-70	GCA_000914635.1
QBP07151.1	002062	Cluster1597_1clades	104	REBECCA_43	Erwinia phage Rebecca	GCA_004521635.1
AUG85831.1	002062	Cluster1597_1clades	104	BOSOLAPHORUS_43	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52142.1	002062	Cluster1597_1clades	104	DM_44	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86151.1	002062	Cluster1597_1clades	104	DESERTFOX_43	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86471.1	002062	Cluster1597_1clades	104	MADMEL_43	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86792.1	002062	Cluster1597_1clades	104	MORTIMER_43	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51824.1	002062	Cluster1597_1clades	104	RAY_43	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51506.1	002062	Cluster1597_1clades	104	SIMMY50_44	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64853.1	002062	Cluster1597_1clades	104	SPECIALG_43	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60275.1	002063	Cluster1598_1clades	104	Ea357_124	Erwinia phage Ea35-70	GCA_000914635.1
QBP07233.1	002063	Cluster1598_1clades	104	REBECCA_126	Erwinia phage Rebecca	GCA_004521635.1
AUG85913.1	002063	Cluster1598_1clades	104	BOSOLAPHORUS_126	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52228.1	002063	Cluster1598_1clades	104	DM_130	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86232.1	002063	Cluster1598_1clades	104	DESERTFOX_125	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86554.1	002063	Cluster1598_1clades	85	MADMEL_126	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86878.1	002063	Cluster1598_1clades	104	MORTIMER_129	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51906.1	002063	Cluster1598_1clades	104	RAY_125	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51590.2	002063	Cluster1598_1clades	104	SIMMY50_128	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64937.1	002063	Cluster1598_1clades	104	SPECIALG_127	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60462.1	002064	Cluster1599_1clades	103	Ea357_308	Erwinia phage Ea35-70	GCA_000914635.1
QBP07419.1	002064	Cluster1599_1clades	103	REBECCA_314	Erwinia phage Rebecca	GCA_004521635.1
AUG86101.1	002064	Cluster1599_1clades	103	BOSOLAPHORUS_315	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52417.1	002064	Cluster1599_1clades	103	DM_318	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86421.1	002064	Cluster1599_1clades	103	DESERTFOX_314	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86742.1	002064	Cluster1599_1clades	103	MADMEL_315	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87067.1	002064	Cluster1599_1clades	103	MORTIMER_319	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52092.1	002064	Cluster1599_1clades	103	RAY_312	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51775.1	002064	Cluster1599_1clades	103	SIMMY50_317	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65127.1	002064	Cluster1599_1clades	103	SPECIALG_316	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13711.1	002065	Cluster1600_1clades	102	Ccr10_gp181c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14056.1	002065	Cluster1600_1clades	102	Ccr2_gp180c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14743.1	002065	Cluster1600_1clades	102	Ccr29_gp187	Caulobacter phage Ccr29	GCA_002619485.1
ARB15098.1	002065	Cluster1600_1clades	102	Ccr32_gp180	Caulobacter phage Ccr32	GCA_002619505.1
ARB15432.1	002065	Cluster1600_1clades	102	Ccr34_gp190	Caulobacter phage Ccr34	GCA_002619525.1
ARB14399.1	002065	Cluster1600_1clades	102	Ccr5_gp179c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87704.1	002065	Cluster1600_1clades	102	CcrKarma_gp187	Caulobacter virus Karma	GCA_000901575.1
AFU87353.1	002065	Cluster1600_1clades	102	CcrMagneto_gp183	Caulobacter virus Magneto	GCA_000903095.1
AFU88500.1	002065	Cluster1600_1clades	102	CcrSwift_gp182	Caulobacter virus Swift	GCA_000899655.1
AFU87017.1	002065	Cluster1600_1clades	102	CbK_gp185	Caulobacter virus phiCbK	GCA_000900535.1
AHI60204.1	002066	Cluster1601_1clades	102	Ea357_054	Erwinia phage Ea35-70	GCA_000914635.1
QBP07163.1	002066	Cluster1601_1clades	102	REBECCA_55	Erwinia phage Rebecca	GCA_004521635.1
AUG85843.1	002066	Cluster1601_1clades	102	BOSOLAPHORUS_55	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52155.1	002066	Cluster1601_1clades	102	DM_57	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86162.1	002066	Cluster1601_1clades	102	DESERTFOX_54	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86483.1	002066	Cluster1601_1clades	102	MADMEL_55	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86804.1	002066	Cluster1601_1clades	102	MORTIMER_55	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51835.1	002066	Cluster1601_1clades	102	RAY_54	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51518.1	002066	Cluster1601_1clades	102	SIMMY50_56	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64866.1	002066	Cluster1601_1clades	102	SPECIALG_56	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60247.1	002067	Cluster1602_1clades	101	Ea357_096	Erwinia phage Ea35-70	GCA_000914635.1
QBP07205.1	002067	Cluster1602_1clades	101	REBECCA_98	Erwinia phage Rebecca	GCA_004521635.1
AUG85884.1	002067	Cluster1602_1clades	101	BOSOLAPHORUS_97	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52199.1	002067	Cluster1602_1clades	101	DM_101	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86203.1	002067	Cluster1602_1clades	101	DESERTFOX_96	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86526.1	002067	Cluster1602_1clades	101	MADMEL_98	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86849.1	002067	Cluster1602_1clades	101	MORTIMER_100	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51877.1	002067	Cluster1602_1clades	101	RAY_96	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51561.1	002067	Cluster1602_1clades	101	SIMMY50_99	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64909.1	002067	Cluster1602_1clades	101	SPECIALG_99	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60408.1	002068	Cluster1603_1clades	101	Ea357_254	Erwinia phage Ea35-70	GCA_000914635.1
QBP07365.1	002068	Cluster1603_1clades	101	REBECCA_260	Erwinia phage Rebecca	GCA_004521635.1
AUG86047.1	002068	Cluster1603_1clades	101	BOSOLAPHORUS_261	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52363.1	002068	Cluster1603_1clades	101	DM_264	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86367.1	002068	Cluster1603_1clades	101	DESERTFOX_260	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86688.1	002068	Cluster1603_1clades	101	MADMEL_261	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87013.1	002068	Cluster1603_1clades	101	MORTIMER_265	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52038.1	002068	Cluster1603_1clades	101	RAY_258	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51721.1	002068	Cluster1603_1clades	101	SIMMY50_263	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65073.1	002068	Cluster1603_1clades	101	SPECIALG_262	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63225.1	002069	Cluster1604_1clades	92	201phi2-1p401	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45083.1	002069	Cluster1604_1clades	100	KTN4_325	Pseudomonas phage KTN4	GCA_002607225.1
QBX32490.1	002069	Cluster1604_1clades	99	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77027.1	002069	Cluster1604_1clades	96	PHABIO_396	Pseudomonas phage Phabio	GCA_002624965.1
AEH03750.1	002069	Cluster1604_1clades	100	327	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02892.1	002069	Cluster1604_1clades	94	PSA21_366	Pseudomonas phage Psa21	GCA_004340405.1
ATN94632.1	002069	Cluster1604_1clades	100	SL2_055	Pseudomonas phage SL2	GCA_002956015.1
QJB22959.1	002069	Cluster1604_1clades	100	fnug_316	Pseudomonas phage fnug	GCA_012837215.1
QEM42063.1	002069	Cluster1604_1clades	99	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83169.1	002069	Cluster1604_1clades	100	PHIKZ268	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64080.1	002070	LON-AAA	100	KVP40.0009	Vibrio phage KVP40	GCA_000843785.1
QHJ74192.1	002070	LON-AAA	100	VH12019_00273	Vibrio phage VH1_2019	GCA_009931825.1
AGB07016.1	002070	LON-AAA	100	CF80_gp229	Vibrio phage VH7D	GCA_000914495.1
QBX06080.1	002070	LON-AAA	100	ValB1HC_126	Vibrio phage ValB1 HC	GCA_004771355.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AJT61094.1	002070	LON-AAA	100	AVU32_gp253	Vibrio phage ValKK3	GCA_001501635.1
AGN30059.1	002070	LON-AAA	100	VPFG_00056	Vibrio phage nt-1	GCA_000910195.2
ALP47200.1	002070	LON-AAA	100	phiGrn1_0124	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47589.1	002070	LON-AAA	100	phiST2_0255	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54706.1	002070	LON-AAA	100	vBValMR10Z_165	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37243.1	002070	LON-AAA	100	pp2_009	Vibriophage phi-pp2	GCA_002630725.1
QCW18609.1	002071	Cluster1606_1clades	95	7t3_088	Salmonella phage 7t3	GCA_006083215.1
AZU98434.1	002071	Cluster1606_1clades	95	CPT_Munch_502	Salmonella phage Munch	GCA_004015485.1
QIG63079.1	002071	Cluster1606_1clades	95	SEPL_466	Salmonella phage SE_PL	GCA_011067555.1
QGT54705.1	002071	Cluster1606_1clades	97	b23_0090	Synechococcus phage B23	GCA_009745195.1
QGT54335.1	002071	Cluster1606_1clades	97	b3_0091	Synechococcus phage B3	GCA_009745215.1
AGB06877.1	002071	Cluster1606_1clades	100	CF80_gp090	Vibrio phage VH7D	GCA_000914495.1
QBX06269.1	002071	Cluster1606_1clades	100	ValB1HC_316	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60895.1	002071	Cluster1606_1clades	100	AVU32_gp054	Vibrio phage ValKK3	GCA_001501635.1
ALP47591.1	002071	Cluster1606_1clades	100	phiST2_0072	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54896.1	002071	Cluster1606_1clades	100	vBValMR10Z_356	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AHI60244.1	002072	Cluster1607_1clades	100	Ea357_093	Erwinia phage Ea35-70	GCA_000914635.1
QBP07202.1	002072	Cluster1607_1clades	100	REBECCA_95	Erwinia phage Rebecca	GCA_004521635.1
AUG85881.1	002072	Cluster1607_1clades	100	BOSOLAPHORUS_94	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52196.1	002072	Cluster1607_1clades	100	DM_98	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86200.1	002072	Cluster1607_1clades	100	DESERTFOX_93	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86523.1	002072	Cluster1607_1clades	100	MADMEL_95	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86846.1	002072	Cluster1607_1clades	100	MORTIMER_97	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51874.1	002072	Cluster1607_1clades	100	RAY_93	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51558.1	002072	Cluster1607_1clades	100	SIMMY50_96	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64906.1	002072	Cluster1607_1clades	100	SPECIALG_96	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13738.1	002073	Cluster1608_1clades	99	Ccr10_gp208c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14083.1	002073	Cluster1608_1clades	99	Ccr2_gp207c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14772.1	002073	Cluster1608_1clades	99	Ccr29_gp216	Caulobacter phage Ccr29	GCA_002619485.1
ARB15116.1	002073	Cluster1608_1clades	99	Ccr32_gp198	Caulobacter phage Ccr32	GCA_002619505.1
ARB15450.1	002073	Cluster1608_1clades	99	Ccr34_gp208	Caulobacter phage Ccr34	GCA_002619525.1
ARB14425.1	002073	Cluster1608_1clades	99	Ccr5_gp205c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87731.1	002073	Cluster1608_1clades	99	CcrKarma_gp214	Caulobacter virus Karma	GCA_000901575.1
AFU87380.1	002073	Cluster1608_1clades	99	CcrMagneto_gp210	Caulobacter virus Magneto	GCA_000903095.1
AFU88527.1	002073	Cluster1608_1clades	99	CcrSwift_gp209	Caulobacter virus Swift	GCA_000899655.1
AFU87035.1	002073	Cluster1608_1clades	99	CbK_gp203	Caulobacter virus phiCbK	GCA_000900535.1
AHI60292.1	002074	TM	99	Ea357_141	Erwinia phage Ea35-70	GCA_000914635.1
QBP07250.1	002074	TM	99	REBECCA_143	Erwinia phage Rebecca	GCA_004521635.1
AUG85930.1	002074	TM	99	BOSOLAPHORUS_143	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52245.1	002074	TM	99	DM_147	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86249.1	002074	TM	99	DESERTFOX_142	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86571.1	002074	TM	99	MADMEL_143	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86895.1	002074	TM	99	MORTIMER_146	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51923.1	002074	TM	99	RAY_142	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51607.1	002074	TM	99	SIMMY50_145	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64954.1	002074	TM	99	SPECIALG_144	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60429.1	002075	Cluster1610_1clades	99	Ea357_275	Erwinia phage Ea35-70	GCA_000914635.1
QBP07386.1	002075	Cluster1610_1clades	99	REBECCA_281	Erwinia phage Rebecca	GCA_004521635.1
AUG86068.1	002075	Cluster1610_1clades	99	BOSOLAPHORUS_282	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52384.1	002075	Cluster1610_1clades	99	DM_285	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86388.1	002075	Cluster1610_1clades	99	DESERTFOX_281	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86709.1	002075	Cluster1610_1clades	99	MADMEL_282	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87034.1	002075	Cluster1610_1clades	99	MORTIMER_286	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52059.1	002075	Cluster1610_1clades	99	RAY_279	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51742.1	002075	Cluster1610_1clades	99	SIMMY50_284	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65094.1	002075	Cluster1610_1clades	99	SPECIALG_283	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13559.1	002076	Cluster1611_1clades	98	Ccr10_gp031	Caulobacter phage Ccr10	GCA_002619445.1
ARB13905.1	002076	Cluster1611_1clades	98	Ccr2_gp030	Caulobacter phage Ccr2	GCA_002619465.1
ARB14594.1	002076	Cluster1611_1clades	98	Ccr29_gp037	Caulobacter phage Ccr29	GCA_002619485.1
ARB14949.1	002076	Cluster1611_1clades	97	Ccr32_gp030	Caulobacter phage Ccr32	GCA_002619505.1
ARB15280.1	002076	Cluster1611_1clades	97	Ccr34_gp031	Caulobacter phage Ccr34	GCA_002619525.1
ARB14248.1	002076	Cluster1611_1clades	98	Ccr5_gp030	Caulobacter phage Ccr5	GCA_002619545.1
AFU87548.1	002076	Cluster1611_1clades	96	CcrKarma_gp031	Caulobacter virus Karma	GCA_000901575.1
AFU87199.1	002076	Cluster1611_1clades	98	CcrMagneto_gp029	Caulobacter virus Magneto	GCA_000903095.1
AFU88345.1	002076	Cluster1611_1clades	96	CcrSwift_gp027	Caulobacter virus Swift	GCA_000899655.1
AFU86862.1	002076	Cluster1611_1clades	97	CbK_gp030	Caulobacter virus phiCbK	GCA_000900535.1
AHI60190.1	002077	SIG+TM	98	Ea357_040	Erwinia phage Ea35-70	GCA_000914635.1
QBP07148.1	002077	SIG+TM	98	REBECCA_40	Erwinia phage Rebecca	GCA_004521635.1
AUG85828.1	002077	SIG+TM	98	BOSOLAPHORUS_40	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52139.1	002077	SIG+TM	98	DM_41	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86148.1	002077	SIG+TM	98	DESERTFOX_40	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86468.1	002077	SIG+TM	98	MADMEL_40	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86789.1	002077	SIG+TM	98	MORTIMER_40	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51821.1	002077	SIG+TM	98	RAY_40	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51503.1	002077	SIG+TM	98	SIMMY50_41	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64850.1	002077	SIG+TM	98	SPECIALG_40	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60231.1	002078	Cluster1613_1clades	98	Ea357_080	Erwinia phage Ea35-70	GCA_000914635.1
QBP07190.1	002078	Cluster1613_1clades	98	REBECCA_82	Erwinia phage Rebecca	GCA_004521635.1
AUG85869.1	002078	Cluster1613_1clades	98	BOSOLAPHORUS_81	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52181.1	002078	Cluster1613_1clades	98	DM_83	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86188.1	002078	Cluster1613_1clades	98	DESERTFOX_80	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86510.1	002078	Cluster1613_1clades	98	MADMEL_82	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86831.1	002078	Cluster1613_1clades	98	MORTIMER_82	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51861.1	002078	Cluster1613_1clades	98	RAY_80	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51545.1	002078	Cluster1613_1clades	98	SIMMY50_83	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64893.1	002078	Cluster1613_1clades	98	SPECIALG_83	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43213.1	002079	Cluster1614_1clades	98	R1080702_207	Cyanophage S-RIM32	GCA_001754165.1
AMO43442.1	002079	Cluster1614_1clades	95	W270710_202	Cyanophage S-RIM44	GCA_002599145.1
AOO11685.1	002079	Cluster1614_1clades	95	ES420910_207	Cyanophage S-RIM44	GCA_002599165.1
AOO11914.1	002079	Cluster1614_1clades	95	Np050604_202	Cyanophage S-RIM44	GCA_002599185.1
AOO12151.1	002079	Cluster1614_1clades	95	Np200711_208	Cyanophage S-RIM44	GCA_002599205.1
AOO12386.1	002079	Cluster1614_1clades	95	Np420711_207	Cyanophage S-RIM44	GCA_002599225.1
AOO12615.1	002079	Cluster1614_1clades	95	Sn080709_202	Cyanophage S-RIM44	GCA_002599245.1
AOO12851.1	002079	Cluster1614_1clades	95	Sn130910_207	Cyanophage S-RIM44	GCA_002599265.1
AOO13081.1	002079	Cluster1614_1clades	95	W2100709_203	Cyanophage S-RIM44	GCA_002599285.1
ADO99301.1	002079	Cluster1614_1clades	95	Syn1_204	Prochlorococcus phage Syn1	GCA_000892495.1
AAQ64263.1	002080	Cluster1615_1clades	97	KVP40.0194	Vibrio phage KVP40	GCA_000843785.1
QIW90579.1	002080	Cluster1615_1clades	97	GCAPEGMB_00232	Vibrio phage V07	GCA_012361095.1
QIW91219.1	002080	Cluster1615_1clades	97	COHAPHLL_00383	Vibrio phage V09	GCA_012361135.1
QHJ74377.1	002080	Cluster1615_1clades	97	VH12019_00050	Vibrio phage VH1_2019	GCA_009931825.1
AGB06874.1	002080	Cluster1615_1clades	80	CF80_gp087	Vibrio phage VH7D	GCA_000914495.1
QBX06272.1	002080	Cluster1615_1clades	94	ValB1HC_319	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60898.1	002080	Cluster1615_1clades	94	AVU32_gp057	Vibrio phage ValKK3	GCA_001501635.1
ALP47266.1	002080	Cluster1615_1clades	80	phiGrn1_0313	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47610.1	002080	Cluster1615_1clades	94	phiST2_0069	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54899.1	002080	Cluster1615_1clades	94	vBValMR10Z_359	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AHI60205.1	002081	Cluster1616_1clades	97	Ea357_055	Erwinia phage Ea35-70	GCA_000914635.1
QBP07164.1	002081	Cluster1616_1clades	97	REBECCA_56	Erwinia phage Rebecca	GCA_004521635.1
AUG85844.1	002081	Cluster1616_1clades	97	BOSOLAPHORUS_56	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52156.1	002081	Cluster1616_1clades	97	DM_58	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86163.1	002081	Cluster1616_1clades	97	DESERTFOX_55	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86484.1	002081	Cluster1616_1clades	97	MADMEL_56	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86805.1	002081	Cluster1616_1clades	97	MORTIMER_56	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51836.1	002081	Cluster1616_1clades	97	RAY_55	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51519.1	002081	Cluster1616_1clades	97	SIMMY50_57	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64867.1	002081	Cluster1616_1clades	97	SPECIALG_57	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43233.1	002082	Cluster1617_1clades	97	R1080702_228	Cyanophage S-RIM32	GCA_001754165.1
AMO43465.1	002082	Cluster1617_1clades	87	W270710_226	Cyanophage S-RIM44	GCA_002599145.1
AOO11705.1	002082	Cluster1617_1clades	87	ES420910_228	Cyanophage S-RIM44	GCA_002599165.1
AOO11937.1	002082	Cluster1617_1clades	87	Np050604_226	Cyanophage S-RIM44	GCA_002599185.1
AOO12171.1	002082	Cluster1617_1clades	87	Np200711_229	Cyanophage S-RIM44	GCA_002599205.1
AOO12406.1	002082	Cluster1617_1clades	87	Np420711_228	Cyanophage S-RIM44	GCA_002599225.1
AOO12638.1	002082	Cluster1617_1clades	87	Sn080709_226	Cyanophage S-RIM44	GCA_002599245.1
AOO12871.1	002082	Cluster1617_1clades	87	Sn130910_228	Cyanophage S-RIM44	GCA_002599265.1
AOO13104.1	002082	Cluster1617_1clades	87	W2100709_227	Cyanophage S-RIM44	GCA_002599285.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADO99326.1	002082	Cluster1617_1clades	87	Syn1_230	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60235.1	002083	Cluster1618_1clades	75	Ea357_084	Erwinia phage Ea35-70	GCA_000914635.1
QBP07194.1	002083	Cluster1618_1clades	97	REBECCA_87	Erwinia phage Rebecca	GCA_004521635.1
AUG85873.1	002083	Cluster1618_1clades	97	BOSOLAPHORUS_86	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52186.1	002083	Cluster1618_1clades	97	DM_88	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86192.1	002083	Cluster1618_1clades	97	DESERTFOX_85	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86515.1	002083	Cluster1618_1clades	97	MADMEL_87	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86836.1	002083	Cluster1618_1clades	97	MORTIMER_87	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51866.1	002083	Cluster1618_1clades	97	RAY_85	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51550.1	002083	Cluster1618_1clades	97	SIMMY50_88	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64898.1	002083	Cluster1618_1clades	97	SPECIALG_88	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60232.1	002084	SIG+TM+TM	96	Ea357_081	Erwinia phage Ea35-70	GCA_000914635.1
QBP07191.1	002084	SIG+TM+TM	96	REBECCA_83	Erwinia phage Rebecca	GCA_004521635.1
AUG85870.1	002084	SIG+TM+TM	96	BOSOLAPHORUS_82	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52182.1	002084	SIG+TM+TM	96	DM_84	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86189.1	002084	SIG+TM+TM	96	DESERTFOX_81	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86511.1	002084	SIG+TM+TM	96	MADMEL_83	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86832.1	002084	SIG+TM+TM	96	MORTIMER_83	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51862.1	002084	SIG+TM+TM	96	RAY_81	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51546.1	002084	SIG+TM+TM	96	SIMMY50_84	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64894.1	002084	SIG+TM+TM	96	SPECIALG_84	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60245.1	002085	HTH	96	Ea357_094	Erwinia phage Ea35-70	GCA_000914635.1
QBP07203.1	002085	HTH	96	REBECCA_96	Erwinia phage Rebecca	GCA_004521635.1
AUG85882.1	002085	HTH	96	BOSOLAPHORUS_95	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52197.1	002085	HTH	96	DM_99	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86201.1	002085	HTH	96	DESERTFOX_94	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86524.1	002085	HTH	96	MADMEL_96	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86847.1	002085	HTH	96	MORTIMER_98	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51875.1	002085	HTH	96	RAY_94	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51559.1	002085	HTH	96	SIMMY50_97	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64907.1	002085	HTH	96	SPECIALG_97	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60384.1	002086	Cluster1621_1clades	96	Ea357_231	Erwinia phage Ea35-70	GCA_000914635.1
QBP07340.1	002086	Cluster1621_1clades	96	REBECCA_235	Erwinia phage Rebecca	GCA_004521635.1
AUG86022.1	002086	Cluster1621_1clades	96	BOSOLAPHORUS_236	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52339.1	002086	Cluster1621_1clades	96	DM_239	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86341.1	002086	Cluster1621_1clades	96	DESERTFOX_234	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86665.1	002086	Cluster1621_1clades	96	MADMEL_237	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86987.1	002086	Cluster1621_1clades	96	MORTIMER_239	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52013.1	002086	Cluster1621_1clades	96	RAY_233	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51697.1	002086	Cluster1621_1clades	96	SIMMY50_238	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65048.1	002086	Cluster1621_1clades	96	SPECIALG_237	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT14169.1	002087	Cluster1622_1clades	75	PBI_121Q_279	Escherichia phage 121Q	GCA_000926855.1
QAY00766.1	002087	Cluster1622_1clades	75	Ecwhy1_492	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34946.1	002087	Cluster1622_1clades	94	ACQ29_gp266	Escherichia phage PBECO4	GCA_001041035.1
BBM61844.1	002087	Cluster1622_1clades	75	EO157G_2550	Escherichia phage SP27	GCA_008033345.1
AXC37048.1	002087	Cluster1622_1clades	75	-	Escherichia phage UB	GCA_003341455.1
QBO61536.1	002087	Cluster1622_1clades	75	G17_00040	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62142.1	002087	Cluster1622_1clades	75	G17_00653	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14150.1	002087	Cluster1622_1clades	75	vBEcoMphAPEC6_gp527c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80155.1	002087	Cluster1622_1clades	75	PSLUR01_00178	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44620.1	002087	Cluster1622_1clades	87	RaK2_00347	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AHI60381.1	002088	Cluster1623_1clades	94	Ea357_228	Erwinia phage Ea35-70	GCA_000914635.1
QBP07338.1	002088	Cluster1623_1clades	94	REBECCA_233	Erwinia phage Rebecca	GCA_004521635.1
AUG86020.1	002088	Cluster1623_1clades	94	BOSOLAPHORUS_234	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52337.1	002088	Cluster1623_1clades	94	DM_237	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86339.1	002088	Cluster1623_1clades	94	DESERTFOX_232	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86663.1	002088	Cluster1623_1clades	94	MADMEL_235	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86984.1	002088	Cluster1623_1clades	94	MORTIMER_236	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52011.1	002088	Cluster1623_1clades	94	RAY_231	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51695.1	002088	Cluster1623_1clades	94	SIMMY50_236	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65046.1	002088	Cluster1623_1clades	94	SPECIALG_235	Erwinia phage vB_EamM_Special G	GCA_002624385.1
APU01619.1	002089	Cluster1624_1clades	67	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28851.1	002089	Cluster1624_1clades	94	AP1_0144	Aeromonas phage AP1	GCA_014183365.1
ATI17255.1	002089	Cluster1624_1clades	71	-	Aeromonas phage AS-szw	GCA_002743635.1
ATI17286.1	002089	Cluster1624_1clades	80	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00336.1	002089	Cluster1624_1clades	71	HWB28_gp216	Aeromonas phage AS-zj	GCA_002627665.1
ASU00310.1	002089	Cluster1624_1clades	80	HWB28_gp242	Aeromonas phage AS-zj	GCA_002627665.1
QAX97728.1	002089	Cluster1624_1clades	85	ASswx1_82	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01425.1	002089	Cluster1624_1clades	77	ASwh1_366	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39177.1	002089	Cluster1624_1clades	85	CC2_030	Aeromonas phage CC2	GCA_000903495.1
ADQ53244.1	002089	Cluster1624_1clades	67	65p236	Aeromonas virus 65	GCA_000893255.1
AHI60239.1	002090	Cluster1625_1clades	92	Ea357_088	Erwinia phage Ea35-70	GCA_000914635.1
QBP07196.1	002090	Cluster1625_1clades	92	REBECCA_89	Erwinia phage Rebecca	GCA_004521635.1
AUG85875.1	002090	Cluster1625_1clades	92	BOSOLAPHORUS_88	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52190.1	002090	Cluster1625_1clades	92	DM_92	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86194.1	002090	Cluster1625_1clades	92	DESERTFOX_87	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86517.1	002090	Cluster1625_1clades	92	MADMEL_89	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86840.1	002090	Cluster1625_1clades	92	MORTIMER_91	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51868.1	002090	Cluster1625_1clades	92	RAY_87	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51552.1	002090	Cluster1625_1clades	92	SIMMY50_90	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64900.1	002090	Cluster1625_1clades	92	SPECIALG_90	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AIT14067.1	002091	Cluster1626_1clades	91	PBI_121Q_177	Escherichia phage 121Q	GCA_000926855.1
QAY00855.1	002091	Cluster1626_1clades	91	Ecwhy1_584	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35026.1	002091	Cluster1626_1clades	91	ACQ29_gp346	Escherichia phage PBECO4	GCA_001041035.1
BBM61750.1	002091	Cluster1626_1clades	91	EO157G_1610	Escherichia phage SP27	GCA_008033345.1
AXC36603.1	002091	Cluster1626_1clades	90	-	Escherichia phage UB	GCA_003341455.1
QBO61632.1	002091	Cluster1626_1clades	91	G17_00136	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80062.1	002091	Cluster1626_1clades	91	PSLUR01_00085	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18611.1	002091	Cluster1626_1clades	86	7t3_090	Salmonella phage 7t3	GCA_006083215.1
AZU98436.1	002091	Cluster1626_1clades	82	CPT_Munch_504	Salmonella phage Munch	GCA_004015485.1
QIG63077.1	002091	Cluster1626_1clades	86	SEPL_464	Salmonella phage SE_PL	GCA_011067555.1
AHI60234.1	002092	Cluster1627_1clades	90	Ea357_083	Erwinia phage Ea35-70	GCA_000914635.1
QBP07193.1	002092	Cluster1627_1clades	90	REBECCA_86	Erwinia phage Rebecca	GCA_004521635.1
AUG85872.1	002092	Cluster1627_1clades	90	BOSOLAPHORUS_85	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52185.1	002092	Cluster1627_1clades	90	DM_87	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86191.1	002092	Cluster1627_1clades	90	DESERTFOX_84	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86514.1	002092	Cluster1627_1clades	90	MADMEL_86	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86835.1	002092	Cluster1627_1clades	90	MORTIMER_86	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51865.1	002092	Cluster1627_1clades	90	RAY_84	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51549.1	002092	Cluster1627_1clades	90	SIMMY50_87	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64897.1	002092	Cluster1627_1clades	90	SPECIALG_87	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63114.1	002093	Cluster1628_1clades	78	201phi2-1p288	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44988.1	002093	Cluster1628_1clades	83	KTN4_230	Pseudomonas phage KTN4	GCA_002607225.1
QBX32378.1	002093	Cluster1628_1clades	76	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76913.1	002093	Cluster1628_1clades	90	PHABIO_282	Pseudomonas phage Phabio	GCA_002624965.1
AEH03648.1	002093	Cluster1628_1clades	81	225	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02784.1	002093	Cluster1628_1clades	77	PSA21_258	Pseudomonas phage Psa21	GCA_004340405.1
ATN94726.1	002093	Cluster1628_1clades	83	SL2_149	Pseudomonas phage SL2	GCA_002956015.1
QJB22866.1	002093	Cluster1628_1clades	83	fnug_223	Pseudomonas phage fnug	GCA_012837215.1
QEM41951.1	002093	Cluster1628_1clades	76	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83090.1	002093	Cluster1628_1clades	83	PHIKZ189	Pseudomonas virus phiKZ	GCA_000842965.1
ARB13781.1	002094	SIG+TM	89	Ccr10_gp251	Caulobacter phage Ccr10	GCA_002619445.1
ARB14126.1	002094	SIG+TM	89	Ccr2_gp250	Caulobacter phage Ccr2	GCA_002619465.1
ARB14820.1	002094	SIG+TM	89	Ccr29_gp264	Caulobacter phage Ccr29	GCA_002619485.1
ARB15160.1	002094	SIG+TM	89	Ccr32_gp242	Caulobacter phage Ccr32	GCA_002619505.1
ARB15494.1	002094	SIG+TM	89	Ccr34_gp252	Caulobacter phage Ccr34	GCA_002619525.1
ARB14468.1	002094	SIG+TM	89	Ccr5_gp248	Caulobacter phage Ccr5	GCA_002619545.1
AFU87777.1	002094	SIG+TM	89	CcrKarma_gp260	Caulobacter virus Karma	GCA_000901575.1
AFU87424.1	002094	SIG+TM	89	CcrMagneto_gp254	Caulobacter virus Magneto	GCA_000903095.1
AFU88571.1	002094	SIG+TM	89	CcrSwift_gp253	Caulobacter virus Swift	GCA_000899655.1
AFU87079.1	002094	SIG+TM	89	CbK_gp247	Caulobacter virus phiCbK	GCA_000900535.1
AHI60184.1	002095	Cluster1630_1clades	89	Ea357_034	Erwinia phage Ea35-70	GCA_000914635.1
QBP07142.1	002095	Cluster1630_1clades	89	REBECCA_34	Erwinia phage Rebecca	GCA_004521635.1
AUG85822.1	002095	Cluster1630_1clades	89	BOSOLAPHORUS_34	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52133.1	002095	Cluster1630_1clades	89	DM_35	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86142.1	002095	Cluster1630_1clades	89	DESERTFOX_34	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86462.1	002095	Cluster1630_1clades	89	MADMEL_34	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86783.1	002095	Cluster1630_1clades	89	MORTIMER_34	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51815.1	002095	Cluster1630_1clades	89	RAY_34	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51497.1	002095	Cluster1630_1clades	89	SIMMY50_35	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64844.1	002095	Cluster1630_1clades	89	SPECIALG_34	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13791.1	002096	Cluster1631_1clades	88	Ccr10_gp261	Caulobacter phage Ccr10	GCA_002619445.1
ARB14136.1	002096	Cluster1631_1clades	88	Ccr2_gp260	Caulobacter phage Ccr2	GCA_002619465.1
ARB14830.1	002096	Cluster1631_1clades	88	Ccr29_gp274	Caulobacter phage Ccr29	GCA_002619485.1
ARB15170.1	002096	Cluster1631_1clades	88	Ccr32_gp252	Caulobacter phage Ccr32	GCA_002619505.1
ARB15504.1	002096	Cluster1631_1clades	88	Ccr34_gp262	Caulobacter phage Ccr34	GCA_002619525.1
ARB14478.1	002096	Cluster1631_1clades	88	Ccr5_gp258	Caulobacter phage Ccr5	GCA_002619545.1
AFU87788.1	002096	Cluster1631_1clades	88	CcrKarma_gp271	Caulobacter virus Karma	GCA_000901575.1
AFU87435.1	002096	Cluster1631_1clades	88	CcrMagneto_gp265	Caulobacter virus Magneto	GCA_000903095.1
AFU88581.1	002096	Cluster1631_1clades	88	CcrSwift_gp263	Caulobacter virus Swift	GCA_000899655.1
AFU87089.1	002096	Cluster1631_1clades	88	CbK_gp257	Caulobacter virus phiCbK	GCA_000900535.1
QGH72004.1	002097	Cluster1632_1clades	46	N1M2_141	Klebsiella phage N1M2	GCA_010092605.1
ABY63208.1	002097	Cluster1632_1clades	87	201phi2-1p383	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44962.1	002097	Cluster1632_1clades	58	KTN4_204	Pseudomonas phage KTN4	GCA_002607225.1
ARV77007.1	002097	Cluster1632_1clades	67	PHABIO_376	Pseudomonas phage Phabio	GCA_002624965.1
AEH03739.1	002097	Cluster1632_1clades	56	316	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94752.1	002097	Cluster1632_1clades	58	SL2_175	Pseudomonas phage SL2	GCA_002956015.1
QJB22840.1	002097	Cluster1632_1clades	58	fnug_197	Pseudomonas phage fnug	GCA_012837215.1
AGC26339.1	002097	Cluster1632_1clades	58	PHIKZ165.1	Pseudomonas virus phiKZ	GCA_000842965.1
ATA65685.1	002097	Cluster1632_1clades	39	2050HW_00350	Serratia phage 2050HW	GCA_002628125.1
QDB71106.1	002097	Cluster1632_1clades	52	CPT_Moabite_074	Serratia phage Moabite	GCA_006384735.1
AHI60352.1	002098	Cluster1633_1clades	56	Ea357_200	Erwinia phage Ea35-70	GCA_000914635.1
QBP07310.1	002098	Cluster1633_1clades	87	REBECCA_205	Erwinia phage Rebecca	GCA_004521635.1
AUG85991.1	002098	Cluster1633_1clades	56	BOSOLAPHORUS_205	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52306.3	002098	Cluster1633_1clades	87	DM_208	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86310.1	002098	Cluster1633_1clades	56	DESERTFOX_203	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86633.1	002098	Cluster1633_1clades	56	MADMEL_205	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86956.1	002098	Cluster1633_1clades	56	MORTIMER_208	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51983.2	002098	Cluster1633_1clades	87	RAY_203	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51667.1	002098	Cluster1633_1clades	56	SIMMY50_206	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65015.3	002098	Cluster1633_1clades	87	SPECIALG_206	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43092.1	002099	Cluster1634_1clades	74	R1080702_083	Cyanophage S-RIM32	GCA_001754165.1
AMO43320.1	002099	Cluster1634_1clades	86	W270710_076	Cyanophage S-RIM44	GCA_002599145.1
AOO11554.1	002099	Cluster1634_1clades	86	ES420910_073	Cyanophage S-RIM44	GCA_002599165.1
AOO11792.1	002099	Cluster1634_1clades	86	Np050604_076	Cyanophage S-RIM44	GCA_002599185.1
AOO12019.1	002099	Cluster1634_1clades	86	Np200711_073	Cyanophage S-RIM44	GCA_002599205.1
AOO12255.1	002099	Cluster1634_1clades	86	Np420711_073	Cyanophage S-RIM44	GCA_002599225.1
AOO12493.1	002099	Cluster1634_1clades	86	Sn080709_076	Cyanophage S-RIM44	GCA_002599245.1
AOO12720.1	002099	Cluster1634_1clades	86	Sn130910_073	Cyanophage S-RIM44	GCA_002599265.1
AOO12958.1	002099	Cluster1634_1clades	86	W2100709_076	Cyanophage S-RIM44	GCA_002599285.1
ADO99176.1	002099	Cluster1634_1clades	86	Syn1_075	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60248.1	002100	Cluster1635_1clades	85	Ea357_097	Erwinia phage Ea35-70	GCA_000914635.1
QBP07206.1	002100	Cluster1635_1clades	85	REBECCA_99	Erwinia phage Rebecca	GCA_004521635.1
AUG85885.1	002100	Cluster1635_1clades	85	BOSOLAPHORUS_98	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52200.1	002100	Cluster1635_1clades	85	DM_102	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86204.1	002100	Cluster1635_1clades	85	DESERTFOX_97	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86527.1	002100	Cluster1635_1clades	85	MADMEL_99	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86850.1	002100	Cluster1635_1clades	85	MORTIMER_101	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51878.1	002100	Cluster1635_1clades	85	RAY_97	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51562.1	002100	Cluster1635_1clades	85	SIMMY50_100	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64910.1	002100	Cluster1635_1clades	85	SPECIALG_100	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43103.1	002101	Cluster1636_1clades	84	R1080702_094	Cyanophage S-RIM32	GCA_001754165.1
AMO43331.1	002101	Cluster1636_1clades	84	W270710_087	Cyanophage S-RIM44	GCA_002599145.1
AOO11564.1	002101	Cluster1636_1clades	84	ES420910_083	Cyanophage S-RIM44	GCA_002599165.1
AOO11803.1	002101	Cluster1636_1clades	84	Np050604_087	Cyanophage S-RIM44	GCA_002599185.1
AOO12029.1	002101	Cluster1636_1clades	84	Np200711_083	Cyanophage S-RIM44	GCA_002599205.1
AOO12265.1	002101	Cluster1636_1clades	84	Np420711_083	Cyanophage S-RIM44	GCA_002599225.1
AOO12504.1	002101	Cluster1636_1clades	84	Sn080709_087	Cyanophage S-RIM44	GCA_002599245.1
AOO12730.1	002101	Cluster1636_1clades	84	Sn130910_083	Cyanophage S-RIM44	GCA_002599265.1
AOO12970.1	002101	Cluster1636_1clades	84	W2100709_088	Cyanophage S-RIM44	GCA_002599285.1
ADO99188.1	002101	Cluster1636_1clades	84	Syn1_087	Prochlorococcus phage Syn1	GCA_000892495.1
AMO43169.1	002102	Cluster1637_1clades	41	R1080702_160	Cyanophage S-RIM32	GCA_001754165.1
AMO43395.1	002102	Cluster1637_1clades	84	W270710_151	Cyanophage S-RIM44	GCA_002599145.1
AOO11639.1	002102	Cluster1637_1clades	84	ES420910_158	Cyanophage S-RIM44	GCA_002599165.1
AOO11867.1	002102	Cluster1637_1clades	84	Np050604_151	Cyanophage S-RIM44	GCA_002599185.1
AOO12105.1	002102	Cluster1637_1clades	84	Np200711_159	Cyanophage S-RIM44	GCA_002599205.1
AOO12340.1	002102	Cluster1637_1clades	84	Np420711_158	Cyanophage S-RIM44	GCA_002599225.1
AOO12568.1	002102	Cluster1637_1clades	84	Sn080709_151	Cyanophage S-RIM44	GCA_002599245.1
AOO12805.1	002102	Cluster1637_1clades	84	Sn130910_158	Cyanophage S-RIM44	GCA_002599265.1
AOO13034.1	002102	Cluster1637_1clades	84	W2100709_152	Cyanophage S-RIM44	GCA_002599285.1
ADO99254.1	002102	Cluster1637_1clades	84	Syn1_153	Prochlorococcus phage Syn1	GCA_000892495.1
AIT14199.1	002103	Cluster1638_1clades	73	PBI_121Q_309	Escherichia phage 121Q	GCA_000926855.1
QAY00740.1	002103	Cluster1638_1clades	84	Ecwhy1_465	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34920.1	002103	Cluster1638_1clades	73	ACQ29_gp240	Escherichia phage PBECO4	GCA_001041035.1
BBM61872.1	002103	Cluster1638_1clades	73	EO157G_2830	Escherichia phage SP27	GCA_008033345.1
AXC37023.1	002103	Cluster1638_1clades	73	-	Escherichia phage UB	GCA_003341455.1
QBO61507.1	002103	Cluster1638_1clades	73	G17_00011	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62113.1	002103	Cluster1638_1clades	73	G17_00624	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14122.1	002103	Cluster1638_1clades	73	vBEcoMphAPEC6_gp499c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80182.1	002103	Cluster1638_1clades	73	PSLUR01_00205	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44631.1	002103	Cluster1638_1clades	78	RaK2_00358	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMO43057.1	002104	Cluster1639_1clades	83	R1080702_048	Cyanophage S-RIM32	GCA_001754165.1
AMO43295.1	002104	Cluster1639_1clades	83	W270710_051	Cyanophage S-RIM44	GCA_002599145.1
AOO11529.1	002104	Cluster1639_1clades	83	ES420910_048	Cyanophage S-RIM44	GCA_002599165.1
AOO11767.1	002104	Cluster1639_1clades	83	Np050604_051	Cyanophage S-RIM44	GCA_002599185.1
AOO11994.1	002104	Cluster1639_1clades	83	Np200711_048	Cyanophage S-RIM44	GCA_002599205.1
AOO12230.1	002104	Cluster1639_1clades	83	Np420711_048	Cyanophage S-RIM44	GCA_002599225.1
AOO12468.1	002104	Cluster1639_1clades	83	Sn080709_051	Cyanophage S-RIM44	GCA_002599245.1
AOO12695.1	002104	Cluster1639_1clades	83	Sn130910_048	Cyanophage S-RIM44	GCA_002599265.1
AOO12933.1	002104	Cluster1639_1clades	83	W2100709_051	Cyanophage S-RIM44	GCA_002599285.1
ADO99149.1	002104	Cluster1639_1clades	83	Syn1_048	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13715.1	002105	Cluster1640_1clades	81	Ccr10_gp185c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14060.1	002105	Cluster1640_1clades	81	Ccr2_gp184c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14747.1	002105	Cluster1640_1clades	81	Ccr29_gp191	Caulobacter phage Ccr29	GCA_002619485.1
ARB15102.1	002105	Cluster1640_1clades	81	Ccr32_gp184	Caulobacter phage Ccr32	GCA_002619505.1
ARB15436.1	002105	Cluster1640_1clades	81	Ccr34_gp194	Caulobacter phage Ccr34	GCA_002619525.1
ARB14403.1	002105	Cluster1640_1clades	81	Ccr5_gp183c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87708.1	002105	Cluster1640_1clades	81	CcrKarma_gp191	Caulobacter virus Karma	GCA_000901575.1
AFU87357.1	002105	Cluster1640_1clades	81	CcrMagneto_gp187	Caulobacter virus Magneto	GCA_000903095.1
AFU88504.1	002105	Cluster1640_1clades	81	CcrSwift_gp186	Caulobacter virus Swift	GCA_000899655.1
AFU87021.1	002105	Cluster1640_1clades	81	CbK_gp189	Caulobacter virus phiCbK	GCA_000900535.1
ARB13765.1	002106	Cluster1641_1clades	80	Ccr10_gp235	Caulobacter phage Ccr10	GCA_002619445.1
ARB14110.1	002106	Cluster1641_1clades	80	Ccr2_gp234	Caulobacter phage Ccr2	GCA_002619465.1
ARB14804.1	002106	Cluster1641_1clades	80	Ccr29_gp248	Caulobacter phage Ccr29	GCA_002619485.1
ARB15144.1	002106	Cluster1641_1clades	80	Ccr32_gp226	Caulobacter phage Ccr32	GCA_002619505.1
ARB15478.1	002106	Cluster1641_1clades	80	Ccr34_gp236	Caulobacter phage Ccr34	GCA_002619525.1
ARB14452.1	002106	Cluster1641_1clades	80	Ccr5_gp232	Caulobacter phage Ccr5	GCA_002619545.1
AFU87760.1	002106	Cluster1641_1clades	80	CcrKarma_gp243	Caulobacter virus Karma	GCA_000901575.1
AFU87407.1	002106	Cluster1641_1clades	80	CcrMagneto_gp237	Caulobacter virus Magneto	GCA_000903095.1
AFU88555.1	002106	Cluster1641_1clades	80	CcrSwift_gp237	Caulobacter virus Swift	GCA_000899655.1
AFU87063.1	002106	Cluster1641_1clades	80	CbK_gp231	Caulobacter virus phiCbK	GCA_000900535.1
AIT14180.1	002107	Cluster1642_1clades	59	PBI_121Q_290	Escherichia phage 121Q	GCA_000926855.1
QAY00757.1	002107	Cluster1642_1clades	59	Ecwhy1_483	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34936.1	002107	Cluster1642_1clades	80	ACQ29_gp256	Escherichia phage PBECO4	GCA_001041035.1
BBM61855.1	002107	Cluster1642_1clades	59	EO157G_2660	Escherichia phage SP27	GCA_008033345.1
AXC37039.1	002107	Cluster1642_1clades	59	-	Escherichia phage UB	GCA_003341455.1
QBO61525.1	002107	Cluster1642_1clades	59	G17_00029	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62131.1	002107	Cluster1642_1clades	59	G17_00642	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14139.1	002107	Cluster1642_1clades	59	vBEcoMphAPEC6_gp516c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80165.1	002107	Cluster1642_1clades	59	PSLUR01_00188	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFA44609.1	002107	Cluster1642_1clades	59	RaK2_00336	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AAQ64382.1	002108	Cluster1643_1clades	79	KVP40.0312	Vibrio phage KVP40	GCA_000843785.1
QIW90697.1	002108	Cluster1643_1clades	79	GCAPEGMB_00355	Vibrio phage V07	GCA_012361095.1
QIW91101.1	002108	Cluster1643_1clades	79	COHAPHLL_00260	Vibrio phage V09	GCA_012361135.1
QBX06159.1	002108	Cluster1643_1clades	79	ValB1HC_206	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61173.1	002108	Cluster1643_1clades	79	AVU32_gp332	Vibrio phage ValKK3	GCA_001501635.1
AGN30361.1	002108	Cluster1643_1clades	80	VPFG_00364	Vibrio phage nt-1	GCA_000910195.2
ALP47268.1	002108	Cluster1643_1clades	79	phiGrn1_0048	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47649.1	002108	Cluster1643_1clades	79	phiST2_0180	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54785.1	002108	Cluster1643_1clades	79	vBValMR10Z_245	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37543.1	002108	Cluster1643_1clades	79	pp2_310	Vibriophage phi-pp2	GCA_002630725.1
AMO43208.1	002109	Cluster1644_1clades	79	R1080702_201	Cyanophage S-RIM32	GCA_001754165.1
AMO43437.1	002109	Cluster1644_1clades	74	W270710_197	Cyanophage S-RIM44	GCA_002599145.1
AOO11680.1	002109	Cluster1644_1clades	74	ES420910_202	Cyanophage S-RIM44	GCA_002599165.1
AOO11909.1	002109	Cluster1644_1clades	74	Np050604_197	Cyanophage S-RIM44	GCA_002599185.1
AOO12146.1	002109	Cluster1644_1clades	74	Np200711_203	Cyanophage S-RIM44	GCA_002599205.1
AOO12381.1	002109	Cluster1644_1clades	74	Np420711_202	Cyanophage S-RIM44	GCA_002599225.1
AOO12610.1	002109	Cluster1644_1clades	74	Sn080709_197	Cyanophage S-RIM44	GCA_002599245.1
AOO12846.1	002109	Cluster1644_1clades	74	Sn130910_202	Cyanophage S-RIM44	GCA_002599265.1
AOO13076.1	002109	Cluster1644_1clades	74	W2100709_198	Cyanophage S-RIM44	GCA_002599285.1
ADO99296.1	002109	Cluster1644_1clades	74	Syn1_199	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13577.1	002110	HTH	78	Ccr10_gp049	Caulobacter phage Ccr10	GCA_002619445.1
ARB13923.1	002110	HTH	78	Ccr2_gp048	Caulobacter phage Ccr2	GCA_002619465.1
ARB14612.1	002110	HTH	78	Ccr29_gp055	Caulobacter phage Ccr29	GCA_002619485.1
ARB14968.1	002110	HTH	78	Ccr32_gp049	Caulobacter phage Ccr32	GCA_002619505.1
ARB15299.1	002110	HTH	78	Ccr34_gp050	Caulobacter phage Ccr34	GCA_002619525.1
ARB14266.1	002110	HTH	78	Ccr5_gp048	Caulobacter phage Ccr5	GCA_002619545.1
AFU87567.1	002110	HTH	78	CcrKarma_gp050	Caulobacter virus Karma	GCA_000901575.1
AFU87217.1	002110	HTH	78	CcrMagneto_gp047	Caulobacter virus Magneto	GCA_000903095.1
AFU88365.1	002110	HTH	77	CcrSwift_gp047	Caulobacter virus Swift	GCA_000899655.1
AFU86881.1	002110	HTH	78	CbK_gp049	Caulobacter virus phiCbK	GCA_000900535.1
ARB13805.1	002111	Cluster1646_1clades	77	Ccr10_gp275	Caulobacter phage Ccr10	GCA_002619445.1
ARB14150.1	002111	Cluster1646_1clades	77	Ccr2_gp274	Caulobacter phage Ccr2	GCA_002619465.1
ARB14844.1	002111	Cluster1646_1clades	77	Ccr29_gp288	Caulobacter phage Ccr29	GCA_002619485.1
ARB15184.1	002111	Cluster1646_1clades	77	Ccr32_gp266	Caulobacter phage Ccr32	GCA_002619505.1
ARB15518.1	002111	Cluster1646_1clades	77	Ccr34_gp276	Caulobacter phage Ccr34	GCA_002619525.1
ARB14493.1	002111	Cluster1646_1clades	77	Ccr5_gp273	Caulobacter phage Ccr5	GCA_002619545.1
AFU87803.1	002111	Cluster1646_1clades	77	CcrKarma_gp286	Caulobacter virus Karma	GCA_000901575.1
AFU87450.1	002111	Cluster1646_1clades	77	CcrMagneto_gp280	Caulobacter virus Magneto	GCA_000903095.1
AFU88595.1	002111	Cluster1646_1clades	77	CcrSwift_gp277	Caulobacter virus Swift	GCA_000899655.1
AFU87103.1	002111	Cluster1646_1clades	77	CbK_gp271	Caulobacter virus phiCbK	GCA_000900535.1
AAQ64388.1	002112	Cluster1647_1clades	76	KVP40.0318	Vibrio phage KVP40	GCA_000843785.1
QIW90702.1	002112	Cluster1647_1clades	76	GCAPEGMB_00382	Vibrio phage V07	GCA_012361095.1
QIW91096.1	002112	Cluster1647_1clades	76	COHAPHLL_00234	Vibrio phage V09	GCA_012361135.1
QHJ74501.1	002112	Cluster1647_1clades	76	VH12019_00200	Vibrio phage VH1_2019	GCA_009931825.1
QBX06154.1	002112	Cluster1647_1clades	76	ValB1HC_200	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61166.1	002112	Cluster1647_1clades	76	AVU32_gp325	Vibrio phage ValKK3	GCA_001501635.1
ALP47275.1	002112	Cluster1647_1clades	76	phiGrn1_0053	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47660.1	002112	Cluster1647_1clades	76	phiST2_0185	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54779.1	002112	Cluster1647_1clades	76	vBValMR10Z_239	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37551.1	002112	Cluster1647_1clades	76	pp2_319	Vibriophage phi-pp2	GCA_002630725.1
ARB13564.1	002113	Cluster1648_1clades	76	Ccr10_gp036	Caulobacter phage Ccr10	GCA_002619445.1
ARB13910.1	002113	Cluster1648_1clades	76	Ccr2_gp035	Caulobacter phage Ccr2	GCA_002619465.1
ARB14599.1	002113	Cluster1648_1clades	76	Ccr29_gp042	Caulobacter phage Ccr29	GCA_002619485.1
ARB14954.1	002113	Cluster1648_1clades	75	Ccr32_gp035	Caulobacter phage Ccr32	GCA_002619505.1
ARB15285.1	002113	Cluster1648_1clades	75	Ccr34_gp036	Caulobacter phage Ccr34	GCA_002619525.1
ARB14253.1	002113	Cluster1648_1clades	76	Ccr5_gp035	Caulobacter phage Ccr5	GCA_002619545.1
AFU87553.1	002113	Cluster1648_1clades	75	CcrKarma_gp036	Caulobacter virus Karma	GCA_000901575.1
AFU87204.1	002113	Cluster1648_1clades	76	CcrMagneto_gp034	Caulobacter virus Magneto	GCA_000903095.1
AFU88350.1	002113	Cluster1648_1clades	75	CcrSwift_gp032	Caulobacter virus Swift	GCA_000899655.1
AFU86867.1	002113	Cluster1648_1clades	75	CbK_gp035	Caulobacter virus phiCbK	GCA_000900535.1
AHI60409.1	002114	Cluster1649_1clades	76	Ea357_255	Erwinia phage Ea35-70	GCA_000914635.1
QBP07366.1	002114	Cluster1649_1clades	76	REBECCA_261	Erwinia phage Rebecca	GCA_004521635.1
AUG86048.1	002114	Cluster1649_1clades	76	BOSOLAPHORUS_262	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52364.2	002114	Cluster1649_1clades	76	DM_265	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86368.1	002114	Cluster1649_1clades	76	DESERTFOX_261	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86689.1	002114	Cluster1649_1clades	76	MADMEL_262	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87014.1	002114	Cluster1649_1clades	76	MORTIMER_266	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52039.1	002114	Cluster1649_1clades	76	RAY_259	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51722.1	002114	Cluster1649_1clades	76	SIMMY50_264	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65074.2	002114	Cluster1649_1clades	76	SPECIALG_263	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13818.1	002115	Cluster1650_1clades	75	Ccr10_gp288	Caulobacter phage Ccr10	GCA_002619445.1
ARB14163.1	002115	Cluster1650_1clades	75	Ccr2_gp287	Caulobacter phage Ccr2	GCA_002619465.1
ARB14857.1	002115	Cluster1650_1clades	75	Ccr29_gp301	Caulobacter phage Ccr29	GCA_002619485.1
ARB15196.1	002115	Cluster1650_1clades	75	Ccr32_gp278	Caulobacter phage Ccr32	GCA_002619505.1
ARB15530.1	002115	Cluster1650_1clades	75	Ccr34_gp288	Caulobacter phage Ccr34	GCA_002619525.1
ARB14505.1	002115	Cluster1650_1clades	75	Ccr5_gp285	Caulobacter phage Ccr5	GCA_002619545.1
AFU87815.1	002115	Cluster1650_1clades	75	CcrKarma_gp298	Caulobacter virus Karma	GCA_000901575.1
AFU87462.1	002115	Cluster1650_1clades	75	CcrMagneto_gp292	Caulobacter virus Magneto	GCA_000903095.1
AFU88607.1	002115	Cluster1650_1clades	75	CcrSwift_gp289	Caulobacter virus Swift	GCA_000899655.1
AFU87115.1	002115	Cluster1650_1clades	75	CbK_gp283	Caulobacter virus phiCbK	GCA_000900535.1
ARB13551.1	002116	Cluster1651_1clades	75	Ccr10_gp023	Caulobacter phage Ccr10	GCA_002619445.1
ARB13897.1	002116	Cluster1651_1clades	75	Ccr2_gp022	Caulobacter phage Ccr2	GCA_002619465.1
ARB14586.1	002116	Cluster1651_1clades	75	Ccr29_gp029	Caulobacter phage Ccr29	GCA_002619485.1
ARB14941.1	002116	Cluster1651_1clades	75	Ccr32_gp022	Caulobacter phage Ccr32	GCA_002619505.1
ARB15272.1	002116	Cluster1651_1clades	75	Ccr34_gp023	Caulobacter phage Ccr34	GCA_002619525.1
ARB14240.1	002116	Cluster1651_1clades	75	Ccr5_gp022	Caulobacter phage Ccr5	GCA_002619545.1
AFU87539.1	002116	Cluster1651_1clades	54	CcrKarma_gp022	Caulobacter virus Karma	GCA_000901575.1
AFU87191.1	002116	Cluster1651_1clades	75	CcrMagneto_gp021	Caulobacter virus Magneto	GCA_000903095.1
AFU88338.1	002116	Cluster1651_1clades	54	CcrSwift_gp020	Caulobacter virus Swift	GCA_000899655.1
AFU86854.1	002116	Cluster1651_1clades	54	CbK_gp022	Caulobacter virus phiCbK	GCA_000900535.1
ARB13775.1	002117	Cluster1652_1clades	74	Ccr10_gp245	Caulobacter phage Ccr10	GCA_002619445.1
ARB14120.1	002117	Cluster1652_1clades	74	Ccr2_gp244	Caulobacter phage Ccr2	GCA_002619465.1
ARB14814.1	002117	Cluster1652_1clades	74	Ccr29_gp258	Caulobacter phage Ccr29	GCA_002619485.1
ARB15154.1	002117	Cluster1652_1clades	64	Ccr32_gp236	Caulobacter phage Ccr32	GCA_002619505.1
ARB15488.1	002117	Cluster1652_1clades	64	Ccr34_gp246	Caulobacter phage Ccr34	GCA_002619525.1
ARB14462.1	002117	Cluster1652_1clades	64	Ccr5_gp242	Caulobacter phage Ccr5	GCA_002619545.1
AFU87770.1	002117	Cluster1652_1clades	74	CcrKarma_gp253	Caulobacter virus Karma	GCA_000901575.1
AFU87417.1	002117	Cluster1652_1clades	74	CcrMagneto_gp247	Caulobacter virus Magneto	GCA_000903095.1
AFU88565.1	002117	Cluster1652_1clades	74	CcrSwift_gp247	Caulobacter virus Swift	GCA_000899655.1
AFU87073.1	002117	Cluster1652_1clades	64	CbK_gp241	Caulobacter virus phiCbK	GCA_000900535.1
ARB13803.1	002118	Cluster1653_1clades	73	Ccr10_gp273	Caulobacter phage Ccr10	GCA_002619445.1
ARB14148.1	002118	Cluster1653_1clades	73	Ccr2_gp272	Caulobacter phage Ccr2	GCA_002619465.1
ARB14842.1	002118	Cluster1653_1clades	73	Ccr29_gp286	Caulobacter phage Ccr29	GCA_002619485.1
ARB15182.1	002118	Cluster1653_1clades	73	Ccr32_gp264	Caulobacter phage Ccr32	GCA_002619505.1
ARB15516.1	002118	Cluster1653_1clades	73	Ccr34_gp274	Caulobacter phage Ccr34	GCA_002619525.1
ARB14490.1	002118	Cluster1653_1clades	73	Ccr5_gp270	Caulobacter phage Ccr5	GCA_002619545.1
AFU87800.1	002118	Cluster1653_1clades	73	CcrKarma_gp283	Caulobacter virus Karma	GCA_000901575.1
AFU87447.1	002118	Cluster1653_1clades	73	CcrMagneto_gp277	Caulobacter virus Magneto	GCA_000903095.1
AFU88592.1	002118	Cluster1653_1clades	73	CcrSwift_gp274	Caulobacter virus Swift	GCA_000899655.1
AFU87101.1	002118	Cluster1653_1clades	73	CbK_gp269	Caulobacter virus phiCbK	GCA_000900535.1
AHI60347.1	002119	DUF1653	73	Ea357_195	Erwinia phage Ea35-70	GCA_000914635.1
QBP07305.1	002119	DUF1653	73	REBECCA_199	Erwinia phage Rebecca	GCA_004521635.1
AUG85986.1	002119	DUF1653	73	BOSOLAPHORUS_199	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52301.2	002119	DUF1653	73	DM_203	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86305.1	002119	DUF1653	73	DESERTFOX_198	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86627.1	002119	DUF1653	73	MADMEL_199	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86951.1	002119	DUF1653	73	MORTIMER_202	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51978.1	002119	DUF1653	73	RAY_197	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51662.1	002119	DUF1653	73	SIMMY50_200	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65009.2	002119	DUF1653	73	SPECIALG_200	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60460.1	002120	Cluster1655_1clades	73	Ea357_306	Erwinia phage Ea35-70	GCA_000914635.1
QBP07417.1	002120	Cluster1655_1clades	73	REBECCA_312	Erwinia phage Rebecca	GCA_004521635.1
AUG86099.1	002120	Cluster1655_1clades	73	BOSOLAPHORUS_313	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ASB43084.1	002120	Cluster1655_1clades	73	DM_316	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86419.1	002120	Cluster1655_1clades	73	DESERTFOX_312	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86740.1	002120	Cluster1655_1clades	73	MADMEL_313	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87065.1	002120	Cluster1655_1clades	73	MORTIMER_317	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52090.1	002120	Cluster1655_1clades	73	RAY_310	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51773.1	002120	Cluster1655_1clades	73	SIMMY50_315	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65125.1	002120	Cluster1655_1clades	73	SPECIALG_314	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43061.1	002121	Cluster1656_1clades	66	R1080702_052	Cyanophage S-RIM32	GCA_001754165.1
AMO43299.1	002121	Cluster1656_1clades	69	W270710_055	Cyanophage S-RIM44	GCA_002599145.1
AOO11533.1	002121	Cluster1656_1clades	69	ES420910_052	Cyanophage S-RIM44	GCA_002599165.1
AOO11771.1	002121	Cluster1656_1clades	69	Np050604_055	Cyanophage S-RIM44	GCA_002599185.1
AOO11998.1	002121	Cluster1656_1clades	69	Np200711_052	Cyanophage S-RIM44	GCA_002599205.1
AOO12234.1	002121	Cluster1656_1clades	69	Np420711_052	Cyanophage S-RIM44	GCA_002599225.1
AOO12472.1	002121	Cluster1656_1clades	69	Sn080709_055	Cyanophage S-RIM44	GCA_002599245.1
AOO12699.1	002121	Cluster1656_1clades	69	Sn130910_052	Cyanophage S-RIM44	GCA_002599265.1
AOO12937.1	002121	Cluster1656_1clades	69	W2100709_055	Cyanophage S-RIM44	GCA_002599285.1
ADO99153.1	002121	Cluster1656_1clades	69	Syn1_052	Prochlorococcus phage Syn1	GCA_000892495.1
AMO43089.1	002122	Cluster1657_1clades	69	R1080702_080	Cyanophage S-RIM32	GCA_001754165.1
AMO43318.1	002122	Cluster1657_1clades	69	W270710_074	Cyanophage S-RIM44	GCA_002599145.1
AOO11551.1	002122	Cluster1657_1clades	69	ES420910_070	Cyanophage S-RIM44	GCA_002599165.1
AOO11790.1	002122	Cluster1657_1clades	69	Np050604_074	Cyanophage S-RIM44	GCA_002599185.1
AOO12016.1	002122	Cluster1657_1clades	69	Np200711_070	Cyanophage S-RIM44	GCA_002599205.1
AOO12252.1	002122	Cluster1657_1clades	69	Np420711_070	Cyanophage S-RIM44	GCA_002599225.1
AOO12491.1	002122	Cluster1657_1clades	69	Sn080709_074	Cyanophage S-RIM44	GCA_002599245.1
AOO12717.1	002122	Cluster1657_1clades	69	Sn130910_070	Cyanophage S-RIM44	GCA_002599265.1
AOO12956.1	002122	Cluster1657_1clades	69	W2100709_074	Cyanophage S-RIM44	GCA_002599285.1
ADO99172.1	002122	Cluster1657_1clades	69	Syn1_071	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13628.1	002123	Cluster1658_1clades	57	Ccr10_gp099	Caulobacter phage Ccr10	GCA_002619445.1
ARB13973.1	002123	Cluster1658_1clades	57	Ccr2_gp098	Caulobacter phage Ccr2	GCA_002619465.1
ARB14662.1	002123	Cluster1658_1clades	57	Ccr29_gp106	Caulobacter phage Ccr29	GCA_002619485.1
ARB15017.1	002123	Cluster1658_1clades	69	Ccr32_gp099	Caulobacter phage Ccr32	GCA_002619505.1
ARB15349.1	002123	Cluster1658_1clades	69	Ccr34_gp107	Caulobacter phage Ccr34	GCA_002619525.1
ARB14317.1	002123	Cluster1658_1clades	57	Ccr5_gp099	Caulobacter phage Ccr5	GCA_002619545.1
AFU87620.1	002123	Cluster1658_1clades	69	CcrKarma_gp103	Caulobacter virus Karma	GCA_000901575.1
AFU87269.1	002123	Cluster1658_1clades	69	CcrMagneto_gp099	Caulobacter virus Magneto	GCA_000903095.1
AFU88416.1	002123	Cluster1658_1clades	69	CcrSwift_gp098	Caulobacter virus Swift	GCA_000899655.1
AFU86934.1	002123	Cluster1658_1clades	69	CbK_gp102	Caulobacter virus phiCbK	GCA_000900535.1
AHI60213.1	002124	Cluster1659_1clades	69	Ea357_062	Erwinia phage Ea35-70	GCA_000914635.1
QBP07171.1	002124	Cluster1659_1clades	69	REBECCA_63	Erwinia phage Rebecca	GCA_004521635.1
AUG85851.1	002124	Cluster1659_1clades	69	BOSOLAPHORUS_63	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52163.2	002124	Cluster1659_1clades	69	DM_65	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86170.1	002124	Cluster1659_1clades	69	DESERTFOX_62	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86492.1	002124	Cluster1659_1clades	69	MADMEL_64	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86813.1	002124	Cluster1659_1clades	69	MORTIMER_64	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51843.1	002124	Cluster1659_1clades	69	RAY_62	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51527.1	002124	Cluster1659_1clades	69	SIMMY50_65	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64875.1	002124	Cluster1659_1clades	69	SPECIALG_65	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60385.1	002125	Cluster1660_1clades	69	Ea357_232	Erwinia phage Ea35-70	GCA_000914635.1
QBP07341.1	002125	Cluster1660_1clades	69	REBECCA_236	Erwinia phage Rebecca	GCA_004521635.1
AUG86023.1	002125	Cluster1660_1clades	69	BOSOLAPHORUS_237	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52340.1	002125	Cluster1660_1clades	69	DM_240	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86342.1	002125	Cluster1660_1clades	69	DESERTFOX_235	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86666.1	002125	Cluster1660_1clades	69	MADMEL_238	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86988.1	002125	Cluster1660_1clades	69	MORTIMER_240	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52014.1	002125	Cluster1660_1clades	69	RAY_234	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51698.1	002125	Cluster1660_1clades	69	SIMMY50_239	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65049.1	002125	Cluster1660_1clades	69	SPECIALG_238	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AAQ64104.1	002126	SIG+TM	68	KVP40.0033	Vibrio phage KVP40	GCA_000843785.1
QIW90427.1	002126	SIG+TM	68	GCAPEGMB_00080	Vibrio phage V07	GCA_012361095.1
QIW91002.1	002126	SIG+TM	68	COHAPHLL_00139	Vibrio phage V09	GCA_012361135.1
QHJ74216.1	002126	SIG+TM	68	VH12019_00297	Vibrio phage VH1_2019	GCA_009931825.1
AGB07040.1	002126	SIG+TM	68	CF80_gp253	Vibrio phage VH7D	GCA_000914495.1
QBX06056.1	002126	SIG+TM	68	ValB1HC_102	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61069.1	002126	SIG+TM	68	AVU32_gp228	Vibrio phage ValKK3	GCA_001501635.1
ALP47297.1	002126	SIG+TM	68	phiGrn1_0148	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47677.1	002126	SIG+TM	68	phiST2_0278	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54682.1	002126	SIG+TM	68	vBValMR10Z_141	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFC21751.1	002127	Cluster1662_1clades	68	GAP32_301	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AIT13931.1	002127	Cluster1662_1clades	55	PBI_121Q_34	Escherichia phage 121Q	GCA_000926855.1
QAY00406.1	002127	Cluster1662_1clades	64	Ecwhy1_125	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35150.1	002127	Cluster1662_1clades	55	ACQ29_gp470	Escherichia phage PBECO4	GCA_001041035.1
BBM61623.1	002127	Cluster1662_1clades	55	EO157G_0340	Escherichia phage SP27	GCA_008033345.1
AXC36723.1	002127	Cluster1662_1clades	55	-	Escherichia phage UB	GCA_003341455.1
AMM43869.1	002127	Cluster1662_1clades	62	CBB_306	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88828.1	002127	Cluster1662_1clades	68	BF_0303	Serratia phage BF	GCA_002619745.1
SOK59112.1	002127	Cluster1662_1clades	64	g304	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58578.1	002127	Cluster1662_1clades	64	g301	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13705.1	002128	Cluster1663_1clades	68	Ccr10_gp175c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14050.1	002128	Cluster1663_1clades	68	Ccr2_gp174c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14737.1	002128	Cluster1663_1clades	68	Ccr29_gp181	Caulobacter phage Ccr29	GCA_002619485.1
ARB15092.1	002128	Cluster1663_1clades	68	Ccr32_gp174	Caulobacter phage Ccr32	GCA_002619505.1
ARB15426.1	002128	Cluster1663_1clades	68	Ccr34_gp184	Caulobacter phage Ccr34	GCA_002619525.1
ARB14393.1	002128	Cluster1663_1clades	68	Ccr5_gp173c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87698.1	002128	Cluster1663_1clades	68	CcrKarma_gp181	Caulobacter virus Karma	GCA_000901575.1
AFU87347.1	002128	Cluster1663_1clades	68	CcrMagneto_gp177	Caulobacter virus Magneto	GCA_000903095.1
AFU88494.1	002128	Cluster1663_1clades	68	CcrSwift_gp176	Caulobacter virus Swift	GCA_000899655.1
AFU87011.1	002128	Cluster1663_1clades	68	CbK_gp179	Caulobacter virus phiCbK	GCA_000900535.1
ABY63100.1	002129	Cluster1664_1clades	66	201phi2-1p272	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44976.1	002129	Cluster1664_1clades	65	KTN4_218	Pseudomonas phage KTN4	GCA_002607225.1
ARV77363.1	002129	Cluster1664_1clades	67	NOXIFER_194	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32366.1	002129	Cluster1664_1clades	64	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76893.1	002129	Cluster1664_1clades	65	PHABIO_262	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02769.1	002129	Cluster1664_1clades	65	PSA21_243	Pseudomonas phage Psa21	GCA_004340405.1
ATN94738.1	002129	Cluster1664_1clades	65	SL2_161	Pseudomonas phage SL2	GCA_002956015.1
QJB22854.1	002129	Cluster1664_1clades	65	fnug_211	Pseudomonas phage fnug	GCA_012837215.1
QEM41940.1	002129	Cluster1664_1clades	64	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26341.1	002129	Cluster1664_1clades	65	PHIKZ177.1	Pseudomonas virus phiKZ	GCA_000842965.1
AIA64908.1	002130	Cluster1665_1clades	56	S13_109	Cronobacter phage S13	GCA_001503575.1
AIT14081.1	002130	Cluster1665_1clades	63	PBI_121Q_191	Escherichia phage 121Q	GCA_000926855.1
QAY00842.1	002130	Cluster1665_1clades	63	Ecwhy1_570	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35013.1	002130	Cluster1665_1clades	63	ACQ29_gp333	Escherichia phage PBECO4	GCA_001041035.1
BBM61764.1	002130	Cluster1665_1clades	63	EO157G_1750	Escherichia phage SP27	GCA_008033345.1
AXC36591.1	002130	Cluster1665_1clades	63	-	Escherichia phage UB	GCA_003341455.1
QBO61618.1	002130	Cluster1665_1clades	63	G17_00122	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13676.1	002130	Cluster1665_1clades	63	vBEcoMphAPEC6_gp046c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80075.1	002130	Cluster1665_1clades	63	PSLUR01_00098	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QHJ79034.1	002130	Cluster1665_1clades	66	-	Myoviridae sp.	GCA_012593985.1
AMO43313.1	002131	Cluster1666_1clades	65	W270710_069	Cyanophage S-RIM44	GCA_002599145.1
AOO11547.1	002131	Cluster1666_1clades	65	ES420910_066	Cyanophage S-RIM44	GCA_002599165.1
AOO11785.1	002131	Cluster1666_1clades	65	Np050604_069	Cyanophage S-RIM44	GCA_002599185.1
AOO12012.1	002131	Cluster1666_1clades	65	Np200711_066	Cyanophage S-RIM44	GCA_002599205.1
AOO12248.1	002131	Cluster1666_1clades	65	Np420711_066	Cyanophage S-RIM44	GCA_002599225.1
AOO12486.1	002131	Cluster1666_1clades	65	Sn080709_069	Cyanophage S-RIM44	GCA_002599245.1
AOO12713.1	002131	Cluster1666_1clades	65	Sn130910_066	Cyanophage S-RIM44	GCA_002599265.1
AOO12951.1	002131	Cluster1666_1clades	65	W2100709_069	Cyanophage S-RIM44	GCA_002599285.1
ADO99167.1	002131	Cluster1666_1clades	65	Syn1_066	Prochlorococcus phage Syn1	GCA_000892495.1
AIX30550.1	002131	Cluster1666_1clades	64	Syn7803US37_73	Synechococcus phage ACG-2014f	GCA_002594065.1
AHI60422.1	002132	Cluster1667_1clades	65	Ea357_268	Erwinia phage Ea35-70	GCA_000914635.1
QBP07379.1	002132	Cluster1667_1clades	65	REBECCA_274	Erwinia phage Rebecca	GCA_004521635.1
AUG86061.1	002132	Cluster1667_1clades	65	BOSOLAPHORUS_275	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52377.1	002132	Cluster1667_1clades	65	DM_278	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86381.1	002132	Cluster1667_1clades	65	DESERTFOX_274	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86702.1	002132	Cluster1667_1clades	65	MADMEL_275	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG87027.1	002132	Cluster1667_1clades	65	MORTIMER_279	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52052.1	002132	Cluster1667_1clades	65	RAY_272	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51735.1	002132	Cluster1667_1clades	65	SIMMY50_277	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANJ65087.1	002132	Cluster1667_1clades	65	SPECIALG_276	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AXQ68207.1	002133	Cluster1668_1clades	62	CcrBL10_gp003	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68525.1	002133	Cluster1668_1clades	62	CcrBL10_gp321	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69038.1	002133	Cluster1668_1clades	63	CcrBL9_gp014	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69554.1	002133	Cluster1668_1clades	63	CcrBL9_gp530	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69598.1	002133	Cluster1668_1clades	63	CcrSC_gp016	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70098.1	002133	Cluster1668_1clades	63	CcrSC_gp516	Caulobacter phage CcrSC	GCA_003443315.1
AFU86487.1	002133	Cluster1668_1clades	62	CcrRogue_gp005	Caulobacter virus Rogue	GCA_000900555.1
AFU86818.1	002133	Cluster1668_1clades	62	CcrRogue_gp336	Caulobacter virus Rogue	GCA_000900555.1
AFU88323.1	002133	Cluster1668_1clades	62	CcrSwift_gp005	Caulobacter virus Swift	GCA_000899655.1
AFU88648.1	002133	Cluster1668_1clades	62	CcrSwift_gp330	Caulobacter virus Swift	GCA_000899655.1
AAQ64123.1	002134	SIG+TM	62	KVP40.0052	Vibrio phage KVP40	GCA_000843785.1
QIW90445.1	002134	SIG+TM	62	GCAPEGMB_00098	Vibrio phage V07	GCA_012361095.1
QIW90984.1	002134	SIG+TM	62	COHAPHLL_00121	Vibrio phage V09	GCA_012361135.1
QHJ74234.1	002134	SIG+TM	62	VH12019_00315	Vibrio phage VH1_2019	GCA_009931825.1
AGB07058.1	002134	SIG+TM	54	CF80_gp271	Vibrio phage VH7D	GCA_000914495.1
QBX06038.1	002134	SIG+TM	62	ValB1HC_084	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61052.1	002134	SIG+TM	62	AVU32_gp211	Vibrio phage ValKK3	GCA_001501635.1
ALP47309.1	002134	SIG+TM	62	phiGrn1_0165	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47689.1	002134	SIG+TM	62	phiST2_0296	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54663.1	002134	SIG+TM	62	vBValMR10Z_122	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AHI60291.1	002135	Cluster1670_1clades	62	Ea357_140	Erwinia phage Ea35-70	GCA_000914635.1
QBP07249.1	002135	Cluster1670_1clades	62	REBECCA_142	Erwinia phage Rebecca	GCA_004521635.1
AUG85929.1	002135	Cluster1670_1clades	62	BOSOLAPHORUS_142	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52244.1	002135	Cluster1670_1clades	62	DM_146	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86248.1	002135	Cluster1670_1clades	62	DESERTFOX_141	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86570.1	002135	Cluster1670_1clades	62	MADMEL_142	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86894.1	002135	Cluster1670_1clades	62	MORTIMER_145	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51922.1	002135	Cluster1670_1clades	62	RAY_141	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51606.1	002135	Cluster1670_1clades	62	SIMMY50_144	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64953.1	002135	Cluster1670_1clades	62	SPECIALG_143	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARB13589.1	002136	Cluster1671_1clades	58	Ccr10_gp061	Caulobacter phage Ccr10	GCA_002619445.1
ARB13935.1	002136	Cluster1671_1clades	58	Ccr2_gp060	Caulobacter phage Ccr2	GCA_002619465.1
ARB14624.1	002136	Cluster1671_1clades	58	Ccr29_gp067	Caulobacter phage Ccr29	GCA_002619485.1
ARB14980.1	002136	Cluster1671_1clades	58	Ccr32_gp061	Caulobacter phage Ccr32	GCA_002619505.1
ARB15311.1	002136	Cluster1671_1clades	58	Ccr34_gp062	Caulobacter phage Ccr34	GCA_002619525.1
ARB14278.1	002136	Cluster1671_1clades	58	Ccr5_gp060	Caulobacter phage Ccr5	GCA_002619545.1
AFU87579.1	002136	Cluster1671_1clades	58	CcrKarma_gp062	Caulobacter virus Karma	GCA_000901575.1
AFU87229.1	002136	Cluster1671_1clades	58	CcrMagneto_gp059	Caulobacter virus Magneto	GCA_000903095.1
AFU88377.1	002136	Cluster1671_1clades	58	CcrSwift_gp059	Caulobacter virus Swift	GCA_000899655.1
AFU86893.1	002136	Cluster1671_1clades	58	CbK_gp061	Caulobacter virus phiCbK	GCA_000900535.1
AHI60153.1	002137	Cluster1672_1clades	58	Ea357_003	Erwinia phage Ea35-70	GCA_000914635.1
QBP07111.1	002137	Cluster1672_1clades	58	REBECCA_3	Erwinia phage Rebecca	GCA_004521635.1
AUG85791.1	002137	Cluster1672_1clades	58	BOSOLAPHORUS_3	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52101.1	002137	Cluster1672_1clades	58	DM_3	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86111.1	002137	Cluster1672_1clades	58	DESERTFOX_3	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86431.1	002137	Cluster1672_1clades	58	MADMEL_3	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86752.1	002137	Cluster1672_1clades	58	MORTIMER_3	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51784.1	002137	Cluster1672_1clades	58	RAY_3	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51465.1	002137	Cluster1672_1clades	58	SIMMY50_3	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64813.1	002137	Cluster1672_1clades	58	SPECIALG_3	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43058.1	002138	Cluster1673_1clades	57	R1080702_049	Cyanophage S-RIM32	GCA_001754165.1
AMO43296.1	002138	Cluster1673_1clades	57	W270710_052	Cyanophage S-RIM44	GCA_002599145.1
AOO11530.1	002138	Cluster1673_1clades	57	ES420910_049	Cyanophage S-RIM44	GCA_002599165.1
AOO11768.1	002138	Cluster1673_1clades	57	Np050604_052	Cyanophage S-RIM44	GCA_002599185.1
AOO11995.1	002138	Cluster1673_1clades	57	Np200711_049	Cyanophage S-RIM44	GCA_002599205.1
AOO12231.1	002138	Cluster1673_1clades	57	Np420711_049	Cyanophage S-RIM44	GCA_002599225.1
AOO12469.1	002138	Cluster1673_1clades	57	Sn080709_052	Cyanophage S-RIM44	GCA_002599245.1
AOO12696.1	002138	Cluster1673_1clades	57	Sn130910_049	Cyanophage S-RIM44	GCA_002599265.1
AOO12934.1	002138	Cluster1673_1clades	57	W2100709_052	Cyanophage S-RIM44	GCA_002599285.1
ADO99150.1	002138	Cluster1673_1clades	57	Syn1_049	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60322.1	002139	Cluster1674_1clades	57	Ea357_171	Erwinia phage Ea35-70	GCA_000914635.1
QBP07281.1	002139	Cluster1674_1clades	57	REBECCA_174	Erwinia phage Rebecca	GCA_004521635.1
AUG85961.1	002139	Cluster1674_1clades	57	BOSOLAPHORUS_174	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52276.1	002139	Cluster1674_1clades	57	DM_178	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86280.1	002139	Cluster1674_1clades	57	DESERTFOX_173	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86602.1	002139	Cluster1674_1clades	57	MADMEL_174	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86926.1	002139	Cluster1674_1clades	57	MORTIMER_177	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51953.1	002139	Cluster1674_1clades	57	RAY_172	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51637.1	002139	Cluster1674_1clades	57	SIMMY50_175	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64984.1	002139	Cluster1674_1clades	57	SPECIALG_174	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43228.1	002140	Cluster1675_1clades	40	R1080702_223	Cyanophage S-RIM32	GCA_001754165.1
AMO43460.1	002140	Cluster1675_1clades	40	W270710_221	Cyanophage S-RIM44	GCA_002599145.1
AOO11700.1	002140	Cluster1675_1clades	40	ES420910_223	Cyanophage S-RIM44	GCA_002599165.1
AOO11932.1	002140	Cluster1675_1clades	40	Np050604_221	Cyanophage S-RIM44	GCA_002599185.1
AOO12166.1	002140	Cluster1675_1clades	40	Np200711_224	Cyanophage S-RIM44	GCA_002599205.1
AOO12401.1	002140	Cluster1675_1clades	40	Np420711_223	Cyanophage S-RIM44	GCA_002599225.1
AOO12633.1	002140	Cluster1675_1clades	40	Sn080709_221	Cyanophage S-RIM44	GCA_002599245.1
AOO12866.1	002140	Cluster1675_1clades	40	Sn130910_223	Cyanophage S-RIM44	GCA_002599265.1
AOO13099.1	002140	Cluster1675_1clades	40	W2100709_222	Cyanophage S-RIM44	GCA_002599285.1
ADO99321.1	002140	Cluster1675_1clades	56	Syn1_225	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13566.1	002141	Cluster1676_1clades	55	Ccr10_gp038	Caulobacter phage Ccr10	GCA_002619445.1
ARB13912.1	002141	Cluster1676_1clades	55	Ccr2_gp037	Caulobacter phage Ccr2	GCA_002619465.1
ARB14601.1	002141	Cluster1676_1clades	55	Ccr29_gp044	Caulobacter phage Ccr29	GCA_002619485.1
ARB14957.1	002141	Cluster1676_1clades	55	Ccr32_gp038	Caulobacter phage Ccr32	GCA_002619505.1
ARB15288.1	002141	Cluster1676_1clades	55	Ccr34_gp039	Caulobacter phage Ccr34	GCA_002619525.1
ARB14255.1	002141	Cluster1676_1clades	55	Ccr5_gp037	Caulobacter phage Ccr5	GCA_002619545.1
AFU87556.1	002141	Cluster1676_1clades	43	CcrKarma_gp039	Caulobacter virus Karma	GCA_000901575.1
AFU87206.1	002141	Cluster1676_1clades	55	CcrMagneto_gp036	Caulobacter virus Magneto	GCA_000903095.1
AFU88353.1	002141	Cluster1676_1clades	39	CcrSwift_gp035	Caulobacter virus Swift	GCA_000899655.1
AFU86870.1	002141	Cluster1676_1clades	43	CbK_gp038	Caulobacter virus phiCbK	GCA_000900535.1
AHI60349.1	002142	Cluster1677_1clades	55	Ea357_197	Erwinia phage Ea35-70	GCA_000914635.1
QBP07307.1	002142	Cluster1677_1clades	55	REBECCA_201	Erwinia phage Rebecca	GCA_004521635.1
AUG85988.1	002142	Cluster1677_1clades	55	BOSOLAPHORUS_201	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52303.1	002142	Cluster1677_1clades	55	DM_205	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86307.1	002142	Cluster1677_1clades	55	DESERTFOX_200	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86629.1	002142	Cluster1677_1clades	55	MADMEL_201	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86953.1	002142	Cluster1677_1clades	55	MORTIMER_204	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51980.1	002142	Cluster1677_1clades	55	RAY_199	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51664.1	002142	Cluster1677_1clades	55	SIMMY50_202	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65011.1	002142	Cluster1677_1clades	55	SPECIALG_202	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMO43093.1	002143	Cluster1678_1clades	53	R1080702_084	Cyanophage S-RIM32	GCA_001754165.1
AMO43321.1	002143	Cluster1678_1clades	54	W270710_077	Cyanophage S-RIM44	GCA_002599145.1
AOO11555.1	002143	Cluster1678_1clades	54	ES420910_074	Cyanophage S-RIM44	GCA_002599165.1
AOO11793.1	002143	Cluster1678_1clades	54	Np050604_077	Cyanophage S-RIM44	GCA_002599185.1
AOO12020.1	002143	Cluster1678_1clades	54	Np200711_074	Cyanophage S-RIM44	GCA_002599205.1
AOO12256.1	002143	Cluster1678_1clades	54	Np420711_074	Cyanophage S-RIM44	GCA_002599225.1
AOO12494.1	002143	Cluster1678_1clades	54	Sn080709_077	Cyanophage S-RIM44	GCA_002599245.1
AOO12721.1	002143	Cluster1678_1clades	54	Sn130910_074	Cyanophage S-RIM44	GCA_002599265.1
AOO12959.1	002143	Cluster1678_1clades	54	W2100709_077	Cyanophage S-RIM44	GCA_002599285.1
ADO99177.1	002143	Cluster1678_1clades	54	Syn1_076	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60288.1	002144	Cluster1679_1clades	54	Ea357_137	Erwinia phage Ea35-70	GCA_000914635.1
QBP07246.1	002144	Cluster1679_1clades	54	REBECCA_139	Erwinia phage Rebecca	GCA_004521635.1
AUG85926.1	002144	Cluster1679_1clades	54	BOSOLAPHORUS_139	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52241.1	002144	Cluster1679_1clades	54	DM_143	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86245.1	002144	Cluster1679_1clades	54	DESERTFOX_138	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86567.1	002144	Cluster1679_1clades	54	MADMEL_139	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86891.1	002144	Cluster1679_1clades	54	MORTIMER_142	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51919.1	002144	Cluster1679_1clades	54	RAY_138	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51603.1	002144	Cluster1679_1clades	54	SIMMY50_141	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64950.1	002144	Cluster1679_1clades	54	SPECIALG_140	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ABY63003.1	002145	Cluster1680_1clades	51	201phi2-1p173	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27177.1	002145	Cluster1680_1clades	54	PPEV_gp083	Pseudomonas phage EL	GCA_000866825.1
ANM44769.1	002145	Cluster1680_1clades	49	KTN4_011	Pseudomonas phage KTN4	GCA_002607225.1
QBX32274.1	002145	Cluster1680_1clades	51	-	Pseudomonas phage PA1C	GCA_004785505.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARV76789.1	002145	Cluster1680_1clades	52	PHABIO_158	Pseudomonas phage Phabio	GCA_002624965.1
AEH03535.1	002145	Cluster1680_1clades	50	111	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94579.1	002145	Cluster1680_1clades	51	SL2_002	Pseudomonas phage SL2	GCA_002956015.1
QJB22654.1	002145	Cluster1680_1clades	51	fnug_11	Pseudomonas phage fnug	GCA_012837215.1
QEM41848.1	002145	Cluster1680_1clades	51	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26303.1	002145	Cluster1680_1clades	49	PHIKZ010.1	Pseudomonas virus phiKZ	GCA_000842965.1
AIT13996.1	002146	Cluster1681_1clades	47	PBI_121Q_99	Escherichia phage 121Q	GCA_000926855.1
QAY00342.1	002146	Cluster1681_1clades	47	Ecwhy1_61	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35088.1	002146	Cluster1681_1clades	47	ACQ29_gp408	Escherichia phage PBECO4	GCA_001041035.1
BBM61687.1	002146	Cluster1681_1clades	47	EO157G_0980	Escherichia phage SP27	GCA_008033345.1
AXC36665.1	002146	Cluster1681_1clades	47	-	Escherichia phage UB	GCA_003341455.1
QBO61697.1	002146	Cluster1681_1clades	47	G17_00208	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80000.1	002146	Cluster1681_1clades	47	PSLUR01_00016	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18613.1	002146	Cluster1681_1clades	52	7t3_092	Salmonella phage 7t3	GCA_006083215.1
AZU98438.1	002146	Cluster1681_1clades	52	CPT_Munch_506	Salmonella phage Munch	GCA_004015485.1
QIG63075.1	002146	Cluster1681_1clades	52	SEPL_462	Salmonella phage SE_PL	GCA_011067555.1
AMO43060.1	002147	Cluster1682_1clades	44	R1080702_051	Cyanophage S-RIM32	GCA_001754165.1
AMO43298.1	002147	Cluster1682_1clades	47	W270710_054	Cyanophage S-RIM44	GCA_002599145.1
AOO11532.1	002147	Cluster1682_1clades	47	ES420910_051	Cyanophage S-RIM44	GCA_002599165.1
AOO11770.1	002147	Cluster1682_1clades	47	Np050604_054	Cyanophage S-RIM44	GCA_002599185.1
AOO11997.1	002147	Cluster1682_1clades	47	Np200711_051	Cyanophage S-RIM44	GCA_002599205.1
AOO12233.1	002147	Cluster1682_1clades	47	Np420711_051	Cyanophage S-RIM44	GCA_002599225.1
AOO12471.1	002147	Cluster1682_1clades	47	Sn080709_054	Cyanophage S-RIM44	GCA_002599245.1
AOO12698.1	002147	Cluster1682_1clades	47	Sn130910_051	Cyanophage S-RIM44	GCA_002599265.1
AOO12936.1	002147	Cluster1682_1clades	47	W2100709_054	Cyanophage S-RIM44	GCA_002599285.1
ADO99152.1	002147	Cluster1682_1clades	47	Syn1_051	Prochlorococcus phage Syn1	GCA_000892495.1
AHI60258.1	002148	Cluster1683_1clades	39	Ea357_107	Erwinia phage Ea35-70	GCA_000914635.1
QBP07215.1	002148	Cluster1683_1clades	47	REBECCA_108	Erwinia phage Rebecca	GCA_004521635.1
AUG85895.1	002148	Cluster1683_1clades	47	BOSOLAPHORUS_108	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52210.1	002148	Cluster1683_1clades	47	DM_112	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86214.1	002148	Cluster1683_1clades	47	DESERTFOX_107	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86536.1	002148	Cluster1683_1clades	47	MADMEL_108	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86861.1	002148	Cluster1683_1clades	47	MORTIMER_112	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51889.1	002148	Cluster1683_1clades	47	RAY_108	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51573.2	002148	Cluster1683_1clades	47	SIMMY50_111	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64920.1	002148	Cluster1683_1clades	47	SPECIALG_110	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AHI60356.1	002149	Cluster1684_1clades	41	Ea357_203	Erwinia phage Ea35-70	GCA_000914635.1
QBP07313.1	002149	Cluster1684_1clades	41	REBECCA_208	Erwinia phage Rebecca	GCA_004521635.1
AUG85994.1	002149	Cluster1684_1clades	41	BOSOLAPHORUS_208	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52311.1	002149	Cluster1684_1clades	41	DM_211	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86313.1	002149	Cluster1684_1clades	41	DESERTFOX_206	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86636.1	002149	Cluster1684_1clades	41	MADMEL_208	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86959.1	002149	Cluster1684_1clades	41	MORTIMER_211	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51986.1	002149	Cluster1684_1clades	41	RAY_206	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51670.1	002149	Cluster1684_1clades	41	SIMMY50_211	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65020.1	002149	Cluster1684_1clades	41	SPECIALG_209	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AAX44399.1	002150	DUF1565	1123	PSSM2_021	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44670.1	002150	DUF1565	617	PSSM2_293	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12307.1	002150	DUF1565	617	PRTG_00154	Prochlorococcus phage P-SSM5	GCA_002991095.1
QGT54935.1	002150	DUF1565	1497	b23_0322	Synechococcus phage B23	GCA_009745195.1
QGT54570.1	002150	DUF1565	1497	b3_0329	Synechococcus phage B3	GCA_009745215.1
QCW23089.1	002150	DUF1565	763	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50723.1	002150	DUF1565	688	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70473.1	002150	DUF1565	836	HOU04_gp074	Synechococcus phage S-T4	GCA_003443335.1
QJT70106.1	002150	DUF1565	1167	SynMITS9220M01_093	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG67149.1	002151	Cluster1687_1clades	674	AD1_105	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79898.1	002151	Cluster1687_1clades	673	JA11_093	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66497.1	002151	Cluster1687_1clades	673	JA13_094	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66822.1	002151	Cluster1687_1clades	673	JA29_096	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67467.1	002151	Cluster1687_1clades	673	JA33_093	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08383.1	002151	Cluster1687_1clades	672	Alexandra_110	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58747.1	002151	Cluster1687_1clades	672	Y3_107	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28580.1	002151	Cluster1687_1clades	673	YOLOSWAG_98	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38301.1	002151	Cluster1687_1clades	1304	BN7874_132	Phage NCTB	GCA_900092385.1
AXH70884.1	002152	Cluster1689_1clades	543	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96887.1	002152	Cluster1689_1clades	173	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96883.1	002152	Cluster1689_1clades	348	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97192.1	002152	Cluster1689_1clades	173	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX97188.1	002152	Cluster1689_1clades	348	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96251.1	002152	Cluster1689_1clades	173	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96247.1	002152	Cluster1689_1clades	348	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96569.1	002152	Cluster1689_1clades	173	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96565.1	002152	Cluster1689_1clades	348	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67188.1	002153	Cluster1690_1clades	255	AD1_144	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79938.1	002153	Cluster1690_1clades	295	JA11_133	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66537.1	002153	Cluster1690_1clades	295	JA13_134	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66862.1	002153	Cluster1690_1clades	295	JA29_136	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67507.1	002153	Cluster1690_1clades	295	JA33_133	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08421.1	002153	Cluster1690_1clades	259	Alexandra_149	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58785.1	002153	Cluster1690_1clades	259	Y3_145	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28623.1	002153	Cluster1690_1clades	244	YOLOSWAG_143	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38423.1	002153	Cluster1690_1clades	483	BN7874_233	Phage NCTB	GCA_900092385.1
AXG67227.1	002154	Cluster1691_1clades	427	AD1_183	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79977.1	002154	Cluster1691_1clades	425	JA11_172	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66575.1	002154	Cluster1691_1clades	425	JA13_172	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66900.1	002154	Cluster1691_1clades	424	JA29_174	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67546.1	002154	Cluster1691_1clades	425	JA33_172	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08456.1	002154	Cluster1691_1clades	429	Alexandra_188	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58824.1	002154	Cluster1691_1clades	427	Y3_184	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28658.1	002154	Cluster1691_1clades	428	YOLOSWAG_179	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38499.1	002154	Cluster1691_1clades	442	BN7874_280	Phage NCTB	GCA_900092385.1
QHJ74358.1	002155	Uri-nuclease	347	VH12019_00031	Vibrio phage VH1_2019	GCA_009931825.1
AGB06850.1	002155	Uri-nuclease	304	CF80_gp063	Vibrio phage VH7D	GCA_000914495.1
QBX06295.1	002155	Uri-nuclease	356	ValB1HC_342	Vibrio phage ValB1 HC	GCA_004771355.1
QBX06296.1	002155	Uri-nuclease	406	ValB1HC_343	Vibrio phage ValB1 HC	GCA_004771355.1
ALP47002.1	002155	Uri-nuclease	356	phiGrn1_0289	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47420.1	002155	Uri-nuclease	249	phiST2_0046	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54922.1	002155	Uri-nuclease	407	vBValMR10Z_382	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AUE22602.1	002156	SIG+Band_7	314	Ah1_00061	Aeromonas phage Ah1	GCA_002957415.1
QAX98639.1	002156	SIG+Band_7	315	ASfcp2_306	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52779.1	002156	SIG+Band_7	315	PX29p060	Aeromonas phage PX29	GCA_000920195.1
ADM80035.1	002156	SIG+Band_7	315	phiAS5_ORF0192	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17724.1	002156	SIG+Band_7	315	Aeh1ORF064c	Aeromonas virus Aeh1	GCA_000843245.1
ANS05974.1	002156	SIG+Band_7	304	ABCD_0138	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97146.1	002156	SIG+Band_7	304	E_138	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78661.1	002156	SIG+Band_7	297	RB43ORF139c	Escherichia virus RB43	GCA_000863505.1
ALY07051.1	002156	SIG+Band_7	321	VmeM32_00060	Vibrio phage vB_VmeM-32	GCA_002608825.1
APU01800.1	002157	RuvB-HTH+35exo	318	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28954.1	002157	RuvB-HTH+35exo	317	AP1_0247	Aeromonas phage AP1	GCA_014183365.1
ATI17505.1	002157	RuvB-HTH+35exo	317	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00492.1	002157	RuvB-HTH+35exo	317	HWB28_gp060	Aeromonas phage AS-zj	GCA_002627665.1
QAX97944.1	002157	RuvB-HTH+35exo	317	ASswx1_302	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01203.1	002157	RuvB-HTH+35exo	318	ASwh1_138	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39490.1	002157	RuvB-HTH+35exo	317	CC2_229	Aeromonas phage CC2	GCA_000903495.1
ADQ53444.1	002157	RuvB-HTH+35exo	318	65p438	Aeromonas virus 65	GCA_000893255.1
QIG57841.1	002157	RuvB-HTH+35exo	301	SEA_PAULODIABOLI_107	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG63315.1	002158	Cluster1697_1clades	314	DAC16_82	Bacteroides phage DAC16	GCA_013387695.1
QIG63571.1	002158	Cluster1697_1clades	230	DAC19_80	Bacteroides phage DAC19	GCA_013387715.1
QIG63576.1	002158	Cluster1697_1clades	314	DAC19_85	Bacteroides phage DAC19	GCA_013387715.1
QIG63832.1	002158	Cluster1697_1clades	230	DAC20_79	Bacteroides phage DAC20	GCA_013387725.1
QIG63837.1	002158	Cluster1697_1clades	314	DAC20_84	Bacteroides phage DAC20	GCA_013387725.1
QIG64094.1	002158	Cluster1697_1clades	230	DAC22_80	Bacteroides phage DAC22	GCA_013387735.1
QIG64099.1	002158	Cluster1697_1clades	314	DAC22_85	Bacteroides phage DAC22	GCA_013387735.1
QIG64354.1	002158	Cluster1697_1clades	223	DAC23_76	Bacteroides phage DAC23	GCA_013387745.1
QIG64359.1	002158	Cluster1697_1clades	314	DAC23_81	Bacteroides phage DAC23	GCA_013387745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63330.1	002159	Cluster1698_1clades	313	DAC16_97	Bacteroides phage DAC16	GCA_013387695.1
QIG63592.1	002159	Cluster1698_1clades	206	DAC19_101	Bacteroides phage DAC19	GCA_013387715.1
QIG63596.1	002159	Cluster1698_1clades	253	DAC19_105	Bacteroides phage DAC19	GCA_013387715.1
QIG63853.1	002159	Cluster1698_1clades	206	DAC20_100	Bacteroides phage DAC20	GCA_013387725.1
QIG63857.1	002159	Cluster1698_1clades	253	DAC20_104	Bacteroides phage DAC20	GCA_013387725.1
QIG64116.1	002159	Cluster1698_1clades	243	DAC22_102	Bacteroides phage DAC22	GCA_013387735.1
QIG64120.1	002159	Cluster1698_1clades	253	DAC22_106	Bacteroides phage DAC22	GCA_013387735.1
QIG64378.1	002159	Cluster1698_1clades	255	DAC23_100	Bacteroides phage DAC23	GCA_013387745.1
QIG64374.1	002159	Cluster1698_1clades	243	DAC23_96	Bacteroides phage DAC23	GCA_013387745.1
AXG67173.1	002160	Cluster1699_1clades	259	AD1_129	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79923.1	002160	Cluster1699_1clades	280	JA11_118	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66522.1	002160	Cluster1699_1clades	280	JA13_119	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66847.1	002160	Cluster1699_1clades	280	JA29_121	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67492.1	002160	Cluster1699_1clades	280	JA33_118	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08406.1	002160	Cluster1699_1clades	280	Alexandra_134	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58770.1	002160	Cluster1699_1clades	271	Y3_130	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28609.1	002160	Cluster1699_1clades	277	YOLOSWAG_128	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38385.1	002160	Cluster1699_1clades	313	BN7874_210	Phage NCTB	GCA_900092385.1
AXG67143.1	002161	Cluster1700_1clades	287	AD1_099	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79892.1	002161	Cluster1700_1clades	248	JA11_087	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66491.1	002161	Cluster1700_1clades	248	JA13_088	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66816.1	002161	Cluster1700_1clades	248	JA29_090	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67461.1	002161	Cluster1700_1clades	248	JA33_087	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08602.1	002161	Cluster1700_1clades	278	Alexandra_104	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58741.1	002161	Cluster1700_1clades	273	Y3_101	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28574.1	002161	Cluster1700_1clades	245	YOLOSWAG_92	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38294.1	002161	Cluster1700_1clades	309	BN7874_125	Phage NCTB	GCA_900092385.1
AXG67190.1	002162	CADHERIN	305	AD1_146	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79940.1	002162	CADHERIN	304	JA11_135	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66539.1	002162	CADHERIN	304	JA13_136	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66864.1	002162	CADHERIN	304	JA29_138	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67509.1	002162	CADHERIN	304	JA33_135	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08423.1	002162	CADHERIN	305	Alexandra_151	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58787.1	002162	CADHERIN	305	Y3_147	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28625.1	002162	CADHERIN	304	YOLOSWAG_145	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38426.1	002162	CADHERIN	307	BN7874_235	Phage NCTB	GCA_900092385.1
AIT13948.1	002163	Cluster1702_1clades	263	PBI_121Q_51	Escherichia phage 121Q	GCA_000926855.1
QAY00389.1	002163	Cluster1702_1clades	264	Ecwhy1_108	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35134.1	002163	Cluster1702_1clades	263	ACQ29_gp454	Escherichia phage PBECO4	GCA_001041035.1
BBM61640.1	002163	Cluster1702_1clades	263	EO157G_0510	Escherichia phage SP27	GCA_008033345.1
AXC36708.1	002163	Cluster1702_1clades	263	-	Escherichia phage UB	GCA_003341455.1
QBO61745.1	002163	Cluster1702_1clades	263	G17_00256	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13790.1	002163	Cluster1702_1clades	263	vBEcoMphAPEC6_gp161c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80542.1	002163	Cluster1702_1clades	263	PSLUR01_00565	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44429.1	002163	Cluster1702_1clades	305	RaK2_00156	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMR59751.1	002164	Cluster1703_1clades	252	SEGD1_102	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96569.1	002164	Cluster1703_1clades	250	G173_gp024	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48129.1	002164	Cluster1703_1clades	250	ASESINO_116	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48403.1	002164	Cluster1703_1clades	237	CAITLIN_108	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48676.1	002164	Cluster1703_1clades	300	CHRISDB_114	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50544.1	002164	Cluster1703_1clades	250	STRATTON_119	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85940.1	002164	Cluster1703_1clades	254	ACEC001_1020	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20808.1	002164	Cluster1703_1clades	252	-	Salmonella phage JN03	GCA_014319805.1
AEP83932.1	002164	Cluster1703_1clades	252	SPN3US_0099	Salmonella phage SPN3US	GCA_001042275.1
AMO43354.1	002165	Cluster1704_1clades	263	W270710_110	Cyanophage S-RIM44	GCA_002599145.1
AOO11598.1	002165	Cluster1704_1clades	280	ES420910_117	Cyanophage S-RIM44	GCA_002599165.1
AOO11826.1	002165	Cluster1704_1clades	263	Np050604_110	Cyanophage S-RIM44	GCA_002599185.1
AOO12063.1	002165	Cluster1704_1clades	280	Np200711_117	Cyanophage S-RIM44	GCA_002599205.1
AOO12299.1	002165	Cluster1704_1clades	280	Np420711_117	Cyanophage S-RIM44	GCA_002599225.1
AOO12527.1	002165	Cluster1704_1clades	263	Sn080709_110	Cyanophage S-RIM44	GCA_002599245.1
AOO12764.1	002165	Cluster1704_1clades	280	Sn130910_117	Cyanophage S-RIM44	GCA_002599265.1
AOO12993.1	002165	Cluster1704_1clades	263	W2100709_111	Cyanophage S-RIM44	GCA_002599285.1
ADO99212.1	002165	Cluster1704_1clades	263	Syn1_111	Prochlorococcus phage Syn1	GCA_000892495.1
ANZ49653.1	002166	SIG+NMT1_3	279	MACHINA_8	Erwinia phage Machina	GCA_002758035.1
AXF51144.1	002166	SIG+NMT1_3	276	WELLINGTON_3	Erwinia phage Wellington	GCA_003344985.1
AFQ96733.1	002166	SIG+NMT1_3	276	G173_gp188	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48031.1	002166	SIG+NMT1_3	278	ASESINO_8	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48307.1	002166	SIG+NMT1_3	277	CAITLIN_7	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ49097.1	002166	SIG+NMT1_3	279	HUXLEY_8	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49365.1	002166	SIG+NMT1_3	276	KWAN_3	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49926.1	002166	SIG+NMT1_3	279	PARSHIK_8	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50443.1	002166	SIG+NMT1_3	276	STRATTON_8	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AFQ96579.1	002167	Cluster1706_1clades	206	G173_gp034	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48419.1	002167	Cluster1706_1clades	202	CAITLIN_124	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ49209.1	002167	Cluster1706_1clades	203	HUXLEY_127	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50037.1	002167	Cluster1706_1clades	203	PARSHIK_128	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50554.1	002167	Cluster1706_1clades	206	STRATTON_129	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ABY63015.1	002167	Cluster1706_1clades	202	201phi2-1p185	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77429.1	002167	Cluster1706_1clades	189	NOXIFER_264	Pseudomonas phage Noxifer	GCA_002625005.1
AGS82188.2	002167	Cluster1706_1clades	272	PaBG_00317	Pseudomonas phage PaBG	GCA_000912555.1
ASV44494.1	002167	Cluster1706_1clades	197	PBI_SCTP2_479	Salicola phage SCTP-2	GCA_002625545.1
ASU03677.1	002168	Cluster1709_1clades	243	JOAD_238	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03434.1	002168	Cluster1709_1clades	243	RISINGSUN_236	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGZ14521.1	002168	Cluster1709_1clades	221	HWC77_gp158	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27287.1	002168	Cluster1709_1clades	222	PPEV_gp193	Pseudomonas phage EL	GCA_000866825.1
QAU04213.1	002168	Cluster1709_1clades	221	HWC03_gp058	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23147.1	002168	Cluster1709_1clades	221	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81019.1	002168	Cluster1709_1clades	221	Aphrodite1_0193	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47580.1	002168	Cluster1709_1clades	221	HWC35_gp186	Vibrio phage USC-1	GCA_006864065.1
BAW98395.1	002168	Cluster1709_1clades	221	FDH33_gp186	Vibrio phage pTD1	GCA_002618825.1
AMS01139.1	002169	Cluster1710_1clades	233	AR9_g054	Bacillus phage AR9	GCA_001743835.1
AMS01140.1	002169	Cluster1710_1clades	230	AR9_g055	Bacillus phage AR9	GCA_001743835.1
AMS01141.1	002169	Cluster1710_1clades	228	AR9_g056	Bacillus phage AR9	GCA_001743835.1
ALN97809.1	002169	Cluster1710_1clades	231	Bp8pS_130	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97810.1	002169	Cluster1710_1clades	224	Bp8pS_131	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97811.1	002169	Cluster1710_1clades	229	Bp8pS_132	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00066.1	002169	Cluster1710_1clades	233	PBI_PBS1_244	Bacillus virus PBS1	GCA_002601325.1
ASU00067.1	002169	Cluster1710_1clades	230	PBI_PBS1_245	Bacillus virus PBS1	GCA_002601325.1
ASU00068.1	002169	Cluster1710_1clades	228	PBI_PBS1_246	Bacillus virus PBS1	GCA_002601325.1
AXG67259.1	002170	Cluster1711_1clades	219	AD1_215	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80006.1	002170	Cluster1711_1clades	183	JA11_201	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66604.1	002170	Cluster1711_1clades	183	JA13_201	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66929.1	002170	Cluster1711_1clades	183	JA29_203	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67575.1	002170	Cluster1711_1clades	183	JA33_201	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08488.1	002170	Cluster1711_1clades	216	Alexandra_225	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58860.1	002170	Cluster1711_1clades	218	Y3_220	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28692.1	002170	Cluster1711_1clades	230	YOLOSWAG_214	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38170.1	002170	Cluster1711_1clades	147	BN7874_001	Phage NCTB	GCA_900092385.1
AXG67176.1	002171	Cluster1713_1clades	224	AD1_132	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79926.1	002171	Cluster1713_1clades	222	JA11_121	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66525.1	002171	Cluster1713_1clades	222	JA13_122	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66850.1	002171	Cluster1713_1clades	222	JA29_124	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67495.1	002171	Cluster1713_1clades	222	JA33_121	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08409.1	002171	Cluster1713_1clades	223	Alexandra_137	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58773.1	002171	Cluster1713_1clades	223	Y3_133	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28612.1	002171	Cluster1713_1clades	225	YOLOSWAG_131	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38391.1	002171	Cluster1713_1clades	226	BN7874_213	Phage NCTB	GCA_900092385.1
ANZ49674.1	002172	Cluster1714_1clades	194	MACHINA_36	Erwinia phage Machina	GCA_002758035.1
AFQ96747.1	002172	Cluster1714_1clades	153	G173_gp202	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48050.1	002172	Cluster1714_1clades	153	ASESINO_37	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48598.1	002172	Cluster1714_1clades	163	CHRISDB_36	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49119.1	002172	Cluster1714_1clades	194	HUXLEY_37	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49947.1	002172	Cluster1714_1clades	194	PARSHIK_38	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50460.1	002172	Cluster1714_1clades	153	STRATTON_35	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85860.1	002172	Cluster1714_1clades	223	ACEC001_0220	Escherichia phage vB_EcoM_EC001	GCA_014131305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXF51100.1	002172	Cluster1714_1clades	223	MLDJOKPK_00146	Salmonella phage SPAsTU	GCA_003183805.1
APU01648.1	002173	Cluster1715_1clades	210	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28886.1	002173	Cluster1715_1clades	205	AP1_0179	Aeromonas phage AP1	GCA_014183365.1
ATI17237.1	002173	Cluster1715_1clades	205	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00350.1	002173	Cluster1715_1clades	205	HWB28_gp202	Aeromonas phage AS-zj	GCA_002627665.1
QAX97680.1	002173	Cluster1715_1clades	205	ASswx1_34	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01468.1	002173	Cluster1715_1clades	215	ASwh1_409	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39211.1	002173	Cluster1715_1clades	205	CC2_081	Aeromonas phage CC2	GCA_000903495.1
ADQ53276.1	002173	Cluster1715_1clades	101	65p268	Aeromonas virus 65	GCA_000893255.1
ADQ53277.1	002173	Cluster1715_1clades	117	65p269	Aeromonas virus 65	GCA_000893255.1
QGZ14533.1	002174	Cluster1716_1clades	211	HWC77_gp170	Photobacterium phage PDCC-1	GCA_009800445.1
QGZ14535.1	002174	Cluster1716_1clades	214	HWC77_gp172	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04201.1	002174	Cluster1716_1clades	211	HWC03_gp046	Vibrio phage 2 TSL-2019	GCA_006964105.1
QAU04199.1	002174	Cluster1716_1clades	214	HWC03_gp044	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23159.1	002174	Cluster1716_1clades	211	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QCW23161.1	002174	Cluster1716_1clades	214	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47569.1	002174	Cluster1716_1clades	212	HWC35_gp175	Vibrio phage USC-1	GCA_006864065.1
QDH47567.1	002174	Cluster1716_1clades	214	HWC35_gp173	Vibrio phage USC-1	GCA_006864065.1
BAW98383.1	002174	Cluster1716_1clades	214	FDH33_gp174	Vibrio phage pTD1	GCA_002618825.1
QMV29173.1	002175	Cluster1717_1clades	161	AP1_0477	Aeromonas phage AP1	GCA_014183365.1
AXQ69153.1	002175	Cluster1717_1clades	168	CcrBL9_gp129	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ68580.1	002175	Cluster1717_1clades	175	CcrPW_gp041	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69707.1	002175	Cluster1717_1clades	168	CcrSC_gp125	Caulobacter phage CcrSC	GCA_003443315.1
QIG57920.1	002175	Cluster1717_1clades	214	SEA_PAULODIABOLI_235	Microbacterium phage PauloDiaboli	GCA_011067425.1
AGR47729.1	002175	Cluster1717_1clades	172	SmphiM12_097	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12983.1	002175	Cluster1717_1clades	172	PHIM19_76	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12623.1	002175	Cluster1717_1clades	172	PHIM7_75	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13355.1	002175	Cluster1717_1clades	172	PHIN3_91	Sinorhizobium phage phiN3	GCA_001501175.1
AAQ64307.1	002176	Cluster1718_1clades	210	KVP40.0238	Vibrio phage KVP40	GCA_000843785.1
AAQ64308.1	002176	Cluster1718_1clades	204	KVP40.0239	Vibrio phage KVP40	GCA_000843785.1
QIW90623.1	002176	Cluster1718_1clades	210	GCAPEGMB_00276	Vibrio phage V07	GCA_012361095.1
QIW90624.1	002176	Cluster1718_1clades	204	GCAPEGMB_00277	Vibrio phage V07	GCA_012361095.1
QIW91175.1	002176	Cluster1718_1clades	204	COHAPHLL_00339	Vibrio phage V09	GCA_012361135.1
QIW91176.1	002176	Cluster1718_1clades	210	COHAPHLL_00340	Vibrio phage V09	GCA_012361135.1
QHJ74418.1	002176	Cluster1718_1clades	210	VH12019_00091	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74419.1	002176	Cluster1718_1clades	204	VH12019_00092	Vibrio phage VH1_2019	GCA_009931825.1
AFN37468.1	002176	Cluster1718_1clades	210	pp2_235	Vibriophage phi-pp2	GCA_002630725.1
AIT14283.1	002177	Cluster1719_1clades	187	PBI_121Q_393	Escherichia phage 121Q	GCA_000926855.1
QAY00655.1	002177	Cluster1719_1clades	188	Ecwhy1_380	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34851.1	002177	Cluster1719_1clades	187	ACQ29_gp171	Escherichia phage PBECO4	GCA_001041035.1
BBM61957.1	002177	Cluster1719_1clades	187	EO157G_3680	Escherichia phage SP27	GCA_008033345.1
AXC36960.1	002177	Cluster1719_1clades	187	-	Escherichia phage UB	GCA_003341455.1
QBO62021.1	002177	Cluster1719_1clades	187	G17_00532	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14042.1	002177	Cluster1719_1clades	187	vBEcoMphAPEC6_gp419c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80270.1	002177	Cluster1719_1clades	187	PSLUR01_00293	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44697.1	002177	Cluster1719_1clades	202	RaK2_00424	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMR59845.1	002178	Cluster1720_1clades	172	SEGD1_198	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49842.1	002178	Cluster1720_1clades	170	MACHINA_204	Erwinia phage Machina	GCA_002758035.1
AGX01821.1	002178	Cluster1720_1clades	202	CF95_gp099	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ48498.1	002178	Cluster1720_1clades	170	CAITLIN_203	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ49286.1	002178	Cluster1720_1clades	170	HUXLEY_204	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50114.1	002178	Cluster1720_1clades	170	PARSHIK_205	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QKN86035.1	002178	Cluster1720_1clades	172	ACEC001_1920	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20884.1	002178	Cluster1720_1clades	172	-	Salmonella phage JN03	GCA_014319805.1
AEP84026.1	002178	Cluster1720_1clades	172	SPN3US_0193	Salmonella phage SPN3US	GCA_001042275.1
AIT13967.1	002179	Cluster1721_1clades	195	PBI_121Q_70	Escherichia phage 121Q	GCA_000926855.1
QAY00370.1	002179	Cluster1721_1clades	195	Ecwhy1_89	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35115.1	002179	Cluster1721_1clades	199	ACQ29_gp435	Escherichia phage PBECO4	GCA_001041035.1
BBM61659.1	002179	Cluster1721_1clades	195	EO157G_0700	Escherichia phage SP27	GCA_008033345.1
AXC36689.1	002179	Cluster1721_1clades	195	-	Escherichia phage UB	GCA_003341455.1
QBO61726.1	002179	Cluster1721_1clades	195	G17_00237	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13771.1	002179	Cluster1721_1clades	195	vBEcoMphAPEC6_gp142c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80561.1	002179	Cluster1721_1clades	199	PSLUR01_00584	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44449.1	002179	Cluster1721_1clades	196	RaK2_00176	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AOO14298.1	002180	Cluster1722_1clades	181	Sn110110_104	Cyanophage S-RIM14	GCA_002599065.1
AOO14947.1	002180	Cluster1722_1clades	181	W1230910_101	Cyanophage S-RIM14	GCA_002599125.1
AIR93444.1	002180	Cluster1722_1clades	199	AVU42_gp106	Prochlorococcus phage P-TIM68	GCA_001503075.1
QGT54889.1	002180	Cluster1722_1clades	182	b23_0276	Synechococcus phage B23	GCA_009745195.1
QGT54524.1	002180	Cluster1722_1clades	182	b3_0283	Synechococcus phage B3	GCA_009745215.1
ASR76175.1	002180	Cluster1722_1clades	196	PBI_BELLAMY_130	Synechococcus phage Bellamy	GCA_002627525.1
QCW22885.1	002180	Cluster1722_1clades	182	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50472.1	002180	Cluster1722_1clades	182	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70117.1	002180	Cluster1722_1clades	182	SynMITS9220M01_104	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG67371.1	002181	Tox-HNH	180	AD1_327	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80123.1	002181	Tox-HNH	180	JA11_318	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66723.1	002181	Tox-HNH	180	JA13_320	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67041.1	002181	Tox-HNH	180	JA29_315	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67692.1	002181	Tox-HNH	180	JA33_318	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08594.1	002181	Tox-HNH	179	Alexandra_346	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28798.1	002181	Tox-HNH	186	YOLOSWAG_330	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38257.1	002181	Tox-HNH	196	BN7874_088	Phage NCTB	GCA_900092385.1
QKE11210.1	002181	Tox-HNH	176	PaBG_00114	Pseudomonas phage PaBG	GCA_000912555.1
AIT14102.1	002182	Cluster1724_1clades	184	PBI_121Q_212	Escherichia phage 121Q	GCA_000926855.1
QAY00820.1	002182	Cluster1724_1clades	184	Ecwhy1_547	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34993.1	002182	Cluster1724_1clades	184	ACQ29_gp313	Escherichia phage PBECO4	GCA_001041035.1
BBM61784.1	002182	Cluster1724_1clades	184	EO157G_1950	Escherichia phage SP27	GCA_008033345.1
AXC36573.1	002182	Cluster1724_1clades	184	-	Escherichia phage UB	GCA_003341455.1
QBO61597.1	002182	Cluster1724_1clades	184	G17_00101	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13656.1	002182	Cluster1724_1clades	184	vBEcoMphAPEC6_gp025c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80096.1	002182	Cluster1724_1clades	184	PSLUR01_00119	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44559.1	002182	Cluster1724_1clades	195	RaK2_00286	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT13977.1	002183	Cluster1725_1clades	142	PBI_121Q_80	Escherichia phage 121Q	GCA_000926855.1
QAY00360.1	002183	Cluster1725_1clades	142	Ecwhy1_79	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35106.1	002183	Cluster1725_1clades	142	ACQ29_gp426	Escherichia phage PBECO4	GCA_001041035.1
BBM61669.1	002183	Cluster1725_1clades	142	EO157G_0800	Escherichia phage SP27	GCA_008033345.1
AXC36681.1	002183	Cluster1725_1clades	142	-	Escherichia phage UB	GCA_003341455.1
QBO61715.1	002183	Cluster1725_1clades	193	G17_00226	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13763.1	002183	Cluster1725_1clades	142	vBEcoMphAPEC6_gp134c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80571.1	002183	Cluster1725_1clades	142	PSLUR01_00594	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44457.1	002183	Cluster1725_1clades	163	RaK2_00184	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFC21608.1	002184	Cluster1726_1clades	191	GAP32_158	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44281.1	002184	Cluster1726_1clades	187	RaK2_00008	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43727.1	002184	Cluster1726_1clades	189	CBB_162	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18863.1	002184	Cluster1726_1clades	173	7t3_0342	Salmonella phage 7t3	GCA_006083215.1
AZU98124.1	002184	Cluster1726_1clades	185	CPT_Munch_180	Salmonella phage Munch	GCA_004015485.1
QIG62858.1	002184	Cluster1726_1clades	173	SEPL_245	Salmonella phage SE_PL	GCA_011067555.1
AQW88682.1	002184	Cluster1726_1clades	191	BF_0157	Serratia phage BF	GCA_002619745.1
SOK58963.1	002184	Cluster1726_1clades	189	g155	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58429.1	002184	Cluster1726_1clades	189	g152	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASU03833.1	002185	Cluster1727_1clades	181	JOAD_82	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03588.1	002185	Cluster1727_1clades	181	RISINGSUN_82	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGZ14433.1	002185	Cluster1727_1clades	188	HWC77_gp070	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27171.1	002185	Cluster1727_1clades	181	PPEV_gp077	Pseudomonas phage EL	GCA_000866825.1
QAU04303.1	002185	Cluster1727_1clades	188	HWC03_gp148	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23275.1	002185	Cluster1727_1clades	188	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81033.1	002185	Cluster1727_1clades	188	Aphrodite1_0070	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47453.1	002185	Cluster1727_1clades	188	HWC35_gp059	Vibrio phage USC-1	GCA_006864065.1
BAW98275.1	002185	Cluster1727_1clades	191	FDH33_gp066	Vibrio phage pTD1	GCA_002618825.1
ASU03896.1	002186	Cluster1728_1clades	161	JOAD_19	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03651.1	002186	Cluster1728_1clades	161	RISINGSUN_19	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGZ14573.1	002186	Cluster1728_1clades	162	HWC77_gp210	Photobacterium phage PDCC-1	GCA_009800445.1
CAG27111.1	002186	Cluster1728_1clades	188	PPEV_gp017	Pseudomonas phage EL	GCA_000866825.1
QAU04160.1	002186	Cluster1728_1clades	162	HWC03_gp005	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23198.1	002186	Cluster1728_1clades	151	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81055.1	002186	Cluster1728_1clades	151	Aphrodite1_0146	Vibrio phage Aphrodite1	GCA_002958015.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDH47531.1	002186	Cluster1728_1clades	151	HWC35_gp137	Vibrio phage USC-1	GCA_006864065.1
BAW98347.1	002186	Cluster1728_1clades	151	FDH33_gp138	Vibrio phage pTD1	GCA_002618825.1
ARB13554.1	002187	Cluster1729_1clades	178	Ccr10_gp026	Caulobacter phage Ccr10	GCA_002619445.1
ARB13900.1	002187	Cluster1729_1clades	178	Ccr2_gp025	Caulobacter phage Ccr2	GCA_002619465.1
ARB14589.1	002187	Cluster1729_1clades	178	Ccr29_gp032	Caulobacter phage Ccr29	GCA_002619485.1
ARB14944.1	002187	Cluster1729_1clades	178	Ccr32_gp025	Caulobacter phage Ccr32	GCA_002619505.1
ARB15275.1	002187	Cluster1729_1clades	178	Ccr34_gp026	Caulobacter phage Ccr34	GCA_002619525.1
ARB14243.1	002187	Cluster1729_1clades	179	Ccr5_gp025	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68226.1	002187	Cluster1729_1clades	175	CcrBL10_gp022	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87542.1	002187	Cluster1729_1clades	118	CcrKarma_gp025	Caulobacter virus Karma	GCA_000901575.1
AFU86857.1	002187	Cluster1729_1clades	178	CbK_gp025	Caulobacter virus phiCbK	GCA_000900535.1
AIT14268.1	002188	Cluster1730_1clades	177	PBI_121Q_378	Escherichia phage 121Q	GCA_000926855.1
QAY00669.1	002188	Cluster1730_1clades	178	Ecwhy1_394	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34864.1	002188	Cluster1730_1clades	177	ACQ29_gp184	Escherichia phage PBECO4	GCA_001041035.1
BBM61943.1	002188	Cluster1730_1clades	178	EO157G_3540	Escherichia phage SP27	GCA_008033345.1
AXC36973.1	002188	Cluster1730_1clades	177	-	Escherichia phage UB	GCA_003341455.1
QBO62036.1	002188	Cluster1730_1clades	177	G17_00547	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14057.1	002188	Cluster1730_1clades	177	vBEcoMphAPEC6_gp434c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80257.1	002188	Cluster1730_1clades	177	PSLUR01_00280	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44671.1	002188	Cluster1730_1clades	177	RaK2_00398	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14413.1	002189	Cluster1731_1clades	159	PBI_121Q_523	Escherichia phage 121Q	GCA_000926855.1
QAY00538.1	002189	Cluster1731_1clades	159	Ecwhy1_259	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34729.1	002189	Cluster1731_1clades	159	ACQ29_gp049	Escherichia phage PBECO4	GCA_001041035.1
BBM62085.1	002189	Cluster1731_1clades	159	EO157G_4960	Escherichia phage SP27	GCA_008033345.1
AXC36845.1	002189	Cluster1731_1clades	159	-	Escherichia phage UB	GCA_003341455.1
QBO61888.1	002189	Cluster1731_1clades	159	G17_00399	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13925.1	002189	Cluster1731_1clades	159	vBEcoMphAPEC6_gp300c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80399.1	002189	Cluster1731_1clades	159	PSLUR01_00422	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44291.1	002189	Cluster1731_1clades	177	RaK2_00018	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ARB13726.1	002190	Cluster1732_1clades	88	Ccr10_gp196c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14071.1	002190	Cluster1732_1clades	88	Ccr2_gp195c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14760.1	002190	Cluster1732_1clades	88	Ccr29_gp204	Caulobacter phage Ccr29	GCA_002619485.1
ARB14414.1	002190	Cluster1732_1clades	88	Ccr5_gp194c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68392.1	002190	Cluster1732_1clades	175	CcrBL10_gp188c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87719.1	002190	Cluster1732_1clades	88	CcrKarma_gp202	Caulobacter virus Karma	GCA_000901575.1
AFU87368.1	002190	Cluster1732_1clades	88	CcrMagneto_gp198	Caulobacter virus Magneto	GCA_000903095.1
AFU86678.1	002190	Cluster1732_1clades	175	CcrRogue_gp196	Caulobacter virus Rogue	GCA_000900555.1
AFU88515.1	002190	Cluster1732_1clades	88	CcrSwift_gp197	Caulobacter virus Swift	GCA_000899655.1
AIT14394.1	002191	Cluster1733_1clades	169	PBI_121Q_504	Escherichia phage 121Q	GCA_000926855.1
QAY00554.1	002191	Cluster1733_1clades	169	Ecwhy1_275	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34748.1	002191	Cluster1733_1clades	169	ACQ29_gp068	Escherichia phage PBECO4	GCA_001041035.1
BBM62065.1	002191	Cluster1733_1clades	169	EO157G_4760	Escherichia phage SP27	GCA_008033345.1
AXC36863.1	002191	Cluster1733_1clades	169	-	Escherichia phage UB	GCA_003341455.1
QBO61908.1	002191	Cluster1733_1clades	169	G17_00419	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13943.1	002191	Cluster1733_1clades	169	vBEcoMphAPEC6_gp319c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80383.1	002191	Cluster1733_1clades	169	PSLUR01_00406	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44275.1	002191	Cluster1733_1clades	162	RaK2_00002	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14289.1	002192	Cluster1734_1clades	169	PBI_121Q_399	Escherichia phage 121Q	GCA_000926855.1
QAY00649.1	002192	Cluster1734_1clades	168	Ecwhy1_374	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34845.1	002192	Cluster1734_1clades	169	ACQ29_gp165	Escherichia phage PBECO4	GCA_001041035.1
BBM61963.1	002192	Cluster1734_1clades	169	EO157G_3740	Escherichia phage SP27	GCA_008033345.1
AXC36954.1	002192	Cluster1734_1clades	169	-	Escherichia phage UB	GCA_003341455.1
QBO62015.1	002192	Cluster1734_1clades	169	G17_00526	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14036.1	002192	Cluster1734_1clades	169	vBEcoMphAPEC6_gp413c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80276.1	002192	Cluster1734_1clades	169	PSLUR01_00299	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44703.1	002192	Cluster1734_1clades	163	RaK2_00430	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMR59765.1	002193	Cluster1735_1clades	156	SEGD1_118	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96582.1	002193	Cluster1735_1clades	157	G173_gp037	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48142.1	002193	Cluster1735_1clades	157	ASESINO_129	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50557.1	002193	Cluster1735_1clades	157	STRATTON_132	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85955.1	002193	Cluster1735_1clades	156	ACEC001_1170	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO63889.1	002193	Cluster1735_1clades	166	Goslar_00096	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QNI20821.1	002193	Cluster1735_1clades	156	-	Salmonella phage JN03	GCA_014319805.1
AWN08995.1	002193	Cluster1735_1clades	160	MLDJOKPK_00043	Salmonella phage SPAsTU	GCA_003183805.1
AEP83947.1	002193	Cluster1735_1clades	156	SPN3US_0114	Salmonella phage SPN3US	GCA_001042275.1
AIT14278.1	002194	Cluster1736_1clades	164	PBI_121Q_388	Escherichia phage 121Q	GCA_000926855.1
QAY00660.1	002194	Cluster1736_1clades	160	Ecwhy1_385	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34856.1	002194	Cluster1736_1clades	160	ACQ29_gp176	Escherichia phage PBECO4	GCA_001041035.1
BBM61952.1	002194	Cluster1736_1clades	161	EO157G_3630	Escherichia phage SP27	GCA_008033345.1
AXC36965.1	002194	Cluster1736_1clades	156	-	Escherichia phage UB	GCA_003341455.1
QBO62026.1	002194	Cluster1736_1clades	164	G17_00537	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14047.1	002194	Cluster1736_1clades	164	vBEcoMphAPEC6_gp424c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80265.1	002194	Cluster1736_1clades	164	PSLUR01_00288	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44692.1	002194	Cluster1736_1clades	163	RaK2_00419	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ANM45105.1	002195	Cluster1737_1clades	137	KTN4_347	Pseudomonas phage KTN4	GCA_002607225.1
ARV77485.1	002195	Cluster1737_1clades	160	NOXIFER_320	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32521.1	002195	Cluster1737_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03775.1	002195	Cluster1737_1clades	138	352	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02911.1	002195	Cluster1737_1clades	144	PSA21_385	Pseudomonas phage Psa21	GCA_004340405.1
ATN94609.1	002195	Cluster1737_1clades	137	SL2_032	Pseudomonas phage SL2	GCA_002956015.1
QJB22981.1	002195	Cluster1737_1clades	137	fnug_338	Pseudomonas phage fnug	GCA_012837215.1
QEM42094.1	002195	Cluster1737_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26360.1	002195	Cluster1737_1clades	52	PHIKZ287.1	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67116.1	002196	Cluster1738_1clades	154	AD1_072	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79873.1	002196	Cluster1738_1clades	155	JA11_068	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66472.1	002196	Cluster1738_1clades	155	JA13_069	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66797.1	002196	Cluster1738_1clades	155	JA29_071	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67442.1	002196	Cluster1738_1clades	155	JA33_068	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08352.1	002196	Cluster1738_1clades	154	Alexandra_74	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58715.1	002196	Cluster1738_1clades	154	Y3_075	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28549.1	002196	Cluster1738_1clades	158	YOLOSWAG_66	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGS82148.1	002196	Cluster1738_1clades	156	PaBG_00275	Pseudomonas phage PaBG	GCA_000912555.1
AFC21458.1	002197	TM	151	GAP32_011	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43576.1	002197	TM	151	CBB_11	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44127.1	002197	TM	151	CBB_564	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18696.1	002197	TM	154	7t3_0175	Salmonella phage 7t3	GCA_006083215.1
AZU97969.1	002197	TM	154	CPT_Munch_025	Salmonella phage Munch	GCA_004015485.1
QIG63009.1	002197	TM	154	SEPL_396	Salmonella phage SE_PL	GCA_011067555.1
AQW88531.1	002197	TM	151	BF_0006	Serratia phage BF	GCA_002619745.1
SOK58813.1	002197	TM	151	g005	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58282.1	002197	TM	151	g005	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14038.1	002198	Cluster1740_1clades	136	PBI_121Q_148	Escherichia phage 121Q	GCA_000926855.1
QAY00305.1	002198	Cluster1740_1clades	145	Ecwhy1_23	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35055.1	002198	Cluster1740_1clades	151	ACQ29_gp375	Escherichia phage PBECO4	GCA_001041035.1
BBM61721.1	002198	Cluster1740_1clades	133	EO157G_1320	Escherichia phage SP27	GCA_008033345.1
AXC36631.1	002198	Cluster1740_1clades	129	-	Escherichia phage UB	GCA_003341455.1
QBO61661.1	002198	Cluster1740_1clades	136	G17_00165	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13713.1	002198	Cluster1740_1clades	136	vBEcoMphAPEC6_gp083c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80033.1	002198	Cluster1740_1clades	136	PSLUR01_00056	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44499.1	002198	Cluster1740_1clades	135	RaK2_00226	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ADM80124.1	002199	SMS-KaiC	60	phiAS5_ORF0281	Aeromonas phage phiAS5	GCA_000887715.1
AXG67069.1	002199	SMS-KaiC	150	AD1_025	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79908.1	002199	SMS-KaiC	103	JA11_103	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66507.1	002199	SMS-KaiC	103	JA13_104	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66832.1	002199	SMS-KaiC	103	JA29_106	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67477.1	002199	SMS-KaiC	103	JA33_103	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08306.1	002199	SMS-KaiC	142	Alexandra_26	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58666.1	002199	SMS-KaiC	140	Y3_026	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28592.1	002199	SMS-KaiC	66	YOLOSWAG_110	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ABY62907.1	002200	Cluster1742_1clades	141	201phi2-1p074	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44817.1	002200	Cluster1742_1clades	142	KTN4_059	Pseudomonas phage KTN4	GCA_002607225.1
QBX32191.1	002200	Cluster1742_1clades	130	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76689.1	002200	Cluster1742_1clades	148	PHABIO_58	Pseudomonas phage Phabio	GCA_002624965.1
AEH03465.1	002200	Cluster1742_1clades	149	038	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02568.1	002200	Cluster1742_1clades	129	PSA21_38	Pseudomonas phage Psa21	GCA_004340405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATN94894.1	002200	Cluster1742_1clades	137	SL2_317	Pseudomonas phage SL2	GCA_002956015.1
QJB22696.1	002200	Cluster1742_1clades	137	fnug_53	Pseudomonas phage fnug	GCA_012837215.1
QEM41769.1	002200	Cluster1742_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AIT14039.1	002201	Cluster1743_1clades	148	PBI_121Q_149	Escherichia phage 121Q	GCA_000926855.1
QAY00304.1	002201	Cluster1743_1clades	148	Ecwhy1_22	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35054.1	002201	Cluster1743_1clades	148	ACQ29_gp374	Escherichia phage PBECO4	GCA_001041035.1
BBM61722.1	002201	Cluster1743_1clades	148	EO157G_1330	Escherichia phage SP27	GCA_008033345.1
AXC36630.1	002201	Cluster1743_1clades	148	-	Escherichia phage UB	GCA_003341455.1
QBO61660.1	002201	Cluster1743_1clades	148	G17_00164	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13712.1	002201	Cluster1743_1clades	148	vBEcoMphAPEC6_gp082c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80034.1	002201	Cluster1743_1clades	148	PSLUR01_00057	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44502.1	002201	Cluster1743_1clades	74	RaK2_00229	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AAX44671.1	002202	TM	113	PSSM2_294	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12306.1	002202	TM	113	PRTG_00153	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIX30746.1	002202	TM	116	Syn7803US37_269	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54936.1	002202	TM	117	b23_0323	Synechococcus phage B23	GCA_009745195.1
QGT54571.1	002202	TM	117	b3_0330	Synechococcus phage B3	GCA_009745215.1
QCW23088.1	002202	TM	114	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50722.1	002202	TM	147	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70472.1	002202	TM	113	HOU04_gp073	Synechococcus phage S-T4	GCA_003443335.1
QJT70107.1	002202	TM	110	SynMITS9220M01_094	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT13982.1	002203	Cluster1745_1clades	134	PBI_121Q_85	Escherichia phage 121Q	GCA_000926855.1
QAY00356.1	002203	Cluster1745_1clades	134	Ecwhy1_75	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35102.1	002203	Cluster1745_1clades	134	ACQ29_gp422	Escherichia phage PBECO4	GCA_001041035.1
BBM61673.1	002203	Cluster1745_1clades	134	EO157G_0840	Escherichia phage SP27	GCA_008033345.1
AXC36677.1	002203	Cluster1745_1clades	134	-	Escherichia phage UB	GCA_003341455.1
QBO61711.1	002203	Cluster1745_1clades	134	G17_00222	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13759.1	002203	Cluster1745_1clades	134	vBEcoMphAPEC6_gp130c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79986.1	002203	Cluster1745_1clades	134	PSLUR01_00002	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44460.1	002203	Cluster1745_1clades	146	RaK2_00187	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ABY63070.1	002204	SIG+FRQ	140	201phi2-1p241	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44950.1	002204	SIG+FRQ	133	KTN4_192	Pseudomonas phage KTN4	GCA_002607225.1
ARV76860.1	002204	SIG+FRQ	139	PHABIO_229	Pseudomonas phage Phabio	GCA_002624965.1
AEH03602.1	002204	SIG+FRQ	138	179	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02739.1	002204	SIG+FRQ	134	PSA21_213	Pseudomonas phage Psa21	GCA_004340405.1
ATN94764.1	002204	SIG+FRQ	133	SL2_187	Pseudomonas phage SL2	GCA_002956015.1
QJB22828.1	002204	SIG+FRQ	133	fnug_185	Pseudomonas phage fnug	GCA_012837215.1
QEM41911.1	002204	SIG+FRQ	136	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83057.1	002204	SIG+FRQ	137	PHIKZ156	Pseudomonas virus phiKZ	GCA_000842965.1
AIT13981.1	002205	Cluster1747_1clades	136	PBI_121Q_84	Escherichia phage 121Q	GCA_000926855.1
QAY00357.1	002205	Cluster1747_1clades	136	Ecwhy1_76	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35103.1	002205	Cluster1747_1clades	110	ACQ29_gp423	Escherichia phage PBECO4	GCA_001041035.1
BBM61672.1	002205	Cluster1747_1clades	136	EO157G_0830	Escherichia phage SP27	GCA_008033345.1
AXC36678.1	002205	Cluster1747_1clades	136	-	Escherichia phage UB	GCA_003341455.1
QBO61712.1	002205	Cluster1747_1clades	136	G17_00223	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13760.1	002205	Cluster1747_1clades	136	vBEcoMphAPEC6_gp131c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79985.1	002205	Cluster1747_1clades	136	PSLUR01_00001	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44459.1	002205	Cluster1747_1clades	140	RaK2_00186	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14400.1	002206	Cluster1748_1clades	139	PBI_121Q_510	Escherichia phage 121Q	GCA_000926855.1
QAY00551.1	002206	Cluster1748_1clades	138	Ecwhy1_272	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34742.1	002206	Cluster1748_1clades	139	ACQ29_gp062	Escherichia phage PBECO4	GCA_001041035.1
BBM62071.1	002206	Cluster1748_1clades	139	EO157G_4820	Escherichia phage SP27	GCA_008033345.1
AXC36857.1	002206	Cluster1748_1clades	139	-	Escherichia phage UB	GCA_003341455.1
QBO61902.1	002206	Cluster1748_1clades	139	G17_00413	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13938.1	002206	Cluster1748_1clades	139	vBEcoMphAPEC6_gp313c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80386.1	002206	Cluster1748_1clades	139	PSLUR01_00409	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44282.1	002206	Cluster1748_1clades	135	RaK2_00009	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14080.1	002207	Cluster1749_1clades	107	PBI_121Q_190	Escherichia phage 121Q	GCA_000926855.1
QAY00843.1	002207	Cluster1749_1clades	116	Ecwhy1_571	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35014.1	002207	Cluster1749_1clades	107	ACQ29_gp334	Escherichia phage PBECO4	GCA_001041035.1
BBM61763.1	002207	Cluster1749_1clades	124	EO157G_1740	Escherichia phage SP27	GCA_008033345.1
AXC36592.1	002207	Cluster1749_1clades	116	-	Escherichia phage UB	GCA_003341455.1
QBO61619.1	002207	Cluster1749_1clades	116	G17_00123	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13677.1	002207	Cluster1749_1clades	116	vBEcoMphAPEC6_gp047c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80074.1	002207	Cluster1749_1clades	116	PSLUR01_00097	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44540.1	002207	Cluster1749_1clades	138	RaK2_00267	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMR59780.1	002208	Cluster1750_1clades	71	SEGD1_133	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59781.1	002208	Cluster1750_1clades	44	SEGD1_134	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96593.1	002208	Cluster1750_1clades	136	G173_gp048	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48158.1	002208	Cluster1750_1clades	136	ASESINO_145	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50570.1	002208	Cluster1750_1clades	136	STRATTON_145	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85969.1	002208	Cluster1750_1clades	127	ACEC001_1310	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20833.1	002208	Cluster1750_1clades	127	-	Salmonella phage JN03	GCA_014319805.1
AWN08986.2	002208	Cluster1750_1clades	128	MLDJOKPK_00023	Salmonella phage SPAsTU	GCA_003183805.1
AEP83962.1	002208	Cluster1750_1clades	127	SPN3US_0129	Salmonella phage SPN3US	GCA_001042275.1
AFC21836.1	002209	Cluster1751_1clades	119	GAP32_384	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44463.1	002209	Cluster1751_1clades	113	RaK2_00190	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43956.1	002209	Cluster1751_1clades	119	CBB_393	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19094.1	002209	Cluster1751_1clades	124	7t3_0576	Salmonella phage 7t3	GCA_006083215.1
AZU98333.1	002209	Cluster1751_1clades	124	CPT_Munch_391	Salmonella phage Munch	GCA_004015485.1
QIG62650.1	002209	Cluster1751_1clades	124	SEPL_037	Salmonella phage SE_PL	GCA_011067555.1
AQW88917.1	002209	Cluster1751_1clades	132	BF_0392	Serratia phage BF	GCA_002619745.1
SOK59207.1	002209	Cluster1751_1clades	128	g399	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58673.1	002209	Cluster1751_1clades	128	g396	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14066.1	002210	Cluster1752_1clades	122	PBI_121Q_176	Escherichia phage 121Q	GCA_000926855.1
QAY00856.1	002210	Cluster1752_1clades	122	Ecwhy1_585	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35027.1	002210	Cluster1752_1clades	122	ACQ29_gp347	Escherichia phage PBECO4	GCA_001041035.1
BBM61749.1	002210	Cluster1752_1clades	122	EO157G_1600	Escherichia phage SP27	GCA_008033345.1
AXC36604.1	002210	Cluster1752_1clades	122	-	Escherichia phage UB	GCA_003341455.1
QBO61633.1	002210	Cluster1752_1clades	122	G17_00137	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13688.1	002210	Cluster1752_1clades	122	vBEcoMphAPEC6_gp058c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80061.1	002210	Cluster1752_1clades	122	PSLUR01_00084	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44523.1	002210	Cluster1752_1clades	130	RaK2_00250	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14410.1	002211	PPP1-HTH	107	PBI_121Q_520	Escherichia phage 121Q	GCA_000926855.1
QAY00541.1	002211	PPP1-HTH	130	Ecwhy1_262	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34732.1	002211	PPP1-HTH	130	ACQ29_gp052	Escherichia phage PBECO4	GCA_001041035.1
BBM62082.1	002211	PPP1-HTH	130	EO157G_4930	Escherichia phage SP27	GCA_008033345.1
AXC36848.1	002211	PPP1-HTH	107	-	Escherichia phage UB	GCA_003341455.1
QBO61891.1	002211	PPP1-HTH	130	G17_00402	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13928.1	002211	PPP1-HTH	130	vBEcoMphAPEC6_gp303c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80396.1	002211	PPP1-HTH	130	PSLUR01_00419	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44289.1	002211	PPP1-HTH	129	RaK2_00016	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14122.1	002212	SIG+TM+TM	123	PBI_121Q_232	Escherichia phage 121Q	GCA_000926855.1
QAY00803.1	002212	SIG+TM+TM	123	Ecwhy1_530	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34978.1	002212	SIG+TM+TM	110	ACQ29_gp298	Escherichia phage PBECO4	GCA_001041035.1
BBM61800.1	002212	SIG+TM+TM	123	EO157G_2110	Escherichia phage SP27	GCA_008033345.1
AXC36558.1	002212	SIG+TM+TM	39	-	Escherichia phage UB	GCA_003341455.1
QBO61579.1	002212	SIG+TM+TM	123	G17_00083	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13643.1	002212	SIG+TM+TM	123	vBEcoMphAPEC6_gp012c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80112.1	002212	SIG+TM+TM	123	PSLUR01_00135	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44588.1	002212	SIG+TM+TM	129	RaK2_00315	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AGH56896.1	002213	TM	120	CPXG_00093	Cyanophage P-RSM6	GCA_000906155.1
AJK27566.1	002213	TM	119	PTIM40_139	Cyanophage P-TIM40	GCA_001470935.1
AGH07603.1	002213	TM	113	CYVG_00159	Cyanophage S-SSM6a	GCA_002710385.1
AGG54501.1	002213	TM	102	CYWG_00217	Cyanophage S-SSM6b	GCA_002710425.1
AGH26235.1	002213	TM	122	CPMG_00134	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44628.1	002213	TM	109	PSSM2_251	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12342.1	002213	TM	109	PRTG_00189	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93557.1	002213	TM	128	AVU42_gp220	Prochlorococcus phage P-TIM68	GCA_001503075.1
QJT70182.1	002213	TM	91	SynMITS9220M01_174	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01402.1	002214	GxC-R	119	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28892.1	002214	GxC-R	122	AP1_0185	Aeromonas phage AP1	GCA_014183365.1
ATI17494.1	002214	GxC-R	122	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00503.1	002214	GxC-R	120	HWB28_gp049	Aeromonas phage AS-zj	GCA_002627665.1
QAX97933.1	002214	GxC-R	120	ASswx1_291	Aeromonas phage Asswx_1	GCA_004146865.1

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QAY01214.1	002214	GxC-R	126	ASwh1_149	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01215.1	002214	GxC-R	106	ASwh1_150	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39393.1	002214	GxC-R	123	CC2_240	Aeromonas phage CC2	GCA_000903495.1
AAR90928.1	002214	GxC-R	119	65p010	Aeromonas virus 65	GCA_000893255.1
AAQ64242.1	002215	ISOCOT	125	KVP40.0173	Vibrio phage KVP40	GCA_000843785.1
QIW90558.1	002215	ISOCOT	102	GCAPEGMB_00211	Vibrio phage V07	GCA_012361095.1
QIW90864.1	002215	ISOCOT	102	COHAPHLL_00001	Vibrio phage V09	GCA_012361135.1
QHJ74356.1	002215	ISOCOT	102	VH12019_00029	Vibrio phage VH1_2019	GCA_009931825.1
AGB06848.1	002215	ISOCOT	102	CF80_gp061	Vibrio phage VH7D	GCA_000914495.1
AJT60926.1	002215	ISOCOT	102	AVU32_gp085	Vibrio phage ValKK3	GCA_001501635.1
ALP47196.1	002215	ISOCOT	102	phiGrn1_0287	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54924.1	002215	ISOCOT	102	vBValMR10Z_384	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37403.1	002215	ISOCOT	102	pp2_170	Vibriophage phi-pp2	GCA_002630725.1
ABY63194.1	002216	Cluster1758_1clades	118	201phi2-1p369	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45070.1	002216	Cluster1758_1clades	124	KTN4_312	Pseudomonas phage KTN4	GCA_002607225.1
QBX32466.1	002216	Cluster1758_1clades	122	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76997.1	002216	Cluster1758_1clades	117	PHABIO_366	Pseudomonas phage Phabio	GCA_002624965.1
AEH03729.1	002216	Cluster1758_1clades	117	306	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94645.1	002216	Cluster1758_1clades	124	SL2_068	Pseudomonas phage SL2	GCA_002956015.1
QJB22945.1	002216	Cluster1758_1clades	124	fnug_302	Pseudomonas phage fnug	GCA_012837215.1
QEM42038.1	002216	Cluster1758_1clades	122	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83159.1	002216	Cluster1758_1clades	124	PHIKZ258	Pseudomonas virus phiKZ	GCA_000842965.1
AGH56809.1	002217	Cluster1759_1clades	124	CPXG_00006	Cyanophage P-RSM6	GCA_000906155.1
AJK27635.1	002217	Cluster1759_1clades	118	PTIM40_231	Cyanophage P-TIM40	GCA_001470935.1
AGH26222.1	002217	Cluster1759_1clades	114	CPMG_00121	Prochlorococcus phage MED4-213	GCA_000904535.1
QGT54979.1	002217	Cluster1759_1clades	116	b23_0373	Synechococcus phage B23	GCA_009745195.1
QGT54614.1	002217	Cluster1759_1clades	116	b3_0379	Synechococcus phage B3	GCA_009745215.1
ASR76300.1	002217	Cluster1759_1clades	119	PBI_BELLAMY_264	Synechococcus phage Bellamy	GCA_002627525.1
QCW23052.1	002217	Cluster1759_1clades	116	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50699.1	002217	Cluster1759_1clades	116	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70247.1	002217	Cluster1759_1clades	120	SynMITS9220M01_241	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ABY63139.1	002218	Cluster1760_1clades	122	201phi2-1p313	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45054.1	002218	Cluster1760_1clades	118	KTN4_296	Pseudomonas phage KTN4	GCA_002607225.1
QBX32397.1	002218	Cluster1760_1clades	119	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76943.1	002218	Cluster1760_1clades	122	PHABIO_312	Pseudomonas phage Phabio	GCA_002624965.1
AEH03663.1	002218	Cluster1760_1clades	123	240	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94661.1	002218	Cluster1760_1clades	118	SL2_084	Pseudomonas phage SL2	GCA_002956015.1
QJB22929.1	002218	Cluster1760_1clades	118	fnug_286	Pseudomonas phage fnug	GCA_012837215.1
QEM41967.1	002218	Cluster1760_1clades	119	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83145.1	002218	Cluster1760_1clades	118	PHIKZ244	Pseudomonas virus phiKZ	GCA_000842965.1
QDH83464.1	002219	Thioredoxin	123	H1O15_gp342	Achromobacter phage Motura	GCA_006964305.1
AND75393.1	002219	Thioredoxin	106	ME3_232	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AMM44954.1	002219	Thioredoxin	104	SP15_156	Bacillus phage SP-15	GCA_001754685.1
QBX06625.1	002219	Thioredoxin	108	BcepSaruman_212	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74593.1	002219	Thioredoxin	108	BcepSauron_213	Burkholderia phage BcepSauron	GCA_005394215.1
BBI90497.1	002219	Thioredoxin	96	HYO65_gp105	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90805.1	002219	Thioredoxin	96	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39353.1	002219	Thioredoxin	93	BPT24_233	Tenacibaculum phage pT24	GCA_002611925.1
QAU04464.1	002219	Thioredoxin	99	ValB1MD_060	Vibrio phage ValB1MD	GCA_004138815.1
ABY63168.1	002220	Cluster1762_1clades	122	201phi2-1p343	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45032.1	002220	Cluster1762_1clades	121	KTN4_274	Pseudomonas phage KTN4	GCA_002607225.1
QBX32422.1	002220	Cluster1762_1clades	121	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76970.1	002220	Cluster1762_1clades	122	PHABIO_339	Pseudomonas phage Phabio	GCA_002624965.1
AEH03692.1	002220	Cluster1762_1clades	122	269	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94682.1	002220	Cluster1762_1clades	121	SL2_105	Pseudomonas phage SL2	GCA_002956015.1
QJB22909.1	002220	Cluster1762_1clades	121	fnug_266	Pseudomonas phage fnug	GCA_012837215.1
QEM41993.1	002220	Cluster1762_1clades	121	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83130.1	002220	Cluster1762_1clades	121	PHIKZ229	Pseudomonas virus phiKZ	GCA_000842965.1
ARB13719.1	002221	SIG+TM	120	Ccr10_gp189c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14064.1	002221	SIG+TM	120	Ccr2_gp188c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14751.1	002221	SIG+TM	120	Ccr29_gp195	Caulobacter phage Ccr29	GCA_002619485.1
ARB14407.1	002221	SIG+TM	120	Ccr5_gp187c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68387.1	002221	SIG+TM	121	CcrBL10_gp183c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87712.1	002221	SIG+TM	120	CcrKarma_gp195	Caulobacter virus Karma	GCA_000901575.1
AFU87361.1	002221	SIG+TM	120	CcrMagneto_gp191	Caulobacter virus Magneto	GCA_000903095.1
AFU86673.1	002221	SIG+TM	121	CcrRogue_gp191	Caulobacter virus Rogue	GCA_000900555.1
AFU88508.1	002221	SIG+TM	120	CcrSwift_gp190	Caulobacter virus Swift	GCA_000899655.1
QBP07223.1	002222	Cluster1764_1clades	120	REBECCA_116	Erwinia phage Rebecca	GCA_004521635.1
AUG85903.1	002222	Cluster1764_1clades	120	BOSOLAPHORUS_116	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52218.1	002222	Cluster1764_1clades	120	DM_120	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86222.1	002222	Cluster1764_1clades	120	DESERTFOX_115	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86544.1	002222	Cluster1764_1clades	120	MADMEL_116	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
AUG86868.1	002222	Cluster1764_1clades	120	MORTIMER_119	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51896.1	002222	Cluster1764_1clades	120	RAY_115	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51580.1	002222	Cluster1764_1clades	120	SIMMY50_118	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64927.1	002222	Cluster1764_1clades	120	SPECIALG_117	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AFC21986.1	002223	SIG+TM+TM	112	GAP32_526	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21987.1	002223	SIG+TM+TM	115	GAP32_526A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44107.1	002223	SIG+TM+TM	112	CBB_544	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89059.1	002223	SIG+TM+TM	120	BF_0534	Serratia phage BF	GCA_002619745.1
AQW89060.1	002223	SIG+TM+TM	113	BF_0535	Serratia phage BF	GCA_002619745.1
SOK59337.1	002223	SIG+TM+TM	117	g529	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59338.1	002223	SIG+TM+TM	115	g530	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58799.1	002223	SIG+TM+TM	117	g522	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58800.1	002223	SIG+TM+TM	115	g523	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14179.1	002224	SIG+INTEGRINBETA	70	PBI_121Q_289	Escherichia phage 121Q	GCA_000926855.1
QAY00758.1	002224	SIG+INTEGRINBETA	70	Ecwhy1_484	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61854.1	002224	SIG+INTEGRINBETA	70	EO157G_2650	Escherichia phage SP27	GCA_008033345.1
AXC37040.1	002224	SIG+INTEGRINBETA	70	-	Escherichia phage UB	GCA_003341455.1
QBO61526.1	002224	SIG+INTEGRINBETA	70	G17_00030	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62132.1	002224	SIG+INTEGRINBETA	70	G17_00643	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14140.1	002224	SIG+INTEGRINBETA	70	vBEcoMphAPEC6_gp517c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80164.1	002224	SIG+INTEGRINBETA	70	PSLUR01_00187	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44602.1	002224	SIG+INTEGRINBETA	119	RaK2_00329	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14064.1	002225	Cluster1767_1clades	102	PBI_121Q_174	Escherichia phage 121Q	GCA_000926855.1
QAY00858.1	002225	Cluster1767_1clades	102	E.Ecwhy1_587	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35029.1	002225	Cluster1767_1clades	102	ACQ29_gp349	Escherichia phage PBECO4	GCA_001041035.1
BBM61747.1	002225	Cluster1767_1clades	102	EO157G_1580	Escherichia phage SP27	GCA_008033345.1
AXC36606.1	002225	Cluster1767_1clades	102	-	Escherichia phage UB	GCA_003341455.1
QBO61635.1	002225	Cluster1767_1clades	102	G17_00139	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13689.1	002225	Cluster1767_1clades	102	vBEcoMphAPEC6_gp059c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80059.1	002225	Cluster1767_1clades	102	PSLUR01_00082	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44530.1	002225	Cluster1767_1clades	115	RaK2_00257	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14117.1	002226	TM+TM+TM	111	PBI_121Q_227	Escherichia phage 121Q	GCA_000926855.1
QAY00807.1	002226	TM+TM+TM	111	Ecwhy1_534	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34981.1	002226	TM+TM+TM	112	ACQ29_gp301	Escherichia phage PBECO4	GCA_001041035.1
BBM61796.1	002226	TM+TM+TM	111	EO157G_2070	Escherichia phage SP27	GCA_008033345.1
AXC36560.1	002226	TM+TM+TM	55	-	Escherichia phage UB	GCA_003341455.1
QBO61583.1	002226	TM+TM+TM	111	G17_00087	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13646.1	002226	TM+TM+TM	111	vBEcoMphAPEC6_gp015c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80108.1	002226	TM+TM+TM	111	PSLUR01_00131	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44585.1	002226	TM+TM+TM	111	RaK2_00312	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14206.1	002227	Cluster1769_1clades	108	PBI_121Q_316	Escherichia phage 121Q	GCA_000926855.1
QAY00732.1	002227	Cluster1769_1clades	111	Ecwhy1_457	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34914.1	002227	Cluster1769_1clades	110	ACQ29_gp234	Escherichia phage PBECO4	GCA_001041035.1
BBM61879.1	002227	Cluster1769_1clades	110	EO157G_2900	Escherichia phage SP27	GCA_008033345.1
AXC37017.1	002227	Cluster1769_1clades	110	-	Escherichia phage UB	GCA_003341455.1
QBO61499.1	002227	Cluster1769_1clades	110	G17_00003	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62105.1	002227	Cluster1769_1clades	110	G17_00616	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14115.1	002227	Cluster1769_1clades	110	vBEcoMphAPEC6_gp492c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80189.1	002227	Cluster1769_1clades	110	PSLUR01_00212	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14240.1	002228	Cluster1770_1clades	105	PBI_121Q_350	Escherichia phage 121Q	GCA_000926855.1
QAY00691.1	002228	Cluster1770_1clades	108	Ecwhy1_416	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00692.1	002228	Cluster1770_1clades	103	Ecwhy1_417	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34887.1	002228	Cluster1770_1clades	99	ACQ29_gp207	Escherichia phage PBECO4	GCA_001041035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBM61918.1	002228	Cluster1770_1clades	103	EO157G_3290	Escherichia phage SP27	GCA_008033345.1
AXC36992.1	002228	Cluster1770_1clades	103	-	Escherichia phage UB	GCA_003341455.1
QBO62064.1	002228	Cluster1770_1clades	103	G17_00575	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14082.1	002228	Cluster1770_1clades	103	vBEcoMphAPEC6_gp459c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80230.1	002228	Cluster1770_1clades	103	PSLUR01_00253	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21664.1	002229	CR-ATPase3	102	GAP32_214	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44330.1	002229	CR-ATPase3	101	RaK2_00057	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43785.1	002229	CR-ATPase3	102	CBB_220	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18935.1	002229	CR-ATPase3	94	7t3_0414	Salmonella phage 7t3	GCA_006083215.1
AZU98190.1	002229	CR-ATPase3	106	CPT_Munch_246	Salmonella phage Munch	GCA_004015485.1
QIG62794.1	002229	CR-ATPase3	94	SEPL_181	Salmonella phage SE_PL	GCA_011067555.1
AQW88741.1	002229	CR-ATPase3	102	BF_0216	Serratia phage BF	GCA_002619745.1
SOK59024.1	002229	CR-ATPase3	102	g216	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58489.1	002229	CR-ATPase3	102	g212	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIX30658.1	002230	Cluster1772_1clades	101	Syn7803US37_181	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76112.1	002230	Cluster1772_1clades	76	PBI_BELLAMY_67	Synechococcus phage Bellamy	GCA_002627525.1
QCW22936.1	002230	Cluster1772_1clades	69	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50621.1	002230	Cluster1772_1clades	69	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59694.1	002230	Cluster1772_1clades	76	S330809_233	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59456.1	002230	Cluster1772_1clades	76	C440309_233	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59931.1	002230	Cluster1772_1clades	76	N231010_232	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70538.1	002230	Cluster1772_1clades	68	HOU04_gp139	Synechococcus phage S-T4	GCA_003443335.1
QJT70054.1	002230	Cluster1772_1clades	67	SynMITS9220M01_041	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14197.1	002231	Cluster1773_1clades	80	PBI_121Q_307	Escherichia phage 121Q	GCA_000926855.1
QAY00742.1	002231	Cluster1773_1clades	80	Ecwhy1_467	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34922.1	002231	Cluster1773_1clades	99	ACQ29_gp242	Escherichia phage PBECO4	GCA_001041035.1
BBM61870.1	002231	Cluster1773_1clades	80	EO157G_2810	Escherichia phage SP27	GCA_008033345.1
AXC37025.1	002231	Cluster1773_1clades	80	-	Escherichia phage UB	GCA_003341455.1
QBO61509.1	002231	Cluster1773_1clades	80	G17_00013	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62115.1	002231	Cluster1773_1clades	80	G17_00626	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14124.1	002231	Cluster1773_1clades	80	vBEcoMphAPEC6_gp501c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80180.1	002231	Cluster1773_1clades	80	PSLUR01_00203	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANM45078.1	002232	Cluster1774_1clades	98	KTN4_320	Pseudomonas phage KTN4	GCA_002607225.1
QBX32485.1	002232	Cluster1774_1clades	86	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77025.1	002232	Cluster1774_1clades	93	PHABIO_394	Pseudomonas phage Phabio	GCA_002624965.1
AEH03747.1	002232	Cluster1774_1clades	90	324	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02889.1	002232	Cluster1774_1clades	93	PSA21_363	Pseudomonas phage Psa21	GCA_004340405.1
ATN94637.1	002232	Cluster1774_1clades	98	SL2_060	Pseudomonas phage SL2	GCA_002956015.1
QJB22953.1	002232	Cluster1774_1clades	98	fnug_310	Pseudomonas phage fnug	GCA_012837215.1
QEM42057.1	002232	Cluster1774_1clades	86	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83166.1	002232	Cluster1774_1clades	98	PHIKZ265	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14000.1	002233	Cluster1775_1clades	96	PBI_121Q_103	Escherichia phage 121Q	GCA_000926855.1
QAY00338.1	002233	Cluster1775_1clades	96	Ecwhy1_57	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35084.1	002233	Cluster1775_1clades	90	ACQ29_gp404	Escherichia phage PBECO4	GCA_001041035.1
BBM61691.1	002233	Cluster1775_1clades	96	EO157G_1020	Escherichia phage SP27	GCA_008033345.1
AXC36661.1	002233	Cluster1775_1clades	96	-	Escherichia phage UB	GCA_003341455.1
QBO61693.1	002233	Cluster1775_1clades	96	G17_00204	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13742.1	002233	Cluster1775_1clades	96	vBEcoMphAPEC6_gp112c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80004.1	002233	Cluster1775_1clades	96	PSLUR01_00020	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44481.1	002233	Cluster1775_1clades	90	RaK2_00208	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14174.1	002234	Cluster1777_1clades	56	PBI_121Q_284	Escherichia phage 121Q	GCA_000926855.1
QAY00762.1	002234	Cluster1777_1clades	90	Ecwhy1_488	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34942.1	002234	Cluster1777_1clades	90	ACQ29_gp262	Escherichia phage PBECO4	GCA_001041035.1
BBM61848.1	002234	Cluster1777_1clades	90	EO157G_2590	Escherichia phage SP27	GCA_008033345.1
AXC37045.1	002234	Cluster1777_1clades	74	-	Escherichia phage UB	GCA_003341455.1
QBO61532.1	002234	Cluster1777_1clades	90	G17_00036	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62138.1	002234	Cluster1777_1clades	90	G17_00649	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14146.1	002234	Cluster1777_1clades	90	vBEcoMphAPEC6_gp523c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80159.1	002234	Cluster1777_1clades	90	PSLUR01_00182	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21493.1	002235	Cluster1778_1clades	89	GAP32_046	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43616.1	002235	Cluster1778_1clades	89	CBB_51	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44167.1	002235	Cluster1778_1clades	89	CBB_604	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18723.1	002235	Cluster1778_1clades	88	7t3_0202	Salmonella phage 7t3	GCA_006083215.1
AZU97995.1	002235	Cluster1778_1clades	88	CPT_Munch_051	Salmonella phage Munch	GCA_004015485.1
QIG62984.1	002235	Cluster1778_1clades	88	SEPL_371	Salmonella phage SE_PL	GCA_011067555.1
AQW88565.1	002235	Cluster1778_1clades	90	BF_0040	Serratia phage BF	GCA_002619745.1
SOK58840.1	002235	Cluster1778_1clades	90	g032	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58300.1	002235	Cluster1778_1clades	90	g023	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14016.1	002236	Cluster1779_1clades	71	PBI_121Q_120	Escherichia phage 121Q	GCA_000926855.1
QAY00323.1	002236	Cluster1779_1clades	88	Ecwhy1_42	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35070.1	002236	Cluster1779_1clades	71	ACQ29_gp390	Escherichia phage PBECO4	GCA_001041035.1
BBM61705.1	002236	Cluster1779_1clades	71	EO157G_1160	Escherichia phage SP27	GCA_008033345.1
AXC36648.1	002236	Cluster1779_1clades	71	-	Escherichia phage UB	GCA_003341455.1
QBO61680.1	002236	Cluster1779_1clades	71	G17_00190	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13728.1	002236	Cluster1779_1clades	71	vBEcoMphAPEC6_gp098c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80017.1	002236	Cluster1779_1clades	71	PSLUR01_00034	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44488.1	002236	Cluster1779_1clades	68	RaK2_00215	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14203.1	002237	Cluster1780_1clades	85	PBI_121Q_313	Escherichia phage 121Q	GCA_000926855.1
QAY00734.1	002237	Cluster1780_1clades	85	Ecwhy1_459	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34915.1	002237	Cluster1780_1clades	72	ACQ29_gp235	Escherichia phage PBECO4	GCA_001041035.1
BBM61877.1	002237	Cluster1780_1clades	85	EO157G_2880	Escherichia phage SP27	GCA_008033345.1
AXC37018.1	002237	Cluster1780_1clades	85	-	Escherichia phage UB	GCA_003341455.1
QBO61501.1	002237	Cluster1780_1clades	85	G17_00005	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62107.1	002237	Cluster1780_1clades	85	G17_00618	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14117.1	002237	Cluster1780_1clades	85	vBEcoMphAPEC6_gp494c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80187.1	002237	Cluster1780_1clades	85	PSLUR01_00210	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ARB13729.1	002238	SIG+TM	79	Ccr10_gp199c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14074.1	002238	SIG+TM	79	Ccr2_gp198c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14763.1	002238	SIG+TM	79	Ccr29_gp207	Caulobacter phage Ccr29	GCA_002619485.1
ARB14416.1	002238	SIG+TM	84	Ccr5_gp196c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68395.1	002238	SIG+TM	80	CcrBL10_gp191c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87722.1	002238	SIG+TM	79	CcrKarma_gp205	Caulobacter virus Karma	GCA_000901575.1
AFU87371.1	002238	SIG+TM	79	CcrMagneto_gp201	Caulobacter virus Magneto	GCA_000903095.1
AFU86681.1	002238	SIG+TM	80	CcrRogue_gp199	Caulobacter virus Rogue	GCA_000900555.1
AFU88518.1	002238	SIG+TM	79	CcrSwift_gp200	Caulobacter virus Swift	GCA_000899655.1
AMO43085.1	002239	Cluster1782_1clades	72	R1080702_076	Cyanophage S-RIM32	GCA_001754165.1
AMO43314.1	002239	Cluster1782_1clades	83	W270710_070	Cyanophage S-RIM44	GCA_002599145.1
AOO11786.1	002239	Cluster1782_1clades	83	Np050604_070	Cyanophage S-RIM44	GCA_002599185.1
AOO12487.1	002239	Cluster1782_1clades	83	Sn080709_070	Cyanophage S-RIM44	GCA_002599245.1
AOO12952.1	002239	Cluster1782_1clades	83	W2100709_070	Cyanophage S-RIM44	GCA_002599285.1
ADO99168.1	002239	Cluster1782_1clades	83	Syn1_067	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59518.1	002239	Cluster1782_1clades	83	S330809_057	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59280.1	002239	Cluster1782_1clades	83	C440309_057	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59756.1	002239	Cluster1782_1clades	83	N231010_057	Synechococcus phage S-CAM4	GCA_002922155.1
AIT14165.1	002240	Cluster1783_1clades	73	PBI_121Q_275	Escherichia phage 121Q	GCA_000926855.1
QAY00771.1	002240	Cluster1783_1clades	83	Ecwhy1_497	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34949.1	002240	Cluster1783_1clades	83	ACQ29_gp269	Escherichia phage PBECO4	GCA_001041035.1
BBM61839.1	002240	Cluster1783_1clades	83	EO157G_2500	Escherichia phage SP27	GCA_008033345.1
AXC37051.1	002240	Cluster1783_1clades	83	-	Escherichia phage UB	GCA_003341455.1
QBO61541.1	002240	Cluster1783_1clades	83	G17_00045	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62147.1	002240	Cluster1783_1clades	83	G17_00658	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14155.1	002240	Cluster1783_1clades	83	vBEcoMphAPEC6_gp532c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80151.1	002240	Cluster1783_1clades	83	PSLUR01_00174	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64082.1	002241	Cluster1784_1clades	81	KVP40.0011	Vibrio phage KVP40	GCA_000843785.1
QHJ74194.1	002241	Cluster1784_1clades	81	VH12019_00275	Vibrio phage VH1_2019	GCA_009931825.1
AGB07018.1	002241	Cluster1784_1clades	66	CF80_gp231	Vibrio phage VH7D	GCA_000914495.1
QBX06078.1	002241	Cluster1784_1clades	81	ValB1HC_124	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61092.1	002241	Cluster1784_1clades	81	AVU32_gp251	Vibrio phage ValKK3	GCA_001501635.1
AGN30061.1	002241	Cluster1784_1clades	81	VPFG_00058	Vibrio phage nt-1	GCA_000910195.2
ALP47260.1	002241	Cluster1784_1clades	81	phiGrn1_0126	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54704.1	002241	Cluster1784_1clades	81	vBValMR10Z_163	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37245.1	002241	Cluster1784_1clades	81	pp2_011	Vibriophage phi-pp2	GCA_002630725.1
AMO43353.1	002242	TM	80	W270710_109	Cyanophage S-RIM44	GCA_002599145.1
AOO11597.1	002242	TM	80	ES420910_116	Cyanophage S-RIM44	GCA_002599165.1
AOO11825.1	002242	TM	80	Np050604_109	Cyanophage S-RIM44	GCA_002599185.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOO12062.1	002242	TM	80	Np200711_116	Cyanophage S-RIM44	GCA_002599205.1
AOO12298.1	002242	TM	80	Np420711_116	Cyanophage S-RIM44	GCA_002599225.1
AOO12526.1	002242	TM	80	Sn080709_109	Cyanophage S-RIM44	GCA_002599245.1
AOO12763.1	002242	TM	80	Sn130910_116	Cyanophage S-RIM44	GCA_002599265.1
AOO12992.1	002242	TM	80	W2100709_110	Cyanophage S-RIM44	GCA_002599285.1
ADO99211.1	002242	TM	80	Syn1_110	Prochlorococcus phage Syn1	GCA_000892495.1
ARB13728.1	002243	Cluster1786_1clades	56	Ccr10_gp198c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14073.1	002243	Cluster1786_1clades	56	Ccr2_gp197c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14762.1	002243	Cluster1786_1clades	56	Ccr29_gp206	Caulobacter phage Ccr29	GCA_002619485.1
ARB15107.1	002243	Cluster1786_1clades	56	Ccr32_gp189	Caulobacter phage Ccr32	GCA_002619505.1
ARB15441.1	002243	Cluster1786_1clades	56	Ccr34_gp199	Caulobacter phage Ccr34	GCA_002619525.1
AFU87721.1	002243	Cluster1786_1clades	78	CcrKarma_gp204	Caulobacter virus Karma	GCA_000901575.1
AFU87370.1	002243	Cluster1786_1clades	78	CcrMagneto_gp200	Caulobacter virus Magneto	GCA_000903095.1
AFU88517.1	002243	Cluster1786_1clades	78	CcrSwift_gp199	Caulobacter virus Swift	GCA_000899655.1
AFU87026.1	002243	Cluster1786_1clades	78	CbK_gp194	Caulobacter virus phiCbK	GCA_000900535.1
AIT14415.1	002244	SIG+TM	69	PBI_121Q_525	Escherichia phage 121Q	GCA_000926855.1
QAY00535.1	002244	SIG+TM	74	Ecwhy1_256	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34727.1	002244	SIG+TM	74	ACQ29_gp047	Escherichia phage PBECO4	GCA_001041035.1
BBM62087.1	002244	SIG+TM	74	EO157G_4980	Escherichia phage SP27	GCA_008033345.1
AXC36843.1	002244	SIG+TM	74	-	Escherichia phage UB	GCA_003341455.1
QBO61886.1	002244	SIG+TM	74	G17_00397	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13923.1	002244	SIG+TM	74	vBEcoMphAPEC6_gp298c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80401.1	002244	SIG+TM	74	PSLUR01_00424	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44295.1	002244	SIG+TM	75	RaK2_00022	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QMV28996.1	002245	Cluster1788_1clades	56	AP1_0289	Aeromonas phage AP1	GCA_014183365.1
ATI17511.1	002245	Cluster1788_1clades	56	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00485.1	002245	Cluster1788_1clades	56	HWB28_gp067	Aeromonas phage AS-zj	GCA_002627665.1
QAX97951.1	002245	Cluster1788_1clades	56	ASswx1_309	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01195.1	002245	Cluster1788_1clades	56	ASwh1_130	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39477.1	002245	Cluster1788_1clades	56	CC2_223	Aeromonas phage CC2	GCA_000903495.1
ADQ53437.1	002245	Cluster1788_1clades	57	65p431	Aeromonas virus 65	GCA_000893255.1
QBX06797.1	002245	Cluster1788_1clades	75	BcepSaruman_384	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74767.1	002245	Cluster1788_1clades	75	BcepSauron_387	Burkholderia phage BcepSauron	GCA_005394215.1
AIT14202.1	002246	Cluster1789_1clades	74	PBI_121Q_312	Escherichia phage 121Q	GCA_000926855.1
QAY00735.1	002246	Cluster1789_1clades	74	Ecwhy1_460	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34916.1	002246	Cluster1789_1clades	74	ACQ29_gp236	Escherichia phage PBECO4	GCA_001041035.1
BBM61876.1	002246	Cluster1789_1clades	74	EO157G_2870	Escherichia phage SP27	GCA_008033345.1
AXC37019.1	002246	Cluster1789_1clades	74	-	Escherichia phage UB	GCA_003341455.1
QBO61502.1	002246	Cluster1789_1clades	74	G17_00006	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62108.1	002246	Cluster1789_1clades	74	G17_00619	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14118.1	002246	Cluster1789_1clades	74	vBEcoMphAPEC6_gp495c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80186.1	002246	Cluster1789_1clades	74	PSLUR01_00209	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMO43316.1	002247	Cluster1790_1clades	73	W270710_072	Cyanophage S-RIM44	GCA_002599145.1
AOO11549.1	002247	Cluster1790_1clades	73	ES420910_068	Cyanophage S-RIM44	GCA_002599165.1
AOO11788.1	002247	Cluster1790_1clades	73	Np050604_072	Cyanophage S-RIM44	GCA_002599185.1
AOO12014.1	002247	Cluster1790_1clades	73	Np200711_068	Cyanophage S-RIM44	GCA_002599205.1
AOO12250.1	002247	Cluster1790_1clades	73	Np420711_068	Cyanophage S-RIM44	GCA_002599225.1
AOO12489.1	002247	Cluster1790_1clades	73	Sn080709_072	Cyanophage S-RIM44	GCA_002599245.1
AOO12715.1	002247	Cluster1790_1clades	73	Sn130910_068	Cyanophage S-RIM44	GCA_002599265.1
AOO12954.1	002247	Cluster1790_1clades	73	W2100709_072	Cyanophage S-RIM44	GCA_002599285.1
ADO99170.1	002247	Cluster1790_1clades	73	Syn1_069	Prochlorococcus phage Syn1	GCA_000892495.1
AIT14062.1	002248	Cluster1791_1clades	66	PBI_121Q_172	Escherichia phage 121Q	GCA_000926855.1
QAY00859.1	002248	Cluster1791_1clades	66	Ecwhy1_588	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35031.1	002248	Cluster1791_1clades	66	ACQ29_gp351	Escherichia phage PBECO4	GCA_001041035.1
BBM61745.1	002248	Cluster1791_1clades	66	EO157G_1560	Escherichia phage SP27	GCA_008033345.1
AXC36608.1	002248	Cluster1791_1clades	66	-	Escherichia phage UB	GCA_003341455.1
QBO61637.1	002248	Cluster1791_1clades	66	G17_00141	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13691.1	002248	Cluster1791_1clades	72	vBEcoMphAPEC6_gp061c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80057.1	002248	Cluster1791_1clades	66	PSLUR01_00080	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44527.1	002248	Cluster1791_1clades	67	RaK2_00254	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ABY62853.1	002249	Cluster1792_1clades	71	201phi2-1p019	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44905.1	002249	Cluster1792_1clades	70	KTN4_147	Pseudomonas phage KTN4	GCA_002607225.1
QBX32163.1	002249	Cluster1792_1clades	67	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76642.1	002249	Cluster1792_1clades	70	PHABIO_11	Pseudomonas phage Phabio	GCA_002624965.1
AEH03460.1	002249	Cluster1792_1clades	65	033	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94808.1	002249	Cluster1792_1clades	70	SL2_231	Pseudomonas phage SL2	GCA_002956015.1
QJB22783.1	002249	Cluster1792_1clades	70	fnug_140	Pseudomonas phage fnug	GCA_012837215.1
QEM41744.1	002249	Cluster1792_1clades	67	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26329.1	002249	Cluster1792_1clades	70	PHIKZ115.2	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14068.1	002250	Cluster1793_1clades	71	PBI_121Q_178	Escherichia phage 121Q	GCA_000926855.1
QAY00854.1	002250	Cluster1793_1clades	71	Ecwhy1_583	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35025.1	002250	Cluster1793_1clades	71	ACQ29_gp345	Escherichia phage PBECO4	GCA_001041035.1
BBM61751.1	002250	Cluster1793_1clades	71	EO157G_1620	Escherichia phage SP27	GCA_008033345.1
AXC36602.1	002250	Cluster1793_1clades	71	-	Escherichia phage UB	GCA_003341455.1
QBO61631.1	002250	Cluster1793_1clades	71	G17_00135	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13687.1	002250	Cluster1793_1clades	71	vBEcoMphAPEC6_gp057c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80063.1	002250	Cluster1793_1clades	71	PSLUR01_00086	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44524.1	002250	Cluster1793_1clades	68	RaK2_00251	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AAQ64198.1	002251	Cluster1794_1clades	66	KVP40.0127	Vibrio phage KVP40	GCA_000843785.1
AGB06804.1	002251	Cluster1794_1clades	69	CF80_gp017	Vibrio phage VH7D	GCA_000914495.1
QBX05962.1	002251	Cluster1794_1clades	69	ValB1HC_008	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60974.1	002251	Cluster1794_1clades	69	AVU32_gp133	Vibrio phage ValKK3	GCA_001501635.1
AGN30177.1	002251	Cluster1794_1clades	69	VPFG_00175	Vibrio phage nt-1	GCA_000910195.2
ALP47295.1	002251	Cluster1794_1clades	69	phiGrn1_0239	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47673.1	002251	Cluster1794_1clades	69	phiST2_0377	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54587.1	002251	Cluster1794_1clades	69	vBValMR10Z_46	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37358.1	002251	Cluster1794_1clades	66	pp2_125	Vibriophage phi-pp2	GCA_002630725.1
AIT14175.1	002252	Cluster1795_1clades	69	PBI_121Q_285	Escherichia phage 121Q	GCA_000926855.1
QAY00761.1	002252	Cluster1795_1clades	69	Ecwhy1_487	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34941.1	002252	Cluster1795_1clades	55	ACQ29_gp261	Escherichia phage PBECO4	GCA_001041035.1
BBM61849.1	002252	Cluster1795_1clades	69	EO157G_2600	Escherichia phage SP27	GCA_008033345.1
AXC37044.1	002252	Cluster1795_1clades	55	-	Escherichia phage UB	GCA_003341455.1
QBO61531.1	002252	Cluster1795_1clades	69	G17_00035	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62137.1	002252	Cluster1795_1clades	69	G17_00648	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14145.1	002252	Cluster1795_1clades	69	vBEcoMphAPEC6_gp522c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80160.1	002252	Cluster1795_1clades	69	PSLUR01_00183	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14070.1	002253	Cluster1796_1clades	66	PBI_121Q_180	Escherichia phage 121Q	GCA_000926855.1
QAY00853.1	002253	Cluster1796_1clades	66	Ecwhy1_581	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35023.1	002253	Cluster1796_1clades	66	ACQ29_gp343	Escherichia phage PBECO4	GCA_001041035.1
BBM61753.1	002253	Cluster1796_1clades	66	EO157G_1640	Escherichia phage SP27	GCA_008033345.1
AXC36600.1	002253	Cluster1796_1clades	66	-	Escherichia phage UB	GCA_003341455.1
QBO61629.1	002253	Cluster1796_1clades	66	G17_00133	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13685.1	002253	Cluster1796_1clades	66	vBEcoMphAPEC6_gp055c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80064.1	002253	Cluster1796_1clades	66	PSLUR01_00087	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44525.1	002253	Cluster1796_1clades	66	RaK2_00252	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14186.1	002254	Cluster1797_1clades	62	PBI_121Q_296	Escherichia phage 121Q	GCA_000926855.1
QAY00752.1	002254	Cluster1797_1clades	62	Ecwhy1_478	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34932.1	002254	Cluster1797_1clades	64	ACQ29_gp252	Escherichia phage PBECO4	GCA_001041035.1
BBM61860.1	002254	Cluster1797_1clades	62	EO157G_2710	Escherichia phage SP27	GCA_008033345.1
AXC37035.1	002254	Cluster1797_1clades	62	-	Escherichia phage UB	GCA_003341455.1
QBO61521.1	002254	Cluster1797_1clades	62	G17_00025	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62127.1	002254	Cluster1797_1clades	62	G17_00638	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14134.1	002254	Cluster1797_1clades	62	vBEcoMphAPEC6_gp511c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80169.1	002254	Cluster1797_1clades	62	PSLUR01_00192	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14201.1	002255	Cluster1798_1clades	63	PBI_121Q_311	Escherichia phage 121Q	GCA_000926855.1
QAY00737.1	002255	Cluster1798_1clades	63	Ecwhy1_462	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34918.1	002255	Cluster1798_1clades	63	ACQ29_gp238	Escherichia phage PBECO4	GCA_001041035.1
BBM61874.1	002255	Cluster1798_1clades	63	EO157G_2850	Escherichia phage SP27	GCA_008033345.1
AXC37021.1	002255	Cluster1798_1clades	63	-	Escherichia phage UB	GCA_003341455.1
QBO61504.1	002255	Cluster1798_1clades	63	G17_00008	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62110.1	002255	Cluster1798_1clades	63	G17_00621	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14120.1	002255	Cluster1798_1clades	63	vBEcoMphAPEC6_gp497c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80184.1	002255	Cluster1798_1clades	63	PSLUR01_00207	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ARB13768.1	002256	Cluster1799_1clades	62	Ccr10_gp238	Caulobacter phage Ccr10	GCA_002619445.1
ARB14113.1	002256	Cluster1799_1clades	62	Ccr2_gp237	Caulobacter phage Ccr2	GCA_002619465.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARB14807.1	002256	Cluster1799_1clades	39	Ccr29_gp251	Caulobacter phage Ccr29	GCA_002619485.1
ARB15147.1	002256	Cluster1799_1clades	62	Ccr32_gp229	Caulobacter phage Ccr32	GCA_002619505.1
ARB15481.1	002256	Cluster1799_1clades	62	Ccr34_gp239	Caulobacter phage Ccr34	GCA_002619525.1
ARB14455.1	002256	Cluster1799_1clades	62	Ccr5_gp235	Caulobacter phage Ccr5	GCA_002619545.1
AFU87763.1	002256	Cluster1799_1clades	62	CcrKarma_gp246	Caulobacter virus Karma	GCA_000901575.1
AFU88558.1	002256	Cluster1799_1clades	62	CcrSwift_gp240	Caulobacter virus Swift	GCA_000899655.1
AFU87066.1	002256	Cluster1799_1clades	62	CbK_gp234	Caulobacter virus phiCbK	GCA_000900535.1
AMR59717.1	002257	Cluster1800_1clades	60	SEGD1_068	Enterobacteria phage SEGD1	GCA_002601865.1
AXF51212.1	002257	Cluster1800_1clades	61	WELLINGTON_82	Erwinia phage Wellington	GCA_003344985.1
AFQ96799.1	002257	Cluster1800_1clades	61	G173_gp254	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48098.1	002257	Cluster1800_1clades	62	ASESINO_85	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ49434.1	002257	Cluster1800_1clades	61	KWAN_82	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50512.1	002257	Cluster1800_1clades	61	STRATTON_87	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85908.1	002257	Cluster1800_1clades	60	ACEC001_0700	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09033.1	002257	Cluster1800_1clades	61	MLDJOKPK_00095	Salmonella phage SPAsTU	GCA_003183805.1
AEP83900.1	002257	Cluster1800_1clades	60	SPN3US_0067	Salmonella phage SPN3US	GCA_001042275.1
AAQ64448.1	002258	DUF1737	57	KVP40.0380	Vibrio phage KVP40	GCA_000843785.1
QIW90393.1	002258	DUF1737	57	GCAPEGMB_00046	Vibrio phage V07	GCA_012361095.1
QIW91036.1	002258	DUF1737	57	COHAPHLL_00173	Vibrio phage V09	GCA_012361135.1
QHJ74560.1	002258	DUF1737	57	VH12019_00260	Vibrio phage VH1_2019	GCA_009931825.1
QBX06093.1	002258	DUF1737	54	ValB1HC_139	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61107.1	002258	DUF1737	54	AVU32_gp266	Vibrio phage ValKK3	GCA_001501635.1
AGN30048.1	002258	DUF1737	54	VPFG_00043	Vibrio phage nt-1	GCA_000910195.2
QNJ54719.1	002258	DUF1737	54	vBValMR10Z_178	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37611.1	002258	DUF1737	57	pp2_379	Vibriophage phi-pp2	GCA_002630725.1
AAQ64295.1	002259	Cluster1802_1clades	55	KVP40.0226	Vibrio phage KVP40	GCA_000843785.1
QIW90611.1	002259	Cluster1802_1clades	55	GCAPEGMB_00264	Vibrio phage V07	GCA_012361095.1
QIW91188.1	002259	Cluster1802_1clades	55	COHAPHLL_00352	Vibrio phage V09	GCA_012361135.1
AGB06913.1	002259	Cluster1802_1clades	56	CF80_gp126	Vibrio phage VH7D	GCA_000914495.1
QBX06233.1	002259	Cluster1802_1clades	56	ValB1HC_280	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60859.1	002259	Cluster1802_1clades	56	AVU32_gp018	Vibrio phage ValKK3	GCA_001501635.1
ALP47699.1	002259	Cluster1802_1clades	56	phiST2_0104	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54858.1	002259	Cluster1802_1clades	56	vBValMR10Z_318	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37456.1	002259	Cluster1802_1clades	55	pp2_223	Vibriophage phi-pp2	GCA_002630725.1
AMO43305.1	002260	Cluster1803_1clades	53	W270710_061	Cyanophage S-RIM44	GCA_002599145.1
AOO11539.1	002260	Cluster1803_1clades	53	ES420910_058	Cyanophage S-RIM44	GCA_002599165.1
AOO11777.1	002260	Cluster1803_1clades	53	Np050604_061	Cyanophage S-RIM44	GCA_002599185.1
AOO12004.1	002260	Cluster1803_1clades	53	Np200711_058	Cyanophage S-RIM44	GCA_002599205.1
AOO12240.1	002260	Cluster1803_1clades	53	Np420711_058	Cyanophage S-RIM44	GCA_002599225.1
AOO12478.1	002260	Cluster1803_1clades	53	Sn080709_061	Cyanophage S-RIM44	GCA_002599245.1
AOO12705.1	002260	Cluster1803_1clades	53	Sn130910_058	Cyanophage S-RIM44	GCA_002599265.1
AOO12943.1	002260	Cluster1803_1clades	53	W2100709_061	Cyanophage S-RIM44	GCA_002599285.1
ADO99159.1	002260	Cluster1803_1clades	53	Syn1_058	Prochlorococcus phage Syn1	GCA_000892495.1
AMO43304.1	002261	Cluster1804_1clades	52	W270710_060	Cyanophage S-RIM44	GCA_002599145.1
AOO11538.1	002261	Cluster1804_1clades	52	ES420910_057	Cyanophage S-RIM44	GCA_002599165.1
AOO11776.1	002261	Cluster1804_1clades	52	Np050604_060	Cyanophage S-RIM44	GCA_002599185.1
AOO12003.1	002261	Cluster1804_1clades	52	Np200711_057	Cyanophage S-RIM44	GCA_002599205.1
AOO12239.1	002261	Cluster1804_1clades	52	Np420711_057	Cyanophage S-RIM44	GCA_002599225.1
AOO12477.1	002261	Cluster1804_1clades	52	Sn080709_060	Cyanophage S-RIM44	GCA_002599245.1
AOO12704.1	002261	Cluster1804_1clades	52	Sn130910_057	Cyanophage S-RIM44	GCA_002599265.1
AOO12942.1	002261	Cluster1804_1clades	52	W2100709_060	Cyanophage S-RIM44	GCA_002599285.1
ADO99158.1	002261	Cluster1804_1clades	52	Syn1_057	Prochlorococcus phage Syn1	GCA_000892495.1
AIT14176.1	002262	Cluster1805_1clades	50	PBI_121Q_286	Escherichia phage 121Q	GCA_000926855.1
AGC34939.1	002262	Cluster1805_1clades	43	ACQ29_gp259	Escherichia phage PBECO4	GCA_001041035.1
BBM61851.1	002262	Cluster1805_1clades	50	EO157G_2620	Escherichia phage SP27	GCA_008033345.1
AXC37042.1	002262	Cluster1805_1clades	50	-	Escherichia phage UB	GCA_003341455.1
QBO61529.1	002262	Cluster1805_1clades	50	G17_00033	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62135.1	002262	Cluster1805_1clades	50	G17_00646	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14144.1	002262	Cluster1805_1clades	50	vBEcoMphAPEC6_gp521c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80162.1	002262	Cluster1805_1clades	50	PSLUR01_00185	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44611.1	002262	Cluster1805_1clades	52	RaK2_00338	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14190.1	002263	Cluster1806_1clades	49	PBI_121Q_300	Escherichia phage 121Q	GCA_000926855.1
QAY00748.1	002263	Cluster1806_1clades	49	Ecwhy1_474	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34928.1	002263	Cluster1806_1clades	49	ACQ29_gp248	Escherichia phage PBECO4	GCA_001041035.1
BBM61864.1	002263	Cluster1806_1clades	49	EO157G_2750	Escherichia phage SP27	GCA_008033345.1
AXC37031.1	002263	Cluster1806_1clades	49	-	Escherichia phage UB	GCA_003341455.1
QBO61516.1	002263	Cluster1806_1clades	49	G17_00020	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62122.1	002263	Cluster1806_1clades	49	G17_00633	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14131.1	002263	Cluster1806_1clades	49	vBEcoMphAPEC6_gp508c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80173.1	002263	Cluster1806_1clades	49	PSLUR01_00196	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14428.1	002264	Cluster1807_1clades	40	PBI_121Q_538	Escherichia phage 121Q	GCA_000926855.1
QAY00520.1	002264	Cluster1807_1clades	39	Ecwhy1_241	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00524.1	002264	Cluster1807_1clades	41	Ecwhy1_245	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34714.1	002264	Cluster1807_1clades	40	ACQ29_gp034	Escherichia phage PBECO4	GCA_001041035.1
BBM62100.1	002264	Cluster1807_1clades	40	EO157G_5110	Escherichia phage SP27	GCA_008033345.1
AXC36833.1	002264	Cluster1807_1clades	40	-	Escherichia phage UB	GCA_003341455.1
QBO61873.1	002264	Cluster1807_1clades	40	G17_00384	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13913.1	002264	Cluster1807_1clades	40	vBEcoMphAPEC6_gp288c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80414.1	002264	Cluster1807_1clades	40	PSLUR01_00437	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMO43451.1	002265	Cluster1808_1clades	39	W270710_212	Cyanophage S-RIM44	GCA_002599145.1
AOO11692.1	002265	Cluster1808_1clades	39	ES420910_215	Cyanophage S-RIM44	GCA_002599165.1
AOO11923.1	002265	Cluster1808_1clades	39	Np050604_212	Cyanophage S-RIM44	GCA_002599185.1
AOO12158.1	002265	Cluster1808_1clades	39	Np200711_216	Cyanophage S-RIM44	GCA_002599205.1
AOO12393.1	002265	Cluster1808_1clades	39	Np420711_215	Cyanophage S-RIM44	GCA_002599225.1
AOO12624.1	002265	Cluster1808_1clades	37	Sn080709_212	Cyanophage S-RIM44	GCA_002599245.1
AOO12858.1	002265	Cluster1808_1clades	39	Sn130910_215	Cyanophage S-RIM44	GCA_002599265.1
AOO13090.1	002265	Cluster1808_1clades	39	W2100709_213	Cyanophage S-RIM44	GCA_002599285.1
ADO99311.1	002265	Cluster1808_1clades	39	Syn1_215	Prochlorococcus phage Syn1	GCA_000892495.1
AMO43356.1	002266	Cluster1809_1clades	37	W270710_112	Cyanophage S-RIM44	GCA_002599145.1
AOO11600.1	002266	Cluster1809_1clades	37	ES420910_119	Cyanophage S-RIM44	GCA_002599165.1
AOO11828.1	002266	Cluster1809_1clades	37	Np050604_112	Cyanophage S-RIM44	GCA_002599185.1
AOO12065.1	002266	Cluster1809_1clades	37	Np200711_119	Cyanophage S-RIM44	GCA_002599205.1
AOO12301.1	002266	Cluster1809_1clades	37	Np420711_119	Cyanophage S-RIM44	GCA_002599225.1
AOO12529.1	002266	Cluster1809_1clades	37	Sn080709_112	Cyanophage S-RIM44	GCA_002599245.1
AOO12766.1	002266	Cluster1809_1clades	37	Sn130910_119	Cyanophage S-RIM44	GCA_002599265.1
AOO12995.1	002266	Cluster1809_1clades	37	W2100709_113	Cyanophage S-RIM44	GCA_002599285.1
ADO99214.1	002266	Cluster1809_1clades	37	Syn1_113	Prochlorococcus phage Syn1	GCA_000892495.1
APU01545.1	002267	gp37_C	1286	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29089.1	002267	gp37_C	396	AP1_0382	Aeromonas phage AP1	GCA_014183365.1
ATI17367.1	002267	gp37_C	1312	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00227.1	002267	gp37_C	1316	HWB28_gp325	Aeromonas phage AS-zj	GCA_002627665.1
QAX97808.1	002267	gp37_C	1316	ASswx1_164	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01355.1	002267	gp37_C	1533	ASwh1_295	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39437.1	002267	gp37_C	1329	CC2_372	Aeromonas phage CC2	GCA_000903495.1
ADQ53167.1	002267	gp37_C	1286	65p159	Aeromonas virus 65	GCA_000893255.1
AXG67154.1	002268	Cluster1811_1clades	1511	AD1_110	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79904.1	002268	Cluster1811_1clades	1507	JA11_099	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66503.1	002268	Cluster1811_1clades	1507	JA13_100	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66828.1	002268	Cluster1811_1clades	1507	JA29_102	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67473.1	002268	Cluster1811_1clades	1507	JA33_099	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08388.1	002268	Cluster1811_1clades	1511	Alexandra_116	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58752.1	002268	Cluster1811_1clades	1508	Y3_112	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28586.1	002268	Cluster1811_1clades	1509	YOLOSWAG_104	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67193.1	002269	Oest_recep	1375	AD1_149	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79945.1	002269	Oest_recep	1320	JA11_140	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66544.1	002269	Oest_recep	1320	JA13_141	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66869.1	002269	Oest_recep	1320	JA29_143	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67514.1	002269	Oest_recep	1320	JA33_140	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08426.1	002269	Oest_recep	1395	Alexandra_154	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58790.1	002269	Oest_recep	1394	Y3_150	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28628.1	002269	Oest_recep	1367	YOLOSWAG_148	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67148.1	002270	SIG+Calx-beta	957	AD1_104	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79897.1	002270	SIG+Calx-beta	1177	JA11_092	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66496.1	002270	SIG+Calx-beta	1177	JA13_093	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66821.1	002270	SIG+Calx-beta	1177	JA29_095	Dickeya phage vB_DsoM_JA29	GCA_003568475.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG67466.1	002270	SIG+Calx-beta	1177	JA33_092	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08382.1	002270	SIG+Calx-beta	958	Alexandra_109	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58746.1	002270	SIG+Calx-beta	958	Y3_106	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28579.1	002270	SIG+Calx-beta	956	YOLOSWAG_97	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFF28262.1	002271	Cluster1814_2clades	1078	PAU_264	Sphingomonas phage PAU	GCA_000902455.1
BBI90396.1	002271	Cluster1814_2clades	257	HYO65_gp004	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90397.1	002271	Cluster1814_2clades	291	HYO65_gp005	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90395.1	002271	Cluster1814_2clades	474	HYO65_gp003	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90703.1	002271	Cluster1814_2clades	474	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90704.1	002271	Cluster1814_2clades	604	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39303.1	002271	Cluster1814_2clades	1076	BPT24_178	Tenacibaculum phage pT24	GCA_002611925.1
prev15ph1000000416	002271	Cluster1814_2clades	752	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGH07642.1	002272	Tail-fiber	1008	CYVG_00199	Cyanophage S-SSM6a	GCA_002710385.1
AGH26192.1	002272	Tail-fiber	938	CPMG_00091	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93401.1	002272	Tail-fiber	875	AVU42_gp015	Prochlorococcus phage P-TIM68	GCA_001503075.1
QGT54640.1	002272	Tail-fiber	766	b23_0012	Synechococcus phage B23	GCA_009745195.1
QGT54270.1	002272	Tail-fiber	766	b3_0012	Synechococcus phage B3	GCA_009745215.1
QCW22916.1	002272	Tail-fiber	792	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50541.1	002272	Tail-fiber	791	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70031.1	002272	Tail-fiber	556	SynMITS9220M01_015	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG67361.1	002273	Cluster1816_1clades	1007	AD1_317	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80113.1	002273	Cluster1816_1clades	990	JA11_308	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66714.1	002273	Cluster1816_1clades	982	JA13_311	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67032.1	002273	Cluster1816_1clades	986	JA29_306	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67683.1	002273	Cluster1816_1clades	990	JA33_309	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08622.1	002273	Cluster1816_1clades	998	Alexandra_334	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58960.1	002273	Cluster1816_1clades	1005	Y3_320	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28787.1	002273	Cluster1816_1clades	993	YOLOSWAG_318	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDB70287.1	002274	Cluster1817_1clades	816	CF8_0119	Aeromonas phage CF8	GCA_006384595.2
QDJ97264.1	002274	Cluster1817_1clades	889	D6_0104	Aeromonas phage D6	GCA_007051205.2
QDH47020.1	002274	Cluster1817_1clades	889	LAh10_36	Aeromonas phage LAh10	GCA_006863975.1
QDJ96878.1	002274	Cluster1817_1clades	804	PS1_0119	Aeromonas phage PS1	GCA_007051165.2
QFR59510.1	002274	Cluster1817_1clades	804	PS2_0119	Aeromonas phage PS2	GCA_009388305.2
QBZ70646.1	002274	Cluster1817_1clades	802	pETSU_065	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71963.1	002274	Cluster1817_1clades	803	N1M2_100	Klebsiella phage N1M2	GCA_010092605.1
AEV89564.1	002274	Cluster1817_1clades	807	OBP_127	Pseudomonas phage OBP	GCA_000896635.1
AXG67264.1	002275	CarboxypepD-reg-IG	589	AD1_220	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80011.1	002275	CarboxypepD-reg-IG	661	JA11_206	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66609.1	002275	CarboxypepD-reg-IG	661	JA13_206	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66934.1	002275	CarboxypepD-reg-IG	661	JA29_208	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67581.1	002275	CarboxypepD-reg-IG	661	JA33_207	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08493.1	002275	CarboxypepD-reg-IG	590	Alexandra_230	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58865.1	002275	CarboxypepD-reg-IG	588	Y3_225	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28697.1	002275	CarboxypepD-reg-IG	576	YOLOSWAG_219	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AUZ94958.1	002276	Cluster1819_1clades	607	FDI40_gp176	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63471.1	002276	Cluster1819_1clades	504	CP21_009	Campylobacter virus CP21	GCA_000902535.1
CCH63475.1	002276	Cluster1819_1clades	435	CP21_013	Campylobacter virus CP21	GCA_000902535.1
CCH63634.1	002276	Cluster1819_1clades	387	CP21_172	Campylobacter virus CP21	GCA_000902535.1
AXH72710.1	002276	Cluster1819_1clades	362	-	Myoviridae sp.	GCA_003657725.1
AXH72715.1	002276	Cluster1819_1clades	392	-	Myoviridae sp.	GCA_003657725.1
QCG76006.1	002276	Cluster1819_1clades	478	EST35_0124	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76007.1	002276	Cluster1819_1clades	581	EST35_0125	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AXG67159.1	002277	Cluster1820_1clades	587	AD1_115	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79909.1	002277	Cluster1820_1clades	592	JA11_104	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66508.1	002277	Cluster1820_1clades	592	JA13_105	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66833.1	002277	Cluster1820_1clades	592	JA29_107	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67478.1	002277	Cluster1820_1clades	592	JA33_104	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08392.1	002277	Cluster1820_1clades	586	Alexandra_120	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58756.1	002277	Cluster1820_1clades	586	Y3_116	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28594.1	002277	Cluster1820_1clades	590	YOLOSWAG_112	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AMO43401.1	002278	Cluster1822_1clades	499	W270710_157	Cyanophage S-RIM44	GCA_002599145.1
AOO11873.1	002278	Cluster1822_1clades	499	Np050604_157	Cyanophage S-RIM44	GCA_002599185.1
AOO12574.1	002278	Cluster1822_1clades	499	Sn080709_157	Cyanophage S-RIM44	GCA_002599245.1
AOO13040.1	002278	Cluster1822_1clades	499	W2100709_158	Cyanophage S-RIM44	GCA_002599285.1
ADO99260.1	002278	Cluster1822_1clades	499	Syn1_159	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59626.1	002278	Cluster1822_1clades	507	S330809_165	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59388.1	002278	Cluster1822_1clades	507	C440309_165	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59864.1	002278	Cluster1822_1clades	507	N231010_165	Synechococcus phage S-CAM4	GCA_002922155.1
QDB70400.1	002279	Cluster1823_1clades	505	CF8_0231	Aeromonas phage CF8	GCA_006384595.2
QDJ97397.1	002279	Cluster1823_1clades	502	D6_0238	Aeromonas phage D6	GCA_007051205.2
QDH47050.1	002279	Cluster1823_1clades	502	LAh10_151	Aeromonas phage LAh10	GCA_006863975.1
QDJ96745.1	002279	Cluster1823_1clades	506	PS1_0234	Aeromonas phage PS1	GCA_007051165.2
QFR59378.1	002279	Cluster1823_1clades	506	PS2_0236	Aeromonas phage PS2	GCA_009388305.2
QBZ70783.1	002279	Cluster1823_1clades	500	pETSU_202	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72089.1	002279	Cluster1823_1clades	505	N1M2_226	Klebsiella phage N1M2	GCA_010092605.1
AEV89718.1	002279	Cluster1823_1clades	505	OBP_281	Pseudomonas phage OBP	GCA_000896635.1
AXG67360.1	002280	Cluster1824_1clades	426	AD1_316	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80112.1	002280	Cluster1824_1clades	422	JA11_307	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66713.1	002280	Cluster1824_1clades	422	JA13_310	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67031.1	002280	Cluster1824_1clades	422	JA29_305	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67682.1	002280	Cluster1824_1clades	422	JA33_308	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08584.1	002280	Cluster1824_1clades	426	Alexandra_333	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58959.1	002280	Cluster1824_1clades	426	Y3_319	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28786.1	002280	Cluster1824_1clades	417	YOLOSWAG_317	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67370.1	002281	Cluster1825_1clades	424	AD1_326	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80122.1	002281	Cluster1825_1clades	396	JA11_317	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66722.1	002281	Cluster1825_1clades	396	JA13_319	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67040.1	002281	Cluster1825_1clades	396	JA29_314	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67691.1	002281	Cluster1825_1clades	396	JA33_317	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08593.1	002281	Cluster1825_1clades	422	Alexandra_345	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58970.1	002281	Cluster1825_1clades	422	Y3_330	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28797.1	002281	Cluster1825_1clades	394	YOLOSWAG_329	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDB70381.1	002282	Cluster1826_1clades	370	CF8_0212	Aeromonas phage CF8	GCA_006384595.2
QDJ97380.1	002282	Cluster1826_1clades	365	D6_0221	Aeromonas phage D6	GCA_007051205.2
QDH47074.1	002282	Cluster1826_1clades	365	LAh10_135	Aeromonas phage LAh10	GCA_006863975.1
QDJ96723.1	002282	Cluster1826_1clades	359	PS1_0212	Aeromonas phage PS1	GCA_007051165.2
QFR59356.1	002282	Cluster1826_1clades	359	PS2_0214	Aeromonas phage PS2	GCA_009388305.2
QBZ70766.1	002282	Cluster1826_1clades	377	pETSU_185	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72072.1	002282	Cluster1826_1clades	367	N1M2_209	Klebsiella phage N1M2	GCA_010092605.1
AEV89701.1	002282	Cluster1826_1clades	368	OBP_264	Pseudomonas phage OBP	GCA_000896635.1
AYD81221.1	002283	MerR-HTH	266	SEA_JUSTBECAUSE_52	Streptomyces phage JustBecause	GCA_003613775.1
AYD81222.1	002283	MerR-HTH	111	SEA_JUSTBECAUSE_53	Streptomyces phage JustBecause	GCA_003613775.1
QJD53624.1	002283	MerR-HTH	266	SEA_KELA_53	Streptomyces phage Kela	GCA_012934305.1
QJD53625.1	002283	MerR-HTH	116	SEA_KELA_54	Streptomyces phage Kela	GCA_012934305.1
QBZ71957.1	002283	MerR-HTH	269	SEA_KRADAL_58	Streptomyces phage Kradal	GCA_004799925.1
QBZ72224.1	002283	MerR-HTH	111	SEA_KRADAL_59	Streptomyces phage Kradal	GCA_004799925.1
AXH66219.1	002283	MerR-HTH	269	SEA_SATIS_58	Streptomyces phage Satis	GCA_003366315.1
AXH66220.1	002283	MerR-HTH	370	SEA_SATIS_59	Streptomyces phage Satis	GCA_003366315.1
ANM44915.1	002284	Cluster1829_1clades	360	KTN4_157	Pseudomonas phage KTN4	GCA_002607225.1
QBX32299.1	002284	Cluster1829_1clades	345	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76820.1	002284	Cluster1829_1clades	336	PHABIO_189	Pseudomonas phage Phabio	GCA_002624965.1
AEH03561.1	002284	Cluster1829_1clades	346	138	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94799.1	002284	Cluster1829_1clades	360	SL2_222	Pseudomonas phage SL2	GCA_002956015.1
QJB22793.1	002284	Cluster1829_1clades	360	fnug_150	Pseudomonas phage fnug	GCA_012837215.1
QEM41872.1	002284	Cluster1829_1clades	345	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83023.1	002284	Cluster1829_1clades	360	PHIKZ122	Pseudomonas virus phiKZ	GCA_000842965.1
AMR59654.1	002285	Cluster1830_1clades	273	SEGD1_003	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49657.1	002285	Cluster1830_1clades	344	MACHINA_19	Erwinia phage Machina	GCA_002758035.1
ANZ49102.1	002285	Cluster1830_1clades	344	HUXLEY_20	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49930.1	002285	Cluster1830_1clades	344	PARSHIK_21	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QKN85842.1	002285	Cluster1830_1clades	273	ACEC001_0050	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20722.1	002285	Cluster1830_1clades	290	-	Salmonella phage JN03	GCA_014319805.1
AWN09088.1	002285	Cluster1830_1clades	271	MLDJOKPK_00163	Salmonella phage SPAsTU	GCA_003183805.1
AEP83837.1	002285	Cluster1830_1clades	273	SPN3US_0004	Salmonella phage SPN3US	GCA_001042275.1
AGH07599.1	002286	SIG+PBP_like_2	325	CYVG_00155	Cyanophage S-SSM6a	GCA_002710385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGG54435.1	002286	SIG+PBP_like_2	325	CYWG_00151	Cyanophage S-SSM6b	GCA_002710425.1
AAX44625.1	002286	SIG+PBP_like_2	321	PSSM2_248	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12346.1	002286	SIG+PBP_like_2	321	PRTG_00193	Prochlorococcus phage P-SSM5	GCA_002991095.1
ASR76267.1	002286	SIG+PBP_like_2	331	PBI_BELLAMY_231	Synechococcus phage Bellamy	GCA_002627525.1
QCW22957.1	002286	SIG+PBP_like_2	322	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50672.1	002286	SIG+PBP_like_2	322	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70221.1	002286	SIG+PBP_like_2	324	SynMITS9220M01_215	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMO43118.1	002287	Cluster1832_1clades	304	R1080702_109	Cyanophage S-RIM32	GCA_001754165.1
AMO43345.1	002287	Cluster1832_1clades	294	W270710_101	Cyanophage S-RIM44	GCA_002599145.1
AOO11817.1	002287	Cluster1832_1clades	294	Np050604_101	Cyanophage S-RIM44	GCA_002599185.1
AOO12518.1	002287	Cluster1832_1clades	294	Sn080709_101	Cyanophage S-RIM44	GCA_002599245.1
AOO12984.1	002287	Cluster1832_1clades	294	W2100709_102	Cyanophage S-RIM44	GCA_002599285.1
AGG54392.1	002287	Cluster1832_1clades	323	CYWG_00108	Cyanophage S-SSM6b	GCA_002710425.1
AGH26124.1	002287	Cluster1832_1clades	325	CPMG_00023	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99203.1	002287	Cluster1832_1clades	294	Syn1_102	Prochlorococcus phage Syn1	GCA_000892495.1
prevph1000000006	002288	PRTase	315	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000012	002288	PRTase	309	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000161	002288	PRTase	306	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000803	002288	PRTase	142	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000007	002288	PRTase	315	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000011	002288	PRTase	309	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000122	002288	PRTase	306	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000550	002288	PRTase	142	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXG67127.1	002289	Cluster1834_1clades	300	AD1_083	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79882.1	002289	Cluster1834_1clades	307	JA11_077	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66481.1	002289	Cluster1834_1clades	307	JA13_078	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66806.1	002289	Cluster1834_1clades	307	JA29_080	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67451.1	002289	Cluster1834_1clades	307	JA33_077	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08363.1	002289	Cluster1834_1clades	299	Alexandra_87	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58726.1	002289	Cluster1834_1clades	267	Y3_086	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28558.1	002289	Cluster1834_1clades	297	YOLOSWAG_75	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDB70374.1	002290	Cluster1835_1clades	227	CF8_0205	Aeromonas phage CF8	GCA_006384595.2
QDJ97371.1	002290	Cluster1835_1clades	243	D6_0212	Aeromonas phage D6	GCA_007051205.2
QDH47116.1	002290	Cluster1835_1clades	243	LAh10_126	Aeromonas phage LAh10	GCA_006863975.1
QDJ96715.1	002290	Cluster1835_1clades	220	PS1_0204	Aeromonas phage PS1	GCA_007051165.2
QFR59348.1	002290	Cluster1835_1clades	220	PS2_0206	Aeromonas phage PS2	GCA_009388305.2
QBZ70757.1	002290	Cluster1835_1clades	277	pETSU_176	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72064.1	002290	Cluster1835_1clades	234	N1M2_201	Klebsiella phage N1M2	GCA_010092605.1
AEV89693.1	002290	Cluster1835_1clades	302	OBP_256	Pseudomonas phage OBP	GCA_000896635.1
AXG67095.1	002291	Cluster1836_1clades	301	AD1_051	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79848.1	002291	Cluster1836_1clades	213	JA11_043	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66448.1	002291	Cluster1836_1clades	213	JA13_045	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66772.1	002291	Cluster1836_1clades	213	JA29_046	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67417.1	002291	Cluster1836_1clades	213	JA33_043	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08331.1	002291	Cluster1836_1clades	218	Alexandra_51	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58695.1	002291	Cluster1836_1clades	245	Y3_055	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28533.1	002291	Cluster1836_1clades	207	YOLOSWAG_49	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AMS01326.1	002292	Cluster1837_1clades	234	AR9_g242	Bacillus phage AR9	GCA_001743835.1
AMS01345.1	002292	Cluster1837_1clades	221	AR9_g261	Bacillus phage AR9	GCA_001743835.1
ALN97977.1	002292	Cluster1837_1clades	240	Bp8pS_298	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97995.1	002292	Cluster1837_1clades	214	Bp8pS_316	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99955.1	002292	Cluster1837_1clades	234	PBI_PBS1_133	Bacillus virus PBS1	GCA_002601325.1
AST99975.1	002292	Cluster1837_1clades	221	PBI_PBS1_154	Bacillus virus PBS1	GCA_002601325.1
CCE26301.1	002292	Cluster1837_1clades	295	g278	Yersinia phage phiR1-37	GCA_000895615.1
CCE26305.1	002292	Cluster1837_1clades	225	g282	Yersinia phage phiR1-37	GCA_000895615.1
AXG67083.1	002293	Cluster1838_1clades	212	AD1_039	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79829.1	002293	Cluster1838_1clades	290	JA11_024	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66428.1	002293	Cluster1838_1clades	290	JA13_025	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66750.1	002293	Cluster1838_1clades	291	JA29_024	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67398.1	002293	Cluster1838_1clades	290	JA33_024	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08316.1	002293	Cluster1838_1clades	198	Alexandra_36	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08317.1	002293	Cluster1838_1clades	217	Alexandra_37	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58681.1	002293	Cluster1838_1clades	224	Y3_041	Erwinia phage vB_EamM_Y3	GCA_002955045.1
APU01613.1	002294	HAD	284	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28865.1	002294	HAD	284	AP1_0158	Aeromonas phage AP1	GCA_014183365.1
ATI17299.1	002294	HAD	284	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00295.1	002294	HAD	284	HWB28_gp257	Aeromonas phage AS-zj	GCA_002627665.1
QAX97742.1	002294	HAD	284	ASswx1_97	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01465.1	002294	HAD	284	ASwh1_406	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39315.1	002294	HAD	284	CC2_014	Aeromonas phage CC2	GCA_000903495.1
ADQ53238.1	002294	HAD	274	65p230	Aeromonas virus 65	GCA_000893255.1
ANZ49886.1	002295	Cluster1840_1clades	284	MACHINA_248	Erwinia phage Machina	GCA_002758035.1
AFQ96700.1	002295	Cluster1840_1clades	275	G173_gp155	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48270.1	002295	Cluster1840_1clades	275	ASESINO_257	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48543.1	002295	Cluster1840_1clades	278	CAITLIN_248	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48820.1	002295	Cluster1840_1clades	274	CHRISDB_258	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49329.1	002295	Cluster1840_1clades	284	HUXLEY_247	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50157.1	002295	Cluster1840_1clades	284	PARSHIK_248	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50682.1	002295	Cluster1840_1clades	275	STRATTON_257	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AYD81322.1	002296	GT	282	SEA_JUSTBECAUSE_157	Streptomyces phage JustBecause	GCA_003613775.1
AYD81217.1	002296	GT	277	SEA_JUSTBECAUSE_48	Streptomyces phage JustBecause	GCA_003613775.1
QJD53725.1	002296	GT	282	SEA_KELA_155	Streptomyces phage Kela	GCA_012934305.1
QJD53620.1	002296	GT	277	SEA_KELA_49	Streptomyces phage Kela	GCA_012934305.1
QBZ72054.1	002296	GT	283	SEA_KRADAL_158	Streptomyces phage Kradal	GCA_004799925.1
QBZ71953.1	002296	GT	282	SEA_KRADAL_54	Streptomyces phage Kradal	GCA_004799925.1
AXH66317.1	002296	GT	283	SEA_SATIS_158	Streptomyces phage Satis	GCA_003366315.1
AXH66215.1	002296	GT	282	SEA_SATIS_54	Streptomyces phage Satis	GCA_003366315.1
AIT14301.1	002297	Cluster1842_1clades	282	PBI_121Q_411	Escherichia phage 121Q	GCA_000926855.1
QAY00637.1	002297	Cluster1842_1clades	282	Ecwhy1_362	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34834.1	002297	Cluster1842_1clades	282	ACQ29_gp154	Escherichia phage PBECO4	GCA_001041035.1
BBM61975.1	002297	Cluster1842_1clades	282	EO157G_3860	Escherichia phage SP27	GCA_008033345.1
AXC36942.1	002297	Cluster1842_1clades	282	-	Escherichia phage UB	GCA_003341455.1
QBO62003.1	002297	Cluster1842_1clades	282	G17_00514	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14024.1	002297	Cluster1842_1clades	282	vBEcoMphAPEC6_gp400c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80288.1	002297	Cluster1842_1clades	283	PSLUR01_00311	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANZ49823.1	002298	Cluster1843_1clades	235	MACHINA_185	Erwinia phage Machina	GCA_002758035.1
AFQ96642.1	002298	Cluster1843_1clades	223	G173_gp097	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48208.1	002298	Cluster1843_1clades	223	ASESINO_195	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48479.1	002298	Cluster1843_1clades	277	CAITLIN_184	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48758.1	002298	Cluster1843_1clades	235	CHRISDB_196	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49267.1	002298	Cluster1843_1clades	235	HUXLEY_185	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50095.1	002298	Cluster1843_1clades	235	PARSHIK_186	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50619.1	002298	Cluster1843_1clades	223	STRATTON_194	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXG67047.1	002299	Cluster1844_1clades	265	AD1_003	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79807.1	002299	Cluster1844_1clades	224	JA11_002	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66405.1	002299	Cluster1844_1clades	259	JA13_002	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66728.1	002299	Cluster1844_1clades	224	JA29_002	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67376.1	002299	Cluster1844_1clades	224	JA33_002	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08285.1	002299	Cluster1844_1clades	263	Alexandra_3	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58643.1	002299	Cluster1844_1clades	267	Y3_003	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28490.1	002299	Cluster1844_1clades	268	YOLOSWAG_3	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01770.1	002300	SIG+TM+TM	262	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28976.1	002300	SIG+TM+TM	183	AP1_0269	Aeromonas phage AP1	GCA_014183365.1
ATI17527.1	002300	SIG+TM+TM	183	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00469.1	002300	SIG+TM+TM	183	HWB28_gp083	Aeromonas phage AS-zj	GCA_002627665.1
QAX97969.1	002300	SIG+TM+TM	183	ASswx1_327	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01171.1	002300	SIG+TM+TM	182	ASwh1_105	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39380.1	002300	SIG+TM+TM	183	CC2_206	Aeromonas phage CC2	GCA_000903495.1
ADQ53413.1	002300	SIG+TM+TM	262	65p406	Aeromonas virus 65	GCA_000893255.1
AXG67339.1	002301	Cluster1846_1clades	228	AD1_295	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80090.1	002301	Cluster1846_1clades	170	JA11_285	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66691.1	002301	Cluster1846_1clades	170	JA13_288	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67011.1	002301	Cluster1846_1clades	170	JA29_285	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67660.1	002301	Cluster1846_1clades	170	JA33_286	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08567.1	002301	Cluster1846_1clades	262	Alexandra_314	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARW58942.1	002301	Cluster1846_1clades	224	Y3_302	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28767.1	002301	Cluster1846_1clades	242	YOLOSWAG_297	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67221.1	002302	Cluster1847_1clades	260	AD1_177	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79971.1	002302	Cluster1847_1clades	255	JA11_166	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66569.1	002302	Cluster1847_1clades	255	JA13_166	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66894.1	002302	Cluster1847_1clades	255	JA29_168	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67540.1	002302	Cluster1847_1clades	255	JA33_166	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08450.1	002302	Cluster1847_1clades	260	Alexandra_182	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58818.1	002302	Cluster1847_1clades	260	Y3_178	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28652.1	002302	Cluster1847_1clades	260	YOLOSWAG_173	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDB70403.1	002303	Cluster1848_1clades	172	CF8_0234	Aeromonas phage CF8	GCA_006384595.2
QDJ97400.1	002303	Cluster1848_1clades	190	D6_0241	Aeromonas phage D6	GCA_007051205.2
QDH47151.1	002303	Cluster1848_1clades	190	LAh10_154	Aeromonas phage LAh10	GCA_006863975.1
QDJ96748.1	002303	Cluster1848_1clades	185	PS1_0237	Aeromonas phage PS1	GCA_007051165.2
QFR59381.1	002303	Cluster1848_1clades	185	PS2_0239	Aeromonas phage PS2	GCA_009388305.2
QBZ70786.1	002303	Cluster1848_1clades	256	pETSU_205	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72092.1	002303	Cluster1848_1clades	199	N1M2_229	Klebsiella phage N1M2	GCA_010092605.1
AEV89721.1	002303	Cluster1848_1clades	218	OBP_284	Pseudomonas phage OBP	GCA_000896635.1
QDB70320.1	002304	Cluster1849_1clades	244	CF8_0151	Aeromonas phage CF8	GCA_006384595.2
QNH80844.1	002304	Cluster1849_1clades	247	D6_0142	Aeromonas phage D6	GCA_007051205.2
QDH47112.1	002304	Cluster1849_1clades	247	LAh10_66	Aeromonas phage LAh10	GCA_006863975.1
QDJ96666.1	002304	Cluster1849_1clades	255	PS1_0155	Aeromonas phage PS1	GCA_007051165.2
QFR59300.1	002304	Cluster1849_1clades	255	PS2_0159	Aeromonas phage PS2	GCA_009388305.2
QBZ70704.1	002304	Cluster1849_1clades	208	pETSU_123	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72016.1	002304	Cluster1849_1clades	209	N1M2_153	Klebsiella phage N1M2	GCA_010092605.1
AEV89630.1	002304	Cluster1849_1clades	209	OBP_193	Pseudomonas phage OBP	GCA_000896635.1
AXG67367.1	002305	Cluster1850_1clades	246	AD1_323	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80119.1	002305	Cluster1850_1clades	113	JA11_314	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66719.1	002305	Cluster1850_1clades	113	JA13_316	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67037.1	002305	Cluster1850_1clades	113	JA29_311	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67688.1	002305	Cluster1850_1clades	113	JA33_314	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08590.1	002305	Cluster1850_1clades	176	Alexandra_341	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58966.1	002305	Cluster1850_1clades	254	Y3_326	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28792.1	002305	Cluster1850_1clades	232	YOLOSWAG_324	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDB70251.1	002306	Cluster1852_1clades	224	CF8_0083	Aeromonas phage CF8	GCA_006384595.2
QDJ97230.1	002306	Cluster1852_1clades	222	D6_0070	Aeromonas phage D6	GCA_007051205.2
QDH47132.1	002306	Cluster1852_1clades	222	LAh10_3	Aeromonas phage LAh10	GCA_006863975.1
QDJ96840.1	002306	Cluster1852_1clades	230	PS1_0081	Aeromonas phage PS1	GCA_007051165.2
QFR59470.1	002306	Cluster1852_1clades	230	PS2_0079	Aeromonas phage PS2	GCA_009388305.2
QBZ70613.1	002306	Cluster1852_1clades	253	pETSU_032	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71929.1	002306	Cluster1852_1clades	251	N1M2_66	Klebsiella phage N1M2	GCA_010092605.1
AEV89529.1	002306	Cluster1852_1clades	252	OBP_092	Pseudomonas phage OBP	GCA_000896635.1
AXG67059.1	002307	Cluster1853_1clades	229	AD1_015	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79818.1	002307	Cluster1853_1clades	214	JA11_013	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66416.1	002307	Cluster1853_1clades	214	JA13_013	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66739.1	002307	Cluster1853_1clades	214	JA29_013	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67387.1	002307	Cluster1853_1clades	214	JA33_013	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08296.1	002307	Cluster1853_1clades	232	Alexandra_15	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58655.1	002307	Cluster1853_1clades	250	Y3_015	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28502.1	002307	Cluster1853_1clades	237	YOLOSWAG_15	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01638.1	002308	Cluster1855_1clades	241	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28878.1	002308	Cluster1855_1clades	128	AP1_0171	Aeromonas phage AP1	GCA_014183365.1
QMV29121.1	002308	Cluster1855_1clades	109	AP1_0418	Aeromonas phage AP1	GCA_014183365.1
ATI17245.1	002308	Cluster1855_1clades	244	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00342.1	002308	Cluster1855_1clades	244	HWB28_gp210	Aeromonas phage AS-zj	GCA_002627665.1
QAX97688.1	002308	Cluster1855_1clades	243	ASswx1_42	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39331.1	002308	Cluster1855_1clades	243	CC2_071	Aeromonas phage CC2	GCA_000903495.1
ADQ53264.1	002308	Cluster1855_1clades	241	65p256	Aeromonas virus 65	GCA_000893255.1
ABY62977.1	002309	Phage_gp49_66	100	201phi2-1p147	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77256.1	002309	Phage_gp49_66	109	NOXIFER_86	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32242.1	002309	Phage_gp49_66	100	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76762.1	002309	Phage_gp49_66	98	PHABIO_131	Pseudomonas phage Phabio	GCA_002624965.1
AEH03512.1	002309	Phage_gp49_66	103	088	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02623.1	002309	Phage_gp49_66	104	PSA21_95	Pseudomonas phage Psa21	GCA_004340405.1
QEM41820.1	002309	Phage_gp49_66	100	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAG41729.1	002309	Phage_gp49_66	234	RSL1_ORF282	Ralstonia phage phiRSL1	GCA_000879455.1
AXG67174.1	002310	Cluster1857_1clades	227	AD1_130	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79924.1	002310	Cluster1857_1clades	228	JA11_119	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66523.1	002310	Cluster1857_1clades	228	JA13_120	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66848.1	002310	Cluster1857_1clades	228	JA29_122	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67493.1	002310	Cluster1857_1clades	228	JA33_119	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08407.1	002310	Cluster1857_1clades	227	Alexandra_135	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58771.1	002310	Cluster1857_1clades	227	Y3_131	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28610.1	002310	Cluster1857_1clades	233	YOLOSWAG_129	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QIG63388.1	002311	TM	233	DAC16_158	Bacteroides phage DAC16	GCA_013387695.1
QIG63651.1	002311	TM	130	DAC19_163	Bacteroides phage DAC19	GCA_013387715.1
QIG63652.1	002311	TM	94	DAC19_164	Bacteroides phage DAC19	GCA_013387715.1
QIG63912.1	002311	TM	130	DAC20_162	Bacteroides phage DAC20	GCA_013387725.1
QIG63913.1	002311	TM	94	DAC20_163	Bacteroides phage DAC20	GCA_013387725.1
QIG64176.1	002311	TM	67	DAC22_165	Bacteroides phage DAC22	GCA_013387735.1
QIG64177.1	002311	TM	64	DAC22_166	Bacteroides phage DAC22	GCA_013387735.1
QIG64432.1	002311	TM	231	DAC23_157	Bacteroides phage DAC23	GCA_013387745.1
QDB70263.1	002312	Cluster1859_1clades	223	CF8_0095	Aeromonas phage CF8	GCA_006384595.2
QDJ97241.1	002312	Cluster1859_1clades	226	D6_0081	Aeromonas phage D6	GCA_007051205.2
QDH47128.1	002312	Cluster1859_1clades	226	LAh10_13	Aeromonas phage LAh10	GCA_006863975.1
QDJ96854.1	002312	Cluster1859_1clades	227	PS1_0095	Aeromonas phage PS1	GCA_007051165.2
QFR59486.1	002312	Cluster1859_1clades	227	PS2_0095	Aeromonas phage PS2	GCA_009388305.2
QBZ70624.1	002312	Cluster1859_1clades	217	pETSU_043	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71940.1	002312	Cluster1859_1clades	217	N1M2_77	Klebsiella phage N1M2	GCA_010092605.1
AEV89540.1	002312	Cluster1859_1clades	216	OBP_103	Pseudomonas phage OBP	GCA_000896635.1
AXQ69198.1	002313	SIG+MAF_flag10	199	CcrBL9_gp174	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87996.1	002313	SIG+MAF_flag10	216	CcrColossus_gp126	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68672.1	002313	SIG+MAF_flag10	216	CcrPW_gp133	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69751.1	002313	SIG+MAF_flag10	199	CcrSC_gp169	Caulobacter phage CcrSC	GCA_003443315.1
BBA65523.1	002313	SIG+MAF_flag10	210	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65522.1	002313	SIG+MAF_flag10	226	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96520.1	002313	SIG+MAF_flag10	226	Xoosp13_334	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96521.1	002313	SIG+MAF_flag10	195	Xoosp13_335	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDB70348.1	002314	Cluster1861_1clades	226	CF8_0179	Aeromonas phage CF8	GCA_006384595.2
QDJ97346.1	002314	Cluster1861_1clades	204	D6_0187	Aeromonas phage D6	GCA_007051205.2
QDH47142.1	002314	Cluster1861_1clades	204	LAh10_105	Aeromonas phage LAh10	GCA_006863975.1
QDJ96699.1	002314	Cluster1861_1clades	199	PS1_0188	Aeromonas phage PS1	GCA_007051165.2
QFR59332.1	002314	Cluster1861_1clades	199	PS2_0190	Aeromonas phage PS2	GCA_009388305.2
QBZ70731.1	002314	Cluster1861_1clades	203	pETSU_150	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72042.1	002314	Cluster1861_1clades	201	N1M2_179	Klebsiella phage N1M2	GCA_010092605.1
AEV89663.1	002314	Cluster1861_1clades	200	OBP_226	Pseudomonas phage OBP	GCA_000896635.1
AIT14146.1	002315	Cluster1862_1clades	223	PBI_121Q_256	Escherichia phage 121Q	GCA_000926855.1
QAY00784.1	002315	Cluster1862_1clades	219	Ecwhy1_511	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34964.1	002315	Cluster1862_1clades	223	ACQ29_gp284	Escherichia phage PBECO4	GCA_001041035.1
BBM61824.1	002315	Cluster1862_1clades	219	EO157G_2350	Escherichia phage SP27	GCA_008033345.1
AXC37057.1	002315	Cluster1862_1clades	221	-	Escherichia phage UB	GCA_003341455.1
QBO61557.1	002315	Cluster1862_1clades	223	G17_00061	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14167.1	002315	Cluster1862_1clades	223	vBEcoMphAPEC6_gp544c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80138.1	002315	Cluster1862_1clades	223	PSLUR01_00161	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14123.1	002316	Cluster1863_1clades	219	PBI_121Q_233	Escherichia phage 121Q	GCA_000926855.1
QAY00801.1	002316	Cluster1863_1clades	216	Ecwhy1_528	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34977.1	002316	Cluster1863_1clades	220	ACQ29_gp297	Escherichia phage PBECO4	GCA_001041035.1
BBM61801.1	002316	Cluster1863_1clades	219	EO157G_2120	Escherichia phage SP27	GCA_008033345.1
AXC36557.1	002316	Cluster1863_1clades	219	-	Escherichia phage UB	GCA_003341455.1
QBO61578.1	002316	Cluster1863_1clades	219	G17_00082	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13642.1	002316	Cluster1863_1clades	219	vBEcoMphAPEC6_gp011c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80113.1	002316	Cluster1863_1clades	219	PSLUR01_00136	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70405.1	002317	Cluster1866_1clades	198	CF8_0236	Aeromonas phage CF8	GCA_006384595.2
QDJ97409.1	002317	Cluster1866_1clades	193	D6_0250	Aeromonas phage D6	GCA_007051205.2
QDH47136.1	002317	Cluster1866_1clades	216	LAh10_162	Aeromonas phage LAh10	GCA_006863975.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ96753.1	002317	Cluster1866_1clades	185	PS1_0242	Aeromonas phage PS1	GCA_007051165.2
QFR59386.1	002317	Cluster1866_1clades	185	PS2_0244	Aeromonas phage PS2	GCA_009388305.2
QBZ70801.1	002317	Cluster1866_1clades	173	pETSU_220	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72101.1	002317	Cluster1866_1clades	200	N1M2_238	Klebsiella phage N1M2	GCA_010092605.1
AEV89738.1	002317	Cluster1866_1clades	200	OBP_301	Pseudomonas phage OBP	GCA_000896635.1
AIT14244.1	002318	Cluster1868_1clades	166	PBI_121Q_354	Escherichia phage 121Q	GCA_000926855.1
QAY00687.1	002318	Cluster1868_1clades	214	Ecwhy1_412	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34883.1	002318	Cluster1868_1clades	180	ACQ29_gp203	Escherichia phage PBECO4	GCA_001041035.1
BBM61922.1	002318	Cluster1868_1clades	170	EO157G_3330	Escherichia phage SP27	GCA_008033345.1
AXC36989.1	002318	Cluster1868_1clades	170	-	Escherichia phage UB	GCA_003341455.1
QBO62060.1	002318	Cluster1868_1clades	170	G17_00571	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14078.1	002318	Cluster1868_1clades	170	vBEcoMphAPEC6_gp455c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80234.1	002318	Cluster1868_1clades	170	PSLUR01_00257	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01460.1	002319	TM	208	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29004.1	002319	TM	211	AP1_0297	Aeromonas phage AP1	GCA_014183365.1
ATI17437.1	002319	TM	211	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00158.1	002319	TM	211	HWB28_gp394	Aeromonas phage AS-zj	GCA_002627665.1
QAX97877.1	002319	TM	211	ASswx1_234	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01273.1	002319	TM	213	ASwh1_210	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39478.1	002319	TM	211	CC2_300	Aeromonas phage CC2	GCA_000903495.1
ADQ53081.1	002319	TM	208	65p071	Aeromonas virus 65	GCA_000893255.1
AIT14341.1	002320	Cluster1870_1clades	209	PBI_121Q_451	Escherichia phage 121Q	GCA_000926855.1
QAY00603.1	002320	Cluster1870_1clades	198	Ecwhy1_326	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34797.1	002320	Cluster1870_1clades	209	ACQ29_gp117	Escherichia phage PBECO4	GCA_001041035.1
BBM62012.1	002320	Cluster1870_1clades	209	EO157G_4230	Escherichia phage SP27	GCA_008033345.1
AXC36914.1	002320	Cluster1870_1clades	209	-	Escherichia phage UB	GCA_003341455.1
QBO61963.1	002320	Cluster1870_1clades	213	G17_00474	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13990.1	002320	Cluster1870_1clades	205	vBEcoMphAPEC6_gp366c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80328.1	002320	Cluster1870_1clades	213	PSLUR01_00351	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01539.1	002321	Cluster1871_1clades	193	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29053.1	002321	Cluster1871_1clades	211	AP1_0346	Aeromonas phage AP1	GCA_014183365.1
ATI17360.1	002321	Cluster1871_1clades	194	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00234.1	002321	Cluster1871_1clades	194	HWB28_gp318	Aeromonas phage AS-zj	GCA_002627665.1
QAX97803.1	002321	Cluster1871_1clades	193	ASswx1_158	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01349.1	002321	Cluster1871_1clades	175	ASwh1_288	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39283.1	002321	Cluster1871_1clades	193	CC2_378	Aeromonas phage CC2	GCA_000903495.1
ADQ53161.1	002321	Cluster1871_1clades	193	65p153	Aeromonas virus 65	GCA_000893255.1
APU01610.1	002322	Cluster1872_1clades	203	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28861.1	002322	Cluster1872_1clades	209	AP1_0154	Aeromonas phage AP1	GCA_014183365.1
ATI17302.1	002322	Cluster1872_1clades	207	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00292.1	002322	Cluster1872_1clades	207	HWB28_gp260	Aeromonas phage AS-zj	GCA_002627665.1
QAX97745.1	002322	Cluster1872_1clades	209	ASswx1_100	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01344.1	002322	Cluster1872_1clades	201	ASwh1_283	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39166.1	002322	Cluster1872_1clades	209	CC2_009	Aeromonas phage CC2	GCA_000903495.1
ADQ53234.1	002322	Cluster1872_1clades	203	65p226	Aeromonas virus 65	GCA_000893255.1
AXG67314.1	002323	Cluster1873_1clades	159	AD1_270	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80066.1	002323	Cluster1873_1clades	206	JA11_261	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66667.1	002323	Cluster1873_1clades	206	JA13_264	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66988.1	002323	Cluster1873_1clades	206	JA29_262	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67636.1	002323	Cluster1873_1clades	206	JA33_262	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08539.1	002323	Cluster1873_1clades	125	Alexandra_282	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58918.1	002323	Cluster1873_1clades	158	Y3_278	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28739.1	002323	Cluster1873_1clades	121	YOLOSWAG_266	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67138.1	002324	Cluster1874_1clades	198	AD1_094	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08374.1	002324	Cluster1874_1clades	198	Alexandra_99	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58737.1	002324	Cluster1874_1clades	198	Y3_097	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28570.1	002324	Cluster1874_1clades	200	YOLOSWAG_87	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38289.1	002324	Cluster1874_1clades	205	BN7874_120	Phage NCTB	GCA_900092385.1
SBV38369.1	002324	Cluster1874_1clades	138	BN7874_199	Phage NCTB	GCA_900092385.1
AGS81977.1	002324	Cluster1874_1clades	143	PaBG_00092	Pseudomonas phage PaBG	GCA_000912555.1
AGS82133.1	002324	Cluster1874_1clades	199	PaBG_00258	Pseudomonas phage PaBG	GCA_000912555.1
AIT14246.1	002325	Cluster1875_1clades	204	PBI_121Q_356	Escherichia phage 121Q	GCA_000926855.1
QAY00686.1	002325	Cluster1875_1clades	202	Ecwhy1_411	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34881.1	002325	Cluster1875_1clades	204	ACQ29_gp201	Escherichia phage PBECO4	GCA_001041035.1
BBM61924.1	002325	Cluster1875_1clades	204	EO157G_3350	Escherichia phage SP27	GCA_008033345.1
AXC36987.1	002325	Cluster1875_1clades	204	-	Escherichia phage UB	GCA_003341455.1
QBO62058.1	002325	Cluster1875_1clades	204	G17_00569	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14076.1	002325	Cluster1875_1clades	204	vBEcoMphAPEC6_gp453c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80236.1	002325	Cluster1875_1clades	204	PSLUR01_00259	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14248.1	002326	Cluster1876_1clades	171	PBI_121Q_358	Escherichia phage 121Q	GCA_000926855.1
QAY00685.1	002326	Cluster1876_1clades	203	Ecwhy1_410	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34879.1	002326	Cluster1876_1clades	171	ACQ29_gp199	Escherichia phage PBECO4	GCA_001041035.1
BBM61926.1	002326	Cluster1876_1clades	172	EO157G_3370	Escherichia phage SP27	GCA_008033345.1
AXC36985.1	002326	Cluster1876_1clades	171	-	Escherichia phage UB	GCA_003341455.1
QBO62056.1	002326	Cluster1876_1clades	171	G17_00567	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14075.1	002326	Cluster1876_1clades	171	vBEcoMphAPEC6_gp452c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80238.1	002326	Cluster1876_1clades	171	PSLUR01_00261	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QGY75121.1	002327	Cluster1877_1clades	191	CF8_0106	Aeromonas phage CF8	GCA_006384595.2
QDJ97252.1	002327	Cluster1877_1clades	179	D6_0092	Aeromonas phage D6	GCA_007051205.2
QDH47159.1	002327	Cluster1877_1clades	179	LAh10_24	Aeromonas phage LAh10	GCA_006863975.1
QDJ96865.1	002327	Cluster1877_1clades	181	PS1_0106	Aeromonas phage PS1	GCA_007051165.2
QFR59497.1	002327	Cluster1877_1clades	181	PS2_0106	Aeromonas phage PS2	GCA_009388305.2
QBZ70634.1	002327	Cluster1877_1clades	203	pETSU_053	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71951.1	002327	Cluster1877_1clades	202	N1M2_88	Klebsiella phage N1M2	GCA_010092605.1
AEV89552.1	002327	Cluster1877_1clades	194	OBP_115	Pseudomonas phage OBP	GCA_000896635.1
AFC21622.1	002328	Cluster1879_1clades	193	GAP32_172	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43740.1	002328	Cluster1879_1clades	202	CBB_175	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18889.1	002328	Cluster1879_1clades	192	7t3_0368	Salmonella phage 7t3	GCA_006083215.1
AZU98147.1	002328	Cluster1879_1clades	192	CPT_Munch_203	Salmonella phage Munch	GCA_004015485.1
QIG62836.1	002328	Cluster1879_1clades	192	SEPL_223	Salmonella phage SE_PL	GCA_011067555.1
AQW88698.1	002328	Cluster1879_1clades	199	BF_0173	Serratia phage BF	GCA_002619745.1
SOK58979.1	002328	Cluster1879_1clades	195	g171	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58445.1	002328	Cluster1879_1clades	195	g168	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14250.1	002329	Cluster1880_1clades	183	PBI_121Q_360	Escherichia phage 121Q	GCA_000926855.1
QAY00683.1	002329	Cluster1880_1clades	201	Ecwhy1_408	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34877.1	002329	Cluster1880_1clades	200	ACQ29_gp197	Escherichia phage PBECO4	GCA_001041035.1
BBM61928.1	002329	Cluster1880_1clades	183	EO157G_3390	Escherichia phage SP27	GCA_008033345.1
AXC36983.1	002329	Cluster1880_1clades	183	-	Escherichia phage UB	GCA_003341455.1
QBO62054.1	002329	Cluster1880_1clades	183	G17_00565	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14073.1	002329	Cluster1880_1clades	183	vBEcoMphAPEC6_gp450c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80240.1	002329	Cluster1880_1clades	183	PSLUR01_00263	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14292.1	002330	Cluster1881_1clades	200	PBI_121Q_402	Escherichia phage 121Q	GCA_000926855.1
QAY00646.1	002330	Cluster1881_1clades	200	Ecwhy1_371	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34842.1	002330	Cluster1881_1clades	200	ACQ29_gp162	Escherichia phage PBECO4	GCA_001041035.1
BBM61966.1	002330	Cluster1881_1clades	200	EO157G_3770	Escherichia phage SP27	GCA_008033345.1
AXC36951.1	002330	Cluster1881_1clades	200	-	Escherichia phage UB	GCA_003341455.1
QBO62012.1	002330	Cluster1881_1clades	200	G17_00523	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14033.1	002330	Cluster1881_1clades	200	vBEcoMphAPEC6_gp410c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80279.1	002330	Cluster1881_1clades	200	PSLUR01_00302	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14272.1	002331	Cluster1882_1clades	188	PBI_121Q_382	Escherichia phage 121Q	GCA_000926855.1
QAY00665.1	002331	Cluster1882_1clades	200	Ecwhy1_390	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34861.1	002331	Cluster1882_1clades	200	ACQ29_gp181	Escherichia phage PBECO4	GCA_001041035.1
BBM61947.1	002331	Cluster1882_1clades	200	EO157G_3580	Escherichia phage SP27	GCA_008033345.1
AXC36970.1	002331	Cluster1882_1clades	200	-	Escherichia phage UB	GCA_003341455.1
QBO62032.1	002331	Cluster1882_1clades	200	G17_00543	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14053.1	002331	Cluster1882_1clades	200	vBEcoMphAPEC6_gp430c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80260.1	002331	Cluster1882_1clades	200	PSLUR01_00283	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70389.1	002332	SIG+Ig_C17orf99	185	CF8_0220	Aeromonas phage CF8	GCA_006384595.2
QDJ97388.1	002332	SIG+Ig_C17orf99	182	D6_0229	Aeromonas phage D6	GCA_007051205.2
QDH47155.1	002332	SIG+Ig_C17orf99	182	LAh10_143	Aeromonas phage LAh10	GCA_006863975.1
QDJ96732.1	002332	SIG+Ig_C17orf99	182	PS1_0221	Aeromonas phage PS1	GCA_007051165.2
QFR59365.1	002332	SIG+Ig_C17orf99	182	PS2_0223	Aeromonas phage PS2	GCA_009388305.2
QBZ70774.1	002332	SIG+Ig_C17orf99	200	pETSU_193	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72080.1	002332	SIG+Ig_C17orf99	183	N1M2_217	Klebsiella phage N1M2	GCA_010092605.1
AEV89709.1	002332	SIG+Ig_C17orf99	184	OBP_272	Pseudomonas phage OBP	GCA_000896635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG67126.1	002333	Cluster1884_1clades	192	AD1_082	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79881.1	002333	Cluster1884_1clades	197	JA11_076	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66480.1	002333	Cluster1884_1clades	197	JA13_077	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66805.1	002333	Cluster1884_1clades	198	JA29_079	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67450.1	002333	Cluster1884_1clades	197	JA33_076	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08362.1	002333	Cluster1884_1clades	112	Alexandra_85	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58725.1	002333	Cluster1884_1clades	193	Y3_085	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28557.1	002333	Cluster1884_1clades	186	YOLOSWAG_74	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01609.1	002334	Cluster1885_1clades	187	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28862.1	002334	Cluster1885_1clades	196	AP1_0155	Aeromonas phage AP1	GCA_014183365.1
ATI17301.1	002334	Cluster1885_1clades	196	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00293.1	002334	Cluster1885_1clades	196	HWB28_gp259	Aeromonas phage AS-zj	GCA_002627665.1
QAX97744.1	002334	Cluster1885_1clades	196	ASswx1_99	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01411.1	002334	Cluster1885_1clades	193	ASwh1_352	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39312.1	002334	Cluster1885_1clades	197	CC2_010	Aeromonas phage CC2	GCA_000903495.1
ADQ53233.1	002334	Cluster1885_1clades	190	65p225	Aeromonas virus 65	GCA_000893255.1
AFC21782.1	002335	Cluster1888_1clades	183	GAP32_332	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43900.1	002335	Cluster1888_1clades	179	CBB_337	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19060.1	002335	Cluster1888_1clades	144	7t3_0540	Salmonella phage 7t3	GCA_006083215.1
AZU98306.1	002335	Cluster1888_1clades	144	CPT_Munch_362	Salmonella phage Munch	GCA_004015485.1
QIG62678.1	002335	Cluster1888_1clades	144	SEPL_065	Salmonella phage SE_PL	GCA_011067555.1
AQW88860.1	002335	Cluster1888_1clades	196	BF_0335	Serratia phage BF	GCA_002619745.1
SOK59144.1	002335	Cluster1888_1clades	188	g336	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58610.1	002335	Cluster1888_1clades	188	g333	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMR59830.1	002336	Cluster1889_1clades	195	SEGD1_183	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96646.1	002336	Cluster1889_1clades	190	G173_gp101	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48212.1	002336	Cluster1889_1clades	190	ASESINO_199	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50623.1	002336	Cluster1889_1clades	190	STRATTON_198	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86020.1	002336	Cluster1889_1clades	195	ACEC001_1790	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20875.1	002336	Cluster1889_1clades	195	-	Salmonella phage JN03	GCA_014319805.1
AWN09158.1	002336	Cluster1889_1clades	192	MLDJOKPK_00262	Salmonella phage SPAsTU	GCA_003183805.1
AEP84012.1	002336	Cluster1889_1clades	195	SPN3US_0179	Salmonella phage SPN3US	GCA_001042275.1
AIT14293.1	002337	Cluster1890_1clades	194	PBI_121Q_403	Escherichia phage 121Q	GCA_000926855.1
QAY00645.1	002337	Cluster1890_1clades	194	Ecwhy1_370	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34841.1	002337	Cluster1890_1clades	194	ACQ29_gp161	Escherichia phage PBECO4	GCA_001041035.1
BBM61967.1	002337	Cluster1890_1clades	194	EO157G_3780	Escherichia phage SP27	GCA_008033345.1
AXC36950.1	002337	Cluster1890_1clades	194	-	Escherichia phage UB	GCA_003341455.1
QBO62011.1	002337	Cluster1890_1clades	194	G17_00522	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14032.1	002337	Cluster1890_1clades	194	vBEcoMphAPEC6_gp409c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80280.1	002337	Cluster1890_1clades	194	PSLUR01_00303	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14286.1	002338	Cluster1891_1clades	194	PBI_121Q_396	Escherichia phage 121Q	GCA_000926855.1
QAY00652.1	002338	Cluster1891_1clades	194	Ecwhy1_377	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34848.1	002338	Cluster1891_1clades	183	ACQ29_gp168	Escherichia phage PBECO4	GCA_001041035.1
BBM61960.1	002338	Cluster1891_1clades	194	EO157G_3710	Escherichia phage SP27	GCA_008033345.1
AXC36957.1	002338	Cluster1891_1clades	183	-	Escherichia phage UB	GCA_003341455.1
QBO62018.1	002338	Cluster1891_1clades	194	G17_00529	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14039.1	002338	Cluster1891_1clades	194	vBEcoMphAPEC6_gp416c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80273.1	002338	Cluster1891_1clades	194	PSLUR01_00296	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT13968.1	002339	Cluster1892_1clades	190	PBI_121Q_71	Escherichia phage 121Q	GCA_000926855.1
QAY00369.1	002339	Cluster1892_1clades	194	Ecwhy1_88	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35114.1	002339	Cluster1892_1clades	190	ACQ29_gp434	Escherichia phage PBECO4	GCA_001041035.1
BBM61660.1	002339	Cluster1892_1clades	193	EO157G_0710	Escherichia phage SP27	GCA_008033345.1
AXC36688.1	002339	Cluster1892_1clades	190	-	Escherichia phage UB	GCA_003341455.1
QDF13770.1	002339	Cluster1892_1clades	190	vBEcoMphAPEC6_gp141c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80562.1	002339	Cluster1892_1clades	190	PSLUR01_00585	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44450.1	002339	Cluster1892_1clades	187	RaK2_00177	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QDB70406.1	002340	Cluster1893_1clades	177	CF8_0237	Aeromonas phage CF8	GCA_006384595.2
QDJ97411.1	002340	Cluster1893_1clades	182	D6_0252	Aeromonas phage D6	GCA_007051205.2
QDH47156.1	002340	Cluster1893_1clades	182	LAh10_164	Aeromonas phage LAh10	GCA_006863975.1
QDJ96754.1	002340	Cluster1893_1clades	174	PS1_0243	Aeromonas phage PS1	GCA_007051165.2
QFR59387.1	002340	Cluster1893_1clades	174	PS2_0245	Aeromonas phage PS2	GCA_009388305.2
QBZ70802.1	002340	Cluster1893_1clades	194	pETSU_221	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72102.1	002340	Cluster1893_1clades	179	N1M2_239	Klebsiella phage N1M2	GCA_010092605.1
AEV89739.1	002340	Cluster1893_1clades	192	OBP_302	Pseudomonas phage OBP	GCA_000896635.1
AIT14290.1	002341	Cluster1894_1clades	179	PBI_121Q_400	Escherichia phage 121Q	GCA_000926855.1
QAY00648.1	002341	Cluster1894_1clades	193	Ecwhy1_373	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34844.1	002341	Cluster1894_1clades	193	ACQ29_gp164	Escherichia phage PBECO4	GCA_001041035.1
BBM61964.1	002341	Cluster1894_1clades	193	EO157G_3750	Escherichia phage SP27	GCA_008033345.1
AXC36953.1	002341	Cluster1894_1clades	193	-	Escherichia phage UB	GCA_003341455.1
QBO62014.1	002341	Cluster1894_1clades	193	G17_00525	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14035.1	002341	Cluster1894_1clades	193	vBEcoMphAPEC6_gp412c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80277.1	002341	Cluster1894_1clades	193	PSLUR01_00300	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14287.1	002342	Cluster1895_1clades	193	PBI_121Q_397	Escherichia phage 121Q	GCA_000926855.1
QAY00651.1	002342	Cluster1895_1clades	192	Ecwhy1_376	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34847.1	002342	Cluster1895_1clades	186	ACQ29_gp167	Escherichia phage PBECO4	GCA_001041035.1
BBM61961.1	002342	Cluster1895_1clades	192	EO157G_3720	Escherichia phage SP27	GCA_008033345.1
AXC36956.1	002342	Cluster1895_1clades	192	-	Escherichia phage UB	GCA_003341455.1
QBO62017.1	002342	Cluster1895_1clades	192	G17_00528	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14038.1	002342	Cluster1895_1clades	193	vBEcoMphAPEC6_gp415c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80274.1	002342	Cluster1895_1clades	193	PSLUR01_00297	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21823.1	002343	Cluster1896_1clades	192	GAP32_372	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43945.1	002343	Cluster1896_1clades	192	CBB_382	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18555.1	002343	Cluster1896_1clades	193	7t3_030	Salmonella phage 7t3	GCA_006083215.1
AZU98384.1	002343	Cluster1896_1clades	193	CPT_Munch_450	Salmonella phage Munch	GCA_004015485.1
QIG63128.1	002343	Cluster1896_1clades	193	SEPL_515	Salmonella phage SE_PL	GCA_011067555.1
AQW88904.1	002343	Cluster1896_1clades	192	BF_0379	Serratia phage BF	GCA_002619745.1
SOK59194.1	002343	Cluster1896_1clades	192	g386	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58658.1	002343	Cluster1896_1clades	192	g381	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01795.1	002344	ACET	189	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28997.1	002344	ACET	188	AP1_0290	Aeromonas phage AP1	GCA_014183365.1
ATI17510.1	002344	ACET	188	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00486.1	002344	ACET	188	HWB28_gp066	Aeromonas phage AS-zj	GCA_002627665.1
QAX97950.1	002344	ACET	188	ASswx1_308	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01198.1	002344	ACET	193	ASwh1_133	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39387.1	002344	ACET	188	CC2_224	Aeromonas phage CC2	GCA_000903495.1
ADQ53439.1	002344	ACET	189	65p433	Aeromonas virus 65	GCA_000893255.1
APU01538.1	002345	Cluster1898_1clades	187	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29071.1	002345	Cluster1898_1clades	193	AP1_0364	Aeromonas phage AP1	GCA_014183365.1
ATI17359.1	002345	Cluster1898_1clades	186	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00235.1	002345	Cluster1898_1clades	186	HWB28_gp317	Aeromonas phage AS-zj	GCA_002627665.1
QAX97802.1	002345	Cluster1898_1clades	186	ASswx1_157	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01348.1	002345	Cluster1898_1clades	189	ASwh1_287	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39442.1	002345	Cluster1898_1clades	186	CC2_379	Aeromonas phage CC2	GCA_000903495.1
ADQ53160.1	002345	Cluster1898_1clades	187	65p152	Aeromonas virus 65	GCA_000893255.1
AIT14285.1	002346	Cluster1899_1clades	192	PBI_121Q_395	Escherichia phage 121Q	GCA_000926855.1
QAY00653.1	002346	Cluster1899_1clades	187	Ecwhy1_378	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34849.1	002346	Cluster1899_1clades	188	ACQ29_gp169	Escherichia phage PBECO4	GCA_001041035.1
BBM61959.1	002346	Cluster1899_1clades	188	EO157G_3700	Escherichia phage SP27	GCA_008033345.1
AXC36958.1	002346	Cluster1899_1clades	188	-	Escherichia phage UB	GCA_003341455.1
QBO62019.1	002346	Cluster1899_1clades	188	G17_00530	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14040.1	002346	Cluster1899_1clades	188	vBEcoMphAPEC6_gp417c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80272.1	002346	Cluster1899_1clades	188	PSLUR01_00295	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14087.1	002347	Cluster1900_1clades	190	PBI_121Q_197	Escherichia phage 121Q	GCA_000926855.1
QAY00835.1	002347	Cluster1900_1clades	190	Ecwhy1_563	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35007.1	002347	Cluster1900_1clades	190	ACQ29_gp327	Escherichia phage PBECO4	GCA_001041035.1
BBM61770.1	002347	Cluster1900_1clades	190	EO157G_1810	Escherichia phage SP27	GCA_008033345.1
AXC36585.1	002347	Cluster1900_1clades	190	-	Escherichia phage UB	GCA_003341455.1
QBO61612.1	002347	Cluster1900_1clades	190	G17_00116	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13670.1	002347	Cluster1900_1clades	190	vBEcoMphAPEC6_gp039c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80081.1	002347	Cluster1900_1clades	190	PSLUR01_00104	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14008.1	002348	Cluster1901_1clades	189	PBI_121Q_111	Escherichia phage 121Q	GCA_000926855.1
QAY00330.1	002348	Cluster1901_1clades	189	Ecwhy1_49	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35076.1	002348	Cluster1901_1clades	189	ACQ29_gp396	Escherichia phage PBECO4	GCA_001041035.1
BBM61699.1	002348	Cluster1901_1clades	72	EO157G_1100	Escherichia phage SP27	GCA_008033345.1
AXC36653.1	002348	Cluster1901_1clades	189	-	Escherichia phage UB	GCA_003341455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBO61685.1	002348	Cluster1901_1clades	189	G17_00196	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13734.1	002348	Cluster1901_1clades	72	vBEcoMphAPEC6_gp104c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80012.1	002348	Cluster1901_1clades	189	PSLUR01_00028	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01651.1	002349	Cluster1902_1clades	150	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28889.1	002349	Cluster1902_1clades	141	AP1_0182	Aeromonas phage AP1	GCA_014183365.1
ATI17234.1	002349	Cluster1902_1clades	141	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00353.1	002349	Cluster1902_1clades	141	HWB28_gp199	Aeromonas phage AS-zj	GCA_002627665.1
QAX97677.1	002349	Cluster1902_1clades	141	ASswx1_31	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01469.1	002349	Cluster1902_1clades	189	ASwh1_410	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39337.1	002349	Cluster1902_1clades	141	CC2_084	Aeromonas phage CC2	GCA_000903495.1
ADQ53281.1	002349	Cluster1902_1clades	150	65p273	Aeromonas virus 65	GCA_000893255.1
AIT14271.1	002350	Cluster1903_1clades	186	PBI_121Q_381	Escherichia phage 121Q	GCA_000926855.1
QAY00666.1	002350	Cluster1903_1clades	184	Ecwhy1_391	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34862.1	002350	Cluster1903_1clades	186	ACQ29_gp182	Escherichia phage PBECO4	GCA_001041035.1
BBM61946.1	002350	Cluster1903_1clades	186	EO157G_3570	Escherichia phage SP27	GCA_008033345.1
AXC36971.1	002350	Cluster1903_1clades	186	-	Escherichia phage UB	GCA_003341455.1
QBO62033.1	002350	Cluster1903_1clades	186	G17_00544	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14054.1	002350	Cluster1903_1clades	186	vBEcoMphAPEC6_gp431c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80259.1	002350	Cluster1903_1clades	186	PSLUR01_00282	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01525.1	002351	A18	184	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28771.1	002351	A18	184	AP1_0053	Aeromonas phage AP1	GCA_014183365.1
ATI17375.1	002351	A18	149	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00219.1	002351	A18	149	HWB28_gp333	Aeromonas phage AS-zj	GCA_002627665.1
QAX97816.1	002351	A18	149	ASswx1_172	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01336.1	002351	A18	178	ASwh1_275	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39431.1	002351	A18	184	CC2_364	Aeromonas phage CC2	GCA_000903495.1
ADQ53147.1	002351	A18	184	65p139	Aeromonas virus 65	GCA_000893255.1
AIT14276.1	002352	Cluster1905_1clades	178	PBI_121Q_386	Escherichia phage 121Q	GCA_000926855.1
QAY00662.1	002352	Cluster1905_1clades	177	Ecwhy1_387	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34858.1	002352	Cluster1905_1clades	178	ACQ29_gp178	Escherichia phage PBECO4	GCA_001041035.1
BBM61950.1	002352	Cluster1905_1clades	178	EO157G_3610	Escherichia phage SP27	GCA_008033345.1
AXC36967.1	002352	Cluster1905_1clades	178	-	Escherichia phage UB	GCA_003341455.1
QBO62028.1	002352	Cluster1905_1clades	178	G17_00539	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14049.1	002352	Cluster1905_1clades	184	vBEcoMphAPEC6_gp426c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80263.1	002352	Cluster1905_1clades	178	PSLUR01_00286	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70283.1	002353	Cluster1906_1clades	183	CF8_0115	Aeromonas phage CF8	GCA_006384595.2
QDJ97260.1	002353	Cluster1906_1clades	184	D6_0100	Aeromonas phage D6	GCA_007051205.2
QDH47153.1	002353	Cluster1906_1clades	184	LAh10_32	Aeromonas phage LAh10	GCA_006863975.1
QDJ96874.1	002353	Cluster1906_1clades	183	PS1_0115	Aeromonas phage PS1	GCA_007051165.2
QFR59506.1	002353	Cluster1906_1clades	183	PS2_0115	Aeromonas phage PS2	GCA_009388305.2
QBZ70642.1	002353	Cluster1906_1clades	182	pETSU_061	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71959.1	002353	Cluster1906_1clades	183	N1M2_96	Klebsiella phage N1M2	GCA_010092605.1
AEV89560.1	002353	Cluster1906_1clades	183	OBP_123	Pseudomonas phage OBP	GCA_000896635.1
AIT14291.1	002354	Cluster1907_1clades	183	PBI_121Q_401	Escherichia phage 121Q	GCA_000926855.1
QAY00647.1	002354	Cluster1907_1clades	183	Ecwhy1_372	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34843.1	002354	Cluster1907_1clades	183	ACQ29_gp163	Escherichia phage PBECO4	GCA_001041035.1
BBM61965.1	002354	Cluster1907_1clades	183	EO157G_3760	Escherichia phage SP27	GCA_008033345.1
AXC36952.1	002354	Cluster1907_1clades	183	-	Escherichia phage UB	GCA_003341455.1
QBO62013.1	002354	Cluster1907_1clades	183	G17_00524	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14034.1	002354	Cluster1907_1clades	183	vBEcoMphAPEC6_gp411c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80278.1	002354	Cluster1907_1clades	183	PSLUR01_00301	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70448.1	002355	Cluster1908_1clades	154	CF8_0036	Aeromonas phage CF8	GCA_006384595.2
QNH80837.1	002355	Cluster1908_1clades	160	D6_0028	Aeromonas phage D6	GCA_007051205.2
QDH47157.1	002355	Cluster1908_1clades	182	LAh10_196	Aeromonas phage LAh10	GCA_006863975.1
QDJ96793.1	002355	Cluster1908_1clades	154	PS1_0034	Aeromonas phage PS1	GCA_007051165.2
QFR59424.1	002355	Cluster1908_1clades	154	PS2_0033	Aeromonas phage PS2	GCA_009388305.2
QBZ70851.1	002355	Cluster1908_1clades	153	pETSU_270	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71883.1	002355	Cluster1908_1clades	151	N1M2_20	Klebsiella phage N1M2	GCA_010092605.1
AEV89477.1	002355	Cluster1908_1clades	151	OBP_040	Pseudomonas phage OBP	GCA_000896635.1
ANM45081.1	002356	Cluster1909_1clades	100	KTN4_323	Pseudomonas phage KTN4	GCA_002607225.1
QBX32514.1	002356	Cluster1909_1clades	113	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77045.1	002356	Cluster1909_1clades	181	PHABIO_414	Pseudomonas phage Phabio	GCA_002624965.1
AEH03771.1	002356	Cluster1909_1clades	116	348	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94634.1	002356	Cluster1909_1clades	100	SL2_057	Pseudomonas phage SL2	GCA_002956015.1
QJB22956.1	002356	Cluster1909_1clades	100	fnug_313	Pseudomonas phage fnug	GCA_012837215.1
QEM42087.1	002356	Cluster1909_1clades	113	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83168.1	002356	Cluster1909_1clades	100	PHIKZ267	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14282.1	002357	Cluster1910_1clades	180	PBI_121Q_392	Escherichia phage 121Q	GCA_000926855.1
QAY00656.1	002357	Cluster1910_1clades	180	Ecwhy1_381	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34852.1	002357	Cluster1910_1clades	180	ACQ29_gp172	Escherichia phage PBECO4	GCA_001041035.1
BBM61956.1	002357	Cluster1910_1clades	180	EO157G_3670	Escherichia phage SP27	GCA_008033345.1
AXC36961.1	002357	Cluster1910_1clades	180	-	Escherichia phage UB	GCA_003341455.1
QBO62022.1	002357	Cluster1910_1clades	180	G17_00533	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14043.1	002357	Cluster1910_1clades	180	vBEcoMphAPEC6_gp420c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80269.1	002357	Cluster1910_1clades	180	PSLUR01_00292	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT13990.1	002358	Cluster1911_1clades	171	PBI_121Q_93	Escherichia phage 121Q	GCA_000926855.1
QAY00348.1	002358	Cluster1911_1clades	180	Ecwhy1_67	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35094.1	002358	Cluster1911_1clades	171	ACQ29_gp414	Escherichia phage PBECO4	GCA_001041035.1
BBM61681.1	002358	Cluster1911_1clades	171	EO157G_0920	Escherichia phage SP27	GCA_008033345.1
AXC36671.1	002358	Cluster1911_1clades	171	-	Escherichia phage UB	GCA_003341455.1
QBO61703.1	002358	Cluster1911_1clades	171	G17_00214	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13750.1	002358	Cluster1911_1clades	171	vBEcoMphAPEC6_gp121c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79994.1	002358	Cluster1911_1clades	171	PSLUR01_00010	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67082.1	002359	Cluster1912_1clades	175	AD1_038	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79828.1	002359	Cluster1912_1clades	150	JA11_023	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66427.1	002359	Cluster1912_1clades	150	JA13_024	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66749.1	002359	Cluster1912_1clades	150	JA29_023	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67397.1	002359	Cluster1912_1clades	150	JA33_023	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08315.1	002359	Cluster1912_1clades	179	Alexandra_35	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58680.1	002359	Cluster1912_1clades	176	Y3_040	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28520.1	002359	Cluster1912_1clades	177	YOLOSWAG_35	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14295.1	002360	Cluster1913_1clades	178	PBI_121Q_405	Escherichia phage 121Q	GCA_000926855.1
QAY00643.1	002360	Cluster1913_1clades	172	Ecwhy1_368	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34839.1	002360	Cluster1913_1clades	172	ACQ29_gp159	Escherichia phage PBECO4	GCA_001041035.1
BBM61969.1	002360	Cluster1913_1clades	172	EO157G_3800	Escherichia phage SP27	GCA_008033345.1
AXC36948.1	002360	Cluster1913_1clades	178	-	Escherichia phage UB	GCA_003341455.1
QBO62009.1	002360	Cluster1913_1clades	178	G17_00520	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14030.1	002360	Cluster1913_1clades	178	vBEcoMphAPEC6_gp407c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80282.1	002360	Cluster1913_1clades	178	PSLUR01_00305	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67248.1	002361	Cluster1914_1clades	178	AD1_204	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79996.1	002361	Cluster1914_1clades	159	JA11_191	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66594.1	002361	Cluster1914_1clades	159	JA13_191	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66919.1	002361	Cluster1914_1clades	159	JA29_193	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67565.1	002361	Cluster1914_1clades	159	JA33_191	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08478.1	002361	Cluster1914_1clades	178	Alexandra_214	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58848.1	002361	Cluster1914_1clades	177	Y3_208	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28678.1	002361	Cluster1914_1clades	155	YOLOSWAG_200	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QDB70273.1	002362	Cluster1915_1clades	176	CF8_0105	Aeromonas phage CF8	GCA_006384595.2
QDJ97251.1	002362	Cluster1915_1clades	178	D6_0091	Aeromonas phage D6	GCA_007051205.2
QDH47162.1	002362	Cluster1915_1clades	178	LAh10_23	Aeromonas phage LAh10	GCA_006863975.1
QDJ96864.1	002362	Cluster1915_1clades	177	PS1_0105	Aeromonas phage PS1	GCA_007051165.2
QFR59496.1	002362	Cluster1915_1clades	177	PS2_0105	Aeromonas phage PS2	GCA_009388305.2
QBZ70633.1	002362	Cluster1915_1clades	172	pETSU_052	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71950.1	002362	Cluster1915_1clades	170	N1M2_87	Klebsiella phage N1M2	GCA_010092605.1
AEV89551.1	002362	Cluster1915_1clades	171	OBP_114	Pseudomonas phage OBP	GCA_000896635.1
AIT13989.1	002363	Imm-SUKH	161	PBI_121Q_92	Escherichia phage 121Q	GCA_000926855.1
QAY00349.1	002363	Imm-SUKH	176	Ecwhy1_68	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35095.1	002363	Imm-SUKH	176	ACQ29_gp415	Escherichia phage PBECO4	GCA_001041035.1
BBM61680.1	002363	Imm-SUKH	161	EO157G_0910	Escherichia phage SP27	GCA_008033345.1
AXC36672.1	002363	Imm-SUKH	176	-	Escherichia phage UB	GCA_003341455.1
QBO61704.1	002363	Imm-SUKH	176	G17_00215	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13751.1	002363	Imm-SUKH	55	vBEcoMphAPEC6_gp122c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79993.1	002363	Imm-SUKH	176	PSLUR01_00009	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01599.1	002364	Cluster1917_1clades	175	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29047.1	002364	Cluster1917_1clades	170	AP1_0340	Aeromonas phage AP1	GCA_014183365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATI17312.1	002364	Cluster1917_1clades	170	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00282.1	002364	Cluster1917_1clades	170	HWB28_gp270	Aeromonas phage AS-zj	GCA_002627665.1
QAX97755.1	002364	Cluster1917_1clades	170	ASswx1_110	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01400.1	002364	Cluster1917_1clades	170	ASwh1_341	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39465.1	002364	Cluster1917_1clades	170	CC2_427	Aeromonas phage CC2	GCA_000903495.1
ADQ53223.1	002364	Cluster1917_1clades	175	65p215	Aeromonas virus 65	GCA_000893255.1
APU01406.1	002365	Cluster1918_1clades	174	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28896.1	002365	Cluster1918_1clades	171	AP1_0189	Aeromonas phage AP1	GCA_014183365.1
ATI17489.1	002365	Cluster1918_1clades	171	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00508.1	002365	Cluster1918_1clades	171	HWB28_gp044	Aeromonas phage AS-zj	GCA_002627665.1
QAX97929.1	002365	Cluster1918_1clades	171	ASswx1_286	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01219.1	002365	Cluster1918_1clades	172	ASwh1_154	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39395.1	002365	Cluster1918_1clades	171	CC2_244	Aeromonas phage CC2	GCA_000903495.1
AAR90924.1	002365	Cluster1918_1clades	174	65p014	Aeromonas virus 65	GCA_000893255.1
AIT14284.1	002366	Cluster1919_1clades	172	PBI_121Q_394	Escherichia phage 121Q	GCA_000926855.1
QAY00654.1	002366	Cluster1919_1clades	172	Ecwhy1_379	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34850.1	002366	Cluster1919_1clades	172	ACQ29_gp170	Escherichia phage PBECO4	GCA_001041035.1
BBM61958.1	002366	Cluster1919_1clades	172	EO157G_3690	Escherichia phage SP27	GCA_008033345.1
AXC36959.1	002366	Cluster1919_1clades	172	-	Escherichia phage UB	GCA_003341455.1
QBO62020.1	002366	Cluster1919_1clades	172	G17_00531	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14041.1	002366	Cluster1919_1clades	172	vBEcoMphAPEC6_gp418c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80271.1	002366	Cluster1919_1clades	172	PSLUR01_00294	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14071.1	002367	Cluster1920_1clades	172	PBI_121Q_181	Escherichia phage 121Q	GCA_000926855.1
QAY00852.1	002367	Cluster1920_1clades	171	Ecwhy1_580	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35022.1	002367	Cluster1920_1clades	172	ACQ29_gp342	Escherichia phage PBECO4	GCA_001041035.1
BBM61754.1	002367	Cluster1920_1clades	172	EO157G_1650	Escherichia phage SP27	GCA_008033345.1
AXC36599.1	002367	Cluster1920_1clades	172	-	Escherichia phage UB	GCA_003341455.1
QBO61628.1	002367	Cluster1920_1clades	172	G17_00132	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13684.1	002367	Cluster1920_1clades	172	vBEcoMphAPEC6_gp054c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80065.1	002367	Cluster1920_1clades	172	PSLUR01_00088	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67164.1	002368	Cluster1921_1clades	167	AD1_120	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79914.1	002368	Cluster1921_1clades	168	JA11_109	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66513.1	002368	Cluster1921_1clades	168	JA13_110	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66838.1	002368	Cluster1921_1clades	168	JA29_112	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67483.1	002368	Cluster1921_1clades	168	JA33_109	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08397.1	002368	Cluster1921_1clades	167	Alexandra_125	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58761.1	002368	Cluster1921_1clades	170	Y3_121	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28599.1	002368	Cluster1921_1clades	167	YOLOSWAG_117	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AMR59835.1	002369	Cluster1922_1clades	166	SEGD1_188	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96653.1	002369	Cluster1922_1clades	169	G173_gp108	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48218.1	002369	Cluster1922_1clades	167	ASESINO_205	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50630.1	002369	Cluster1922_1clades	169	STRATTON_205	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86025.1	002369	Cluster1922_1clades	166	ACEC001_1840	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20880.1	002369	Cluster1922_1clades	166	-	Salmonella phage JN03	GCA_014319805.1
AWN09154.1	002369	Cluster1922_1clades	166	MLDJOKPK_00256	Salmonella phage SPAsTU	GCA_003183805.1
AEP84017.1	002369	Cluster1922_1clades	166	SPN3US_0184	Salmonella phage SPN3US	GCA_001042275.1
AXG67141.1	002370	TM	169	AD1_097	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79890.1	002370	TM	163	JA11_085	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66489.1	002370	TM	163	JA13_086	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66814.1	002370	TM	163	JA29_088	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67459.1	002370	TM	163	JA33_085	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08377.1	002370	TM	168	Alexandra_102	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58740.1	002370	TM	168	Y3_100	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28573.1	002370	TM	161	YOLOSWAG_90	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14243.1	002371	Cluster1924_1clades	168	PBI_121Q_353	Escherichia phage 121Q	GCA_000926855.1
QAY00688.1	002371	Cluster1924_1clades	165	Ecwhy1_413	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34884.1	002371	Cluster1924_1clades	165	ACQ29_gp204	Escherichia phage PBECO4	GCA_001041035.1
BBM61921.1	002371	Cluster1924_1clades	168	EO157G_3320	Escherichia phage SP27	GCA_008033345.1
AXC36990.1	002371	Cluster1924_1clades	168	-	Escherichia phage UB	GCA_003341455.1
QBO62061.1	002371	Cluster1924_1clades	168	G17_00572	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14079.1	002371	Cluster1924_1clades	168	vBEcoMphAPEC6_gp456c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80233.1	002371	Cluster1924_1clades	168	PSLUR01_00256	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67220.1	002372	Cluster1925_1clades	164	AD1_176	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79970.1	002372	Cluster1925_1clades	166	JA11_165	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66568.1	002372	Cluster1925_1clades	166	JA13_165	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66893.1	002372	Cluster1925_1clades	166	JA29_167	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67539.1	002372	Cluster1925_1clades	166	JA33_165	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08604.1	002372	Cluster1925_1clades	165	Alexandra_181	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58817.1	002372	Cluster1925_1clades	165	Y3_177	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28651.1	002372	Cluster1925_1clades	166	YOLOSWAG_172	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67054.1	002373	Cluster1926_1clades	165	AD1_010	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79813.1	002373	Cluster1926_1clades	154	JA11_008	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66411.1	002373	Cluster1926_1clades	154	JA13_008	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66734.1	002373	Cluster1926_1clades	153	JA29_008	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67382.1	002373	Cluster1926_1clades	154	JA33_008	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08618.1	002373	Cluster1926_1clades	166	Alexandra_10	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58650.1	002373	Cluster1926_1clades	162	Y3_010	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28497.1	002373	Cluster1926_1clades	126	YOLOSWAG_10	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QIG66029.1	002374	SIG+TM	139	phiOC_p387	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47899.1	002374	SIG+TM	165	SmphiM12_267	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13106.1	002374	SIG+TM	147	PHIM19_201	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13107.1	002374	SIG+TM	165	PHIM19_202	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12746.1	002374	SIG+TM	147	PHIM7_201	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12747.1	002374	SIG+TM	165	PHIM7_202	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13476.1	002374	SIG+TM	147	PHIN3_213	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13477.1	002374	SIG+TM	165	PHIN3_214	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67131.1	002375	Cluster1928_1clades	165	AD1_087	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79886.1	002375	Cluster1928_1clades	165	JA11_081	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66485.1	002375	Cluster1928_1clades	165	JA13_082	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66810.1	002375	Cluster1928_1clades	165	JA29_084	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67455.1	002375	Cluster1928_1clades	165	JA33_081	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08367.1	002375	Cluster1928_1clades	165	Alexandra_91	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58730.1	002375	Cluster1928_1clades	165	Y3_090	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28562.1	002375	Cluster1928_1clades	164	YOLOSWAG_79	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFC21589.1	002376	Cluster1929_1clades	147	GAP32_139	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43708.1	002376	Cluster1929_1clades	148	CBB_143	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18847.1	002376	Cluster1929_1clades	165	7t3_0326	Salmonella phage 7t3	GCA_006083215.1
AZU98109.1	002376	Cluster1929_1clades	147	CPT_Munch_165	Salmonella phage Munch	GCA_004015485.1
QIG62873.1	002376	Cluster1929_1clades	147	SEPL_260	Salmonella phage SE_PL	GCA_011067555.1
AQW88663.1	002376	Cluster1929_1clades	148	BF_0138	Serratia phage BF	GCA_002619745.1
SOK58944.1	002376	Cluster1929_1clades	148	g136	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58410.1	002376	Cluster1929_1clades	148	g133	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000423	002377	Cluster1930_1clades	166	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000424	002377	Cluster1930_1clades	147	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000425	002377	Cluster1930_1clades	153	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000431	002377	Cluster1930_1clades	151	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000334	002377	Cluster1930_1clades	166	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000335	002377	Cluster1930_1clades	147	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000336	002377	Cluster1930_1clades	153	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000343	002377	Cluster1930_1clades	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AIT14281.1	002378	Cluster1931_1clades	163	PBI_121Q_391	Escherichia phage 121Q	GCA_000926855.1
QAY00657.1	002378	Cluster1931_1clades	160	Ecwhy1_382	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34853.1	002378	Cluster1931_1clades	160	ACQ29_gp173	Escherichia phage PBECO4	GCA_001041035.1
BBM61955.1	002378	Cluster1931_1clades	160	EO157G_3660	Escherichia phage SP27	GCA_008033345.1
AXC36962.1	002378	Cluster1931_1clades	160	-	Escherichia phage UB	GCA_003341455.1
QBO62023.1	002378	Cluster1931_1clades	163	G17_00534	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14044.1	002378	Cluster1931_1clades	163	vBEcoMphAPEC6_gp421c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80268.1	002378	Cluster1931_1clades	163	PSLUR01_00291	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70297.1	002379	Cluster1932_1clades	162	CF8_0129	Aeromonas phage CF8	GCA_006384595.2
QDJ97274.1	002379	Cluster1932_1clades	145	D6_0114	Aeromonas phage D6	GCA_007051205.2
QDH47189.1	002379	Cluster1932_1clades	145	LAh10_46	Aeromonas phage LAh10	GCA_006863975.1
QDJ96891.1	002379	Cluster1932_1clades	159	PS1_0132	Aeromonas phage PS1	GCA_007051165.2
QFR59521.1	002379	Cluster1932_1clades	159	PS2_0130	Aeromonas phage PS2	GCA_009388305.2
QBZ70660.1	002379	Cluster1932_1clades	150	pETSU_079	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71976.1	002379	Cluster1932_1clades	149	N1M2_113	Klebsiella phage N1M2	GCA_010092605.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEV89577.1	002379	Cluster1932_1clades	146	OBP_140	Pseudomonas phage OBP	GCA_000896635.1
QDB70456.1	002380	Cluster1933_1clades	162	CF8_0044	Aeromonas phage CF8	GCA_006384595.2
QDJ97197.1	002380	Cluster1933_1clades	162	D6_0037	Aeromonas phage D6	GCA_007051205.2
QDH47171.1	002380	Cluster1933_1clades	162	LAh10_203	Aeromonas phage LAh10	GCA_006863975.1
QDJ96798.1	002380	Cluster1933_1clades	159	PS1_0039	Aeromonas phage PS1	GCA_007051165.2
QFR59429.1	002380	Cluster1933_1clades	159	PS2_0038	Aeromonas phage PS2	GCA_009388305.2
QBZ70860.1	002380	Cluster1933_1clades	157	pETSU_279	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71891.1	002380	Cluster1933_1clades	158	N1M2_28	Klebsiella phage N1M2	GCA_010092605.1
AEV89486.1	002380	Cluster1933_1clades	155	OBP_049	Pseudomonas phage OBP	GCA_000896635.1
AIT14277.1	002381	Cluster1934_1clades	158	PBI_121Q_387	Escherichia phage 121Q	GCA_000926855.1
QAY00661.1	002381	Cluster1934_1clades	160	Ecwhy1_386	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34857.1	002381	Cluster1934_1clades	158	ACQ29_gp177	Escherichia phage PBECO4	GCA_001041035.1
BBM61951.1	002381	Cluster1934_1clades	158	EO157G_3620	Escherichia phage SP27	GCA_008033345.1
AXC36966.1	002381	Cluster1934_1clades	158	-	Escherichia phage UB	GCA_003341455.1
QBO62027.1	002381	Cluster1934_1clades	158	G17_00538	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14048.1	002381	Cluster1934_1clades	158	vBEcoMphAPEC6_gp425c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80264.1	002381	Cluster1934_1clades	158	PSLUR01_00287	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67359.1	002382	Cluster1935_1clades	153	AD1_315	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80111.1	002382	Cluster1935_1clades	158	JA11_306	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66712.1	002382	Cluster1935_1clades	158	JA13_309	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67030.1	002382	Cluster1935_1clades	158	JA29_304	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67681.1	002382	Cluster1935_1clades	158	JA33_307	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08583.1	002382	Cluster1935_1clades	153	Alexandra_332	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58958.1	002382	Cluster1935_1clades	159	Y3_318	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28785.1	002382	Cluster1935_1clades	155	YOLOSWAG_316	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67145.1	002383	Cluster1936_1clades	158	AD1_101	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79894.1	002383	Cluster1936_1clades	152	JA11_089	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66493.1	002383	Cluster1936_1clades	152	JA13_090	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66818.1	002383	Cluster1936_1clades	152	JA29_092	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67463.1	002383	Cluster1936_1clades	152	JA33_089	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08379.1	002383	Cluster1936_1clades	158	Alexandra_106	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58743.1	002383	Cluster1936_1clades	158	Y3_103	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28576.1	002383	Cluster1936_1clades	157	YOLOSWAG_94	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGB06895.1	002384	TM	157	CF80_gp108	Vibrio phage VH7D	GCA_000914495.1
QBX06251.1	002384	TM	137	ValB1HC_298	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04499.1	002384	TM	141	ValB1MD_146	Vibrio phage ValB1MD	GCA_004138815.1
AJT60877.1	002384	TM	157	AVU32_gp036	Vibrio phage ValKK3	GCA_001501635.1
AGN30270.1	002384	TM	135	VPFG_00271	Vibrio phage nt-1	GCA_000910195.2
ALP47118.1	002384	TM	157	phiGrn1_0333	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47519.1	002384	TM	147	phiST2_0088	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54878.1	002384	TM	137	vBValMR10Z_338	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AXG67181.1	002385	Cluster1938_1clades	140	AD1_137	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79931.1	002385	Cluster1938_1clades	157	JA11_126	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66530.1	002385	Cluster1938_1clades	157	JA13_127	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66855.1	002385	Cluster1938_1clades	157	JA29_129	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67500.1	002385	Cluster1938_1clades	157	JA33_126	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08414.1	002385	Cluster1938_1clades	133	Alexandra_142	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58778.1	002385	Cluster1938_1clades	137	Y3_138	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28616.1	002385	Cluster1938_1clades	132	YOLOSWAG_136	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67169.1	002386	Cluster1939_1clades	144	AD1_125	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79919.1	002386	Cluster1939_1clades	132	JA11_114	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66518.1	002386	Cluster1939_1clades	132	JA13_115	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66843.1	002386	Cluster1939_1clades	128	JA29_117	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67488.1	002386	Cluster1939_1clades	132	JA33_114	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08402.1	002386	Cluster1939_1clades	154	Alexandra_130	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58766.1	002386	Cluster1939_1clades	144	Y3_126	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28605.1	002386	Cluster1939_1clades	133	YOLOSWAG_124	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01605.1	002387	Cluster1940_1clades	152	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28857.1	002387	Cluster1940_1clades	153	AP1_0150	Aeromonas phage AP1	GCA_014183365.1
ATI17306.1	002387	Cluster1940_1clades	153	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00288.1	002387	Cluster1940_1clades	153	HWB28_gp264	Aeromonas phage AS-zj	GCA_002627665.1
QAX97749.1	002387	Cluster1940_1clades	153	ASswx1_104	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01406.1	002387	Cluster1940_1clades	153	ASwh1_347	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39310.1	002387	Cluster1940_1clades	153	CC2_005	Aeromonas phage CC2	GCA_000903495.1
ADQ53229.1	002387	Cluster1940_1clades	152	65p221	Aeromonas virus 65	GCA_000893255.1
APU01611.1	002388	Cluster1941_1clades	145	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28863.1	002388	Cluster1941_1clades	153	AP1_0156	Aeromonas phage AP1	GCA_014183365.1
ATI17300.1	002388	Cluster1941_1clades	153	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00294.1	002388	Cluster1941_1clades	153	HWB28_gp258	Aeromonas phage AS-zj	GCA_002627665.1
QAX97743.1	002388	Cluster1941_1clades	153	ASswx1_98	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01415.1	002388	Cluster1941_1clades	148	ASwh1_356	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39313.1	002388	Cluster1941_1clades	153	CC2_011	Aeromonas phage CC2	GCA_000903495.1
ADQ53235.1	002388	Cluster1941_1clades	145	65p227	Aeromonas virus 65	GCA_000893255.1
AXG67336.1	002389	Cluster1942_1clades	152	AD1_292	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80085.1	002389	Cluster1942_1clades	147	JA11_280	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66686.1	002389	Cluster1942_1clades	147	JA13_283	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67006.1	002389	Cluster1942_1clades	146	JA29_280	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67655.1	002389	Cluster1942_1clades	147	JA33_281	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08564.1	002389	Cluster1942_1clades	153	Alexandra_308	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58937.1	002389	Cluster1942_1clades	148	Y3_297	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28762.1	002389	Cluster1942_1clades	145	YOLOSWAG_292	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14048.1	002390	Cluster1943_1clades	151	PBI_121Q_158	Escherichia phage 121Q	GCA_000926855.1
QAY00295.1	002390	Cluster1943_1clades	152	Ecwhy1_13	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35045.1	002390	Cluster1943_1clades	146	ACQ29_gp365	Escherichia phage PBECO4	GCA_001041035.1
BBM61731.1	002390	Cluster1943_1clades	151	EO157G_1420	Escherichia phage SP27	GCA_008033345.1
AXC36622.1	002390	Cluster1943_1clades	151	-	Escherichia phage UB	GCA_003341455.1
QBO61651.1	002390	Cluster1943_1clades	151	G17_00155	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13704.1	002390	Cluster1943_1clades	151	vBEcoMphAPEC6_gp074c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80043.1	002390	Cluster1943_1clades	151	PSLUR01_00066	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMR59862.1	002391	Cluster1944_1clades	135	SEGD1_215	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96678.1	002391	Cluster1944_1clades	108	G173_gp133	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48244.1	002391	Cluster1944_1clades	109	ASESINO_231	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50658.1	002391	Cluster1944_1clades	108	STRATTON_233	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86051.1	002391	Cluster1944_1clades	135	ACEC001_2080	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20899.1	002391	Cluster1944_1clades	152	-	Salmonella phage JN03	GCA_014319805.1
AWN09136.1	002391	Cluster1944_1clades	138	MLDJOKPK_00229	Salmonella phage SPAsTU	GCA_003183805.1
AEP84044.1	002391	Cluster1944_1clades	135	SPN3US_0211	Salmonella phage SPN3US	GCA_001042275.1
AIT13991.1	002392	Cluster1945_1clades	151	PBI_121Q_94	Escherichia phage 121Q	GCA_000926855.1
QAY00347.1	002392	Cluster1945_1clades	151	Ecwhy1_66	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35093.1	002392	Cluster1945_1clades	151	ACQ29_gp413	Escherichia phage PBECO4	GCA_001041035.1
BBM61682.1	002392	Cluster1945_1clades	151	EO157G_0930	Escherichia phage SP27	GCA_008033345.1
AXC36670.1	002392	Cluster1945_1clades	151	-	Escherichia phage UB	GCA_003341455.1
QBO61702.1	002392	Cluster1945_1clades	151	G17_00213	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13749.1	002392	Cluster1945_1clades	151	vBEcoMphAPEC6_gp120c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79995.1	002392	Cluster1945_1clades	151	PSLUR01_00011	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT13985.1	002393	Cluster1946_1clades	146	PBI_121Q_88	Escherichia phage 121Q	GCA_000926855.1
QAY00353.1	002393	Cluster1946_1clades	151	Ecwhy1_72	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35099.1	002393	Cluster1946_1clades	146	ACQ29_gp419	Escherichia phage PBECO4	GCA_001041035.1
BBM61676.1	002393	Cluster1946_1clades	146	EO157G_0870	Escherichia phage SP27	GCA_008033345.1
AXC36676.1	002393	Cluster1946_1clades	113	-	Escherichia phage UB	GCA_003341455.1
QBO61708.1	002393	Cluster1946_1clades	146	G17_00219	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13756.1	002393	Cluster1946_1clades	146	vBEcoMphAPEC6_gp127c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79989.1	002393	Cluster1946_1clades	146	PSLUR01_00005	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01551.1	002394	SIG+TM+TM	149	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29009.1	002394	SIG+TM+TM	149	AP1_0302	Aeromonas phage AP1	GCA_014183365.1
ATI17350.1	002394	SIG+TM+TM	149	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00243.1	002394	SIG+TM+TM	149	HWB28_gp309	Aeromonas phage AS-zj	GCA_002627665.1
QAX97795.1	002394	SIG+TM+TM	149	ASswx1_150	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01360.1	002394	SIG+TM+TM	149	ASwh1_300	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39446.1	002394	SIG+TM+TM	149	CC2_387	Aeromonas phage CC2	GCA_000903495.1
ADQ53173.1	002394	SIG+TM+TM	149	65p165	Aeromonas virus 65	GCA_000893255.1
AWY08477.1	002395	Cluster1948_2clades	148	Alexandra_213	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXG67247.1	002395	Cluster1948_2clades	149	AD1_203	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79994.1	002395	Cluster1948_2clades	144	JA11_189	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66592.1	002395	Cluster1948_2clades	144	JA13_189	Dickeya phage vB_DsoM_JA13	GCA_003568455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG66917.1	002395	Cluster1948_2clades	144	JA29_191	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67563.1	002395	Cluster1948_2clades	144	JA33_189	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ARW58845.1	002395	Cluster1948_2clades	145	Y3_205	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28677.1	002395	Cluster1948_2clades	146	YOLOSWAG_198	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01585.1	002396	Cluster1949_1clades	140	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29042.1	002396	Cluster1949_1clades	148	AP1_0335	Aeromonas phage AP1	GCA_014183365.1
ATI17318.1	002396	Cluster1949_1clades	148	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00276.1	002396	Cluster1949_1clades	148	HWB28_gp276	Aeromonas phage AS-zj	GCA_002627665.1
QAX97761.1	002396	Cluster1949_1clades	148	ASswx1_116	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01387.1	002396	Cluster1949_1clades	142	ASwh1_327	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39295.1	002396	Cluster1949_1clades	148	CC2_421	Aeromonas phage CC2	GCA_000903495.1
ADQ53208.1	002396	Cluster1949_1clades	140	65p200	Aeromonas virus 65	GCA_000893255.1
APU01668.1	002397	Cluster1950_1clades	96	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29025.1	002397	Cluster1950_1clades	96	AP1_0318	Aeromonas phage AP1	GCA_014183365.1
ATI17626.1	002397	Cluster1950_1clades	96	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00369.1	002397	Cluster1950_1clades	96	HWB28_gp183	Aeromonas phage AS-zj	GCA_002627665.1
QAX97661.1	002397	Cluster1950_1clades	96	ASswx1_15	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01079.1	002397	Cluster1950_1clades	88	ASwh1_11	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39470.1	002397	Cluster1950_1clades	96	CC2_100	Aeromonas phage CC2	GCA_000903495.1
ADQ53299.1	002397	Cluster1950_1clades	147	65p291	Aeromonas virus 65	GCA_000893255.1
AIT13993.1	002398	Cluster1951_1clades	147	PBI_121Q_96	Escherichia phage 121Q	GCA_000926855.1
QAY00345.1	002398	Cluster1951_1clades	147	Ecwhy1_64	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35091.1	002398	Cluster1951_1clades	147	ACQ29_gp411	Escherichia phage PBECO4	GCA_001041035.1
BBM61684.1	002398	Cluster1951_1clades	147	EO157G_0950	Escherichia phage SP27	GCA_008033345.1
AXC36668.1	002398	Cluster1951_1clades	147	-	Escherichia phage UB	GCA_003341455.1
QBO61700.1	002398	Cluster1951_1clades	147	G17_00211	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA79997.1	002398	Cluster1951_1clades	147	PSLUR01_00013	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44471.1	002398	Cluster1951_1clades	144	RaK2_00198	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ANM45124.1	002399	Cluster1952_1clades	137	KTN4_366	Pseudomonas phage KTN4	GCA_002607225.1
QBX32545.1	002399	Cluster1952_1clades	137	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76977.1	002399	Cluster1952_1clades	129	PHABIO_346	Pseudomonas phage Phabio	GCA_002624965.1
AEH03799.1	002399	Cluster1952_1clades	146	376	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94587.1	002399	Cluster1952_1clades	137	SL2_010	Pseudomonas phage SL2	GCA_002956015.1
QJB23001.1	002399	Cluster1952_1clades	137	fnug_358	Pseudomonas phage fnug	GCA_012837215.1
QEM42116.1	002399	Cluster1952_1clades	137	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83205.1	002399	Cluster1952_1clades	137	PHIKZ304	Pseudomonas virus phiKZ	GCA_000842965.1
AFC21794.1	002400	Cluster1953_1clades	136	GAP32_344	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43914.1	002400	Cluster1953_1clades	146	CBB_351	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19074.1	002400	Cluster1953_1clades	74	7t3_0554	Salmonella phage 7t3	GCA_006083215.1
AZU98317.1	002400	Cluster1953_1clades	74	CPT_Munch_373	Salmonella phage Munch	GCA_004015485.1
QIG62667.1	002400	Cluster1953_1clades	74	SEPL_054	Salmonella phage SE_PL	GCA_011067555.1
AQW88875.1	002400	Cluster1953_1clades	115	BF_0350	Serratia phage BF	GCA_002619745.1
SOK59160.1	002400	Cluster1953_1clades	97	g352	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58628.1	002400	Cluster1953_1clades	97	g351	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMR59771.1	002401	Cluster1954_1clades	131	SEGD1_124	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96589.1	002401	Cluster1954_1clades	144	G173_gp044	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48150.1	002401	Cluster1954_1clades	146	ASESINO_137	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50566.1	002401	Cluster1954_1clades	144	STRATTON_141	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85961.1	002401	Cluster1954_1clades	131	ACEC001_1230	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20825.1	002401	Cluster1954_1clades	127	-	Salmonella phage JN03	GCA_014319805.1
AXF51063.1	002401	Cluster1954_1clades	133	MLDJOKPK_00033	Salmonella phage SPAsTU	GCA_003183805.1
AEP83954.1	002401	Cluster1954_1clades	127	SPN3US_0121	Salmonella phage SPN3US	GCA_001042275.1
AXG67160.1	002402	Cluster1955_1clades	136	AD1_116	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79910.1	002402	Cluster1955_1clades	146	JA11_105	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66509.1	002402	Cluster1955_1clades	146	JA13_106	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66834.1	002402	Cluster1955_1clades	146	JA29_108	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67479.1	002402	Cluster1955_1clades	146	JA33_105	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08393.1	002402	Cluster1955_1clades	144	Alexandra_121	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58757.1	002402	Cluster1955_1clades	144	Y3_117	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28595.1	002402	Cluster1955_1clades	144	YOLOSWAG_113	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01734.1	002403	Cluster1956_1clades	144	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28734.1	002403	Cluster1956_1clades	145	AP1_0016	Aeromonas phage AP1	GCA_014183365.1
ATI17564.1	002403	Cluster1956_1clades	141	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00432.1	002403	Cluster1956_1clades	141	HWB28_gp120	Aeromonas phage AS-zj	GCA_002627665.1
QAX98004.1	002403	Cluster1956_1clades	145	ASswx1_364	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01410.1	002403	Cluster1956_1clades	146	ASwh1_351	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39366.1	002403	Cluster1956_1clades	141	CC2_170	Aeromonas phage CC2	GCA_000903495.1
ADQ53376.1	002403	Cluster1956_1clades	144	65p368	Aeromonas virus 65	GCA_000893255.1
AIT14427.1	002404	Cluster1957_1clades	140	PBI_121Q_537	Escherichia phage 121Q	GCA_000926855.1
QAY00521.1	002404	Cluster1957_1clades	145	Ecwhy1_242	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34715.1	002404	Cluster1957_1clades	140	ACQ29_gp035	Escherichia phage PBECO4	GCA_001041035.1
BBM62099.1	002404	Cluster1957_1clades	140	EO157G_5100	Escherichia phage SP27	GCA_008033345.1
AXC36834.1	002404	Cluster1957_1clades	58	-	Escherichia phage UB	GCA_003341455.1
QBO61874.1	002404	Cluster1957_1clades	140	G17_00385	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13914.1	002404	Cluster1957_1clades	140	vBEcoMphAPEC6_gp289c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80413.1	002404	Cluster1957_1clades	140	PSLUR01_00436	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01674.1	002405	Cluster1958_1clades	100	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01082.1	002405	Cluster1958_1clades	100	ASwh1_14	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53308.1	002405	Cluster1958_1clades	54	65p300	Aeromonas virus 65	GCA_000893255.1
AFC21617.1	002405	Cluster1958_1clades	144	GAP32_167	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43735.1	002405	Cluster1958_1clades	143	CBB_170	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88693.1	002405	Cluster1958_1clades	131	BF_0168	Serratia phage BF	GCA_002619745.1
SOK58974.1	002405	Cluster1958_1clades	134	g166	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58440.1	002405	Cluster1958_1clades	134	g163	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67213.1	002406	Cluster1959_1clades	144	AD1_169	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79963.1	002406	Cluster1959_1clades	142	JA11_158	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66561.1	002406	Cluster1959_1clades	142	JA13_158	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66886.1	002406	Cluster1959_1clades	142	JA29_160	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67532.1	002406	Cluster1959_1clades	142	JA33_158	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08603.1	002406	Cluster1959_1clades	144	Alexandra_174	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58810.1	002406	Cluster1959_1clades	144	Y3_170	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28805.1	002406	Cluster1959_1clades	144	YOLOSWAG_165	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01739.1	002407	Cluster1960_1clades	142	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28729.1	002407	Cluster1960_1clades	136	AP1_0011	Aeromonas phage AP1	GCA_014183365.1
ATI17559.1	002407	Cluster1960_1clades	136	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00438.1	002407	Cluster1960_1clades	136	HWB28_gp114	Aeromonas phage AS-zj	GCA_002627665.1
QAX97999.1	002407	Cluster1960_1clades	136	ASswx1_359	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01141.1	002407	Cluster1960_1clades	138	ASwh1_75	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39370.1	002407	Cluster1960_1clades	136	CC2_176	Aeromonas phage CC2	GCA_000903495.1
ADQ53382.1	002407	Cluster1960_1clades	142	65p374	Aeromonas virus 65	GCA_000893255.1
AIT14288.1	002408	Alpha_E1_glycop	142	PBI_121Q_398	Escherichia phage 121Q	GCA_000926855.1
QAY00650.1	002408	Alpha_E1_glycop	142	Ecwhy1_375	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34846.1	002408	Alpha_E1_glycop	142	ACQ29_gp166	Escherichia phage PBECO4	GCA_001041035.1
BBM61962.1	002408	Alpha_E1_glycop	142	EO157G_3730	Escherichia phage SP27	GCA_008033345.1
AXC36955.1	002408	Alpha_E1_glycop	98	-	Escherichia phage UB	GCA_003341455.1
QBO62016.1	002408	Alpha_E1_glycop	142	G17_00527	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14037.1	002408	Alpha_E1_glycop	142	vBEcoMphAPEC6_gp414c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80275.1	002408	Alpha_E1_glycop	142	PSLUR01_00298	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14036.1	002409	Cluster1962_1clades	142	PBI_121Q_146	Escherichia phage 121Q	GCA_000926855.1
QAY00306.1	002409	Cluster1962_1clades	138	Ecwhy1_24	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35056.1	002409	Cluster1962_1clades	142	ACQ29_gp376	Escherichia phage PBECO4	GCA_001041035.1
BBM61719.1	002409	Cluster1962_1clades	139	EO157G_1300	Escherichia phage SP27	GCA_008033345.1
AXC36632.1	002409	Cluster1962_1clades	139	-	Escherichia phage UB	GCA_003341455.1
QBO61663.1	002409	Cluster1962_1clades	139	G17_00167	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13714.1	002409	Cluster1962_1clades	139	vBEcoMphAPEC6_gp084c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80031.1	002409	Cluster1962_1clades	139	PSLUR01_00054	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70371.1	002410	DUF3523	140	CF8_0203	Aeromonas phage CF8	GCA_006384595.2
QDJ96845.1	002410	DUF3523	142	PS1_0086	Aeromonas phage PS1	GCA_007051165.2
QDJ96713.1	002410	DUF3523	141	PS1_0202	Aeromonas phage PS1	GCA_007051165.2
QFR59475.1	002410	DUF3523	142	PS2_0084	Aeromonas phage PS2	GCA_009388305.2
QFR59346.1	002410	DUF3523	141	PS2_0204	Aeromonas phage PS2	GCA_009388305.2
QBZ70753.1	002410	DUF3523	109	pETSU_172	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72060.1	002410	DUF3523	115	N1M2_197	Klebsiella phage N1M2	GCA_010092605.1
AEV89687.1	002410	DUF3523	132	OBP_250	Pseudomonas phage OBP	GCA_000896635.1
ANM45059.1	002411	SIG+HSORC6	119	KTN4_301	Pseudomonas phage KTN4	GCA_002607225.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX32457.1	002411	SIG+HSORC6	118	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76993.1	002411	SIG+HSORC6	116	PHABIO_362	Pseudomonas phage Phabio	GCA_002624965.1
AEH03726.1	002411	SIG+HSORC6	116	303	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94656.1	002411	SIG+HSORC6	119	SL2_079	Pseudomonas phage SL2	GCA_002956015.1
QJB22934.1	002411	SIG+HSORC6	119	fnug_291	Pseudomonas phage fnug	GCA_012837215.1
QEM42029.1	002411	SIG+HSORC6	142	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83149.1	002411	SIG+HSORC6	119	PHIKZ248	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14052.1	002412	SIG+TM+TM	141	PBI_121Q_162	Escherichia phage 121Q	GCA_000926855.1
QAY00291.1	002412	SIG+TM+TM	141	Ecwhy1_9	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35041.1	002412	SIG+TM+TM	141	ACQ29_gp361	Escherichia phage PBECO4	GCA_001041035.1
BBM61735.1	002412	SIG+TM+TM	141	EO157G_1460	Escherichia phage SP27	GCA_008033345.1
AXC36618.1	002412	SIG+TM+TM	106	-	Escherichia phage UB	GCA_003341455.1
QBO61647.1	002412	SIG+TM+TM	141	G17_00151	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13701.1	002412	SIG+TM+TM	141	vBEcoMphAPEC6_gp071c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80047.1	002412	SIG+TM+TM	141	PSLUR01_00070	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67187.1	002413	Cluster1966_1clades	136	AD1_143	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79937.1	002413	Cluster1966_1clades	140	JA11_132	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66536.1	002413	Cluster1966_1clades	140	JA13_133	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66861.1	002413	Cluster1966_1clades	140	JA29_135	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67506.1	002413	Cluster1966_1clades	140	JA33_132	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08420.1	002413	Cluster1966_1clades	140	Alexandra_148	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58784.1	002413	Cluster1966_1clades	138	Y3_144	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28622.1	002413	Cluster1966_1clades	139	YOLOSWAG_142	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14094.1	002414	Cluster1967_1clades	139	PBI_121Q_204	Escherichia phage 121Q	GCA_000926855.1
QAY00827.1	002414	Cluster1967_1clades	137	Ecwhy1_554	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35000.1	002414	Cluster1967_1clades	78	ACQ29_gp320	Escherichia phage PBECO4	GCA_001041035.1
BBM61776.1	002414	Cluster1967_1clades	139	EO157G_1870	Escherichia phage SP27	GCA_008033345.1
AXC36579.1	002414	Cluster1967_1clades	139	-	Escherichia phage UB	GCA_003341455.1
QBO61605.1	002414	Cluster1967_1clades	139	G17_00109	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13663.1	002414	Cluster1967_1clades	139	vBEcoMphAPEC6_gp032c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80088.1	002414	Cluster1967_1clades	139	PSLUR01_00111	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14417.1	002415	Cluster1968_1clades	129	PBI_121Q_527	Escherichia phage 121Q	GCA_000926855.1
QAY00533.1	002415	Cluster1968_1clades	129	Ecwhy1_254	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34725.1	002415	Cluster1968_1clades	129	ACQ29_gp045	Escherichia phage PBECO4	GCA_001041035.1
BBM62089.1	002415	Cluster1968_1clades	129	EO157G_5000	Escherichia phage SP27	GCA_008033345.1
QBO61884.1	002415	Cluster1968_1clades	129	G17_00395	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13922.1	002415	Cluster1968_1clades	129	vBEcoMphAPEC6_gp297c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80403.1	002415	Cluster1968_1clades	129	PSLUR01_00426	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44297.1	002415	Cluster1968_1clades	138	RaK2_00024	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AUE22690.1	002416	Cluster1969_1clades	137	Ah1_00149	Aeromonas phage Ah1	GCA_002957415.1
QAX98414.1	002416	Cluster1969_1clades	137	ASfcp2_70	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98415.1	002416	Cluster1969_1clades	128	ASfcp2_71	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52869.1	002416	Cluster1969_1clades	137	PX29p150	Aeromonas phage PX29	GCA_000920195.1
ADQ52870.1	002416	Cluster1969_1clades	128	PX29p151	Aeromonas phage PX29	GCA_000920195.1
ADM80132.1	002416	Cluster1969_1clades	133	phiAS5_ORF0289	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17817.1	002416	Cluster1969_1clades	137	Aeh1ORF152c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17818.1	002416	Cluster1969_1clades	128	Aeh1ORF153c	Aeromonas virus Aeh1	GCA_000843245.1
AIT14280.1	002417	Cluster1970_1clades	137	PBI_121Q_390	Escherichia phage 121Q	GCA_000926855.1
QAY00658.1	002417	Cluster1970_1clades	137	Ecwhy1_383	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34854.1	002417	Cluster1970_1clades	134	ACQ29_gp174	Escherichia phage PBECO4	GCA_001041035.1
BBM61954.1	002417	Cluster1970_1clades	137	EO157G_3650	Escherichia phage SP27	GCA_008033345.1
AXC36963.1	002417	Cluster1970_1clades	137	-	Escherichia phage UB	GCA_003341455.1
QBO62024.1	002417	Cluster1970_1clades	137	G17_00535	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14045.1	002417	Cluster1970_1clades	137	vBEcoMphAPEC6_gp422c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80267.1	002417	Cluster1970_1clades	137	PSLUR01_00290	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14297.1	002418	Cluster1971_1clades	95	PBI_121Q_407	Escherichia phage 121Q	GCA_000926855.1
QAY00641.1	002418	Cluster1971_1clades	137	Ecwhy1_366	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34837.1	002418	Cluster1971_1clades	95	ACQ29_gp157	Escherichia phage PBECO4	GCA_001041035.1
BBM61971.1	002418	Cluster1971_1clades	137	EO157G_3820	Escherichia phage SP27	GCA_008033345.1
AXC36946.1	002418	Cluster1971_1clades	95	-	Escherichia phage UB	GCA_003341455.1
QBO62007.1	002418	Cluster1971_1clades	137	G17_00518	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14028.1	002418	Cluster1971_1clades	95	vBEcoMphAPEC6_gp405c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80284.1	002418	Cluster1971_1clades	137	PSLUR01_00307	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70253.1	002419	Cluster1972_1clades	117	CF8_0085	Aeromonas phage CF8	GCA_006384595.2
QNH80842.1	002419	Cluster1972_1clades	69	D6_0072	Aeromonas phage D6	GCA_007051205.2
QDH47231.1	002419	Cluster1972_1clades	106	LAh10_5	Aeromonas phage LAh10	GCA_006863975.1
QDJ96842.1	002419	Cluster1972_1clades	119	PS1_0083	Aeromonas phage PS1	GCA_007051165.2
QFR59472.1	002419	Cluster1972_1clades	119	PS2_0081	Aeromonas phage PS2	GCA_009388305.2
QBZ70615.1	002419	Cluster1972_1clades	109	pETSU_034	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71931.1	002419	Cluster1972_1clades	110	N1M2_68	Klebsiella phage N1M2	GCA_010092605.1
AEV89531.1	002419	Cluster1972_1clades	136	OBP_094	Pseudomonas phage OBP	GCA_000896635.1
AIT14384.1	002420	Cluster1973_1clades	136	PBI_121Q_494	Escherichia phage 121Q	GCA_000926855.1
QAY00564.1	002420	Cluster1973_1clades	136	Ecwhy1_285	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34758.1	002420	Cluster1973_1clades	136	ACQ29_gp078	Escherichia phage PBECO4	GCA_001041035.1
BBM62055.1	002420	Cluster1973_1clades	136	EO157G_4660	Escherichia phage SP27	GCA_008033345.1
AXC36873.1	002420	Cluster1973_1clades	136	-	Escherichia phage UB	GCA_003341455.1
QBO61919.1	002420	Cluster1973_1clades	136	G17_00430	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13952.1	002420	Cluster1973_1clades	136	vBEcoMphAPEC6_gp328c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80372.1	002420	Cluster1973_1clades	136	PSLUR01_00395	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14353.1	002421	Cluster1974_1clades	134	PBI_121Q_463	Escherichia phage 121Q	GCA_000926855.1
QAY00591.1	002421	Cluster1974_1clades	127	Ecwhy1_314	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34786.1	002421	Cluster1974_1clades	134	ACQ29_gp106	Escherichia phage PBECO4	GCA_001041035.1
BBM62024.1	002421	Cluster1974_1clades	134	EO157G_4350	Escherichia phage SP27	GCA_008033345.1
AXC36902.1	002421	Cluster1974_1clades	134	-	Escherichia phage UB	GCA_003341455.1
QBO61951.1	002421	Cluster1974_1clades	134	G17_00462	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13978.1	002421	Cluster1974_1clades	134	vBEcoMphAPEC6_gp354c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80340.1	002421	Cluster1974_1clades	134	PSLUR01_00363	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14010.1	002422	Cluster1975_1clades	134	PBI_121Q_113	Escherichia phage 121Q	GCA_000926855.1
QAY00328.1	002422	Cluster1975_1clades	134	Ecwhy1_47	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35074.1	002422	Cluster1975_1clades	134	ACQ29_gp394	Escherichia phage PBECO4	GCA_001041035.1
BBM61701.1	002422	Cluster1975_1clades	134	EO157G_1120	Escherichia phage SP27	GCA_008033345.1
AXC36651.1	002422	Cluster1975_1clades	134	-	Escherichia phage UB	GCA_003341455.1
QBO61683.1	002422	Cluster1975_1clades	134	G17_00194	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13732.1	002422	Cluster1975_1clades	134	vBEcoMphAPEC6_gp102c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80014.1	002422	Cluster1975_1clades	134	PSLUR01_00030	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67102.1	002423	ASCH	132	AD1_058	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79859.1	002423	ASCH	133	JA11_054	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66458.1	002423	ASCH	133	JA13_055	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66781.1	002423	ASCH	133	JA29_055	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67428.1	002423	ASCH	133	JA33_054	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08338.1	002423	ASCH	134	Alexandra_58	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58700.1	002423	ASCH	133	Y3_060	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28536.1	002423	ASCH	133	YOLOSWAG_52	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67358.1	002424	Cluster1977_1clades	126	AD1_314	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80110.1	002424	Cluster1977_1clades	120	JA11_305	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66711.1	002424	Cluster1977_1clades	120	JA13_308	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67029.1	002424	Cluster1977_1clades	124	JA29_303	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67680.1	002424	Cluster1977_1clades	120	JA33_306	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08582.1	002424	Cluster1977_1clades	127	Alexandra_331	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58957.1	002424	Cluster1977_1clades	109	Y3_317	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28784.1	002424	Cluster1977_1clades	133	YOLOSWAG_315	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ANM44910.1	002425	Cluster1978_1clades	122	KTN4_152	Pseudomonas phage KTN4	GCA_002607225.1
QBX32294.1	002425	Cluster1978_1clades	133	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03554.1	002425	Cluster1978_1clades	127	130	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02694.1	002425	Cluster1978_1clades	129	PSA21_167	Pseudomonas phage Psa21	GCA_004340405.1
ATN94804.1	002425	Cluster1978_1clades	122	SL2_227	Pseudomonas phage SL2	GCA_002956015.1
QJB22788.1	002425	Cluster1978_1clades	122	fnug_145	Pseudomonas phage fnug	GCA_012837215.1
QEM41868.1	002425	Cluster1978_1clades	133	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26334.1	002425	Cluster1978_1clades	122	PHIKZ117.4	Pseudomonas virus phiKZ	GCA_000842965.1
APU01517.1	002426	Cluster1979_1clades	131	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28777.1	002426	Cluster1979_1clades	132	AP1_0069	Aeromonas phage AP1	GCA_014183365.1
ATI17380.1	002426	Cluster1979_1clades	132	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00213.1	002426	Cluster1979_1clades	117	HWB28_gp339	Aeromonas phage AS-zj	GCA_002627665.1
QAX97822.1	002426	Cluster1979_1clades	132	ASswx1_178	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01328.1	002426	Cluster1979_1clades	130	ASwh1_266	Aeromonas phage Aswh_1	GCA_004146945.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN39429.1	002426	Cluster1979_1clades	131	CC2_358	Aeromonas phage CC2	GCA_000903495.1
ADQ53140.1	002426	Cluster1979_1clades	131	65p132	Aeromonas virus 65	GCA_000893255.1
AIT14424.1	002427	Cluster1980_1clades	126	PBI_121Q_534	Escherichia phage 121Q	GCA_000926855.1
QAY00526.1	002427	Cluster1980_1clades	126	Ecwhy1_247	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34718.1	002427	Cluster1980_1clades	126	ACQ29_gp038	Escherichia phage PBECO4	GCA_001041035.1
BBM62096.1	002427	Cluster1980_1clades	131	EO157G_5070	Escherichia phage SP27	GCA_008033345.1
AXC36836.1	002427	Cluster1980_1clades	131	-	Escherichia phage UB	GCA_003341455.1
QBO61877.1	002427	Cluster1980_1clades	131	G17_00388	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13916.1	002427	Cluster1980_1clades	131	vBEcoMphAPEC6_gp291c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80410.1	002427	Cluster1980_1clades	131	PSLUR01_00433	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70452.1	002428	Cluster1981_1clades	126	CF8_0040	Aeromonas phage CF8	GCA_006384595.2
QDJ97193.1	002428	Cluster1981_1clades	131	D6_0033	Aeromonas phage D6	GCA_007051205.2
QDH47201.1	002428	Cluster1981_1clades	131	LAh10_200	Aeromonas phage LAh10	GCA_006863975.1
QDJ96795.1	002428	Cluster1981_1clades	123	PS1_0036	Aeromonas phage PS1	GCA_007051165.2
QFR59426.1	002428	Cluster1981_1clades	123	PS2_0035	Aeromonas phage PS2	GCA_009388305.2
QBZ70856.1	002428	Cluster1981_1clades	125	pETSU_275	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71888.1	002428	Cluster1981_1clades	124	N1M2_25	Klebsiella phage N1M2	GCA_010092605.1
AEV89482.1	002428	Cluster1981_1clades	128	OBP_045	Pseudomonas phage OBP	GCA_000896635.1
APU01753.1	002429	NACHT	128	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29058.1	002429	NACHT	130	AP1_0351	Aeromonas phage AP1	GCA_014183365.1
ATI17543.1	002429	NACHT	130	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00454.1	002429	NACHT	130	HWB28_gp098	Aeromonas phage AS-zj	GCA_002627665.1
QAX97984.1	002429	NACHT	130	ASswx1_343	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01156.1	002429	NACHT	124	ASwh1_90	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39374.1	002429	NACHT	130	CC2_192	Aeromonas phage CC2	GCA_000903495.1
ADQ53395.1	002429	NACHT	91	65p388	Aeromonas virus 65	GCA_000893255.1
AIT14007.1	002430	Cluster1983_1clades	130	PBI_121Q_110	Escherichia phage 121Q	GCA_000926855.1
QAY00331.1	002430	Cluster1983_1clades	130	Ecwhy1_50	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35077.1	002430	Cluster1983_1clades	130	ACQ29_gp397	Escherichia phage PBECO4	GCA_001041035.1
BBM61698.1	002430	Cluster1983_1clades	130	EO157G_1090	Escherichia phage SP27	GCA_008033345.1
AXC36654.1	002430	Cluster1983_1clades	130	-	Escherichia phage UB	GCA_003341455.1
QBO61686.1	002430	Cluster1983_1clades	130	G17_00197	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13735.1	002430	Cluster1983_1clades	130	vBEcoMphAPEC6_gp105c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80011.1	002430	Cluster1983_1clades	130	PSLUR01_00027	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIW90584.1	002431	Cluster1984_1clades	124	GCAPEGMB_00237	Vibrio phage V07	GCA_012361095.1
AGB06884.1	002431	Cluster1984_1clades	107	CF80_gp097	Vibrio phage VH7D	GCA_000914495.1
QBX06262.1	002431	Cluster1984_1clades	130	ValB1HC_309	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60888.1	002431	Cluster1984_1clades	130	AVU32_gp047	Vibrio phage ValKK3	GCA_001501635.1
AGN30257.1	002431	Cluster1984_1clades	127	VPFG_00258	Vibrio phage nt-1	GCA_000910195.2
ALP47186.1	002431	Cluster1984_1clades	107	phiGrn1_0322	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47575.1	002431	Cluster1984_1clades	107	phiST2_0078	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54889.1	002431	Cluster1984_1clades	130	vBValMR10Z_349	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AXG67334.1	002432	Cluster1985_1clades	100	AD1_290	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80083.1	002432	Cluster1985_1clades	98	JA11_278	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66684.1	002432	Cluster1985_1clades	98	JA13_281	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67004.1	002432	Cluster1985_1clades	98	JA29_278	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67653.1	002432	Cluster1985_1clades	98	JA33_279	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08562.1	002432	Cluster1985_1clades	100	Alexandra_306	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58935.1	002432	Cluster1985_1clades	100	Y3_295	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28811.1	002432	Cluster1985_1clades	130	YOLOSWAG_289	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67374.1	002433	Cluster1986_1clades	123	AD1_330	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80126.1	002433	Cluster1986_1clades	118	JA11_321	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66726.1	002433	Cluster1986_1clades	118	JA13_323	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67044.1	002433	Cluster1986_1clades	118	JA29_318	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67695.1	002433	Cluster1986_1clades	118	JA33_321	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08597.1	002433	Cluster1986_1clades	123	Alexandra_349	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58973.1	002433	Cluster1986_1clades	123	Y3_333	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28813.1	002433	Cluster1986_1clades	130	YOLOSWAG_333	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01669.1	002434	Cluster1987_1clades	110	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29027.1	002434	Cluster1987_1clades	110	AP1_0320	Aeromonas phage AP1	GCA_014183365.1
ATI17625.1	002434	Cluster1987_1clades	130	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00371.1	002434	Cluster1987_1clades	110	HWB28_gp181	Aeromonas phage AS-zj	GCA_002627665.1
QAX97659.1	002434	Cluster1987_1clades	130	ASswx1_13	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01081.1	002434	Cluster1987_1clades	109	ASwh1_13	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39343.1	002434	Cluster1987_1clades	110	CC2_101	Aeromonas phage CC2	GCA_000903495.1
ADQ53300.1	002434	Cluster1987_1clades	110	65p292	Aeromonas virus 65	GCA_000893255.1
ARB13673.1	002435	Cluster1988_1clades	114	Ccr10_gp144c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14018.1	002435	Cluster1988_1clades	114	Ccr2_gp143c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14706.1	002435	Cluster1988_1clades	114	Ccr29_gp150	Caulobacter phage Ccr29	GCA_002619485.1
ARB15061.1	002435	Cluster1988_1clades	114	Ccr32_gp143	Caulobacter phage Ccr32	GCA_002619505.1
ARB15395.1	002435	Cluster1988_1clades	114	Ccr34_gp153	Caulobacter phage Ccr34	GCA_002619525.1
ARB14361.1	002435	Cluster1988_1clades	114	Ccr5_gp142c	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68343.1	002435	Cluster1988_1clades	129	CcrBL10_gp139c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86627.1	002435	Cluster1988_1clades	129	CcrRogue_gp145	Caulobacter virus Rogue	GCA_000900555.1
APU01574.1	002436	Cluster1989_1clades	128	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28948.1	002436	Cluster1989_1clades	127	AP1_0241	Aeromonas phage AP1	GCA_014183365.1
ATI17333.1	002436	Cluster1989_1clades	127	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00261.1	002436	Cluster1989_1clades	127	HWB28_gp291	Aeromonas phage AS-zj	GCA_002627665.1
QAX97777.1	002436	Cluster1989_1clades	127	ASswx1_132	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01377.1	002436	Cluster1989_1clades	127	ASwh1_317	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39454.1	002436	Cluster1989_1clades	127	CC2_406	Aeromonas phage CC2	GCA_000903495.1
ADQ53198.1	002436	Cluster1989_1clades	128	65p190	Aeromonas virus 65	GCA_000893255.1
AXG67052.1	002437	Cluster1990_1clades	128	AD1_008	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79812.1	002437	Cluster1990_1clades	124	JA11_007	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66410.1	002437	Cluster1990_1clades	124	JA13_007	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66733.1	002437	Cluster1990_1clades	124	JA29_007	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67381.1	002437	Cluster1990_1clades	124	JA33_007	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08290.1	002437	Cluster1990_1clades	128	Alexandra_8	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58648.1	002437	Cluster1990_1clades	127	Y3_008	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28495.1	002437	Cluster1990_1clades	126	YOLOSWAG_8	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFC21825.1	002438	Cluster1991_1clades	108	GAP32_374	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43946.1	002438	Cluster1991_1clades	108	CBB_383	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QBX32170.1	002438	Cluster1991_1clades	115	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03461.1	002438	Cluster1991_1clades	108	034	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41750.1	002438	Cluster1991_1clades	115	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAS04998.1	002438	Cluster1991_1clades	114	AVU11_gp206	Ralstonia phage RSF1	GCA_001500875.1
QKE54524.1	002438	Cluster1991_1clades	128	ACSA002_2080	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AQW88905.1	002438	Cluster1991_1clades	112	BF_0380	Serratia phage BF	GCA_002619745.1
AXG67118.1	002439	TM+TM	102	AD1_074	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79875.1	002439	TM+TM	109	JA11_070	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66474.1	002439	TM+TM	109	JA13_071	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66799.1	002439	TM+TM	109	JA29_073	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67444.1	002439	TM+TM	109	JA33_070	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08354.1	002439	TM+TM	100	Alexandra_76	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58717.1	002439	TM+TM	101	Y3_077	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28551.1	002439	TM+TM	127	YOLOSWAG_68	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67207.1	002440	Cluster1993_1clades	123	AD1_163	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79958.1	002440	Cluster1993_1clades	127	JA11_153	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66557.1	002440	Cluster1993_1clades	127	JA13_154	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66882.1	002440	Cluster1993_1clades	127	JA29_156	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67527.1	002440	Cluster1993_1clades	127	JA33_153	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08438.1	002440	Cluster1993_1clades	122	Alexandra_168	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58803.1	002440	Cluster1993_1clades	123	Y3_163	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28641.1	002440	Cluster1993_1clades	123	YOLOSWAG_161	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14079.1	002441	SIG+TM+TM	125	PBI_121Q_189	Escherichia phage 121Q	GCA_000926855.1
QAY00844.1	002441	SIG+TM+TM	127	Ecwhy1_572	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35015.1	002441	SIG+TM+TM	125	ACQ29_gp335	Escherichia phage PBECO4	GCA_001041035.1
BBM61762.1	002441	SIG+TM+TM	125	EO157G_1730	Escherichia phage SP27	GCA_008033345.1
QBO61620.1	002441	SIG+TM+TM	125	G17_00124	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13678.1	002441	SIG+TM+TM	125	vBEcoMphAPEC6_gp048c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80073.1	002441	SIG+TM+TM	125	PSLUR01_00096	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44539.1	002441	SIG+TM+TM	118	RaK2_00266	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AHI60254.1	002442	Cluster1995_1clades	126	Ea357_103	Erwinia phage Ea35-70	GCA_000914635.1
AUG85891.1	002442	Cluster1995_1clades	126	BOSOLAPHORUS_104	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52206.1	002442	Cluster1995_1clades	126	DM_108	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUG86210.1	002442	Cluster1995_1clades	126	DESERTFOX_103	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86856.1	002442	Cluster1995_1clades	126	MORTIMER_107	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51884.1	002442	Cluster1995_1clades	126	RAY_103	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51568.1	002442	Cluster1995_1clades	126	SIMMY50_106	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64916.1	002442	Cluster1995_1clades	126	SPECIALG_106	Erwinia phage vB_EamM_Special G	GCA_002624385.1
AMR59861.1	002443	Cluster1996_1clades	123	SEGD1_214	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96676.1	002443	Cluster1996_1clades	125	G173_gp131	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48242.1	002443	Cluster1996_1clades	125	ASESINO_229	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50656.1	002443	Cluster1996_1clades	125	STRATTON_231	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86050.1	002443	Cluster1996_1clades	123	ACEC001_2070	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20898.1	002443	Cluster1996_1clades	123	-	Salmonella phage JN03	GCA_014319805.1
AWN09137.1	002443	Cluster1996_1clades	123	MLDJOKPK_00230	Salmonella phage SPAsTU	GCA_003183805.1
AEP84043.1	002443	Cluster1996_1clades	123	SPN3US_0210	Salmonella phage SPN3US	GCA_001042275.1
APU01536.1	002444	RF3_C	124	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29072.1	002444	RF3_C	124	AP1_0365	Aeromonas phage AP1	GCA_014183365.1
ATI17357.1	002444	RF3_C	124	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00237.1	002444	RF3_C	124	HWB28_gp315	Aeromonas phage AS-zj	GCA_002627665.1
QAX97801.1	002444	RF3_C	124	ASswx1_156	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01346.1	002444	RF3_C	124	ASwh1_285	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39443.1	002444	RF3_C	124	CC2_381	Aeromonas phage CC2	GCA_000903495.1
ADQ53158.1	002444	RF3_C	124	65p150	Aeromonas virus 65	GCA_000893255.1
APU01743.1	002445	GxC-R	124	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28922.1	002445	GxC-R	124	AP1_0215	Aeromonas phage AP1	GCA_014183365.1
ATI17555.1	002445	GxC-R	124	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00442.1	002445	GxC-R	124	HWB28_gp110	Aeromonas phage AS-zj	GCA_002627665.1
QAX97995.1	002445	GxC-R	124	ASswx1_355	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01145.1	002445	GxC-R	124	ASwh1_79	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39246.1	002445	GxC-R	124	CC2_180	Aeromonas phage CC2	GCA_000903495.1
ADQ53446.1	002445	GxC-R	60	65p378	Aeromonas virus 65	GCA_000893255.1
AGR47876.2	002446	Cluster1999_1clades	39	SmphiM12_244	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47877.1	002446	Cluster1999_1clades	123	SmphiM12_245	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13077.2	002446	Cluster1999_1clades	120	PHIM19_172	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13078.1	002446	Cluster1999_1clades	123	PHIM19_173	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12717.2	002446	Cluster1999_1clades	120	PHIM7_172	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12718.1	002446	Cluster1999_1clades	123	PHIM7_173	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13447.1	002446	Cluster1999_1clades	120	PHIN3_184	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13448.1	002446	Cluster1999_1clades	45	PHIN3_185	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14041.1	002447	Cluster2000_1clades	123	PBI_121Q_151	Escherichia phage 121Q	GCA_000926855.1
QAY00302.1	002447	Cluster2000_1clades	63	Ecwhy1_20	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35052.1	002447	Cluster2000_1clades	95	ACQ29_gp372	Escherichia phage PBECO4	GCA_001041035.1
BBM61724.1	002447	Cluster2000_1clades	123	EO157G_1350	Escherichia phage SP27	GCA_008033345.1
AXC36628.1	002447	Cluster2000_1clades	95	-	Escherichia phage UB	GCA_003341455.1
QBO61658.1	002447	Cluster2000_1clades	123	G17_00162	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80036.1	002447	Cluster2000_1clades	123	PSLUR01_00059	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44504.1	002447	Cluster2000_1clades	109	RaK2_00231	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXG67347.1	002448	Cluster2001_1clades	99	AD1_303	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80049.1	002448	Cluster2001_1clades	116	JA11_244	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66648.1	002448	Cluster2001_1clades	116	JA13_245	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66972.1	002448	Cluster2001_1clades	116	JA29_246	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67619.1	002448	Cluster2001_1clades	116	JA33_245	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08574.1	002448	Cluster2001_1clades	99	Alexandra_323	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58950.1	002448	Cluster2001_1clades	99	Y3_310	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28776.1	002448	Cluster2001_1clades	123	YOLOSWAG_306	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01665.1	002449	Cluster2002_1clades	122	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29023.1	002449	Cluster2002_1clades	116	AP1_0316	Aeromonas phage AP1	GCA_014183365.1
ATI17628.1	002449	Cluster2002_1clades	116	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00367.1	002449	Cluster2002_1clades	116	HWB28_gp185	Aeromonas phage AS-zj	GCA_002627665.1
QAX97663.1	002449	Cluster2002_1clades	116	ASswx1_17	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01076.1	002449	Cluster2002_1clades	118	ASwh1_8	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39342.1	002449	Cluster2002_1clades	115	CC2_098	Aeromonas phage CC2	GCA_000903495.1
ADQ53297.1	002449	Cluster2002_1clades	122	65p289	Aeromonas virus 65	GCA_000893255.1
APU01495.1	002450	Cluster2003_1clades	119	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28961.1	002450	Cluster2003_1clades	82	AP1_0254	Aeromonas phage AP1	GCA_014183365.1
ATI17402.1	002450	Cluster2003_1clades	121	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00193.1	002450	Cluster2003_1clades	120	HWB28_gp359	Aeromonas phage AS-zj	GCA_002627665.1
QAX97842.1	002450	Cluster2003_1clades	121	ASswx1_199	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01310.1	002450	Cluster2003_1clades	114	ASwh1_247	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39275.1	002450	Cluster2003_1clades	122	CC2_336	Aeromonas phage CC2	GCA_000903495.1
ADQ53116.1	002450	Cluster2003_1clades	119	65p108	Aeromonas virus 65	GCA_000893255.1
AXQ69045.1	002451	Cluster2004_1clades	106	CcrBL9_gp021	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69561.1	002451	Cluster2004_1clades	106	CcrBL9_gp537	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88298.1	002451	Cluster2004_1clades	122	CcrColossus_gp428	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68973.1	002451	Cluster2004_1clades	122	CcrPW_gp434c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69605.1	002451	Cluster2004_1clades	102	CcrSC_gp023	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70105.1	002451	Cluster2004_1clades	102	CcrSC_gp523	Caulobacter phage CcrSC	GCA_003443315.1
AFU87534.1	002451	Cluster2004_1clades	100	CcrKarma_gp017	Caulobacter virus Karma	GCA_000901575.1
AFU87867.1	002451	Cluster2004_1clades	100	CcrKarma_gp350	Caulobacter virus Karma	GCA_000901575.1
AIT14120.1	002452	SIG+TM+TM	122	PBI_121Q_230	Escherichia phage 121Q	GCA_000926855.1
QAY00805.1	002452	SIG+TM+TM	122	Ecwhy1_532	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34979.1	002452	SIG+TM+TM	122	ACQ29_gp299	Escherichia phage PBECO4	GCA_001041035.1
BBM61798.1	002452	SIG+TM+TM	122	EO157G_2090	Escherichia phage SP27	GCA_008033345.1
AXC36559.1	002452	SIG+TM+TM	122	-	Escherichia phage UB	GCA_003341455.1
QBO61581.1	002452	SIG+TM+TM	122	G17_00085	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13644.1	002452	SIG+TM+TM	122	vBEcoMphAPEC6_gp013c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80110.1	002452	SIG+TM+TM	122	PSLUR01_00133	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67232.1	002453	DUF2778	121	AD1_188	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79983.1	002453	DUF2778	121	JA11_178	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66581.1	002453	DUF2778	121	JA13_178	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66906.1	002453	DUF2778	121	JA29_180	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67552.1	002453	DUF2778	121	JA33_178	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08461.1	002453	DUF2778	121	Alexandra_195	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58831.1	002453	DUF2778	121	Y3_191	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28665.1	002453	DUF2778	121	YOLOSWAG_186	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67280.1	002454	Cluster2007_1clades	103	AD1_236	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80024.1	002454	Cluster2007_1clades	93	JA11_219	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66623.1	002454	Cluster2007_1clades	93	JA13_220	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66947.1	002454	Cluster2007_1clades	93	JA29_221	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67594.1	002454	Cluster2007_1clades	93	JA33_220	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08613.1	002454	Cluster2007_1clades	121	Alexandra_245	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58880.1	002454	Cluster2007_1clades	105	Y3_240	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28713.1	002454	Cluster2007_1clades	107	YOLOSWAG_235	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14078.1	002455	Cluster2008_1clades	109	PBI_121Q_188	Escherichia phage 121Q	GCA_000926855.1
QAY00845.1	002455	Cluster2008_1clades	121	Ecwhy1_573	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35016.1	002455	Cluster2008_1clades	109	ACQ29_gp336	Escherichia phage PBECO4	GCA_001041035.1
BBM61761.1	002455	Cluster2008_1clades	119	EO157G_1720	Escherichia phage SP27	GCA_008033345.1
AXC36593.1	002455	Cluster2008_1clades	119	-	Escherichia phage UB	GCA_003341455.1
QBO61621.1	002455	Cluster2008_1clades	119	G17_00125	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80072.1	002455	Cluster2008_1clades	119	PSLUR01_00095	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44538.1	002455	Cluster2008_1clades	111	RaK2_00265	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14279.1	002456	Cluster2009_1clades	111	PBI_121Q_389	Escherichia phage 121Q	GCA_000926855.1
QAY00659.1	002456	Cluster2009_1clades	119	Ecwhy1_384	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34855.1	002456	Cluster2009_1clades	120	ACQ29_gp175	Escherichia phage PBECO4	GCA_001041035.1
BBM61953.1	002456	Cluster2009_1clades	120	EO157G_3640	Escherichia phage SP27	GCA_008033345.1
AXC36964.1	002456	Cluster2009_1clades	72	-	Escherichia phage UB	GCA_003341455.1
QBO62025.1	002456	Cluster2009_1clades	120	G17_00536	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14046.1	002456	Cluster2009_1clades	111	vBEcoMphAPEC6_gp423c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80266.1	002456	Cluster2009_1clades	120	PSLUR01_00289	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14273.1	002457	Cluster2010_1clades	120	PBI_121Q_383	Escherichia phage 121Q	GCA_000926855.1
QAY00664.1	002457	Cluster2010_1clades	119	Ecwhy1_389	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34860.1	002457	Cluster2010_1clades	120	ACQ29_gp180	Escherichia phage PBECO4	GCA_001041035.1
BBM61948.1	002457	Cluster2010_1clades	120	EO157G_3590	Escherichia phage SP27	GCA_008033345.1
AXC36969.1	002457	Cluster2010_1clades	120	-	Escherichia phage UB	GCA_003341455.1
QBO62031.1	002457	Cluster2010_1clades	120	G17_00542	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14052.1	002457	Cluster2010_1clades	120	vBEcoMphAPEC6_gp429c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80261.1	002457	Cluster2010_1clades	120	PSLUR01_00284	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21796.1	002458	Cluster2011_1clades	115	GAP32_346	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43916.1	002458	Cluster2011_1clades	115	CBB_353	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19075.1	002458	Cluster2011_1clades	66	7t3_0555	Salmonella phage 7t3	GCA_006083215.1
AZU98318.1	002458	Cluster2011_1clades	66	CPT_Munch_374	Salmonella phage Munch	GCA_004015485.1
QIG62666.1	002458	Cluster2011_1clades	66	SEPL_053	Salmonella phage SE_PL	GCA_011067555.1
AQW88877.1	002458	Cluster2011_1clades	120	BF_0352	Serratia phage BF	GCA_002619745.1
SOK59162.1	002458	Cluster2011_1clades	120	g354	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58630.1	002458	Cluster2011_1clades	120	g353	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14382.1	002459	TM+TM	119	PBI_121Q_492	Escherichia phage 121Q	GCA_000926855.1
QAY00566.1	002459	TM+TM	119	Ecwhy1_287	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34759.1	002459	TM+TM	119	ACQ29_gp079	Escherichia phage PBECO4	GCA_001041035.1
BBM62053.1	002459	TM+TM	119	EO157G_4640	Escherichia phage SP27	GCA_008033345.1
AXC36874.1	002459	TM+TM	119	-	Escherichia phage UB	GCA_003341455.1
QBO61920.1	002459	TM+TM	119	G17_00431	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13953.1	002459	TM+TM	119	vBEcoMphAPEC6_gp329c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80371.1	002459	TM+TM	119	PSLUR01_00394	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01600.1	002460	Cluster2013_1clades	115	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29120.1	002460	Cluster2013_1clades	49	AP1_0417	Aeromonas phage AP1	GCA_014183365.1
QMV29171.1	002460	Cluster2013_1clades	53	AP1_0474	Aeromonas phage AP1	GCA_014183365.1
ATI17311.1	002460	Cluster2013_1clades	119	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00283.1	002460	Cluster2013_1clades	119	HWB28_gp269	Aeromonas phage AS-zj	GCA_002627665.1
QAX97754.1	002460	Cluster2013_1clades	119	ASswx1_109	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01401.1	002460	Cluster2013_1clades	118	ASwh1_342	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53224.1	002460	Cluster2013_1clades	115	65p216	Aeromonas virus 65	GCA_000893255.1
APU01572.1	002461	Cluster2014_1clades	109	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29082.1	002461	Cluster2014_1clades	113	AP1_0375	Aeromonas phage AP1	GCA_014183365.1
ATI17445.1	002461	Cluster2014_1clades	111	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00150.1	002461	Cluster2014_1clades	111	HWB28_gp402	Aeromonas phage AS-zj	GCA_002627665.1
QAX97885.1	002461	Cluster2014_1clades	118	ASswx1_242	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01452.1	002461	Cluster2014_1clades	103	ASwh1_393	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39412.1	002461	Cluster2014_1clades	118	CC2_291	Aeromonas phage CC2	GCA_000903495.1
ADQ53195.1	002461	Cluster2014_1clades	109	65p187	Aeromonas virus 65	GCA_000893255.1
APU01711.1	002462	Cluster2015_1clades	112	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28910.1	002462	Cluster2015_1clades	112	AP1_0203	Aeromonas phage AP1	GCA_014183365.1
ATI17585.1	002462	Cluster2015_1clades	112	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00412.1	002462	Cluster2015_1clades	112	HWB28_gp140	Aeromonas phage AS-zj	GCA_002627665.1
QAX98024.1	002462	Cluster2015_1clades	112	ASswx1_384	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01122.1	002462	Cluster2015_1clades	113	ASwh1_55	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39359.1	002462	Cluster2015_1clades	115	CC2_148	Aeromonas phage CC2	GCA_000903495.1
ADQ53350.1	002462	Cluster2015_1clades	116	65p342	Aeromonas virus 65	GCA_000893255.1
AIT14249.1	002463	Cluster2016_1clades	113	PBI_121Q_359	Escherichia phage 121Q	GCA_000926855.1
QAY00684.1	002463	Cluster2016_1clades	114	Ecwhy1_409	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34878.1	002463	Cluster2016_1clades	114	ACQ29_gp198	Escherichia phage PBECO4	GCA_001041035.1
BBM61927.1	002463	Cluster2016_1clades	114	EO157G_3380	Escherichia phage SP27	GCA_008033345.1
AXC36984.1	002463	Cluster2016_1clades	114	-	Escherichia phage UB	GCA_003341455.1
QBO62055.1	002463	Cluster2016_1clades	114	G17_00566	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14074.1	002463	Cluster2016_1clades	113	vBEcoMphAPEC6_gp451c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80239.1	002463	Cluster2016_1clades	114	PSLUR01_00262	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14083.1	002464	Cluster2017_1clades	114	PBI_121Q_193	Escherichia phage 121Q	GCA_000926855.1
QAY00840.1	002464	Cluster2017_1clades	114	Ecwhy1_568	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35011.1	002464	Cluster2017_1clades	114	ACQ29_gp331	Escherichia phage PBECO4	GCA_001041035.1
BBM61766.1	002464	Cluster2017_1clades	114	EO157G_1770	Escherichia phage SP27	GCA_008033345.1
AXC36589.1	002464	Cluster2017_1clades	114	-	Escherichia phage UB	GCA_003341455.1
QBO61616.1	002464	Cluster2017_1clades	114	G17_00120	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13674.1	002464	Cluster2017_1clades	114	vBEcoMphAPEC6_gp044c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80077.1	002464	Cluster2017_1clades	114	PSLUR01_00100	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67179.1	002465	SIG+MreB_Mbl	114	AD1_135	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79929.1	002465	SIG+MreB_Mbl	114	JA11_124	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66528.1	002465	SIG+MreB_Mbl	114	JA13_125	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66853.1	002465	SIG+MreB_Mbl	114	JA29_127	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67498.1	002465	SIG+MreB_Mbl	114	JA33_124	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08412.1	002465	SIG+MreB_Mbl	114	Alexandra_140	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58776.1	002465	SIG+MreB_Mbl	114	Y3_136	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28614.1	002465	SIG+MreB_Mbl	114	YOLOSWAG_134	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14232.1	002466	CyaA	113	PBI_121Q_342	Escherichia phage 121Q	GCA_000926855.1
QAY00703.1	002466	CyaA	113	Ecwhy1_428	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34893.1	002466	CyaA	88	ACQ29_gp213	Escherichia phage PBECO4	GCA_001041035.1
BBM61908.1	002466	CyaA	114	EO157G_3190	Escherichia phage SP27	GCA_008033345.1
AXC36998.1	002466	CyaA	88	-	Escherichia phage UB	GCA_003341455.1
QBO62073.1	002466	CyaA	114	G17_00584	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14089.1	002466	CyaA	114	vBEcoMphAPEC6_gp466c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80221.1	002466	CyaA	114	PSLUR01_00244	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ABY63216.1	002467	Cluster2020_1clades	78	201phi2-1p392	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44770.1	002467	Cluster2020_1clades	113	KTN4_012	Pseudomonas phage KTN4	GCA_002607225.1
QBX32275.1	002467	Cluster2020_1clades	113	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76794.1	002467	Cluster2020_1clades	92	PHABIO_163	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02666.1	002467	Cluster2020_1clades	102	PSA21_139	Pseudomonas phage Psa21	GCA_004340405.1
QJB22656.1	002467	Cluster2020_1clades	113	fnug_13	Pseudomonas phage fnug	GCA_012837215.1
QEM41849.1	002467	Cluster2020_1clades	113	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82912.1	002467	Cluster2020_1clades	113	PHIKZ011	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14098.1	002468	SIG+TM+TM	113	PBI_121Q_208	Escherichia phage 121Q	GCA_000926855.1
QAY00824.1	002468	SIG+TM+TM	113	Ecwhy1_551	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34996.1	002468	SIG+TM+TM	113	ACQ29_gp316	Escherichia phage PBECO4	GCA_001041035.1
BBM61780.1	002468	SIG+TM+TM	113	EO157G_1910	Escherichia phage SP27	GCA_008033345.1
AXC36576.1	002468	SIG+TM+TM	113	-	Escherichia phage UB	GCA_003341455.1
QBO61601.1	002468	SIG+TM+TM	113	G17_00105	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13660.1	002468	SIG+TM+TM	113	vBEcoMphAPEC6_gp029c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80092.1	002468	SIG+TM+TM	113	PSLUR01_00115	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14275.1	002469	Cluster2022_1clades	113	PBI_121Q_385	Escherichia phage 121Q	GCA_000926855.1
QAY00663.1	002469	Cluster2022_1clades	112	Ecwhy1_388	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34859.1	002469	Cluster2022_1clades	93	ACQ29_gp179	Escherichia phage PBECO4	GCA_001041035.1
BBM61949.1	002469	Cluster2022_1clades	111	EO157G_3600	Escherichia phage SP27	GCA_008033345.1
AXC36968.1	002469	Cluster2022_1clades	63	-	Escherichia phage UB	GCA_003341455.1
QBO62029.1	002469	Cluster2022_1clades	113	G17_00540	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14050.1	002469	Cluster2022_1clades	103	vBEcoMphAPEC6_gp427c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80262.1	002469	Cluster2022_1clades	111	PSLUR01_00285	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70291.1	002470	Cluster2023_1clades	105	CF8_0123	Aeromonas phage CF8	GCA_006384595.2
QDJ97268.1	002470	Cluster2023_1clades	109	D6_0108	Aeromonas phage D6	GCA_007051205.2
QDH47229.1	002470	Cluster2023_1clades	109	LAh10_40	Aeromonas phage LAh10	GCA_006863975.1
QDJ96882.1	002470	Cluster2023_1clades	106	PS1_0123	Aeromonas phage PS1	GCA_007051165.2
QFR59514.1	002470	Cluster2023_1clades	106	PS2_0123	Aeromonas phage PS2	GCA_009388305.2
QBZ70654.1	002470	Cluster2023_1clades	106	pETSU_073	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71970.1	002470	Cluster2023_1clades	112	N1M2_107	Klebsiella phage N1M2	GCA_010092605.1
AEV89571.1	002470	Cluster2023_1clades	112	OBP_134	Pseudomonas phage OBP	GCA_000896635.1
AMR59710.1	002471	Cluster2024_1clades	109	SEGD1_061	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96788.1	002471	Cluster2024_1clades	112	G173_gp243	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48089.1	002471	Cluster2024_1clades	112	ASESINO_76	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50500.1	002471	Cluster2024_1clades	112	STRATTON_75	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85900.1	002471	Cluster2024_1clades	109	ACEC001_0620	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20775.1	002471	Cluster2024_1clades	99	-	Salmonella phage JN03	GCA_014319805.1
AXF51092.1	002471	Cluster2024_1clades	109	MLDJOKPK_00105	Salmonella phage SPAsTU	GCA_003183805.1
AEP83892.1	002471	Cluster2024_1clades	99	SPN3US_0059	Salmonella phage SPN3US	GCA_001042275.1
AGH56894.1	002472	TM	69	CPXG_00091	Cyanophage P-RSM6	GCA_000906155.1
AJK27552.1	002472	TM	69	PTIM40_125	Cyanophage P-TIM40	GCA_001470935.1
AGH07605.1	002472	TM	49	CYVG_00161	Cyanophage S-SSM6a	GCA_002710385.1
AGG54414.1	002472	TM	69	CYWG_00130	Cyanophage S-SSM6b	GCA_002710425.1
AGH26205.1	002472	TM	69	CPMG_00104	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44545.1	002472	TM	100	PSSM2_167	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12426.1	002472	TM	100	PRTG_00276	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93476.1	002472	TM	112	AVU42_gp139	Prochlorococcus phage P-TIM68	GCA_001503075.1
APU01728.1	002473	Cluster2026_1clades	111	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28740.1	002473	Cluster2026_1clades	95	AP1_0022	Aeromonas phage AP1	GCA_014183365.1
ATI17568.1	002473	Cluster2026_1clades	95	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00428.1	002473	Cluster2026_1clades	95	HWB28_gp124	Aeromonas phage AS-zj	GCA_002627665.1
QAX98008.1	002473	Cluster2026_1clades	94	ASswx1_368	Aeromonas phage Asswx_1	GCA_004146865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY01134.1	002473	Cluster2026_1clades	111	ASwh1_68	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39301.1	002473	Cluster2026_1clades	94	CC2_164	Aeromonas phage CC2	GCA_000903495.1
ADQ53369.1	002473	Cluster2026_1clades	111	65p361	Aeromonas virus 65	GCA_000893255.1
AXG67051.1	002474	Cluster2027_1clades	111	AD1_007	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79811.1	002474	Cluster2027_1clades	102	JA11_006	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66409.1	002474	Cluster2027_1clades	102	JA13_006	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66732.1	002474	Cluster2027_1clades	102	JA29_006	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67380.1	002474	Cluster2027_1clades	102	JA33_006	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08289.1	002474	Cluster2027_1clades	111	Alexandra_7	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58647.1	002474	Cluster2027_1clades	97	Y3_007	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28494.1	002474	Cluster2027_1clades	108	YOLOSWAG_7	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14342.1	002475	Cys_Met_Meta_PP	109	PBI_121Q_452	Escherichia phage 121Q	GCA_000926855.1
QAY00602.1	002475	Cys_Met_Meta_PP	94	Ecwhy1_325	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34796.1	002475	Cys_Met_Meta_PP	109	ACQ29_gp116	Escherichia phage PBECO4	GCA_001041035.1
BBM62013.1	002475	Cys_Met_Meta_PP	111	EO157G_4240	Escherichia phage SP27	GCA_008033345.1
AXC36913.1	002475	Cys_Met_Meta_PP	109	-	Escherichia phage UB	GCA_003341455.1
QBO61962.1	002475	Cys_Met_Meta_PP	109	G17_00473	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13989.1	002475	Cys_Met_Meta_PP	109	vBEcoMphAPEC6_gp365c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80329.1	002475	Cys_Met_Meta_PP	109	PSLUR01_00352	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01458.1	002476	Cluster2029_1clades	101	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29006.1	002476	Cluster2029_1clades	107	AP1_0299	Aeromonas phage AP1	GCA_014183365.1
ATI17439.1	002476	Cluster2029_1clades	107	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00156.1	002476	Cluster2029_1clades	107	HWB28_gp396	Aeromonas phage AS-zj	GCA_002627665.1
QAX97879.1	002476	Cluster2029_1clades	107	ASswx1_236	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01271.1	002476	Cluster2029_1clades	111	ASwh1_208	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39417.1	002476	Cluster2029_1clades	107	CC2_298	Aeromonas phage CC2	GCA_000903495.1
ADQ53079.1	002476	Cluster2029_1clades	105	65p069	Aeromonas virus 65	GCA_000893255.1
AXG67058.1	002477	Cluster2030_1clades	71	AD1_014	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79817.1	002477	Cluster2030_1clades	104	JA11_012	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66415.1	002477	Cluster2030_1clades	104	JA13_012	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66738.1	002477	Cluster2030_1clades	104	JA29_012	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67386.1	002477	Cluster2030_1clades	104	JA33_012	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08295.1	002477	Cluster2030_1clades	110	Alexandra_14	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58654.1	002477	Cluster2030_1clades	110	Y3_014	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28501.1	002477	Cluster2030_1clades	110	YOLOSWAG_14	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01691.1	002478	SIG+TM	90	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28828.1	002478	SIG+TM	89	AP1_0121	Aeromonas phage AP1	GCA_014183365.1
ATI17600.1	002478	SIG+TM	90	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00397.1	002478	SIG+TM	90	HWB28_gp155	Aeromonas phage AS-zj	GCA_002627665.1
QAX98039.1	002478	SIG+TM	89	ASswx1_399	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01106.1	002478	SIG+TM	88	ASwh1_38	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39356.1	002478	SIG+TM	90	CC2_131	Aeromonas phage CC2	GCA_000903495.1
ADQ53329.1	002478	SIG+TM	109	65p321	Aeromonas virus 65	GCA_000893255.1
AIT14163.1	002479	DUF1033	94	PBI_121Q_273	Escherichia phage 121Q	GCA_000926855.1
QAY00774.1	002479	DUF1033	86	Ecwhy1_500	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34952.1	002479	DUF1033	108	ACQ29_gp272	Escherichia phage PBECO4	GCA_001041035.1
BBM61836.1	002479	DUF1033	95	EO157G_2470	Escherichia phage SP27	GCA_008033345.1
AXC37054.1	002479	DUF1033	95	-	Escherichia phage UB	GCA_003341455.1
QBO61543.1	002479	DUF1033	94	G17_00047	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62149.1	002479	DUF1033	94	G17_00660	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14156.1	002479	DUF1033	93	vBEcoMphAPEC6_gp533c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AIT14018.1	002480	Cluster2033_1clades	72	PBI_121Q_122	Escherichia phage 121Q	GCA_000926855.1
QAY00322.1	002480	Cluster2033_1clades	72	Ecwhy1_40	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35069.1	002480	Cluster2033_1clades	108	ACQ29_gp389	Escherichia phage PBECO4	GCA_001041035.1
BBM61706.1	002480	Cluster2033_1clades	108	EO157G_1170	Escherichia phage SP27	GCA_008033345.1
AXC36647.1	002480	Cluster2033_1clades	72	-	Escherichia phage UB	GCA_003341455.1
QBO61678.1	002480	Cluster2033_1clades	72	G17_00188	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13727.1	002480	Cluster2033_1clades	108	vBEcoMphAPEC6_gp097c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80019.1	002480	Cluster2033_1clades	72	PSLUR01_00036	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMR59763.1	002481	Cluster2034_1clades	101	SEGD1_116	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96580.1	002481	Cluster2034_1clades	104	G173_gp035	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48140.1	002481	Cluster2034_1clades	97	ASESINO_127	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50555.1	002481	Cluster2034_1clades	104	STRATTON_130	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85953.1	002481	Cluster2034_1clades	101	ACEC001_1150	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20820.1	002481	Cluster2034_1clades	101	-	Salmonella phage JN03	GCA_014319805.1
AWN08997.1	002481	Cluster2034_1clades	108	MLDJOKPK_00045	Salmonella phage SPAsTU	GCA_003183805.1
AEP83945.1	002481	Cluster2034_1clades	101	SPN3US_0112	Salmonella phage SPN3US	GCA_001042275.1
APU01579.1	002482	Cluster2035_1clades	93	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28966.1	002482	Cluster2035_1clades	92	AP1_0259	Aeromonas phage AP1	GCA_014183365.1
ATI17328.1	002482	Cluster2035_1clades	92	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00266.1	002482	Cluster2035_1clades	92	HWB28_gp286	Aeromonas phage AS-zj	GCA_002627665.1
QAX97771.1	002482	Cluster2035_1clades	92	ASswx1_126	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01343.1	002482	Cluster2035_1clades	108	ASwh1_282	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01382.1	002482	Cluster2035_1clades	94	ASwh1_322	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39292.1	002482	Cluster2035_1clades	92	CC2_411	Aeromonas phage CC2	GCA_000903495.1
APU01576.1	002483	FamB-divDNAPol	100	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28963.1	002483	FamB-divDNAPol	106	AP1_0256	Aeromonas phage AP1	GCA_014183365.1
ATI17331.1	002483	FamB-divDNAPol	106	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00263.1	002483	FamB-divDNAPol	106	HWB28_gp289	Aeromonas phage AS-zj	GCA_002627665.1
QAX97774.1	002483	FamB-divDNAPol	104	ASswx1_129	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01376.1	002483	FamB-divDNAPol	108	ASwh1_316	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39456.1	002483	FamB-divDNAPol	106	CC2_408	Aeromonas phage CC2	GCA_000903495.1
ADQ53200.1	002483	FamB-divDNAPol	100	65p192	Aeromonas virus 65	GCA_000893255.1
APU01561.1	002484	Cluster2037_1clades	76	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28939.1	002484	Cluster2037_1clades	107	AP1_0232	Aeromonas phage AP1	GCA_014183365.1
ATI17341.1	002484	Cluster2037_1clades	103	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00252.1	002484	Cluster2037_1clades	103	HWB28_gp300	Aeromonas phage AS-zj	GCA_002627665.1
QAX97786.1	002484	Cluster2037_1clades	103	ASswx1_141	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01368.1	002484	Cluster2037_1clades	103	ASwh1_308	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39450.1	002484	Cluster2037_1clades	103	CC2_397	Aeromonas phage CC2	GCA_000903495.1
ADQ53184.1	002484	Cluster2037_1clades	100	65p176	Aeromonas virus 65	GCA_000893255.1
APU01658.1	002485	Cluster2038_1clades	106	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29109.1	002485	Cluster2038_1clades	70	AP1_0402	Aeromonas phage AP1	GCA_014183365.1
ATI17228.1	002485	Cluster2038_1clades	103	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00359.1	002485	Cluster2038_1clades	103	HWB28_gp193	Aeromonas phage AS-zj	GCA_002627665.1
QAX97671.1	002485	Cluster2038_1clades	103	ASswx1_25	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01070.1	002485	Cluster2038_1clades	106	ASwh1_2	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39469.1	002485	Cluster2038_1clades	103	CC2_090	Aeromonas phage CC2	GCA_000903495.1
ADQ53289.1	002485	Cluster2038_1clades	106	65p281	Aeromonas virus 65	GCA_000893255.1
AGH07692.1	002486	Cluster2039_1clades	90	CYVG_00249	Cyanophage S-SSM6a	GCA_002710385.1
AGG54326.1	002486	Cluster2039_1clades	106	CYWG_00042	Cyanophage S-SSM6b	GCA_002710425.1
AAX44463.1	002486	Cluster2039_1clades	80	PSSM2_085	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12190.1	002486	Cluster2039_1clades	80	PRTG_00032	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93621.1	002486	Cluster2039_1clades	84	AVU42_gp076	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIX30551.1	002486	Cluster2039_1clades	85	Syn7803US37_74	Synechococcus phage ACG-2014f	GCA_002594065.1
AXQ70410.1	002486	Cluster2039_1clades	83	HOU04_gp011	Synechococcus phage S-T4	GCA_003443335.1
AXQ70612.1	002486	Cluster2039_1clades	83	HOU04_gp011	Synechococcus phage S-T4	GCA_003443335.1
AIT14234.1	002487	Cluster2040_1clades	106	PBI_121Q_344	Escherichia phage 121Q	GCA_000926855.1
QAY00699.1	002487	Cluster2040_1clades	103	Ecwhy1_424	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34891.1	002487	Cluster2040_1clades	105	ACQ29_gp211	Escherichia phage PBECO4	GCA_001041035.1
BBM61911.1	002487	Cluster2040_1clades	106	EO157G_3220	Escherichia phage SP27	GCA_008033345.1
AXC36994.1	002487	Cluster2040_1clades	106	-	Escherichia phage UB	GCA_003341455.1
QBO62070.1	002487	Cluster2040_1clades	106	G17_00581	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14086.1	002487	Cluster2040_1clades	106	vBEcoMphAPEC6_gp463c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80223.1	002487	Cluster2040_1clades	103	PSLUR01_00246	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMR59826.1	002488	Cluster2041_1clades	105	SEGD1_179	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96641.1	002488	Cluster2041_1clades	105	G173_gp096	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48207.1	002488	Cluster2041_1clades	105	ASESINO_194	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50618.1	002488	Cluster2041_1clades	105	STRATTON_193	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86015.1	002488	Cluster2041_1clades	105	ACEC001_1740	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20870.1	002488	Cluster2041_1clades	105	-	Salmonella phage JN03	GCA_014319805.1
AWN09161.1	002488	Cluster2041_1clades	105	MLDJOKPK_00267	Salmonella phage SPAsTU	GCA_003183805.1
AEP84007.1	002488	Cluster2041_1clades	105	SPN3US_0174	Salmonella phage SPN3US	GCA_001042275.1
AGH56947.1	002489	Cluster2042_1clades	76	CPXG_00144	Cyanophage P-RSM6	GCA_000906155.1
AJK27496.1	002489	Cluster2042_1clades	86	PTIM40_69	Cyanophage P-TIM40	GCA_001470935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH07681.1	002489	Cluster2042_1clades	98	CYVG_00238	Cyanophage S-SSM6a	GCA_002710385.1
AGG54324.1	002489	Cluster2042_1clades	105	CYWG_00040	Cyanophage S-SSM6b	GCA_002710425.1
AGH26160.1	002489	Cluster2042_1clades	82	CPMG_00059	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44464.1	002489	Cluster2042_1clades	95	PSSM2_086	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12189.1	002489	Cluster2042_1clades	95	PRTG_00031	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93607.1	002489	Cluster2042_1clades	74	AVU42_gp062	Prochlorococcus phage P-TIM68	GCA_001503075.1
APU01477.1	002490	Cluster2043_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29111.1	002490	Cluster2043_1clades	101	AP1_0408	Aeromonas phage AP1	GCA_014183365.1
ATI17420.1	002490	Cluster2043_1clades	101	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00176.1	002490	Cluster2043_1clades	101	HWB28_gp376	Aeromonas phage AS-zj	GCA_002627665.1
QAX97860.1	002490	Cluster2043_1clades	101	ASswx1_217	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01290.1	002490	Cluster2043_1clades	105	ASwh1_227	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39306.1	002490	Cluster2043_1clades	101	CC2_317	Aeromonas phage CC2	GCA_000903495.1
ADQ53100.1	002490	Cluster2043_1clades	102	65p090	Aeromonas virus 65	GCA_000893255.1
AFC21910.1	002491	Cluster2044_1clades	82	GAP32_453A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44034.1	002491	Cluster2044_1clades	83	CBB_471	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18570.1	002491	Cluster2044_1clades	80	7t3_049	Salmonella phage 7t3	GCA_006083215.1
AZU98399.1	002491	Cluster2044_1clades	80	CPT_Munch_467	Salmonella phage Munch	GCA_004015485.1
QIG63114.1	002491	Cluster2044_1clades	80	SEPL_501	Salmonella phage SE_PL	GCA_011067555.1
AQW88994.1	002491	Cluster2044_1clades	88	BF_0469	Serratia phage BF	GCA_002619745.1
SOK59275.1	002491	Cluster2044_1clades	105	g467	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58740.1	002491	Cluster2044_1clades	103	g463	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14118.1	002492	SIG+TM+TM	59	PBI_121Q_228	Escherichia phage 121Q	GCA_000926855.1
AIT14119.1	002492	SIG+TM+TM	55	PBI_121Q_229	Escherichia phage 121Q	GCA_000926855.1
QAY00806.1	002492	SIG+TM+TM	104	Ecwhy1_533	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34980.1	002492	SIG+TM+TM	104	ACQ29_gp300	Escherichia phage PBECO4	GCA_001041035.1
BBM61797.1	002492	SIG+TM+TM	104	EO157G_2080	Escherichia phage SP27	GCA_008033345.1
QBO61582.1	002492	SIG+TM+TM	104	G17_00086	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13645.1	002492	SIG+TM+TM	104	vBEcoMphAPEC6_gp014c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80109.1	002492	SIG+TM+TM	104	PSLUR01_00132	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14332.1	002493	Cluster2046_1clades	104	PBI_121Q_442	Escherichia phage 121Q	GCA_000926855.1
QAY00610.1	002493	Cluster2046_1clades	103	Ecwhy1_334	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34806.1	002493	Cluster2046_1clades	103	ACQ29_gp126	Escherichia phage PBECO4	GCA_001041035.1
BBM62004.1	002493	Cluster2046_1clades	103	EO157G_4150	Escherichia phage SP27	GCA_008033345.1
AXC36918.1	002493	Cluster2046_1clades	103	-	Escherichia phage UB	GCA_003341455.1
QBO61972.1	002493	Cluster2046_1clades	104	G17_00483	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13997.1	002493	Cluster2046_1clades	103	vBEcoMphAPEC6_gp373c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80319.1	002493	Cluster2046_1clades	104	PSLUR01_00342	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67117.1	002494	Cluster2047_1clades	103	AD1_073	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79874.1	002494	Cluster2047_1clades	93	JA11_069	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66473.1	002494	Cluster2047_1clades	93	JA13_070	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66798.1	002494	Cluster2047_1clades	93	JA29_072	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67443.1	002494	Cluster2047_1clades	93	JA33_069	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08353.1	002494	Cluster2047_1clades	98	Alexandra_75	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58716.1	002494	Cluster2047_1clades	97	Y3_076	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28550.1	002494	Cluster2047_1clades	104	YOLOSWAG_67	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14315.1	002495	Cluster2048_1clades	103	PBI_121Q_425	Escherichia phage 121Q	GCA_000926855.1
QAY00623.1	002495	Cluster2048_1clades	103	Ecwhy1_348	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34820.1	002495	Cluster2048_1clades	103	ACQ29_gp140	Escherichia phage PBECO4	GCA_001041035.1
BBM61989.1	002495	Cluster2048_1clades	103	EO157G_4000	Escherichia phage SP27	GCA_008033345.1
AXC36929.1	002495	Cluster2048_1clades	65	-	Escherichia phage UB	GCA_003341455.1
QBO61989.1	002495	Cluster2048_1clades	103	G17_00500	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14010.1	002495	Cluster2048_1clades	103	vBEcoMphAPEC6_gp386c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80302.1	002495	Cluster2048_1clades	103	PSLUR01_00325	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01571.1	002496	Cluster2049_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28843.1	002496	Cluster2049_1clades	98	AP1_0136	Aeromonas phage AP1	GCA_014183365.1
ATI17275.1	002496	Cluster2049_1clades	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00318.1	002496	Cluster2049_1clades	98	HWB28_gp234	Aeromonas phage AS-zj	GCA_002627665.1
QAX97717.1	002496	Cluster2049_1clades	98	ASswx1_71	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01373.1	002496	Cluster2049_1clades	100	ASwh1_313	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39324.1	002496	Cluster2049_1clades	98	CC2_041	Aeromonas phage CC2	GCA_000903495.1
ADQ53194.1	002496	Cluster2049_1clades	102	65p186	Aeromonas virus 65	GCA_000893255.1
AIT14327.1	002497	Cluster2050_1clades	87	PBI_121Q_437	Escherichia phage 121Q	GCA_000926855.1
QAY00614.1	002497	Cluster2050_1clades	102	Ecwhy1_338	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34810.1	002497	Cluster2050_1clades	95	ACQ29_gp130	Escherichia phage PBECO4	GCA_001041035.1
BBM62000.1	002497	Cluster2050_1clades	87	EO157G_4110	Escherichia phage SP27	GCA_008033345.1
AXC36921.1	002497	Cluster2050_1clades	87	-	Escherichia phage UB	GCA_003341455.1
QBO61977.1	002497	Cluster2050_1clades	102	G17_00488	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14001.1	002497	Cluster2050_1clades	87	vBEcoMphAPEC6_gp377c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80314.1	002497	Cluster2050_1clades	102	PSLUR01_00337	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01583.1	002498	Cluster2051_1clades	101	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28968.1	002498	Cluster2051_1clades	100	AP1_0261	Aeromonas phage AP1	GCA_014183365.1
ATI17326.1	002498	Cluster2051_1clades	100	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00268.1	002498	Cluster2051_1clades	100	HWB28_gp284	Aeromonas phage AS-zj	GCA_002627665.1
QAX97769.1	002498	Cluster2051_1clades	100	ASswx1_124	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01385.1	002498	Cluster2051_1clades	99	ASwh1_325	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39458.1	002498	Cluster2051_1clades	100	CC2_413	Aeromonas phage CC2	GCA_000903495.1
ADQ53206.1	002498	Cluster2051_1clades	101	65p198	Aeromonas virus 65	GCA_000893255.1
AIT14346.1	002499	Cluster2052_1clades	89	PBI_121Q_456	Escherichia phage 121Q	GCA_000926855.1
QAY00598.1	002499	Cluster2052_1clades	101	Ecwhy1_321	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34793.1	002499	Cluster2052_1clades	89	ACQ29_gp113	Escherichia phage PBECO4	GCA_001041035.1
BBM62017.1	002499	Cluster2052_1clades	89	EO157G_4280	Escherichia phage SP27	GCA_008033345.1
AXC36909.1	002499	Cluster2052_1clades	89	-	Escherichia phage UB	GCA_003341455.1
QBO61958.1	002499	Cluster2052_1clades	89	G17_00469	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13985.1	002499	Cluster2052_1clades	89	vBEcoMphAPEC6_gp361c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80333.1	002499	Cluster2052_1clades	89	PSLUR01_00356	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14310.1	002500	Cluster2053_1clades	99	PBI_121Q_420	Escherichia phage 121Q	GCA_000926855.1
QAY00628.1	002500	Cluster2053_1clades	95	Ecwhy1_353	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34825.1	002500	Cluster2053_1clades	95	ACQ29_gp145	Escherichia phage PBECO4	GCA_001041035.1
BBM61984.1	002500	Cluster2053_1clades	95	EO157G_3950	Escherichia phage SP27	GCA_008033345.1
AXC36933.1	002500	Cluster2053_1clades	95	-	Escherichia phage UB	GCA_003341455.1
QBO61994.1	002500	Cluster2053_1clades	95	G17_00505	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14015.1	002500	Cluster2053_1clades	80	vBEcoMphAPEC6_gp391c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80297.1	002500	Cluster2053_1clades	95	PSLUR01_00320	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01797.1	002501	Cluster2054_1clades	98	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29000.1	002501	Cluster2054_1clades	98	AP1_0293	Aeromonas phage AP1	GCA_014183365.1
ATI17508.1	002501	Cluster2054_1clades	97	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00489.1	002501	Cluster2054_1clades	98	HWB28_gp063	Aeromonas phage AS-zj	GCA_002627665.1
QAX97947.1	002501	Cluster2054_1clades	98	ASswx1_305	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01201.1	002501	Cluster2054_1clades	98	ASwh1_136	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39389.1	002501	Cluster2054_1clades	97	CC2_227	Aeromonas phage CC2	GCA_000903495.1
ADQ53441.1	002501	Cluster2054_1clades	98	65p435	Aeromonas virus 65	GCA_000893255.1
AIT14002.1	002502	Cluster2055_1clades	98	PBI_121Q_105	Escherichia phage 121Q	GCA_000926855.1
QAY00336.1	002502	Cluster2055_1clades	98	Ecwhy1_55	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35082.1	002502	Cluster2055_1clades	98	ACQ29_gp402	Escherichia phage PBECO4	GCA_001041035.1
BBM61693.1	002502	Cluster2055_1clades	98	EO157G_1040	Escherichia phage SP27	GCA_008033345.1
AXC36659.1	002502	Cluster2055_1clades	98	-	Escherichia phage UB	GCA_003341455.1
QBO61691.1	002502	Cluster2055_1clades	98	G17_00202	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13740.1	002502	Cluster2055_1clades	98	vBEcoMphAPEC6_gp110c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80006.1	002502	Cluster2055_1clades	98	PSLUR01_00022	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67215.1	002503	Cluster2056_1clades	97	AD1_171	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79965.1	002503	Cluster2056_1clades	89	JA11_160	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66563.1	002503	Cluster2056_1clades	89	JA13_160	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66888.1	002503	Cluster2056_1clades	89	JA29_162	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67534.1	002503	Cluster2056_1clades	89	JA33_160	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08445.1	002503	Cluster2056_1clades	98	Alexandra_176	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58812.1	002503	Cluster2056_1clades	72	Y3_172	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28646.1	002503	Cluster2056_1clades	97	YOLOSWAG_167	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01792.1	002504	Cluster2057_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28994.1	002504	Cluster2057_1clades	97	AP1_0287	Aeromonas phage AP1	GCA_014183365.1
ATI17513.1	002504	Cluster2057_1clades	97	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00483.1	002504	Cluster2057_1clades	97	HWB28_gp069	Aeromonas phage AS-zj	GCA_002627665.1
QAX97953.1	002504	Cluster2057_1clades	97	ASswx1_311	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01193.1	002504	Cluster2057_1clades	91	ASwh1_128	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39385.1	002504	Cluster2057_1clades	79	CC2_221	Aeromonas phage CC2	GCA_000903495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADQ53435.1	002504	Cluster2057_1clades	97	65p429	Aeromonas virus 65	GCA_000893255.1
AIT14085.1	002505	Cluster2058_1clades	97	PBI_121Q_195	Escherichia phage 121Q	GCA_000926855.1
QAY00838.1	002505	Cluster2058_1clades	97	Ecwhy1_566	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35009.1	002505	Cluster2058_1clades	97	ACQ29_gp329	Escherichia phage PBECO4	GCA_001041035.1
BBM61768.1	002505	Cluster2058_1clades	97	EO157G_1790	Escherichia phage SP27	GCA_008033345.1
AXC36587.1	002505	Cluster2058_1clades	97	-	Escherichia phage UB	GCA_003341455.1
QBO61614.1	002505	Cluster2058_1clades	97	G17_00118	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13672.1	002505	Cluster2058_1clades	97	vBEcoMphAPEC6_gp041c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80079.1	002505	Cluster2058_1clades	97	PSLUR01_00102	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14063.1	002506	Cluster2059_1clades	97	PBI_121Q_173	Escherichia phage 121Q	GCA_000926855.1
AGC35030.1	002506	Cluster2059_1clades	92	ACQ29_gp350	Escherichia phage PBECO4	GCA_001041035.1
BBM61746.1	002506	Cluster2059_1clades	92	EO157G_1570	Escherichia phage SP27	GCA_008033345.1
AXC36607.1	002506	Cluster2059_1clades	92	-	Escherichia phage UB	GCA_003341455.1
QBO61636.1	002506	Cluster2059_1clades	92	G17_00140	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13690.1	002506	Cluster2059_1clades	92	vBEcoMphAPEC6_gp060c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80058.1	002506	Cluster2059_1clades	92	PSLUR01_00081	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44526.1	002506	Cluster2059_1clades	93	RaK2_00253	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFC21837.1	002507	Cluster2060_1clades	77	GAP32_385	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43957.1	002507	Cluster2060_1clades	77	CBB_394	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19095.1	002507	Cluster2060_1clades	97	7t3_0577	Salmonella phage 7t3	GCA_006083215.1
AZU98334.1	002507	Cluster2060_1clades	97	CPT_Munch_392	Salmonella phage Munch	GCA_004015485.1
QIG62649.1	002507	Cluster2060_1clades	97	SEPL_036	Salmonella phage SE_PL	GCA_011067555.1
AQW88918.1	002507	Cluster2060_1clades	82	BF_0393	Serratia phage BF	GCA_002619745.1
SOK59208.1	002507	Cluster2060_1clades	74	g400	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58674.1	002507	Cluster2060_1clades	75	g397	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT13987.1	002508	Cluster2061_1clades	96	PBI_121Q_90	Escherichia phage 121Q	GCA_000926855.1
QAY00351.1	002508	Cluster2061_1clades	95	Ecwhy1_70	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35097.1	002508	Cluster2061_1clades	95	ACQ29_gp417	Escherichia phage PBECO4	GCA_001041035.1
BBM61678.1	002508	Cluster2061_1clades	83	EO157G_0890	Escherichia phage SP27	GCA_008033345.1
AXC36674.1	002508	Cluster2061_1clades	83	-	Escherichia phage UB	GCA_003341455.1
QBO61706.1	002508	Cluster2061_1clades	83	G17_00217	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13753.1	002508	Cluster2061_1clades	83	vBEcoMphAPEC6_gp124c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79991.1	002508	Cluster2061_1clades	83	PSLUR01_00007	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14106.1	002509	Cluster2062_1clades	89	PBI_121Q_216	Escherichia phage 121Q	GCA_000926855.1
QAY00816.1	002509	Cluster2062_1clades	90	Ecwhy1_543	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34990.1	002509	Cluster2062_1clades	93	ACQ29_gp310	Escherichia phage PBECO4	GCA_001041035.1
BBM61788.1	002509	Cluster2062_1clades	89	EO157G_1990	Escherichia phage SP27	GCA_008033345.1
AXC36570.1	002509	Cluster2062_1clades	95	-	Escherichia phage UB	GCA_003341455.1
QBO61593.1	002509	Cluster2062_1clades	89	G17_00097	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13654.1	002509	Cluster2062_1clades	89	vBEcoMphAPEC6_gp023c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80100.1	002509	Cluster2062_1clades	89	PSLUR01_00123	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUE22797.1	002510	Cluster2063_1clades	94	Ah1_00279	Aeromonas phage Ah1	GCA_002957415.1
QAX98512.1	002510	Cluster2063_1clades	94	ASfcp2_176	Aeromonas phage AsFcp_2	GCA_004146885.1
QAY01165.1	002510	Cluster2063_1clades	95	ASwh1_99	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ52974.1	002510	Cluster2063_1clades	94	PX29p255	Aeromonas phage PX29	GCA_000920195.1
ADM79900.1	002510	Cluster2063_1clades	94	phiAS5_ORF0057	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17924.1	002510	Cluster2063_1clades	94	rIII	Aeromonas virus Aeh1	GCA_000843245.1
AIA64838.1	002510	Cluster2063_1clades	93	S13_039	Cronobacter phage S13	GCA_001503575.1
QHJ78824.1	002510	Cluster2063_1clades	93	-	Myoviridae sp.	GCA_012593985.1
APU01541.1	002511	Cluster2064_1clades	90	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29051.1	002511	Cluster2064_1clades	88	AP1_0344	Aeromonas phage AP1	GCA_014183365.1
ATI17362.1	002511	Cluster2064_1clades	88	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00232.1	002511	Cluster2064_1clades	88	HWB28_gp320	Aeromonas phage AS-zj	GCA_002627665.1
QAX97804.1	002511	Cluster2064_1clades	88	ASswx1_160	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01350.1	002511	Cluster2064_1clades	95	ASwh1_290	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39440.1	002511	Cluster2064_1clades	88	CC2_376	Aeromonas phage CC2	GCA_000903495.1
ADQ53163.1	002511	Cluster2064_1clades	90	65p155	Aeromonas virus 65	GCA_000893255.1
APU01723.1	002512	Cluster2065_1clades	94	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28744.1	002512	Cluster2065_1clades	91	AP1_0026	Aeromonas phage AP1	GCA_014183365.1
ATI17573.1	002512	Cluster2065_1clades	91	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00423.1	002512	Cluster2065_1clades	91	HWB28_gp129	Aeromonas phage AS-zj	GCA_002627665.1
QAX98013.1	002512	Cluster2065_1clades	91	ASswx1_373	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01129.1	002512	Cluster2065_1clades	94	ASwh1_62	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39363.1	002512	Cluster2065_1clades	91	CC2_159	Aeromonas phage CC2	GCA_000903495.1
ADQ53363.1	002512	Cluster2065_1clades	94	65p355	Aeromonas virus 65	GCA_000893255.1
AIT14034.1	002513	Cluster2066_1clades	94	PBI_121Q_144	Escherichia phage 121Q	GCA_000926855.1
QAY00307.1	002513	Cluster2066_1clades	94	Ecwhy1_25	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35057.1	002513	Cluster2066_1clades	94	ACQ29_gp377	Escherichia phage PBECO4	GCA_001041035.1
BBM61718.1	002513	Cluster2066_1clades	94	EO157G_1290	Escherichia phage SP27	GCA_008033345.1
AXC36633.1	002513	Cluster2066_1clades	94	-	Escherichia phage UB	GCA_003341455.1
QBO61665.1	002513	Cluster2066_1clades	94	G17_00169	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13715.1	002513	Cluster2066_1clades	94	vBEcoMphAPEC6_gp085c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80030.1	002513	Cluster2066_1clades	94	PSLUR01_00053	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14323.1	002514	Phage-cap-E	93	PBI_121Q_433	Escherichia phage 121Q	GCA_000926855.1
QAY00617.1	002514	Phage-cap-E	93	Ecwhy1_341	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34814.1	002514	Phage-cap-E	93	ACQ29_gp134	Escherichia phage PBECO4	GCA_001041035.1
BBM61996.1	002514	Phage-cap-E	94	EO157G_4070	Escherichia phage SP27	GCA_008033345.1
AXC36924.1	002514	Phage-cap-E	93	-	Escherichia phage UB	GCA_003341455.1
QBO61981.1	002514	Phage-cap-E	93	G17_00492	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14005.1	002514	Phage-cap-E	93	vBEcoMphAPEC6_gp381c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80310.1	002514	Phage-cap-E	93	PSLUR01_00333	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01617.1	002515	Cluster2068_1clades	93	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29096.1	002515	Cluster2068_1clades	93	AP1_0389	Aeromonas phage AP1	GCA_014183365.1
ATI17294.1	002515	Cluster2068_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00302.1	002515	Cluster2068_1clades	93	HWB28_gp250	Aeromonas phage AS-zj	GCA_002627665.1
QAX97736.1	002515	Cluster2068_1clades	93	ASswx1_90	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01419.1	002515	Cluster2068_1clades	93	ASwh1_360	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39317.1	002515	Cluster2068_1clades	93	CC2_021	Aeromonas phage CC2	GCA_000903495.1
ADQ53242.1	002515	Cluster2068_1clades	93	65p234	Aeromonas virus 65	GCA_000893255.1
AIT14412.1	002516	Cluster2069_1clades	93	PBI_121Q_522	Escherichia phage 121Q	GCA_000926855.1
QAY00539.1	002516	Cluster2069_1clades	93	Ecwhy1_260	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34730.1	002516	Cluster2069_1clades	93	ACQ29_gp050	Escherichia phage PBECO4	GCA_001041035.1
BBM62084.1	002516	Cluster2069_1clades	93	EO157G_4950	Escherichia phage SP27	GCA_008033345.1
AXC36846.1	002516	Cluster2069_1clades	93	-	Escherichia phage UB	GCA_003341455.1
QBO61889.1	002516	Cluster2069_1clades	93	G17_00400	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13926.1	002516	Cluster2069_1clades	93	vBEcoMphAPEC6_gp301c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80398.1	002516	Cluster2069_1clades	93	PSLUR01_00421	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14096.1	002517	Cluster2070_1clades	93	PBI_121Q_206	Escherichia phage 121Q	GCA_000926855.1
QAY00826.1	002517	Cluster2070_1clades	91	Ecwhy1_553	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34998.1	002517	Cluster2070_1clades	93	ACQ29_gp318	Escherichia phage PBECO4	GCA_001041035.1
BBM61778.1	002517	Cluster2070_1clades	93	EO157G_1890	Escherichia phage SP27	GCA_008033345.1
AXC36577.1	002517	Cluster2070_1clades	93	-	Escherichia phage UB	GCA_003341455.1
QBO61603.1	002517	Cluster2070_1clades	93	G17_00107	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13661.1	002517	Cluster2070_1clades	93	vBEcoMphAPEC6_gp030c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80090.1	002517	Cluster2070_1clades	93	PSLUR01_00113	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01496.1	002518	Cluster2071_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28960.1	002518	Cluster2071_1clades	91	AP1_0253	Aeromonas phage AP1	GCA_014183365.1
ATI17401.1	002518	Cluster2071_1clades	91	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00194.1	002518	Cluster2071_1clades	91	HWB28_gp358	Aeromonas phage AS-zj	GCA_002627665.1
QAX97841.1	002518	Cluster2071_1clades	91	ASswx1_198	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01311.1	002518	Cluster2071_1clades	91	ASwh1_248	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39426.1	002518	Cluster2071_1clades	91	CC2_337	Aeromonas phage CC2	GCA_000903495.1
ADQ53117.1	002518	Cluster2071_1clades	86	65p109	Aeromonas virus 65	GCA_000893255.1
AIT14312.1	002519	Cluster2072_1clades	91	PBI_121Q_422	Escherichia phage 121Q	GCA_000926855.1
QAY00626.1	002519	Cluster2072_1clades	89	Ecwhy1_351	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34823.1	002519	Cluster2072_1clades	91	ACQ29_gp143	Escherichia phage PBECO4	GCA_001041035.1
BBM61986.1	002519	Cluster2072_1clades	91	EO157G_3970	Escherichia phage SP27	GCA_008033345.1
AXC36931.1	002519	Cluster2072_1clades	50	-	Escherichia phage UB	GCA_003341455.1
QBO61992.1	002519	Cluster2072_1clades	91	G17_00503	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14013.1	002519	Cluster2072_1clades	91	vBEcoMphAPEC6_gp389c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80299.1	002519	Cluster2072_1clades	91	PSLUR01_00322	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGB06879.1	002520	Cluster2073_1clades	86	CF80_gp092	Vibrio phage VH7D	GCA_000914495.1
QBX06267.1	002520	Cluster2073_1clades	86	ValB1HC_314	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60893.1	002520	Cluster2073_1clades	86	AVU32_gp052	Vibrio phage ValKK3	GCA_001501635.1
AGN30253.1	002520	Cluster2073_1clades	91	VPFG_00254	Vibrio phage nt-1	GCA_000910195.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALP47246.1	002520	Cluster2073_1clades	86	phiGrn1_0317	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47631.1	002520	Cluster2073_1clades	86	phiST2_0073	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54894.1	002520	Cluster2073_1clades	86	vBValMR10Z_354	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ALY07185.1	002520	Cluster2073_1clades	88	VmeM32_00199	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFO71328.1	002521	Cluster2074_1clades	65	CR5_108	Cronobacter phage CR5	GCA_000910235.1
AMR59882.1	002521	Cluster2074_1clades	83	SEGD1_235	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07537.1	002521	Cluster2074_1clades	87	DERBICUS_111	Erwinia phage Derbicus	GCA_004521655.1
ANZ48960.1	002521	Cluster2074_1clades	87	EARLPHILLIPIV_111	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50302.1	002521	Cluster2074_1clades	91	PHOBOS_112	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QKN86072.1	002521	Cluster2074_1clades	83	ACEC001_2290	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09121.1	002521	Cluster2074_1clades	83	MLDJOKPK_00209	Salmonella phage SPAsTU	GCA_003183805.1
AEP84064.1	002521	Cluster2074_1clades	83	SPN3US_0231	Salmonella phage SPN3US	GCA_001042275.1
AFC21975.1	002522	CCTBP	90	GAP32_515	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44097.1	002522	CCTBP	90	CBB_534	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18716.1	002522	CCTBP	90	7t3_0195	Salmonella phage 7t3	GCA_006083215.1
AZU97989.1	002522	CCTBP	90	CPT_Munch_045	Salmonella phage Munch	GCA_004015485.1
QIG62990.1	002522	CCTBP	90	SEPL_377	Salmonella phage SE_PL	GCA_011067555.1
AQW89053.1	002522	CCTBP	90	BF_0528	Serratia phage BF	GCA_002619745.1
SOK59331.1	002522	CCTBP	90	g523	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58793.1	002522	CCTBP	90	g516	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14001.1	002523	Cluster2076_1clades	89	PBI_121Q_104	Escherichia phage 121Q	GCA_000926855.1
QAY00337.1	002523	Cluster2076_1clades	89	Ecwhy1_56	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35083.1	002523	Cluster2076_1clades	89	ACQ29_gp403	Escherichia phage PBECO4	GCA_001041035.1
BBM61692.1	002523	Cluster2076_1clades	89	EO157G_1030	Escherichia phage SP27	GCA_008033345.1
AXC36660.1	002523	Cluster2076_1clades	89	-	Escherichia phage UB	GCA_003341455.1
QBO61692.1	002523	Cluster2076_1clades	89	G17_00203	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13741.1	002523	Cluster2076_1clades	89	vBEcoMphAPEC6_gp111c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80005.1	002523	Cluster2076_1clades	89	PSLUR01_00021	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01681.1	002524	Cluster2077_1clades	87	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28842.1	002524	Cluster2077_1clades	87	AP1_0135	Aeromonas phage AP1	GCA_014183365.1
ATI17274.1	002524	Cluster2077_1clades	87	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00319.1	002524	Cluster2077_1clades	87	HWB28_gp233	Aeromonas phage AS-zj	GCA_002627665.1
QAX97716.1	002524	Cluster2077_1clades	87	ASswx1_70	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01094.1	002524	Cluster2077_1clades	89	ASwh1_26	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39466.1	002524	Cluster2077_1clades	87	CC2_042	Aeromonas phage CC2	GCA_000903495.1
ADQ53317.1	002524	Cluster2077_1clades	87	65p309	Aeromonas virus 65	GCA_000893255.1
APU01589.1	002525	Cluster2078_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28973.1	002525	Cluster2078_1clades	78	AP1_0266	Aeromonas phage AP1	GCA_014183365.1
ATI17321.1	002525	Cluster2078_1clades	78	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00273.1	002525	Cluster2078_1clades	76	HWB28_gp279	Aeromonas phage AS-zj	GCA_002627665.1
QAX97764.1	002525	Cluster2078_1clades	78	ASswx1_119	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01392.1	002525	Cluster2078_1clades	71	ASwh1_333	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39311.1	002525	Cluster2078_1clades	78	CC2_418	Aeromonas phage CC2	GCA_000903495.1
ADQ53213.1	002525	Cluster2078_1clades	88	65p205	Aeromonas virus 65	GCA_000893255.1
APU01462.1	002526	Cluster2079_1clades	51	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29002.1	002526	Cluster2079_1clades	88	AP1_0295	Aeromonas phage AP1	GCA_014183365.1
ATI17435.1	002526	Cluster2079_1clades	88	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00160.1	002526	Cluster2079_1clades	88	HWB28_gp392	Aeromonas phage AS-zj	GCA_002627665.1
QAX97875.1	002526	Cluster2079_1clades	88	ASswx1_232	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01274.1	002526	Cluster2079_1clades	87	ASwh1_211	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39418.1	002526	Cluster2079_1clades	88	CC2_302	Aeromonas phage CC2	GCA_000903495.1
ADQ53084.1	002526	Cluster2079_1clades	87	65p074	Aeromonas virus 65	GCA_000893255.1
AIT14313.1	002527	Cluster2080_1clades	88	PBI_121Q_423	Escherichia phage 121Q	GCA_000926855.1
QAY00625.1	002527	Cluster2080_1clades	86	Ecwhy1_350	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34822.1	002527	Cluster2080_1clades	88	ACQ29_gp142	Escherichia phage PBECO4	GCA_001041035.1
BBM61987.1	002527	Cluster2080_1clades	88	EO157G_3980	Escherichia phage SP27	GCA_008033345.1
AXC36930.1	002527	Cluster2080_1clades	88	-	Escherichia phage UB	GCA_003341455.1
QBO61991.1	002527	Cluster2080_1clades	88	G17_00502	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14012.1	002527	Cluster2080_1clades	88	vBEcoMphAPEC6_gp388c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80300.1	002527	Cluster2080_1clades	88	PSLUR01_00323	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14084.1	002528	Cluster2081_1clades	88	PBI_121Q_194	Escherichia phage 121Q	GCA_000926855.1
QAY00839.1	002528	Cluster2081_1clades	88	Ecwhy1_567	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35010.1	002528	Cluster2081_1clades	88	ACQ29_gp330	Escherichia phage PBECO4	GCA_001041035.1
BBM61767.1	002528	Cluster2081_1clades	88	EO157G_1780	Escherichia phage SP27	GCA_008033345.1
AXC36588.1	002528	Cluster2081_1clades	88	-	Escherichia phage UB	GCA_003341455.1
QBO61615.1	002528	Cluster2081_1clades	88	G17_00119	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13673.1	002528	Cluster2081_1clades	88	vBEcoMphAPEC6_gp043c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80078.1	002528	Cluster2081_1clades	88	PSLUR01_00101	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01640.1	002529	Cluster2082_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28882.1	002529	Cluster2082_1clades	88	AP1_0175	Aeromonas phage AP1	GCA_014183365.1
ATI17241.1	002529	Cluster2082_1clades	88	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00346.1	002529	Cluster2082_1clades	88	HWB28_gp206	Aeromonas phage AS-zj	GCA_002627665.1
QAX97684.1	002529	Cluster2082_1clades	88	ASswx1_38	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01466.1	002529	Cluster2082_1clades	87	ASwh1_407	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39332.1	002529	Cluster2082_1clades	87	CC2_076	Aeromonas phage CC2	GCA_000903495.1
ADQ53266.1	002529	Cluster2082_1clades	86	65p258	Aeromonas virus 65	GCA_000893255.1
QAY00736.1	002530	Cluster2083_1clades	87	Ecwhy1_461	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34917.1	002530	Cluster2083_1clades	70	ACQ29_gp237	Escherichia phage PBECO4	GCA_001041035.1
BBM61875.1	002530	Cluster2083_1clades	87	EO157G_2860	Escherichia phage SP27	GCA_008033345.1
AXC37020.1	002530	Cluster2083_1clades	87	-	Escherichia phage UB	GCA_003341455.1
QBO61503.1	002530	Cluster2083_1clades	87	G17_00007	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62109.1	002530	Cluster2083_1clades	87	G17_00620	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14119.1	002530	Cluster2083_1clades	87	vBEcoMphAPEC6_gp496c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80185.1	002530	Cluster2083_1clades	88	PSLUR01_00208	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01685.1	002531	Cluster2084_1clades	87	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28818.1	002531	Cluster2084_1clades	87	AP1_0111	Aeromonas phage AP1	GCA_014183365.1
ATI17608.1	002531	Cluster2084_1clades	87	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00388.1	002531	Cluster2084_1clades	87	HWB28_gp164	Aeromonas phage AS-zj	GCA_002627665.1
QAX98049.1	002531	Cluster2084_1clades	87	ASswx1_409	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01096.1	002531	Cluster2084_1clades	87	ASwh1_28	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39351.1	002531	Cluster2084_1clades	87	CC2_120	Aeromonas phage CC2	GCA_000903495.1
ADQ53321.1	002531	Cluster2084_1clades	87	65p313	Aeromonas virus 65	GCA_000893255.1
APU01584.1	002532	Cluster2085_1clades	73	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28969.1	002532	Cluster2085_1clades	76	AP1_0262	Aeromonas phage AP1	GCA_014183365.1
ATI17325.1	002532	Cluster2085_1clades	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00269.1	002532	Cluster2085_1clades	76	HWB28_gp283	Aeromonas phage AS-zj	GCA_002627665.1
QAX97768.1	002532	Cluster2085_1clades	76	ASswx1_123	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01386.1	002532	Cluster2085_1clades	76	ASwh1_326	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39459.1	002532	Cluster2085_1clades	76	CC2_414	Aeromonas phage CC2	GCA_000903495.1
ADQ53207.1	002532	Cluster2085_1clades	86	65p199	Aeromonas virus 65	GCA_000893255.1
APU01635.1	002533	Cluster2086_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28845.1	002533	Cluster2086_1clades	86	AP1_0138	Aeromonas phage AP1	GCA_014183365.1
ATI17277.1	002533	Cluster2086_1clades	86	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00316.1	002533	Cluster2086_1clades	86	HWB28_gp236	Aeromonas phage AS-zj	GCA_002627665.1
QAX97719.1	002533	Cluster2086_1clades	86	ASswx1_73	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01453.1	002533	Cluster2086_1clades	85	ASwh1_394	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39323.1	002533	Cluster2086_1clades	86	CC2_039	Aeromonas phage CC2	GCA_000903495.1
ADQ53261.1	002533	Cluster2086_1clades	86	65p253	Aeromonas virus 65	GCA_000893255.1
APU01639.1	002534	Cluster2087_1clades	74	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28879.1	002534	Cluster2087_1clades	74	AP1_0172	Aeromonas phage AP1	GCA_014183365.1
ATI17244.1	002534	Cluster2087_1clades	74	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00343.1	002534	Cluster2087_1clades	74	HWB28_gp209	Aeromonas phage AS-zj	GCA_002627665.1
QAX97687.1	002534	Cluster2087_1clades	72	ASswx1_41	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01462.1	002534	Cluster2087_1clades	75	ASwh1_403	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39207.1	002534	Cluster2087_1clades	72	CC2_073	Aeromonas phage CC2	GCA_000903495.1
ADQ53265.1	002534	Cluster2087_1clades	86	65p257	Aeromonas virus 65	GCA_000893255.1
APU01780.1	002535	Cluster2088_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29065.1	002535	Cluster2088_1clades	85	AP1_0358	Aeromonas phage AP1	GCA_014183365.1
ATI17521.1	002535	Cluster2088_1clades	85	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00475.1	002535	Cluster2088_1clades	85	HWB28_gp077	Aeromonas phage AS-zj	GCA_002627665.1
QAX97963.1	002535	Cluster2088_1clades	85	ASswx1_321	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01181.1	002535	Cluster2088_1clades	86	ASwh1_116	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39476.1	002535	Cluster2088_1clades	85	CC2_211	Aeromonas phage CC2	GCA_000903495.1
ADQ53423.1	002535	Cluster2088_1clades	86	65p416	Aeromonas virus 65	GCA_000893255.1
APU01781.1	002536	Cluster2089_1clades	83	-	Aeromonas phage 65.2	GCA_002618145.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QMV29064.1	002536	Cluster2089_1clades	86	AP1_0357	Aeromonas phage AP1	GCA_014183365.1
ATI17520.1	002536	Cluster2089_1clades	86	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00476.1	002536	Cluster2089_1clades	86	HWB28_gp076	Aeromonas phage AS-zj	GCA_002627665.1
QAX97962.1	002536	Cluster2089_1clades	86	ASswx1_320	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01180.1	002536	Cluster2089_1clades	83	ASwh1_115	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39381.1	002536	Cluster2089_1clades	86	CC2_212	Aeromonas phage CC2	GCA_000903495.1
ADQ53424.1	002536	Cluster2089_1clades	83	65p417	Aeromonas virus 65	GCA_000893255.1
APU01427.1	002537	AQSYN	85	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28760.1	002537	AQSYN	86	AP1_0042	Aeromonas phage AP1	GCA_014183365.1
ATI17471.1	002537	AQSYN	86	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00526.1	002537	AQSYN	86	HWB28_gp026	Aeromonas phage AS-zj	GCA_002627665.1
QAX97911.1	002537	AQSYN	86	ASswx1_268	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01239.1	002537	AQSYN	85	ASwh1_174	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39401.1	002537	AQSYN	86	CC2_264	Aeromonas phage CC2	GCA_000903495.1
AAR90902.1	002537	AQSYN	85	65p036	Aeromonas virus 65	GCA_000893255.1
AIT14054.1	002538	Cluster2091_1clades	86	PBI_121Q_164	Escherichia phage 121Q	GCA_000926855.1
QAY00289.1	002538	Cluster2091_1clades	86	Ecwhy1_7	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35039.1	002538	Cluster2091_1clades	86	ACQ29_gp359	Escherichia phage PBECO4	GCA_001041035.1
BBM61737.1	002538	Cluster2091_1clades	86	EO157G_1480	Escherichia phage SP27	GCA_008033345.1
AXC36616.1	002538	Cluster2091_1clades	86	-	Escherichia phage UB	GCA_003341455.1
QBO61645.1	002538	Cluster2091_1clades	86	G17_00149	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13699.1	002538	Cluster2091_1clades	86	vBEcoMphAPEC6_gp069c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80049.1	002538	Cluster2091_1clades	86	PSLUR01_00072	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01558.1	002539	Cluster2092_1clades	85	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28937.1	002539	Cluster2092_1clades	85	AP1_0230	Aeromonas phage AP1	GCA_014183365.1
ATI17343.1	002539	Cluster2092_1clades	85	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00250.1	002539	Cluster2092_1clades	85	HWB28_gp302	Aeromonas phage AS-zj	GCA_002627665.1
QAX97788.1	002539	Cluster2092_1clades	85	ASswx1_143	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01366.1	002539	Cluster2092_1clades	85	ASwh1_306	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39308.1	002539	Cluster2092_1clades	85	CC2_395	Aeromonas phage CC2	GCA_000903495.1
ADQ53181.1	002539	Cluster2092_1clades	85	65p173	Aeromonas virus 65	GCA_000893255.1
AIT14025.1	002540	Cluster2093_1clades	85	PBI_121Q_134	Escherichia phage 121Q	GCA_000926855.1
QAY00314.1	002540	Cluster2093_1clades	85	Ecwhy1_32	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35063.1	002540	Cluster2093_1clades	85	ACQ29_gp383	Escherichia phage PBECO4	GCA_001041035.1
BBM61712.1	002540	Cluster2093_1clades	85	EO157G_1230	Escherichia phage SP27	GCA_008033345.1
AXC36640.1	002540	Cluster2093_1clades	85	-	Escherichia phage UB	GCA_003341455.1
QBO61672.1	002540	Cluster2093_1clades	85	G17_00177	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13721.1	002540	Cluster2093_1clades	85	vBEcoMphAPEC6_gp091c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80024.1	002540	Cluster2093_1clades	85	PSLUR01_00046	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AJK27554.1	002541	Cluster2094_1clades	74	PTIM40_127	Cyanophage P-TIM40	GCA_001470935.1
AGH07469.1	002541	Cluster2094_1clades	74	CYVG_00025	Cyanophage S-SSM6a	GCA_002710385.1
AGG54408.1	002541	Cluster2094_1clades	77	CYWG_00124	Cyanophage S-SSM6b	GCA_002710425.1
AGH26208.1	002541	Cluster2094_1clades	78	CPMG_00107	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44422.1	002541	Cluster2094_1clades	59	PSSM2_044	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12228.1	002541	Cluster2094_1clades	59	PRTG_00070	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93469.1	002541	Cluster2094_1clades	85	AVU42_gp130	Prochlorococcus phage P-TIM68	GCA_001503075.1
QJT70128.1	002541	Cluster2094_1clades	68	SynMITS9220M01_115	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14100.1	002542	Cluster2095_1clades	84	PBI_121Q_210	Escherichia phage 121Q	GCA_000926855.1
QAY00822.1	002542	Cluster2095_1clades	85	Ecwhy1_549	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34995.1	002542	Cluster2095_1clades	84	ACQ29_gp315	Escherichia phage PBECO4	GCA_001041035.1
BBM61782.1	002542	Cluster2095_1clades	84	EO157G_1930	Escherichia phage SP27	GCA_008033345.1
AXC36575.1	002542	Cluster2095_1clades	84	-	Escherichia phage UB	GCA_003341455.1
QBO61599.1	002542	Cluster2095_1clades	84	G17_00103	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13658.1	002542	Cluster2095_1clades	84	vBEcoMphAPEC6_gp027c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80094.1	002542	Cluster2095_1clades	84	PSLUR01_00117	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14336.1	002543	Cluster2096_1clades	84	PBI_121Q_446	Escherichia phage 121Q	GCA_000926855.1
QAY00607.1	002543	Cluster2096_1clades	83	Ecwhy1_331	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34802.1	002543	Cluster2096_1clades	83	ACQ29_gp122	Escherichia phage PBECO4	GCA_001041035.1
BBM62007.1	002543	Cluster2096_1clades	83	EO157G_4180	Escherichia phage SP27	GCA_008033345.1
AXC36915.1	002543	Cluster2096_1clades	83	-	Escherichia phage UB	GCA_003341455.1
QBO61968.1	002543	Cluster2096_1clades	83	G17_00479	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13994.1	002543	Cluster2096_1clades	83	vBEcoMphAPEC6_gp370c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80323.1	002543	Cluster2096_1clades	83	PSLUR01_00346	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01577.1	002544	Cluster2097_1clades	80	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28964.1	002544	Cluster2097_1clades	80	AP1_0257	Aeromonas phage AP1	GCA_014183365.1
ATI17330.1	002544	Cluster2097_1clades	80	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00264.1	002544	Cluster2097_1clades	84	HWB28_gp288	Aeromonas phage AS-zj	GCA_002627665.1
QAX97773.1	002544	Cluster2097_1clades	80	ASswx1_128	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01375.1	002544	Cluster2097_1clades	82	ASwh1_315	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39291.1	002544	Cluster2097_1clades	80	CC2_409	Aeromonas phage CC2	GCA_000903495.1
ADQ53201.1	002544	Cluster2097_1clades	39	65p193	Aeromonas virus 65	GCA_000893255.1
APU01522.1	002545	Cluster2098_1clades	82	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28774.1	002545	Cluster2098_1clades	83	AP1_0056	Aeromonas phage AP1	GCA_014183365.1
ATI17378.1	002545	Cluster2098_1clades	83	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00216.1	002545	Cluster2098_1clades	83	HWB28_gp336	Aeromonas phage AS-zj	GCA_002627665.1
QAX97819.1	002545	Cluster2098_1clades	83	ASswx1_175	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01334.1	002545	Cluster2098_1clades	83	ASwh1_273	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39307.1	002545	Cluster2098_1clades	83	CC2_361	Aeromonas phage CC2	GCA_000903495.1
ADQ53144.1	002545	Cluster2098_1clades	82	65p136	Aeromonas virus 65	GCA_000893255.1
AIT14217.1	002546	Cluster2099_1clades	83	PBI_121Q_327	Escherichia phage 121Q	GCA_000926855.1
QAY00721.1	002546	Cluster2099_1clades	83	Ecwhy1_446	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34904.1	002546	Cluster2099_1clades	49	ACQ29_gp224	Escherichia phage PBECO4	GCA_001041035.1
BBM61890.1	002546	Cluster2099_1clades	82	EO157G_3010	Escherichia phage SP27	GCA_008033345.1
AXC37009.1	002546	Cluster2099_1clades	40	-	Escherichia phage UB	GCA_003341455.1
QBO62092.1	002546	Cluster2099_1clades	82	G17_00603	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14105.1	002546	Cluster2099_1clades	83	vBEcoMphAPEC6_gp482c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80202.1	002546	Cluster2099_1clades	82	PSLUR01_00225	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14344.1	002547	Cluster2100_1clades	83	PBI_121Q_454	Escherichia phage 121Q	GCA_000926855.1
QAY00600.1	002547	Cluster2100_1clades	72	Ecwhy1_323	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34795.1	002547	Cluster2100_1clades	71	ACQ29_gp115	Escherichia phage PBECO4	GCA_001041035.1
BBM62015.1	002547	Cluster2100_1clades	83	EO157G_4260	Escherichia phage SP27	GCA_008033345.1
AXC36911.1	002547	Cluster2100_1clades	71	-	Escherichia phage UB	GCA_003341455.1
QBO61960.1	002547	Cluster2100_1clades	83	G17_00471	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13987.1	002547	Cluster2100_1clades	83	vBEcoMphAPEC6_gp363c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80331.1	002547	Cluster2100_1clades	83	PSLUR01_00354	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01556.1	002548	Cluster2101_1clades	81	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29087.1	002548	Cluster2101_1clades	82	AP1_0380	Aeromonas phage AP1	GCA_014183365.1
ATI17345.1	002548	Cluster2101_1clades	82	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00248.1	002548	Cluster2101_1clades	82	HWB28_gp304	Aeromonas phage AS-zj	GCA_002627665.1
QAX97790.1	002548	Cluster2101_1clades	82	ASswx1_145	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01364.1	002548	Cluster2101_1clades	82	ASwh1_304	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39448.1	002548	Cluster2101_1clades	82	CC2_393	Aeromonas phage CC2	GCA_000903495.1
ADQ53179.1	002548	Cluster2101_1clades	81	65p171	Aeromonas virus 65	GCA_000893255.1
ARB13725.1	002549	Cluster2102_1clades	82	Ccr10_gp195c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14070.1	002549	Cluster2102_1clades	60	Ccr2_gp194c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14759.1	002549	Cluster2102_1clades	82	Ccr29_gp203	Caulobacter phage Ccr29	GCA_002619485.1
ARB14413.1	002549	Cluster2102_1clades	82	Ccr5_gp193c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87718.1	002549	Cluster2102_1clades	82	CcrKarma_gp201	Caulobacter virus Karma	GCA_000901575.1
AFU87367.1	002549	Cluster2102_1clades	82	CcrMagneto_gp197	Caulobacter virus Magneto	GCA_000903095.1
AFU86677.1	002549	Cluster2102_1clades	81	CcrRogue_gp195	Caulobacter virus Rogue	GCA_000900555.1
AFU88514.1	002549	Cluster2102_1clades	82	CcrSwift_gp196	Caulobacter virus Swift	GCA_000899655.1
APU01549.1	002550	Cluster2103_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29011.1	002550	Cluster2103_1clades	79	AP1_0304	Aeromonas phage AP1	GCA_014183365.1
ATI17352.1	002550	Cluster2103_1clades	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00241.1	002550	Cluster2103_1clades	79	HWB28_gp311	Aeromonas phage AS-zj	GCA_002627665.1
QAX97797.1	002550	Cluster2103_1clades	79	ASswx1_152	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01358.1	002550	Cluster2103_1clades	80	ASwh1_298	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39285.1	002550	Cluster2103_1clades	81	CC2_385	Aeromonas phage CC2	GCA_000903495.1
ADQ53171.1	002550	Cluster2103_1clades	78	65p163	Aeromonas virus 65	GCA_000893255.1
APU01594.1	002551	SIG+TM	80	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29043.1	002551	SIG+TM	76	AP1_0336	Aeromonas phage AP1	GCA_014183365.1
ATI17317.1	002551	SIG+TM	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00277.1	002551	SIG+TM	76	HWB28_gp275	Aeromonas phage AS-zj	GCA_002627665.1
QAX97760.1	002551	SIG+TM	76	ASswx1_115	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01394.1	002551	SIG+TM	80	ASwh1_335	Aeromonas phage Aswh_1	GCA_004146945.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFN39463.1	002551	SIG+TM	76	CC2_422	Aeromonas phage CC2	GCA_000903495.1
ADQ53218.1	002551	SIG+TM	80	65p210	Aeromonas virus 65	GCA_000893255.1
AFC21880.1	002552	Cluster2105_1clades	80	GAP32_427	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44010.1	002552	Cluster2105_1clades	80	CBB_447	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18537.1	002552	Cluster2105_1clades	80	7t3_04	Salmonella phage 7t3	GCA_006083215.1
AZU98370.1	002552	Cluster2105_1clades	80	CPT_Munch_430	Salmonella phage Munch	GCA_004015485.1
QIG63143.1	002552	Cluster2105_1clades	80	SEPL_530	Salmonella phage SE_PL	GCA_011067555.1
AQW88967.1	002552	Cluster2105_1clades	80	BF_0442	Serratia phage BF	GCA_002619745.1
SOK59256.1	002552	Cluster2105_1clades	80	g448	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58721.1	002552	Cluster2105_1clades	80	g444	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01768.1	002553	Cluster2106_1clades	79	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28978.1	002553	Cluster2106_1clades	74	AP1_0271	Aeromonas phage AP1	GCA_014183365.1
ATI17529.1	002553	Cluster2106_1clades	74	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00467.1	002553	Cluster2106_1clades	74	HWB28_gp085	Aeromonas phage AS-zj	GCA_002627665.1
QAX97971.1	002553	Cluster2106_1clades	74	ASswx1_329	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01169.1	002553	Cluster2106_1clades	77	ASwh1_103	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39378.1	002553	Cluster2106_1clades	74	CC2_204	Aeromonas phage CC2	GCA_000903495.1
ADQ53411.1	002553	Cluster2106_1clades	79	65p404	Aeromonas virus 65	GCA_000893255.1
APU01724.1	002554	Cluster2107_1clades	77	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28742.1	002554	Cluster2107_1clades	79	AP1_0024	Aeromonas phage AP1	GCA_014183365.1
ATI17571.1	002554	Cluster2107_1clades	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00425.1	002554	Cluster2107_1clades	79	HWB28_gp127	Aeromonas phage AS-zj	GCA_002627665.1
QAX98011.1	002554	Cluster2107_1clades	79	ASswx1_371	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01130.1	002554	Cluster2107_1clades	77	ASwh1_63	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39364.1	002554	Cluster2107_1clades	79	CC2_161	Aeromonas phage CC2	GCA_000903495.1
ADQ53364.1	002554	Cluster2107_1clades	77	65p356	Aeromonas virus 65	GCA_000893255.1
APU01624.1	002555	Cluster2108_1clades	79	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29032.1	002555	Cluster2108_1clades	76	AP1_0325	Aeromonas phage AP1	GCA_014183365.1
ATI17260.1	002555	Cluster2108_1clades	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00331.1	002555	Cluster2108_1clades	76	HWB28_gp221	Aeromonas phage AS-zj	GCA_002627665.1
QAX97700.1	002555	Cluster2108_1clades	76	ASswx1_54	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01436.1	002555	Cluster2108_1clades	74	ASwh1_377	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39196.1	002555	Cluster2108_1clades	76	CC2_056	Aeromonas phage CC2	GCA_000903495.1
ADQ53249.1	002555	Cluster2108_1clades	54	65p241	Aeromonas virus 65	GCA_000893255.1
AXG67119.1	002556	Cluster2109_1clades	79	AD1_075	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79876.1	002556	Cluster2109_1clades	79	JA11_071	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66475.1	002556	Cluster2109_1clades	79	JA13_072	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66800.1	002556	Cluster2109_1clades	79	JA29_074	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67445.1	002556	Cluster2109_1clades	79	JA33_071	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08355.1	002556	Cluster2109_1clades	79	Alexandra_78	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58718.1	002556	Cluster2109_1clades	79	Y3_078	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28552.1	002556	Cluster2109_1clades	79	YOLOSWAG_69	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14376.1	002557	Cluster2110_1clades	76	PBI_121Q_486	Escherichia phage 121Q	GCA_000926855.1
QAY00572.1	002557	Cluster2110_1clades	77	Ecwhy1_293	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34764.1	002557	Cluster2110_1clades	52	ACQ29_gp084	Escherichia phage PBECO4	GCA_001041035.1
BBM62047.1	002557	Cluster2110_1clades	77	EO157G_4580	Escherichia phage SP27	GCA_008033345.1
AXC36879.1	002557	Cluster2110_1clades	77	-	Escherichia phage UB	GCA_003341455.1
QBO61926.1	002557	Cluster2110_1clades	77	G17_00437	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13958.1	002557	Cluster2110_1clades	77	vBEcoMphAPEC6_gp334c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80365.1	002557	Cluster2110_1clades	77	PSLUR01_00388	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01578.1	002558	Cluster2111_1clades	76	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28940.1	002558	Cluster2111_1clades	75	AP1_0233	Aeromonas phage AP1	GCA_014183365.1
ATI17340.1	002558	Cluster2111_1clades	75	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00253.1	002558	Cluster2111_1clades	75	HWB28_gp299	Aeromonas phage AS-zj	GCA_002627665.1
QAX97785.1	002558	Cluster2111_1clades	75	ASswx1_140	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01379.1	002558	Cluster2111_1clades	72	ASwh1_319	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39289.1	002558	Cluster2111_1clades	75	CC2_398	Aeromonas phage CC2	GCA_000903495.1
ADQ53202.1	002558	Cluster2111_1clades	76	65p194	Aeromonas virus 65	GCA_000893255.1
APU01622.1	002559	Cluster2112_1clades	74	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29030.1	002559	Cluster2112_1clades	76	AP1_0323	Aeromonas phage AP1	GCA_014183365.1
ATI17261.1	002559	Cluster2112_1clades	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00329.1	002559	Cluster2112_1clades	76	HWB28_gp223	Aeromonas phage AS-zj	GCA_002627665.1
QAX97701.1	002559	Cluster2112_1clades	75	ASswx1_55	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01437.1	002559	Cluster2112_1clades	75	ASwh1_378	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39194.1	002559	Cluster2112_1clades	76	CC2_054	Aeromonas phage CC2	GCA_000903495.1
ADQ53247.1	002559	Cluster2112_1clades	74	65p239	Aeromonas virus 65	GCA_000893255.1
AIT14159.1	002560	Cluster2113_1clades	76	PBI_121Q_269	Escherichia phage 121Q	GCA_000926855.1
QAY00776.1	002560	Cluster2113_1clades	76	Ecwhy1_503	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34955.1	002560	Cluster2113_1clades	76	ACQ29_gp275	Escherichia phage PBECO4	GCA_001041035.1
BBM61833.1	002560	Cluster2113_1clades	76	EO157G_2440	Escherichia phage SP27	GCA_008033345.1
QBO61546.1	002560	Cluster2113_1clades	76	G17_00050	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62152.1	002560	Cluster2113_1clades	76	G17_00663	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14159.1	002560	Cluster2113_1clades	76	vBEcoMphAPEC6_gp536c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80148.1	002560	Cluster2113_1clades	76	PSLUR01_00171	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14059.1	002561	Cluster2114_1clades	76	PBI_121Q_169	Escherichia phage 121Q	GCA_000926855.1
QAY00285.1	002561	Cluster2114_1clades	75	Ecwhy1_2	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35034.1	002561	Cluster2114_1clades	76	ACQ29_gp354	Escherichia phage PBECO4	GCA_001041035.1
BBM61742.1	002561	Cluster2114_1clades	76	EO157G_1530	Escherichia phage SP27	GCA_008033345.1
AXC36611.1	002561	Cluster2114_1clades	76	-	Escherichia phage UB	GCA_003341455.1
QBO61640.1	002561	Cluster2114_1clades	76	G17_00144	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13694.1	002561	Cluster2114_1clades	76	vBEcoMphAPEC6_gp064c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80054.1	002561	Cluster2114_1clades	76	PSLUR01_00077	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01430.1	002562	Cluster2115_1clades	75	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28763.1	002562	Cluster2115_1clades	74	AP1_0045	Aeromonas phage AP1	GCA_014183365.1
ATI17468.1	002562	Cluster2115_1clades	74	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00529.1	002562	Cluster2115_1clades	74	HWB28_gp023	Aeromonas phage AS-zj	GCA_002627665.1
QAX97908.1	002562	Cluster2115_1clades	74	ASswx1_265	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01242.1	002562	Cluster2115_1clades	75	ASwh1_177	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39403.1	002562	Cluster2115_1clades	74	CC2_267	Aeromonas phage CC2	GCA_000903495.1
AAR90899.1	002562	Cluster2115_1clades	75	65p039	Aeromonas virus 65	GCA_000893255.1
AIT14047.1	002563	Cluster2116_1clades	75	PBI_121Q_157	Escherichia phage 121Q	GCA_000926855.1
QAY00296.1	002563	Cluster2116_1clades	75	Ecwhy1_14	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35046.1	002563	Cluster2116_1clades	75	ACQ29_gp366	Escherichia phage PBECO4	GCA_001041035.1
BBM61730.1	002563	Cluster2116_1clades	75	EO157G_1410	Escherichia phage SP27	GCA_008033345.1
AXC36623.1	002563	Cluster2116_1clades	75	-	Escherichia phage UB	GCA_003341455.1
QBO61652.1	002563	Cluster2116_1clades	75	G17_00156	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13705.1	002563	Cluster2116_1clades	75	vBEcoMphAPEC6_gp075c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80042.1	002563	Cluster2116_1clades	75	PSLUR01_00065	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21888.1	002564	Cluster2117_1clades	74	GAP32_434	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44016.1	002564	Cluster2117_1clades	74	CBB_453	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18560.1	002564	Cluster2117_1clades	74	7t3_037	Salmonella phage 7t3	GCA_006083215.1
AZU98389.1	002564	Cluster2117_1clades	74	CPT_Munch_456	Salmonella phage Munch	GCA_004015485.1
QIG63123.1	002564	Cluster2117_1clades	74	SEPL_510	Salmonella phage SE_PL	GCA_011067555.1
AQW88976.1	002564	Cluster2117_1clades	74	BF_0451	Serratia phage BF	GCA_002619745.1
SOK59260.1	002564	Cluster2117_1clades	74	g452	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58725.1	002564	Cluster2117_1clades	74	g448	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14086.1	002565	Cluster2118_1clades	73	PBI_121Q_196	Escherichia phage 121Q	GCA_000926855.1
QAY00837.1	002565	Cluster2118_1clades	74	Ecwhy1_565	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35008.1	002565	Cluster2118_1clades	73	ACQ29_gp328	Escherichia phage PBECO4	GCA_001041035.1
BBM61769.1	002565	Cluster2118_1clades	73	EO157G_1800	Escherichia phage SP27	GCA_008033345.1
AXC36586.1	002565	Cluster2118_1clades	73	-	Escherichia phage UB	GCA_003341455.1
QBO61613.1	002565	Cluster2118_1clades	73	G17_00117	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13671.1	002565	Cluster2118_1clades	73	vBEcoMphAPEC6_gp040c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80080.1	002565	Cluster2118_1clades	73	PSLUR01_00103	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01424.1	002566	Cluster2119_1clades	71	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28757.1	002566	Cluster2119_1clades	73	AP1_0039	Aeromonas phage AP1	GCA_014183365.1
ATI17474.1	002566	Cluster2119_1clades	73	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00523.1	002566	Cluster2119_1clades	73	HWB28_gp029	Aeromonas phage AS-zj	GCA_002627665.1
QAX97914.1	002566	Cluster2119_1clades	73	ASswx1_271	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01236.1	002566	Cluster2119_1clades	74	ASwh1_171	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39399.1	002566	Cluster2119_1clades	73	CC2_261	Aeromonas phage CC2	GCA_000903495.1
AAR90905.1	002566	Cluster2119_1clades	71	65p033	Aeromonas virus 65	GCA_000893255.1
AAX44410.1	002567	Cluster2120_1clades	68	PSSM2_032	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12241.1	002567	Cluster2120_1clades	68	PRTG_00083	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93583.1	002567	Cluster2120_1clades	73	AVU42_gp019	Prochlorococcus phage P-TIM68	GCA_001503075.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASR76068.1	002567	Cluster2120_1clades	60	PBI_BELLAMY_21	Synechococcus phage Bellamy	GCA_002627525.1
QCW22912.1	002567	Cluster2120_1clades	72	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50546.1	002567	Cluster2120_1clades	74	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70433.1	002567	Cluster2120_1clades	64	HOU04_gp034	Synechococcus phage S-T4	GCA_003443335.1
QJT70037.1	002567	Cluster2120_1clades	60	SynMITS9220M01_021	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01637.1	002568	Cluster2121_1clades	53	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28835.1	002568	Cluster2121_1clades	74	AP1_0128	Aeromonas phage AP1	GCA_014183365.1
ATI17268.1	002568	Cluster2121_1clades	51	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00324.1	002568	Cluster2121_1clades	51	HWB28_gp228	Aeromonas phage AS-zj	GCA_002627665.1
QAX97708.1	002568	Cluster2121_1clades	51	ASswx1_62	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01456.1	002568	Cluster2121_1clades	53	ASwh1_397	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39189.1	002568	Cluster2121_1clades	51	CC2_049	Aeromonas phage CC2	GCA_000903495.1
ADQ53263.1	002568	Cluster2121_1clades	53	65p255	Aeromonas virus 65	GCA_000893255.1
AIT14230.1	002569	Cluster2122_1clades	73	PBI_121Q_340	Escherichia phage 121Q	GCA_000926855.1
QAY00705.1	002569	Cluster2122_1clades	73	Ecwhy1_430	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34895.1	002569	Cluster2122_1clades	73	ACQ29_gp215	Escherichia phage PBECO4	GCA_001041035.1
BBM61906.1	002569	Cluster2122_1clades	73	EO157G_3170	Escherichia phage SP27	GCA_008033345.1
AXC36999.1	002569	Cluster2122_1clades	73	-	Escherichia phage UB	GCA_003341455.1
QBO62075.1	002569	Cluster2122_1clades	73	G17_00586	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14091.1	002569	Cluster2122_1clades	73	vBEcoMphAPEC6_gp468c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80219.1	002569	Cluster2122_1clades	73	PSLUR01_00242	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14072.1	002570	Cluster2123_1clades	73	PBI_121Q_182	Escherichia phage 121Q	GCA_000926855.1
QAY00851.1	002570	Cluster2123_1clades	73	Ecwhy1_579	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35021.1	002570	Cluster2123_1clades	47	ACQ29_gp341	Escherichia phage PBECO4	GCA_001041035.1
BBM61755.1	002570	Cluster2123_1clades	73	EO157G_1660	Escherichia phage SP27	GCA_008033345.1
AXC36598.1	002570	Cluster2123_1clades	47	-	Escherichia phage UB	GCA_003341455.1
QBO61627.1	002570	Cluster2123_1clades	73	G17_00131	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13683.1	002570	Cluster2123_1clades	73	vBEcoMphAPEC6_gp053c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80066.1	002570	Cluster2123_1clades	73	PSLUR01_00089	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AOO14399.1	002571	Cluster2124_1clades	73	Sn110110_206	Cyanophage S-RIM14	GCA_002599065.1
AOO15048.1	002571	Cluster2124_1clades	73	W1230910_203	Cyanophage S-RIM14	GCA_002599125.1
AIX30725.1	002571	Cluster2124_1clades	70	Syn7803US37_248	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76297.1	002571	Cluster2124_1clades	72	PBI_BELLAMY_261	Synechococcus phage Bellamy	GCA_002627525.1
AOV59676.1	002571	Cluster2124_1clades	69	S330809_215	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59438.1	002571	Cluster2124_1clades	46	C440309_215	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59913.1	002571	Cluster2124_1clades	47	N231010_214	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70242.1	002571	Cluster2124_1clades	60	SynMITS9220M01_236	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXG67049.1	002572	Cluster2125_1clades	71	AD1_005	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79809.1	002572	Cluster2125_1clades	71	JA11_004	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66407.1	002572	Cluster2125_1clades	71	JA13_004	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66730.1	002572	Cluster2125_1clades	71	JA29_004	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67378.1	002572	Cluster2125_1clades	71	JA33_004	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08287.1	002572	Cluster2125_1clades	70	Alexandra_5	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58645.1	002572	Cluster2125_1clades	70	Y3_005	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28492.1	002572	Cluster2125_1clades	73	YOLOSWAG_5	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01680.1	002573	Cluster2126_1clades	66	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28815.1	002573	Cluster2126_1clades	70	AP1_0108	Aeromonas phage AP1	GCA_014183365.1
ATI17611.1	002573	Cluster2126_1clades	70	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00385.1	002573	Cluster2126_1clades	70	HWB28_gp167	Aeromonas phage AS-zj	GCA_002627665.1
QAX98053.1	002573	Cluster2126_1clades	70	ASswx1_413	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01093.1	002573	Cluster2126_1clades	73	ASwh1_25	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39349.1	002573	Cluster2126_1clades	70	CC2_116	Aeromonas phage CC2	GCA_000903495.1
ADQ53316.1	002573	Cluster2126_1clades	66	65p308	Aeromonas virus 65	GCA_000893255.1
AOO14213.1	002574	SIG+TM	70	Sn110110_019	Cyanophage S-RIM14	GCA_002599065.1
AOO14865.1	002574	SIG+TM	70	W1230910_019	Cyanophage S-RIM14	GCA_002599125.1
ADK66270.1	002574	SIG+TM	71	PSSM2_089.1	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12185.1	002574	SIG+TM	71	PRTG_00027	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59517.1	002574	SIG+TM	71	S330809_056	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59279.1	002574	SIG+TM	71	C440309_056	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59755.1	002574	SIG+TM	71	N231010_056	Synechococcus phage S-CAM4	GCA_002922155.1
QJT70145.1	002574	SIG+TM	73	SynMITS9220M01_132	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14073.1	002575	Cluster2128_1clades	72	PBI_121Q_183	Escherichia phage 121Q	GCA_000926855.1
QAY00850.1	002575	Cluster2128_1clades	72	Ecwhy1_578	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35020.1	002575	Cluster2128_1clades	72	ACQ29_gp340	Escherichia phage PBECO4	GCA_001041035.1
BBM61756.1	002575	Cluster2128_1clades	72	EO157G_1670	Escherichia phage SP27	GCA_008033345.1
AXC36597.1	002575	Cluster2128_1clades	72	-	Escherichia phage UB	GCA_003341455.1
QBO61626.1	002575	Cluster2128_1clades	72	G17_00130	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13682.1	002575	Cluster2128_1clades	72	vBEcoMphAPEC6_gp052c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80067.1	002575	Cluster2128_1clades	72	PSLUR01_00090	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGH56915.1	002576	Cluster2129_2clades	71	CPXG_00112	Cyanophage P-RSM6	GCA_000906155.1
AJK27549.1	002576	Cluster2129_2clades	71	PTIM40_122	Cyanophage P-TIM40	GCA_001470935.1
AGH07592.1	002576	Cluster2129_2clades	71	CYVG_00148	Cyanophage S-SSM6a	GCA_002710385.1
AGG54444.1	002576	Cluster2129_2clades	67	CYWG_00160	Cyanophage S-SSM6b	GCA_002710425.1
AGH26240.1	002576	Cluster2129_2clades	72	CPMG_00139	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44659.1	002576	Cluster2129_2clades	66	PSSM2_282	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12316.1	002576	Cluster2129_2clades	66	PRTG_00163	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93569.1	002576	Cluster2129_2clades	68	-	Prochlorococcus phage P-TIM68	GCA_001503075.1
AXG67276.1	002577	Cluster2130_1clades	71	AD1_232	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80021.1	002577	Cluster2130_1clades	58	JA11_216	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66620.1	002577	Cluster2130_1clades	58	JA13_217	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66944.1	002577	Cluster2130_1clades	58	JA29_218	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67591.1	002577	Cluster2130_1clades	58	JA33_217	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08501.1	002577	Cluster2130_1clades	71	Alexandra_241	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58876.1	002577	Cluster2130_1clades	72	Y3_236	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28710.1	002577	Cluster2130_1clades	71	YOLOSWAG_232	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01563.1	002578	Cluster2131_1clades	68	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28943.1	002578	Cluster2131_1clades	68	AP1_0236	Aeromonas phage AP1	GCA_014183365.1
ATI17338.1	002578	Cluster2131_1clades	68	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00256.1	002578	Cluster2131_1clades	68	HWB28_gp296	Aeromonas phage AS-zj	GCA_002627665.1
QAX97782.1	002578	Cluster2131_1clades	68	ASswx1_137	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01369.1	002578	Cluster2131_1clades	72	ASwh1_309	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39451.1	002578	Cluster2131_1clades	68	CC2_401	Aeromonas phage CC2	GCA_000903495.1
ADQ53186.1	002578	Cluster2131_1clades	68	65p178	Aeromonas virus 65	GCA_000893255.1
APU01636.1	002579	Cluster2132_1clades	71	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29117.1	002579	Cluster2132_1clades	68	AP1_0414	Aeromonas phage AP1	GCA_014183365.1
ATI17250.1	002579	Cluster2132_1clades	68	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00338.1	002579	Cluster2132_1clades	68	HWB28_gp214	Aeromonas phage AS-zj	GCA_002627665.1
QAX97694.1	002579	Cluster2132_1clades	68	ASswx1_48	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01457.1	002579	Cluster2132_1clades	71	ASwh1_398	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39329.1	002579	Cluster2132_1clades	68	CC2_064	Aeromonas phage CC2	GCA_000903495.1
ADQ53262.1	002579	Cluster2132_1clades	71	65p254	Aeromonas virus 65	GCA_000893255.1
AIT14208.1	002580	Cluster2133_1clades	69	PBI_121Q_318	Escherichia phage 121Q	GCA_000926855.1
QAY00730.1	002580	Cluster2133_1clades	69	Ecwhy1_455	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34912.1	002580	Cluster2133_1clades	69	ACQ29_gp232	Escherichia phage PBECO4	GCA_001041035.1
BBM61881.1	002580	Cluster2133_1clades	69	EO157G_2920	Escherichia phage SP27	GCA_008033345.1
QBO61497.1	002580	Cluster2133_1clades	69	G17_00001	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62103.1	002580	Cluster2133_1clades	69	G17_00614	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14113.1	002580	Cluster2133_1clades	69	vBEcoMphAPEC6_gp490c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80191.1	002580	Cluster2133_1clades	69	PSLUR01_00214	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG67204.1	002581	Cluster2134_1clades	64	AD1_160	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79955.1	002581	Cluster2134_1clades	69	JA11_150	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66554.1	002581	Cluster2134_1clades	69	JA13_151	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66879.1	002581	Cluster2134_1clades	69	JA29_153	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67524.1	002581	Cluster2134_1clades	69	JA33_150	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08436.1	002581	Cluster2134_1clades	64	Alexandra_165	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58801.1	002581	Cluster2134_1clades	69	Y3_161	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28639.1	002581	Cluster2134_1clades	64	YOLOSWAG_159	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14058.1	002582	Cluster2135_1clades	45	PBI_121Q_168	Escherichia phage 121Q	GCA_000926855.1
QAY00286.1	002582	Cluster2135_1clades	69	Ecwhy1_3	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35035.1	002582	Cluster2135_1clades	45	ACQ29_gp355	Escherichia phage PBECO4	GCA_001041035.1
BBM61741.1	002582	Cluster2135_1clades	69	EO157G_1520	Escherichia phage SP27	GCA_008033345.1
AXC36612.1	002582	Cluster2135_1clades	45	-	Escherichia phage UB	GCA_003341455.1
QBO61641.1	002582	Cluster2135_1clades	69	G17_00145	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13695.1	002582	Cluster2135_1clades	69	vBEcoMphAPEC6_gp065c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80053.1	002582	Cluster2135_1clades	69	PSLUR01_00076	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIT14211.1	002583	Cluster2136_1clades	49	PBI_121Q_321	Escherichia phage 121Q	GCA_000926855.1
QAY00727.1	002583	Cluster2136_1clades	69	Ecwhy1_452	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34908.1	002583	Cluster2136_1clades	53	ACQ29_gp228	Escherichia phage PBECO4	GCA_001041035.1
BBM61884.1	002583	Cluster2136_1clades	69	EO157G_2950	Escherichia phage SP27	GCA_008033345.1
AXC37013.1	002583	Cluster2136_1clades	50	-	Escherichia phage UB	GCA_003341455.1
QBO62100.1	002583	Cluster2136_1clades	69	G17_00611	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14110.1	002583	Cluster2136_1clades	69	vBEcoMphAPEC6_gp487c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80194.1	002583	Cluster2136_1clades	69	PSLUR01_00217	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64379.1	002584	Cluster2137_1clades	68	KVP40.0308	Vibrio phage KVP40	GCA_000843785.1
QIW90694.1	002584	Cluster2137_1clades	68	GCAPEGMB_00347	Vibrio phage V07	GCA_012361095.1
QIW91104.1	002584	Cluster2137_1clades	68	COHAPHLL_00268	Vibrio phage V09	GCA_012361135.1
QHJ74491.1	002584	Cluster2137_1clades	67	VH12019_00164	Vibrio phage VH1_2019	GCA_009931825.1
QBX06160.1	002584	Cluster2137_1clades	68	ValB1HC_207	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61177.1	002584	Cluster2137_1clades	68	AVU32_gp336	Vibrio phage ValKK3	GCA_001501635.1
QNJ54786.1	002584	Cluster2137_1clades	68	vBValMR10Z_246	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37540.1	002584	Cluster2137_1clades	67	pp2_307	Vibriophage phi-pp2	GCA_002630725.1
AIT14420.1	002585	Cluster2138_1clades	67	PBI_121Q_530	Escherichia phage 121Q	GCA_000926855.1
QAY00530.1	002585	Cluster2138_1clades	67	Ecwhy1_251	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34722.1	002585	Cluster2138_1clades	67	ACQ29_gp042	Escherichia phage PBECO4	GCA_001041035.1
BBM62092.1	002585	Cluster2138_1clades	67	EO157G_5030	Escherichia phage SP27	GCA_008033345.1
AXC36840.1	002585	Cluster2138_1clades	67	-	Escherichia phage UB	GCA_003341455.1
QBO61881.1	002585	Cluster2138_1clades	67	G17_00392	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80406.1	002585	Cluster2138_1clades	67	PSLUR01_00429	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44300.1	002585	Cluster2138_1clades	68	RaK2_00027	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMR59905.1	002586	Cluster2139_1clades	67	SEGD1_258	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49903.1	002586	Cluster2139_1clades	57	MACHINA_265	Erwinia phage Machina	GCA_002758035.1
ANZ48287.1	002586	Cluster2139_1clades	68	ASESINO_274	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ49346.1	002586	Cluster2139_1clades	57	HUXLEY_264	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50174.1	002586	Cluster2139_1clades	57	PARSHIK_265	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QKN86094.1	002586	Cluster2139_1clades	67	ACEC001_2510	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09100.1	002586	Cluster2139_1clades	68	MLDJOKPK_00187	Salmonella phage SPAsTU	GCA_003183805.1
AEP84086.1	002586	Cluster2139_1clades	67	SPN3US_0253	Salmonella phage SPN3US	GCA_001042275.1
AXG67147.1	002587	Cluster2140_1clades	67	AD1_103	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79896.1	002587	Cluster2140_1clades	66	JA11_091	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66495.1	002587	Cluster2140_1clades	66	JA13_092	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66820.1	002587	Cluster2140_1clades	66	JA29_094	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67465.1	002587	Cluster2140_1clades	66	JA33_091	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08381.1	002587	Cluster2140_1clades	67	Alexandra_108	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58745.1	002587	Cluster2140_1clades	67	Y3_105	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28578.1	002587	Cluster2140_1clades	68	YOLOSWAG_96	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14155.1	002588	Cluster2141_1clades	63	PBI_121Q_265	Escherichia phage 121Q	GCA_000926855.1
QAY00780.1	002588	Cluster2141_1clades	68	Ecwhy1_507	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00781.1	002588	Cluster2141_1clades	63	Ecwhy1_508	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34960.1	002588	Cluster2141_1clades	63	ACQ29_gp280	Escherichia phage PBECO4	GCA_001041035.1
BBM61829.1	002588	Cluster2141_1clades	63	EO157G_2400	Escherichia phage SP27	GCA_008033345.1
QBO61550.1	002588	Cluster2141_1clades	63	G17_00054	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14163.1	002588	Cluster2141_1clades	63	vBEcoMphAPEC6_gp540c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80144.1	002588	Cluster2141_1clades	66	PSLUR01_00167	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01694.1	002589	Cluster2142_1clades	67	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28830.1	002589	Cluster2142_1clades	66	AP1_0123	Aeromonas phage AP1	GCA_014183365.1
ATI17597.1	002589	Cluster2142_1clades	66	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00400.1	002589	Cluster2142_1clades	66	HWB28_gp152	Aeromonas phage AS-zj	GCA_002627665.1
QAX98037.1	002589	Cluster2142_1clades	66	ASswx1_397	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01108.1	002589	Cluster2142_1clades	65	ASwh1_40	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39228.1	002589	Cluster2142_1clades	66	CC2_134	Aeromonas phage CC2	GCA_000903495.1
ADQ53332.1	002589	Cluster2142_1clades	67	65p324	Aeromonas virus 65	GCA_000893255.1
APU01742.1	002590	Cluster2143_1clades	67	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28923.1	002590	Cluster2143_1clades	63	AP1_0216	Aeromonas phage AP1	GCA_014183365.1
ATI17556.1	002590	Cluster2143_1clades	63	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00441.1	002590	Cluster2143_1clades	63	HWB28_gp111	Aeromonas phage AS-zj	GCA_002627665.1
QAX97996.1	002590	Cluster2143_1clades	63	ASswx1_356	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39371.1	002590	Cluster2143_1clades	63	CC2_179	Aeromonas phage CC2	GCA_000903495.1
QGY75127.1	002590	Cluster2143_1clades	66	CF8_0167	Aeromonas phage CF8	GCA_006384595.2
ADQ53385.1	002590	Cluster2143_1clades	67	65p377	Aeromonas virus 65	GCA_000893255.1
APU01590.1	002591	Cluster2144_1clades	66	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28974.1	002591	Cluster2144_1clades	66	AP1_0267	Aeromonas phage AP1	GCA_014183365.1
ATI17320.1	002591	Cluster2144_1clades	66	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00274.1	002591	Cluster2144_1clades	66	HWB28_gp278	Aeromonas phage AS-zj	GCA_002627665.1
QAX97763.1	002591	Cluster2144_1clades	66	ASswx1_118	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01393.1	002591	Cluster2144_1clades	67	ASwh1_334	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39461.1	002591	Cluster2144_1clades	66	CC2_419	Aeromonas phage CC2	GCA_000903495.1
ADQ53214.1	002591	Cluster2144_1clades	66	65p206	Aeromonas virus 65	GCA_000893255.1
APU01741.1	002592	Cluster2145_1clades	63	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28924.1	002592	Cluster2145_1clades	63	AP1_0217	Aeromonas phage AP1	GCA_014183365.1
ATI17557.1	002592	Cluster2145_1clades	63	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00440.1	002592	Cluster2145_1clades	63	HWB28_gp112	Aeromonas phage AS-zj	GCA_002627665.1
QAX97997.1	002592	Cluster2145_1clades	63	ASswx1_357	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01144.1	002592	Cluster2145_1clades	64	ASwh1_78	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39245.1	002592	Cluster2145_1clades	66	CC2_178	Aeromonas phage CC2	GCA_000903495.1
ADQ53384.1	002592	Cluster2145_1clades	63	65p376	Aeromonas virus 65	GCA_000893255.1
AIT14209.1	002593	Cluster2146_1clades	65	PBI_121Q_319	Escherichia phage 121Q	GCA_000926855.1
QAY00729.1	002593	Cluster2146_1clades	65	Ecwhy1_454	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34910.1	002593	Cluster2146_1clades	65	ACQ29_gp230	Escherichia phage PBECO4	GCA_001041035.1
BBM61882.1	002593	Cluster2146_1clades	65	EO157G_2930	Escherichia phage SP27	GCA_008033345.1
AXC37015.1	002593	Cluster2146_1clades	65	-	Escherichia phage UB	GCA_003341455.1
QBO62102.1	002593	Cluster2146_1clades	65	G17_00613	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14112.1	002593	Cluster2146_1clades	65	vBEcoMphAPEC6_gp489c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80192.1	002593	Cluster2146_1clades	65	PSLUR01_00215	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT13998.1	002594	Cluster2147_1clades	65	PBI_121Q_101	Escherichia phage 121Q	GCA_000926855.1
QAY00340.1	002594	Cluster2147_1clades	65	Ecwhy1_59	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35086.1	002594	Cluster2147_1clades	59	ACQ29_gp406	Escherichia phage PBECO4	GCA_001041035.1
BBM61689.1	002594	Cluster2147_1clades	65	EO157G_1000	Escherichia phage SP27	GCA_008033345.1
AXC36663.1	002594	Cluster2147_1clades	65	-	Escherichia phage UB	GCA_003341455.1
QBO61695.1	002594	Cluster2147_1clades	65	G17_00206	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13744.1	002594	Cluster2147_1clades	65	vBEcoMphAPEC6_gp114c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80002.1	002594	Cluster2147_1clades	65	PSLUR01_00018	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14501.1	002595	Cluster2148_1clades	49	PBI_121Q_611	Escherichia phage 121Q	GCA_000926855.1
QAY00448.1	002595	Cluster2148_1clades	65	Ecwhy1_168	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35191.1	002595	Cluster2148_1clades	49	ACQ29_gp511	Escherichia phage PBECO4	GCA_001041035.1
BBM62173.1	002595	Cluster2148_1clades	49	EO157G_5840	Escherichia phage SP27	GCA_008033345.1
AXC36762.1	002595	Cluster2148_1clades	49	-	Escherichia phage UB	GCA_003341455.1
QBO61802.1	002595	Cluster2148_1clades	49	G17_00313	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13846.1	002595	Cluster2148_1clades	49	vBEcoMphAPEC6_gp217c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80485.1	002595	Cluster2148_1clades	49	PSLUR01_00508	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01581.1	002596	Cluster2149_1clades	59	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28965.1	002596	Cluster2149_1clades	61	AP1_0258	Aeromonas phage AP1	GCA_014183365.1
ATI17329.1	002596	Cluster2149_1clades	61	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00265.1	002596	Cluster2149_1clades	61	HWB28_gp287	Aeromonas phage AS-zj	GCA_002627665.1
QAX97772.1	002596	Cluster2149_1clades	61	ASswx1_127	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01380.1	002596	Cluster2149_1clades	65	ASwh1_320	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39457.1	002596	Cluster2149_1clades	63	CC2_410	Aeromonas phage CC2	GCA_000903495.1
ADQ53204.1	002596	Cluster2149_1clades	59	65p196	Aeromonas virus 65	GCA_000893255.1
AAQ64288.1	002597	Cluster2150_1clades	64	KVP40.0219	Vibrio phage KVP40	GCA_000843785.1
QIW90604.1	002597	Cluster2150_1clades	64	GCAPEGMB_00257	Vibrio phage V07	GCA_012361095.1
QIW91195.1	002597	Cluster2150_1clades	64	COHAPHLL_00359	Vibrio phage V09	GCA_012361135.1
QHJ74400.1	002597	Cluster2150_1clades	64	VH12019_00073	Vibrio phage VH1_2019	GCA_009931825.1
QBX06240.1	002597	Cluster2150_1clades	64	ValB1HC_287	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60866.1	002597	Cluster2150_1clades	64	AVU32_gp025	Vibrio phage ValKK3	GCA_001501635.1
QNJ54866.1	002597	Cluster2150_1clades	63	vBValMR10Z_326	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37449.1	002597	Cluster2150_1clades	64	pp2_216	Vibriophage phi-pp2	GCA_002630725.1
AIT13976.1	002598	Cluster2151_1clades	64	PBI_121Q_79	Escherichia phage 121Q	GCA_000926855.1
QAY00361.1	002598	Cluster2151_1clades	64	Ecwhy1_80	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35107.1	002598	Cluster2151_1clades	64	ACQ29_gp427	Escherichia phage PBECO4	GCA_001041035.1
BBM61668.1	002598	Cluster2151_1clades	64	EO157G_0790	Escherichia phage SP27	GCA_008033345.1
AXC36682.1	002598	Cluster2151_1clades	64	-	Escherichia phage UB	GCA_003341455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBO61716.1	002598	Cluster2151_1clades	64	G17_00227	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80570.1	002598	Cluster2151_1clades	64	PSLUR01_00593	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44456.1	002598	Cluster2151_1clades	64	RaK2_00183	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14033.1	002599	Cluster2152_1clades	63	PBI_121Q_143	Escherichia phage 121Q	GCA_000926855.1
QAY00308.1	002599	Cluster2152_1clades	63	Ecwhy1_26	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35058.1	002599	Cluster2152_1clades	56	ACQ29_gp378	Escherichia phage PBECO4	GCA_001041035.1
BBM61717.1	002599	Cluster2152_1clades	63	EO157G_1280	Escherichia phage SP27	GCA_008033345.1
AXC36634.1	002599	Cluster2152_1clades	63	-	Escherichia phage UB	GCA_003341455.1
QBO61666.1	002599	Cluster2152_1clades	63	G17_00170	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13716.1	002599	Cluster2152_1clades	63	vBEcoMphAPEC6_gp086c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80029.1	002599	Cluster2152_1clades	63	PSLUR01_00052	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14270.1	002600	Cluster2153_1clades	63	PBI_121Q_380	Escherichia phage 121Q	GCA_000926855.1
QAY00667.1	002600	Cluster2153_1clades	63	Ecwhy1_392	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34863.1	002600	Cluster2153_1clades	44	ACQ29_gp183	Escherichia phage PBECO4	GCA_001041035.1
BBM61945.1	002600	Cluster2153_1clades	63	EO157G_3560	Escherichia phage SP27	GCA_008033345.1
AXC36972.1	002600	Cluster2153_1clades	43	-	Escherichia phage UB	GCA_003341455.1
QBO62034.1	002600	Cluster2153_1clades	63	G17_00545	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14055.1	002600	Cluster2153_1clades	63	vBEcoMphAPEC6_gp432c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80258.1	002600	Cluster2153_1clades	63	PSLUR01_00281	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMO43270.1	002601	Cluster2154_1clades	48	W270710_025	Cyanophage S-RIM44	GCA_002599145.1
AOO11742.1	002601	Cluster2154_1clades	48	Np050604_025	Cyanophage S-RIM44	GCA_002599185.1
AOO12443.1	002601	Cluster2154_1clades	48	Sn080709_025	Cyanophage S-RIM44	GCA_002599245.1
AOO12908.1	002601	Cluster2154_1clades	48	W2100709_025	Cyanophage S-RIM44	GCA_002599285.1
ADO99127.1	002601	Cluster2154_1clades	62	Syn1_025	Prochlorococcus phage Syn1	GCA_000892495.1
AOV59680.1	002601	Cluster2154_1clades	48	S330809_219	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59442.1	002601	Cluster2154_1clades	56	C440309_219	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59917.1	002601	Cluster2154_1clades	56	N231010_218	Synechococcus phage S-CAM4	GCA_002922155.1
APU01756.1	002602	Cluster2155_1clades	62	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29076.1	002602	Cluster2155_1clades	61	AP1_0369	Aeromonas phage AP1	GCA_014183365.1
ATI17540.1	002602	Cluster2155_1clades	61	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00457.1	002602	Cluster2155_1clades	61	HWB28_gp095	Aeromonas phage AS-zj	GCA_002627665.1
QAX97981.1	002602	Cluster2155_1clades	61	ASswx1_340	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01159.1	002602	Cluster2155_1clades	60	ASwh1_93	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39254.1	002602	Cluster2155_1clades	61	CC2_194	Aeromonas phage CC2	GCA_000903495.1
ADQ53398.1	002602	Cluster2155_1clades	62	65p391	Aeromonas virus 65	GCA_000893255.1
APU01419.1	002603	Cluster2156_1clades	62	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28810.1	002603	Cluster2156_1clades	62	AP1_0103	Aeromonas phage AP1	GCA_014183365.1
ATI17479.1	002603	Cluster2156_1clades	62	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00518.1	002603	Cluster2156_1clades	62	HWB28_gp034	Aeromonas phage AS-zj	GCA_002627665.1
QAX97919.1	002603	Cluster2156_1clades	62	ASswx1_276	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01231.1	002603	Cluster2156_1clades	62	ASwh1_166	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39156.1	002603	Cluster2156_1clades	62	CC2_256	Aeromonas phage CC2	GCA_000903495.1
AAR90910.1	002603	Cluster2156_1clades	44	65p028	Aeromonas virus 65	GCA_000893255.1
AIT14061.1	002604	Cluster2157_1clades	60	PBI_121Q_171	Escherichia phage 121Q	GCA_000926855.1
QAY00860.1	002604	Cluster2157_1clades	60	Ecwhy1_589	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35032.1	002604	Cluster2157_1clades	41	ACQ29_gp352	Escherichia phage PBECO4	GCA_001041035.1
BBM61744.1	002604	Cluster2157_1clades	60	EO157G_1550	Escherichia phage SP27	GCA_008033345.1
AXC36609.1	002604	Cluster2157_1clades	60	-	Escherichia phage UB	GCA_003341455.1
QBO61638.1	002604	Cluster2157_1clades	60	G17_00142	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13692.1	002604	Cluster2157_1clades	60	vBEcoMphAPEC6_gp062c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80056.1	002604	Cluster2157_1clades	60	PSLUR01_00079	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANZ49652.1	002605	Cluster2158_1clades	60	MACHINA_7	Erwinia phage Machina	GCA_002758035.1
AXF51143.1	002605	Cluster2158_1clades	56	WELLINGTON_2	Erwinia phage Wellington	GCA_003344985.1
ANZ48030.1	002605	Cluster2158_1clades	60	ASESINO_7	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48306.1	002605	Cluster2158_1clades	59	CAITLIN_6	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48578.1	002605	Cluster2158_1clades	59	CHRISDB_7	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49096.1	002605	Cluster2158_1clades	60	HUXLEY_7	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49364.1	002605	Cluster2158_1clades	56	KWAN_2	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49925.1	002605	Cluster2158_1clades	60	PARSHIK_7	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QAX96937.1	002606	Cluster2159_1clades	59	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96936.1	002606	Cluster2159_1clades	60	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97242.1	002606	Cluster2159_1clades	59	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX97241.1	002606	Cluster2159_1clades	60	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96301.1	002606	Cluster2159_1clades	59	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96300.1	002606	Cluster2159_1clades	60	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96619.1	002606	Cluster2159_1clades	59	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96618.1	002606	Cluster2159_1clades	60	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
APU01735.1	002607	Cluster2160_1clades	59	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28733.1	002607	Cluster2160_1clades	59	AP1_0015	Aeromonas phage AP1	GCA_014183365.1
ATI17563.1	002607	Cluster2160_1clades	59	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00433.1	002607	Cluster2160_1clades	59	HWB28_gp119	Aeromonas phage AS-zj	GCA_002627665.1
QAX98003.1	002607	Cluster2160_1clades	59	ASswx1_363	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01138.1	002607	Cluster2160_1clades	57	ASwh1_72	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39367.1	002607	Cluster2160_1clades	59	CC2_171	Aeromonas phage CC2	GCA_000903495.1
ADQ53377.1	002607	Cluster2160_1clades	59	65p369	Aeromonas virus 65	GCA_000893255.1
APU01451.1	002608	DUF2685	57	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29079.1	002608	DUF2685	57	AP1_0372	Aeromonas phage AP1	GCA_014183365.1
ATI17448.1	002608	DUF2685	57	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00148.1	002608	DUF2685	57	HWB28_gp002	Aeromonas phage AS-zj	GCA_002627665.1
QAX97888.1	002608	DUF2685	57	ASswx1_245	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01263.1	002608	DUF2685	57	ASwh1_199	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39272.1	002608	DUF2685	59	CC2_288	Aeromonas phage CC2	GCA_000903495.1
ADQ53071.1	002608	DUF2685	57	65p061	Aeromonas virus 65	GCA_000893255.1
AIT14377.1	002609	Cluster2162_1clades	56	PBI_121Q_487	Escherichia phage 121Q	GCA_000926855.1
QAY00571.1	002609	Cluster2162_1clades	56	Ecwhy1_292	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34763.1	002609	Cluster2162_1clades	56	ACQ29_gp083	Escherichia phage PBECO4	GCA_001041035.1
BBM62048.1	002609	Cluster2162_1clades	56	EO157G_4590	Escherichia phage SP27	GCA_008033345.1
AXC36878.1	002609	Cluster2162_1clades	56	-	Escherichia phage UB	GCA_003341455.1
QBO61925.1	002609	Cluster2162_1clades	56	G17_00436	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13957.1	002609	Cluster2162_1clades	56	vBEcoMphAPEC6_gp333c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80366.1	002609	Cluster2162_1clades	56	PSLUR01_00389	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT13995.1	002610	Cluster2163_1clades	56	PBI_121Q_98	Escherichia phage 121Q	GCA_000926855.1
QAY00343.1	002610	Cluster2163_1clades	56	Ecwhy1_62	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35089.1	002610	Cluster2163_1clades	56	ACQ29_gp409	Escherichia phage PBECO4	GCA_001041035.1
BBM61686.1	002610	Cluster2163_1clades	56	EO157G_0970	Escherichia phage SP27	GCA_008033345.1
AXC36666.1	002610	Cluster2163_1clades	56	-	Escherichia phage UB	GCA_003341455.1
QBO61698.1	002610	Cluster2163_1clades	56	G17_00209	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13746.1	002610	Cluster2163_1clades	56	vBEcoMphAPEC6_gp116c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79999.1	002610	Cluster2163_1clades	56	PSLUR01_00015	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21974.1	002611	Cluster2164_1clades	55	GAP32_514	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44096.1	002611	Cluster2164_1clades	55	CBB_533	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18715.1	002611	Cluster2164_1clades	50	7t3_0194	Salmonella phage 7t3	GCA_006083215.1
AZU97988.1	002611	Cluster2164_1clades	50	CPT_Munch_044	Salmonella phage Munch	GCA_004015485.1
QIG62991.1	002611	Cluster2164_1clades	50	SEPL_378	Salmonella phage SE_PL	GCA_011067555.1
AQW89052.1	002611	Cluster2164_1clades	55	BF_0527	Serratia phage BF	GCA_002619745.1
SOK59330.1	002611	Cluster2164_1clades	55	g522	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58792.1	002611	Cluster2164_1clades	55	g515	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01684.1	002612	TM+TM	54	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28817.1	002612	TM+TM	54	AP1_0110	Aeromonas phage AP1	GCA_014183365.1
ATI17609.1	002612	TM+TM	54	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00387.1	002612	TM+TM	54	HWB28_gp165	Aeromonas phage AS-zj	GCA_002627665.1
QAX98050.1	002612	TM+TM	54	ASswx1_410	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01103.1	002612	TM+TM	54	ASwh1_35	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39225.1	002612	TM+TM	54	CC2_119	Aeromonas phage CC2	GCA_000903495.1
ADQ53320.1	002612	TM+TM	54	65p312	Aeromonas virus 65	GCA_000893255.1
AIT14021.1	002613	Cluster2166_1clades	54	PBI_121Q_127	Escherichia phage 121Q	GCA_000926855.1
QAY00318.1	002613	Cluster2166_1clades	54	Ecwhy1_36	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35066.1	002613	Cluster2166_1clades	54	ACQ29_gp386	Escherichia phage PBECO4	GCA_001041035.1
BBM61709.1	002613	Cluster2166_1clades	54	EO157G_1200	Escherichia phage SP27	GCA_008033345.1
AXC36643.1	002613	Cluster2166_1clades	54	-	Escherichia phage UB	GCA_003341455.1
QBO61675.1	002613	Cluster2166_1clades	54	G17_00183	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13724.1	002613	Cluster2166_1clades	54	vBEcoMphAPEC6_gp094c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80021.1	002613	Cluster2166_1clades	54	PSLUR01_00040	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01472.1	002614	Cluster2167_1clades	51	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28786.1	002614	Cluster2167_1clades	51	AP1_0079	Aeromonas phage AP1	GCA_014183365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATI17425.1	002614	Cluster2167_1clades	51	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00170.1	002614	Cluster2167_1clades	51	HWB28_gp382	Aeromonas phage AS-zj	GCA_002627665.1
QAX97865.1	002614	Cluster2167_1clades	51	ASswx1_222	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01285.1	002614	Cluster2167_1clades	51	ASwh1_222	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39422.1	002614	Cluster2167_1clades	51	CC2_312	Aeromonas phage CC2	GCA_000903495.1
ADQ53095.1	002614	Cluster2167_1clades	51	65p085	Aeromonas virus 65	GCA_000893255.1
AIT14006.1	002615	Cluster2168_1clades	49	PBI_121Q_109	Escherichia phage 121Q	GCA_000926855.1
QAY00332.1	002615	Cluster2168_1clades	49	Ecwhy1_51	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35078.1	002615	Cluster2168_1clades	49	ACQ29_gp398	Escherichia phage PBECO4	GCA_001041035.1
BBM61697.1	002615	Cluster2168_1clades	49	EO157G_1080	Escherichia phage SP27	GCA_008033345.1
AXC36655.1	002615	Cluster2168_1clades	49	-	Escherichia phage UB	GCA_003341455.1
QBO61687.1	002615	Cluster2168_1clades	49	G17_00198	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13736.1	002615	Cluster2168_1clades	49	vBEcoMphAPEC6_gp106c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80010.1	002615	Cluster2168_1clades	49	PSLUR01_00026	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14419.1	002616	TM	43	PBI_121Q_529	Escherichia phage 121Q	GCA_000926855.1
QAY00531.1	002616	TM	43	Ecwhy1_252	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34723.1	002616	TM	48	ACQ29_gp043	Escherichia phage PBECO4	GCA_001041035.1
BBM62091.1	002616	TM	43	EO157G_5020	Escherichia phage SP27	GCA_008033345.1
AXC36841.1	002616	TM	43	-	Escherichia phage UB	GCA_003341455.1
QBO61882.1	002616	TM	43	G17_00393	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13920.1	002616	TM	43	vBEcoMphAPEC6_gp295c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80405.1	002616	TM	43	PSLUR01_00428	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT13994.1	002617	Cluster2170_1clades	47	PBI_121Q_97	Escherichia phage 121Q	GCA_000926855.1
QAY00344.1	002617	Cluster2170_1clades	47	Ecwhy1_63	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35090.1	002617	Cluster2170_1clades	47	ACQ29_gp410	Escherichia phage PBECO4	GCA_001041035.1
BBM61685.1	002617	Cluster2170_1clades	47	EO157G_0960	Escherichia phage SP27	GCA_008033345.1
AXC36667.1	002617	Cluster2170_1clades	47	-	Escherichia phage UB	GCA_003341455.1
QBO61699.1	002617	Cluster2170_1clades	47	G17_00210	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13747.1	002617	Cluster2170_1clades	47	vBEcoMphAPEC6_gp117c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79998.1	002617	Cluster2170_1clades	47	PSLUR01_00014	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21915.1	002618	Cluster2171_1clades	42	GAP32_458	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44041.1	002618	Cluster2171_1clades	42	CBB_478	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18639.1	002618	Cluster2171_1clades	42	7t3_0118	Salmonella phage 7t3	GCA_006083215.1
AZU98464.1	002618	Cluster2171_1clades	42	CPT_Munch_532	Salmonella phage Munch	GCA_004015485.1
QIG63050.1	002618	Cluster2171_1clades	42	SEPL_437	Salmonella phage SE_PL	GCA_011067555.1
AQW88997.1	002618	Cluster2171_1clades	43	BF_0472	Serratia phage BF	GCA_002619745.1
SOK59280.1	002618	Cluster2171_1clades	43	g472	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58745.1	002618	Cluster2171_1clades	43	g468	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01550.1	002619	Cluster2172_1clades	37	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29010.1	002619	Cluster2172_1clades	36	AP1_0303	Aeromonas phage AP1	GCA_014183365.1
ATI17351.1	002619	Cluster2172_1clades	36	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00242.1	002619	Cluster2172_1clades	36	HWB28_gp310	Aeromonas phage AS-zj	GCA_002627665.1
QAX97796.1	002619	Cluster2172_1clades	36	ASswx1_151	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01359.1	002619	Cluster2172_1clades	40	ASwh1_299	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39286.1	002619	Cluster2172_1clades	36	CC2_386	Aeromonas phage CC2	GCA_000903495.1
ADQ53172.1	002619	Cluster2172_1clades	37	65p164	Aeromonas virus 65	GCA_000893255.1
AMO43322.1	002620	Cluster2173_1clades	39	W270710_078	Cyanophage S-RIM44	GCA_002599145.1
AOO11556.1	002620	Cluster2173_1clades	39	ES420910_075	Cyanophage S-RIM44	GCA_002599165.1
AOO11794.1	002620	Cluster2173_1clades	39	Np050604_078	Cyanophage S-RIM44	GCA_002599185.1
AOO12021.1	002620	Cluster2173_1clades	39	Np200711_075	Cyanophage S-RIM44	GCA_002599205.1
AOO12257.1	002620	Cluster2173_1clades	39	Np420711_075	Cyanophage S-RIM44	GCA_002599225.1
AOO12495.1	002620	Cluster2173_1clades	39	Sn080709_078	Cyanophage S-RIM44	GCA_002599245.1
AOO12722.1	002620	Cluster2173_1clades	39	Sn130910_075	Cyanophage S-RIM44	GCA_002599265.1
AOO12960.1	002620	Cluster2173_1clades	39	W2100709_078	Cyanophage S-RIM44	GCA_002599285.1
QGZ14475.1	002621	IG	1507	HWC77_gp112	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04259.1	002621	IG	1508	HWC03_gp104	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23104.1	002621	IG	1227	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80912.1	002621	IG	1507	Aphrodite1_0027	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47412.1	002621	IG	1227	HWC35_gp018	Vibrio phage USC-1	GCA_006864065.1
BAW98229.1	002621	IG	1423	FDH33_gp020	Vibrio phage pTD1	GCA_002618825.1
BAW98369.1	002621	IG	1726	FDH33_gp160	Vibrio phage pTD1	GCA_002618825.1
AGH07544.1	002622	Peptidase-S8	738	CYVG_00100	Cyanophage S-SSM6a	GCA_002710385.1
AAX44674.1	002622	Peptidase-S8	611	PSSM2_297	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12303.1	002622	Peptidase-S8	611	PRTG_00150	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59651.1	002622	Peptidase-S8	682	S330809_190	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59413.1	002622	Peptidase-S8	681	C440309_190	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59889.1	002622	Peptidase-S8	682	N231010_190	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70469.1	002622	Peptidase-S8	588	HOU04_gp070	Synechococcus phage S-T4	GCA_003443335.1
prevph1000000633	002623	MA	79	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000695	002623	MA	163	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000703	002623	MA	211	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000450	002623	MA	149	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000476	002623	MA	450	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000480	002623	MA	228	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000482	002623	MA	553	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXG67258.1	002624	TVPOL	350	AD1_214	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80005.1	002624	TVPOL	405	JA11_200	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66603.1	002624	TVPOL	284	JA13_200	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66928.1	002624	TVPOL	545	JA29_202	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67574.1	002624	TVPOL	405	JA33_200	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08487.1	002624	TVPOL	525	Alexandra_224	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58859.1	002624	TVPOL	538	Y3_219	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AEO93569.1	002625	HAD	202	G_310	Bacillus virus G	GCA_000917535.1
BAG41684.1	002625	HAD	240	RSL1_ORF235	Ralstonia phage phiRSL1	GCA_000879455.1
QGT54958.1	002625	HAD	457	b23_0352	Synechococcus phage B23	GCA_009745195.1
QGT54593.1	002625	HAD	457	b3_0358	Synechococcus phage B3	GCA_009745215.1
ASR76242.1	002625	HAD	385	PBI_BELLAMY_206	Synechococcus phage Bellamy	GCA_002627525.1
ASR76245.1	002625	HAD	524	PBI_BELLAMY_209	Synechococcus phage Bellamy	GCA_002627525.1
QJT70198.1	002625	HAD	385	SynMITS9220M01_192	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AAQ64434.1	002626	Cluster2184_1clades	484	KVP40.0366	Vibrio phage KVP40	GCA_000843785.1
QIW90380.1	002626	Cluster2184_1clades	484	GCAPEGMB_00033	Vibrio phage V07	GCA_012361095.1
QIW91049.1	002626	Cluster2184_1clades	484	COHAPHLL_00186	Vibrio phage V09	GCA_012361135.1
QBX06107.1	002626	Cluster2184_1clades	484	ValB1HC_153	Vibrio phage ValB1 HC	GCA_004771355.1
AGN30036.1	002626	Cluster2184_1clades	486	VPFG_00031	Vibrio phage nt-1	GCA_000910195.2
QNJ54732.1	002626	Cluster2184_1clades	484	vBValMR10Z_192	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37598.1	002626	Cluster2184_1clades	484	pp2_366	Vibriophage phi-pp2	GCA_002630725.1
APU01513.1	002627	GT	398	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22621.1	002627	GT	399	Ah1_00080	Aeromonas phage Ah1	GCA_002957415.1
ADM80061.1	002627	GT	399	phiAS5_ORF0218	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53136.1	002627	GT	398	65p128	Aeromonas virus 65	GCA_000893255.1
AAQ17748.1	002627	GT	399	Aeh1ORF087c	Aeromonas virus Aeh1	GCA_000843245.1
BBI90601.1	002627	GT	471	HYO65_gp209	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90908.1	002627	GT	471	-	Tenacibaculum phage PTm5	GCA_009730715.1
AGX01946.1	002628	Cluster2186_1clades	454	CF95_gp224	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65359.1	002628	Cluster2186_1clades	167	2050HW_00024	Serratia phage 2050HW	GCA_002628125.1
ATA65360.1	002628	Cluster2186_1clades	218	2050HW_00025	Serratia phage 2050HW	GCA_002628125.1
ATA65564.1	002628	Cluster2186_1clades	423	2050HW_00229	Serratia phage 2050HW	GCA_002628125.1
QDB71146.1	002628	Cluster2186_1clades	411	CPT_Moabite_116	Serratia phage Moabite	GCA_006384735.1
QDB71329.1	002628	Cluster2186_1clades	423	CPT_Moabite_299	Serratia phage Moabite	GCA_006384735.1
QFP93084.1	002628	Cluster2186_1clades	443	-	Serratia phage PCH45	GCA_009187865.1
AMS01112.1	002629	BirA-HTH	314	AR9_g027	Bacillus phage AR9	GCA_001743835.1
ALN97755.1	002629	BirA-HTH	171	Bp8pS_076	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97760.1	002629	BirA-HTH	152	Bp8pS_081	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97761.1	002629	BirA-HTH	110	Bp8pS_082	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97970.1	002629	BirA-HTH	230	Bp8pS_291	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97971.1	002629	BirA-HTH	447	Bp8pS_292	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00034.1	002629	BirA-HTH	264	PBI_PBS1_212	Bacillus virus PBS1	GCA_002601325.1
AFU87975.1	002630	Cluster2188_1clades	399	CcrColossus_gp105	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68652.1	002630	Cluster2188_1clades	399	CcrPW_gp113	Caulobacter phage CcrPW	GCA_003443275.1
AFC21801.1	002630	Cluster2188_1clades	340	GAP32_351	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43922.1	002630	Cluster2188_1clades	339	CBB_359	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88882.1	002630	Cluster2188_1clades	333	BF_0357	Serratia phage BF	GCA_002619745.1
SOK59168.1	002630	Cluster2188_1clades	333	g360	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58636.1	002630	Cluster2188_1clades	333	g359	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH07731.1	002631	Cluster2190_1clades	261	CYVG_00288	Cyanophage S-SSM6a	GCA_002710385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH07732.1	002631	Cluster2190_1clades	264	CYVG_00289	Cyanophage S-SSM6a	GCA_002710385.1
AGH07733.1	002631	Cluster2190_1clades	262	CYVG_00290	Cyanophage S-SSM6a	GCA_002710385.1
AAX44681.1	002631	Cluster2190_1clades	356	PSSM2_304	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44683.1	002631	Cluster2190_1clades	355	PSSM2_306	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12293.1	002631	Cluster2190_1clades	355	PRTG_00140	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12295.1	002631	Cluster2190_1clades	356	PRTG_00142	Prochlorococcus phage P-SSM5	GCA_002991095.1
AHI60257.1	002632	Cluster2191_1clades	191	Ea357_106	Erwinia phage Ea35-70	GCA_000914635.1
AUG85894.1	002632	Cluster2191_1clades	191	BOSOLAPHORUS_107	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52209.1	002632	Cluster2191_1clades	191	DM_111	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86860.1	002632	Cluster2191_1clades	183	MORTIMER_111	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH51888.1	002632	Cluster2191_1clades	183	RAY_107	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51572.1	002632	Cluster2191_1clades	182	SIMMY50_110	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
QKE54405.1	002632	Cluster2191_1clades	356	ACSA002_0910	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AFQ96789.1	002633	Cluster2192_1clades	354	G173_gp244	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48090.1	002633	Cluster2192_1clades	354	ASESINO_77	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50501.1	002633	Cluster2192_1clades	354	STRATTON_76	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85901.1	002633	Cluster2192_1clades	196	ACEC001_0630	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20776.1	002633	Cluster2192_1clades	196	-	Salmonella phage JN03	GCA_014319805.1
AXF51091.1	002633	Cluster2192_1clades	196	MLDJOKPK_00104	Salmonella phage SPAsTU	GCA_003183805.1
AEP83893.1	002633	Cluster2192_1clades	196	SPN3US_0060	Salmonella phage SPN3US	GCA_001042275.1
ASV44228.1	002634	Cluster2194_1clades	299	PBI_SCTP2_213	Salicola phage SCTP-2	GCA_002625545.1
ASV44229.1	002634	Cluster2194_1clades	322	PBI_SCTP2_214	Salicola phage SCTP-2	GCA_002625545.1
ASV44231.1	002634	Cluster2194_1clades	225	PBI_SCTP2_216	Salicola phage SCTP-2	GCA_002625545.1
ASV44232.1	002634	Cluster2194_1clades	323	PBI_SCTP2_217	Salicola phage SCTP-2	GCA_002625545.1
ASV44233.1	002634	Cluster2194_1clades	300	PBI_SCTP2_218	Salicola phage SCTP-2	GCA_002625545.1
ASV44234.1	002634	Cluster2194_1clades	329	PBI_SCTP2_219	Salicola phage SCTP-2	GCA_002625545.1
ASV44414.1	002634	Cluster2194_1clades	304	PBI_SCTP2_399	Salicola phage SCTP-2	GCA_002625545.1
AFQ96599.1	002635	SIG+FamB-divDNAPol	306	G173_gp054	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48163.1	002635	SIG+FamB-divDNAPol	302	ASESINO_150	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48438.1	002635	SIG+FamB-divDNAPol	134	CAITLIN_143	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48714.1	002635	SIG+FamB-divDNAPol	276	CHRISDB_152	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50576.1	002635	SIG+FamB-divDNAPol	306	STRATTON_151	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85975.1	002635	SIG+FamB-divDNAPol	129	ACEC001_1370	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51054.1	002635	SIG+FamB-divDNAPol	134	MLDJOKPK_00015	Salmonella phage SPAsTU	GCA_003183805.1
AXH72900.1	002636	SIG+Pentapeptide	186	-	Myoviridae sp.	GCA_003657725.1
QGT54796.1	002636	SIG+Pentapeptide	118	b23_0181	Synechococcus phage B23	GCA_009745195.1
QGT54801.1	002636	SIG+Pentapeptide	306	b23_0186	Synechococcus phage B23	GCA_009745195.1
QGT54839.1	002636	SIG+Pentapeptide	178	b23_0224	Synechococcus phage B23	GCA_009745195.1
QGT54426.1	002636	SIG+Pentapeptide	118	b3_0182	Synechococcus phage B3	GCA_009745215.1
QGT54431.1	002636	SIG+Pentapeptide	306	b3_0187	Synechococcus phage B3	GCA_009745215.1
QGT54473.1	002636	SIG+Pentapeptide	198	b3_0230	Synechococcus phage B3	GCA_009745215.1
AXG67062.1	002637	Asn_synthase	289	AD1_018	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08300.1	002637	Asn_synthase	289	Alexandra_19	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58658.1	002637	Asn_synthase	290	Y3_018	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28504.1	002637	Asn_synthase	291	YOLOSWAG_17	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGS82056.1	002637	Asn_synthase	274	PaBG_00180	Pseudomonas phage PaBG	GCA_000912555.1
QCW22934.1	002637	Asn_synthase	271	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50619.1	002637	Asn_synthase	271	-	Synechococcus phage S-B43	GCA_006869725.1
AOO14229.1	002638	DUF2207	253	Sn110110_035	Cyanophage S-RIM14	GCA_002599065.1
AOO14881.1	002638	DUF2207	253	W1230910_035	Cyanophage S-RIM14	GCA_002599125.1
BAW19114.1	002638	DUF2207	215	FDH28_gp281	Ralstonia phage RP12	GCA_002617345.1
BAW19400.1	002638	DUF2207	203	-	Ralstonia phage RP31	GCA_002617365.1
AOV59563.1	002638	DUF2207	272	S330809_102	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59325.1	002638	DUF2207	272	C440309_102	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59801.1	002638	DUF2207	272	N231010_102	Synechococcus phage S-CAM4	GCA_002922155.1
APU01662.1	002639	Cluster2203_1clades	253	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29019.1	002639	Cluster2203_1clades	57	AP1_0312	Aeromonas phage AP1	GCA_014183365.1
ATI17632.1	002639	Cluster2203_1clades	161	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00363.1	002639	Cluster2203_1clades	161	HWB28_gp189	Aeromonas phage AS-zj	GCA_002627665.1
QAX97667.1	002639	Cluster2203_1clades	161	ASswx1_21	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39148.1	002639	Cluster2203_1clades	161	CC2_094	Aeromonas phage CC2	GCA_000903495.1
ADQ53293.1	002639	Cluster2203_1clades	253	65p285	Aeromonas virus 65	GCA_000893255.1
ANZ49655.1	002640	ParBC	110	MACHINA_10	Erwinia phage Machina	GCA_002758035.1
ANZ49100.1	002640	ParBC	110	HUXLEY_11	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49928.1	002640	ParBC	110	PARSHIK_10	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
CAG27169.1	002640	ParBC	119	PPEV_gp075	Pseudomonas phage EL	GCA_000866825.1
QBJ02745.1	002640	ParBC	94	PSA21_219	Pseudomonas phage Psa21	GCA_004340405.1
QCG76022.1	002640	ParBC	249	EST35_0140	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QFP93211.1	002640	ParBC	138	-	Serratia phage PCH45	GCA_009187865.1
AXG67353.1	002641	Cluster2205_1clades	243	AD1_309	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80104.1	002641	Cluster2205_1clades	247	JA11_299	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66705.1	002641	Cluster2205_1clades	247	JA13_302	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67024.1	002641	Cluster2205_1clades	245	JA29_298	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67674.1	002641	Cluster2205_1clades	247	JA33_300	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08579.1	002641	Cluster2205_1clades	242	Alexandra_328	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28780.1	002641	Cluster2205_1clades	237	YOLOSWAG_311	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AAX44645.1	002642	Glyco_transf_6	231	PSSM2_268	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12326.1	002642	Glyco_transf_6	231	PRTG_00173	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIX30706.1	002642	Glyco_transf_6	243	Syn7803US37_229	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54954.1	002642	Glyco_transf_6	240	b23_0348	Synechococcus phage B23	GCA_009745195.1
QGT54589.1	002642	Glyco_transf_6	240	b3_0354	Synechococcus phage B3	GCA_009745215.1
ASR76238.1	002642	Glyco_transf_6	238	PBI_BELLAMY_202	Synechococcus phage Bellamy	GCA_002627525.1
QJT70195.1	002642	Glyco_transf_6	240	SynMITS9220M01_189	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AGH56980.1	002643	JOR	232	CPXG_00177	Cyanophage P-RSM6	GCA_000906155.1
AGH56982.1	002643	JOR	234	CPXG_00179	Cyanophage P-RSM6	GCA_000906155.1
AJK27479.1	002643	JOR	240	PTIM40_52	Cyanophage P-TIM40	GCA_001470935.1
AOO11589.1	002643	JOR	241	ES420910_108	Cyanophage S-RIM44	GCA_002599165.1
AOO12054.1	002643	JOR	241	Np200711_108	Cyanophage S-RIM44	GCA_002599205.1
AOO12290.1	002643	JOR	241	Np420711_108	Cyanophage S-RIM44	GCA_002599225.1
AOO12755.1	002643	JOR	241	Sn130910_108	Cyanophage S-RIM44	GCA_002599265.1
AIR93402.1	002644	Cluster2208_1clades	227	AVU42_gp016	Prochlorococcus phage P-TIM68	GCA_001503075.1
QGT54641.1	002644	Cluster2208_1clades	212	b23_0013	Synechococcus phage B23	GCA_009745195.1
QGT54271.1	002644	Cluster2208_1clades	212	b3_0013	Synechococcus phage B3	GCA_009745215.1
ASR76065.1	002644	Cluster2208_1clades	208	PBI_BELLAMY_18	Synechococcus phage Bellamy	GCA_002627525.1
QCW22915.1	002644	Cluster2208_1clades	191	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50542.1	002644	Cluster2208_1clades	191	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70033.1	002644	Cluster2208_1clades	181	SynMITS9220M01_017	Synechococcus phage SynMITS9220M01	GCA_013187275.1
APU01740.1	002645	Cluster2210_1clades	222	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28925.1	002645	Cluster2210_1clades	220	AP1_0218	Aeromonas phage AP1	GCA_014183365.1
ATI17558.1	002645	Cluster2210_1clades	222	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00439.1	002645	Cluster2210_1clades	222	HWB28_gp113	Aeromonas phage AS-zj	GCA_002627665.1
QAX97998.1	002645	Cluster2210_1clades	225	ASswx1_358	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39244.1	002645	Cluster2210_1clades	225	CC2_177	Aeromonas phage CC2	GCA_000903495.1
ADQ53383.1	002645	Cluster2210_1clades	222	65p375	Aeromonas virus 65	GCA_000893255.1
AFU88135.1	002646	SIG+DUF262	174	CcrColossus_gp265	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68811.1	002646	SIG+DUF262	223	CcrPW_gp272	Caulobacter phage CcrPW	GCA_003443275.1
ASV44327.1	002646	SIG+DUF262	180	PBI_SCTP2_312	Salicola phage SCTP-2	GCA_002625545.1
AGR47710.2	002646	SIG+DUF262	175	SmphiM12_078	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12966.1	002646	SIG+DUF262	175	PHIM19_59	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12606.1	002646	SIG+DUF262	175	PHIM7_58	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13339.1	002646	SIG+DUF262	175	PHIN3_74	Sinorhizobium phage phiN3	GCA_001501175.1
ANM44966.1	002647	Cluster2212_1clades	218	KTN4_208	Pseudomonas phage KTN4	GCA_002607225.1
QBX32356.1	002647	Cluster2212_1clades	211	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03620.1	002647	Cluster2212_1clades	152	197	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94748.1	002647	Cluster2212_1clades	218	SL2_171	Pseudomonas phage SL2	GCA_002956015.1
QJB22844.1	002647	Cluster2212_1clades	218	fnug_201	Pseudomonas phage fnug	GCA_012837215.1
QEM41930.1	002647	Cluster2212_1clades	211	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83069.1	002647	Cluster2212_1clades	218	PHIKZ168	Pseudomonas virus phiKZ	GCA_000842965.1
APU01514.1	002648	Cluster2213_1clades	140	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28778.1	002648	Cluster2213_1clades	129	AP1_0070	Aeromonas phage AP1	GCA_014183365.1
ATI17381.1	002648	Cluster2213_1clades	129	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00212.1	002648	Cluster2213_1clades	129	HWB28_gp340	Aeromonas phage AS-zj	GCA_002627665.1
QAY01326.1	002648	Cluster2213_1clades	215	ASwh1_264	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39280.1	002648	Cluster2213_1clades	129	CC2_357	Aeromonas phage CC2	GCA_000903495.1
ADQ53137.1	002648	Cluster2213_1clades	140	65p129	Aeromonas virus 65	GCA_000893255.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANM45009.1	002649	Cluster2215_1clades	200	KTN4_251	Pseudomonas phage KTN4	GCA_002607225.1
QBX32407.1	002649	Cluster2215_1clades	192	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03676.1	002649	Cluster2215_1clades	197	253	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94705.1	002649	Cluster2215_1clades	200	SL2_128	Pseudomonas phage SL2	GCA_002956015.1
QJB22887.1	002649	Cluster2215_1clades	200	fnug_244	Pseudomonas phage fnug	GCA_012837215.1
QEM41978.1	002649	Cluster2215_1clades	192	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83110.1	002649	Cluster2215_1clades	200	PHIKZ209	Pseudomonas virus phiKZ	GCA_000842965.1
QDJ97198.1	002650	Cluster2216_1clades	152	D6_0038	Aeromonas phage D6	GCA_007051205.2
QDH47182.1	002650	Cluster2216_1clades	152	LAh10_204	Aeromonas phage LAh10	GCA_006863975.1
QDJ96799.1	002650	Cluster2216_1clades	148	PS1_0040	Aeromonas phage PS1	GCA_007051165.2
QFR59430.1	002650	Cluster2216_1clades	148	PS2_0039	Aeromonas phage PS2	GCA_009388305.2
QBZ70861.1	002650	Cluster2216_1clades	192	pETSU_280	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71892.1	002650	Cluster2216_1clades	189	N1M2_29	Klebsiella phage N1M2	GCA_010092605.1
AEV89487.1	002650	Cluster2216_1clades	200	OBP_050	Pseudomonas phage OBP	GCA_000896635.1
QDB70246.1	002651	Cluster2217_1clades	164	CF8_0078	Aeromonas phage CF8	GCA_006384595.2
QDJ97227.1	002651	Cluster2217_1clades	168	D6_0067	Aeromonas phage D6	GCA_007051205.2
QDJ96836.1	002651	Cluster2217_1clades	170	PS1_0077	Aeromonas phage PS1	GCA_007051165.2
QFR59466.1	002651	Cluster2217_1clades	170	PS2_0075	Aeromonas phage PS2	GCA_009388305.2
QBZ70607.1	002651	Cluster2217_1clades	176	pETSU_026	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71923.1	002651	Cluster2217_1clades	186	N1M2_60	Klebsiella phage N1M2	GCA_010092605.1
AEV89524.1	002651	Cluster2217_1clades	194	OBP_087	Pseudomonas phage OBP	GCA_000896635.1
AIT14325.1	002652	Cluster2218_1clades	192	PBI_121Q_435	Escherichia phage 121Q	GCA_000926855.1
AGC34812.1	002652	Cluster2218_1clades	192	ACQ29_gp132	Escherichia phage PBECO4	GCA_001041035.1
BBM61998.1	002652	Cluster2218_1clades	192	EO157G_4090	Escherichia phage SP27	GCA_008033345.1
AXC36923.1	002652	Cluster2218_1clades	192	-	Escherichia phage UB	GCA_003341455.1
QBO61979.1	002652	Cluster2218_1clades	192	G17_00490	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14003.1	002652	Cluster2218_1clades	192	vBEcoMphAPEC6_gp379c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80312.1	002652	Cluster2218_1clades	192	PSLUR01_00335	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANZ49766.1	002653	Cluster2219_1clades	188	MACHINA_128	Erwinia phage Machina	GCA_002758035.1
AXF51276.1	002653	Cluster2219_1clades	162	WELLINGTON_147	Erwinia phage Wellington	GCA_003344985.1
ANZ48421.1	002653	Cluster2219_1clades	190	CAITLIN_126	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48693.1	002653	Cluster2219_1clades	182	CHRISDB_131	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49211.1	002653	Cluster2219_1clades	188	HUXLEY_129	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49499.1	002653	Cluster2219_1clades	166	KWAN_147	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50039.1	002653	Cluster2219_1clades	188	PARSHIK_130	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOO14333.1	002654	SIG+CR-HNH3	129	Sn110110_139	Cyanophage S-RIM14	GCA_002599065.1
AMO43214.1	002654	SIG+CR-HNH3	188	R1080702_208	Cyanophage S-RIM32	GCA_001754165.1
AMO43266.1	002654	SIG+CR-HNH3	133	W270710_021	Cyanophage S-RIM44	GCA_002599145.1
AOO11738.1	002654	SIG+CR-HNH3	133	Np050604_021	Cyanophage S-RIM44	GCA_002599185.1
AOO12439.1	002654	SIG+CR-HNH3	133	Sn080709_021	Cyanophage S-RIM44	GCA_002599245.1
AOO12904.1	002654	SIG+CR-HNH3	133	W2100709_021	Cyanophage S-RIM44	GCA_002599285.1
ADO99123.1	002654	SIG+CR-HNH3	133	Syn1_021	Prochlorococcus phage Syn1	GCA_000892495.1
ANZ49833.1	002655	Cluster2221_1clades	188	MACHINA_195	Erwinia phage Machina	GCA_002758035.1
AXF51332.1	002655	Cluster2221_1clades	169	WELLINGTON_204	Erwinia phage Wellington	GCA_003344985.1
ANZ48489.1	002655	Cluster2221_1clades	180	CAITLIN_194	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48768.1	002655	Cluster2221_1clades	179	CHRISDB_206	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49277.1	002655	Cluster2221_1clades	188	HUXLEY_195	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49557.1	002655	Cluster2221_1clades	169	KWAN_205	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50105.1	002655	Cluster2221_1clades	188	PARSHIK_196	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AFQ96644.1	002656	Cluster2222_1clades	186	G173_gp099	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48210.1	002656	Cluster2222_1clades	187	ASESINO_197	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50621.1	002656	Cluster2222_1clades	186	STRATTON_196	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86018.1	002656	Cluster2222_1clades	187	ACEC001_1770	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20873.1	002656	Cluster2222_1clades	187	-	Salmonella phage JN03	GCA_014319805.1
AXF51128.1	002656	Cluster2222_1clades	187	MLDJOKPK_00264	Salmonella phage SPAsTU	GCA_003183805.1
AEP84010.1	002656	Cluster2222_1clades	187	SPN3US_0177	Salmonella phage SPN3US	GCA_001042275.1
APU01564.1	002657	Cluster2223_1clades	183	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28944.1	002657	Cluster2223_1clades	184	AP1_0237	Aeromonas phage AP1	GCA_014183365.1
ATI17337.1	002657	Cluster2223_1clades	184	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00257.1	002657	Cluster2223_1clades	184	HWB28_gp295	Aeromonas phage AS-zj	GCA_002627665.1
QAX97781.1	002657	Cluster2223_1clades	184	ASswx1_136	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39485.1	002657	Cluster2223_1clades	184	CC2_402	Aeromonas phage CC2	GCA_000903495.1
ADQ53187.1	002657	Cluster2223_1clades	183	65p179	Aeromonas virus 65	GCA_000893255.1
AXQ69122.1	002658	Cluster2224_1clades	161	CcrBL9_gp098	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87929.1	002658	Cluster2224_1clades	152	CcrColossus_gp059	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68601.1	002658	Cluster2224_1clades	153	CcrPW_gp062	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69676.1	002658	Cluster2224_1clades	161	CcrSC_gp094	Caulobacter phage CcrSC	GCA_003443315.1
ARV77204.1	002658	Cluster2224_1clades	125	NOXIFER_33	Pseudomonas phage Noxifer	GCA_002625005.1
AGS82102.1	002658	Cluster2224_1clades	133	PaBG_00227	Pseudomonas phage PaBG	GCA_000912555.1
BAG41723.1	002658	Cluster2224_1clades	180	RSL1_ORF276	Ralstonia phage phiRSL1	GCA_000879455.1
QDB70244.1	002659	Cluster2225_1clades	167	CF8_0076	Aeromonas phage CF8	GCA_006384595.2
QDJ97226.1	002659	Cluster2225_1clades	180	D6_0066	Aeromonas phage D6	GCA_007051205.2
QDJ96833.1	002659	Cluster2225_1clades	164	PS1_0074	Aeromonas phage PS1	GCA_007051165.2
QFR59463.1	002659	Cluster2225_1clades	164	PS2_0072	Aeromonas phage PS2	GCA_009388305.2
QBZ70605.1	002659	Cluster2225_1clades	132	pETSU_024	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71921.1	002659	Cluster2225_1clades	141	N1M2_58	Klebsiella phage N1M2	GCA_010092605.1
AEV89522.1	002659	Cluster2225_1clades	146	OBP_085	Pseudomonas phage OBP	GCA_000896635.1
AIT14024.1	002660	Cluster2226_1clades	123	PBI_121Q_130	Escherichia phage 121Q	GCA_000926855.1
QAY00316.1	002660	Cluster2226_1clades	123	Ecwhy1_34	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35064.1	002660	Cluster2226_1clades	119	ACQ29_gp384	Escherichia phage PBECO4	GCA_001041035.1
BBM61711.1	002660	Cluster2226_1clades	129	EO157G_1220	Escherichia phage SP27	GCA_008033345.1
QBO61673.1	002660	Cluster2226_1clades	127	G17_00181	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13722.1	002660	Cluster2226_1clades	127	vBEcoMphAPEC6_gp092c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80023.1	002660	Cluster2226_1clades	180	PSLUR01_00042	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14245.1	002661	Cluster2227_1clades	167	PBI_121Q_355	Escherichia phage 121Q	GCA_000926855.1
AGC34882.1	002661	Cluster2227_1clades	176	ACQ29_gp202	Escherichia phage PBECO4	GCA_001041035.1
BBM61923.1	002661	Cluster2227_1clades	179	EO157G_3340	Escherichia phage SP27	GCA_008033345.1
AXC36988.1	002661	Cluster2227_1clades	179	-	Escherichia phage UB	GCA_003341455.1
QBO62059.1	002661	Cluster2227_1clades	179	G17_00570	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14077.1	002661	Cluster2227_1clades	175	vBEcoMphAPEC6_gp454c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80235.1	002661	Cluster2227_1clades	175	PSLUR01_00258	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANZ49887.1	002662	Cluster2228_1clades	166	MACHINA_249	Erwinia phage Machina	GCA_002758035.1
AXF51388.1	002662	Cluster2228_1clades	165	WELLINGTON_262	Erwinia phage Wellington	GCA_003344985.1
ANZ48544.1	002662	Cluster2228_1clades	171	CAITLIN_249	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48821.1	002662	Cluster2228_1clades	163	CHRISDB_259	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49330.1	002662	Cluster2228_1clades	166	HUXLEY_248	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49614.1	002662	Cluster2228_1clades	165	KWAN_262	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50158.1	002662	Cluster2228_1clades	166	PARSHIK_249	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ABY62890.1	002663	MACRODOMAIN	170	201phi2-1p057	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44809.1	002663	MACRODOMAIN	170	KTN4_051	Pseudomonas phage KTN4	GCA_002607225.1
ARV76675.1	002663	MACRODOMAIN	157	PHABIO_44	Pseudomonas phage Phabio	GCA_002624965.1
AEH03452.1	002663	MACRODOMAIN	156	025	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94902.1	002663	MACRODOMAIN	170	SL2_325	Pseudomonas phage SL2	GCA_002956015.1
QJB22688.1	002663	MACRODOMAIN	170	fnug_45	Pseudomonas phage fnug	GCA_012837215.1
AAL82939.1	002663	MACRODOMAIN	170	PHIKZ038	Pseudomonas virus phiKZ	GCA_000842965.1
AGB06946.1	002664	Cluster2230_1clades	168	CF80_gp159	Vibrio phage VH7D	GCA_000914495.1
QBX06200.1	002664	Cluster2230_1clades	168	ValB1HC_247	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61217.1	002664	Cluster2230_1clades	168	AVU32_gp376	Vibrio phage ValKK3	GCA_001501635.1
AGN30317.1	002664	Cluster2230_1clades	168	VPFG_00319	Vibrio phage nt-1	GCA_000910195.2
ALP47100.1	002664	Cluster2230_1clades	168	phiGrn1_0005	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47483.1	002664	Cluster2230_1clades	168	phiST2_0137	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54825.1	002664	Cluster2230_1clades	168	vBValMR10Z_285	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ANZ48750.1	002665	Cluster2231_1clades	85	CHRISDB_188	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49258.1	002665	Cluster2231_1clades	97	HUXLEY_176	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49259.1	002665	Cluster2231_1clades	107	HUXLEY_177	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49535.1	002665	Cluster2231_1clades	125	KWAN_183	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50087.1	002665	Cluster2231_1clades	111	PARSHIK_178	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50357.1	002665	Cluster2231_1clades	87	PHOBOS_167	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50358.1	002665	Cluster2231_1clades	166	PHOBOS_168	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM44776.1	002666	Cluster2233_1clades	159	KTN4_018	Pseudomonas phage KTN4	GCA_002607225.1
QBX32497.1	002666	Cluster2233_1clades	159	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03754.1	002666	Cluster2233_1clades	161	331	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94930.1	002666	Cluster2233_1clades	159	SL2_353	Pseudomonas phage SL2	GCA_002956015.1
QJB22661.1	002666	Cluster2233_1clades	159	fnug_18	Pseudomonas phage fnug	GCA_012837215.1
QEM42070.1	002666	Cluster2233_1clades	159	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAL82917.1	002666	Cluster2233_1clades	159	PHIKZ016	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45018.1	002667	Cluster2234_1clades	158	KTN4_260	Pseudomonas phage KTN4	GCA_002607225.1
QBX32409.1	002667	Cluster2234_1clades	155	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03679.1	002667	Cluster2234_1clades	160	256	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94696.1	002667	Cluster2234_1clades	158	SL2_119	Pseudomonas phage SL2	GCA_002956015.1
QJB22895.1	002667	Cluster2234_1clades	158	fnug_252	Pseudomonas phage fnug	GCA_012837215.1
QEM41980.1	002667	Cluster2234_1clades	155	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83117.1	002667	Cluster2234_1clades	158	PHIKZ216	Pseudomonas virus phiKZ	GCA_000842965.1
AGH57016.1	002668	Cluster2235_1clades	159	CPXG_00213	Cyanophage P-RSM6	GCA_000906155.1
AJK27434.1	002668	Cluster2235_1clades	155	PTIM40_7	Cyanophage P-TIM40	GCA_001470935.1
AGG54366.1	002668	Cluster2235_1clades	146	CYWG_00082	Cyanophage S-SSM6b	GCA_002710425.1
ASR76117.1	002668	Cluster2235_1clades	145	PBI_BELLAMY_72	Synechococcus phage Bellamy	GCA_002627525.1
QCW23086.1	002668	Cluster2235_1clades	129	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50577.1	002668	Cluster2235_1clades	122	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70058.1	002668	Cluster2235_1clades	138	SynMITS9220M01_045	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARB13810.1	002669	Cluster2236_1clades	76	Ccr10_gp280	Caulobacter phage Ccr10	GCA_002619445.1
ARB14155.1	002669	Cluster2236_1clades	76	Ccr2_gp279	Caulobacter phage Ccr2	GCA_002619465.1
ARB14849.1	002669	Cluster2236_1clades	76	Ccr29_gp293	Caulobacter phage Ccr29	GCA_002619485.1
AFU88281.1	002669	Cluster2236_1clades	75	CcrColossus_gp411	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88302.1	002669	Cluster2236_1clades	158	CcrColossus_gp432	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68957.1	002669	Cluster2236_1clades	75	CcrPW_gp418c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68977.1	002669	Cluster2236_1clades	159	CcrPW_gp438c	Caulobacter phage CcrPW	GCA_003443275.1
AXH72910.1	002670	SIG+DPBB_1	141	-	Myoviridae sp.	GCA_003657725.1
AGR47977.1	002670	SIG+DPBB_1	108	SmphiM12_345	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13165.2	002670	SIG+DPBB_1	120	PHIM19_260	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12805.1	002670	SIG+DPBB_1	120	PHIM7_260	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13528.1	002670	SIG+DPBB_1	120	PHIN3_265	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54966.1	002670	SIG+DPBB_1	159	b23_0360	Synechococcus phage B23	GCA_009745195.1
QGT54601.1	002670	SIG+DPBB_1	159	b3_0366	Synechococcus phage B3	GCA_009745215.1
AIT14049.1	002671	Cluster2238_1clades	144	PBI_121Q_159	Escherichia phage 121Q	GCA_000926855.1
QAY00294.1	002671	Cluster2238_1clades	147	Ecwhy1_12	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35044.1	002671	Cluster2238_1clades	144	ACQ29_gp364	Escherichia phage PBECO4	GCA_001041035.1
BBM61732.1	002671	Cluster2238_1clades	158	EO157G_1430	Escherichia phage SP27	GCA_008033345.1
AXC36621.1	002671	Cluster2238_1clades	158	-	Escherichia phage UB	GCA_003341455.1
QBO61650.1	002671	Cluster2238_1clades	158	G17_00154	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80044.1	002671	Cluster2238_1clades	158	PSLUR01_00067	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64256.1	002672	Cluster2239_1clades	155	KVP40.0187	Vibrio phage KVP40	GCA_000843785.1
QIW90572.1	002672	Cluster2239_1clades	155	GCAPEGMB_00225	Vibrio phage V07	GCA_012361095.1
QIW91226.1	002672	Cluster2239_1clades	155	COHAPHLL_00390	Vibrio phage V09	GCA_012361135.1
QHJ74370.1	002672	Cluster2239_1clades	155	VH12019_00043	Vibrio phage VH1_2019	GCA_009931825.1
AGB06866.1	002672	Cluster2239_1clades	155	CF80_gp079	Vibrio phage VH7D	GCA_000914495.1
ALP47503.1	002672	Cluster2239_1clades	155	phiST2_0061	Vibrio phage phi-ST2	GCA_002757135.1
AFN37418.1	002672	Cluster2239_1clades	155	pp2_185	Vibriophage phi-pp2	GCA_002630725.1
APU01650.1	002673	Cluster2240_1clades	155	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28888.1	002673	Cluster2240_1clades	155	AP1_0181	Aeromonas phage AP1	GCA_014183365.1
ATI17235.1	002673	Cluster2240_1clades	155	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00352.1	002673	Cluster2240_1clades	155	HWB28_gp200	Aeromonas phage AS-zj	GCA_002627665.1
QAX97678.1	002673	Cluster2240_1clades	155	ASswx1_32	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39336.1	002673	Cluster2240_1clades	155	CC2_083	Aeromonas phage CC2	GCA_000903495.1
ADQ53279.1	002673	Cluster2240_1clades	155	65p271	Aeromonas virus 65	GCA_000893255.1
QIG63310.1	002674	Cluster2241_1clades	155	DAC16_77	Bacteroides phage DAC16	GCA_013387695.1
QIG63569.1	002674	Cluster2241_1clades	88	DAC19_78	Bacteroides phage DAC19	GCA_013387715.1
QIG63570.1	002674	Cluster2241_1clades	71	DAC19_79	Bacteroides phage DAC19	GCA_013387715.1
QIG63830.1	002674	Cluster2241_1clades	88	DAC20_77	Bacteroides phage DAC20	GCA_013387725.1
QIG63831.1	002674	Cluster2241_1clades	71	DAC20_78	Bacteroides phage DAC20	GCA_013387725.1
QIG64092.1	002674	Cluster2241_1clades	88	DAC22_78	Bacteroides phage DAC22	GCA_013387735.1
QIG64093.1	002674	Cluster2241_1clades	71	DAC22_79	Bacteroides phage DAC22	GCA_013387735.1
APU01750.1	002675	Cluster2242_1clades	152	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28915.1	002675	Cluster2242_1clades	149	AP1_0208	Aeromonas phage AP1	GCA_014183365.1
ATI17548.1	002675	Cluster2242_1clades	149	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00449.1	002675	Cluster2242_1clades	143	HWB28_gp103	Aeromonas phage AS-zj	GCA_002627665.1
QAX97989.1	002675	Cluster2242_1clades	149	ASswx1_348	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39372.1	002675	Cluster2242_1clades	149	CC2_187	Aeromonas phage CC2	GCA_000903495.1
ADQ53391.1	002675	Cluster2242_1clades	152	65p384	Aeromonas virus 65	GCA_000893255.1
AIT13984.1	002676	Cluster2244_1clades	151	PBI_121Q_87	Escherichia phage 121Q	GCA_000926855.1
QAY00354.1	002676	Cluster2244_1clades	150	Ecwhy1_73	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35100.1	002676	Cluster2244_1clades	151	ACQ29_gp420	Escherichia phage PBECO4	GCA_001041035.1
BBM61675.1	002676	Cluster2244_1clades	151	EO157G_0860	Escherichia phage SP27	GCA_008033345.1
QBO61709.1	002676	Cluster2244_1clades	151	G17_00220	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13757.1	002676	Cluster2244_1clades	151	vBEcoMphAPEC6_gp128c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79988.1	002676	Cluster2244_1clades	151	PSLUR01_00004	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGB06828.1	002677	Cluster2245_1clades	138	CF80_gp041	Vibrio phage VH7D	GCA_000914495.1
QBX06318.1	002677	Cluster2245_1clades	151	ValB1HC_365	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60949.1	002677	Cluster2245_1clades	151	AVU32_gp108	Vibrio phage ValKK3	GCA_001501635.1
AGN30201.1	002677	Cluster2245_1clades	146	VPFG_00201	Vibrio phage nt-1	GCA_000910195.2
ALP47129.1	002677	Cluster2245_1clades	151	phiGrn1_0265	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47514.1	002677	Cluster2245_1clades	151	phiST2_0024	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54561.1	002677	Cluster2245_1clades	151	vBValMR10Z_20	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
APU01647.1	002678	HSORC6	150	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28885.1	002678	HSORC6	144	AP1_0178	Aeromonas phage AP1	GCA_014183365.1
ATI17238.1	002678	HSORC6	145	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00349.1	002678	HSORC6	145	HWB28_gp203	Aeromonas phage AS-zj	GCA_002627665.1
QAX97681.1	002678	HSORC6	145	ASswx1_35	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39334.1	002678	HSORC6	145	CC2_080	Aeromonas phage CC2	GCA_000903495.1
ADQ53275.1	002678	HSORC6	150	65p267	Aeromonas virus 65	GCA_000893255.1
AIT14416.1	002679	Cluster2247_1clades	150	PBI_121Q_526	Escherichia phage 121Q	GCA_000926855.1
QAY00534.1	002679	Cluster2247_1clades	147	Ecwhy1_255	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34726.1	002679	Cluster2247_1clades	150	ACQ29_gp046	Escherichia phage PBECO4	GCA_001041035.1
BBM62088.1	002679	Cluster2247_1clades	150	EO157G_4990	Escherichia phage SP27	GCA_008033345.1
AXC36842.1	002679	Cluster2247_1clades	150	-	Escherichia phage UB	GCA_003341455.1
QBO61885.1	002679	Cluster2247_1clades	150	G17_00396	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80402.1	002679	Cluster2247_1clades	150	PSLUR01_00425	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMR59786.1	002680	Cluster2248_1clades	148	SEGD1_139	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96601.1	002680	Cluster2248_1clades	142	G173_gp056	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50578.1	002680	Cluster2248_1clades	142	STRATTON_153	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85976.1	002680	Cluster2248_1clades	148	ACEC001_1380	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20837.1	002680	Cluster2248_1clades	148	-	Salmonella phage JN03	GCA_014319805.1
AXF51053.1	002680	Cluster2248_1clades	142	MLDJOKPK_00014	Salmonella phage SPAsTU	GCA_003183805.1
AEP83968.1	002680	Cluster2248_1clades	148	SPN3US_0135	Salmonella phage SPN3US	GCA_001042275.1
ANM45093.1	002681	Cluster2249_1clades	146	KTN4_335	Pseudomonas phage KTN4	GCA_002607225.1
QBX32500.1	002681	Cluster2249_1clades	147	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03757.1	002681	Cluster2249_1clades	144	334	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94622.1	002681	Cluster2249_1clades	145	SL2_045	Pseudomonas phage SL2	GCA_002956015.1
QJB22969.1	002681	Cluster2249_1clades	146	fnug_326	Pseudomonas phage fnug	GCA_012837215.1
QEM42073.1	002681	Cluster2249_1clades	147	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83179.1	002681	Cluster2249_1clades	146	PHIKZ278	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ69154.1	002682	Cluster2250_1clades	144	CcrBL9_gp130	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ68625.1	002682	Cluster2250_1clades	145	CcrPW_gp086	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69708.1	002682	Cluster2250_1clades	136	CcrSC_gp126	Caulobacter phage CcrSC	GCA_003443315.1
AGR47728.2	002682	Cluster2250_1clades	78	SmphiM12_096	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12982.1	002682	Cluster2250_1clades	78	PHIM19_75	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12622.1	002682	Cluster2250_1clades	78	PHIM7_74	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13354.1	002682	Cluster2250_1clades	78	PHIN3_90	Sinorhizobium phage phiN3	GCA_001501175.1
APU01408.1	002683	Cluster2251_1clades	142	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28898.1	002683	Cluster2251_1clades	144	AP1_0191	Aeromonas phage AP1	GCA_014183365.1
ASU00510.1	002683	Cluster2251_1clades	143	HWB28_gp042	Aeromonas phage AS-zj	GCA_002627665.1
QAY01221.1	002683	Cluster2251_1clades	138	ASwh1_156	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39396.1	002683	Cluster2251_1clades	143	CC2_246	Aeromonas phage CC2	GCA_000903495.1
AAR90922.1	002683	Cluster2251_1clades	89	65p016	Aeromonas virus 65	GCA_000893255.1
AAR90921.1	002683	Cluster2251_1clades	69	65p017	Aeromonas virus 65	GCA_000893255.1
AUE22796.1	002684	Cluster2253_1clades	143	Ah1_00278	Aeromonas phage Ah1	GCA_002957415.1
QAX98511.1	002684	Cluster2253_1clades	142	ASfcp2_175	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52973.1	002684	Cluster2253_1clades	142	PX29p254	Aeromonas phage PX29	GCA_000920195.1
ADM79899.1	002684	Cluster2253_1clades	139	phiAS5_ORF0056	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17923.1	002684	Cluster2253_1clades	142	Aeh1ORF259c	Aeromonas virus Aeh1	GCA_000843245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIA64839.1	002684	Cluster2253_1clades	140	S13_040	Cronobacter phage S13	GCA_001503575.1
QHJ78823.1	002684	Cluster2253_1clades	113	-	Myoviridae sp.	GCA_012593985.1
APU01567.1	002685	Cluster2255_1clades	139	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28946.1	002685	Cluster2255_1clades	138	AP1_0239	Aeromonas phage AP1	GCA_014183365.1
ATI17335.1	002685	Cluster2255_1clades	138	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00259.1	002685	Cluster2255_1clades	138	HWB28_gp293	Aeromonas phage AS-zj	GCA_002627665.1
QAX97779.1	002685	Cluster2255_1clades	137	ASswx1_134	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39452.1	002685	Cluster2255_1clades	137	CC2_404	Aeromonas phage CC2	GCA_000903495.1
ADQ53190.1	002685	Cluster2255_1clades	139	65p182	Aeromonas virus 65	GCA_000893255.1
AIT14055.1	002686	Cluster2256_1clades	139	PBI_121Q_165	Escherichia phage 121Q	GCA_000926855.1
QAY00288.1	002686	Cluster2256_1clades	139	Ecwhy1_6	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35038.1	002686	Cluster2256_1clades	139	ACQ29_gp358	Escherichia phage PBECO4	GCA_001041035.1
BBM61738.1	002686	Cluster2256_1clades	139	EO157G_1490	Escherichia phage SP27	GCA_008033345.1
QBO61644.1	002686	Cluster2256_1clades	139	G17_00148	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13698.1	002686	Cluster2256_1clades	139	vBEcoMphAPEC6_gp068c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80050.1	002686	Cluster2256_1clades	139	PSLUR01_00073	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMS01308.1	002687	Flavodoxin_NdrI	139	AR9_g224	Bacillus phage AR9	GCA_001743835.1
ALN97958.1	002687	Flavodoxin_NdrI	124	Bp8pS_279	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93352.1	002687	Flavodoxin_NdrI	123	G_81	Bacillus virus G	GCA_000917535.1
AST99937.1	002687	Flavodoxin_NdrI	139	PBI_PBS1_115	Bacillus virus PBS1	GCA_002601325.1
QIG57903.1	002687	Flavodoxin_NdrI	130	SEA_PAULODIABOLI_217	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG66023.1	002687	Flavodoxin_NdrI	124	phiOC_p381	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AFF28243.1	002687	Flavodoxin_NdrI	123	PAU_245	Sphingomonas phage PAU	GCA_000902455.1
QDH83467.1	002688	PP-binding	81	H1O15_gp339	Achromobacter phage Motura	GCA_006964305.1
AFC21609.1	002688	PP-binding	84	GAP32_159	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43728.1	002688	PP-binding	138	CBB_163	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAG41529.1	002688	PP-binding	87	RSL1_ORF083	Ralstonia phage phiRSL1	GCA_000879455.1
AQW88683.1	002688	PP-binding	134	BF_0158	Serratia phage BF	GCA_002619745.1
SOK58964.1	002688	PP-binding	138	g156	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58430.1	002688	PP-binding	138	g153	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QAY01182.1	002689	Cluster2259_1clades	120	ASwh1_117	Aeromonas phage Aswh_1	GCA_004146945.1
AUZ94999.1	002689	Cluster2259_1clades	129	FDI40_gp217	Agrobacterium phage Atu_ph07	GCA_002628245.1
QHJ78877.1	002689	Cluster2259_1clades	121	-	Myoviridae sp.	GCA_012593985.1
AGR47969.1	002689	Cluster2259_1clades	136	SmphiM12_337	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13160.1	002689	Cluster2259_1clades	136	PHIM19_255	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12800.1	002689	Cluster2259_1clades	136	PHIM7_255	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13522.1	002689	Cluster2259_1clades	136	PHIN3_259	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14426.1	002690	Cluster2260_1clades	136	PBI_121Q_536	Escherichia phage 121Q	GCA_000926855.1
QAY00522.1	002690	Cluster2260_1clades	135	Ecwhy1_243	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34716.1	002690	Cluster2260_1clades	135	ACQ29_gp036	Escherichia phage PBECO4	GCA_001041035.1
BBM62098.1	002690	Cluster2260_1clades	136	EO157G_5090	Escherichia phage SP27	GCA_008033345.1
QBO61875.1	002690	Cluster2260_1clades	136	G17_00386	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13915.1	002690	Cluster2260_1clades	136	vBEcoMphAPEC6_gp290c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80412.1	002690	Cluster2260_1clades	136	PSLUR01_00435	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QAY00701.1	002691	Cluster2261_1clades	120	Ecwhy1_426	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34892.1	002691	Cluster2261_1clades	123	ACQ29_gp212	Escherichia phage PBECO4	GCA_001041035.1
BBM61909.1	002691	Cluster2261_1clades	134	EO157G_3200	Escherichia phage SP27	GCA_008033345.1
AXC36997.1	002691	Cluster2261_1clades	123	-	Escherichia phage UB	GCA_003341455.1
QBO62072.1	002691	Cluster2261_1clades	134	G17_00583	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14088.1	002691	Cluster2261_1clades	134	vBEcoMphAPEC6_gp465c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80222.1	002691	Cluster2261_1clades	131	PSLUR01_00245	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14237.1	002692	Cluster2262_1clades	128	PBI_121Q_347	Escherichia phage 121Q	GCA_000926855.1
QAY00696.1	002692	Cluster2262_1clades	134	Ecwhy1_421	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34889.1	002692	Cluster2262_1clades	128	ACQ29_gp209	Escherichia phage PBECO4	GCA_001041035.1
BBM61914.1	002692	Cluster2262_1clades	130	EO157G_3250	Escherichia phage SP27	GCA_008033345.1
QBO62068.1	002692	Cluster2262_1clades	128	G17_00579	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14084.1	002692	Cluster2262_1clades	128	vBEcoMphAPEC6_gp461c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80225.1	002692	Cluster2262_1clades	128	PSLUR01_00248	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14026.1	002693	Cluster2263_1clades	133	PBI_121Q_135	Escherichia phage 121Q	GCA_000926855.1
AXC36639.1	002693	Cluster2263_1clades	133	-	Escherichia phage UB	GCA_003341455.1
QBO61671.1	002693	Cluster2263_1clades	133	G17_00176	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13720.1	002693	Cluster2263_1clades	133	vBEcoMphAPEC6_gp090c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QCW19121.1	002693	Cluster2263_1clades	133	7t3_0605	Salmonella phage 7t3	GCA_006083215.1
AZU98358.1	002693	Cluster2263_1clades	133	CPT_Munch_418	Salmonella phage Munch	GCA_004015485.1
QIG62624.1	002693	Cluster2263_1clades	133	SEPI_011	Salmonella phage SE_PL	GCA_011067555.1
AIT13980.1	002694	Cluster2264_1clades	131	PBI_121Q_83	Escherichia phage 121Q	GCA_000926855.1
QAY00358.1	002694	Cluster2264_1clades	131	Ecwhy1_77	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35104.1	002694	Cluster2264_1clades	131	ACQ29_gp424	Escherichia phage PBECO4	GCA_001041035.1
BBM61671.1	002694	Cluster2264_1clades	131	EO157G_0820	Escherichia phage SP27	GCA_008033345.1
AXC36679.1	002694	Cluster2264_1clades	82	-	Escherichia phage UB	GCA_003341455.1
QBO61713.1	002694	Cluster2264_1clades	131	G17_00224	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13761.1	002694	Cluster2264_1clades	131	vBEcoMphAPEC6_gp132c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
APU01566.1	002695	Cluster2265_1clades	124	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28945.1	002695	Cluster2265_1clades	131	AP1_0238	Aeromonas phage AP1	GCA_014183365.1
ATI17336.1	002695	Cluster2265_1clades	127	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00258.1	002695	Cluster2265_1clades	127	HWB28_gp294	Aeromonas phage AS-zj	GCA_002627665.1
QAX97780.1	002695	Cluster2265_1clades	127	ASswx1_135	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39486.1	002695	Cluster2265_1clades	126	CC2_403	Aeromonas phage CC2	GCA_000903495.1
ADQ53189.1	002695	Cluster2265_1clades	124	65p181	Aeromonas virus 65	GCA_000893255.1
AMO43119.1	002696	Cluster2266_1clades	118	R1080702_110	Cyanophage S-RIM32	GCA_001754165.1
AMO43346.1	002696	Cluster2266_1clades	121	W270710_102	Cyanophage S-RIM44	GCA_002599145.1
AOO11818.1	002696	Cluster2266_1clades	121	Np050604_102	Cyanophage S-RIM44	GCA_002599185.1
AOO12519.1	002696	Cluster2266_1clades	121	Sn080709_102	Cyanophage S-RIM44	GCA_002599245.1
AOO12985.1	002696	Cluster2266_1clades	121	W2100709_103	Cyanophage S-RIM44	GCA_002599285.1
AGH26123.1	002696	Cluster2266_1clades	130	CPMG_00022	Prochlorococcus phage MED4-213	GCA_000904535.1
ADO99204.1	002696	Cluster2266_1clades	121	Syn1_103	Prochlorococcus phage Syn1	GCA_000892495.1
QDB70459.1	002697	Cluster2267_1clades	104	CF8_0046	Aeromonas phage CF8	GCA_006384595.2
QDJ97200.1	002697	Cluster2267_1clades	105	D6_0040	Aeromonas phage D6	GCA_007051205.2
QDH47202.1	002697	Cluster2267_1clades	130	LAh10_206	Aeromonas phage LAh10	GCA_006863975.1
QDJ96801.1	002697	Cluster2267_1clades	100	PS1_0042	Aeromonas phage PS1	GCA_007051165.2
QFR59432.1	002697	Cluster2267_1clades	100	PS2_0041	Aeromonas phage PS2	GCA_009388305.2
QGH71894.1	002697	Cluster2267_1clades	105	N1M2_31	Klebsiella phage N1M2	GCA_010092605.1
AEV89489.1	002697	Cluster2267_1clades	100	OBP_052	Pseudomonas phage OBP	GCA_000896635.1
APU01687.1	002698	Cluster2268_1clades	118	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28823.1	002698	Cluster2268_1clades	128	AP1_0116	Aeromonas phage AP1	GCA_014183365.1
ATI17603.1	002698	Cluster2268_1clades	128	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00393.1	002698	Cluster2268_1clades	128	HWB28_gp159	Aeromonas phage AS-zj	GCA_002627665.1
QAX98044.1	002698	Cluster2268_1clades	128	ASswx1_404	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39354.1	002698	Cluster2268_1clades	127	CC2_126	Aeromonas phage CC2	GCA_000903495.1
ADQ53323.1	002698	Cluster2268_1clades	118	65p315	Aeromonas virus 65	GCA_000893255.1
AIT14352.1	002699	Cluster2269_1clades	125	PBI_121Q_462	Escherichia phage 121Q	GCA_000926855.1
AGC34787.1	002699	Cluster2269_1clades	127	ACQ29_gp107	Escherichia phage PBECO4	GCA_001041035.1
BBM62023.1	002699	Cluster2269_1clades	127	EO157G_4340	Escherichia phage SP27	GCA_008033345.1
AXC36903.1	002699	Cluster2269_1clades	127	-	Escherichia phage UB	GCA_003341455.1
QBO61952.1	002699	Cluster2269_1clades	127	G17_00463	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13979.1	002699	Cluster2269_1clades	90	vBEcoMphAPEC6_gp355c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80339.1	002699	Cluster2269_1clades	127	PSLUR01_00362	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFQ96692.1	002700	Cluster2270_1clades	125	G173_gp147	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48261.1	002700	Cluster2270_1clades	124	ASESINO_248	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50674.1	002700	Cluster2270_1clades	125	STRATTON_249	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86067.1	002700	Cluster2270_1clades	120	ACEC001_2240	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20913.1	002700	Cluster2270_1clades	120	-	Salmonella phage JN03	GCA_014319805.1
AXF51112.1	002700	Cluster2270_1clades	120	MLDJOKPK_00214	Salmonella phage SPAsTU	GCA_003183805.1
AEP84059.1	002700	Cluster2270_1clades	120	SPN3US_0226	Salmonella phage SPN3US	GCA_001042275.1
AIT13983.1	002701	Cluster2271_1clades	125	PBI_121Q_86	Escherichia phage 121Q	GCA_000926855.1
QAY00355.1	002701	Cluster2271_1clades	124	Ecwhy1_74	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35101.1	002701	Cluster2271_1clades	125	ACQ29_gp421	Escherichia phage PBECO4	GCA_001041035.1
BBM61674.1	002701	Cluster2271_1clades	125	EO157G_0850	Escherichia phage SP27	GCA_008033345.1
QBO61710.1	002701	Cluster2271_1clades	125	G17_00221	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13758.1	002701	Cluster2271_1clades	125	vBEcoMphAPEC6_gp129c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA79987.1	002701	Cluster2271_1clades	125	PSLUR01_00003	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01534.1	002702	Cluster2272_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29074.1	002702	Cluster2272_1clades	122	AP1_0367	Aeromonas phage AP1	GCA_014183365.1
ATI17355.1	002702	Cluster2272_1clades	123	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00239.1	002702	Cluster2272_1clades	123	HWB28_gp313	Aeromonas phage AS-zj	GCA_002627665.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX97799.1	002702	Cluster2272_1clades	123	ASswx1_154	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39445.1	002702	Cluster2272_1clades	118	CC2_383	Aeromonas phage CC2	GCA_000903495.1
ADQ53156.1	002702	Cluster2272_1clades	123	65p148	Aeromonas virus 65	GCA_000893255.1
QIW91095.1	002703	Cluster2273_1clades	122	COHAPHLL_00232	Vibrio phage V09	GCA_012361135.1
QBX06153.1	002703	Cluster2273_1clades	122	ValB1HC_199	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61165.1	002703	Cluster2273_1clades	122	AVU32_gp324	Vibrio phage ValKK3	GCA_001501635.1
ALP47161.1	002703	Cluster2273_1clades	122	phiGrn1_0054	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47654.1	002703	Cluster2273_1clades	77	phiST2_0186	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54778.1	002703	Cluster2273_1clades	122	vBValMR10Z_238	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37552.1	002703	Cluster2273_1clades	122	pp2_320	Vibriophage phi-pp2	GCA_002630725.1
AYD81449.1	002704	Cluster2274_1clades	122	SEA_JUSTBECAUSE_294	Streptomyces phage JustBecause	GCA_003613775.1
QJD53835.1	002704	Cluster2274_1clades	110	SEA_KELA_275	Streptomyces phage Kela	GCA_012934305.1
QJD53854.1	002704	Cluster2274_1clades	122	SEA_KELA_294	Streptomyces phage Kela	GCA_012934305.1
QBZ72164.1	002704	Cluster2274_1clades	108	SEA_KRADAL_278	Streptomyces phage Kradal	GCA_004799925.1
QBZ72185.1	002704	Cluster2274_1clades	118	SEA_KRADAL_299	Streptomyces phage Kradal	GCA_004799925.1
AXH66427.1	002704	Cluster2274_1clades	108	SEA_SATIS_278	Streptomyces phage Satis	GCA_003366315.1
AXH66448.1	002704	Cluster2274_1clades	118	SEA_SATIS_299	Streptomyces phage Satis	GCA_003366315.1
AIT13938.1	002705	SIG+TM	110	PBI_121Q_41	Escherichia phage 121Q	GCA_000926855.1
QAY00399.1	002705	SIG+TM	122	Ecwhy1_118	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35144.1	002705	SIG+TM	116	ACQ29_gp464	Escherichia phage PBECO4	GCA_001041035.1
BBM61630.1	002705	SIG+TM	122	EO157G_0410	Escherichia phage SP27	GCA_008033345.1
QBO61755.1	002705	SIG+TM	122	G17_00266	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13800.1	002705	SIG+TM	122	vBEcoMphAPEC6_gp171c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80532.1	002705	SIG+TM	122	PSLUR01_00555	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ABY63145.1	002706	SIG+TM	90	201phi2-1p320	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM44782.1	002706	SIG+TM	96	KTN4_024	Pseudomonas phage KTN4	GCA_002607225.1
AFH14896.1	002706	SIG+TM	89	Lu11_0358	Pseudomonas phage Lu11	GCA_000897175.1
ARV77276.1	002706	SIG+TM	121	NOXIFER_107	Pseudomonas phage Noxifer	GCA_002625005.1
QHJ86128.1	002706	SIG+TM	87	KKIINIFJ_00217	Pseudomonas phage PN05	GCA_009931935.1
QBJ02948.1	002706	SIG+TM	107	PSA21_129	Pseudomonas phage Psa21	GCA_004340405.1
QEM41859.1	002706	SIG+TM	101	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AXG67296.1	002707	Cluster2277_1clades	120	AD1_252	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80037.1	002707	Cluster2277_1clades	105	JA11_232	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66636.1	002707	Cluster2277_1clades	105	JA13_233	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66960.1	002707	Cluster2277_1clades	105	JA29_234	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67607.1	002707	Cluster2277_1clades	105	JA33_233	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08521.1	002707	Cluster2277_1clades	121	Alexandra_264	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58899.1	002707	Cluster2277_1clades	121	Y3_259	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AIT14318.1	002708	Cluster2278_1clades	87	PBI_121Q_428	Escherichia phage 121Q	GCA_000926855.1
AGC34818.1	002708	Cluster2278_1clades	87	ACQ29_gp138	Escherichia phage PBECO4	GCA_001041035.1
BBM61992.1	002708	Cluster2278_1clades	87	EO157G_4030	Escherichia phage SP27	GCA_008033345.1
AXC36927.1	002708	Cluster2278_1clades	87	-	Escherichia phage UB	GCA_003341455.1
QBO61986.1	002708	Cluster2278_1clades	87	G17_00497	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14009.1	002708	Cluster2278_1clades	120	vBEcoMphAPEC6_gp385c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80305.1	002708	Cluster2278_1clades	87	PSLUR01_00328	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01575.1	002709	Cluster2279_1clades	119	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28962.1	002709	Cluster2279_1clades	55	AP1_0255	Aeromonas phage AP1	GCA_014183365.1
ATI17332.1	002709	Cluster2279_1clades	118	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00262.1	002709	Cluster2279_1clades	118	HWB28_gp290	Aeromonas phage AS-zj	GCA_002627665.1
QAX97776.1	002709	Cluster2279_1clades	117	ASswx1_131	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39455.1	002709	Cluster2279_1clades	118	CC2_407	Aeromonas phage CC2	GCA_000903495.1
ADQ53199.1	002709	Cluster2279_1clades	119	65p191	Aeromonas virus 65	GCA_000893255.1
AFC21982.1	002710	SIG+TM+TM	107	GAP32_522	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21983.1	002710	SIG+TM+TM	119	GAP32_523	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44102.1	002710	SIG+TM+TM	107	CBB_539	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44103.1	002710	SIG+TM+TM	62	CBB_540	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89056.1	002710	SIG+TM+TM	115	BF_0531	Serratia phage BF	GCA_002619745.1
SOK59334.1	002710	SIG+TM+TM	115	g526	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58796.1	002710	SIG+TM+TM	115	g519	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14109.1	002711	Cluster2281_1clades	119	PBI_121Q_219	Escherichia phage 121Q	GCA_000926855.1
AGC34988.1	002711	Cluster2281_1clades	119	ACQ29_gp308	Escherichia phage PBECO4	GCA_001041035.1
BBM61791.1	002711	Cluster2281_1clades	119	EO157G_2020	Escherichia phage SP27	GCA_008033345.1
AXC36567.1	002711	Cluster2281_1clades	119	-	Escherichia phage UB	GCA_003341455.1
QBO61590.1	002711	Cluster2281_1clades	119	G17_00094	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13652.1	002711	Cluster2281_1clades	119	vBEcoMphAPEC6_gp021c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80102.1	002711	Cluster2281_1clades	119	PSLUR01_00125	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AND75242.1	002712	HU-IHF	94	ME3_81	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83596.1	002712	HU-IHF	111	0305phi8-36p033	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93498.1	002712	HU-IHF	95	G_239	Bacillus virus G	GCA_000917535.1
AYD81312.1	002712	HU-IHF	119	SEA_JUSTBECAUSE_147	Streptomyces phage JustBecause	GCA_003613775.1
QJD53715.1	002712	HU-IHF	119	SEA_KELA_145	Streptomyces phage Kela	GCA_012934305.1
QBZ72042.1	002712	HU-IHF	119	SEA_KRADAL_146	Streptomyces phage Kradal	GCA_004799925.1
AXH66305.1	002712	HU-IHF	119	SEA_SATIS_146	Streptomyces phage Satis	GCA_003366315.1
APU01710.1	002713	MIB_HERC2+DUF1778	118	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28909.1	002713	MIB_HERC2+DUF1778	80	AP1_0202	Aeromonas phage AP1	GCA_014183365.1
ATI17586.1	002713	MIB_HERC2+DUF1778	80	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00411.1	002713	MIB_HERC2+DUF1778	80	HWB28_gp141	Aeromonas phage AS-zj	GCA_002627665.1
QAX98025.1	002713	MIB_HERC2+DUF1778	79	ASswx1_385	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39236.1	002713	MIB_HERC2+DUF1778	75	CC2_147	Aeromonas phage CC2	GCA_000903495.1
ADQ53349.1	002713	MIB_HERC2+DUF1778	118	65p341	Aeromonas virus 65	GCA_000893255.1
AFC21666.1	002714	FAM76	117	GAP32_216	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43787.1	002714	FAM76	109	CBB_222	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18937.1	002714	FAM76	99	7t3_0416	Salmonella phage 7t3	GCA_006083215.1
AZU98192.1	002714	FAM76	99	CPT_Munch_248	Salmonella phage Munch	GCA_004015485.1
AQW88743.1	002714	FAM76	115	BF_0218	Serratia phage BF	GCA_002619745.1
SOK59026.1	002714	FAM76	112	g218	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58491.1	002714	FAM76	112	g214	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGB06838.1	002715	Cluster2285_1clades	116	CF80_gp051	Vibrio phage VH7D	GCA_000914495.1
QBX06308.1	002715	Cluster2285_1clades	116	ValB1HC_355	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60939.1	002715	Cluster2285_1clades	116	AVU32_gp098	Vibrio phage ValKK3	GCA_001501635.1
AGN30211.1	002715	Cluster2285_1clades	115	VPFG_00211	Vibrio phage nt-1	GCA_000910195.2
ALP47168.1	002715	Cluster2285_1clades	116	phiGrn1_0275	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47559.1	002715	Cluster2285_1clades	116	phiST2_0034	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54551.1	002715	Cluster2285_1clades	116	vBValMR10Z_10	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AIT14116.1	002716	TM+TM+TM	115	PBI_121Q_226	Escherichia phage 121Q	GCA_000926855.1
QAY00808.1	002716	TM+TM+TM	115	Ecwhy1_535	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34982.1	002716	TM+TM+TM	115	ACQ29_gp302	Escherichia phage PBECO4	GCA_001041035.1
BBM61795.1	002716	TM+TM+TM	115	EO157G_2060	Escherichia phage SP27	GCA_008033345.1
QBO61584.1	002716	TM+TM+TM	115	G17_00088	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13647.1	002716	TM+TM+TM	115	vBEcoMphAPEC6_gp016c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80107.1	002716	TM+TM+TM	115	PSLUR01_00130	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ARB13846.1	002717	Cluster2287_1clades	113	Ccr10_gp316	Caulobacter phage Ccr10	GCA_002619445.1
ARB14191.1	002717	Cluster2287_1clades	113	Ccr2_gp315	Caulobacter phage Ccr2	GCA_002619465.1
ARB14885.1	002717	Cluster2287_1clades	113	Ccr29_gp329	Caulobacter phage Ccr29	GCA_002619485.1
ARB15223.1	002717	Cluster2287_1clades	113	Ccr32_gp305	Caulobacter phage Ccr32	GCA_002619505.1
ARB15557.1	002717	Cluster2287_1clades	113	Ccr34_gp315	Caulobacter phage Ccr34	GCA_002619525.1
AFU88635.1	002717	Cluster2287_1clades	113	CcrSwift_gp317	Caulobacter virus Swift	GCA_000899655.1
AFU87142.1	002717	Cluster2287_1clades	113	CbK_gp310	Caulobacter virus phiCbK	GCA_000900535.1
AIT14242.1	002718	Cluster2288_1clades	113	PBI_121Q_352	Escherichia phage 121Q	GCA_000926855.1
QAY00689.1	002718	Cluster2288_1clades	113	Ecwhy1_414	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34885.1	002718	Cluster2288_1clades	113	ACQ29_gp205	Escherichia phage PBECO4	GCA_001041035.1
BBM61920.1	002718	Cluster2288_1clades	113	EO157G_3310	Escherichia phage SP27	GCA_008033345.1
QBO62062.1	002718	Cluster2288_1clades	113	G17_00573	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14080.1	002718	Cluster2288_1clades	113	vBEcoMphAPEC6_gp457c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80232.1	002718	Cluster2288_1clades	113	PSLUR01_00255	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01457.1	002719	Cluster2289_1clades	105	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29099.1	002719	Cluster2289_1clades	60	AP1_0392	Aeromonas phage AP1	GCA_014183365.1
ATI17440.1	002719	Cluster2289_1clades	111	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00155.1	002719	Cluster2289_1clades	111	HWB28_gp397	Aeromonas phage AS-zj	GCA_002627665.1
QAX97880.1	002719	Cluster2289_1clades	111	ASswx1_237	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39416.1	002719	Cluster2289_1clades	104	CC2_297	Aeromonas phage CC2	GCA_000903495.1
ADQ53078.1	002719	Cluster2289_1clades	105	65p068	Aeromonas virus 65	GCA_000893255.1
APU01717.1	002720	Cluster2290_1clades	108	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28749.1	002720	Cluster2290_1clades	110	AP1_0031	Aeromonas phage AP1	GCA_014183365.1
ATI17579.1	002720	Cluster2290_1clades	110	-	Aeromonas phage AS-szw	GCA_002743635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU00418.1	002720	Cluster2290_1clades	110	HWB28_gp134	Aeromonas phage AS-zj	GCA_002627665.1
QAX98018.1	002720	Cluster2290_1clades	104	ASswx1_378	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39361.1	002720	Cluster2290_1clades	110	CC2_154	Aeromonas phage CC2	GCA_000903495.1
ADQ53357.1	002720	Cluster2290_1clades	108	65p349	Aeromonas virus 65	GCA_000893255.1
AFC21848.1	002721	Cluster2291_1clades	109	GAP32_396	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QCW19102.1	002721	Cluster2291_1clades	110	7t3_0584	Salmonella phage 7t3	GCA_006083215.1
AZU98341.1	002721	Cluster2291_1clades	110	CPT_Munch_399	Salmonella phage Munch	GCA_004015485.1
QIG62643.1	002721	Cluster2291_1clades	110	SEPL_030	Salmonella phage SE_PL	GCA_011067555.1
AQW88928.1	002721	Cluster2291_1clades	110	BF_0403	Serratia phage BF	GCA_002619745.1
SOK59217.1	002721	Cluster2291_1clades	110	g409	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58683.1	002721	Cluster2291_1clades	110	g406	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01623.1	002722	DUF5417	91	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17278.1	002722	DUF5417	92	-	Aeromonas phage AS-szw	GCA_002743635.1
ADQ53248.1	002722	DUF5417	91	65p240	Aeromonas virus 65	GCA_000893255.1
ANS06115.1	002722	DUF5417	92	ABCD_0168	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97180.1	002722	DUF5417	108	E_172	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70790.1	002722	DUF5417	82	phiC120_c84	Escherichia phage phiC120	GCA_002621185.1
AAX78698.1	002722	DUF5417	92	RB43ORF176c	Escherichia virus RB43	GCA_000863505.1
QAY00751.1	002723	Cluster2293_1clades	107	Ecwhy1_477	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34931.1	002723	Cluster2293_1clades	107	ACQ29_gp251	Escherichia phage PBECO4	GCA_001041035.1
BBM61861.1	002723	Cluster2293_1clades	107	EO157G_2720	Escherichia phage SP27	GCA_008033345.1
AXC37034.1	002723	Cluster2293_1clades	107	-	Escherichia phage UB	GCA_003341455.1
QBO61520.1	002723	Cluster2293_1clades	107	G17_00024	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62126.1	002723	Cluster2293_1clades	107	G17_00637	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80170.1	002723	Cluster2293_1clades	107	PSLUR01_00193	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01562.1	002724	Cluster2294_1clades	104	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28941.1	002724	Cluster2294_1clades	105	AP1_0234	Aeromonas phage AP1	GCA_014183365.1
ATI17339.1	002724	Cluster2294_1clades	105	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00254.1	002724	Cluster2294_1clades	105	HWB28_gp298	Aeromonas phage AS-zj	GCA_002627665.1
QAX97784.1	002724	Cluster2294_1clades	105	ASswx1_139	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39484.1	002724	Cluster2294_1clades	105	CC2_399	Aeromonas phage CC2	GCA_000903495.1
ADQ53185.1	002724	Cluster2294_1clades	104	65p177	Aeromonas virus 65	GCA_000893255.1
AIR93415.1	002725	Cluster2295_1clades	105	AVU42_gp033	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22984.1	002725	Cluster2295_1clades	95	-	Synechococcus phage S-B05	GCA_006083695.1
AOV59657.1	002725	Cluster2295_1clades	83	S330809_196	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59419.1	002725	Cluster2295_1clades	83	C440309_196	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59894.1	002725	Cluster2295_1clades	83	N231010_195	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70466.1	002725	Cluster2295_1clades	88	HOU04_gp067	Synechococcus phage S-T4	GCA_003443335.1
QJT70049.1	002725	Cluster2295_1clades	94	SynMITS9220M01_036	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ALN97691.1	002726	Cluster2296_1clades	105	Bp8pS_012	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93545.1	002726	Cluster2296_1clades	92	G_286	Bacillus virus G	GCA_000917535.1
AXQ69170.1	002726	Cluster2296_1clades	86	CcrBL9_gp146	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88002.1	002726	Cluster2296_1clades	87	CcrColossus_gp132	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68678.1	002726	Cluster2296_1clades	87	CcrPW_gp139	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69724.1	002726	Cluster2296_1clades	86	CcrSC_gp142	Caulobacter phage CcrSC	GCA_003443315.1
BBA65304.1	002726	Cluster2296_1clades	83	-	Xanthomonas phage XacN1	GCA_003173815.1
AIT14265.1	002727	Cluster2297_1clades	104	PBI_121Q_375	Escherichia phage 121Q	GCA_000926855.1
QAY00672.1	002727	Cluster2297_1clades	104	Ecwhy1_397	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34867.1	002727	Cluster2297_1clades	104	ACQ29_gp187	Escherichia phage PBECO4	GCA_001041035.1
BBM61940.1	002727	Cluster2297_1clades	104	EO157G_3510	Escherichia phage SP27	GCA_008033345.1
QBO62039.1	002727	Cluster2297_1clades	104	G17_00550	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14060.1	002727	Cluster2297_1clades	104	vBEcoMphAPEC6_gp437c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80254.1	002727	Cluster2297_1clades	104	PSLUR01_00277	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64251.1	002728	Cluster2298_1clades	103	KVP40.0182	Vibrio phage KVP40	GCA_000843785.1
QIW90567.1	002728	Cluster2298_1clades	103	GCAPEGMB_00220	Vibrio phage V07	GCA_012361095.1
QIW91232.1	002728	Cluster2298_1clades	103	COHAPHLL_00396	Vibrio phage V09	GCA_012361135.1
QHJ74365.1	002728	Cluster2298_1clades	103	VH12019_00038	Vibrio phage VH1_2019	GCA_009931825.1
AJT60913.1	002728	Cluster2298_1clades	102	AVU32_gp072	Vibrio phage ValKK3	GCA_001501635.1
AGN30240.1	002728	Cluster2298_1clades	101	VPFG_00241	Vibrio phage nt-1	GCA_000910195.2
AFN37412.1	002728	Cluster2298_1clades	103	pp2_179	Vibriophage phi-pp2	GCA_002630725.1
AIT14314.1	002729	Cluster2299_1clades	103	PBI_121Q_424	Escherichia phage 121Q	GCA_000926855.1
QAY00624.1	002729	Cluster2299_1clades	83	Ecwhy1_349	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34821.1	002729	Cluster2299_1clades	86	ACQ29_gp141	Escherichia phage PBECO4	GCA_001041035.1
BBM61988.1	002729	Cluster2299_1clades	103	EO157G_3990	Escherichia phage SP27	GCA_008033345.1
QBO61990.1	002729	Cluster2299_1clades	103	G17_00501	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14011.1	002729	Cluster2299_1clades	103	vBEcoMphAPEC6_gp387c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80301.1	002729	Cluster2299_1clades	103	PSLUR01_00324	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14339.1	002730	Cluster2300_1clades	101	PBI_121Q_449	Escherichia phage 121Q	GCA_000926855.1
QAY00604.1	002730	Cluster2300_1clades	101	Ecwhy1_328	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34799.1	002730	Cluster2300_1clades	101	ACQ29_gp119	Escherichia phage PBECO4	GCA_001041035.1
BBM62010.1	002730	Cluster2300_1clades	101	EO157G_4210	Escherichia phage SP27	GCA_008033345.1
QBO61965.1	002730	Cluster2300_1clades	101	G17_00476	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13991.1	002730	Cluster2300_1clades	101	vBEcoMphAPEC6_gp367c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80326.1	002730	Cluster2300_1clades	101	PSLUR01_00349	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28821.1	002731	Cluster2301_1clades	95	AP1_0114	Aeromonas phage AP1	GCA_014183365.1
ATI17605.1	002731	Cluster2301_1clades	95	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00391.1	002731	Cluster2301_1clades	95	HWB28_gp161	Aeromonas phage AS-zj	GCA_002627665.1
QAX98046.1	002731	Cluster2301_1clades	95	ASswx1_406	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01099.1	002731	Cluster2301_1clades	94	ASwh1_31	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39353.1	002731	Cluster2301_1clades	95	CC2_124	Aeromonas phage CC2	GCA_000903495.1
ARM70955.1	002731	Cluster2301_1clades	101	phiC120_c250	Escherichia phage phiC120	GCA_002621185.1
AXQ69046.1	002732	TM	99	CcrBL9_gp022	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69562.1	002732	TM	99	CcrBL9_gp538	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87891.1	002732	TM	95	CcrColossus_gp021	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68562.1	002732	TM	95	CcrPW_gp023	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69011.1	002732	TM	95	CcrPW_gp472	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69606.1	002732	TM	101	CcrSC_gp024	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70106.1	002732	TM	101	CcrSC_gp524	Caulobacter phage CcrSC	GCA_003443315.1
QIG63237.1	002733	S1	101	DAC16_4	Bacteroides phage DAC16	GCA_013387695.1
QIG63495.1	002733	S1	101	DAC19_4	Bacteroides phage DAC19	GCA_013387715.1
QIG63757.1	002733	S1	101	DAC20_4	Bacteroides phage DAC20	GCA_013387725.1
QIG64018.1	002733	S1	101	DAC22_4	Bacteroides phage DAC22	GCA_013387735.1
QIG64282.1	002733	S1	101	DAC23_4	Bacteroides phage DAC23	GCA_013387745.1
prevph1000000797	002733	S1	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000545	002733	S1	73	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AIT14337.1	002734	Cluster2304_1clades	100	PBI_121Q_447	Escherichia phage 121Q	GCA_000926855.1
QAY00606.1	002734	Cluster2304_1clades	100	Ecwhy1_330	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34801.1	002734	Cluster2304_1clades	100	ACQ29_gp121	Escherichia phage PBECO4	GCA_001041035.1
BBM62008.1	002734	Cluster2304_1clades	100	EO157G_4190	Escherichia phage SP27	GCA_008033345.1
QBO61967.1	002734	Cluster2304_1clades	100	G17_00478	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13993.1	002734	Cluster2304_1clades	100	vBEcoMphAPEC6_gp369c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80324.1	002734	Cluster2304_1clades	100	PSLUR01_00347	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14324.1	002735	Cluster2305_1clades	100	PBI_121Q_434	Escherichia phage 121Q	GCA_000926855.1
QAY00616.1	002735	Cluster2305_1clades	99	Ecwhy1_340	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34813.1	002735	Cluster2305_1clades	100	ACQ29_gp133	Escherichia phage PBECO4	GCA_001041035.1
BBM61997.1	002735	Cluster2305_1clades	100	EO157G_4080	Escherichia phage SP27	GCA_008033345.1
QBO61980.1	002735	Cluster2305_1clades	100	G17_00491	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14004.1	002735	Cluster2305_1clades	100	vBEcoMphAPEC6_gp380c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80311.1	002735	Cluster2305_1clades	100	PSLUR01_00334	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01676.1	002736	Cluster2306_1clades	98	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29063.1	002736	Cluster2306_1clades	98	AP1_0356	Aeromonas phage AP1	GCA_014183365.1
ATI17618.1	002736	Cluster2306_1clades	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00378.1	002736	Cluster2306_1clades	98	HWB28_gp174	Aeromonas phage AS-zj	GCA_002627665.1
QAX97652.1	002736	Cluster2306_1clades	98	ASswx1_6	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39346.1	002736	Cluster2306_1clades	98	CC2_108	Aeromonas phage CC2	GCA_000903495.1
ADQ53310.1	002736	Cluster2306_1clades	98	65p302	Aeromonas virus 65	GCA_000893255.1
AIT14338.1	002737	Cluster2307_1clades	98	PBI_121Q_448	Escherichia phage 121Q	GCA_000926855.1
QAY00605.1	002737	Cluster2307_1clades	98	Ecwhy1_329	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34800.1	002737	Cluster2307_1clades	98	ACQ29_gp120	Escherichia phage PBECO4	GCA_001041035.1
BBM62009.1	002737	Cluster2307_1clades	98	EO157G_4200	Escherichia phage SP27	GCA_008033345.1
QBO61966.1	002737	Cluster2307_1clades	98	G17_00477	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13992.1	002737	Cluster2307_1clades	98	vBEcoMphAPEC6_gp368c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80325.1	002737	Cluster2307_1clades	98	PSLUR01_00348	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01799.1	002738	Cluster2308_1clades	73	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28953.1	002738	Cluster2308_1clades	97	AP1_0246	Aeromonas phage AP1	GCA_014183365.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATI17506.1	002738	Cluster2308_1clades	97	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00491.1	002738	Cluster2308_1clades	97	HWB28_gp061	Aeromonas phage AS-zj	GCA_002627665.1
QAX97945.1	002738	Cluster2308_1clades	97	ASswx1_303	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39390.1	002738	Cluster2308_1clades	96	CC2_228	Aeromonas phage CC2	GCA_000903495.1
ADQ53443.1	002738	Cluster2308_1clades	73	65p437	Aeromonas virus 65	GCA_000893255.1
ARB13723.1	002739	Cluster2309_1clades	44	Ccr10_gp193c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14068.1	002739	Cluster2309_1clades	44	Ccr2_gp192c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14757.1	002739	Cluster2309_1clades	44	Ccr29_gp201	Caulobacter phage Ccr29	GCA_002619485.1
ARB14411.1	002739	Cluster2309_1clades	44	Ccr5_gp191c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87716.1	002739	Cluster2309_1clades	96	CcrKarma_gp199	Caulobacter virus Karma	GCA_000901575.1
AFU87365.1	002739	Cluster2309_1clades	44	CcrMagneto_gp195	Caulobacter virus Magneto	GCA_000903095.1
AFU88512.1	002739	Cluster2309_1clades	44	CcrSwift_gp194	Caulobacter virus Swift	GCA_000899655.1
AIT14319.1	002740	Cluster2310_1clades	83	PBI_121Q_429	Escherichia phage 121Q	GCA_000926855.1
QAY00620.1	002740	Cluster2310_1clades	96	Ecwhy1_345	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34817.1	002740	Cluster2310_1clades	83	ACQ29_gp137	Escherichia phage PBECO4	GCA_001041035.1
BBM61993.1	002740	Cluster2310_1clades	96	EO157G_4040	Escherichia phage SP27	GCA_008033345.1
QBO61985.1	002740	Cluster2310_1clades	96	G17_00496	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14008.1	002740	Cluster2310_1clades	96	vBEcoMphAPEC6_gp384c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80306.1	002740	Cluster2310_1clades	96	PSLUR01_00329	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01580.1	002741	Cluster2311_1clades	80	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22651.1	002741	Cluster2311_1clades	95	Ah1_00110	Aeromonas phage Ah1	GCA_002957415.1
QAX98377.1	002741	Cluster2311_1clades	95	ASfcp2_31	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52830.1	002741	Cluster2311_1clades	95	PX29p111	Aeromonas phage PX29	GCA_000920195.1
ADM80090.1	002741	Cluster2311_1clades	91	phiAS5_ORF0247	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53203.1	002741	Cluster2311_1clades	71	65p195	Aeromonas virus 65	GCA_000893255.1
AAQ17777.1	002741	Cluster2311_1clades	95	Aeh1ORF115c	Aeromonas virus Aeh1	GCA_000843245.1
AFA44544.1	002742	Cluster2312_1clades	94	RaK2_00271	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18595.1	002742	Cluster2312_1clades	95	7t3_074	Salmonella phage 7t3	GCA_006083215.1
AZU98423.1	002742	Cluster2312_1clades	95	CPT_Munch_491	Salmonella phage Munch	GCA_004015485.1
QIG63090.1	002742	Cluster2312_1clades	95	SEPL_477	Salmonella phage SE_PL	GCA_011067555.1
AQW89041.1	002742	Cluster2312_1clades	90	BF_0516	Serratia phage BF	GCA_002619745.1
SOK59317.1	002742	Cluster2312_1clades	90	g509	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58779.1	002742	Cluster2312_1clades	90	g502	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67142.1	002743	SIG+Tox-Ribonuclease	94	AD1_098	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79891.1	002743	SIG+Tox-Ribonuclease	91	JA11_086	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66490.1	002743	SIG+Tox-Ribonuclease	91	JA13_087	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66815.1	002743	SIG+Tox-Ribonuclease	91	JA29_089	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67460.1	002743	SIG+Tox-Ribonuclease	91	JA33_086	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08601.1	002743	SIG+Tox-Ribonuclease	94	Alexandra_103	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28815.1	002743	SIG+Tox-Ribonuclease	87	YOLOSWAG_91	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14321.1	002744	Cluster2314_1clades	92	PBI_121Q_431	Escherichia phage 121Q	GCA_000926855.1
QAY00618.1	002744	Cluster2314_1clades	94	Ecwhy1_343	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34816.1	002744	Cluster2314_1clades	92	ACQ29_gp136	Escherichia phage PBECO4	GCA_001041035.1
BBM61994.1	002744	Cluster2314_1clades	92	EO157G_4050	Escherichia phage SP27	GCA_008033345.1
QBO61983.1	002744	Cluster2314_1clades	92	G17_00494	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14007.1	002744	Cluster2314_1clades	92	vBEcoMphAPEC6_gp383c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80308.1	002744	Cluster2314_1clades	92	PSLUR01_00331	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AXG66418.1	002745	Cluster2315_1clades	73	JA13_015	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AWY08305.1	002745	Cluster2315_1clades	87	Alexandra_25	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANH52148.1	002745	Cluster2315_1clades	68	DM_50	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
ANH51512.1	002745	Cluster2315_1clades	68	SIMMY50_50	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64859.1	002745	Cluster2315_1clades	68	SPECIALG_49	Erwinia phage vB_EamM_Special G	GCA_002624385.1
ARW58665.1	002745	Cluster2315_1clades	93	Y3_025	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QKE54419.1	002745	Cluster2315_1clades	79	ACSA002_1050	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AIT14231.1	002746	Cluster2316_1clades	80	PBI_121Q_341	Escherichia phage 121Q	GCA_000926855.1
QAY00704.1	002746	Cluster2316_1clades	93	Ecwhy1_429	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34894.1	002746	Cluster2316_1clades	86	ACQ29_gp214	Escherichia phage PBECO4	GCA_001041035.1
BBM61907.1	002746	Cluster2316_1clades	80	EO157G_3180	Escherichia phage SP27	GCA_008033345.1
QBO62074.1	002746	Cluster2316_1clades	80	G17_00585	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14090.1	002746	Cluster2316_1clades	83	vBEcoMphAPEC6_gp467c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80220.1	002746	Cluster2316_1clades	80	PSLUR01_00243	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUE22683.1	002747	Cluster2317_1clades	92	Ah1_00142	Aeromonas phage Ah1	GCA_002957415.1
QAX98409.1	002747	Cluster2317_1clades	92	ASfcp2_65	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52865.1	002747	Cluster2317_1clades	92	PX29p146	Aeromonas phage PX29	GCA_000920195.1
ADM80125.1	002747	Cluster2317_1clades	92	phiAS5_ORF0282	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17811.1	002747	Cluster2317_1clades	92	rI.1	Aeromonas virus Aeh1	GCA_000843245.1
AIA64994.1	002747	Cluster2317_1clades	90	S13_197	Cronobacter phage S13	GCA_001503575.1
QHJ78937.1	002747	Cluster2317_1clades	89	-	Myoviridae sp.	GCA_012593985.1
APU01707.1	002748	Cluster2318_1clades	92	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28905.1	002748	Cluster2318_1clades	92	AP1_0198	Aeromonas phage AP1	GCA_014183365.1
ATI17590.1	002748	Cluster2318_1clades	92	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00407.1	002748	Cluster2318_1clades	92	HWB28_gp145	Aeromonas phage AS-zj	GCA_002627665.1
QAX98029.1	002748	Cluster2318_1clades	92	ASswx1_389	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39358.1	002748	Cluster2318_1clades	92	CC2_142	Aeromonas phage CC2	GCA_000903495.1
ADQ53346.1	002748	Cluster2318_1clades	92	65p338	Aeromonas virus 65	GCA_000893255.1
AGB06918.1	002749	Cluster2319_1clades	92	CF80_gp131	Vibrio phage VH7D	GCA_000914495.1
QBX06228.1	002749	Cluster2319_1clades	92	ValB1HC_275	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60854.1	002749	Cluster2319_1clades	92	AVU32_gp013	Vibrio phage ValKK3	GCA_001501635.1
AGN30290.1	002749	Cluster2319_1clades	92	VPFG_00291	Vibrio phage nt-1	GCA_000910195.2
ALP47226.1	002749	Cluster2319_1clades	92	phiGrn1_0354	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47615.1	002749	Cluster2319_1clades	92	phiST2_0109	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54853.1	002749	Cluster2319_1clades	92	vBValMR10Z_313	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AIT14439.1	002750	Cluster2320_1clades	89	PBI_121Q_549	Escherichia phage 121Q	GCA_000926855.1
QAY00510.1	002750	Cluster2320_1clades	92	Ecwhy1_231	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34704.1	002750	Cluster2320_1clades	89	ACQ29_gp024	Escherichia phage PBECO4	GCA_001041035.1
BBM62110.1	002750	Cluster2320_1clades	89	EO157G_5210	Escherichia phage SP27	GCA_008033345.1
QBO61863.1	002750	Cluster2320_1clades	89	G17_00374	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13904.1	002750	Cluster2320_1clades	89	vBEcoMphAPEC6_gp279c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80424.1	002750	Cluster2320_1clades	89	PSLUR01_00447	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG65933.1	002751	Cluster2321_1clades	73	phiOC_p291	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ANM44907.1	002751	Cluster2321_1clades	51	KTN4_149	Pseudomonas phage KTN4	GCA_002607225.1
ARV76811.1	002751	Cluster2321_1clades	87	PHABIO_180	Pseudomonas phage Phabio	GCA_002624965.1
ATN94806.1	002751	Cluster2321_1clades	91	SL2_229	Pseudomonas phage SL2	GCA_002956015.1
QJB22785.1	002751	Cluster2321_1clades	91	fnug_142	Pseudomonas phage fnug	GCA_012837215.1
AAL83017.1	002751	Cluster2321_1clades	91	PHIKZ116	Pseudomonas virus phiKZ	GCA_000842965.1
QDJ96270.1	002751	Cluster2321_1clades	82	Xoosp13_83	Xanthomonas phage Xoo-sp13	GCA_013364725.1
APU01705.1	002752	Cluster2322_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28901.1	002752	Cluster2322_1clades	86	AP1_0194	Aeromonas phage AP1	GCA_014183365.1
ATI17594.1	002752	Cluster2322_1clades	86	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00403.1	002752	Cluster2322_1clades	91	HWB28_gp149	Aeromonas phage AS-zj	GCA_002627665.1
QAX98033.1	002752	Cluster2322_1clades	86	ASswx1_393	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39300.1	002752	Cluster2322_1clades	86	CC2_138	Aeromonas phage CC2	GCA_000903495.1
ADQ53344.1	002752	Cluster2322_1clades	86	65p336	Aeromonas virus 65	GCA_000893255.1
AIT14216.1	002753	Cluster2323_1clades	90	PBI_121Q_326	Escherichia phage 121Q	GCA_000926855.1
QAY00722.1	002753	Cluster2323_1clades	90	Ecwhy1_447	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34905.1	002753	Cluster2323_1clades	90	ACQ29_gp225	Escherichia phage PBECO4	GCA_001041035.1
BBM61889.1	002753	Cluster2323_1clades	90	EO157G_3000	Escherichia phage SP27	GCA_008033345.1
AXC37010.1	002753	Cluster2323_1clades	90	-	Escherichia phage UB	GCA_003341455.1
QBO62093.1	002753	Cluster2323_1clades	83	G17_00604	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80201.1	002753	Cluster2323_1clades	83	PSLUR01_00224	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUG86108.1	002754	Cluster2324_1clades	90	BOSOLAPHORUS_84	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
ANH52184.1	002754	Cluster2324_1clades	90	DM_86	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86428.1	002754	Cluster2324_1clades	90	DESERTFOX_83	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG86513.1	002754	Cluster2324_1clades	90	MADMEL_85	Erwinia phage vB_EamM_MadMel	GCA_002957755.1
ANH51864.1	002754	Cluster2324_1clades	90	RAY_83	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ANH51548.1	002754	Cluster2324_1clades	90	SIMMY50_86	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ64896.1	002754	Cluster2324_1clades	90	SPECIALG_86	Erwinia phage vB_EamM_Special G	GCA_002624385.1
APU01775.1	002755	Cluster2325_1clades	89	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29067.1	002755	Cluster2325_1clades	61	AP1_0360	Aeromonas phage AP1	GCA_014183365.1
ATI17524.1	002755	Cluster2325_1clades	61	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00472.1	002755	Cluster2325_1clades	61	HWB28_gp080	Aeromonas phage AS-zj	GCA_002627665.1
QAX97966.1	002755	Cluster2325_1clades	61	ASswx1_324	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39259.1	002755	Cluster2325_1clades	61	CC2_209	Aeromonas phage CC2	GCA_000903495.1
ADQ53418.1	002755	Cluster2325_1clades	89	65p411	Aeromonas virus 65	GCA_000893255.1
AIT14076.1	002756	SIG+TM	80	PBI_121Q_186	Escherichia phage 121Q	GCA_000926855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY00847.1	002756	SIG+TM	80	Ecwhy1_575	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61759.1	002756	SIG+TM	80	EO157G_1700	Escherichia phage SP27	GCA_008033345.1
QBO61623.1	002756	SIG+TM	80	G17_00127	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13680.1	002756	SIG+TM	80	vBEcoMphAPEC6_gp050c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80070.1	002756	SIG+TM	80	PSLUR01_00093	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44536.1	002756	SIG+TM	89	RaK2_00263	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
APU01657.1	002757	TM	68	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17230.1	002757	TM	88	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00357.1	002757	TM	88	HWB28_gp195	Aeromonas phage AS-zj	GCA_002627665.1
QAX97673.1	002757	TM	88	ASswx1_27	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01104.1	002757	TM	86	ASwh1_36	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39213.1	002757	TM	82	CC2_088	Aeromonas phage CC2	GCA_000903495.1
ADQ53288.1	002757	TM	75	65p280	Aeromonas virus 65	GCA_000893255.1
AIT14236.1	002758	Cluster2328_1clades	75	PBI_121Q_346	Escherichia phage 121Q	GCA_000926855.1
QAY00697.1	002758	Cluster2328_1clades	87	Ecwhy1_422	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34890.1	002758	Cluster2328_1clades	49	ACQ29_gp210	Escherichia phage PBECO4	GCA_001041035.1
BBM61913.1	002758	Cluster2328_1clades	88	EO157G_3240	Escherichia phage SP27	GCA_008033345.1
QBO62069.1	002758	Cluster2328_1clades	88	G17_00580	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14085.1	002758	Cluster2328_1clades	88	vBEcoMphAPEC6_gp462c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80224.1	002758	Cluster2328_1clades	87	PSLUR01_00247	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28970.1	002759	Cluster2329_1clades	83	AP1_0263	Aeromonas phage AP1	GCA_014183365.1
ATI17324.1	002759	Cluster2329_1clades	83	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00270.1	002759	Cluster2329_1clades	83	HWB28_gp282	Aeromonas phage AS-zj	GCA_002627665.1
QAX97767.1	002759	Cluster2329_1clades	83	ASswx1_122	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01389.1	002759	Cluster2329_1clades	76	ASwh1_330	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39460.1	002759	Cluster2329_1clades	83	CC2_415	Aeromonas phage CC2	GCA_000903495.1
ADQ53211.1	002759	Cluster2329_1clades	87	65p203	Aeromonas virus 65	GCA_000893255.1
APU01593.1	002760	Cluster2330_1clades	86	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29041.1	002760	Cluster2330_1clades	70	AP1_0334	Aeromonas phage AP1	GCA_014183365.1
ATI17319.1	002760	Cluster2330_1clades	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00275.1	002760	Cluster2330_1clades	80	HWB28_gp277	Aeromonas phage AS-zj	GCA_002627665.1
QAX97762.1	002760	Cluster2330_1clades	76	ASswx1_117	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39462.1	002760	Cluster2330_1clades	76	CC2_420	Aeromonas phage CC2	GCA_000903495.1
ADQ53217.1	002760	Cluster2330_1clades	86	65p209	Aeromonas virus 65	GCA_000893255.1
AIT14335.1	002761	Cluster2331_1clades	86	PBI_121Q_445	Escherichia phage 121Q	GCA_000926855.1
QAY00608.1	002761	Cluster2331_1clades	86	Ecwhy1_332	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34803.1	002761	Cluster2331_1clades	86	ACQ29_gp123	Escherichia phage PBECO4	GCA_001041035.1
BBM62006.1	002761	Cluster2331_1clades	86	EO157G_4170	Escherichia phage SP27	GCA_008033345.1
AXC36916.1	002761	Cluster2331_1clades	86	-	Escherichia phage UB	GCA_003341455.1
QBO61969.1	002761	Cluster2331_1clades	86	G17_00480	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80322.1	002761	Cluster2331_1clades	86	PSLUR01_00345	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGB06820.1	002762	Cluster2332_1clades	85	CF80_gp033	Vibrio phage VH7D	GCA_000914495.1
QBX06327.1	002762	Cluster2332_1clades	85	ValB1HC_374	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04450.1	002762	Cluster2332_1clades	84	ValB1MD_030	Vibrio phage ValB1MD	GCA_004138815.1
AJT60957.1	002762	Cluster2332_1clades	85	AVU32_gp116	Vibrio phage ValKK3	GCA_001501635.1
ALP47249.1	002762	Cluster2332_1clades	85	phiGrn1_0256	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47633.1	002762	Cluster2332_1clades	85	phiST2_0013	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54570.1	002762	Cluster2332_1clades	85	vBValMR10Z_29	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AUE22572.1	002763	Cluster2333_1clades	76	Ah1_00031	Aeromonas phage Ah1	GCA_002957415.1
QAX98608.1	002763	Cluster2333_1clades	81	ASfcp2_275	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52745.1	002763	Cluster2333_1clades	81	PX29p026	Aeromonas phage PX29	GCA_000920195.1
ADM80001.1	002763	Cluster2333_1clades	83	phiAS5_ORF0158	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17687.1	002763	Cluster2333_1clades	76	Aeh1hmmORF01c	Aeromonas virus Aeh1	GCA_000843245.1
AIA65038.1	002763	Cluster2333_1clades	70	S13_241	Cronobacter phage S13	GCA_001503575.1
QHJ78894.1	002763	Cluster2333_1clades	73	-	Myoviridae sp.	GCA_012593985.1
APU01527.1	002764	Cluster2334_1clades	83	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28769.1	002764	Cluster2334_1clades	83	AP1_0051	Aeromonas phage AP1	GCA_014183365.1
ATI17373.1	002764	Cluster2334_1clades	83	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00221.1	002764	Cluster2334_1clades	83	HWB28_gp331	Aeromonas phage AS-zj	GCA_002627665.1
QAX97814.1	002764	Cluster2334_1clades	83	ASswx1_170	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39433.1	002764	Cluster2334_1clades	83	CC2_366	Aeromonas phage CC2	GCA_000903495.1
ADQ53149.1	002764	Cluster2334_1clades	83	65p141	Aeromonas virus 65	GCA_000893255.1
APU01666.1	002765	Cluster2335_1clades	79	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29024.1	002765	Cluster2335_1clades	76	AP1_0317	Aeromonas phage AP1	GCA_014183365.1
ATI17627.1	002765	Cluster2335_1clades	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00368.1	002765	Cluster2335_1clades	76	HWB28_gp184	Aeromonas phage AS-zj	GCA_002627665.1
QAX97662.1	002765	Cluster2335_1clades	76	ASswx1_16	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39217.1	002765	Cluster2335_1clades	76	CC2_099	Aeromonas phage CC2	GCA_000903495.1
ADQ53298.1	002765	Cluster2335_1clades	83	65p290	Aeromonas virus 65	GCA_000893255.1
QCW19038.1	002766	Cluster2336_1clades	67	7t3_0518	Salmonella phage 7t3	GCA_006083215.1
AZU98285.1	002766	Cluster2336_1clades	67	CPT_Munch_341	Salmonella phage Munch	GCA_004015485.1
QIG62699.1	002766	Cluster2336_1clades	67	SEPL_086	Salmonella phage SE_PL	GCA_011067555.1
AQW88838.1	002766	Cluster2336_1clades	65	BF_0313	Serratia phage BF	GCA_002619745.1
QAU04486.1	002766	Cluster2336_1clades	83	ValB1MD_115	Vibrio phage ValB1MD	GCA_004138815.1
SOK59122.1	002766	Cluster2336_1clades	65	g314	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58588.1	002766	Cluster2336_1clades	65	g311	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGB06880.1	002767	SIG+TM	81	CF80_gp093	Vibrio phage VH7D	GCA_000914495.1
QBX06266.1	002767	SIG+TM	80	ValB1HC_313	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60892.1	002767	SIG+TM	81	AVU32_gp051	Vibrio phage ValKK3	GCA_001501635.1
AGN30256.1	002767	SIG+TM	80	VPFG_00257	Vibrio phage nt-1	GCA_000910195.2
ALP47261.1	002767	SIG+TM	81	phiGrn1_0318	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47642.1	002767	SIG+TM	81	phiST2_0074	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54893.1	002767	SIG+TM	81	vBValMR10Z_353	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
APU01632.1	002768	Cluster2338_1clades	80	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22825.1	002768	Cluster2338_1clades	71	Ah1_00307	Aeromonas phage Ah1	GCA_002957415.1
QAX98540.1	002768	Cluster2338_1clades	71	ASfcp2_204	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53003.1	002768	Cluster2338_1clades	71	PX29p284	Aeromonas phage PX29	GCA_000920195.1
ADM79926.1	002768	Cluster2338_1clades	73	phiAS5_ORF0083	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53258.1	002768	Cluster2338_1clades	80	65p250	Aeromonas virus 65	GCA_000893255.1
AAQ17955.1	002768	Cluster2338_1clades	71	Aeh1ORF286c	Aeromonas virus Aeh1	GCA_000843245.1
ARB13721.1	002769	Cluster2339_1clades	79	Ccr10_gp191c	Caulobacter phage Ccr10	GCA_002619445.1
ARB14066.1	002769	Cluster2339_1clades	79	Ccr2_gp190c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14755.1	002769	Cluster2339_1clades	79	Ccr29_gp199	Caulobacter phage Ccr29	GCA_002619485.1
ARB14409.1	002769	Cluster2339_1clades	79	Ccr5_gp189c	Caulobacter phage Ccr5	GCA_002619545.1
AFU87714.1	002769	Cluster2339_1clades	79	CcrKarma_gp197	Caulobacter virus Karma	GCA_000901575.1
AFU87363.1	002769	Cluster2339_1clades	79	CcrMagneto_gp193	Caulobacter virus Magneto	GCA_000903095.1
AFU88510.1	002769	Cluster2339_1clades	79	CcrSwift_gp192	Caulobacter virus Swift	GCA_000899655.1
AIT14110.1	002770	Cluster2340_1clades	79	PBI_121Q_220	Escherichia phage 121Q	GCA_000926855.1
QAY00812.1	002770	Cluster2340_1clades	79	Ecwhy1_539	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34987.1	002770	Cluster2340_1clades	78	ACQ29_gp307	Escherichia phage PBECO4	GCA_001041035.1
AXC36566.1	002770	Cluster2340_1clades	79	-	Escherichia phage UB	GCA_003341455.1
QBO61589.1	002770	Cluster2340_1clades	78	G17_00093	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13651.1	002770	Cluster2340_1clades	79	vBEcoMphAPEC6_gp020c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80103.1	002770	Cluster2340_1clades	79	PSLUR01_00126	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01654.1	002771	Cluster2341_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28891.1	002771	Cluster2341_1clades	78	AP1_0184	Aeromonas phage AP1	GCA_014183365.1
ATI17231.1	002771	Cluster2341_1clades	78	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00356.1	002771	Cluster2341_1clades	78	HWB28_gp196	Aeromonas phage AS-zj	GCA_002627665.1
QAX97674.1	002771	Cluster2341_1clades	78	ASswx1_28	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39339.1	002771	Cluster2341_1clades	78	CC2_087	Aeromonas phage CC2	GCA_000903495.1
ADQ53284.1	002771	Cluster2341_1clades	78	65p276	Aeromonas virus 65	GCA_000893255.1
APU01763.1	002772	Cluster2342_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28984.1	002772	Cluster2342_1clades	71	AP1_0277	Aeromonas phage AP1	GCA_014183365.1
ATI17535.1	002772	Cluster2342_1clades	71	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00461.1	002772	Cluster2342_1clades	71	HWB28_gp091	Aeromonas phage AS-zj	GCA_002627665.1
QAX97976.1	002772	Cluster2342_1clades	71	ASswx1_335	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39255.1	002772	Cluster2342_1clades	71	CC2_198	Aeromonas phage CC2	GCA_000903495.1
ADQ53406.1	002772	Cluster2342_1clades	78	65p399	Aeromonas virus 65	GCA_000893255.1
AIT14162.1	002773	Cluster2343_1clades	78	PBI_121Q_272	Escherichia phage 121Q	GCA_000926855.1
QAY00770.1	002773	Cluster2343_1clades	78	Ecwhy1_496	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61840.1	002773	Cluster2343_1clades	78	EO157G_2510	Escherichia phage SP27	GCA_008033345.1
QBO61540.1	002773	Cluster2343_1clades	78	G17_00044	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62146.1	002773	Cluster2343_1clades	78	G17_00657	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14154.1	002773	Cluster2343_1clades	78	vBEcoMphAPEC6_gp531c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80152.1	002773	Cluster2343_1clades	78	PSLUR01_00175	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
APU01762.1	002774	Cluster2344_1clades	73	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28985.1	002774	Cluster2344_1clades	76	AP1_0278	Aeromonas phage AP1	GCA_014183365.1
ATI17536.1	002774	Cluster2344_1clades	76	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00460.1	002774	Cluster2344_1clades	76	HWB28_gp092	Aeromonas phage AS-zj	GCA_002627665.1
QAX97977.1	002774	Cluster2344_1clades	76	ASswx1_336	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39376.1	002774	Cluster2344_1clades	76	CC2_197	Aeromonas phage CC2	GCA_000903495.1
ADQ53405.1	002774	Cluster2344_1clades	73	65p398	Aeromonas virus 65	GCA_000893255.1
AXG67342.1	002775	Cluster2345_1clades	75	AD1_298	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80061.1	002775	Cluster2345_1clades	72	JA11_256	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66660.1	002775	Cluster2345_1clades	72	JA13_257	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66983.1	002775	Cluster2345_1clades	72	JA29_257	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67631.1	002775	Cluster2345_1clades	72	JA33_257	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08569.1	002775	Cluster2345_1clades	76	Alexandra_317	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58945.1	002775	Cluster2345_1clades	72	Y3_305	Erwinia phage vB_EamM_Y3	GCA_002955045.1
APU01744.1	002776	SIG+TM	72	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28921.1	002776	SIG+TM	71	AP1_0214	Aeromonas phage AP1	GCA_014183365.1
ATI17554.1	002776	SIG+TM	71	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00443.1	002776	SIG+TM	71	HWB28_gp109	Aeromonas phage AS-zj	GCA_002627665.1
QAX97994.1	002776	SIG+TM	71	ASswx1_354	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01146.1	002776	SIG+TM	76	ASwh1_80	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39247.1	002776	SIG+TM	71	CC2_181	Aeromonas phage CC2	GCA_000903495.1
APU01726.1	002777	Cluster2347_1clades	75	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28741.1	002777	Cluster2347_1clades	73	AP1_0023	Aeromonas phage AP1	GCA_014183365.1
ATI17570.1	002777	Cluster2347_1clades	73	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00426.1	002777	Cluster2347_1clades	73	HWB28_gp126	Aeromonas phage AS-zj	GCA_002627665.1
QAX98010.1	002777	Cluster2347_1clades	73	ASswx1_370	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39474.1	002777	Cluster2347_1clades	73	CC2_162	Aeromonas phage CC2	GCA_000903495.1
ADQ53367.1	002777	Cluster2347_1clades	75	65p359	Aeromonas virus 65	GCA_000893255.1
APU01511.1	002778	Cluster2348_1clades	72	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28782.1	002778	Cluster2348_1clades	74	AP1_0075	Aeromonas phage AP1	GCA_014183365.1
ATI17385.1	002778	Cluster2348_1clades	74	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00208.1	002778	Cluster2348_1clades	74	HWB28_gp344	Aeromonas phage AS-zj	GCA_002627665.1
QAX97827.1	002778	Cluster2348_1clades	74	ASswx1_183	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39278.1	002778	Cluster2348_1clades	74	CC2_352	Aeromonas phage CC2	GCA_000903495.1
ADQ53134.1	002778	Cluster2348_1clades	72	65p126	Aeromonas virus 65	GCA_000893255.1
ARB13609.1	002779	Cluster2349_1clades	74	Ccr10_gp081	Caulobacter phage Ccr10	GCA_002619445.1
ARB13955.1	002779	Cluster2349_1clades	74	Ccr2_gp080	Caulobacter phage Ccr2	GCA_002619465.1
ARB14298.1	002779	Cluster2349_1clades	74	Ccr5_gp080	Caulobacter phage Ccr5	GCA_002619545.1
AFU87599.1	002779	Cluster2349_1clades	74	CcrKarma_gp082	Caulobacter virus Karma	GCA_000901575.1
AFU87249.1	002779	Cluster2349_1clades	74	CcrMagneto_gp079	Caulobacter virus Magneto	GCA_000903095.1
AFU86564.1	002779	Cluster2349_1clades	73	CcrRogue_gp082	Caulobacter virus Rogue	GCA_000900555.1
AFU86913.1	002779	Cluster2349_1clades	74	CbK_gp081	Caulobacter virus phiCbK	GCA_000900535.1
AFC21971.1	002780	Cluster2350_1clades	61	GAP32_511	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44094.1	002780	Cluster2350_1clades	62	CBB_531	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18713.1	002780	Cluster2350_1clades	64	7t3_0192	Salmonella phage 7t3	GCA_006083215.1
AZU97986.1	002780	Cluster2350_1clades	64	CPT_Munch_042	Salmonella phage Munch	GCA_004015485.1
QIG62993.1	002780	Cluster2350_1clades	64	SEPL_380	Salmonella phage SE_PL	GCA_011067555.1
SOK59328.1	002780	Cluster2350_1clades	74	g520	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58790.1	002780	Cluster2350_1clades	74	g513	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13612.1	002781	Cluster2351_1clades	68	Ccr10_gp347	Caulobacter phage Ccr10	GCA_002619445.1
ARB14301.1	002781	Cluster2351_1clades	68	Ccr5_gp083	Caulobacter phage Ccr5	GCA_002619545.1
AFU87603.1	002781	Cluster2351_1clades	68	CcrKarma_gp086	Caulobacter virus Karma	GCA_000901575.1
AFU87252.1	002781	Cluster2351_1clades	68	CcrMagneto_gp082	Caulobacter virus Magneto	GCA_000903095.1
AFU86567.1	002781	Cluster2351_1clades	73	CcrRogue_gp085	Caulobacter virus Rogue	GCA_000900555.1
AFU88399.1	002781	Cluster2351_1clades	68	CcrSwift_gp081	Caulobacter virus Swift	GCA_000899655.1
AFU86917.1	002781	Cluster2351_1clades	68	CbK_gp085	Caulobacter virus phiCbK	GCA_000900535.1
AIT14226.1	002782	Cluster2352_1clades	73	PBI_121Q_336	Escherichia phage 121Q	GCA_000926855.1
QAY00710.1	002782	Cluster2352_1clades	71	Ecwhy1_435	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34897.1	002782	Cluster2352_1clades	73	ACQ29_gp217	Escherichia phage PBECO4	GCA_001041035.1
BBM61902.1	002782	Cluster2352_1clades	71	EO157G_3130	Escherichia phage SP27	GCA_008033345.1
AXC37003.1	002782	Cluster2352_1clades	71	-	Escherichia phage UB	GCA_003341455.1
QBO62079.1	002782	Cluster2352_1clades	73	G17_00590	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80215.1	002782	Cluster2352_1clades	73	PSLUR01_00238	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44784.1	002783	Cluster2353_1clades	72	RaK2_00511	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18836.1	002783	Cluster2353_1clades	61	7t3_0315	Salmonella phage 7t3	GCA_006083215.1
AZU98099.1	002783	Cluster2353_1clades	61	CPT_Munch_155	Salmonella phage Munch	GCA_004015485.1
QIG62883.1	002783	Cluster2353_1clades	61	SEPL_270	Salmonella phage SE_PL	GCA_011067555.1
AQW88653.1	002783	Cluster2353_1clades	62	BF_0128	Serratia phage BF	GCA_002619745.1
SOK58933.1	002783	Cluster2353_1clades	62	g125	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58398.1	002783	Cluster2353_1clades	62	g121	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGB06862.1	002784	Cluster2354_1clades	72	CF80_gp075	Vibrio phage VH7D	GCA_000914495.1
QBX06283.1	002784	Cluster2354_1clades	68	ValB1HC_330	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60910.1	002784	Cluster2354_1clades	68	AVU32_gp069	Vibrio phage ValKK3	GCA_001501635.1
AGN30244.1	002784	Cluster2354_1clades	69	VPFG_00245	Vibrio phage nt-1	GCA_000910195.2
ALP47296.1	002784	Cluster2354_1clades	68	phiGrn1_0302	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47678.1	002784	Cluster2354_1clades	68	phiST2_0058	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54910.1	002784	Cluster2354_1clades	68	vBValMR10Z_370	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AGH07555.1	002785	Cluster2355_1clades	70	CYVG_00111	Cyanophage S-SSM6a	GCA_002710385.1
AAX44443.1	002785	Cluster2355_1clades	68	PSSM2_065	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12209.1	002785	Cluster2355_1clades	68	PRTG_00051	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93590.1	002785	Cluster2355_1clades	72	AVU42_gp039	Prochlorococcus phage P-TIM68	GCA_001503075.1
AOV59643.1	002785	Cluster2355_1clades	68	S330809_182	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59405.1	002785	Cluster2355_1clades	68	C440309_182	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59881.1	002785	Cluster2355_1clades	68	N231010_182	Synechococcus phage S-CAM4	GCA_002922155.1
AIT14196.1	002786	HTH	72	PBI_121Q_306	Escherichia phage 121Q	GCA_000926855.1
QAY00743.1	002786	HTH	72	Ecwhy1_468	Escherichia phage Ecwhy_1	GCA_004146585.1
AXC37026.1	002786	HTH	72	-	Escherichia phage UB	GCA_003341455.1
QBO61510.1	002786	HTH	72	G17_00014	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62116.1	002786	HTH	72	G17_00627	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14125.1	002786	HTH	72	vBEcoMphAPEC6_gp502c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80179.1	002786	HTH	72	PSLUR01_00202	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14219.1	002787	Cluster2357_1clades	72	PBI_121Q_329	Escherichia phage 121Q	GCA_000926855.1
QAY00719.1	002787	Cluster2357_1clades	72	Ecwhy1_444	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61892.1	002787	Cluster2357_1clades	72	EO157G_3030	Escherichia phage SP27	GCA_008033345.1
AXC37008.1	002787	Cluster2357_1clades	51	-	Escherichia phage UB	GCA_003341455.1
QBO62090.1	002787	Cluster2357_1clades	72	G17_00601	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14103.1	002787	Cluster2357_1clades	72	vBEcoMphAPEC6_gp480c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80204.1	002787	Cluster2357_1clades	72	PSLUR01_00227	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14074.1	002788	Cluster2358_1clades	71	PBI_121Q_184	Escherichia phage 121Q	GCA_000926855.1
QAY00849.1	002788	Cluster2358_1clades	70	Ecwhy1_577	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35019.1	002788	Cluster2358_1clades	71	ACQ29_gp339	Escherichia phage PBECO4	GCA_001041035.1
BBM61757.1	002788	Cluster2358_1clades	71	EO157G_1680	Escherichia phage SP27	GCA_008033345.1
AXC36596.1	002788	Cluster2358_1clades	51	-	Escherichia phage UB	GCA_003341455.1
QBO61625.1	002788	Cluster2358_1clades	71	G17_00129	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80068.1	002788	Cluster2358_1clades	71	PSLUR01_00091	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14218.1	002789	Cluster2359_1clades	71	PBI_121Q_328	Escherichia phage 121Q	GCA_000926855.1
QAY00720.1	002789	Cluster2359_1clades	71	Ecwhy1_445	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34903.1	002789	Cluster2359_1clades	52	ACQ29_gp223	Escherichia phage PBECO4	GCA_001041035.1
BBM61891.1	002789	Cluster2359_1clades	71	EO157G_3020	Escherichia phage SP27	GCA_008033345.1
QBO62091.1	002789	Cluster2359_1clades	71	G17_00602	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14104.1	002789	Cluster2359_1clades	71	vBEcoMphAPEC6_gp481c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80203.1	002789	Cluster2359_1clades	71	PSLUR01_00226	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ARB13681.1	002790	Cluster2360_1clades	71	Ccr10_gp346	Caulobacter phage Ccr10	GCA_002619445.1
ARB14026.1	002790	Cluster2360_1clades	71	Ccr2_gp342c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14369.1	002790	Cluster2360_1clades	71	Ccr5_gp339	Caulobacter phage Ccr5	GCA_002619545.1
AFU87674.1	002790	Cluster2360_1clades	67	CcrKarma_gp157	Caulobacter virus Karma	GCA_000901575.1
AFU87323.1	002790	Cluster2360_1clades	67	CcrMagneto_gp153	Caulobacter virus Magneto	GCA_000903095.1
AFU88470.1	002790	Cluster2360_1clades	67	CcrSwift_gp152	Caulobacter virus Swift	GCA_000899655.1
AFU86987.1	002790	Cluster2360_1clades	67	CbK_gp155	Caulobacter virus phiCbK	GCA_000900535.1
AMR59840.1	002791	SIG+TM	67	SEGD1_193	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96658.1	002791	SIG+TM	70	G173_gp113	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48222.1	002791	SIG+TM	70	ASESINO_209	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50635.1	002791	SIG+TM	70	STRATTON_210	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN86029.1	002791	SIG+TM	63	ACEC001_1880	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09149.1	002791	SIG+TM	68	MLDJOKPK_00251	Salmonella phage SPAsTU	GCA_003183805.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEP84021.1	002791	SIG+TM	67	SPN3US_0188	Salmonella phage SPN3US	GCA_001042275.1
ANM44780.1	002792	SIG+TM	69	KTN4_022	Pseudomonas phage KTN4	GCA_002607225.1
ANM44788.1	002792	SIG+TM	69	KTN4_030	Pseudomonas phage KTN4	GCA_002607225.1
QBX32289.1	002792	SIG+TM	69	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94926.1	002792	SIG+TM	69	SL2_349	Pseudomonas phage SL2	GCA_002956015.1
QJB22665.1	002792	SIG+TM	69	fnug_22	Pseudomonas phage fnug	GCA_012837215.1
QEM41863.1	002792	SIG+TM	69	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82920.1	002792	SIG+TM	69	PHIKZ019	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14042.1	002793	Cluster2363_1clades	43	PBI_121Q_152	Escherichia phage 121Q	GCA_000926855.1
QAY00301.1	002793	Cluster2363_1clades	67	Ecwhy1_19	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35051.1	002793	Cluster2363_1clades	43	ACQ29_gp371	Escherichia phage PBECO4	GCA_001041035.1
BBM61725.1	002793	Cluster2363_1clades	62	EO157G_1360	Escherichia phage SP27	GCA_008033345.1
QBO61657.1	002793	Cluster2363_1clades	67	G17_00161	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13710.1	002793	Cluster2363_1clades	69	vBEcoMphAPEC6_gp080c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80037.1	002793	Cluster2363_1clades	67	PSLUR01_00060	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21495.1	002794	Cluster2364_1clades	66	GAP32_047A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QCW18726.1	002794	Cluster2364_1clades	68	7t3_0205	Salmonella phage 7t3	GCA_006083215.1
AZU97997.1	002794	Cluster2364_1clades	68	CPT_Munch_053	Salmonella phage Munch	GCA_004015485.1
QIG62982.1	002794	Cluster2364_1clades	68	SEPL_369	Salmonella phage SE_PL	GCA_011067555.1
AQW88567.1	002794	Cluster2364_1clades	68	BF_0042	Serratia phage BF	GCA_002619745.1
SOK58842.1	002794	Cluster2364_1clades	66	g034	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58303.1	002794	Cluster2364_1clades	66	g026	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01523.1	002795	SIG+TM	51	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28773.1	002795	SIG+TM	61	AP1_0055	Aeromonas phage AP1	GCA_014183365.1
ATI17377.1	002795	SIG+TM	61	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00217.1	002795	SIG+TM	61	HWB28_gp335	Aeromonas phage AS-zj	GCA_002627665.1
QAX97818.1	002795	SIG+TM	61	ASswx1_174	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39282.1	002795	SIG+TM	61	CC2_362	Aeromonas phage CC2	GCA_000903495.1
ADQ53145.1	002795	SIG+TM	67	65p137	Aeromonas virus 65	GCA_000893255.1
AIT14317.1	002796	Cluster2366_1clades	66	PBI_121Q_427	Escherichia phage 121Q	GCA_000926855.1
AGC34819.1	002796	Cluster2366_1clades	66	ACQ29_gp139	Escherichia phage PBECO4	GCA_001041035.1
BBM61991.1	002796	Cluster2366_1clades	66	EO157G_4020	Escherichia phage SP27	GCA_008033345.1
AXC36928.1	002796	Cluster2366_1clades	66	-	Escherichia phage UB	GCA_003341455.1
QBO61987.1	002796	Cluster2366_1clades	66	G17_00498	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80304.1	002796	Cluster2366_1clades	66	PSLUR01_00327	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFA44727.1	002796	Cluster2366_1clades	66	RaK2_00454	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AIT14210.1	002797	Cluster2367_1clades	64	PBI_121Q_320	Escherichia phage 121Q	GCA_000926855.1
QAY00728.1	002797	Cluster2367_1clades	66	Ecwhy1_453	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34909.1	002797	Cluster2367_1clades	66	ACQ29_gp229	Escherichia phage PBECO4	GCA_001041035.1
BBM61883.1	002797	Cluster2367_1clades	66	EO157G_2940	Escherichia phage SP27	GCA_008033345.1
QBO62101.1	002797	Cluster2367_1clades	66	G17_00612	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14111.1	002797	Cluster2367_1clades	66	vBEcoMphAPEC6_gp488c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80193.1	002797	Cluster2367_1clades	66	PSLUR01_00216	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14204.1	002798	Cluster2368_1clades	66	PBI_121Q_314	Escherichia phage 121Q	GCA_000926855.1
QAY00733.1	002798	Cluster2368_1clades	66	Ecwhy1_458	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61878.1	002798	Cluster2368_1clades	66	EO157G_2890	Escherichia phage SP27	GCA_008033345.1
QBO61500.1	002798	Cluster2368_1clades	66	G17_00004	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62106.1	002798	Cluster2368_1clades	66	G17_00617	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14116.1	002798	Cluster2368_1clades	66	vBEcoMphAPEC6_gp493c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80188.1	002798	Cluster2368_1clades	66	PSLUR01_00211	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMR59718.1	002799	Cluster2369_1clades	62	SEGD1_069	Enterobacteria phage SEGD1	GCA_002601865.1
AFQ96800.1	002799	Cluster2369_1clades	56	G173_gp255	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48099.1	002799	Cluster2369_1clades	57	ASESINO_86	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50513.1	002799	Cluster2369_1clades	56	STRATTON_88	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QKN85909.1	002799	Cluster2369_1clades	62	ACEC001_0710	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09032.1	002799	Cluster2369_1clades	62	MLDJOKPK_00094	Salmonella phage SPAsTU	GCA_003183805.1
AEP83901.1	002799	Cluster2369_1clades	62	SPN3US_0068	Salmonella phage SPN3US	GCA_001042275.1
APU01721.1	002800	Cluster2370_1clades	56	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28745.1	002800	Cluster2370_1clades	61	AP1_0027	Aeromonas phage AP1	GCA_014183365.1
ATI17574.1	002800	Cluster2370_1clades	61	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00422.1	002800	Cluster2370_1clades	61	HWB28_gp130	Aeromonas phage AS-zj	GCA_002627665.1
QAX98014.1	002800	Cluster2370_1clades	61	ASswx1_374	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39240.1	002800	Cluster2370_1clades	61	CC2_158	Aeromonas phage CC2	GCA_000903495.1
ADQ53361.1	002800	Cluster2370_1clades	58	65p353	Aeromonas virus 65	GCA_000893255.1
AIT14425.1	002801	Cluster2371_1clades	61	PBI_121Q_535	Escherichia phage 121Q	GCA_000926855.1
QAY00523.1	002801	Cluster2371_1clades	61	Ecwhy1_244	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34717.1	002801	Cluster2371_1clades	41	ACQ29_gp037	Escherichia phage PBECO4	GCA_001041035.1
BBM62097.1	002801	Cluster2371_1clades	61	EO157G_5080	Escherichia phage SP27	GCA_008033345.1
AXC36835.1	002801	Cluster2371_1clades	41	-	Escherichia phage UB	GCA_003341455.1
QBO61876.1	002801	Cluster2371_1clades	61	G17_00387	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80411.1	002801	Cluster2371_1clades	61	PSLUR01_00434	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01704.1	002802	Cluster2372_1clades	59	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28900.1	002802	Cluster2372_1clades	60	AP1_0193	Aeromonas phage AP1	GCA_014183365.1
ATI17595.1	002802	Cluster2372_1clades	60	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00402.1	002802	Cluster2372_1clades	60	HWB28_gp150	Aeromonas phage AS-zj	GCA_002627665.1
QAX98034.1	002802	Cluster2372_1clades	60	ASswx1_394	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39153.1	002802	Cluster2372_1clades	60	CC2_137	Aeromonas phage CC2	GCA_000903495.1
ADQ53343.1	002802	Cluster2372_1clades	59	65p335	Aeromonas virus 65	GCA_000893255.1
APU01448.1	002803	Cluster2373_1clades	58	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28933.1	002803	Cluster2373_1clades	58	AP1_0226	Aeromonas phage AP1	GCA_014183365.1
ATI17451.1	002803	Cluster2373_1clades	58	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00145.1	002803	Cluster2373_1clades	58	HWB28_gp005	Aeromonas phage AS-zj	GCA_002627665.1
QAX97891.1	002803	Cluster2373_1clades	58	ASswx1_248	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39409.1	002803	Cluster2373_1clades	58	CC2_285	Aeromonas phage CC2	GCA_000903495.1
ADQ53068.1	002803	Cluster2373_1clades	58	65p058	Aeromonas virus 65	GCA_000893255.1
AGB06853.1	002804	Cluster2374_1clades	57	CF80_gp066	Vibrio phage VH7D	GCA_000914495.1
QBX06292.1	002804	Cluster2374_1clades	57	ValB1HC_339	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60922.1	002804	Cluster2374_1clades	57	AVU32_gp081	Vibrio phage ValKK3	GCA_001501635.1
ALP47317.1	002804	Cluster2374_1clades	57	phiGrn1_0292	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47697.1	002804	Cluster2374_1clades	57	phiST2_0049	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54919.1	002804	Cluster2374_1clades	57	vBValMR10Z_379	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37406.1	002804	Cluster2374_1clades	57	pp2_173	Vibriophage phi-pp2	GCA_002630725.1
AIT14170.1	002805	Cluster2375_1clades	47	PBI_121Q_280	Escherichia phage 121Q	GCA_000926855.1
BBM61845.1	002805	Cluster2375_1clades	47	EO157G_2560	Escherichia phage SP27	GCA_008033345.1
AXC37047.1	002805	Cluster2375_1clades	47	-	Escherichia phage UB	GCA_003341455.1
QBO61535.1	002805	Cluster2375_1clades	47	G17_00039	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62141.1	002805	Cluster2375_1clades	47	G17_00652	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14149.1	002805	Cluster2375_1clades	57	vBEcoMphAPEC6_gp526c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80156.1	002805	Cluster2375_1clades	47	PSLUR01_00179	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QDB70399.1	002806	Cluster2376_1clades	54	CF8_0230	Aeromonas phage CF8	GCA_006384595.2
QDJ97396.1	002806	Cluster2376_1clades	55	D6_0237	Aeromonas phage D6	GCA_007051205.2
QDJ96744.1	002806	Cluster2376_1clades	54	PS1_0233	Aeromonas phage PS1	GCA_007051165.2
QFR59377.1	002806	Cluster2376_1clades	54	PS2_0235	Aeromonas phage PS2	GCA_009388305.2
QBZ70782.1	002806	Cluster2376_1clades	54	pETSU_201	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72088.1	002806	Cluster2376_1clades	55	N1M2_225	Klebsiella phage N1M2	GCA_010092605.1
AEV89717.1	002806	Cluster2376_1clades	54	OBP_280	Pseudomonas phage OBP	GCA_000896635.1
QMV28914.1	002807	Cluster2377_1clades	37	AP1_0207	Aeromonas phage AP1	GCA_014183365.1
ATI17547.1	002807	Cluster2377_1clades	51	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00450.1	002807	Cluster2377_1clades	51	HWB28_gp102	Aeromonas phage AS-zj	GCA_002627665.1
QAX97988.1	002807	Cluster2377_1clades	51	ASswx1_347	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01153.1	002807	Cluster2377_1clades	49	ASwh1_87	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39252.1	002807	Cluster2377_1clades	51	CC2_188	Aeromonas phage CC2	GCA_000903495.1
ADQ53392.1	002807	Cluster2377_1clades	36	65p385	Aeromonas virus 65	GCA_000893255.1
AGB06846.1	002808	TM	40	CF80_gp059	Vibrio phage VH7D	GCA_000914495.1
QBX06299.1	002808	TM	40	ValB1HC_346	Vibrio phage ValB1 HC	GCA_004771355.1
AIE13771.1	002808	TM	48	-	Vibrio phage nt-1	GCA_000910195.2
ALP47335.1	002808	TM	40	phiGrn1_0285	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47718.1	002808	TM	40	phiST2_0043	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54926.1	002808	TM	40	vBValMR10Z_386	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37402.1	002808	TM	40	pp2_169	Vibriophage phi-pp2	GCA_002630725.1
APU01482.1	002809	Cluster2379_1clades	45	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28722.1	002809	Cluster2379_1clades	47	AP1_004	Aeromonas phage AP1	GCA_014183365.1
ATI17415.1	002809	Cluster2379_1clades	47	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00181.1	002809	Cluster2379_1clades	47	HWB28_gp371	Aeromonas phage AS-zj	GCA_002627665.1
QAX97855.1	002809	Cluster2379_1clades	47	ASswx1_212	Aeromonas phage Asswx_1	GCA_004146865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY01295.1	002809	Cluster2379_1clades	47	ASwh1_232	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39145.1	002809	Cluster2379_1clades	47	CC2_322	Aeromonas phage CC2	GCA_000903495.1
AHI60397.1	002810	Cluster2380_1clades	43	Ea357_244	Erwinia phage Ea35-70	GCA_000914635.1
ASB43081.1	002810	Cluster2380_1clades	43	DM_253	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86355.1	002810	Cluster2380_1clades	43	DESERTFOX_248	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG87001.1	002810	Cluster2380_1clades	43	MORTIMER_253	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
ANH52027.1	002810	Cluster2380_1clades	43	RAY_247	Erwinia phage vB_EamM_RAY	GCA_002624345.1
ASB43077.1	002810	Cluster2380_1clades	43	SIMMY50_252	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANJ65062.1	002810	Cluster2380_1clades	43	SPECIALG_251	Erwinia phage vB_EamM_Special G	GCA_002624385.1
APU01796.1	002811	Cluster2381_1clades	37	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28999.1	002811	Cluster2381_1clades	37	AP1_0292	Aeromonas phage AP1	GCA_014183365.1
ASU00488.1	002811	Cluster2381_1clades	37	HWB28_gp064	Aeromonas phage AS-zj	GCA_002627665.1
QAX97948.1	002811	Cluster2381_1clades	37	ASswx1_306	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01200.1	002811	Cluster2381_1clades	37	ASwh1_135	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39388.1	002811	Cluster2381_1clades	37	CC2_226	Aeromonas phage CC2	GCA_000903495.1
ADQ53440.1	002811	Cluster2381_1clades	37	65p434	Aeromonas virus 65	GCA_000893255.1
QGZ14551.1	002812	BactIG+BactIG	2550	HWC77_gp188	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04183.1	002812	BactIG+BactIG	2549	HWC03_gp028	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23176.1	002812	BactIG+BactIG	2550	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80909.1	002812	BactIG+BactIG	2548	Aphrodite1_0166	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47553.1	002812	BactIG+BactIG	2550	HWC35_gp159	Vibrio phage USC-1	GCA_006864065.1
BAW98368.1	002812	BactIG+BactIG	1630	FDH33_gp159	Vibrio phage pTD1	GCA_002618825.1
AUE22859.1	002813	Cluster2383_1clades	582	Ah1_00341	Aeromonas phage Ah1	GCA_002957415.1
AUE22858.1	002813	Cluster2383_1clades	792	Ah1_00340	Aeromonas phage Ah1	GCA_002957415.1
QAX98569.1	002813	Cluster2383_1clades	1282	ASfcp2_235	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53033.1	002813	Cluster2383_1clades	1242	PX29p316	Aeromonas phage PX29	GCA_000920195.1
ADM79958.1	002813	Cluster2383_1clades	1331	phiAS5_ORF0115	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17987.1	002813	Cluster2383_1clades	1303	Aeh1ORF318w	Aeromonas virus Aeh1	GCA_000843245.1
QGZ14451.1	002814	Cluster2384_1clades	1086	HWC77_gp088	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04283.1	002814	Cluster2384_1clades	1086	HWC03_gp128	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23294.1	002814	Cluster2384_1clades	1089	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80914.1	002814	Cluster2384_1clades	1089	Aphrodite1_0051	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47434.1	002814	Cluster2384_1clades	1089	HWC35_gp040	Vibrio phage USC-1	GCA_006864065.1
BAW98255.1	002814	Cluster2384_1clades	1081	FDH33_gp046	Vibrio phage pTD1	GCA_002618825.1
QGZ14453.1	002815	Cluster2386_1clades	851	HWC77_gp090	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04281.1	002815	Cluster2386_1clades	851	HWC03_gp126	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23296.1	002815	Cluster2386_1clades	836	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80919.1	002815	Cluster2386_1clades	836	Aphrodite1_0049	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47432.1	002815	Cluster2386_1clades	836	HWC35_gp038	Vibrio phage USC-1	GCA_006864065.1
BAW98253.1	002815	Cluster2386_1clades	836	FDH33_gp044	Vibrio phage pTD1	GCA_002618825.1
ABY63278.1	002816	Cluster2387_1clades	768	201phi2-1p455	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45123.1	002816	Cluster2387_1clades	627	KTN4_365	Pseudomonas phage KTN4	GCA_002607225.1
ARV77500.1	002816	Cluster2387_1clades	335	NOXIFER_335	Pseudomonas phage Noxifer	GCA_002625005.1
ATN94588.1	002816	Cluster2387_1clades	630	SL2_011	Pseudomonas phage SL2	GCA_002956015.1
QJB23000.1	002816	Cluster2387_1clades	646	fnug_357	Pseudomonas phage fnug	GCA_012837215.1
AAL83204.1	002816	Cluster2387_1clades	646	PHIKZ303	Pseudomonas virus phiKZ	GCA_000842965.1
QGT54963.1	002817	HtrL_YibB	268	b23_0357	Synechococcus phage B23	GCA_009745195.1
QGT54598.1	002817	HtrL_YibB	268	b3_0363	Synechococcus phage B3	GCA_009745215.1
ASR76257.1	002817	HtrL_YibB	268	PBI_BELLAMY_221	Synechococcus phage Bellamy	GCA_002627525.1
QJT70208.1	002817	HtrL_YibB	268	SynMITS9220M01_202	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBA65478.1	002817	HtrL_YibB	546	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96486.1	002817	HtrL_YibB	546	Xoosp13_300	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGH56996.1	002818	Cluster2392_1clades	444	CPXG_00193	Cyanophage P-RSM6	GCA_000906155.1
AJK27464.1	002818	Cluster2392_1clades	446	PTIM40_37	Cyanophage P-TIM40	GCA_001470935.1
AOO14220.1	002818	Cluster2392_1clades	439	Sn110110_026	Cyanophage S-RIM14	GCA_002599065.1
AOO14872.1	002818	Cluster2392_1clades	439	W1230910_026	Cyanophage S-RIM14	GCA_002599125.1
AGG54345.1	002818	Cluster2392_1clades	438	CYWG_00061	Cyanophage S-SSM6b	GCA_002710425.1
AGH26186.1	002818	Cluster2392_1clades	533	CPMG_00085	Prochlorococcus phage MED4-213	GCA_000904535.1
AXH70830.1	002819	Cluster2393_1clades	518	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96663.1	002819	Cluster2393_1clades	533	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96981.1	002819	Cluster2393_1clades	533	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96027.1	002819	Cluster2393_1clades	533	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96345.1	002819	Cluster2393_1clades	533	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21076.1	002819	Cluster2393_1clades	489	-	Vibrio phage vB_pir03	GCA_014319855.1
ANS05991.1	002820	GDSL	246	ABCD_0225	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64934.1	002820	GDSL	508	S13_135	Cronobacter phage S13	GCA_001503575.1
AON97242.1	002820	GDSL	167	E_234	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ASU03778.1	002820	GDSL	493	JOAD_137	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03534.1	002820	GDSL	493	RISINGSUN_136	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AAX78759.1	002820	GDSL	61	RB43ORF237w	Escherichia virus RB43	GCA_000863505.1
QGZ14419.1	002821	Cluster2397_1clades	475	HWC77_gp056	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04317.1	002821	Cluster2397_1clades	475	HWC03_gp162	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23261.1	002821	Cluster2397_1clades	470	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80949.1	002821	Cluster2397_1clades	479	Aphrodite1_0084	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47467.1	002821	Cluster2397_1clades	470	HWC35_gp073	Vibrio phage USC-1	GCA_006864065.1
BAW98288.1	002821	Cluster2397_1clades	508	FDH33_gp079	Vibrio phage pTD1	GCA_002618825.1
QGZ14518.1	002822	Cluster2398_1clades	497	HWC77_gp155	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04216.1	002822	Cluster2398_1clades	497	HWC03_gp061	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23144.1	002822	Cluster2398_1clades	496	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80945.1	002822	Cluster2398_1clades	496	Aphrodite1_0196	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47583.1	002822	Cluster2398_1clades	496	HWC35_gp189	Vibrio phage USC-1	GCA_006864065.1
BAW98398.1	002822	Cluster2398_1clades	495	FDH33_gp189	Vibrio phage pTD1	GCA_002618825.1
QGZ14414.1	002823	Cluster2399_1clades	472	HWC77_gp051	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04322.1	002823	Cluster2399_1clades	472	HWC03_gp167	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23256.1	002823	Cluster2399_1clades	470	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80953.1	002823	Cluster2399_1clades	470	Aphrodite1_0089	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47472.1	002823	Cluster2399_1clades	470	HWC35_gp078	Vibrio phage USC-1	GCA_006864065.1
BAW98293.1	002823	Cluster2399_1clades	472	FDH33_gp084	Vibrio phage pTD1	GCA_002618825.1
AGB07114.1	002824	Cluster2400_1clades	458	CF80_gp327	Vibrio phage VH7D	GCA_000914495.1
QBX05980.1	002824	Cluster2400_1clades	458	ValB1HC_026	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60993.1	002824	Cluster2400_1clades	458	AVU32_gp152	Vibrio phage ValKK3	GCA_001501635.1
AGN30158.1	002824	Cluster2400_1clades	451	VPFG_00156	Vibrio phage nt-1	GCA_000910195.2
ALP46986.1	002824	Cluster2400_1clades	458	phiGrn1_0220	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54605.1	002824	Cluster2400_1clades	458	vBValMR10Z_64	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QGZ14484.1	002825	Cluster2401_1clades	452	HWC77_gp121	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04250.1	002825	Cluster2401_1clades	452	HWC03_gp095	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23113.1	002825	Cluster2401_1clades	451	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80955.1	002825	Cluster2401_1clades	451	Aphrodite1_0018	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47403.1	002825	Cluster2401_1clades	451	HWC35_gp009	Vibrio phage USC-1	GCA_006864065.1
BAW98220.1	002825	Cluster2401_1clades	452	FDH33_gp011	Vibrio phage pTD1	GCA_002618825.1
AFC21581.1	002826	S4	420	GAP32_131	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AXH72861.1	002826	S4	399	-	Myoviridae sp.	GCA_003657725.1
AMM43697.1	002826	S4	421	CBB_132	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88650.1	002826	S4	420	BF_0125	Serratia phage BF	GCA_002619745.1
SOK58930.1	002826	S4	421	g122	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58395.1	002826	S4	421	g118	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14461.1	002827	SIG+TMEM71	412	HWC77_gp098	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04273.1	002827	SIG+TMEM71	412	HWC03_gp118	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23304.1	002827	SIG+TMEM71	414	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80965.1	002827	SIG+TMEM71	414	Aphrodite1_0041	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47424.1	002827	SIG+TMEM71	414	HWC35_gp030	Vibrio phage USC-1	GCA_006864065.1
BAW98245.1	002827	SIG+TMEM71	418	FDH33_gp036	Vibrio phage pTD1	GCA_002618825.1
AMO43176.1	002828	Cluster2404_1clades	414	R1080702_167	Cyanophage S-RIM32	GCA_001754165.1
AOO11645.1	002828	Cluster2404_1clades	410	ES420910_164	Cyanophage S-RIM44	GCA_002599165.1
AOO12111.1	002828	Cluster2404_1clades	410	Np200711_165	Cyanophage S-RIM44	GCA_002599205.1
AOO12346.1	002828	Cluster2404_1clades	410	Np420711_164	Cyanophage S-RIM44	GCA_002599225.1
AOO12811.1	002828	Cluster2404_1clades	410	Sn130910_164	Cyanophage S-RIM44	GCA_002599265.1
QJT70166.1	002828	Cluster2404_1clades	386	SynMITS9220M01_154	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXH71042.1	002829	Cluster2405_1clades	413	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96792.1	002829	Cluster2405_1clades	412	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97111.1	002829	Cluster2405_1clades	412	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96157.1	002829	Cluster2405_1clades	412	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96475.1	002829	Cluster2405_1clades	412	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20952.1	002829	Cluster2405_1clades	403	-	Vibrio phage vB_pir03	GCA_014319855.1
QGZ14474.1	002830	Cluster2406_1clades	394	HWC77_gp111	Photobacterium phage PDCC-1	GCA_009800445.1

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QAU04260.1	002830	Cluster2406_1clades	394	HWC03_gp105	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23103.1	002830	Cluster2406_1clades	395	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80970.1	002830	Cluster2406_1clades	394	Aphrodite1_0028	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47413.1	002830	Cluster2406_1clades	395	HWC35_gp019	Vibrio phage USC-1	GCA_006864065.1
BAW98230.1	002830	Cluster2406_1clades	398	FDH33_gp021	Vibrio phage pTD1	GCA_002618825.1
QGZ14568.1	002831	HTH_18+HTH_18	392	HWC77_gp205	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04165.1	002831	HTH_18+HTH_18	392	HWC03_gp010	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23192.1	002831	HTH_18+HTH_18	392	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80971.1	002831	HTH_18+HTH_18	392	Aphrodite1_0150	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47537.1	002831	HTH_18+HTH_18	392	HWC35_gp143	Vibrio phage USC-1	GCA_006864065.1
BAW98351.1	002831	HTH_18+HTH_18	382	FDH33_gp142	Vibrio phage pTD1	GCA_002618825.1
QIG65761.1	002832	Cluster2408_1clades	360	phiOC_p096	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QCG76073.1	002832	Cluster2408_1clades	372	EST35_0192	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AGR47890.1	002832	Cluster2408_1clades	388	SmphiM12_258	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13091.1	002832	Cluster2408_1clades	388	PHIM19_186	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12731.1	002832	Cluster2408_1clades	388	PHIM7_186	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13461.1	002832	Cluster2408_1clades	388	PHIN3_198	Sinorhizobium phage phiN3	GCA_001501175.1
QGZ14468.1	002833	Cluster2409_1clades	385	HWC77_gp105	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04266.1	002833	Cluster2409_1clades	385	HWC03_gp111	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23099.1	002833	Cluster2409_1clades	381	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80973.1	002833	Cluster2409_1clades	381	Aphrodite1_0034	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47417.1	002833	Cluster2409_1clades	381	HWC35_gp023	Vibrio phage USC-1	GCA_006864065.1
BAW98237.1	002833	Cluster2409_1clades	386	FDH33_gp028	Vibrio phage pTD1	GCA_002618825.1
QDB70285.1	002834	Cluster2410_1clades	354	CF8_0117	Aeromonas phage CF8	GCA_006384595.2
QDJ96876.1	002834	Cluster2410_1clades	342	PS1_0117	Aeromonas phage PS1	GCA_007051165.2
QFR59508.1	002834	Cluster2410_1clades	342	PS2_0117	Aeromonas phage PS2	GCA_009388305.2
QBZ70644.1	002834	Cluster2410_1clades	365	pETSU_063	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71961.1	002834	Cluster2410_1clades	277	N1M2_98	Klebsiella phage N1M2	GCA_010092605.1
AEV89562.1	002834	Cluster2410_1clades	371	OBP_125	Pseudomonas phage OBP	GCA_000896635.1
QGZ14488.1	002835	Cluster2411_1clades	363	HWC77_gp125	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04246.1	002835	Cluster2411_1clades	363	HWC03_gp091	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23117.1	002835	Cluster2411_1clades	362	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80978.1	002835	Cluster2411_1clades	363	Aphrodite1_0014	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47399.1	002835	Cluster2411_1clades	362	HWC35_gp005	Vibrio phage USC-1	GCA_006864065.1
BAW98216.1	002835	Cluster2411_1clades	360	FDH33_gp007	Vibrio phage pTD1	GCA_002618825.1
AWY08369.1	002836	Cluster2412_1clades	351	Alexandra_93	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08370.1	002836	Cluster2412_1clades	347	Alexandra_95	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58732.1	002836	Cluster2412_1clades	340	Y3_092	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58733.1	002836	Cluster2412_1clades	352	Y3_093	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28563.1	002836	Cluster2412_1clades	358	YOLOSWAG_80	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28565.1	002836	Cluster2412_1clades	345	YOLOSWAG_82	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QGZ14435.1	002837	Cluster2413_1clades	356	HWC77_gp072	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04301.1	002837	Cluster2413_1clades	356	HWC03_gp146	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23277.1	002837	Cluster2413_1clades	356	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80980.1	002837	Cluster2413_1clades	356	Aphrodite1_0068	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47451.1	002837	Cluster2413_1clades	356	HWC35_gp057	Vibrio phage USC-1	GCA_006864065.1
BAW98273.1	002837	Cluster2413_1clades	357	FDH33_gp064	Vibrio phage pTD1	GCA_002618825.1
BAW19128.1	002838	Cluster2414_1clades	182	FDH28_gp267	Ralstonia phage RP12	GCA_002617345.1
BAW19044.1	002838	Cluster2414_1clades	184	FDH28_gp070	Ralstonia phage RP12	GCA_002617345.1
BAW19414.1	002838	Cluster2414_1clades	182	-	Ralstonia phage RP31	GCA_002617365.1
BAW19329.1	002838	Cluster2414_1clades	184	-	Ralstonia phage RP31	GCA_002617365.1
BAS04962.1	002838	Cluster2414_1clades	354	AVU11_gp170	Ralstonia phage RSF1	GCA_001500875.1
BAQ02687.1	002838	Cluster2414_1clades	353	AVU38_gp159	Ralstonia phage RSL2	GCA_001503055.1
AFF28091.1	002839	Cluster2415_2clades	315	PAU_93	Sphingomonas phage PAU	GCA_000902455.1
BBI90414.1	002839	Cluster2415_2clades	297	HYO65_gp022	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90722.1	002839	Cluster2415_2clades	297	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39257.1	002839	Cluster2415_2clades	306	BPT24_132	Tenacibaculum phage pT24	GCA_002611925.1
prevph1000000846	002839	Cluster2415_2clades	265	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000588	002839	Cluster2415_2clades	350	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QGZ14562.1	002840	Cluster2416_1clades	347	HWC77_gp199	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04171.1	002840	Cluster2416_1clades	347	HWC03_gp016	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23187.1	002840	Cluster2416_1clades	334	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80986.1	002840	Cluster2416_1clades	334	Aphrodite1_0156	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47542.1	002840	Cluster2416_1clades	334	HWC35_gp148	Vibrio phage USC-1	GCA_006864065.1
BAW98356.1	002840	Cluster2416_1clades	315	FDH33_gp147	Vibrio phage pTD1	GCA_002618825.1
AXH70788.1	002841	Cluster2417_1clades	315	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96733.1	002841	Cluster2417_1clades	316	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97052.1	002841	Cluster2417_1clades	316	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96098.1	002841	Cluster2417_1clades	316	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96416.1	002841	Cluster2417_1clades	316	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21007.1	002841	Cluster2417_1clades	343	-	Vibrio phage vB_pir03	GCA_014319855.1
ANM44775.1	002842	Cluster2418_1clades	333	KTN4_017	Pseudomonas phage KTN4	GCA_002607225.1
QBX32285.1	002842	Cluster2418_1clades	342	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94931.1	002842	Cluster2418_1clades	333	SL2_354	Pseudomonas phage SL2	GCA_002956015.1
QJB22660.1	002842	Cluster2418_1clades	333	fnug_17	Pseudomonas phage fnug	GCA_012837215.1
QEM41858.1	002842	Cluster2418_1clades	342	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82916.1	002842	Cluster2418_1clades	333	PHIKZ015	Pseudomonas virus phiKZ	GCA_000842965.1
AAQ64343.1	002843	TM	333	KVP40.0274	Vibrio phage KVP40	GCA_000843785.1
QIW90657.1	002843	TM	333	GCAPEGMB_00310	Vibrio phage V07	GCA_012361095.1
QIW91141.1	002843	TM	333	COHAPHLL_00305	Vibrio phage V09	GCA_012361135.1
QHJ74452.1	002843	TM	333	VH12019_00125	Vibrio phage VH1_2019	GCA_009931825.1
AGN30320.1	002843	TM	327	VPFG_00322	Vibrio phage nt-1	GCA_000910195.2
AFN37503.1	002843	TM	333	pp2_270	Vibriophage phi-pp2	GCA_002630725.1
QIG65678.1	002844	Cluster2421_1clades	268	phiOC_p012	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47674.1	002844	Cluster2421_1clades	325	SmphiM12_042	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12937.1	002844	Cluster2421_1clades	325	PHIM19_30	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12577.1	002844	Cluster2421_1clades	325	PHIM7_29	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13309.1	002844	Cluster2421_1clades	325	PHIN3_44	Sinorhizobium phage phiN3	GCA_001501175.1
AIX30755.1	002844	Cluster2421_1clades	252	Syn7803US37_278	Synechococcus phage ACG-2014f	GCA_002594065.1
QGZ14463.1	002845	HTH_18	322	HWC77_gp100	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04271.1	002845	HTH_18	322	HWC03_gp116	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23094.1	002845	HTH_18	322	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80987.1	002845	HTH_18	322	Aphrodite1_0039	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47422.1	002845	HTH_18	322	HWC35_gp028	Vibrio phage USC-1	GCA_006864065.1
BAW98242.1	002845	HTH_18	314	FDH33_gp033	Vibrio phage pTD1	GCA_002618825.1
AXH70863.1	002846	TM+SpoIID	289	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96942.1	002846	TM+SpoIID	288	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97247.1	002846	TM+SpoIID	288	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96306.1	002846	TM+SpoIID	288	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96624.1	002846	TM+SpoIID	288	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21115.1	002846	TM+SpoIID	317	-	Vibrio phage vB_pir03	GCA_014319855.1
ABY63245.1	002847	Cluster2424_1clades	222	201phi2-1p421	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32519.1	002847	Cluster2424_1clades	229	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77053.1	002847	Cluster2424_1clades	242	PHABIO_422	Pseudomonas phage Phabio	GCA_002624965.1
AEH03773.1	002847	Cluster2424_1clades	315	350	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02909.1	002847	Cluster2424_1clades	222	PSA21_383	Pseudomonas phage Psa21	GCA_004340405.1
QEM42092.1	002847	Cluster2424_1clades	229	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDB70256.1	002848	Cluster2425_1clades	192	CF8_0088	Aeromonas phage CF8	GCA_006384595.2
QDJ97410.1	002848	Cluster2425_1clades	178	D6_0251	Aeromonas phage D6	GCA_007051205.2
QDH47163.1	002848	Cluster2425_1clades	178	LAh10_163	Aeromonas phage LAh10	GCA_006863975.1
QDJ96847.1	002848	Cluster2425_1clades	182	PS1_0088	Aeromonas phage PS1	GCA_007051165.2
QFR59477.1	002848	Cluster2425_1clades	314	PS2_0086	Aeromonas phage PS2	GCA_009388305.2
QFR59478.1	002848	Cluster2425_1clades	189	PS2_0087	Aeromonas phage PS2	GCA_009388305.2
AGR47971.3	002849	Cluster2426_1clades	201	SmphiM12_339	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13161.2	002849	Cluster2426_1clades	227	PHIM19_256	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12801.1	002849	Cluster2426_1clades	227	PHIM7_256	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13524.2	002849	Cluster2426_1clades	227	PHIN3_261	Sinorhizobium phage phiN3	GCA_001501175.1
BBA65405.1	002849	Cluster2426_1clades	305	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96430.1	002849	Cluster2426_1clades	301	Xoosp13_244	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGB06868.1	002850	Cluster2427_1clades	304	CF80_gp081	Vibrio phage VH7D	GCA_000914495.1
QBX06278.1	002850	Cluster2427_1clades	304	ValB1HC_325	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60904.1	002850	Cluster2427_1clades	304	AVU32_gp063	Vibrio phage ValKK3	GCA_001501635.1
ALP47023.1	002850	Cluster2427_1clades	304	phiGrn1_0306	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47422.1	002850	Cluster2427_1clades	247	phiST2_0063	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54905.1	002850	Cluster2427_1clades	304	vBValMR10Z_365	Vibrio phage vB_ValM_R10Z	GCA_014337545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU88153.1	002851	RADICAL-SAM	301	CcrColossus_gp283	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68828.1	002851	RADICAL-SAM	301	CcrPW_gp289	Caulobacter phage CcrPW	GCA_003443275.1
AXH72902.1	002851	RADICAL-SAM	293	-	Myoviridae sp.	GCA_003657725.1
ABY63257.1	002851	RADICAL-SAM	302	201phi2-1p434	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77075.1	002851	RADICAL-SAM	296	PHABIO_444	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02924.1	002851	RADICAL-SAM	293	PSA21_398	Pseudomonas phage Psa21	GCA_004340405.1
AXH70843.1	002852	Cluster2429_1clades	294	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96649.1	002852	Cluster2429_1clades	302	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96967.1	002852	Cluster2429_1clades	302	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96013.1	002852	Cluster2429_1clades	302	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96331.1	002852	Cluster2429_1clades	302	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21091.1	002852	Cluster2429_1clades	293	-	Vibrio phage vB_pir03	GCA_014319855.1
AMS01126.1	002853	Cluster2430_1clades	300	AR9_g041	Bacillus phage AR9	GCA_001743835.1
AMS01127.1	002853	Cluster2430_1clades	300	AR9_g042	Bacillus phage AR9	GCA_001743835.1
AMS01128.1	002853	Cluster2430_1clades	148	AR9_g043	Bacillus phage AR9	GCA_001743835.1
ASU00050.1	002853	Cluster2430_1clades	301	PBI_PBS1_228	Bacillus virus PBS1	GCA_002601325.1
ASU00051.1	002853	Cluster2430_1clades	300	PBI_PBS1_229	Bacillus virus PBS1	GCA_002601325.1
ASU00052.1	002853	Cluster2430_1clades	148	PBI_PBS1_230	Bacillus virus PBS1	GCA_002601325.1
AFC21486.1	002854	DUF932	295	GAP32_039	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44161.1	002854	DUF932	295	CBB_45	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43610.1	002854	DUF932	295	CBB_598	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88561.1	002854	DUF932	297	BF_0036	Serratia phage BF	GCA_002619745.1
SOK58836.1	002854	DUF932	297	g028	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58296.1	002854	DUF932	297	g019	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14422.1	002855	Cluster2433_1clades	279	HWC77_gp059	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04313.1	002855	Cluster2433_1clades	279	HWC03_gp158	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23265.1	002855	Cluster2433_1clades	279	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81000.1	002855	Cluster2433_1clades	279	Aphrodite1_0080	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47463.1	002855	Cluster2433_1clades	279	HWC35_gp069	Vibrio phage USC-1	GCA_006864065.1
BAW98284.1	002855	Cluster2433_1clades	290	FDH33_gp075	Vibrio phage pTD1	GCA_002618825.1
AXH70880.1	002856	Cluster2434_1clades	288	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96927.1	002856	Cluster2434_1clades	274	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97232.1	002856	Cluster2434_1clades	274	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96291.1	002856	Cluster2434_1clades	274	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96609.1	002856	Cluster2434_1clades	274	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21130.1	002856	Cluster2434_1clades	284	-	Vibrio phage vB_pir03	GCA_014319855.1
AXH70752.1	002857	Cluster2435_1clades	285	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96782.1	002857	Cluster2435_1clades	288	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97101.1	002857	Cluster2435_1clades	288	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96147.1	002857	Cluster2435_1clades	288	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96465.1	002857	Cluster2435_1clades	288	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20962.1	002857	Cluster2435_1clades	279	-	Vibrio phage vB_pir03	GCA_014319855.1
AGH07574.1	002858	BACTERIALFRINGE	278	CYVG_00130	Cyanophage S-SSM6a	GCA_002710385.1
AIR93520.1	002858	BACTERIALFRINGE	271	AVU42_gp183	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93519.1	002858	BACTERIALFRINGE	282	AVU42_gp182	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22964.1	002858	BACTERIALFRINGE	272	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50566.1	002858	BACTERIALFRINGE	272	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70505.1	002858	BACTERIALFRINGE	268	HOU04_gp106	Synechococcus phage S-T4	GCA_003443335.1
QDB70372.1	002859	VCX_VCY	251	CF8_0204	Aeromonas phage CF8	GCA_006384595.2
QDJ96714.1	002859	VCX_VCY	269	PS1_0203	Aeromonas phage PS1	GCA_007051165.2
QFR59347.1	002859	VCX_VCY	269	PS2_0205	Aeromonas phage PS2	GCA_009388305.2
QBZ70754.1	002859	VCX_VCY	281	pETSU_173	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72061.1	002859	VCX_VCY	240	N1M2_198	Klebsiella phage N1M2	GCA_010092605.1
AEV89689.1	002859	VCX_VCY	220	OBP_252	Pseudomonas phage OBP	GCA_000896635.1
AXH70995.1	002860	35exo	276	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96696.1	002860	35exo	256	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97014.1	002860	35exo	256	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96060.1	002860	35exo	256	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96378.1	002860	35exo	256	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21266.1	002860	35exo	225	-	Vibrio phage vB_pir03	GCA_014319855.1
AXH70832.1	002861	Cluster2439_1clades	275	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96661.1	002861	Cluster2439_1clades	275	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96979.1	002861	Cluster2439_1clades	275	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96025.1	002861	Cluster2439_1clades	275	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96343.1	002861	Cluster2439_1clades	275	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21079.1	002861	Cluster2439_1clades	273	-	Vibrio phage vB_pir03	GCA_014319855.1
QGZ14491.1	002862	Cluster2440_1clades	259	HWC77_gp128	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04243.1	002862	Cluster2440_1clades	259	HWC03_gp088	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23120.1	002862	Cluster2440_1clades	259	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81004.1	002862	Cluster2440_1clades	259	Aphrodite1_0011	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47396.1	002862	Cluster2440_1clades	259	HWC35_gp002	Vibrio phage USC-1	GCA_006864065.1
BAW98213.1	002862	Cluster2440_1clades	264	FDH33_gp004	Vibrio phage pTD1	GCA_002618825.1
AXH70786.1	002863	Cluster2441_1clades	241	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96734.1	002863	Cluster2441_1clades	261	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97053.1	002863	Cluster2441_1clades	261	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96099.1	002863	Cluster2441_1clades	261	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96417.1	002863	Cluster2441_1clades	261	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21005.1	002863	Cluster2441_1clades	233	-	Vibrio phage vB_pir03	GCA_014319855.1
QGZ14567.1	002864	Cluster2442_1clades	259	HWC77_gp204	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04166.1	002864	Cluster2442_1clades	259	HWC03_gp011	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23191.1	002864	Cluster2442_1clades	259	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81005.1	002864	Cluster2442_1clades	259	Aphrodite1_0151	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47538.1	002864	Cluster2442_1clades	259	HWC35_gp144	Vibrio phage USC-1	GCA_006864065.1
BAW98352.1	002864	Cluster2442_1clades	255	FDH33_gp143	Vibrio phage pTD1	GCA_002618825.1
QGZ14438.1	002865	Cluster2443_1clades	245	HWC77_gp075	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04296.1	002865	Cluster2443_1clades	245	HWC03_gp141	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23282.1	002865	Cluster2443_1clades	249	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81008.1	002865	Cluster2443_1clades	249	Aphrodite1_0063	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47446.1	002865	Cluster2443_1clades	249	HWC35_gp052	Vibrio phage USC-1	GCA_006864065.1
BAW98268.1	002865	Cluster2443_1clades	258	FDH33_gp059	Vibrio phage pTD1	GCA_002618825.1
QBX06471.1	002866	Cluster2444_1clades	135	BcepSaruman_058	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74438.1	002866	Cluster2444_1clades	135	BcepSauron_058	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ69055.1	002866	Cluster2444_1clades	256	CcrBL9_gp031	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69571.1	002866	Cluster2444_1clades	256	CcrBL9_gp547	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69614.1	002866	Cluster2444_1clades	256	CcrSC_gp032	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70114.1	002866	Cluster2444_1clades	256	CcrSC_gp532	Caulobacter phage CcrSC	GCA_003443315.1
QGT54955.1	002867	Cluster2445_1clades	241	b23_0349	Synechococcus phage B23	GCA_009745195.1
QGT54961.1	002867	Cluster2445_1clades	256	b23_0355	Synechococcus phage B23	GCA_009745195.1
QGT54590.1	002867	Cluster2445_1clades	241	b3_0355	Synechococcus phage B3	GCA_009745215.1
QGT54596.1	002867	Cluster2445_1clades	256	b3_0361	Synechococcus phage B3	GCA_009745215.1
ASR76244.1	002867	Cluster2445_1clades	250	PBI_BELLAMY_208	Synechococcus phage Bellamy	GCA_002627525.1
QJT70200.1	002867	Cluster2445_1clades	250	SynMITS9220M01_194	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QGZ14392.1	002868	Cluster2447_1clades	254	HWC77_gp029	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04344.1	002868	Cluster2447_1clades	254	HWC03_gp189	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23232.1	002868	Cluster2447_1clades	241	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81011.1	002868	Cluster2447_1clades	241	Aphrodite1_0113	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47496.1	002868	Cluster2447_1clades	241	HWC35_gp102	Vibrio phage USC-1	GCA_006864065.1
BAW98316.1	002868	Cluster2447_1clades	254	FDH33_gp107	Vibrio phage pTD1	GCA_002618825.1
QGZ14566.1	002869	Cluster2448_1clades	252	HWC77_gp203	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04167.1	002869	Cluster2448_1clades	252	HWC03_gp012	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23190.1	002869	Cluster2448_1clades	252	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81006.1	002869	Cluster2448_1clades	252	Aphrodite1_0152	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47539.1	002869	Cluster2448_1clades	252	HWC35_gp145	Vibrio phage USC-1	GCA_006864065.1
BAW98354.1	002869	Cluster2448_1clades	251	FDH33_gp145	Vibrio phage pTD1	GCA_002618825.1
QGZ14476.1	002870	Cluster2449_1clades	250	HWC77_gp113	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04258.1	002870	Cluster2449_1clades	250	HWC03_gp103	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23105.1	002870	Cluster2449_1clades	250	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81007.1	002870	Cluster2449_1clades	250	Aphrodite1_0026	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47411.1	002870	Cluster2449_1clades	252	HWC35_gp017	Vibrio phage USC-1	GCA_006864065.1
BAW98228.1	002870	Cluster2449_1clades	235	FDH33_gp019	Vibrio phage pTD1	GCA_002618825.1
AYD81326.1	002871	Cluster2450_1clades	192	SEA_JUSTBECAUSE_161	Streptomyces phage JustBecause	GCA_003613775.1
AYD81327.1	002871	Cluster2450_1clades	119	SEA_JUSTBECAUSE_162	Streptomyces phage JustBecause	GCA_003613775.1
QJD53729.1	002871	Cluster2450_1clades	192	SEA_KELA_159	Streptomyces phage Kela	GCA_012934305.1
QJD53730.1	002871	Cluster2450_1clades	119	SEA_KELA_160	Streptomyces phage Kela	GCA_012934305.1
QBZ72056.1	002871	Cluster2450_1clades	250	SEA_KRADAL_160	Streptomyces phage Kradal	GCA_004799925.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH66319.1	002871	Cluster2450_1clades	250	SEA_SATIS_160	Streptomyces phage Satis	GCA_003366315.1
QGZ14401.1	002872	Cluster2451_1clades	240	HWC77_gp038	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04335.1	002872	Cluster2451_1clades	240	HWC03_gp180	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23241.1	002872	Cluster2451_1clades	240	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81013.1	002872	Cluster2451_1clades	240	Aphrodite1_0104	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47487.1	002872	Cluster2451_1clades	240	HWC35_gp093	Vibrio phage USC-1	GCA_006864065.1
BAW98307.1	002872	Cluster2451_1clades	243	FDH33_gp098	Vibrio phage pTD1	GCA_002618825.1
QDB70319.1	002873	Cluster2453_1clades	241	CF8_0150	Aeromonas phage CF8	GCA_006384595.2
QDJ96665.1	002873	Cluster2453_1clades	233	PS1_0154	Aeromonas phage PS1	GCA_007051165.2
QFR59299.1	002873	Cluster2453_1clades	233	PS2_0158	Aeromonas phage PS2	GCA_009388305.2
QBZ70696.1	002873	Cluster2453_1clades	234	pETSU_115	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72011.1	002873	Cluster2453_1clades	230	N1M2_148	Klebsiella phage N1M2	GCA_010092605.1
AEV89621.1	002873	Cluster2453_1clades	226	OBP_184	Pseudomonas phage OBP	GCA_000896635.1
AXG67321.1	002874	Cluster2454_1clades	239	AD1_277	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79823.1	002874	Cluster2454_1clades	240	JA11_018	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66422.1	002874	Cluster2454_1clades	240	JA13_019	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66744.1	002874	Cluster2454_1clades	239	JA29_018	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67392.1	002874	Cluster2454_1clades	240	JA33_018	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ARW58670.1	002874	Cluster2454_1clades	236	Y3_030	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67096.1	002875	Cluster2455_1clades	219	AD1_052	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79843.1	002875	Cluster2455_1clades	239	JA11_038	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66443.1	002875	Cluster2455_1clades	239	JA13_040	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66767.1	002875	Cluster2455_1clades	239	JA29_041	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67412.1	002875	Cluster2455_1clades	239	JA33_038	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ARW58701.1	002875	Cluster2455_1clades	211	Y3_061	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QDB70411.1	002876	Cluster2456_1clades	220	CF8_0242	Aeromonas phage CF8	GCA_006384595.2
QDJ96756.1	002876	Cluster2456_1clades	232	PS1_0245	Aeromonas phage PS1	GCA_007051165.2
QFR59389.1	002876	Cluster2456_1clades	232	PS2_0247	Aeromonas phage PS2	GCA_009388305.2
QBZ70804.1	002876	Cluster2456_1clades	234	pETSU_223	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72104.1	002876	Cluster2456_1clades	224	N1M2_241	Klebsiella phage N1M2	GCA_010092605.1
AEV89743.1	002876	Cluster2456_1clades	235	OBP_306	Pseudomonas phage OBP	GCA_000896635.1
AXH70904.1	002877	Cluster2457_1clades	227	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96880.1	002877	Cluster2457_1clades	233	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97185.1	002877	Cluster2457_1clades	233	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96244.1	002877	Cluster2457_1clades	233	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96562.1	002877	Cluster2457_1clades	233	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21143.1	002877	Cluster2457_1clades	223	-	Vibrio phage vB_pir03	GCA_014319855.1
QMV28750.1	002878	Cluster2458_1clades	220	AP1_0032	Aeromonas phage AP1	GCA_014183365.1
ATI17580.1	002878	Cluster2458_1clades	220	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00417.1	002878	Cluster2458_1clades	220	HWB28_gp135	Aeromonas phage AS-zj	GCA_002627665.1
QAX98019.1	002878	Cluster2458_1clades	220	ASswx1_379	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01124.1	002878	Cluster2458_1clades	232	ASwh1_57	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39239.1	002878	Cluster2458_1clades	220	CC2_153	Aeromonas phage CC2	GCA_000903495.1
AXH70819.1	002879	Cluster2459_1clades	223	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96678.1	002879	Cluster2459_1clades	227	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96996.1	002879	Cluster2459_1clades	227	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96042.1	002879	Cluster2459_1clades	227	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96360.1	002879	Cluster2459_1clades	227	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21064.1	002879	Cluster2459_1clades	232	-	Vibrio phage vB_pir03	GCA_014319855.1
QGZ14492.1	002880	Cluster2460_1clades	224	HWC77_gp129	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04242.1	002880	Cluster2460_1clades	224	HWC03_gp087	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23121.1	002880	Cluster2460_1clades	224	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81018.1	002880	Cluster2460_1clades	224	Aphrodite1_0010	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47395.1	002880	Cluster2460_1clades	225	HWC35_gp001	Vibrio phage USC-1	GCA_006864065.1
BAW98212.1	002880	Cluster2460_1clades	229	FDH33_gp003	Vibrio phage pTD1	GCA_002618825.1
AYD80059.1	002881	Cluster2461_1clades	226	JA11_254	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AYD80060.1	002881	Cluster2461_1clades	223	JA11_255	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66659.1	002881	Cluster2461_1clades	223	JA13_256	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66982.1	002881	Cluster2461_1clades	223	JA29_256	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67629.1	002881	Cluster2461_1clades	226	JA33_255	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67630.1	002881	Cluster2461_1clades	223	JA33_256	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGH56988.1	002882	Cluster2462_1clades	221	CPXG_00185	Cyanophage P-RSM6	GCA_000906155.1
AJK27472.1	002882	Cluster2462_1clades	135	PTIM40_45	Cyanophage P-TIM40	GCA_001470935.1
AOO11581.1	002882	Cluster2462_1clades	153	ES420910_100	Cyanophage S-RIM44	GCA_002599165.1
AOO12046.1	002882	Cluster2462_1clades	153	Np200711_100	Cyanophage S-RIM44	GCA_002599205.1
AOO12282.1	002882	Cluster2462_1clades	153	Np420711_100	Cyanophage S-RIM44	GCA_002599225.1
AOO12747.1	002882	Cluster2462_1clades	153	Sn130910_100	Cyanophage S-RIM44	GCA_002599265.1
AXH70761.1	002883	Cluster2463_1clades	217	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96773.1	002883	Cluster2463_1clades	221	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97092.1	002883	Cluster2463_1clades	221	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96138.1	002883	Cluster2463_1clades	221	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96456.1	002883	Cluster2463_1clades	221	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20970.1	002883	Cluster2463_1clades	219	-	Vibrio phage vB_pir03	GCA_014319855.1
QGZ14526.1	002884	Cluster2464_1clades	219	HWC77_gp163	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04208.1	002884	Cluster2464_1clades	220	HWC03_gp053	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23152.1	002884	Cluster2464_1clades	219	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81020.1	002884	Cluster2464_1clades	219	Aphrodite1_0188	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47576.1	002884	Cluster2464_1clades	219	HWC35_gp182	Vibrio phage USC-1	GCA_006864065.1
BAW98391.1	002884	Cluster2464_1clades	219	FDH33_gp182	Vibrio phage pTD1	GCA_002618825.1
AXQ68496.1	002885	Cluster2466_1clades	215	CcrBL10_gp292	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69364.1	002885	Cluster2466_1clades	134	CcrBL9_gp340	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69924.1	002885	Cluster2466_1clades	120	CcrSC_gp342	Caulobacter phage CcrSC	GCA_003443315.1
AFU87826.1	002885	Cluster2466_1clades	218	CcrKarma_gp309	Caulobacter virus Karma	GCA_000901575.1
AFU87473.1	002885	Cluster2466_1clades	218	CcrMagneto_gp303	Caulobacter virus Magneto	GCA_000903095.1
AFU88618.1	002885	Cluster2466_1clades	218	CcrSwift_gp300	Caulobacter virus Swift	GCA_000899655.1
QGZ14467.1	002886	Cluster2467_1clades	215	HWC77_gp104	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04267.1	002886	Cluster2467_1clades	215	HWC03_gp112	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23098.1	002886	Cluster2467_1clades	214	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81022.1	002886	Cluster2467_1clades	214	Aphrodite1_0035	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47418.1	002886	Cluster2467_1clades	214	HWC35_gp024	Vibrio phage USC-1	GCA_006864065.1
BAW98238.1	002886	Cluster2467_1clades	214	FDH33_gp029	Vibrio phage pTD1	GCA_002618825.1
QDB70427.1	002887	Cluster2469_1clades	210	CF8_0014	Aeromonas phage CF8	GCA_006384595.2
QDJ96778.1	002887	Cluster2469_1clades	204	PS1_0019	Aeromonas phage PS1	GCA_007051165.2
QFR59410.1	002887	Cluster2469_1clades	204	PS2_0019	Aeromonas phage PS2	GCA_009388305.2
QBZ70821.1	002887	Cluster2469_1clades	204	pETSU_240	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72119.1	002887	Cluster2469_1clades	204	N1M2_259	Klebsiella phage N1M2	GCA_010092605.1
AEV89453.1	002887	Cluster2469_1clades	201	OBP_016	Pseudomonas phage OBP	GCA_000896635.1
QGZ14381.1	002888	Cluster2470_1clades	207	HWC77_gp018	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04355.1	002888	Cluster2470_1clades	207	HWC03_gp200	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23221.1	002888	Cluster2470_1clades	208	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81026.1	002888	Cluster2470_1clades	208	Aphrodite1_0124	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47507.1	002888	Cluster2470_1clades	208	HWC35_gp113	Vibrio phage USC-1	GCA_006864065.1
BAW98326.1	002888	Cluster2470_1clades	206	FDH33_gp117	Vibrio phage pTD1	GCA_002618825.1
AXQ68213.1	002889	Cluster2472_1clades	206	CcrBL10_gp009	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68531.1	002889	Cluster2472_1clades	206	CcrBL10_gp327	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86493.1	002889	Cluster2472_1clades	206	CcrRogue_gp011	Caulobacter virus Rogue	GCA_000900555.1
AFU86824.1	002889	Cluster2472_1clades	206	CcrRogue_gp342	Caulobacter virus Rogue	GCA_000900555.1
AFU88328.1	002889	Cluster2472_1clades	206	CcrSwift_gp010	Caulobacter virus Swift	GCA_000899655.1
AFU88653.1	002889	Cluster2472_1clades	206	CcrSwift_gp335	Caulobacter virus Swift	GCA_000899655.1
QGZ14507.1	002890	Cluster2473_1clades	203	HWC77_gp144	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04227.1	002890	Cluster2473_1clades	203	HWC03_gp072	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23135.1	002890	Cluster2473_1clades	204	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81029.1	002890	Cluster2473_1clades	200	Aphrodite1_0205	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47592.1	002890	Cluster2473_1clades	204	HWC35_gp198	Vibrio phage USC-1	GCA_006864065.1
BAW98407.1	002890	Cluster2473_1clades	204	FDH33_gp198	Vibrio phage pTD1	GCA_002618825.1
QDB70335.1	002891	Cluster2474_1clades	152	CF8_0165	Aeromonas phage CF8	GCA_006384595.2
QDJ97303.1	002891	Cluster2474_1clades	204	D6_0143	Aeromonas phage D6	GCA_007051205.2
QDH47141.1	002891	Cluster2474_1clades	204	LAh10_67	Aeromonas phage LAh10	GCA_006863975.1
QDJ96687.1	002891	Cluster2474_1clades	157	PS1_0176	Aeromonas phage PS1	GCA_007051165.2
QFR59320.1	002891	Cluster2474_1clades	152	PS2_0178	Aeromonas phage PS2	GCA_009388305.2
AEV89533.1	002891	Cluster2474_1clades	155	OBP_096	Pseudomonas phage OBP	GCA_000896635.1
AUE22745.1	002892	Cluster2475_1clades	62	Ah1_00227	Aeromonas phage Ah1	GCA_002957415.1
AUE22746.1	002892	Cluster2475_1clades	120	Ah1_00228	Aeromonas phage Ah1	GCA_002957415.1
QAX98462.1	002892	Cluster2475_1clades	122	ASfcp2_122	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52922.1	002892	Cluster2475_1clades	201	PX29p203	Aeromonas phage PX29	GCA_000920195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADM79846.1	002892	Cluster2475_1clades	201	phiAS5_ORF0003	Aeromonas phage phiAS5	GCA_000887715.1
AAP04361.1	002892	Cluster2475_1clades	201	Aeh1ORF208w	Aeromonas virus Aeh1	GCA_000843245.1
CAG27192.1	002893	Cluster2476_1clades	178	PPEV_gp098	Pseudomonas phage EL	GCA_000866825.1
ANM44773.1	002893	Cluster2476_1clades	135	KTN4_015	Pseudomonas phage KTN4	GCA_002607225.1
QBX32280.1	002893	Cluster2476_1clades	200	-	Pseudomonas phage PA1C	GCA_004785505.1
QJB22658.1	002893	Cluster2476_1clades	200	fnug_15	Pseudomonas phage fnug	GCA_012837215.1
QEM41854.1	002893	Cluster2476_1clades	200	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82914.1	002893	Cluster2476_1clades	135	PHIKZ013	Pseudomonas virus phiKZ	GCA_000842965.1
BAS04983.2	002894	SIG+SPRY	155	AVU11_agp38	Ralstonia phage RSF1	GCA_001500875.1
BAS04982.1	002894	SIG+SPRY	194	AVU11_gp190	Ralstonia phage RSF1	GCA_001500875.1
BAS04793.1	002894	SIG+SPRY	196	AVU11_gp001	Ralstonia phage RSF1	GCA_001500875.1
BAQ02709.2	002894	SIG+SPRY	191	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02708.1	002894	SIG+SPRY	198	AVU38_gp180	Ralstonia phage RSL2	GCA_001503055.1
BAQ02529.2	002894	SIG+SPRY	90	-	Ralstonia phage RSL2	GCA_001503055.1
QGZ14556.1	002895	Cluster2479_1clades	197	HWC77_gp193	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04177.1	002895	Cluster2479_1clades	197	HWC03_gp022	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23181.1	002895	Cluster2479_1clades	197	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81031.1	002895	Cluster2479_1clades	197	Aphrodite1_0161	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47548.1	002895	Cluster2479_1clades	182	HWC35_gp154	Vibrio phage USC-1	GCA_006864065.1
BAW98361.1	002895	Cluster2479_1clades	197	FDH33_gp152	Vibrio phage pTD1	GCA_002618825.1
QGZ14537.1	002896	Cluster2480_1clades	189	HWC77_gp174	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04197.1	002896	Cluster2480_1clades	189	HWC03_gp042	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23163.1	002896	Cluster2480_1clades	189	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81032.1	002896	Cluster2480_1clades	189	Aphrodite1_0178	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47565.1	002896	Cluster2480_1clades	189	HWC35_gp171	Vibrio phage USC-1	GCA_006864065.1
BAW98380.1	002896	Cluster2480_1clades	138	FDH33_gp171	Vibrio phage pTD1	GCA_002618825.1
ANM44787.1	002897	Cluster2481_1clades	184	KTN4_029	Pseudomonas phage KTN4	GCA_002607225.1
QBX32288.1	002897	Cluster2481_1clades	184	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03551.1	002897	Cluster2481_1clades	139	127	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94923.1	002897	Cluster2481_1clades	187	SL2_346	Pseudomonas phage SL2	GCA_002956015.1
QEM41862.1	002897	Cluster2481_1clades	184	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82923.1	002897	Cluster2481_1clades	187	PHIKZ022	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ68340.1	002898	Cluster2482_1clades	118	CcrBL10_gp136	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69475.1	002898	Cluster2482_1clades	184	CcrBL9_gp451	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88179.1	002898	Cluster2482_1clades	123	CcrColossus_gp309	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68856.1	002898	Cluster2482_1clades	124	CcrPW_gp317	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70024.1	002898	Cluster2482_1clades	184	CcrSC_gp442	Caulobacter phage CcrSC	GCA_003443315.1
AFU86625.1	002898	Cluster2482_1clades	129	CcrRogue_gp143	Caulobacter virus Rogue	GCA_000900555.1
AYD79847.1	002899	tRNA-synt_2c	86	JA11_042	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66447.1	002899	tRNA-synt_2c	86	JA13_044	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66771.1	002899	tRNA-synt_2c	86	JA29_045	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67416.1	002899	tRNA-synt_2c	86	JA33_042	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGX01758.1	002899	tRNA-synt_2c	183	CF95_gp036	Erwinia phage PhiEaH1	GCA_000914555.1
QDB71265.1	002899	tRNA-synt_2c	132	CPT_Moabite_235	Serratia phage Moabite	GCA_006384735.1
AXQ68209.1	002900	Cluster2485_1clades	179	CcrBL10_gp005	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68527.1	002900	Cluster2485_1clades	179	CcrBL10_gp323	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86489.1	002900	Cluster2485_1clades	179	CcrRogue_gp007	Caulobacter virus Rogue	GCA_000900555.1
AFU86820.1	002900	Cluster2485_1clades	179	CcrRogue_gp338	Caulobacter virus Rogue	GCA_000900555.1
AFU88324.1	002900	Cluster2485_1clades	179	CcrSwift_gp006	Caulobacter virus Swift	GCA_000899655.1
AFU88649.1	002900	Cluster2485_1clades	179	CcrSwift_gp331	Caulobacter virus Swift	GCA_000899655.1
BAW19149.1	002901	Cluster2486_1clades	106	FDH28_gp246	Ralstonia phage RP12	GCA_002617345.1
BAW19145.1	002901	Cluster2486_1clades	144	FDH28_gp250	Ralstonia phage RP12	GCA_002617345.1
BAW19144.1	002901	Cluster2486_1clades	179	FDH28_gp251	Ralstonia phage RP12	GCA_002617345.1
BAW19435.1	002901	Cluster2486_1clades	106	-	Ralstonia phage RP31	GCA_002617365.1
BAW19431.1	002901	Cluster2486_1clades	144	-	Ralstonia phage RP31	GCA_002617365.1
BAW19430.1	002901	Cluster2486_1clades	179	-	Ralstonia phage RP31	GCA_002617365.1
AGB06939.1	002902	Cluster2487_1clades	177	CF80_gp152	Vibrio phage VH7D	GCA_000914495.1
QBX06207.1	002902	Cluster2487_1clades	177	ValB1HC_254	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61224.1	002902	Cluster2487_1clades	177	AVU32_gp383	Vibrio phage ValKK3	GCA_001501635.1
ALP47172.1	002902	Cluster2487_1clades	115	phiGrn1_0375	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47472.1	002902	Cluster2487_1clades	177	phiST2_0130	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54832.1	002902	Cluster2487_1clades	177	vBValMR10Z_292	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QGZ14490.1	002903	Cluster2488_1clades	170	HWC77_gp127	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04244.1	002903	Cluster2488_1clades	170	HWC03_gp089	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23119.1	002903	Cluster2488_1clades	170	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81039.1	002903	Cluster2488_1clades	170	Aphrodite1_0012	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47397.1	002903	Cluster2488_1clades	170	HWC35_gp003	Vibrio phage USC-1	GCA_006864065.1
BAW98214.1	002903	Cluster2488_1clades	174	FDH33_gp005	Vibrio phage pTD1	GCA_002618825.1
QGZ14480.1	002904	Cluster2489_1clades	174	HWC77_gp117	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04254.1	002904	Cluster2489_1clades	174	HWC03_gp099	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23109.1	002904	Cluster2489_1clades	165	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81044.1	002904	Cluster2489_1clades	165	Aphrodite1_0022	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47407.1	002904	Cluster2489_1clades	165	HWC35_gp013	Vibrio phage USC-1	GCA_006864065.1
BAW98224.1	002904	Cluster2489_1clades	173	FDH33_gp015	Vibrio phage pTD1	GCA_002618825.1
QGZ14528.1	002905	SIG+TM	172	HWC77_gp165	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04206.1	002905	SIG+TM	172	HWC03_gp051	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23154.1	002905	SIG+TM	172	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81038.1	002905	SIG+TM	172	Aphrodite1_0186	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47574.1	002905	SIG+TM	172	HWC35_gp180	Vibrio phage USC-1	GCA_006864065.1
BAW98389.1	002905	SIG+TM	172	FDH33_gp180	Vibrio phage pTD1	GCA_002618825.1
QGZ14423.1	002906	Cluster2491_1clades	165	HWC77_gp060	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04312.1	002906	Cluster2491_1clades	165	HWC03_gp157	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23266.1	002906	Cluster2491_1clades	165	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81045.1	002906	Cluster2491_1clades	165	Aphrodite1_0079	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47462.1	002906	Cluster2491_1clades	165	HWC35_gp068	Vibrio phage USC-1	GCA_006864065.1
BAW98283.1	002906	Cluster2491_1clades	171	FDH33_gp074	Vibrio phage pTD1	GCA_002618825.1
QGZ14503.1	002907	Cluster2492_1clades	171	HWC77_gp140	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04231.1	002907	Cluster2492_1clades	171	HWC03_gp076	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23132.1	002907	Cluster2492_1clades	170	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81040.1	002907	Cluster2492_1clades	170	Aphrodite1_0208	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47595.1	002907	Cluster2492_1clades	170	HWC35_gp201	Vibrio phage USC-1	GCA_006864065.1
BAW98410.1	002907	Cluster2492_1clades	171	FDH33_gp201	Vibrio phage pTD1	GCA_002618825.1
ANM45094.1	002908	Cluster2493_1clades	170	KTN4_336	Pseudomonas phage KTN4	GCA_002607225.1
QBX32508.1	002908	Cluster2493_1clades	171	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94619.1	002908	Cluster2493_1clades	170	SL2_042	Pseudomonas phage SL2	GCA_002956015.1
QJB22970.1	002908	Cluster2493_1clades	170	fnug_327	Pseudomonas phage fnug	GCA_012837215.1
QEM42080.1	002908	Cluster2493_1clades	171	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83180.1	002908	Cluster2493_1clades	170	PHIKZ279	Pseudomonas virus phiKZ	GCA_000842965.1
QGZ14481.1	002909	Cluster2494_1clades	165	HWC77_gp118	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04253.1	002909	Cluster2494_1clades	170	HWC03_gp098	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23110.1	002909	Cluster2494_1clades	156	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81053.1	002909	Cluster2494_1clades	156	Aphrodite1_0021	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47406.1	002909	Cluster2494_1clades	156	HWC35_gp012	Vibrio phage USC-1	GCA_006864065.1
BAW98223.1	002909	Cluster2494_1clades	153	FDH33_gp014	Vibrio phage pTD1	GCA_002618825.1
QGZ14424.1	002910	Cluster2495_1clades	168	HWC77_gp061	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04311.1	002910	Cluster2495_1clades	168	HWC03_gp156	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23267.1	002910	Cluster2495_1clades	168	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81042.1	002910	Cluster2495_1clades	168	Aphrodite1_0078	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47461.1	002910	Cluster2495_1clades	168	HWC35_gp067	Vibrio phage USC-1	GCA_006864065.1
BAW98282.1	002910	Cluster2495_1clades	120	FDH33_gp073	Vibrio phage pTD1	GCA_002618825.1
AXH70816.1	002911	Cluster2496_1clades	168	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96681.1	002911	Cluster2496_1clades	163	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96999.1	002911	Cluster2496_1clades	163	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96045.1	002911	Cluster2496_1clades	163	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96363.1	002911	Cluster2496_1clades	163	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21061.1	002911	Cluster2496_1clades	158	-	Vibrio phage vB_pir03	GCA_014319855.1
QGZ14482.1	002912	Cluster2497_1clades	163	HWC77_gp119	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04252.1	002912	Cluster2497_1clades	163	HWC03_gp097	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23111.1	002912	Cluster2497_1clades	163	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81046.1	002912	Cluster2497_1clades	163	Aphrodite1_0020	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47405.1	002912	Cluster2497_1clades	163	HWC35_gp011	Vibrio phage USC-1	GCA_006864065.1
BAW98222.1	002912	Cluster2497_1clades	167	FDH33_gp013	Vibrio phage pTD1	GCA_002618825.1
QGZ14462.1	002913	Cluster2498_1clades	160	HWC77_gp099	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04272.1	002913	Cluster2498_1clades	160	HWC03_gp117	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23305.1	002913	Cluster2498_1clades	160	-	Vibrio phage 5 TSL-2019	GCA_006964265.1

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AUR81048.1	002913	Cluster2498_1clades	160	Aphrodite1_0040	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47423.1	002913	Cluster2498_1clades	160	HWC35_gp029	Vibrio phage USC-1	GCA_006864065.1
BAW98244.1	002913	Cluster2498_1clades	166	FDH33_gp035	Vibrio phage pTD1	GCA_002618825.1
QDB70386.1	002914	Cluster2499_1clades	165	CF8_0217	Aeromonas phage CF8	GCA_006384595.2
QDJ96728.1	002914	Cluster2499_1clades	150	PS1_0217	Aeromonas phage PS1	GCA_007051165.2
QFR59361.1	002914	Cluster2499_1clades	150	PS2_0219	Aeromonas phage PS2	GCA_009388305.2
QBZ70771.1	002914	Cluster2499_1clades	151	pETSU_190	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72077.1	002914	Cluster2499_1clades	158	N1M2_214	Klebsiella phage N1M2	GCA_010092605.1
AEV89706.1	002914	Cluster2499_1clades	151	OBP_269	Pseudomonas phage OBP	GCA_000896635.1
AYD79824.1	002915	Cluster2500_1clades	84	JA11_019	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66423.1	002915	Cluster2500_1clades	84	JA13_020	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66745.1	002915	Cluster2500_1clades	77	JA29_019	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67393.1	002915	Cluster2500_1clades	84	JA33_019	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QKE54409.1	002915	Cluster2500_1clades	163	ACSA002_0950	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QFP93264.1	002915	Cluster2500_1clades	49	-	Serratia phage PCH45	GCA_009187865.1
QGZ14527.1	002916	Cluster2501_1clades	160	HWC77_gp164	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04207.1	002916	Cluster2501_1clades	161	HWC03_gp052	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23153.1	002916	Cluster2501_1clades	160	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81049.1	002916	Cluster2501_1clades	160	Aphrodite1_0187	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47575.1	002916	Cluster2501_1clades	160	HWC35_gp181	Vibrio phage USC-1	GCA_006864065.1
BAW98390.1	002916	Cluster2501_1clades	75	FDH33_gp181	Vibrio phage pTD1	GCA_002618825.1
QGZ14525.1	002917	Cluster2502_1clades	157	HWC77_gp162	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04209.1	002917	Cluster2502_1clades	157	HWC03_gp054	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23151.1	002917	Cluster2502_1clades	160	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81050.1	002917	Cluster2502_1clades	160	Aphrodite1_0189	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47577.1	002917	Cluster2502_1clades	160	HWC35_gp183	Vibrio phage USC-1	GCA_006864065.1
BAW98392.1	002917	Cluster2502_1clades	157	FDH33_gp183	Vibrio phage pTD1	GCA_002618825.1
QCW19126.1	002918	Cluster2503_1clades	147	7t3_0611	Salmonella phage 7t3	GCA_006083215.1
AZU98363.1	002918	Cluster2503_1clades	147	CPT_Munch_423	Salmonella phage Munch	GCA_004015485.1
QIG62619.1	002918	Cluster2503_1clades	147	SEPL_006	Salmonella phage SE_PL	GCA_011067555.1
AQW88951.1	002918	Cluster2503_1clades	159	BF_0426	Serratia phage BF	GCA_002619745.1
SOK59237.1	002918	Cluster2503_1clades	154	g429	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58703.1	002918	Cluster2503_1clades	154	g426	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14529.1	002919	Cluster2504_1clades	158	HWC77_gp166	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04205.1	002919	Cluster2504_1clades	158	HWC03_gp050	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23155.1	002919	Cluster2504_1clades	159	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81051.1	002919	Cluster2504_1clades	159	Aphrodite1_0185	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47573.1	002919	Cluster2504_1clades	149	HWC35_gp179	Vibrio phage USC-1	GCA_006864065.1
BAW98388.1	002919	Cluster2504_1clades	154	FDH33_gp179	Vibrio phage pTD1	GCA_002618825.1
QGZ14371.1	002920	Cluster2505_1clades	158	HWC77_gp008	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04365.1	002920	Cluster2505_1clades	158	HWC03_gp210	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23211.1	002920	Cluster2505_1clades	158	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81052.1	002920	Cluster2505_1clades	158	Aphrodite1_0134	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47517.1	002920	Cluster2505_1clades	158	HWC35_gp123	Vibrio phage USC-1	GCA_006864065.1
BAW98336.1	002920	Cluster2505_1clades	156	FDH33_gp127	Vibrio phage pTD1	GCA_002618825.1
QGZ14439.1	002921	SIG+TM+TM+TM	157	HWC77_gp076	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04295.1	002921	SIG+TM+TM+TM	155	HWC03_gp140	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23283.1	002921	SIG+TM+TM+TM	147	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81059.1	002921	SIG+TM+TM+TM	147	Aphrodite1_0062	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47445.1	002921	SIG+TM+TM+TM	147	HWC35_gp051	Vibrio phage USC-1	GCA_006864065.1
BAW98267.1	002921	SIG+TM+TM+TM	140	FDH33_gp058	Vibrio phage pTD1	GCA_002618825.1
QDJ96581.1	002922	Ntox48	155	Xoosp13_395	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96583.1	002922	Ntox48	119	Xoosp13_397	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96584.1	002922	Ntox48	74	Xoosp13_398	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96585.1	002922	Ntox48	78	Xoosp13_399	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96586.1	002922	Ntox48	131	Xoosp13_400	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96587.1	002922	Ntox48	153	Xoosp13_401	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGZ14426.1	002923	Cluster2509_1clades	149	HWC77_gp063	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04309.1	002923	Cluster2509_1clades	149	HWC03_gp154	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23269.1	002923	Cluster2509_1clades	152	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81054.1	002923	Cluster2509_1clades	152	Aphrodite1_0076	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47459.1	002923	Cluster2509_1clades	152	HWC35_gp065	Vibrio phage USC-1	GCA_006864065.1
BAW98280.1	002923	Cluster2509_1clades	146	FDH33_gp071	Vibrio phage pTD1	GCA_002618825.1
QGZ14479.1	002924	Cluster2510_1clades	150	HWC77_gp116	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04255.1	002924	Cluster2510_1clades	150	HWC03_gp100	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23108.1	002924	Cluster2510_1clades	150	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81056.1	002924	Cluster2510_1clades	150	Aphrodite1_0023	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47408.1	002924	Cluster2510_1clades	150	HWC35_gp014	Vibrio phage USC-1	GCA_006864065.1
BAW98225.1	002924	Cluster2510_1clades	151	FDH33_gp016	Vibrio phage pTD1	GCA_002618825.1
ANM44995.1	002925	Cluster2512_1clades	120	KTN4_237	Pseudomonas phage KTN4	GCA_002607225.1
ARV76920.1	002925	Cluster2512_1clades	126	PHABIO_289	Pseudomonas phage Phabio	GCA_002624965.1
AEH03651.1	002925	Cluster2512_1clades	149	228	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94719.1	002925	Cluster2512_1clades	120	SL2_142	Pseudomonas phage SL2	GCA_002956015.1
QJB22873.1	002925	Cluster2512_1clades	120	fnug_230	Pseudomonas phage fnug	GCA_012837215.1
AAL83097.1	002925	Cluster2512_1clades	120	PHIKZ196	Pseudomonas virus phiKZ	GCA_000842965.1
QGZ14457.1	002926	Cluster2513_1clades	149	HWC77_gp094	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04277.1	002926	Cluster2513_1clades	149	HWC03_gp122	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23300.1	002926	Cluster2513_1clades	147	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81058.1	002926	Cluster2513_1clades	147	Aphrodite1_0045	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47428.1	002926	Cluster2513_1clades	147	HWC35_gp034	Vibrio phage USC-1	GCA_006864065.1
BAW98249.1	002926	Cluster2513_1clades	149	FDH33_gp040	Vibrio phage pTD1	GCA_002618825.1
QGZ14394.1	002927	Cluster2514_1clades	114	HWC77_gp031	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04342.1	002927	Cluster2514_1clades	146	HWC03_gp187	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23234.1	002927	Cluster2514_1clades	128	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81072.1	002927	Cluster2514_1clades	132	Aphrodite1_0111	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47494.1	002927	Cluster2514_1clades	128	HWC35_gp100	Vibrio phage USC-1	GCA_006864065.1
BAW98314.1	002927	Cluster2514_1clades	149	FDH33_gp105	Vibrio phage pTD1	GCA_002618825.1
QGZ14389.1	002928	Cluster2515_1clades	146	HWC77_gp026	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04347.1	002928	Cluster2515_1clades	146	HWC03_gp192	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23229.1	002928	Cluster2515_1clades	146	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81061.1	002928	Cluster2515_1clades	146	Aphrodite1_0116	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47499.1	002928	Cluster2515_1clades	146	HWC35_gp105	Vibrio phage USC-1	GCA_006864065.1
BAW98319.1	002928	Cluster2515_1clades	149	FDH33_gp110	Vibrio phage pTD1	GCA_002618825.1
QGZ14387.1	002929	Cluster2516_1clades	147	HWC77_gp024	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04349.1	002929	Cluster2516_1clades	147	HWC03_gp194	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23227.1	002929	Cluster2516_1clades	138	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81065.1	002929	Cluster2516_1clades	138	Aphrodite1_0118	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47501.1	002929	Cluster2516_1clades	145	HWC35_gp107	Vibrio phage USC-1	GCA_006864065.1
BAW98320.1	002929	Cluster2516_1clades	108	FDH33_gp111	Vibrio phage pTD1	GCA_002618825.1
QGZ14364.1	002930	Cluster2517_1clades	145	HWC77_gp001	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04372.1	002930	Cluster2517_1clades	145	HWC03_gp217	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23203.1	002930	Cluster2517_1clades	145	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81062.1	002930	Cluster2517_1clades	145	Aphrodite1_0141	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47525.1	002930	Cluster2517_1clades	145	HWC35_gp131	Vibrio phage USC-1	GCA_006864065.1
BAW98342.1	002930	Cluster2517_1clades	146	FDH33_gp133	Vibrio phage pTD1	GCA_002618825.1
AIT14407.1	002931	Cluster2518_1clades	142	PBI_121Q_517	Escherichia phage 121Q	GCA_000926855.1
QAY00545.1	002931	Cluster2518_1clades	142	Ecwhy1_266	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34736.1	002931	Cluster2518_1clades	127	ACQ29_gp056	Escherichia phage PBECO4	GCA_001041035.1
BBM62078.1	002931	Cluster2518_1clades	142	EO157G_4890	Escherichia phage SP27	GCA_008033345.1
QBO61895.1	002931	Cluster2518_1clades	142	G17_00406	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80392.1	002931	Cluster2518_1clades	142	PSLUR01_00415	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANM45074.1	002932	Cluster2520_1clades	140	KTN4_316	Pseudomonas phage KTN4	GCA_002607225.1
QBX32465.1	002932	Cluster2520_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94641.1	002932	Cluster2520_1clades	140	SL2_064	Pseudomonas phage SL2	GCA_002956015.1
QJB22949.1	002932	Cluster2520_1clades	140	fnug_306	Pseudomonas phage fnug	GCA_012837215.1
QEM42037.1	002932	Cluster2520_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83162.1	002932	Cluster2520_1clades	140	PHIKZ261	Pseudomonas virus phiKZ	GCA_000842965.1
AFC21459.1	002933	Cluster2521_1clades	140	GAP32_012	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43579.1	002933	Cluster2521_1clades	140	CBB_14	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44130.1	002933	Cluster2521_1clades	140	CBB_567	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88533.1	002933	Cluster2521_1clades	134	BF_0008	Serratia phage BF	GCA_002619745.1
SOK58815.1	002933	Cluster2521_1clades	136	g007	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58283.1	002933	Cluster2521_1clades	136	g006	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXH71034.1	002934	Cluster2522_1clades	138	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96802.1	002934	Cluster2522_1clades	137	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX97121.1	002934	Cluster2522_1clades	137	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96167.1	002934	Cluster2522_1clades	137	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96485.1	002934	Cluster2522_1clades	137	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21277.1	002934	Cluster2522_1clades	137	-	Vibrio phage vB_pir03	GCA_014319855.1
ANZ49743.1	002935	Cluster2523_1clades	119	MACHINA_105	Erwinia phage Machina	GCA_002758035.1
ANZ48669.1	002935	Cluster2523_1clades	117	CHRISDB_107	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49188.1	002935	Cluster2523_1clades	119	HUXLEY_106	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50016.1	002935	Cluster2523_1clades	119	PARSHIK_107	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
BAQ02695.1	002935	Cluster2523_1clades	138	AVU38_gp167	Ralstonia phage RSL2	GCA_001503055.1
AXF51079.1	002935	Cluster2523_1clades	108	MLDJOKPK_00065	Salmonella phage SPAsTU	GCA_003183805.1
QGZ14425.1	002936	Cluster2524_1clades	134	HWC77_gp062	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04310.1	002936	Cluster2524_1clades	134	HWC03_gp155	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23268.1	002936	Cluster2524_1clades	134	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81069.1	002936	Cluster2524_1clades	134	Aphrodite1_0077	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47460.1	002936	Cluster2524_1clades	134	HWC35_gp066	Vibrio phage USC-1	GCA_006864065.1
BAW98281.1	002936	Cluster2524_1clades	137	FDH33_gp072	Vibrio phage pTD1	GCA_002618825.1
QGZ14541.1	002937	Cluster2525_1clades	123	HWC77_gp178	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04193.1	002937	Cluster2525_1clades	123	HWC03_gp038	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23167.1	002937	Cluster2525_1clades	123	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81076.1	002937	Cluster2525_1clades	123	Aphrodite1_0175	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47562.1	002937	Cluster2525_1clades	137	HWC35_gp168	Vibrio phage USC-1	GCA_006864065.1
BAW98378.1	002937	Cluster2525_1clades	137	FDH33_gp169	Vibrio phage pTD1	GCA_002618825.1
AMR59901.1	002938	Cluster2526_1clades	132	SEGD1_254	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ48284.1	002938	Cluster2526_1clades	134	ASESINO_271	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
QKN86090.1	002938	Cluster2526_1clades	132	ACEC001_2470	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20933.1	002938	Cluster2526_1clades	132	-	Salmonella phage JN03	GCA_014319805.1
AWN09104.1	002938	Cluster2526_1clades	136	MLDJOKPK_00191	Salmonella phage SPAsTU	GCA_003183805.1
AEP84082.1	002938	Cluster2526_1clades	132	SPN3US_0249	Salmonella phage SPN3US	GCA_001042275.1
AAQ64380.1	002939	Cluster2527_1clades	134	KVP40.0310	Vibrio phage KVP40	GCA_000843785.1
QIW90695.1	002939	Cluster2527_1clades	125	GCAPEGMB_00348	Vibrio phage V07	GCA_012361095.1
QIW91103.1	002939	Cluster2527_1clades	125	COHAPHLL_00267	Vibrio phage V09	GCA_012361135.1
AJT61176.1	002939	Cluster2527_1clades	125	AVU32_gp335	Vibrio phage ValKK3	GCA_001501635.1
ALP47544.1	002939	Cluster2527_1clades	125	phiST2_0177	Vibrio phage phi-ST2	GCA_002757135.1
AFN37541.1	002939	Cluster2527_1clades	125	pp2_308	Vibriophage phi-pp2	GCA_002630725.1
QGZ14560.1	002940	Cluster2528_1clades	130	HWC77_gp197	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04173.1	002940	Cluster2528_1clades	130	HWC03_gp018	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23185.1	002940	Cluster2528_1clades	130	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81073.1	002940	Cluster2528_1clades	130	Aphrodite1_0158	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47544.1	002940	Cluster2528_1clades	130	HWC35_gp150	Vibrio phage USC-1	GCA_006864065.1
BAW98358.1	002940	Cluster2528_1clades	134	FDH33_gp149	Vibrio phage pTD1	GCA_002618825.1
QBX06803.1	002941	Cluster2529_1clades	126	BcepSaruman_390	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06804.1	002941	Cluster2529_1clades	134	BcepSaruman_391	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06805.1	002941	Cluster2529_1clades	127	BcepSaruman_392	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74772.1	002941	Cluster2529_1clades	126	BcepSauron_392	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74773.1	002941	Cluster2529_1clades	134	BcepSauron_393	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74774.1	002941	Cluster2529_1clades	127	BcepSauron_394	Burkholderia phage BcepSauron	GCA_005394215.1
ANM44771.1	002942	Cluster2530_1clades	132	KTN4_013	Pseudomonas phage KTN4	GCA_002607225.1
QBX32278.1	002942	Cluster2530_1clades	117	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03537.1	002942	Cluster2530_1clades	126	113	Pseudomonas phage PhiPA3	GCA_001502095.1
QJB22657.1	002942	Cluster2530_1clades	132	fnug_14	Pseudomonas phage fnug	GCA_012837215.1
QEM41852.1	002942	Cluster2530_1clades	128	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82913.1	002942	Cluster2530_1clades	132	PHIKZ012	Pseudomonas virus phiKZ	GCA_000842965.1
AXH72545.1	002943	Cluster2531_1clades	131	-	Myoviridae sp.	GCA_003657725.1
AXH72454.1	002943	Cluster2531_1clades	132	-	Myoviridae sp.	GCA_003657725.1
AGR48108.1	002943	Cluster2531_1clades	120	SmphiM12_476	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13654.1	002943	Cluster2531_1clades	120	PHIN3_391	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54753.1	002943	Cluster2531_1clades	120	b23_0138	Synechococcus phage B23	GCA_009745195.1
QGT54383.1	002943	Cluster2531_1clades	120	b3_0139	Synechococcus phage B3	GCA_009745215.1
QIG63271.1	002944	K1377	131	DAC16_38	Bacteroides phage DAC16	GCA_013387695.1
QIG63532.1	002944	K1377	131	DAC19_41	Bacteroides phage DAC19	GCA_013387715.1
QIG63793.1	002944	K1377	131	DAC20_40	Bacteroides phage DAC20	GCA_013387725.1
QIG64054.1	002944	K1377	131	DAC22_40	Bacteroides phage DAC22	GCA_013387735.1
QIG64315.1	002944	K1377	131	DAC23_37	Bacteroides phage DAC23	GCA_013387745.1
AKF13645.1	002944	K1377	112	PHIN3_382	Sinorhizobium phage phiN3	GCA_001501175.1
ANM44778.1	002945	Cluster2533_1clades	130	KTN4_020	Pseudomonas phage KTN4	GCA_002607225.1
QBX32353.1	002945	Cluster2533_1clades	130	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94928.1	002945	Cluster2533_1clades	130	SL2_351	Pseudomonas phage SL2	GCA_002956015.1
QJB22663.1	002945	Cluster2533_1clades	130	fnug_20	Pseudomonas phage fnug	GCA_012837215.1
QEM41927.1	002945	Cluster2533_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82918.1	002945	Cluster2533_1clades	130	PHIKZ017	Pseudomonas virus phiKZ	GCA_000842965.1
QGZ14448.1	002946	Cluster2535_1clades	129	HWC77_gp085	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04286.1	002946	Cluster2535_1clades	129	HWC03_gp131	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23291.1	002946	Cluster2535_1clades	129	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81074.1	002946	Cluster2535_1clades	129	Aphrodite1_0054	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47437.1	002946	Cluster2535_1clades	129	HWC35_gp043	Vibrio phage USC-1	GCA_006864065.1
BAW98258.1	002946	Cluster2535_1clades	126	FDH33_gp049	Vibrio phage pTD1	GCA_002618825.1
AFC21478.1	002947	Cluster2536_1clades	121	GAP32_030	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44152.1	002947	Cluster2536_1clades	128	CBB_36	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43601.1	002947	Cluster2536_1clades	128	CBB_589	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88550.1	002947	Cluster2536_1clades	106	BF_0025	Serratia phage BF	GCA_002619745.1
SOK58823.1	002947	Cluster2536_1clades	113	g015	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58290.1	002947	Cluster2536_1clades	118	g013	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01615.1	002948	Cluster2537_1clades	123	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17291.1	002948	Cluster2537_1clades	120	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00305.1	002948	Cluster2537_1clades	119	HWB28_gp247	Aeromonas phage AS-zj	GCA_002627665.1
QAX97733.1	002948	Cluster2537_1clades	119	ASswx1_87	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39319.1	002948	Cluster2537_1clades	117	CC2_025	Aeromonas phage CC2	GCA_000903495.1
ADQ53240.1	002948	Cluster2537_1clades	123	65p232	Aeromonas virus 65	GCA_000893255.1
ANM45048.1	002949	Cluster2538_1clades	97	KTN4_290	Pseudomonas phage KTN4	GCA_002607225.1
AFH14600.1	002949	Cluster2538_1clades	89	Lu11_0069A	Pseudomonas phage Lu11	GCA_000897175.1
AEH03702.1	002949	Cluster2538_1clades	85	279	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94667.1	002949	Cluster2538_1clades	97	SL2_090	Pseudomonas phage SL2	GCA_002956015.1
QJB22923.1	002949	Cluster2538_1clades	97	fnug_280	Pseudomonas phage fnug	GCA_012837215.1
AGC26352.1	002949	Cluster2538_1clades	122	PHIKZ238.1	Pseudomonas virus phiKZ	GCA_000842965.1
QAX98381.1	002950	Phage_30_8	104	ASfcp2_35	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52834.1	002950	Phage_30_8	104	PX29p115	Aeromonas phage PX29	GCA_000920195.1
ADM80093.1	002950	Phage_30_8	105	phiAS5_ORF0250	Aeromonas phage phiAS5	GCA_000887715.1
AIA64922.1	002950	Phage_30_8	120	S13_123	Cronobacter phage S13	GCA_001503575.1
ARM70765.1	002950	Phage_30_8	122	phiC120_c59	Escherichia phage phiC120	GCA_002621185.1
QHJ79018.1	002950	Phage_30_8	116	-	Myoviridae sp.	GCA_012593985.1
QGZ14441.1	002951	Cluster2540_1clades	121	HWC77_gp078	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04293.1	002951	Cluster2540_1clades	121	HWC03_gp138	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23284.1	002951	Cluster2540_1clades	121	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81078.1	002951	Cluster2540_1clades	121	Aphrodite1_0061	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47444.1	002951	Cluster2540_1clades	121	HWC35_gp050	Vibrio phage USC-1	GCA_006864065.1
BAW98265.1	002951	Cluster2540_1clades	120	FDH33_gp056	Vibrio phage pTD1	GCA_002618825.1
AFC21786.1	002952	Cluster2541_1clades	110	GAP32_336	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QHJ79005.1	002952	Cluster2541_1clades	120	-	Myoviridae sp.	GCA_012593985.1
AMM43904.1	002952	Cluster2541_1clades	110	CBB_341	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88864.1	002952	Cluster2541_1clades	108	BF_0339	Serratia phage BF	GCA_002619745.1
SOK59148.1	002952	Cluster2541_1clades	109	g340	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58614.1	002952	Cluster2541_1clades	109	g337	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14396.1	002953	SIG+TM+TM	115	HWC77_gp033	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04340.1	002953	SIG+TM+TM	115	HWC03_gp185	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23236.1	002953	SIG+TM+TM	119	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81079.1	002953	SIG+TM+TM	119	Aphrodite1_0109	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47492.1	002953	SIG+TM+TM	119	HWC35_gp098	Vibrio phage USC-1	GCA_006864065.1
BAW98312.1	002953	SIG+TM+TM	116	FDH33_gp103	Vibrio phage pTD1	GCA_002618825.1
ANM45096.1	002954	Cluster2543_1clades	118	KTN4_338	Pseudomonas phage KTN4	GCA_002607225.1
QBX32161.1	002954	Cluster2543_1clades	119	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94617.1	002954	Cluster2543_1clades	118	SL2_040	Pseudomonas phage SL2	GCA_002956015.1
QJB22972.1	002954	Cluster2543_1clades	118	fnug_329	Pseudomonas phage fnug	GCA_012837215.1
QEM41742.1	002954	Cluster2543_1clades	119	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83182.1	002954	Cluster2543_1clades	118	PHIKZ281	Pseudomonas virus phiKZ	GCA_000842965.1
QGZ14574.1	002955	Cluster2544_1clades	109	HWC77_gp211	Photobacterium phage PDCC-1	GCA_009800445.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAU04159.1	002955	Cluster2544_1clades	109	HWC03_gp004	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23199.1	002955	Cluster2544_1clades	109	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81086.1	002955	Cluster2544_1clades	109	Aphrodite1_0145	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47529.1	002955	Cluster2544_1clades	103	HWC35_gp135	Vibrio phage USC-1	GCA_006864065.1
BAW98345.1	002955	Cluster2544_1clades	118	FDH33_gp136	Vibrio phage pTD1	GCA_002618825.1
QDB70328.1	002956	Cluster2545_1clades	117	CF8_0158	Aeromonas phage CF8	GCA_006384595.2
QDJ96672.1	002956	Cluster2545_1clades	116	PS1_0161	Aeromonas phage PS1	GCA_007051165.2
QFR59306.1	002956	Cluster2545_1clades	116	PS2_0165	Aeromonas phage PS2	GCA_009388305.2
QBZ70711.1	002956	Cluster2545_1clades	116	pETSU_130	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72021.1	002956	Cluster2545_1clades	115	N1M2_158	Klebsiella phage N1M2	GCA_010092605.1
AEV89639.1	002956	Cluster2545_1clades	116	OBP_202	Pseudomonas phage OBP	GCA_000896635.1
AUE22614.1	002957	Cluster2546_1clades	111	Ah1_00073	Aeromonas phage Ah1	GCA_002957415.1
ADQ52798.1	002957	Cluster2546_1clades	109	PX29p079	Aeromonas phage PX29	GCA_000920195.1
ADM80054.1	002957	Cluster2546_1clades	110	phiAS5_ORF0211	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17741.1	002957	Cluster2546_1clades	111	Aeh1ORF080c	Aeromonas virus Aeh1	GCA_000843245.1
AIA65056.1	002957	Cluster2546_1clades	116	S13_259	Cronobacter phage S13	GCA_001503575.1
QHJ78873.1	002957	Cluster2546_1clades	109	-	Myoviridae sp.	GCA_012593985.1
AFC21481.1	002958	Cluster2547_1clades	114	GAP32_033	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44155.1	002958	Cluster2547_1clades	112	CBB_39	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43604.1	002958	Cluster2547_1clades	112	CBB_592	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88553.1	002958	Cluster2547_1clades	116	BF_0028	Serratia phage BF	GCA_002619745.1
SOK58826.1	002958	Cluster2547_1clades	116	g018	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58293.1	002958	Cluster2547_1clades	116	g016	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14430.1	002959	Cluster2548_1clades	115	HWC77_gp067	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04306.1	002959	Cluster2548_1clades	115	HWC03_gp151	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23272.1	002959	Cluster2548_1clades	116	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81081.1	002959	Cluster2548_1clades	116	Aphrodite1_0073	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47456.1	002959	Cluster2548_1clades	116	HWC35_gp062	Vibrio phage USC-1	GCA_006864065.1
BAW98278.1	002959	Cluster2548_1clades	113	FDH33_gp069	Vibrio phage pTD1	GCA_002618825.1
QGZ14386.1	002960	Cluster2549_1clades	107	HWC77_gp023	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04350.1	002960	Cluster2549_1clades	107	HWC03_gp195	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23226.1	002960	Cluster2549_1clades	116	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81082.1	002960	Cluster2549_1clades	116	Aphrodite1_0119	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47502.1	002960	Cluster2549_1clades	116	HWC35_gp108	Vibrio phage USC-1	GCA_006864065.1
BAW98321.1	002960	Cluster2549_1clades	115	FDH33_gp112	Vibrio phage pTD1	GCA_002618825.1
QGZ14494.1	002961	Cluster2550_1clades	109	HWC77_gp131	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04240.1	002961	Cluster2550_1clades	109	HWC03_gp085	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23123.1	002961	Cluster2550_1clades	109	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81084.1	002961	Cluster2550_1clades	109	Aphrodite1_0008	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47604.1	002961	Cluster2550_1clades	109	HWC35_gp210	Vibrio phage USC-1	GCA_006864065.1
BAW98210.1	002961	Cluster2550_1clades	116	FDH33_gp001	Vibrio phage pTD1	GCA_002618825.1
ANM45025.1	002962	Cluster2551_1clades	110	KTN4_267	Pseudomonas phage KTN4	GCA_002607225.1
QBX32416.1	002962	Cluster2551_1clades	116	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94689.1	002962	Cluster2551_1clades	110	SL2_112	Pseudomonas phage SL2	GCA_002956015.1
QJB22902.1	002962	Cluster2551_1clades	110	fnug_259	Pseudomonas phage fnug	GCA_012837215.1
QEM41987.1	002962	Cluster2551_1clades	116	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83123.1	002962	Cluster2551_1clades	110	PHIKZ222	Pseudomonas virus phiKZ	GCA_000842965.1
QIG65808.1	002963	Cluster2552_1clades	106	phiOC_p143	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ASV44427.1	002963	Cluster2552_1clades	64	PBI_SCTP2_412	Salicola phage SCTP-2	GCA_002625545.1
AGR48058.1	002963	Cluster2552_1clades	114	SmphiM12_426	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13237.1	002963	Cluster2552_1clades	114	PHIM19_332	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12877.1	002963	Cluster2552_1clades	114	PHIM7_332	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13600.1	002963	Cluster2552_1clades	114	PHIN3_337	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14099.1	002964	SIG+TM+TM	114	PBI_121Q_209	Escherichia phage 121Q	GCA_000926855.1
QAY00823.1	002964	SIG+TM+TM	114	Ecwhy1_550	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61781.1	002964	SIG+TM+TM	114	EO157G_1920	Escherichia phage SP27	GCA_008033345.1
QBO61600.1	002964	SIG+TM+TM	114	G17_00104	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13659.1	002964	SIG+TM+TM	114	vBEcoMphAPEC6_gp028c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80093.1	002964	SIG+TM+TM	114	PSLUR01_00116	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28854.1	002965	Cluster2554_1clades	46	AP1_0147	Aeromonas phage AP1	GCA_014183365.1
QMV29142.1	002965	Cluster2554_1clades	47	AP1_0439	Aeromonas phage AP1	GCA_014183365.1
ATI17289.1	002965	Cluster2554_1clades	114	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00307.1	002965	Cluster2554_1clades	111	HWB28_gp245	Aeromonas phage AS-zj	GCA_002627665.1
QAX97731.1	002965	Cluster2554_1clades	111	ASswx1_85	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39175.1	002965	Cluster2554_1clades	111	CC2_027	Aeromonas phage CC2	GCA_000903495.1
AIT14097.1	002966	SIG+TM+TM	112	PBI_121Q_207	Escherichia phage 121Q	GCA_000926855.1
QAY00825.1	002966	SIG+TM+TM	112	Ecwhy1_552	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34997.1	002966	SIG+TM+TM	112	ACQ29_gp317	Escherichia phage PBECO4	GCA_001041035.1
BBM61779.1	002966	SIG+TM+TM	112	EO157G_1900	Escherichia phage SP27	GCA_008033345.1
QBO61602.1	002966	SIG+TM+TM	112	G17_00106	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80091.1	002966	SIG+TM+TM	112	PSLUR01_00114	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QGZ14478.1	002967	Cluster2556_1clades	110	HWC77_gp115	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04256.1	002967	Cluster2556_1clades	110	HWC03_gp101	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23107.1	002967	Cluster2556_1clades	110	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81083.1	002967	Cluster2556_1clades	110	Aphrodite1_0024	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47409.1	002967	Cluster2556_1clades	110	HWC35_gp015	Vibrio phage USC-1	GCA_006864065.1
BAW98226.1	002967	Cluster2556_1clades	108	FDH33_gp017	Vibrio phage pTD1	GCA_002618825.1
AGH56959.1	002968	Cluster2557_1clades	80	CPXG_00156	Cyanophage P-RSM6	GCA_000906155.1
AJK27504.1	002968	Cluster2557_1clades	92	PTIM40_77	Cyanophage P-TIM40	GCA_001470935.1
AGG54315.1	002968	Cluster2557_1clades	78	CYWG_00031	Cyanophage S-SSM6b	GCA_002710425.1
AAX44477.1	002968	Cluster2557_1clades	83	PSSM2_099	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12175.1	002968	Cluster2557_1clades	83	PRTG_00017	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93622.1	002968	Cluster2557_1clades	109	AVU42_gp077	Prochlorococcus phage P-TIM68	GCA_001503075.1
ARB13881.1	002969	Cluster2558_1clades	97	Ccr2_gp006	Caulobacter phage Ccr2	GCA_002619465.1
ARB14204.1	002969	Cluster2558_1clades	97	Ccr2_gp328	Caulobacter phage Ccr2	GCA_002619465.1
AFU87874.1	002969	Cluster2558_1clades	96	CcrColossus_gp004	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68543.1	002969	Cluster2558_1clades	97	CcrPW_gp004	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68993.1	002969	Cluster2558_1clades	97	CcrPW_gp454	Caulobacter phage CcrPW	GCA_003443275.1
AXH72672.1	002969	Cluster2558_1clades	109	-	Myoviridae sp.	GCA_003657725.1
AXG67318.1	002970	Cluster2559_1clades	105	AD1_274	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80070.1	002970	Cluster2559_1clades	102	JA11_265	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66671.1	002970	Cluster2559_1clades	102	JA13_268	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67640.1	002970	Cluster2559_1clades	102	JA33_266	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08543.1	002970	Cluster2559_1clades	105	Alexandra_287	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58917.1	002970	Cluster2559_1clades	108	Y3_277	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QGZ14431.1	002971	Cluster2560_1clades	101	HWC77_gp068	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04305.1	002971	Cluster2560_1clades	101	HWC03_gp150	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23273.1	002971	Cluster2560_1clades	108	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81087.1	002971	Cluster2560_1clades	108	Aphrodite1_0072	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47455.1	002971	Cluster2560_1clades	108	HWC35_gp061	Vibrio phage USC-1	GCA_006864065.1
BAW98277.1	002971	Cluster2560_1clades	56	FDH33_gp068	Vibrio phage pTD1	GCA_002618825.1
QGZ14575.1	002972	Cluster2561_1clades	108	HWC77_gp212	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04158.1	002972	Cluster2561_1clades	108	HWC03_gp003	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23200.1	002972	Cluster2561_1clades	108	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81088.1	002972	Cluster2561_1clades	108	Aphrodite1_0144	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47528.1	002972	Cluster2561_1clades	108	HWC35_gp134	Vibrio phage USC-1	GCA_006864065.1
BAW98344.1	002972	Cluster2561_1clades	68	FDH33_gp135	Vibrio phage pTD1	GCA_002618825.1
AGB06847.1	002973	Cluster2562_1clades	107	CF80_gp060	Vibrio phage VH7D	GCA_000914495.1
QBX06298.1	002973	Cluster2562_1clades	100	ValB1HC_345	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60927.1	002973	Cluster2562_1clades	107	AVU32_gp086	Vibrio phage ValKK3	GCA_001501635.1
ALP47302.1	002973	Cluster2562_1clades	66	phiGrn1_0286	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47683.1	002973	Cluster2562_1clades	66	phiST2_0044	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54925.1	002973	Cluster2562_1clades	107	vBValMR10Z_385	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QCW18589.1	002974	MAPKK1_Int	96	7t3_068	Salmonella phage 7t3	GCA_006083215.1
AZU98417.1	002974	MAPKK1_Int	96	CPT_Munch_485	Salmonella phage Munch	GCA_004015485.1
QIG63096.1	002974	MAPKK1_Int	96	SEPL_483	Salmonella phage SE_PL	GCA_011067555.1
AQW89042.1	002974	MAPKK1_Int	106	BF_0517	Serratia phage BF	GCA_002619745.1
SOK59318.1	002974	MAPKK1_Int	103	g510	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58780.1	002974	MAPKK1_Int	103	g503	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14489.1	002975	Cluster2564_1clades	98	HWC77_gp126	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04245.1	002975	Cluster2564_1clades	83	HWC03_gp090	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23118.1	002975	Cluster2564_1clades	98	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81094.1	002975	Cluster2564_1clades	98	Aphrodite1_0013	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47398.1	002975	Cluster2564_1clades	98	HWC35_gp004	Vibrio phage USC-1	GCA_006864065.1
BAW98215.1	002975	Cluster2564_1clades	106	FDH33_gp006	Vibrio phage pTD1	GCA_002618825.1

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QGZ14460.1	002976	Cluster2565_1clades	102	HWC77_gp097	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04274.1	002976	Cluster2565_1clades	102	HWC03_gp119	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23303.1	002976	Cluster2565_1clades	100	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81092.1	002976	Cluster2565_1clades	100	Aphrodite1_0042	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47425.1	002976	Cluster2565_1clades	100	HWC35_gp031	Vibrio phage USC-1	GCA_006864065.1
BAW98246.1	002976	Cluster2565_1clades	106	FDH33_gp037	Vibrio phage pTD1	GCA_002618825.1
AGB06851.1	002977	Cluster2566_1clades	105	CF80_gp064	Vibrio phage VH7D	GCA_000914495.1
QBX06294.1	002977	Cluster2566_1clades	105	ValB1HC_341	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60924.1	002977	Cluster2566_1clades	105	AVU32_gp083	Vibrio phage ValKK3	GCA_001501635.1
ALP47191.1	002977	Cluster2566_1clades	105	phiGrn1_0290	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47582.1	002977	Cluster2566_1clades	105	phiST2_0047	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54921.1	002977	Cluster2566_1clades	105	vBValMR10Z_381	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QMV29095.1	002978	Cluster2567_1clades	102	AP1_0388	Aeromonas phage AP1	GCA_014183365.1
ATI17293.1	002978	Cluster2567_1clades	102	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00303.1	002978	Cluster2567_1clades	102	HWB28_gp249	Aeromonas phage AS-zj	GCA_002627665.1
QAX97735.1	002978	Cluster2567_1clades	99	ASswx1_89	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01420.1	002978	Cluster2567_1clades	103	ASwh1_361	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39172.1	002978	Cluster2567_1clades	101	CC2_022	Aeromonas phage CC2	GCA_000903495.1
AIT14266.1	002979	Cluster2568_1clades	102	PBI_121Q_376	Escherichia phage 121Q	GCA_000926855.1
AGC34866.1	002979	Cluster2568_1clades	102	ACQ29_gp186	Escherichia phage PBECO4	GCA_001041035.1
AXC36975.1	002979	Cluster2568_1clades	102	-	Escherichia phage UB	GCA_003341455.1
QBO62038.1	002979	Cluster2568_1clades	102	G17_00549	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14059.1	002979	Cluster2568_1clades	102	vBEcoMphAPEC6_gp436c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80255.1	002979	Cluster2568_1clades	102	PSLUR01_00278	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AYD80032.1	002980	Cluster2569_1clades	82	JA11_227	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66631.1	002980	Cluster2569_1clades	82	JA13_228	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66955.1	002980	Cluster2569_1clades	82	JA29_229	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67602.1	002980	Cluster2569_1clades	82	JA33_228	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08510.1	002980	Cluster2569_1clades	86	Alexandra_253	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28807.1	002980	Cluster2569_1clades	101	YOLOSWAG_241	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
APU01798.1	002981	Cluster2570_1clades	95	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17507.1	002981	Cluster2570_1clades	94	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00490.1	002981	Cluster2570_1clades	94	HWB28_gp062	Aeromonas phage AS-zj	GCA_002627665.1
QAX97946.1	002981	Cluster2570_1clades	94	ASswx1_304	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01202.1	002981	Cluster2570_1clades	101	ASwh1_137	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53442.1	002981	Cluster2570_1clades	95	65p436	Aeromonas virus 65	GCA_000893255.1
QGZ14542.1	002982	Cluster2571_1clades	99	HWC77_gp179	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04192.1	002982	Cluster2571_1clades	99	HWC03_gp037	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23168.1	002982	Cluster2571_1clades	99	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81093.1	002982	Cluster2571_1clades	99	Aphrodite1_0174	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47561.1	002982	Cluster2571_1clades	99	HWC35_gp167	Vibrio phage USC-1	GCA_006864065.1
BAW98377.1	002982	Cluster2571_1clades	75	FDH33_gp168	Vibrio phage pTD1	GCA_002618825.1
AIT13973.1	002983	Cluster2572_1clades	53	PBI_121Q_76	Escherichia phage 121Q	GCA_000926855.1
QAY00364.1	002983	Cluster2572_1clades	81	Ecwhy1_83	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61665.1	002983	Cluster2572_1clades	53	EO157G_0760	Escherichia phage SP27	GCA_008033345.1
QBO61719.1	002983	Cluster2572_1clades	53	G17_00230	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13766.1	002983	Cluster2572_1clades	99	vBEcoMphAPEC6_gp137c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80567.1	002983	Cluster2572_1clades	53	PSLUR01_00590	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AOO14216.1	002984	Cluster2573_1clades	98	Sn110110_022	Cyanophage S-RIM14	GCA_002599065.1
AOO14868.1	002984	Cluster2573_1clades	98	W1230910_022	Cyanophage S-RIM14	GCA_002599125.1
AGG54467.1	002984	Cluster2573_1clades	97	CYWG_00183	Cyanophage S-SSM6b	GCA_002710425.1
AIX30640.1	002984	Cluster2573_1clades	96	Syn7803US37_163	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23085.1	002984	Cluster2573_1clades	95	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50576.1	002984	Cluster2573_1clades	95	-	Synechococcus phage S-B43	GCA_006869725.1
QMV29094.1	002985	Cluster2574_1clades	93	AP1_0387	Aeromonas phage AP1	GCA_014183365.1
ATI17290.1	002985	Cluster2574_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00306.1	002985	Cluster2574_1clades	93	HWB28_gp246	Aeromonas phage AS-zj	GCA_002627665.1
QAX97732.1	002985	Cluster2574_1clades	93	ASswx1_86	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01422.1	002985	Cluster2574_1clades	98	ASwh1_363	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39174.1	002985	Cluster2574_1clades	93	CC2_026	Aeromonas phage CC2	GCA_000903495.1
ANM45119.1	002986	Cluster2575_1clades	95	KTN4_361	Pseudomonas phage KTN4	GCA_002607225.1
QBX32542.1	002986	Cluster2575_1clades	95	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03788.1	002986	Cluster2575_1clades	97	365	Pseudomonas phage PhiPA3	GCA_001502095.1
QJB22996.1	002986	Cluster2575_1clades	95	fnug_353	Pseudomonas phage fnug	GCA_012837215.1
QEM42113.1	002986	Cluster2575_1clades	95	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26367.1	002986	Cluster2575_1clades	95	PHIKZ299.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGB06875.1	002987	Cluster2576_1clades	97	CF80_gp088	Vibrio phage VH7D	GCA_000914495.1
QBX06271.1	002987	Cluster2576_1clades	97	ValB1HC_318	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60897.1	002987	Cluster2576_1clades	97	AVU32_gp056	Vibrio phage ValKK3	GCA_001501635.1
ALP47213.1	002987	Cluster2576_1clades	97	phiGrn1_0314	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47604.1	002987	Cluster2576_1clades	97	phiST2_0070	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54898.1	002987	Cluster2576_1clades	97	vBValMR10Z_358	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AGR47920.2	002988	Cluster2577_1clades	57	SmphiM12_288	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47921.2	002988	Cluster2577_1clades	48	SmphiM12_289	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13123.1	002988	Cluster2577_1clades	57	PHIM19_218	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13124.1	002988	Cluster2577_1clades	48	PHIM19_219	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12763.1	002988	Cluster2577_1clades	97	PHIM7_218	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13493.2	002988	Cluster2577_1clades	97	PHIN3_230	Sinorhizobium phage phiN3	GCA_001501175.1
QGZ14485.1	002989	Cluster2578_1clades	95	HWC77_gp122	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04249.1	002989	Cluster2578_1clades	95	HWC03_gp094	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23114.1	002989	Cluster2578_1clades	96	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81095.1	002989	Cluster2578_1clades	96	Aphrodite1_0017	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47402.1	002989	Cluster2578_1clades	96	HWC35_gp008	Vibrio phage USC-1	GCA_006864065.1
BAW98219.1	002989	Cluster2578_1clades	96	FDH33_gp010	Vibrio phage pTD1	GCA_002618825.1
QMV28827.1	002990	Cluster2579_1clades	91	AP1_0120	Aeromonas phage AP1	GCA_014183365.1
ATI17601.1	002990	Cluster2579_1clades	91	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00395.1	002990	Cluster2579_1clades	91	HWB28_gp157	Aeromonas phage AS-zj	GCA_002627665.1
QAX98040.1	002990	Cluster2579_1clades	91	ASswx1_400	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01107.1	002990	Cluster2579_1clades	92	ASwh1_39	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39152.1	002990	Cluster2579_1clades	95	CC2_130	Aeromonas phage CC2	GCA_000903495.1
ANM44935.1	002991	Cluster2580_1clades	75	KTN4_177	Pseudomonas phage KTN4	GCA_002607225.1
ARV77312.1	002991	Cluster2580_1clades	84	NOXIFER_143	Pseudomonas phage Noxifer	GCA_002625005.1
QBJ02721.1	002991	Cluster2580_1clades	65	PSA21_195	Pseudomonas phage Psa21	GCA_004340405.1
ATN94779.1	002991	Cluster2580_1clades	81	SL2_202	Pseudomonas phage SL2	GCA_002956015.1
QJB22813.1	002991	Cluster2580_1clades	95	fnug_170	Pseudomonas phage fnug	GCA_012837215.1
AGC26335.1	002991	Cluster2580_1clades	95	PHIKZ141.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGH56848.1	002992	TM	91	CPXG_00045	Cyanophage P-RSM6	GCA_000906155.1
AJK27602.1	002992	TM	82	PTIM40_180	Cyanophage P-TIM40	GCA_001470935.1
AGH07585.1	002992	TM	94	CYVG_00141	Cyanophage S-SSM6a	GCA_002710385.1
AGN12423.1	002992	TM	54	PRTG_00272	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93630.1	002992	TM	65	AVU42_gp134	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW23005.1	002992	TM	67	-	Synechococcus phage S-B05	GCA_006083695.1
APU01540.1	002993	Cluster2582_1clades	91	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29052.1	002993	Cluster2582_1clades	84	AP1_0345	Aeromonas phage AP1	GCA_014183365.1
ATI17361.1	002993	Cluster2582_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00233.1	002993	Cluster2582_1clades	93	HWB28_gp319	Aeromonas phage AS-zj	GCA_002627665.1
AFN39441.1	002993	Cluster2582_1clades	84	CC2_377	Aeromonas phage CC2	GCA_000903495.1
ADQ53162.1	002993	Cluster2582_1clades	91	65p154	Aeromonas virus 65	GCA_000893255.1
AUZ95211.1	002994	Cluster2583_1clades	74	FDI40_gp452	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65958.1	002994	Cluster2583_1clades	92	phiOC_p316	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47994.1	002994	Cluster2583_1clades	92	SmphiM12_362	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13181.1	002994	Cluster2583_1clades	92	PHIM19_276	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12820.1	002994	Cluster2583_1clades	92	PHIM7_275	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13543.1	002994	Cluster2583_1clades	92	PHIN3_280	Sinorhizobium phage phiN3	GCA_001501175.1
AXQ69448.1	002995	Cluster2584_1clades	92	CcrBL9_gp424	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69998.1	002995	Cluster2584_1clades	92	CcrSC_gp416	Caulobacter phage CcrSC	GCA_003443315.1
AYD81366.1	002995	Cluster2584_1clades	74	SEA_JUSTBECAUSE_211	Streptomyces phage JustBecause	GCA_003613775.1
QJD53769.1	002995	Cluster2584_1clades	74	SEA_KELA_209	Streptomyces phage Kela	GCA_012934305.1
QBZ72098.1	002995	Cluster2584_1clades	78	SEA_KRADAL_212	Streptomyces phage Kradal	GCA_004799925.1
AXH66359.1	002995	Cluster2584_1clades	78	SEA_SATIS_210	Streptomyces phage Satis	GCA_003366315.1
QGZ14456.1	002996	Cluster2585_1clades	91	HWC77_gp093	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04278.1	002996	Cluster2585_1clades	91	HWC03_gp123	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23299.1	002996	Cluster2585_1clades	90	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81096.1	002996	Cluster2585_1clades	90	Aphrodite1_0046	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47429.1	002996	Cluster2585_1clades	90	HWC35_gp035	Vibrio phage USC-1	GCA_006864065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAW98250.1	002996	Cluster2585_1clades	81	FDH33_gp041	Vibrio phage pTD1	GCA_002618825.1
QMV28860.1	002997	Cluster2586_1clades	89	AP1_0153	Aeromonas phage AP1	GCA_014183365.1
ATI17303.1	002997	Cluster2586_1clades	89	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00291.1	002997	Cluster2586_1clades	89	HWB28_gp261	Aeromonas phage AS-zj	GCA_002627665.1
QAX97746.1	002997	Cluster2586_1clades	89	ASswx1_101	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39165.1	002997	Cluster2586_1clades	89	CC2_008	Aeromonas phage CC2	GCA_000903495.1
ANS06138.1	002997	Cluster2586_1clades	84	ABCD_0125	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
QMV28840.1	002998	Cluster2587_1clades	88	AP1_0133	Aeromonas phage AP1	GCA_014183365.1
ATI17272.1	002998	Cluster2587_1clades	87	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00321.1	002998	Cluster2587_1clades	88	HWB28_gp231	Aeromonas phage AS-zj	GCA_002627665.1
QAX97713.1	002998	Cluster2587_1clades	87	ASswx1_67	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01454.1	002998	Cluster2587_1clades	87	ASwh1_395	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39185.1	002998	Cluster2587_1clades	87	CC2_044	Aeromonas phage CC2	GCA_000903495.1
QDB70306.1	002999	Cluster2588_1clades	87	CF8_0138	Aeromonas phage CF8	GCA_006384595.2
QDJ96900.1	002999	Cluster2588_1clades	86	PS1_0141	Aeromonas phage PS1	GCA_007051165.2
QFR59530.1	002999	Cluster2588_1clades	86	PS2_0139	Aeromonas phage PS2	GCA_009388305.2
QBZ70671.1	002999	Cluster2588_1clades	88	pETSU_090	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71986.1	002999	Cluster2588_1clades	87	N1M2_123	Klebsiella phage N1M2	GCA_010092605.1
AEV89587.1	002999	Cluster2588_1clades	87	OBP_150	Pseudomonas phage OBP	GCA_000896635.1
AFC21462.1	003000	Cluster2589_1clades	84	GAP32_015	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44135.1	003000	Cluster2589_1clades	84	CBB_19	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43584.1	003000	Cluster2589_1clades	84	CBB_572	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88536.1	003000	Cluster2589_1clades	87	BF_0011	Serratia phage BF	GCA_002619745.1
SOK58817.1	003000	Cluster2589_1clades	86	g009	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58285.1	003000	Cluster2589_1clades	86	g008	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14364.1	003001	SIG+TM	86	PBI_121Q_474	Escherichia phage 121Q	GCA_000926855.1
QAY00584.1	003001	SIG+TM	86	Ecwhy1_305	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM62034.1	003001	SIG+TM	86	EO157G_4450	Escherichia phage SP27	GCA_008033345.1
AXC36892.1	003001	SIG+TM	86	-	Escherichia phage UB	GCA_003341455.1
QBO61941.1	003001	SIG+TM	86	G17_00452	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80350.1	003001	SIG+TM	86	PSLUR01_00373	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28998.1	003002	Cluster2591_1clades	85	AP1_0291	Aeromonas phage AP1	GCA_014183365.1
ATI17509.1	003002	Cluster2591_1clades	85	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00487.1	003002	Cluster2591_1clades	85	HWB28_gp065	Aeromonas phage AS-zj	GCA_002627665.1
QAX97949.1	003002	Cluster2591_1clades	85	ASswx1_307	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01199.1	003002	Cluster2591_1clades	85	ASwh1_134	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39264.1	003002	Cluster2591_1clades	85	CC2_225	Aeromonas phage CC2	GCA_000903495.1
QAY00711.1	003003	Cluster2592_1clades	85	Ecwhy1_436	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34898.1	003003	Cluster2592_1clades	63	ACQ29_gp218	Escherichia phage PBECO4	GCA_001041035.1
BBM61900.1	003003	Cluster2592_1clades	80	EO157G_3110	Escherichia phage SP27	GCA_008033345.1
QBO62081.1	003003	Cluster2592_1clades	80	G17_00592	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14095.1	003003	Cluster2592_1clades	80	vBEcoMphAPEC6_gp472c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80213.1	003003	Cluster2592_1clades	80	PSLUR01_00236	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANM44765.1	003004	Cluster2593_1clades	78	KTN4_007	Pseudomonas phage KTN4	GCA_002607225.1
QBX32511.1	003004	Cluster2593_1clades	78	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03541.1	003004	Cluster2593_1clades	78	117	Pseudomonas phage PhiPA3	GCA_001502095.1
QJB22650.1	003004	Cluster2593_1clades	85	fnug_7	Pseudomonas phage fnug	GCA_012837215.1
QEM42084.1	003004	Cluster2593_1clades	78	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82908.1	003004	Cluster2593_1clades	78	PHIKZ007	Pseudomonas virus phiKZ	GCA_000842965.1
AJK27544.1	003005	Cluster2594_1clades	70	PTIM40_117	Cyanophage P-TIM40	GCA_001470935.1
AMO43199.1	003005	Cluster2594_1clades	50	R1080702_190	Cyanophage S-RIM32	GCA_001754165.1
AGG54411.1	003005	Cluster2594_1clades	69	CYWG_00127	Cyanophage S-SSM6b	GCA_002710425.1
AIX30733.1	003005	Cluster2594_1clades	84	Syn7803US37_256	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW23036.1	003005	Cluster2594_1clades	69	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70184.1	003005	Cluster2594_1clades	70	SynMITS9220M01_176	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ANM44897.1	003006	Cluster2595_1clades	83	KTN4_139	Pseudomonas phage KTN4	GCA_002607225.1
AEH03544.1	003006	Cluster2595_1clades	70	120	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02679.1	003006	Cluster2595_1clades	69	PSA21_152	Pseudomonas phage Psa21	GCA_004340405.1
ATN94816.1	003006	Cluster2595_1clades	83	SL2_239	Pseudomonas phage SL2	GCA_002956015.1
QJB22775.1	003006	Cluster2595_1clades	83	fnug_132	Pseudomonas phage fnug	GCA_012837215.1
AGC26327.1	003006	Cluster2595_1clades	83	PHIKZ109.1	Pseudomonas virus phiKZ	GCA_000842965.1
AFC21541.1	003007	Cluster2596_1clades	81	GAP32_093	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
ARM70947.1	003007	Cluster2596_1clades	78	phiC120_c242	Escherichia phage phiC120	GCA_002621185.1
AMM43660.1	003007	Cluster2596_1clades	81	CBB_95	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88611.1	003007	Cluster2596_1clades	83	BF_0086	Serratia phage BF	GCA_002619745.1
SOK58888.1	003007	Cluster2596_1clades	76	g080	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58351.1	003007	Cluster2596_1clades	76	g074	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01755.1	003008	SFII-RAD3	79	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17541.1	003008	SFII-RAD3	83	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00456.1	003008	SFII-RAD3	83	HWB28_gp096	Aeromonas phage AS-zj	GCA_002627665.1
QAX97982.1	003008	SFII-RAD3	83	ASswx1_341	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01158.1	003008	SFII-RAD3	83	ASwh1_92	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53397.1	003008	SFII-RAD3	79	65p390	Aeromonas virus 65	GCA_000893255.1
AIT14222.1	003009	Cluster2598_1clades	71	PBI_121Q_332	Escherichia phage 121Q	GCA_000926855.1
QAY00715.1	003009	Cluster2598_1clades	83	Ecwhy1_440	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61897.1	003009	Cluster2598_1clades	83	EO157G_3080	Escherichia phage SP27	GCA_008033345.1
QBO62085.1	003009	Cluster2598_1clades	71	G17_00596	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14098.1	003009	Cluster2598_1clades	71	vBEcoMphAPEC6_gp475c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80209.1	003009	Cluster2598_1clades	71	PSLUR01_00232	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64180.1	003010	SIG+TM	82	KVP40.0109	Vibrio phage KVP40	GCA_000843785.1
QIW90503.1	003010	SIG+TM	77	GCAPEGMB_00156	Vibrio phage V07	GCA_012361095.1
QIW90926.1	003010	SIG+TM	77	COHAPHLL_00063	Vibrio phage V09	GCA_012361135.1
QHJ74291.1	003010	SIG+TM	62	VH12019_00372	Vibrio phage VH1_2019	GCA_009931825.1
AGN30159.1	003010	SIG+TM	77	VPFG_00157	Vibrio phage nt-1	GCA_000910195.2
AFN37338.1	003010	SIG+TM	77	pp2_105	Vibriophage phi-pp2	GCA_002630725.1
AIT14220.1	003011	Cluster2600_1clades	76	PBI_121Q_330	Escherichia phage 121Q	GCA_000926855.1
QAY00717.1	003011	Cluster2600_1clades	82	Ecwhy1_442	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61894.1	003011	Cluster2600_1clades	76	EO157G_3050	Escherichia phage SP27	GCA_008033345.1
QBO62088.1	003011	Cluster2600_1clades	76	G17_00599	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14101.1	003011	Cluster2600_1clades	76	vBEcoMphAPEC6_gp478c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80206.1	003011	Cluster2600_1clades	76	PSLUR01_00229	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64335.1	003012	Cluster2601_1clades	80	KVP40.0266	Vibrio phage KVP40	GCA_000843785.1
QIW90650.1	003012	Cluster2601_1clades	80	GCAPEGMB_00303	Vibrio phage V07	GCA_012361095.1
QIW91149.1	003012	Cluster2601_1clades	80	COHAPHLL_00313	Vibrio phage V09	GCA_012361135.1
QHJ74445.1	003012	Cluster2601_1clades	80	VH12019_00118	Vibrio phage VH1_2019	GCA_009931825.1
AGN30311.1	003012	Cluster2601_1clades	81	VPFG_00313	Vibrio phage nt-1	GCA_000910195.2
AFN37495.1	003012	Cluster2601_1clades	80	pp2_262	Vibriophage phi-pp2	GCA_002630725.1
AAQ64269.1	003013	Cluster2602_1clades	80	KVP40.0200	Vibrio phage KVP40	GCA_000843785.1
QIW90586.1	003013	Cluster2602_1clades	80	GCAPEGMB_00239	Vibrio phage V07	GCA_012361095.1
QIW91213.1	003013	Cluster2602_1clades	80	COHAPHLL_00377	Vibrio phage V09	GCA_012361135.1
QHJ74383.1	003013	Cluster2602_1clades	80	VH12019_00056	Vibrio phage VH1_2019	GCA_009931825.1
AGN30260.1	003013	Cluster2602_1clades	80	VPFG_00261	Vibrio phage nt-1	GCA_000910195.2
AFN37430.1	003013	Cluster2602_1clades	80	pp2_197	Vibriophage phi-pp2	GCA_002630725.1
AYD81424.1	003014	Cluster2603_1clades	77	SEA_JUSTBECAUSE_269	Streptomyces phage JustBecause	GCA_003613775.1
QJD53829.1	003014	Cluster2603_1clades	77	SEA_KELA_269	Streptomyces phage Kela	GCA_012934305.1
QBZ72155.1	003014	Cluster2603_1clades	76	SEA_KRADAL_269	Streptomyces phage Kradal	GCA_004799925.1
QBZ72156.1	003014	Cluster2603_1clades	80	SEA_KRADAL_270	Streptomyces phage Kradal	GCA_004799925.1
AXH66418.1	003014	Cluster2603_1clades	76	SEA_SATIS_269	Streptomyces phage Satis	GCA_003366315.1
AXH66419.1	003014	Cluster2603_1clades	80	SEA_SATIS_270	Streptomyces phage Satis	GCA_003366315.1
AAX44471.1	003015	Cluster2604_1clades	76	PSSM2_093	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12181.1	003015	Cluster2604_1clades	76	PRTG_00023	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93592.1	003015	Cluster2604_1clades	77	AVU42_gp041	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22999.1	003015	Cluster2604_1clades	77	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50650.1	003015	Cluster2604_1clades	77	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70062.1	003015	Cluster2604_1clades	80	SynMITS9220M01_049	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ANM45120.1	003016	Cluster2605_1clades	73	KTN4_362	Pseudomonas phage KTN4	GCA_002607225.1
QBX32543.1	003016	Cluster2605_1clades	73	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03787.1	003016	Cluster2605_1clades	79	364	Pseudomonas phage PhiPA3	GCA_001502095.1
QJB22997.1	003016	Cluster2605_1clades	73	fnug_354	Pseudomonas phage fnug	GCA_012837215.1
QEM42114.1	003016	Cluster2605_1clades	73	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83201.2	003016	Cluster2605_1clades	73	PHIKZ300	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14253.1	003017	Cluster2606_1clades	78	PBI_121Q_363	Escherichia phage 121Q	GCA_000926855.1
QAY00681.1	003017	Cluster2606_1clades	71	Ecwhy1_406	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61931.1	003017	Cluster2606_1clades	69	EO157G_3420	Escherichia phage SP27	GCA_008033345.1
QBO62051.1	003017	Cluster2606_1clades	74	G17_00562	Escherichia phage vB_EcoM_G17	GCA_004521135.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDF14071.1	003017	Cluster2606_1clades	74	vBEcoMphAPEC6_gp448c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80243.1	003017	Cluster2606_1clades	74	PSLUR01_00266	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28908.1	003018	Cluster2607_1clades	78	AP1_0201	Aeromonas phage AP1	GCA_014183365.1
ATI17587.1	003018	Cluster2607_1clades	78	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00410.1	003018	Cluster2607_1clades	78	HWB28_gp142	Aeromonas phage AS-zj	GCA_002627665.1
QAX98026.1	003018	Cluster2607_1clades	78	ASswx1_386	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01117.1	003018	Cluster2607_1clades	66	ASwh1_49	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39235.1	003018	Cluster2607_1clades	57	CC2_146	Aeromonas phage CC2	GCA_000903495.1
AFC21901.1	003019	Cluster2608_1clades	73	GAP32_446	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44030.1	003019	Cluster2608_1clades	72	CBB_467	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88986.1	003019	Cluster2608_1clades	75	BF_0461	Serratia phage BF	GCA_002619745.1
BBA65505.1	003019	Cluster2608_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1
SOK59267.1	003019	Cluster2608_1clades	76	g459	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58732.1	003019	Cluster2608_1clades	73	g455	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28858.1	003020	Cluster2609_1clades	68	AP1_0151	Aeromonas phage AP1	GCA_014183365.1
ATI17305.1	003020	Cluster2609_1clades	68	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00289.1	003020	Cluster2609_1clades	68	HWB28_gp263	Aeromonas phage AS-zj	GCA_002627665.1
QAX97748.1	003020	Cluster2609_1clades	68	ASswx1_103	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01408.1	003020	Cluster2609_1clades	77	ASwh1_349	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39163.1	003020	Cluster2609_1clades	68	CC2_006	Aeromonas phage CC2	GCA_000903495.1
AJK27488.1	003021	Cluster2610_1clades	64	PTIM40_62	Cyanophage P-TIM40	GCA_001470935.1
AGH07484.1	003021	Cluster2610_1clades	76	CYVG_00040	Cyanophage S-SSM6a	GCA_002710385.1
AGH26302.1	003021	Cluster2610_1clades	76	CPMG_00202	Prochlorococcus phage MED4-213	GCA_000904535.1
AIX30522.1	003021	Cluster2610_1clades	65	Syn7803US37_45	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76106.1	003021	Cluster2610_1clades	70	PBI_BELLAMY_61	Synechococcus phage Bellamy	GCA_002627525.1
QJT70240.1	003021	Cluster2610_1clades	76	SynMITS9220M01_234	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14225.1	003022	Cluster2611_1clades	73	PBI_121Q_335	Escherichia phage 121Q	GCA_000926855.1
BBM61901.1	003022	Cluster2611_1clades	76	EO157G_3120	Escherichia phage SP27	GCA_008033345.1
AXC37004.1	003022	Cluster2611_1clades	69	-	Escherichia phage UB	GCA_003341455.1
QBO62080.1	003022	Cluster2611_1clades	76	G17_00591	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14094.1	003022	Cluster2611_1clades	76	vBEcoMphAPEC6_gp471c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80214.1	003022	Cluster2611_1clades	76	PSLUR01_00237	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28975.1	003023	Cluster2612_1clades	65	AP1_0268	Aeromonas phage AP1	GCA_014183365.1
ATI17526.1	003023	Cluster2612_1clades	65	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00470.1	003023	Cluster2612_1clades	65	HWB28_gp082	Aeromonas phage AS-zj	GCA_002627665.1
QAX97968.1	003023	Cluster2612_1clades	65	ASswx1_326	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01173.1	003023	Cluster2612_1clades	76	ASwh1_107	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39258.1	003023	Cluster2612_1clades	65	CC2_207	Aeromonas phage CC2	GCA_000903495.1
QMV28859.1	003024	Cluster2613_1clades	75	AP1_0152	Aeromonas phage AP1	GCA_014183365.1
ATI17304.1	003024	Cluster2613_1clades	75	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00290.1	003024	Cluster2613_1clades	75	HWB28_gp262	Aeromonas phage AS-zj	GCA_002627665.1
QAX97747.1	003024	Cluster2613_1clades	75	ASswx1_102	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01409.1	003024	Cluster2613_1clades	69	ASwh1_350	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39164.1	003024	Cluster2613_1clades	75	CC2_007	Aeromonas phage CC2	GCA_000903495.1
QMV28820.1	003025	Cluster2614_1clades	75	AP1_0113	Aeromonas phage AP1	GCA_014183365.1
ATI17606.1	003025	Cluster2614_1clades	75	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00390.1	003025	Cluster2614_1clades	75	HWB28_gp162	Aeromonas phage AS-zj	GCA_002627665.1
QAX98047.1	003025	Cluster2614_1clades	75	ASswx1_407	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01098.1	003025	Cluster2614_1clades	72	ASwh1_30	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39494.1	003025	Cluster2614_1clades	75	CC2_123	Aeromonas phage CC2	GCA_000903495.1
ANM44815.1	003026	Cluster2615_1clades	75	KTN4_057	Pseudomonas phage KTN4	GCA_002607225.1
QBX32187.1	003026	Cluster2615_1clades	74	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94896.1	003026	Cluster2615_1clades	75	SL2_319	Pseudomonas phage SL2	GCA_002956015.1
QJB22694.1	003026	Cluster2615_1clades	75	fnug_51	Pseudomonas phage fnug	GCA_012837215.1
QEM41765.1	003026	Cluster2615_1clades	74	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26312.1	003026	Cluster2615_1clades	75	PHIKZ041.3	Pseudomonas virus phiKZ	GCA_000842965.1
AAX44458.1	003027	Cluster2616_1clades	64	PSSM2_080	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12195.1	003027	Cluster2616_1clades	75	PRTG_00037	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93603.1	003027	Cluster2616_1clades	67	AVU42_gp058	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22847.1	003027	Cluster2616_1clades	67	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50705.1	003027	Cluster2616_1clades	67	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70081.1	003027	Cluster2616_1clades	68	SynMITS9220M01_068	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14139.1	003028	Cluster2617_1clades	75	PBI_121Q_249	Escherichia phage 121Q	GCA_000926855.1
QAY00788.1	003028	Cluster2617_1clades	75	Ecwhy1_515	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61815.1	003028	Cluster2617_1clades	75	EO157G_2260	Escherichia phage SP27	GCA_008033345.1
QBO61565.1	003028	Cluster2617_1clades	75	G17_00069	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14171.1	003028	Cluster2617_1clades	75	vBEcoMphAPEC6_gp548c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80129.1	003028	Cluster2617_1clades	75	PSLUR01_00152	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGH56914.1	003029	Cluster2618_1clades	55	CPXG_00111	Cyanophage P-RSM6	GCA_000906155.1
AGH07512.1	003029	Cluster2618_1clades	56	CYVG_00068	Cyanophage S-SSM6a	GCA_002710385.1
AGH26232.1	003029	Cluster2618_1clades	53	CPMG_00131	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44606.1	003029	Cluster2618_1clades	74	PSSM2_229	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12364.1	003029	Cluster2618_1clades	74	PRTG_00211	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93546.1	003029	Cluster2618_1clades	57	AVU42_gp208	Prochlorococcus phage P-TIM68	GCA_001503075.1
QMV28841.1	003030	SIG+TM	73	AP1_0134	Aeromonas phage AP1	GCA_014183365.1
ATI17273.1	003030	SIG+TM	73	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00320.1	003030	SIG+TM	73	HWB28_gp232	Aeromonas phage AS-zj	GCA_002627665.1
QAX97714.1	003030	SIG+TM	73	ASswx1_68	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39325.1	003030	SIG+TM	73	CC2_043	Aeromonas phage CC2	GCA_000903495.1
ADQ53257.1	003030	SIG+TM	74	65p249	Aeromonas virus 65	GCA_000893255.1
AIT14164.1	003031	Cluster2620_1clades	74	PBI_121Q_274	Escherichia phage 121Q	GCA_000926855.1
AGC34951.1	003031	Cluster2620_1clades	68	ACQ29_gp271	Escherichia phage PBECO4	GCA_001041035.1
BBM61837.1	003031	Cluster2620_1clades	70	EO157G_2480	Escherichia phage SP27	GCA_008033345.1
AXC37053.1	003031	Cluster2620_1clades	68	-	Escherichia phage UB	GCA_003341455.1
QBO61542.1	003031	Cluster2620_1clades	67	G17_00046	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62148.1	003031	Cluster2620_1clades	67	G17_00659	Escherichia phage vB_EcoM_G17	GCA_004521135.1
ARB14955.1	003032	Cluster2621_1clades	71	Ccr32_gp036	Caulobacter phage Ccr32	GCA_002619505.1
ARB15286.1	003032	Cluster2621_1clades	71	Ccr34_gp037	Caulobacter phage Ccr34	GCA_002619525.1
AFU87554.1	003032	Cluster2621_1clades	71	CcrKarma_gp037	Caulobacter virus Karma	GCA_000901575.1
AFU86510.1	003032	Cluster2621_1clades	70	CcrRogue_gp028	Caulobacter virus Rogue	GCA_000900555.1
AFU88351.1	003032	Cluster2621_1clades	71	CcrSwift_gp033	Caulobacter virus Swift	GCA_000899655.1
AFU86868.1	003032	Cluster2621_1clades	71	CbK_gp036	Caulobacter virus phiCbK	GCA_000900535.1
AIT14229.1	003033	Cluster2622_1clades	71	PBI_121Q_339	Escherichia phage 121Q	GCA_000926855.1
QAY00706.1	003033	Cluster2622_1clades	71	Ecwhy1_431	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61905.1	003033	Cluster2622_1clades	71	EO157G_3160	Escherichia phage SP27	GCA_008033345.1
QBO62076.1	003033	Cluster2622_1clades	71	G17_00587	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14092.1	003033	Cluster2622_1clades	71	vBEcoMphAPEC6_gp469c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80218.1	003033	Cluster2622_1clades	71	PSLUR01_00241	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14343.1	003034	SIG+TM	71	PBI_121Q_453	Escherichia phage 121Q	GCA_000926855.1
BBM62014.1	003034	SIG+TM	71	EO157G_4250	Escherichia phage SP27	GCA_008033345.1
AXC36912.1	003034	SIG+TM	71	-	Escherichia phage UB	GCA_003341455.1
QBO61961.1	003034	SIG+TM	71	G17_00472	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13988.1	003034	SIG+TM	71	vBEcoMphAPEC6_gp364c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80330.1	003034	SIG+TM	71	PSLUR01_00353	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIW90678.1	003035	Cluster2624_1clades	71	GCAPEGMB_00331	Vibrio phage V07	GCA_012361095.1
QIW91120.1	003035	Cluster2624_1clades	71	COHAPHLL_00284	Vibrio phage V09	GCA_012361135.1
QHJ74473.1	003035	Cluster2624_1clades	71	VH12019_00146	Vibrio phage VH1_2019	GCA_009931825.1
QBX06178.1	003035	Cluster2624_1clades	66	ValB1HC_225	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61195.1	003035	Cluster2624_1clades	66	AVU32_gp354	Vibrio phage ValKK3	GCA_001501635.1
ALP47682.1	003035	Cluster2624_1clades	66	phiST2_0158	Vibrio phage phi-ST2	GCA_002757135.1
AOO14256.1	003036	Cluster2625_1clades	66	Sn110110_062	Cyanophage S-RIM14	GCA_002599065.1
AOO14908.1	003036	Cluster2625_1clades	66	W1230910_062	Cyanophage S-RIM14	GCA_002599125.1
AMO43063.1	003036	Cluster2625_1clades	67	R1080702_054	Cyanophage S-RIM32	GCA_001754165.1
QDH50612.1	003036	Cluster2625_1clades	70	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70412.1	003036	Cluster2625_1clades	67	HOU04_gp013	Synechococcus phage S-T4	GCA_003443335.1
AXQ70614.1	003036	Cluster2625_1clades	67	HOU04_gp013	Synechococcus phage S-T4	GCA_003443335.1
AIT14141.1	003037	Cluster2626_1clades	69	PBI_121Q_251	Escherichia phage 121Q	GCA_000926855.1
QAY00782.1	003037	Cluster2626_1clades	68	Ecwhy1_509	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34961.1	003037	Cluster2626_1clades	51	ACQ29_gp281	Escherichia phage PBECO4	GCA_001041035.1
BBM61816.1	003037	Cluster2626_1clades	69	EO157G_2270	Escherichia phage SP27	GCA_008033345.1
QBO61563.1	003037	Cluster2626_1clades	69	G17_00067	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80131.1	003037	Cluster2626_1clades	69	PSLUR01_00154	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14252.1	003038	Cluster2627_1clades	69	PBI_121Q_362	Escherichia phage 121Q	GCA_000926855.1
QAY00682.1	003038	Cluster2627_1clades	67	Ecwhy1_407	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61930.1	003038	Cluster2627_1clades	67	EO157G_3410	Escherichia phage SP27	GCA_008033345.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBO62052.1	003038	Cluster2627_1clades	69	G17_00563	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14072.1	003038	Cluster2627_1clades	67	vBEcoMphAPEC6_gp449c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80242.1	003038	Cluster2627_1clades	69	PSLUR01_00265	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21467.1	003039	Cluster2628_1clades	67	GAP32_019	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44139.1	003039	Cluster2628_1clades	67	CBB_23	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43588.1	003039	Cluster2628_1clades	67	CBB_576	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88542.1	003039	Cluster2628_1clades	67	BF_0017	Serratia phage BF	GCA_002619745.1
SOK58819.1	003039	Cluster2628_1clades	69	g011	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58287.1	003039	Cluster2628_1clades	69	g010	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB14491.1	003040	Cluster2629_1clades	68	Ccr5_gp271	Caulobacter phage Ccr5	GCA_002619545.1
AXQ68469.1	003040	Cluster2629_1clades	68	CcrBL10_gp265	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87801.1	003040	Cluster2629_1clades	64	CcrKarma_gp284	Caulobacter virus Karma	GCA_000901575.1
AFU87448.1	003040	Cluster2629_1clades	64	CcrMagneto_gp278	Caulobacter virus Magneto	GCA_000903095.1
AFU86754.1	003040	Cluster2629_1clades	68	CcrRogue_gp272	Caulobacter virus Rogue	GCA_000900555.1
AFU88593.1	003040	Cluster2629_1clades	64	CcrSwift_gp275	Caulobacter virus Swift	GCA_000899655.1
APU01652.1	003041	Cluster2630_1clades	67	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17233.1	003041	Cluster2630_1clades	63	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00354.1	003041	Cluster2630_1clades	63	HWB28_gp198	Aeromonas phage AS-zj	GCA_002627665.1
QAX97676.1	003041	Cluster2630_1clades	63	ASswx1_30	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39212.1	003041	Cluster2630_1clades	63	CC2_085	Aeromonas phage CC2	GCA_000903495.1
ADQ53282.1	003041	Cluster2630_1clades	67	65p274	Aeromonas virus 65	GCA_000893255.1
AGH56818.1	003042	TM	65	CPXG_00015	Cyanophage P-RSM6	GCA_000906155.1
AGH07583.1	003042	TM	67	CYVG_00139	Cyanophage S-SSM6a	GCA_002710385.1
AGH26244.1	003042	TM	57	CPMG_00143	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44655.1	003042	TM	65	PSSM2_278	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12319.1	003042	TM	65	PRTG_00166	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93542.1	003042	TM	64	AVU42_gp205	Prochlorococcus phage P-TIM68	GCA_001503075.1
AOO14324.1	003043	Cluster2632_1clades	58	Sn110110_130	Cyanophage S-RIM14	GCA_002599065.1
AOO14973.1	003043	Cluster2632_1clades	58	W1230910_127	Cyanophage S-RIM14	GCA_002599125.1
AIX30727.1	003043	Cluster2632_1clades	66	Syn7803US37_250	Synechococcus phage ACG-2014f	GCA_002594065.1
AOV59690.1	003043	Cluster2632_1clades	56	S330809_229	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59452.1	003043	Cluster2632_1clades	56	C440309_229	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59927.1	003043	Cluster2632_1clades	56	N231010_228	Synechococcus phage S-CAM4	GCA_002922155.1
AGB06793.1	003044	Cluster2633_1clades	64	CF80_gp006	Vibrio phage VH7D	GCA_000914495.1
QAU04578.1	003044	Cluster2633_1clades	66	ValB1MD_327	Vibrio phage ValB1MD	GCA_004138815.1
AJT60985.1	003044	Cluster2633_1clades	64	AVU32_gp144	Vibrio phage ValKK3	GCA_001501635.1
ALP47306.1	003044	Cluster2633_1clades	64	phiGrn1_0228	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47685.1	003044	Cluster2633_1clades	64	phiST2_0363	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54598.1	003044	Cluster2633_1clades	64	vBValMR10Z_57	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AGB07061.1	003045	Cluster2634_1clades	65	CF80_gp274	Vibrio phage VH7D	GCA_000914495.1
QBX06035.1	003045	Cluster2634_1clades	65	ValB1HC_081	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61049.1	003045	Cluster2634_1clades	65	AVU32_gp208	Vibrio phage ValKK3	GCA_001501635.1
ALP47303.1	003045	Cluster2634_1clades	65	phiGrn1_0168	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47684.1	003045	Cluster2634_1clades	65	phiST2_0299	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54660.1	003045	Cluster2634_1clades	65	vBValMR10Z_119	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
APU01518.1	003046	Cluster2635_1clades	64	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28776.1	003046	Cluster2635_1clades	64	AP1_0064	Aeromonas phage AP1	GCA_014183365.1
ATI17379.1	003046	Cluster2635_1clades	64	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00214.1	003046	Cluster2635_1clades	64	HWB28_gp338	Aeromonas phage AS-zj	GCA_002627665.1
QAY01330.1	003046	Cluster2635_1clades	64	ASwh1_269	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53141.1	003046	Cluster2635_1clades	64	65p133	Aeromonas virus 65	GCA_000893255.1
AIT14247.1	003047	Cluster2636_1clades	64	PBI_121Q_357	Escherichia phage 121Q	GCA_000926855.1
AGC34880.1	003047	Cluster2636_1clades	64	ACQ29_gp200	Escherichia phage PBECO4	GCA_001041035.1
BBM61925.1	003047	Cluster2636_1clades	64	EO157G_3360	Escherichia phage SP27	GCA_008033345.1
AXC36986.1	003047	Cluster2636_1clades	64	-	Escherichia phage UB	GCA_003341455.1
QBO62057.1	003047	Cluster2636_1clades	64	G17_00568	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80237.1	003047	Cluster2636_1clades	64	PSLUR01_00260	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28743.1	003048	Cluster2637_1clades	53	AP1_0025	Aeromonas phage AP1	GCA_014183365.1
ATI17572.1	003048	Cluster2637_1clades	53	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00424.1	003048	Cluster2637_1clades	53	HWB28_gp128	Aeromonas phage AS-zj	GCA_002627665.1
QAX98366.1	003048	Cluster2637_1clades	62	ASfcp2_20	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98012.1	003048	Cluster2637_1clades	53	ASswx1_372	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39154.1	003048	Cluster2637_1clades	53	CC2_160	Aeromonas phage CC2	GCA_000903495.1
AXG67317.1	003049	Cluster2638_1clades	61	AD1_273	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80071.1	003049	Cluster2638_1clades	46	JA11_266	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66672.1	003049	Cluster2638_1clades	46	JA13_269	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66992.1	003049	Cluster2638_1clades	45	JA29_266	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67641.1	003049	Cluster2638_1clades	46	JA33_267	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08546.1	003049	Cluster2638_1clades	42	Alexandra_290	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AGC34925.1	003050	Cluster2639_1clades	60	ACQ29_gp245	Escherichia phage PBECO4	GCA_001041035.1
BBM61866.1	003050	Cluster2639_1clades	60	EO157G_2770	Escherichia phage SP27	GCA_008033345.1
AXC37029.1	003050	Cluster2639_1clades	60	-	Escherichia phage UB	GCA_003341455.1
QBO61514.1	003050	Cluster2639_1clades	60	G17_00018	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62120.1	003050	Cluster2639_1clades	60	G17_00631	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80175.1	003050	Cluster2639_1clades	60	PSLUR01_00198	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14144.1	003051	Cluster2640_1clades	60	PBI_121Q_254	Escherichia phage 121Q	GCA_000926855.1
BBM61819.1	003051	Cluster2640_1clades	60	EO157G_2300	Escherichia phage SP27	GCA_008033345.1
BBM61821.1	003051	Cluster2640_1clades	59	EO157G_2320	Escherichia phage SP27	GCA_008033345.1
QBO61559.1	003051	Cluster2640_1clades	60	G17_00063	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14169.1	003051	Cluster2640_1clades	60	vBEcoMphAPEC6_gp546c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80136.1	003051	Cluster2640_1clades	60	PSLUR01_00159	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28881.1	003052	Cluster2641_1clades	59	AP1_0174	Aeromonas phage AP1	GCA_014183365.1
ATI17242.1	003052	Cluster2641_1clades	59	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00345.1	003052	Cluster2641_1clades	59	HWB28_gp207	Aeromonas phage AS-zj	GCA_002627665.1
QAX97685.1	003052	Cluster2641_1clades	59	ASswx1_39	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01463.1	003052	Cluster2641_1clades	59	ASwh1_404	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39209.1	003052	Cluster2641_1clades	59	CC2_075	Aeromonas phage CC2	GCA_000903495.1
AGH56897.1	003053	Cluster2642_1clades	54	CPXG_00094	Cyanophage P-RSM6	GCA_000906155.1
AGH07580.1	003053	Cluster2642_1clades	55	CYVG_00136	Cyanophage S-SSM6a	GCA_002710385.1
AGH26209.1	003053	Cluster2642_1clades	54	CPMG_00108	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44660.1	003053	Cluster2642_1clades	40	PSSM2_283	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12315.1	003053	Cluster2642_1clades	54	PRTG_00162	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93556.1	003053	Cluster2642_1clades	58	AVU42_gp219	Prochlorococcus phage P-TIM68	GCA_001503075.1
AAQ64181.1	003054	Cluster2643_1clades	56	KVP40.0110	Vibrio phage KVP40	GCA_000843785.1
QIW90504.1	003054	Cluster2643_1clades	56	GCAPEGMB_00157	Vibrio phage V07	GCA_012361095.1
QIW90925.1	003054	Cluster2643_1clades	56	COHAPHLL_00062	Vibrio phage V09	GCA_012361135.1
QHJ74293.1	003054	Cluster2643_1clades	56	VH12019_00374	Vibrio phage VH1_2019	GCA_009931825.1
AGN30161.1	003054	Cluster2643_1clades	54	VPFG_00159	Vibrio phage nt-1	GCA_000910195.2
AFN37339.1	003054	Cluster2643_1clades	56	pp2_106	Vibriophage phi-pp2	GCA_002630725.1
QGZ14517.1	003055	Cluster2644_1clades	53	HWC77_gp154	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04217.1	003055	Cluster2644_1clades	53	HWC03_gp062	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23143.1	003055	Cluster2644_1clades	53	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81099.1	003055	Cluster2644_1clades	53	Aphrodite1_0197	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47584.1	003055	Cluster2644_1clades	53	HWC35_gp190	Vibrio phage USC-1	GCA_006864065.1
BAW98399.1	003055	Cluster2644_1clades	54	FDH33_gp190	Vibrio phage pTD1	GCA_002618825.1
AIT14069.1	003056	TM	48	PBI_121Q_179	Escherichia phage 121Q	GCA_000926855.1
AGC35024.1	003056	TM	48	ACQ29_gp344	Escherichia phage PBECO4	GCA_001041035.1
BBM61752.1	003056	TM	48	EO157G_1630	Escherichia phage SP27	GCA_008033345.1
AXC36601.1	003056	TM	48	-	Escherichia phage UB	GCA_003341455.1
QBO61630.1	003056	TM	48	G17_00134	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13686.1	003056	TM	48	vBEcoMphAPEC6_gp056c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QAY00760.1	003057	Cluster2646_1clades	48	Ecwhy1_486	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61850.1	003057	Cluster2646_1clades	48	EO157G_2610	Escherichia phage SP27	GCA_008033345.1
AXC37043.1	003057	Cluster2646_1clades	48	-	Escherichia phage UB	GCA_003341455.1
QBO61530.1	003057	Cluster2646_1clades	48	G17_00034	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62136.1	003057	Cluster2646_1clades	48	G17_00647	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80161.1	003057	Cluster2646_1clades	48	PSLUR01_00184	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
APU01672.1	003058	Cluster2647_1clades	46	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29016.1	003058	Cluster2647_1clades	46	AP1_0309	Aeromonas phage AP1	GCA_014183365.1
ATI17622.1	003058	Cluster2647_1clades	46	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00374.1	003058	Cluster2647_1clades	46	HWB28_gp178	Aeromonas phage AS-zj	GCA_002627665.1
QAX97656.1	003058	Cluster2647_1clades	46	ASswx1_10	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39219.1	003058	Cluster2647_1clades	46	CC2_104	Aeromonas phage CC2	GCA_000903495.1
QCW19117.1	003059	TM	46	7t3_0600	Salmonella phage 7t3	GCA_006083215.1
AZU98354.1	003059	TM	46	CPT_Munch_413	Salmonella phage Munch	GCA_004015485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG62628.1	003059	TM	46	SEPL_015	Salmonella phage SE_PL	GCA_011067555.1
AQW88953.1	003059	TM	43	BF_0428	Serratia phage BF	GCA_002619745.1
SOK59238.1	003059	TM	43	g430	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58704.1	003059	TM	43	g427	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB15053.1	003060	Cluster2649_1clades	45	Ccr32_gp135	Caulobacter phage Ccr32	GCA_002619505.1
ARB15386.1	003060	Cluster2649_1clades	45	Ccr34_gp144	Caulobacter phage Ccr34	GCA_002619525.1
AFU87658.1	003060	Cluster2649_1clades	45	CcrKarma_gp141	Caulobacter virus Karma	GCA_000901575.1
AFU87307.1	003060	Cluster2649_1clades	45	CcrMagneto_gp137	Caulobacter virus Magneto	GCA_000903095.1
AFU88454.1	003060	Cluster2649_1clades	45	CcrSwift_gp136	Caulobacter virus Swift	GCA_000899655.1
AFU86971.1	003060	Cluster2649_1clades	45	CbK_gp139	Caulobacter virus phiCbK	GCA_000900535.1
AIT14177.1	003061	Cluster2650_1clades	45	PBI_121Q_287	Escherichia phage 121Q	GCA_000926855.1
AGC34938.1	003061	Cluster2650_1clades	44	ACQ29_gp258	Escherichia phage PBECO4	GCA_001041035.1
BBM61852.1	003061	Cluster2650_1clades	45	EO157G_2630	Escherichia phage SP27	GCA_008033345.1
QBO61528.1	003061	Cluster2650_1clades	45	G17_00032	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62134.1	003061	Cluster2650_1clades	45	G17_00645	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14142.1	003061	Cluster2650_1clades	44	vBEcoMphAPEC6_gp519c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AIT14397.1	003062	Cluster2651_1clades	42	PBI_121Q_507	Escherichia phage 121Q	GCA_000926855.1
AGC34745.1	003062	Cluster2651_1clades	42	ACQ29_gp065	Escherichia phage PBECO4	GCA_001041035.1
BBM62068.1	003062	Cluster2651_1clades	42	EO157G_4790	Escherichia phage SP27	GCA_008033345.1
AXC36860.1	003062	Cluster2651_1clades	42	-	Escherichia phage UB	GCA_003341455.1
QBO61905.1	003062	Cluster2651_1clades	42	G17_00416	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13940.1	003062	Cluster2651_1clades	42	vBEcoMphAPEC6_gp315c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QMV29036.1	003063	SIG+TM	41	AP1_0329	Aeromonas phage AP1	GCA_014183365.1
ATI17256.1	003063	SIG+TM	41	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00335.1	003063	SIG+TM	41	HWB28_gp217	Aeromonas phage AS-zj	GCA_002627665.1
QAX97697.1	003063	SIG+TM	41	ASswx1_51	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01441.1	003063	SIG+TM	41	ASwh1_382	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39199.1	003063	SIG+TM	41	CC2_061	Aeromonas phage CC2	GCA_000903495.1
AIT14030.1	003064	Cluster2653_1clades	37	PBI_121Q_139	Escherichia phage 121Q	GCA_000926855.1
QAY00311.1	003064	Cluster2653_1clades	37	Ecwhy1_29	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35061.1	003064	Cluster2653_1clades	37	ACQ29_gp381	Escherichia phage PBECO4	GCA_001041035.1
AXC36637.1	003064	Cluster2653_1clades	37	-	Escherichia phage UB	GCA_003341455.1
QBO61669.1	003064	Cluster2653_1clades	37	G17_00174	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80026.1	003064	Cluster2653_1clades	37	PSLUR01_00048	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QGZ14550.1	003065	CarboxypepD-reg-IG	3527	HWC77_gp187	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04184.1	003065	CarboxypepD-reg-IG	3908	HWC03_gp029	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23175.1	003065	CarboxypepD-reg-IG	3529	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80908.1	003065	CarboxypepD-reg-IG	3529	Aphrodite1_0167	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47554.1	003065	CarboxypepD-reg-IG	3529	HWC35_gp160	Vibrio phage USC-1	GCA_006864065.1
QIG63392.1	003066	Cluster2655_1clades	1693	DAC16_162	Bacteroides phage DAC16	GCA_013387695.1
QIG63656.1	003066	Cluster2655_1clades	2223	DAC19_168	Bacteroides phage DAC19	GCA_013387715.1
QIG63917.1	003066	Cluster2655_1clades	2223	DAC20_167	Bacteroides phage DAC20	GCA_013387725.1
QIG64181.1	003066	Cluster2655_1clades	2223	DAC22_170	Bacteroides phage DAC22	GCA_013387735.1
QIG64437.1	003066	Cluster2655_1clades	2699	DAC23_162	Bacteroides phage DAC23	GCA_013387745.1
AGH56923.1	003067	Mtd_N	2538	CPXG_00120	Cyanophage P-RSM6	GCA_000906155.1
AJK27534.1	003067	Mtd_N	2301	PTIM40_107	Cyanophage P-TIM40	GCA_001470935.1
AOO14293.1	003067	Mtd_N	2330	Sn110110_099	Cyanophage S-RIM14	GCA_002599065.1
AOO14942.1	003067	Mtd_N	2228	W1230910_096	Cyanophage S-RIM14	GCA_002599125.1
AGG54291.1	003067	Mtd_N	1931	CYWG_00007	Cyanophage S-SSM6b	GCA_002710425.1
QIG65714.1	003068	DUF4815+DUF4815	1942	phiOC_p048	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47761.1	003068	DUF4815+DUF4815	1802	SmphiM12_129	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12997.1	003068	DUF4815+DUF4815	1802	PHIM19_91	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12637.1	003068	DUF4815+DUF4815	1801	PHIM7_90	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13370.1	003068	DUF4815+DUF4815	1802	PHIN3_105	Sinorhizobium phage phiN3	GCA_001501175.1
AXH70882.1	003069	Cluster2659_1clades	1043	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96801.1	003069	Cluster2659_1clades	1444	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97120.1	003069	Cluster2659_1clades	1444	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96166.1	003069	Cluster2659_1clades	1444	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96484.1	003069	Cluster2659_1clades	1444	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63391.1	003070	Collagen	1115	DAC16_161	Bacteroides phage DAC16	GCA_013387695.1
QIG63655.1	003070	Collagen	1114	DAC19_167	Bacteroides phage DAC19	GCA_013387715.1
QIG63916.1	003070	Collagen	1114	DAC20_166	Bacteroides phage DAC20	GCA_013387725.1
QIG64180.1	003070	Collagen	1115	DAC22_169	Bacteroides phage DAC22	GCA_013387735.1
QIG64435.1	003070	Collagen	1114	DAC23_160	Bacteroides phage DAC23	GCA_013387745.1
AGN12302.1	003071	Cupredoxin	590	PRTG_00149	Prochlorococcus phage P-SSM5	GCA_002991095.1
QCW22875.1	003071	Cupredoxin	517	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50482.1	003071	Cupredoxin	315	-	Synechococcus phage S-B43	GCA_006869725.1
QDB70331.1	003072	Cluster2666_1clades	1068	CF8_0161	Aeromonas phage CF8	GCA_006384595.2
QDJ97326.2	003072	Cluster2666_1clades	1077	D6_0165	Aeromonas phage D6	GCA_007051205.2
QDH47016.1	003072	Cluster2666_1clades	1077	LAh10_86	Aeromonas phage LAh10	GCA_006863975.1
QDJ96680.1	003072	Cluster2666_1clades	1049	PS1_0169	Aeromonas phage PS1	GCA_007051165.2
QFR59315.1	003072	Cluster2666_1clades	1049	PS2_0174	Aeromonas phage PS2	GCA_009388305.2
AFF28264.1	003073	IG+IG	875	PAU_266	Sphingomonas phage PAU	GCA_000902455.1
BBI90400.1	003073	IG+IG	722	HYO65_gp008	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90708.1	003073	IG+IG	225	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90707.1	003073	IG+IG	460	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39304.1	003073	IG+IG	1070	BPT24_179	Tenacibaculum phage pT24	GCA_002611925.1
QIG63314.1	003074	Polysacc_deac_3	954	DAC16_81	Bacteroides phage DAC16	GCA_013387695.1
QIG63575.1	003074	Polysacc_deac_3	954	DAC19_84	Bacteroides phage DAC19	GCA_013387715.1
QIG63836.1	003074	Polysacc_deac_3	954	DAC20_83	Bacteroides phage DAC20	GCA_013387725.1
QIG64098.1	003074	Polysacc_deac_3	954	DAC22_84	Bacteroides phage DAC22	GCA_013387735.1
QIG64358.1	003074	Polysacc_deac_3	954	DAC23_80	Bacteroides phage DAC23	GCA_013387745.1
QIG63454.1	003075	SIG+TM	934	DAC16_225	Bacteroides phage DAC16	GCA_013387695.1
QIG63717.1	003075	SIG+TM	934	DAC19_230	Bacteroides phage DAC19	GCA_013387715.1
QIG63978.1	003075	SIG+TM	934	DAC20_229	Bacteroides phage DAC20	GCA_013387725.1
QIG64242.1	003075	SIG+TM	934	DAC22_232	Bacteroides phage DAC22	GCA_013387735.1
QIG64498.1	003075	SIG+TM	934	DAC23_224	Bacteroides phage DAC23	GCA_013387745.1
AXQ68323.1	003076	SIG+CADHERIN	857	CcrBL10_gp119	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69177.1	003076	SIG+CADHERIN	786	CcrBL9_gp153	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ68626.1	003076	SIG+CADHERIN	802	CcrPW_gp087	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69730.1	003076	SIG+CADHERIN	782	CcrSC_gp148	Caulobacter phage CcrSC	GCA_003443315.1
AFU86608.1	003076	SIG+CADHERIN	897	CcrRogue_gp126	Caulobacter virus Rogue	GCA_000900555.1
AFF28267.1	003077	Cluster2672_2clades	536	PAU_269	Sphingomonas phage PAU	GCA_000902455.1
BBI90403.1	003077	Cluster2672_2clades	524	HYO65_gp011	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90711.1	003077	Cluster2672_2clades	375	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39307.1	003077	Cluster2672_2clades	550	BPT24_182	Tenacibaculum phage pT24	GCA_002611925.1
prev15ph1000000354	003077	Cluster2672_2clades	874	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44860.1	003078	SPRY	850	SP15_061	Bacillus phage SP-15	GCA_001754685.1
AMM44861.1	003078	SPRY	551	SP15_062	Bacillus phage SP-15	GCA_001754685.1
AMM44862.1	003078	SPRY	762	SP15_063	Bacillus phage SP-15	GCA_001754685.1
AEO93625.1	003078	SPRY	731	G_366	Bacillus virus G	GCA_000917535.1
BAE47813.1	003078	SPRY	388	CST115	Clostridium phage c-st	GCA_000865225.1
QAU04299.1	003079	Cluster2674_1clades	830	HWC03_gp144	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23279.1	003079	Cluster2674_1clades	827	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80920.1	003079	Cluster2674_1clades	827	Aphrodite1_0066	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47449.1	003079	Cluster2674_1clades	827	HWC35_gp055	Vibrio phage USC-1	GCA_006864065.1
BAW98271.1	003079	Cluster2674_1clades	815	FDH33_gp062	Vibrio phage pTD1	GCA_002618825.1
QIG63446.1	003080	Cluster2675_1clades	805	DAC16_217	Bacteroides phage DAC16	GCA_013387695.1
QIG63709.1	003080	Cluster2675_1clades	805	DAC19_222	Bacteroides phage DAC19	GCA_013387715.1
QIG63970.1	003080	Cluster2675_1clades	805	DAC20_221	Bacteroides phage DAC20	GCA_013387725.1
QIG64234.1	003080	Cluster2675_1clades	805	DAC22_224	Bacteroides phage DAC22	GCA_013387735.1
QIG64490.1	003080	Cluster2675_1clades	805	DAC23_216	Bacteroides phage DAC23	GCA_013387745.1
QIG63455.1	003081	Cluster2676_1clades	755	DAC16_226	Bacteroides phage DAC16	GCA_013387695.1
QIG63718.1	003081	Cluster2676_1clades	755	DAC19_231	Bacteroides phage DAC19	GCA_013387715.1
QIG63979.1	003081	Cluster2676_1clades	755	DAC20_230	Bacteroides phage DAC20	GCA_013387725.1
QIG64243.1	003081	Cluster2676_1clades	755	DAC22_233	Bacteroides phage DAC22	GCA_013387735.1
QIG64499.1	003081	Cluster2676_1clades	755	DAC23_225	Bacteroides phage DAC23	GCA_013387745.1
AGH56995.1	003082	Cluster2677_1clades	727	CPXG_00192	Cyanophage P-RSM6	GCA_000906155.1
AJK27465.1	003082	Cluster2677_1clades	734	PTIM40_38	Cyanophage P-TIM40	GCA_001470935.1
AOO14221.1	003082	Cluster2677_1clades	492	Sn110110_027	Cyanophage S-RIM14	GCA_002599065.1
AOO14873.1	003082	Cluster2677_1clades	492	W1230910_027	Cyanophage S-RIM14	GCA_002599125.1
AGG54344.1	003082	Cluster2677_1clades	496	CYWG_00060	Cyanophage S-SSM6b	GCA_002710425.1
AFO71364.1	003083	GP38	722	CR5_144	Cronobacter phage CR5	GCA_000910235.1
AMR59805.1	003083	GP38	725	SEGD1_158	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ50335.1	003083	GP38	719	PHOBOS_145	Erwinia phage vB_EamM_Phobos	GCA_001743635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QKN85993.1	003083	GP38	722	ACEC001_1540	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AEP83988.1	003083	GP38	725	SPN3US_0155	Salmonella phage SPN3US	GCA_001042275.1
ANS05932.1	003084	PspA	690	ABCD_0195	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64955.1	003084	PspA	684	S13_156	Cronobacter phage S13	GCA_001503575.1
AON97209.1	003084	PspA	695	E_201	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78727.1	003084	PspA	690	RB43ORF205w	Escherichia virus RB43	GCA_000863505.1
QHJ78979.1	003084	PspA	676	-	Myoviridae sp.	GCA_012593985.1
QBX06607.1	003085	MuB-ATPase	635	BcepSaruman_194	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06794.1	003085	MuB-ATPase	626	BcepSaruman_381	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74573.1	003085	MuB-ATPase	635	BcepSauron_193	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74764.1	003085	MuB-ATPase	679	BcepSauron_384	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41741.1	003085	MuB-ATPase	604	RSL1_ORF295	Ralstonia phage phiRSL1	GCA_000879455.1
QGT54880.1	003086	SIG+DUF192	376	b23_0266	Synechococcus phage B23	GCA_009745195.1
QGT54515.1	003086	SIG+DUF192	376	b3_0273	Synechococcus phage B3	GCA_009745215.1
ASR76168.1	003086	SIG+DUF192	618	PBI_BELLAMY_123	Synechococcus phage Bellamy	GCA_002627525.1
AXQ70586.1	003086	SIG+DUF192	499	HOU04_gp187	Synechococcus phage S-T4	GCA_003443335.1
QJT70110.1	003086	SIG+DUF192	665	SynMITS9220M01_097	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFF28015.1	003087	Cluster2684_2clades	576	PAU_17	Sphingomonas phage PAU	GCA_000902455.1
BBI90565.1	003087	Cluster2684_2clades	574	HYO65_gp173	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90873.1	003087	Cluster2684_2clades	585	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39363.1	003087	Cluster2684_2clades	579	BPT24_243	Tenacibaculum phage pT24	GCA_002611925.1
prev15ph1000000405	003087	Cluster2684_2clades	639	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFC21793.1	003088	Cluster2685_1clades	482	GAP32_343	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43912.1	003088	Cluster2685_1clades	574	CBB_349	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88873.1	003088	Cluster2685_1clades	594	BF_0348	Serratia phage BF	GCA_002619745.1
SOK59157.1	003088	Cluster2685_1clades	594	g349	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58623.1	003088	Cluster2685_1clades	630	g346	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63445.1	003089	Cluster2686_1clades	625	DAC16_216	Bacteroides phage DAC16	GCA_013387695.1
QIG63708.1	003089	Cluster2686_1clades	625	DAC19_221	Bacteroides phage DAC19	GCA_013387715.1
QIG63969.1	003089	Cluster2686_1clades	625	DAC20_220	Bacteroides phage DAC20	GCA_013387725.1
QIG64233.1	003089	Cluster2686_1clades	625	DAC22_223	Bacteroides phage DAC22	GCA_013387735.1
QIG64489.1	003089	Cluster2686_1clades	625	DAC23_215	Bacteroides phage DAC23	GCA_013387745.1
QGZ14429.1	003090	Cluster2687_1clades	560	HWC77_gp066	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04307.1	003090	Cluster2687_1clades	620	HWC03_gp152	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23271.1	003090	Cluster2687_1clades	620	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80934.1	003090	Cluster2687_1clades	607	Aphrodite1_0074	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47457.1	003090	Cluster2687_1clades	620	HWC35_gp063	Vibrio phage USC-1	GCA_006864065.1
QIG63317.1	003091	MA	596	DAC16_84	Bacteroides phage DAC16	GCA_013387695.1
QIG63578.1	003091	MA	596	DAC19_87	Bacteroides phage DAC19	GCA_013387715.1
QIG63839.1	003091	MA	596	DAC20_86	Bacteroides phage DAC20	GCA_013387725.1
QIG64101.1	003091	MA	596	DAC22_87	Bacteroides phage DAC22	GCA_013387735.1
QIG64361.1	003091	MA	596	DAC23_83	Bacteroides phage DAC23	GCA_013387745.1
AXH70979.1	003092	SIG+DUF4849	574	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96921.1	003092	SIG+DUF4849	586	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97226.1	003092	SIG+DUF4849	586	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96285.1	003092	SIG+DUF4849	586	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96603.1	003092	SIG+DUF4849	586	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QHJ74493.1	003093	Cluster2691_1clades	571	VH12019_00166	Vibrio phage VH1_2019	GCA_009931825.1
AGB06973.1	003093	Cluster2691_1clades	571	CF80_gp186	Vibrio phage VH7D	GCA_000914495.1
AJT61174.1	003093	Cluster2691_1clades	571	AVU32_gp333	Vibrio phage ValKK3	GCA_001501635.1
ALP46973.1	003093	Cluster2691_1clades	571	phiGrn1_0046	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47354.1	003093	Cluster2691_1clades	571	phiST2_0179	Vibrio phage phi-ST2	GCA_002757135.1
QIG63426.1	003094	Cluster2694_1clades	552	DAC16_196	Bacteroides phage DAC16	GCA_013387695.1
QIG63690.1	003094	Cluster2694_1clades	552	DAC19_202	Bacteroides phage DAC19	GCA_013387715.1
QIG63951.1	003094	Cluster2694_1clades	552	DAC20_201	Bacteroides phage DAC20	GCA_013387725.1
QIG64215.1	003094	Cluster2694_1clades	552	DAC22_204	Bacteroides phage DAC22	GCA_013387735.1
QIG64471.1	003094	Cluster2694_1clades	552	DAC23_196	Bacteroides phage DAC23	GCA_013387745.1
QIG63422.1	003095	Portal	544	DAC16_192	Bacteroides phage DAC16	GCA_013387695.1
QIG63686.1	003095	Portal	544	DAC19_198	Bacteroides phage DAC19	GCA_013387715.1
QIG63947.1	003095	Portal	544	DAC20_197	Bacteroides phage DAC20	GCA_013387725.1
QIG64211.1	003095	Portal	544	DAC22_200	Bacteroides phage DAC22	GCA_013387735.1
QIG64467.1	003095	Portal	544	DAC23_192	Bacteroides phage DAC23	GCA_013387745.1
AXF51325.1	003096	Cluster2697_1clades	524	WELLINGTON_197	Erwinia phage Wellington	GCA_003344985.1
AFQ96647.1	003096	Cluster2697_1clades	434	G173_gp102	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48213.1	003096	Cluster2697_1clades	428	ASESINO_200	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ49550.1	003096	Cluster2697_1clades	524	KWAN_198	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50624.1	003096	Cluster2697_1clades	443	STRATTON_199	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QGZ14487.1	003097	Cluster2698_1clades	507	HWC77_gp124	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04247.1	003097	Cluster2698_1clades	506	HWC03_gp092	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23116.1	003097	Cluster2698_1clades	507	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80944.1	003097	Cluster2698_1clades	507	Aphrodite1_0015	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47400.1	003097	Cluster2698_1clades	507	HWC35_gp006	Vibrio phage USC-1	GCA_006864065.1
QBO63956.1	003098	Cluster2699_1clades	297	Goslar_00163	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
BAW19056.1	003098	Cluster2699_1clades	214	FDH28_gp082	Ralstonia phage RP12	GCA_002617345.1
BAW19341.1	003098	Cluster2699_1clades	204	-	Ralstonia phage RP31	GCA_002617365.1
BAS04886.2	003098	Cluster2699_1clades	307	AVU11_gp094	Ralstonia phage RSF1	GCA_001500875.1
BAQ02613.2	003098	Cluster2699_1clades	507	-	Ralstonia phage RSL2	GCA_001503055.1
AOO14227.1	003099	Cluster2700_1clades	497	Sn110110_033	Cyanophage S-RIM14	GCA_002599065.1
AOO14879.1	003099	Cluster2700_1clades	497	W1230910_033	Cyanophage S-RIM14	GCA_002599125.1
AOV59561.1	003099	Cluster2700_1clades	455	S330809_100	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59323.1	003099	Cluster2700_1clades	455	C440309_100	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59799.1	003099	Cluster2700_1clades	401	N231010_100	Synechococcus phage S-CAM4	GCA_002922155.1
QIG63433.1	003100	DUF5309	467	DAC16_204	Bacteroides phage DAC16	GCA_013387695.1
QIG63697.1	003100	DUF5309	492	DAC19_210	Bacteroides phage DAC19	GCA_013387715.1
QIG63958.1	003100	DUF5309	492	DAC20_209	Bacteroides phage DAC20	GCA_013387725.1
QIG64222.1	003100	DUF5309	492	DAC22_212	Bacteroides phage DAC22	GCA_013387735.1
QIG64478.1	003100	DUF5309	492	DAC23_204	Bacteroides phage DAC23	GCA_013387745.1
QNI21190.1	003101	Cluster2704_1clades	425	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21191.1	003101	Cluster2704_1clades	433	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21195.1	003101	Cluster2704_1clades	449	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21194.1	003101	Cluster2704_1clades	452	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21193.1	003101	Cluster2704_1clades	465	-	Vibrio phage vB_pir03	GCA_014319855.1
QAX96657.1	003102	Cluster2706_1clades	441	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96975.1	003102	Cluster2706_1clades	441	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96021.1	003102	Cluster2706_1clades	441	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96339.1	003102	Cluster2706_1clades	441	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI21084.1	003102	Cluster2706_1clades	448	-	Vibrio phage vB_pir03	GCA_014319855.1
QIG63473.1	003103	SF2-DUF3427A	445	DAC16_244	Bacteroides phage DAC16	GCA_013387695.1
QIG63736.1	003103	SF2-DUF3427A	445	DAC19_249	Bacteroides phage DAC19	GCA_013387715.1
QIG63997.1	003103	SF2-DUF3427A	445	DAC20_248	Bacteroides phage DAC20	GCA_013387725.1
QIG64261.1	003103	SF2-DUF3427A	445	DAC22_251	Bacteroides phage DAC22	GCA_013387735.1
QIG64517.1	003103	SF2-DUF3427A	445	DAC23_243	Bacteroides phage DAC23	GCA_013387745.1
QIG63479.1	003104	Cluster2708_1clades	440	DAC16_250	Bacteroides phage DAC16	GCA_013387695.1
QIG63742.1	003104	Cluster2708_1clades	440	DAC19_255	Bacteroides phage DAC19	GCA_013387715.1
QIG64003.1	003104	Cluster2708_1clades	440	DAC20_254	Bacteroides phage DAC20	GCA_013387725.1
QIG64267.1	003104	Cluster2708_1clades	440	DAC22_257	Bacteroides phage DAC22	GCA_013387735.1
QIG64524.1	003104	Cluster2708_1clades	440	DAC23_250	Bacteroides phage DAC23	GCA_013387745.1
AFF28253.1	003105	Cluster2709_2clades	413	PAU_255	Sphingomonas phage PAU	GCA_000902455.1
BBI90627.1	003105	Cluster2709_2clades	401	HYO65_gp235	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90933.1	003105	Cluster2709_2clades	401	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39289.1	003105	Cluster2709_2clades	368	BPT24_163	Tenacibaculum phage pT24	GCA_002611925.1
prevph1000000449	003105	Cluster2709_2clades	266	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AMR59827.1	003106	Cluster2710_1clades	412	SEGD1_180	Enterobacteria phage SEGD1	GCA_002601865.1
QKN86016.1	003106	Cluster2710_1clades	412	ACEC001_1750	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20871.1	003106	Cluster2710_1clades	411	-	Salmonella phage JN03	GCA_014319805.1
AXF51129.1	003106	Cluster2710_1clades	333	MLDJOKPK_00266	Salmonella phage SPAsTU	GCA_003183805.1
AEP84008.1	003106	Cluster2710_1clades	412	SPN3US_0175	Salmonella phage SPN3US	GCA_001042275.1
QDH83679.1	003107	Tail-P2-I	406	H1O15_gp132	Achromobacter phage Motura	GCA_006964305.1
QBX06676.1	003107	Tail-P2-I	272	BcepSaruman_263	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74646.1	003107	Tail-P2-I	274	BcepSauron_266	Burkholderia phage BcepSauron	GCA_005394215.1
QHJ85932.1	003107	Tail-P2-I	319	KKIINIFJ_00020	Pseudomonas phage PN05	GCA_009931935.1
BAG41646.1	003107	Tail-P2-I	412	RSL1_ORF197	Ralstonia phage phiRSL1	GCA_000879455.1
SBV38358.1	003108	Cluster2712_1clades	355	BN7874_189	Phage NCTB	GCA_900092385.1
SBV38359.1	003108	Cluster2712_1clades	382	BN7874_190	Phage NCTB	GCA_900092385.1
SBV38360.1	003108	Cluster2712_1clades	358	BN7874_191	Phage NCTB	GCA_900092385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SBV38364.1	003108	Cluster2712_1clades	402	BN7874_195	Phage NCTB	GCA_900092385.1
SBV38365.1	003108	Cluster2712_1clades	362	BN7874_196	Phage NCTB	GCA_900092385.1
QIG63451.1	003109	Baseplate_J	399	DAC16_222	Bacteroides phage DAC16	GCA_013387695.1
QIG63714.1	003109	Baseplate_J	399	DAC19_227	Bacteroides phage DAC19	GCA_013387715.1
QIG63975.1	003109	Baseplate_J	399	DAC20_226	Bacteroides phage DAC20	GCA_013387725.1
QIG64239.1	003109	Baseplate_J	399	DAC22_229	Bacteroides phage DAC22	GCA_013387735.1
QIG64495.1	003109	Baseplate_J	399	DAC23_221	Bacteroides phage DAC23	GCA_013387745.1
QIG63452.1	003110	Cluster2714_1clades	398	DAC16_223	Bacteroides phage DAC16	GCA_013387695.1
QIG63715.1	003110	Cluster2714_1clades	398	DAC19_228	Bacteroides phage DAC19	GCA_013387715.1
QIG63976.1	003110	Cluster2714_1clades	398	DAC20_227	Bacteroides phage DAC20	GCA_013387725.1
QIG64240.1	003110	Cluster2714_1clades	398	DAC22_230	Bacteroides phage DAC22	GCA_013387735.1
QIG64496.1	003110	Cluster2714_1clades	398	DAC23_222	Bacteroides phage DAC23	GCA_013387745.1
QIG63411.1	003111	Cluster2715_1clades	395	DAC16_181	Bacteroides phage DAC16	GCA_013387695.1
QIG63675.1	003111	Cluster2715_1clades	395	DAC19_187	Bacteroides phage DAC19	GCA_013387715.1
QIG63936.1	003111	Cluster2715_1clades	395	DAC20_186	Bacteroides phage DAC20	GCA_013387725.1
QIG64200.1	003111	Cluster2715_1clades	395	DAC22_189	Bacteroides phage DAC22	GCA_013387735.1
QIG64456.1	003111	Cluster2715_1clades	395	DAC23_181	Bacteroides phage DAC23	GCA_013387745.1
AMO43392.1	003112	Cluster2716_1clades	374	W270710_148	Cyanophage S-RIM44	GCA_002599145.1
AOO11864.1	003112	Cluster2716_1clades	374	Np050604_148	Cyanophage S-RIM44	GCA_002599185.1
AOO12565.1	003112	Cluster2716_1clades	374	Sn080709_148	Cyanophage S-RIM44	GCA_002599245.1
AOO13031.1	003112	Cluster2716_1clades	374	W2100709_149	Cyanophage S-RIM44	GCA_002599285.1
ADO99250.1	003112	Cluster2716_1clades	392	Syn1_149	Prochlorococcus phage Syn1	GCA_000892495.1
AXH70885.1	003113	Cluster2717_1clades	381	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96888.1	003113	Cluster2717_1clades	391	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97193.1	003113	Cluster2717_1clades	391	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96252.1	003113	Cluster2717_1clades	391	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96570.1	003113	Cluster2717_1clades	391	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AAQ64330.1	003114	RADICAL-SAM	374	KVP40.0261	Vibrio phage KVP40	GCA_000843785.1
QIW90645.1	003114	RADICAL-SAM	374	GCAPEGMB_00298	Vibrio phage V07	GCA_012361095.1
QIW91154.1	003114	RADICAL-SAM	374	COHAPHLL_00318	Vibrio phage V09	GCA_012361135.1
QHJ74440.1	003114	RADICAL-SAM	374	VH12019_00113	Vibrio phage VH1_2019	GCA_009931825.1
AFN37489.1	003114	RADICAL-SAM	374	pp2_256	Vibriophage phi-pp2	GCA_002630725.1
CCH63708.1	003115	REase	333	CP21_248	Campylobacter virus CP21	GCA_000902535.1
BBI90632.1	003115	REase	261	HYO65_gp240	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90938.1	003115	REase	212	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000823	003115	REase	234	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000567	003115	REase	373	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFC21524.1	003116	Cluster2721_1clades	365	GAP32_076	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43644.1	003116	Cluster2721_1clades	370	CBB_79	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88593.1	003116	Cluster2721_1clades	351	BF_0068	Serratia phage BF	GCA_002619745.1
SOK58869.1	003116	Cluster2721_1clades	354	g061	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58332.1	003116	Cluster2721_1clades	354	g055	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGT54907.1	003117	Cluster2723_1clades	361	b23_0294	Synechococcus phage B23	GCA_009745195.1
QGT54990.1	003117	Cluster2723_1clades	223	b23_0384	Synechococcus phage B23	GCA_009745195.1
QGT54542.1	003117	Cluster2723_1clades	361	b3_0301	Synechococcus phage B3	GCA_009745215.1
QGT54625.1	003117	Cluster2723_1clades	223	b3_0390	Synechococcus phage B3	GCA_009745215.1
QCW23010.1	003117	Cluster2723_1clades	163	-	Synechococcus phage S-B05	GCA_006083695.1
AXH70762.1	003118	Cluster2724_1clades	354	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96770.1	003118	Cluster2724_1clades	357	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97089.1	003118	Cluster2724_1clades	357	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96135.1	003118	Cluster2724_1clades	357	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96453.1	003118	Cluster2724_1clades	357	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83672.1	003119	Cluster2725_1clades	352	H1O15_gp139	Achromobacter phage Motura	GCA_006964305.1
QBX06670.1	003119	Cluster2725_1clades	313	BcepSaruman_257	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74640.1	003119	Cluster2725_1clades	313	BcepSauron_260	Burkholderia phage BcepSauron	GCA_005394215.1
QHJ85967.1	003119	Cluster2725_1clades	241	KKIINIFJ_00055	Pseudomonas phage PN05	GCA_009931935.1
BAG41652.1	003119	Cluster2725_1clades	304	RSL1_ORF203	Ralstonia phage phiRSL1	GCA_000879455.1
QIG63420.1	003120	PAD_porph	350	DAC16_190	Bacteroides phage DAC16	GCA_013387695.1
QIG63684.1	003120	PAD_porph	350	DAC19_196	Bacteroides phage DAC19	GCA_013387715.1
QIG63945.1	003120	PAD_porph	350	DAC20_195	Bacteroides phage DAC20	GCA_013387725.1
QIG64209.1	003120	PAD_porph	350	DAC22_198	Bacteroides phage DAC22	GCA_013387735.1
QIG64465.1	003120	PAD_porph	350	DAC23_190	Bacteroides phage DAC23	GCA_013387745.1
BAW19112.1	003121	SIG+TM+TM+TM+TM+TM+TM	346	FDH28_gp283	Ralstonia phage RP12	GCA_002617345.1
BAW19398.1	003121	SIG+TM+TM+TM+TM+TM+TM	346	-	Ralstonia phage RP31	GCA_002617365.1
AOV59646.1	003121	SIG+TM+TM+TM+TM+TM+TM	346	S330809_185	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59408.1	003121	SIG+TM+TM+TM+TM+TM+TM	331	C440309_185	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59884.1	003121	SIG+TM+TM+TM+TM+TM+TM	346	N231010_185	Synechococcus phage S-CAM4	GCA_002922155.1
AFC21965.1	003122	Cluster2729_1clades	332	GAP32_505	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44088.1	003122	Cluster2729_1clades	336	CBB_525	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89045.1	003122	Cluster2729_1clades	346	BF_0520	Serratia phage BF	GCA_002619745.1
SOK59320.1	003122	Cluster2729_1clades	317	g512	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58782.1	003122	Cluster2729_1clades	313	g505	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QAU04297.1	003123	Cluster2731_1clades	342	HWC03_gp142	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23281.1	003123	Cluster2731_1clades	334	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80985.1	003123	Cluster2731_1clades	334	Aphrodite1_0064	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47447.1	003123	Cluster2731_1clades	334	HWC35_gp053	Vibrio phage USC-1	GCA_006864065.1
BAW98269.1	003123	Cluster2731_1clades	323	FDH33_gp060	Vibrio phage pTD1	GCA_002618825.1
QGZ14477.1	003124	Cluster2732_1clades	339	HWC77_gp114	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04257.1	003124	Cluster2732_1clades	339	HWC03_gp102	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23106.1	003124	Cluster2732_1clades	339	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR80983.1	003124	Cluster2732_1clades	339	Aphrodite1_0025	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47410.1	003124	Cluster2732_1clades	339	HWC35_gp016	Vibrio phage USC-1	GCA_006864065.1
QBX32325.1	003125	Mtd_N	339	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03587.1	003125	Mtd_N	232	164	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02725.1	003125	Mtd_N	201	PSA21_199	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02726.1	003125	Mtd_N	160	PSA21_200	Pseudomonas phage Psa21	GCA_004340405.1
QEM41898.1	003125	Mtd_N	339	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDH83478.1	003126	Cluster2734_1clades	339	H1O15_gp328	Achromobacter phage Motura	GCA_006964305.1
QBX06579.1	003126	Cluster2734_1clades	326	BcepSaruman_166	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74545.1	003126	Cluster2734_1clades	326	BcepSauron_165	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41447.1	003126	Cluster2734_1clades	178	RSL1_ORF002	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41448.1	003126	Cluster2734_1clades	188	RSL1_ORF003	Ralstonia phage phiRSL1	GCA_000879455.1
AEO93504.1	003127	ABC-ATPase	209	G_245	Bacillus virus G	GCA_000917535.1
prevph1000000427	003127	ABC-ATPase	330	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000429	003127	ABC-ATPase	102	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000338	003127	ABC-ATPase	330	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000341	003127	ABC-ATPase	102	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG63467.1	003128	Cluster2736_1clades	325	DAC16_238	Bacteroides phage DAC16	GCA_013387695.1
QIG63730.1	003128	Cluster2736_1clades	325	DAC19_243	Bacteroides phage DAC19	GCA_013387715.1
QIG63991.1	003128	Cluster2736_1clades	325	DAC20_242	Bacteroides phage DAC20	GCA_013387725.1
QIG64255.1	003128	Cluster2736_1clades	325	DAC22_245	Bacteroides phage DAC22	GCA_013387735.1
QIG64511.1	003128	Cluster2736_1clades	325	DAC23_237	Bacteroides phage DAC23	GCA_013387745.1
ALY07043.1	003129	Cluster2738_1clades	320	VmeM32_00052	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07154.1	003129	Cluster2738_1clades	199	VmeM32_00168	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07168.1	003129	Cluster2738_1clades	240	VmeM32_00182	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07183.1	003129	Cluster2738_1clades	240	VmeM32_00197	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07191.1	003129	Cluster2738_1clades	154	VmeM32_00205	Vibrio phage vB_VmeM-32	GCA_002608825.1
QDH83685.1	003130	SIG+PBPB	306	H1O15_gp276	Achromobacter phage Motura	GCA_006964305.1
BAW19167.1	003130	SIG+PBPB	306	FDH28_gp228	Ralstonia phage RP12	GCA_002617345.1
BAW19453.1	003130	SIG+PBPB	306	-	Ralstonia phage RP31	GCA_002617365.1
BAG41546.1	003130	SIG+PBPB	316	RSL1_ORF101	Ralstonia phage phiRSL1	GCA_000879455.1
QAU04479.1	003130	SIG+PBPB	313	ValB1MD_093	Vibrio phage ValB1MD	GCA_004138815.1
QIG65765.1	003131	Glyco_trans_1_4	312	phiOC_p100	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47888.1	003131	Glyco_trans_1_4	315	SmphiM12_256	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13090.1	003131	Glyco_trans_1_4	315	PHIM19_185	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12730.1	003131	Glyco_trans_1_4	315	PHIM7_185	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13460.1	003131	Glyco_trans_1_4	315	PHIN3_197	Sinorhizobium phage phiN3	GCA_001501175.1
QIG63437.1	003132	Cluster2741_1clades	315	DAC16_208	Bacteroides phage DAC16	GCA_013387695.1
QIG63700.1	003132	Cluster2741_1clades	315	DAC19_213	Bacteroides phage DAC19	GCA_013387715.1
QIG63961.1	003132	Cluster2741_1clades	315	DAC20_212	Bacteroides phage DAC20	GCA_013387725.1
QIG64225.1	003132	Cluster2741_1clades	315	DAC22_215	Bacteroides phage DAC22	GCA_013387735.1
QIG64481.1	003132	Cluster2741_1clades	315	DAC23_207	Bacteroides phage DAC23	GCA_013387745.1
AOO14228.1	003133	Cluster2742_1clades	302	Sn110110_034	Cyanophage S-RIM14	GCA_002599065.1
AOO14880.1	003133	Cluster2742_1clades	302	W1230910_034	Cyanophage S-RIM14	GCA_002599125.1
AOV59562.1	003133	Cluster2742_1clades	287	S330809_101	Synechococcus phage S-CAM4	GCA_002366065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59324.1	003133	Cluster2742_1clades	310	C440309_101	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59800.1	003133	Cluster2742_1clades	310	N231010_101	Synechococcus phage S-CAM4	GCA_002922155.1
ANZ49775.1	003134	Cluster2743_1clades	300	MACHINA_137	Erwinia phage Machina	GCA_002758035.1
ANZ48429.1	003134	Cluster2743_1clades	308	CAITLIN_134	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48704.1	003134	Cluster2743_1clades	297	CHRISDB_142	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49219.1	003134	Cluster2743_1clades	300	HUXLEY_137	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50047.1	003134	Cluster2743_1clades	300	PARSHIK_138	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AMR59755.1	003135	Cluster2744_1clades	218	SEGD1_106	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85944.1	003135	Cluster2744_1clades	308	ACEC001_1060	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20812.1	003135	Cluster2744_1clades	218	-	Salmonella phage JN03	GCA_014319805.1
AXF51075.1	003135	Cluster2744_1clades	219	MLDJOKPK_00054	Salmonella phage SPAsTU	GCA_003183805.1
AEP83936.1	003135	Cluster2744_1clades	218	SPN3US_0103	Salmonella phage SPN3US	GCA_001042275.1
QIG63450.1	003136	Cluster2745_1clades	307	DAC16_221	Bacteroides phage DAC16	GCA_013387695.1
QIG63713.1	003136	Cluster2745_1clades	307	DAC19_226	Bacteroides phage DAC19	GCA_013387715.1
QIG63974.1	003136	Cluster2745_1clades	307	DAC20_225	Bacteroides phage DAC20	GCA_013387725.1
QIG64238.1	003136	Cluster2745_1clades	307	DAC22_228	Bacteroides phage DAC22	GCA_013387735.1
QIG64494.1	003136	Cluster2745_1clades	307	DAC23_220	Bacteroides phage DAC23	GCA_013387745.1
QIG63425.1	003137	MuF	303	DAC16_195	Bacteroides phage DAC16	GCA_013387695.1
QIG63689.1	003137	MuF	303	DAC19_201	Bacteroides phage DAC19	GCA_013387715.1
QIG63950.1	003137	MuF	303	DAC20_200	Bacteroides phage DAC20	GCA_013387725.1
QIG64214.1	003137	MuF	303	DAC22_203	Bacteroides phage DAC22	GCA_013387735.1
QIG64470.1	003137	MuF	303	DAC23_195	Bacteroides phage DAC23	GCA_013387745.1
QBX06630.1	003138	35exo	297	BcepSaruman_217	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74599.1	003138	35exo	296	BcepSauron_219	Burkholderia phage BcepSauron	GCA_005394215.1
BBI90663.1	003138	35exo	220	HYO65_gp271	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90968.1	003138	35exo	220	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAU04456.1	003138	35exo	214	ValB1MD_040	Vibrio phage ValB1MD	GCA_004138815.1
QIG63478.1	003139	Cluster2749_1clades	297	DAC16_249	Bacteroides phage DAC16	GCA_013387695.1
QIG63741.1	003139	Cluster2749_1clades	292	DAC19_254	Bacteroides phage DAC19	GCA_013387715.1
QIG64002.1	003139	Cluster2749_1clades	292	DAC20_253	Bacteroides phage DAC20	GCA_013387725.1
QIG64266.1	003139	Cluster2749_1clades	292	DAC22_256	Bacteroides phage DAC22	GCA_013387735.1
QIG64523.1	003139	Cluster2749_1clades	292	DAC23_249	Bacteroides phage DAC23	GCA_013387745.1
AUE22623.1	003140	Cluster2750_1clades	292	Ah1_00082	Aeromonas phage Ah1	GCA_002957415.1
QAX98350.1	003140	Cluster2750_1clades	292	ASfcp2_4	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52806.1	003140	Cluster2750_1clades	292	PX29p087	Aeromonas phage PX29	GCA_000920195.1
ADM80063.1	003140	Cluster2750_1clades	271	phiAS5_ORF0220	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17750.1	003140	Cluster2750_1clades	292	Aeh1ORF089c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63344.1	003141	Cluster2751_1clades	291	DAC16_111	Bacteroides phage DAC16	GCA_013387695.1
QIG63610.1	003141	Cluster2751_1clades	291	DAC19_119	Bacteroides phage DAC19	GCA_013387715.1
QIG63871.1	003141	Cluster2751_1clades	291	DAC20_118	Bacteroides phage DAC20	GCA_013387725.1
QIG64134.1	003141	Cluster2751_1clades	291	DAC22_120	Bacteroides phage DAC22	GCA_013387735.1
QIG64391.1	003141	Cluster2751_1clades	291	DAC23_113	Bacteroides phage DAC23	GCA_013387745.1
QIG63488.1	003142	Cluster2752_1clades	289	DAC16_259	Bacteroides phage DAC16	GCA_013387695.1
QIG63750.1	003142	Cluster2752_1clades	289	DAC19_263	Bacteroides phage DAC19	GCA_013387715.1
QIG64011.1	003142	Cluster2752_1clades	289	DAC20_262	Bacteroides phage DAC20	GCA_013387725.1
QIG64275.1	003142	Cluster2752_1clades	289	DAC22_265	Bacteroides phage DAC22	GCA_013387735.1
QIG64532.1	003142	Cluster2752_1clades	289	DAC23_258	Bacteroides phage DAC23	GCA_013387745.1
AGH56836.1	003143	Cluster2753_1clades	125	CPXG_00033	Cyanophage P-RSM6	GCA_000906155.1
AJK27609.1	003143	Cluster2753_1clades	122	PTIM40_191	Cyanophage P-TIM40	GCA_001470935.1
AOO14376.1	003143	Cluster2753_1clades	286	Sn110110_182	Cyanophage S-RIM14	GCA_002599065.1
AOO15024.1	003143	Cluster2753_1clades	286	W1230910_178	Cyanophage S-RIM14	GCA_002599125.1
AGG54426.1	003143	Cluster2753_1clades	288	CYWG_00142	Cyanophage S-SSM6b	GCA_002710425.1
AJK27475.1	003144	Cluster2754_1clades	288	PTIM40_48	Cyanophage P-TIM40	GCA_001470935.1
AOO11584.1	003144	Cluster2754_1clades	235	ES420910_103	Cyanophage S-RIM44	GCA_002599165.1
AOO12049.1	003144	Cluster2754_1clades	235	Np200711_103	Cyanophage S-RIM44	GCA_002599205.1
AOO12285.1	003144	Cluster2754_1clades	235	Np420711_103	Cyanophage S-RIM44	GCA_002599225.1
AOO12750.1	003144	Cluster2754_1clades	235	Sn130910_103	Cyanophage S-RIM44	GCA_002599265.1
AFF28290.1	003145	PDDEXK_1	287	PAU_293	Sphingomonas phage PAU	GCA_000902455.1
BBI90530.1	003145	PDDEXK_1	258	HYO65_gp138	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90838.1	003145	PDDEXK_1	225	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000138	003145	PDDEXK_1	242	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000106	003145	PDDEXK_1	288	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAQ64325.1	003146	Cluster2756_1clades	253	KVP40.0256	Vibrio phage KVP40	GCA_000843785.1
QIW90640.1	003146	Cluster2756_1clades	284	GCAPEGMB_00293	Vibrio phage V07	GCA_012361095.1
QIW91159.1	003146	Cluster2756_1clades	284	COHAPHLL_00323	Vibrio phage V09	GCA_012361135.1
QHJ74435.1	003146	Cluster2756_1clades	284	VH12019_00108	Vibrio phage VH1_2019	GCA_009931825.1
AFN37484.1	003146	Cluster2756_1clades	284	pp2_251	Vibriophage phi-pp2	GCA_002630725.1
AXQ69171.1	003147	RNA_pol_A_CTD	192	CcrBL9_gp147	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88003.1	003147	RNA_pol_A_CTD	284	CcrColossus_gp133	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68679.1	003147	RNA_pol_A_CTD	284	CcrPW_gp140	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69725.1	003147	RNA_pol_A_CTD	192	CcrSC_gp143	Caulobacter phage CcrSC	GCA_003443315.1
BBA65305.1	003147	RNA_pol_A_CTD	196	-	Xanthomonas phage XacN1	GCA_003173815.1
QIG63456.1	003148	Cluster2758_1clades	283	DAC16_227	Bacteroides phage DAC16	GCA_013387695.1
QIG63719.1	003148	Cluster2758_1clades	283	DAC19_232	Bacteroides phage DAC19	GCA_013387715.1
QIG63980.1	003148	Cluster2758_1clades	283	DAC20_231	Bacteroides phage DAC20	GCA_013387725.1
QIG64244.1	003148	Cluster2758_1clades	283	DAC22_234	Bacteroides phage DAC22	GCA_013387735.1
QIG64500.1	003148	Cluster2758_1clades	283	DAC23_226	Bacteroides phage DAC23	GCA_013387745.1
QIG63431.1	003149	Cluster2759_1clades	282	DAC16_202	Bacteroides phage DAC16	GCA_013387695.1
QIG63695.1	003149	Cluster2759_1clades	282	DAC19_208	Bacteroides phage DAC19	GCA_013387715.1
QIG63956.1	003149	Cluster2759_1clades	282	DAC20_207	Bacteroides phage DAC20	GCA_013387725.1
QIG64220.1	003149	Cluster2759_1clades	282	DAC22_210	Bacteroides phage DAC22	GCA_013387735.1
QIG64476.1	003149	Cluster2759_1clades	282	DAC23_202	Bacteroides phage DAC23	GCA_013387745.1
QDH83569.1	003150	Cluster2760_1clades	281	H1O15_gp219	Achromobacter phage Motura	GCA_006964305.1
AFH14851.1	003150	Cluster2760_1clades	266	Lu11_0313	Pseudomonas phage Lu11	GCA_000897175.1
QBZ72162.1	003150	Cluster2760_1clades	237	SEA_KRADAL_276	Streptomyces phage Kradal	GCA_004799925.1
AXH66425.1	003150	Cluster2760_1clades	237	SEA_SATIS_276	Streptomyces phage Satis	GCA_003366315.1
QDJ96288.1	003150	Cluster2760_1clades	234	Xoosp13_101	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QIG63468.1	003151	PS_Dcarbxylase	281	DAC16_239	Bacteroides phage DAC16	GCA_013387695.1
QIG63731.1	003151	PS_Dcarbxylase	281	DAC19_244	Bacteroides phage DAC19	GCA_013387715.1
QIG63992.1	003151	PS_Dcarbxylase	281	DAC20_243	Bacteroides phage DAC20	GCA_013387725.1
QIG64256.1	003151	PS_Dcarbxylase	281	DAC22_246	Bacteroides phage DAC22	GCA_013387735.1
QIG64512.1	003151	PS_Dcarbxylase	281	DAC23_238	Bacteroides phage DAC23	GCA_013387745.1
ASV44703.1	003152	Cluster2762_1clades	255	FDI40_gp097	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21979.1	003152	Cluster2762_1clades	277	GAP32_519	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AAX44414.1	003152	Cluster2762_1clades	193	PSSM2_036	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12237.1	003152	Cluster2762_1clades	193	PRTG_00079	Prochlorococcus phage P-SSM5	GCA_002991095.1
SOK58357.1	003152	Cluster2762_1clades	281	g080	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ABY63271.1	003153	Cluster2764_1clades	192	201phi2-1p448	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77387.1	003153	Cluster2764_1clades	277	NOXIFER_222	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32536.1	003153	Cluster2764_1clades	187	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77085.1	003153	Cluster2764_1clades	185	PHABIO_457	Pseudomonas phage Phabio	GCA_002624965.1
QEM42110.1	003153	Cluster2764_1clades	187	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63279.1	003154	ParB	274	DAC16_46	Bacteroides phage DAC16	GCA_013387695.1
QIG63541.1	003154	ParB	274	DAC19_50	Bacteroides phage DAC19	GCA_013387715.1
QIG63802.1	003154	ParB	274	DAC20_49	Bacteroides phage DAC20	GCA_013387725.1
QIG64063.1	003154	ParB	274	DAC22_49	Bacteroides phage DAC22	GCA_013387735.1
QIG64324.1	003154	ParB	274	DAC23_46	Bacteroides phage DAC23	GCA_013387745.1
QIG63447.1	003155	Cluster2768_1clades	269	DAC16_218	Bacteroides phage DAC16	GCA_013387695.1
QIG63710.1	003155	Cluster2768_1clades	269	DAC19_223	Bacteroides phage DAC19	GCA_013387715.1
QIG63971.1	003155	Cluster2768_1clades	269	DAC20_222	Bacteroides phage DAC20	GCA_013387725.1
QIG64235.1	003155	Cluster2768_1clades	269	DAC22_225	Bacteroides phage DAC22	GCA_013387735.1
QIG64491.1	003155	Cluster2768_1clades	269	DAC23_217	Bacteroides phage DAC23	GCA_013387745.1
AFC21967.1	003156	Cluster2769_1clades	267	GAP32_507	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44090.1	003156	Cluster2769_1clades	264	CBB_527	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89047.1	003156	Cluster2769_1clades	266	BF_0522	Serratia phage BF	GCA_002619745.1
SOK59322.1	003156	Cluster2769_1clades	267	g514	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58784.1	003156	Cluster2769_1clades	267	g507	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21964.1	003157	Cluster2770_1clades	266	GAP32_504	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44087.1	003157	Cluster2770_1clades	267	CBB_524	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89044.1	003157	Cluster2770_1clades	264	BF_0519	Serratia phage BF	GCA_002619745.1
SOK59319.1	003157	Cluster2770_1clades	264	g511	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58781.1	003157	Cluster2770_1clades	264	g504	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21984.1	003158	Cluster2771_1clades	254	GAP32_524	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44105.1	003158	Cluster2771_1clades	256	CBB_542	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89057.1	003158	Cluster2771_1clades	266	BF_0532	Serratia phage BF	GCA_002619745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK59335.1	003158	Cluster2771_1clades	259	g527	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58797.1	003158	Cluster2771_1clades	260	g520	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63276.1	003159	Cluster2772_1clades	265	DAC16_43	Bacteroides phage DAC16	GCA_013387695.1
QIG63538.1	003159	Cluster2772_1clades	266	DAC19_47	Bacteroides phage DAC19	GCA_013387715.1
QIG63799.1	003159	Cluster2772_1clades	266	DAC20_46	Bacteroides phage DAC20	GCA_013387725.1
QIG64060.1	003159	Cluster2772_1clades	266	DAC22_46	Bacteroides phage DAC22	GCA_013387735.1
QIG64321.1	003159	Cluster2772_1clades	266	DAC23_43	Bacteroides phage DAC23	GCA_013387745.1
AXG67091.1	003160	SIG+ParB	236	AD1_047	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08325.1	003160	SIG+ParB	233	Alexandra_45	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58689.1	003160	SIG+ParB	234	Y3_049	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28527.1	003160	SIG+ParB	226	YOLOSWAG_42	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGS82052.1	003160	SIG+ParB	265	PaBG_00176	Pseudomonas phage PaBG	GCA_000912555.1
QIG63380.1	003161	Cluster2774_1clades	265	DAC16_147	Bacteroides phage DAC16	GCA_013387695.1
QIG63644.1	003161	Cluster2774_1clades	265	DAC19_153	Bacteroides phage DAC19	GCA_013387715.1
QIG63905.1	003161	Cluster2774_1clades	265	DAC20_152	Bacteroides phage DAC20	GCA_013387725.1
QIG64169.1	003161	Cluster2774_1clades	241	DAC22_155	Bacteroides phage DAC22	GCA_013387735.1
QIG64425.1	003161	Cluster2774_1clades	265	DAC23_147	Bacteroides phage DAC23	GCA_013387745.1
AGH07499.1	003162	CTP_transf_like	154	CYVG_00055	Cyanophage S-SSM6a	GCA_002710385.1
AIR93485.1	003162	CTP_transf_like	153	AVU42_gp149	Prochlorococcus phage P-TIM68	GCA_001503075.1
QHJ86124.1	003163	CTP_transf_like+MannoseP_isomer	264	KKIINIFJ_00213	Pseudomonas phage PN05	GCA_009931935.1
QCW23027.1	003164	MannoseP_isomer	115	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50518.1	003164	MannoseP_isomer	115	-	Synechococcus phage S-B43	GCA_006869725.1
QIG63383.1	003165	Cluster2776_1clades	264	DAC16_150	Bacteroides phage DAC16	GCA_013387695.1
QIG63647.1	003165	Cluster2776_1clades	264	DAC19_156	Bacteroides phage DAC19	GCA_013387715.1
QIG63908.1	003165	Cluster2776_1clades	264	DAC20_155	Bacteroides phage DAC20	GCA_013387725.1
QIG64172.1	003165	Cluster2776_1clades	264	DAC22_158	Bacteroides phage DAC22	GCA_013387735.1
QIG64428.1	003165	Cluster2776_1clades	264	DAC23_150	Bacteroides phage DAC23	GCA_013387745.1
QIG63436.1	003166	Cluster2777_1clades	263	DAC16_207	Bacteroides phage DAC16	GCA_013387695.1
QIG63699.1	003166	Cluster2777_1clades	263	DAC19_212	Bacteroides phage DAC19	GCA_013387715.1
QIG63960.1	003166	Cluster2777_1clades	263	DAC20_211	Bacteroides phage DAC20	GCA_013387725.1
QIG64224.1	003166	Cluster2777_1clades	263	DAC22_214	Bacteroides phage DAC22	GCA_013387735.1
QIG64480.1	003166	Cluster2777_1clades	263	DAC23_206	Bacteroides phage DAC23	GCA_013387745.1
QIG63458.1	003167	Cluster2778_1clades	263	DAC16_229	Bacteroides phage DAC16	GCA_013387695.1
QIG63721.1	003167	Cluster2778_1clades	263	DAC19_234	Bacteroides phage DAC19	GCA_013387715.1
QIG63982.1	003167	Cluster2778_1clades	263	DAC20_233	Bacteroides phage DAC20	GCA_013387725.1
QIG64246.1	003167	Cluster2778_1clades	263	DAC22_236	Bacteroides phage DAC22	GCA_013387735.1
QIG64502.1	003167	Cluster2778_1clades	263	DAC23_228	Bacteroides phage DAC23	GCA_013387745.1
QGZ14486.1	003168	Cluster2779_1clades	251	HWC77_gp123	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04248.1	003168	Cluster2779_1clades	251	HWC03_gp093	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23115.1	003168	Cluster2779_1clades	251	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47401.1	003168	Cluster2779_1clades	251	HWC35_gp007	Vibrio phage USC-1	GCA_006864065.1
BAW98218.1	003168	Cluster2779_1clades	260	FDH33_gp009	Vibrio phage pTD1	GCA_002618825.1
AUE22814.1	003169	CCDC158	259	Ah1_00296	Aeromonas phage Ah1	GCA_002957415.1
QAX98527.1	003169	CCDC158	259	ASfcp2_191	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52990.1	003169	CCDC158	259	PX29p271	Aeromonas phage PX29	GCA_000920195.1
ADM79915.1	003169	CCDC158	246	phiAS5_ORF0072	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17942.1	003169	CCDC158	259	Aeh1ORF277c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21513.1	003170	Cluster2781_1clades	252	GAP32_065	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43634.1	003170	Cluster2781_1clades	257	CBB_69	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88585.1	003170	Cluster2781_1clades	257	BF_0060	Serratia phage BF	GCA_002619745.1
SOK58860.1	003170	Cluster2781_1clades	256	g052	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58322.1	003170	Cluster2781_1clades	256	g045	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63239.1	003171	ATHOOK	249	DAC16_6	Bacteroides phage DAC16	GCA_013387695.1
QIG63497.1	003171	ATHOOK	256	DAC19_6	Bacteroides phage DAC19	GCA_013387715.1
QIG63759.1	003171	ATHOOK	256	DAC20_6	Bacteroides phage DAC20	GCA_013387725.1
QIG64020.1	003171	ATHOOK	256	DAC22_6	Bacteroides phage DAC22	GCA_013387735.1
QIG64284.1	003171	ATHOOK	249	DAC23_6	Bacteroides phage DAC23	GCA_013387745.1
ANZ49757.1	003172	Cluster2783_1clades	253	MACHINA_119	Erwinia phage Machina	GCA_002758035.1
ANZ48414.1	003172	Cluster2783_1clades	254	CAITLIN_119	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48686.1	003172	Cluster2783_1clades	252	CHRISDB_124	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49201.1	003172	Cluster2783_1clades	253	HUXLEY_119	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50029.1	003172	Cluster2783_1clades	253	PARSHIK_120	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOO11586.1	003173	Cluster2784_1clades	254	ES420910_105	Cyanophage S-RIM44	GCA_002599165.1
AOO12051.1	003173	Cluster2784_1clades	254	Np200711_105	Cyanophage S-RIM44	GCA_002599205.1
AOO12287.1	003173	Cluster2784_1clades	254	Np420711_105	Cyanophage S-RIM44	GCA_002599225.1
AOO12752.1	003173	Cluster2784_1clades	254	Sn130910_105	Cyanophage S-RIM44	GCA_002599265.1
AGG54389.1	003173	Cluster2784_1clades	216	CYWG_00105	Cyanophage S-SSM6b	GCA_002710425.1
AMR59706.1	003174	Cluster2785_1clades	251	SEGD1_057	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85896.1	003174	Cluster2785_1clades	251	ACEC001_0580	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20771.1	003174	Cluster2785_1clades	253	-	Salmonella phage JN03	GCA_014319805.1
AWN09042.1	003174	Cluster2785_1clades	251	MLDJOKPK_00110	Salmonella phage SPAsTU	GCA_003183805.1
AEP83888.1	003174	Cluster2785_1clades	251	SPN3US_0055	Salmonella phage SPN3US	GCA_001042275.1
AGR47997.1	003175	RelA-SpoT	250	SmphiM12_365	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13184.1	003175	RelA-SpoT	250	PHIM19_279	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12823.1	003175	RelA-SpoT	120	PHIM7_278	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12824.1	003175	RelA-SpoT	130	PHIM7_279	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13546.1	003175	RelA-SpoT	250	PHIN3_283	Sinorhizobium phage phiN3	GCA_001501175.1
AUE22558.1	003176	Cluster2788_1clades	241	Ah1_00017	Aeromonas phage Ah1	GCA_002957415.1
QAX98596.1	003176	Cluster2788_1clades	241	ASfcp2_263	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52732.1	003176	Cluster2788_1clades	241	PX29p013	Aeromonas phage PX29	GCA_000920195.1
ADM79985.1	003176	Cluster2788_1clades	247	phiAS5_ORF0142	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17670.1	003176	Cluster2788_1clades	241	Aeh1ORF014c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63246.1	003177	Cluster2789_1clades	245	DAC16_13	Bacteroides phage DAC16	GCA_013387695.1
QIG63508.1	003177	Cluster2789_1clades	245	DAC19_17	Bacteroides phage DAC19	GCA_013387715.1
QIG63770.1	003177	Cluster2789_1clades	245	DAC20_17	Bacteroides phage DAC20	GCA_013387725.1
QIG64031.1	003177	Cluster2789_1clades	245	DAC22_17	Bacteroides phage DAC22	GCA_013387735.1
QIG64292.1	003177	Cluster2789_1clades	246	DAC23_14	Bacteroides phage DAC23	GCA_013387745.1
ANZ49918.1	003178	SIG+ArdCN-kineto	126	MACHINA_280	Erwinia phage Machina	GCA_002758035.1
AXF51418.1	003178	SIG+ArdCN-kineto	245	WELLINGTON_294	Erwinia phage Wellington	GCA_003344985.1
ANZ49361.1	003178	SIG+ArdCN-kineto	126	HUXLEY_279	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49643.1	003178	SIG+ArdCN-kineto	245	KWAN_292	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50189.1	003178	SIG+ArdCN-kineto	126	PARSHIK_280	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QIG63449.1	003179	Cluster2791_1clades	245	DAC16_220	Bacteroides phage DAC16	GCA_013387695.1
QIG63712.1	003179	Cluster2791_1clades	245	DAC19_225	Bacteroides phage DAC19	GCA_013387715.1
QIG63973.1	003179	Cluster2791_1clades	245	DAC20_224	Bacteroides phage DAC20	GCA_013387725.1
QIG64237.1	003179	Cluster2791_1clades	245	DAC22_227	Bacteroides phage DAC22	GCA_013387735.1
QIG64493.1	003179	Cluster2791_1clades	245	DAC23_219	Bacteroides phage DAC23	GCA_013387745.1
ANM45107.1	003180	Cluster2792_1clades	243	KTN4_349	Pseudomonas phage KTN4	GCA_002607225.1
QBJ02916.1	003180	Cluster2792_1clades	243	PSA21_390	Pseudomonas phage Psa21	GCA_004340405.1
ATN94607.1	003180	Cluster2792_1clades	243	SL2_030	Pseudomonas phage SL2	GCA_002956015.1
QJB22983.1	003180	Cluster2792_1clades	243	fnug_340	Pseudomonas phage fnug	GCA_012837215.1
AAL83190.1	003180	Cluster2792_1clades	243	PHIKZ289	Pseudomonas virus phiKZ	GCA_000842965.1
QIG63438.1	003181	Cluster2793_1clades	243	DAC16_209	Bacteroides phage DAC16	GCA_013387695.1
QIG63701.1	003181	Cluster2793_1clades	243	DAC19_214	Bacteroides phage DAC19	GCA_013387715.1
QIG63962.1	003181	Cluster2793_1clades	243	DAC20_213	Bacteroides phage DAC20	GCA_013387725.1
QIG64226.1	003181	Cluster2793_1clades	243	DAC22_216	Bacteroides phage DAC22	GCA_013387735.1
QIG64482.1	003181	Cluster2793_1clades	243	DAC23_208	Bacteroides phage DAC23	GCA_013387745.1
AFC21940.1	003182	Cluster2794_1clades	242	GAP32_482	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44067.1	003182	Cluster2794_1clades	241	CBB_504	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89022.1	003182	Cluster2794_1clades	207	BF_0497	Serratia phage BF	GCA_002619745.1
SOK59303.1	003182	Cluster2794_1clades	207	g495	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58768.1	003182	Cluster2794_1clades	207	g491	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QHJ86143.1	003183	DUF2786	242	KKIINIFJ_00232	Pseudomonas phage PN05	GCA_009931935.1
AGR47992.1	003183	DUF2786	236	SmphiM12_360	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13179.1	003183	DUF2786	236	PHIM19_274	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12818.1	003183	DUF2786	236	PHIM7_273	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13541.1	003183	DUF2786	236	PHIN3_278	Sinorhizobium phage phiN3	GCA_001501175.1
QIG63359.1	003184	Cluster2796_1clades	242	DAC16_126	Bacteroides phage DAC16	GCA_013387695.1
QIG63624.1	003184	Cluster2796_1clades	242	DAC19_133	Bacteroides phage DAC19	GCA_013387715.1
QIG63885.1	003184	Cluster2796_1clades	242	DAC20_132	Bacteroides phage DAC20	GCA_013387725.1
QIG64148.1	003184	Cluster2796_1clades	242	DAC22_134	Bacteroides phage DAC22	GCA_013387735.1
QIG64405.1	003184	Cluster2796_1clades	242	DAC23_127	Bacteroides phage DAC23	GCA_013387745.1
AGG54350.1	003185	Cluster2797_1clades	194	CYWG_00066	Cyanophage S-SSM6b	GCA_002710425.1
AGH26310.1	003185	Cluster2797_1clades	218	CPMG_00211	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44705.1	003185	Cluster2797_1clades	229	PSSM2_327	Prochlorococcus phage P-SSM2	GCA_000859585.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAX44706.1	003185	Cluster2797_1clades	241	PSSM2_328	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12270.1	003185	Cluster2797_1clades	241	PRTG_00116	Prochlorococcus phage P-SSM5	GCA_002991095.1
QIG63453.1	003186	TM	236	DAC16_224	Bacteroides phage DAC16	GCA_013387695.1
QIG63716.1	003186	TM	236	DAC19_229	Bacteroides phage DAC19	GCA_013387715.1
QIG63977.1	003186	TM	236	DAC20_228	Bacteroides phage DAC20	GCA_013387725.1
QIG64241.1	003186	TM	236	DAC22_231	Bacteroides phage DAC22	GCA_013387735.1
QIG64497.1	003186	TM	236	DAC23_223	Bacteroides phage DAC23	GCA_013387745.1
AFC21845.1	003187	Cluster2800_1clades	233	GAP32_393	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43965.1	003187	Cluster2800_1clades	234	CBB_402	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88925.1	003187	Cluster2800_1clades	233	BF_0400	Serratia phage BF	GCA_002619745.1
SOK59213.1	003187	Cluster2800_1clades	233	g405	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58679.1	003187	Cluster2800_1clades	233	g402	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21931.1	003188	Cluster2801_1clades	225	GAP32_473	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44057.1	003188	Cluster2801_1clades	228	CBB_494	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89011.1	003188	Cluster2801_1clades	234	BF_0486	Serratia phage BF	GCA_002619745.1
SOK59292.1	003188	Cluster2801_1clades	232	g484	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58757.1	003188	Cluster2801_1clades	232	g480	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56910.1	003189	Fe_bilin_red	223	CPXG_00107	Cyanophage P-RSM6	GCA_000906155.1
AGH07477.1	003189	Fe_bilin_red	210	CYVG_00033	Cyanophage S-SSM6a	GCA_002710385.1
AGH26204.1	003189	Fe_bilin_red	209	CPMG_00103	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44436.1	003189	Fe_bilin_red	233	PSSM2_058	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12216.1	003189	Fe_bilin_red	233	PRTG_00058	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGH56832.1	003190	Heme_oxygenase	232	CPXG_00029	Cyanophage P-RSM6	GCA_000906155.1
AGH07607.1	003190	Heme_oxygenase	231	CYVG_00164	Cyanophage S-SSM6a	GCA_002710385.1
AGH26239.1	003190	Heme_oxygenase	230	CPMG_00138	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44668.1	003190	Heme_oxygenase	233	PSSM2_291	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12309.1	003190	Heme_oxygenase	233	PRTG_00156	Prochlorococcus phage P-SSM5	GCA_002991095.1
AUE22750.1	003191	Cluster2805_1clades	201	Ah1_00232	Aeromonas phage Ah1	GCA_002957415.1
QAX98467.1	003191	Cluster2805_1clades	204	ASfcp2_127	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52927.1	003191	Cluster2805_1clades	204	PX29p208	Aeromonas phage PX29	GCA_000920195.1
ADM79851.1	003191	Cluster2805_1clades	231	phiAS5_ORF0008	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17875.1	003191	Cluster2805_1clades	201	Aeh1ORF213c	Aeromonas virus Aeh1	GCA_000843245.1
AND75345.1	003192	Cluster2806_1clades	230	ME3_184	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ95127.1	003192	Cluster2806_1clades	156	FDI40_gp368	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGR47882.1	003192	Cluster2806_1clades	127	SmphiM12_250	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13083.1	003192	Cluster2806_1clades	127	PHIM19_178	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12723.1	003192	Cluster2806_1clades	127	PHIM7_178	Sinorhizobium phage phiM7	GCA_002622405.1
QIG63248.1	003193	Cluster2807_1clades	229	DAC16_15	Bacteroides phage DAC16	GCA_013387695.1
QIG63510.1	003193	Cluster2807_1clades	229	DAC19_19	Bacteroides phage DAC19	GCA_013387715.1
QIG63772.1	003193	Cluster2807_1clades	229	DAC20_19	Bacteroides phage DAC20	GCA_013387725.1
QIG64033.1	003193	Cluster2807_1clades	229	DAC22_19	Bacteroides phage DAC22	GCA_013387735.1
QIG64294.1	003193	Cluster2807_1clades	229	DAC23_16	Bacteroides phage DAC23	GCA_013387745.1
QIG63404.1	003194	Cluster2809_1clades	228	DAC16_174	Bacteroides phage DAC16	GCA_013387695.1
QIG63668.1	003194	Cluster2809_1clades	228	DAC19_180	Bacteroides phage DAC19	GCA_013387715.1
QIG63929.1	003194	Cluster2809_1clades	228	DAC20_179	Bacteroides phage DAC20	GCA_013387725.1
QIG64193.1	003194	Cluster2809_1clades	228	DAC22_182	Bacteroides phage DAC22	GCA_013387735.1
QIG64449.1	003194	Cluster2809_1clades	228	DAC23_174	Bacteroides phage DAC23	GCA_013387745.1
QIG63414.1	003195	ZNR	227	DAC16_184	Bacteroides phage DAC16	GCA_013387695.1
QIG63678.1	003195	ZNR	227	DAC19_190	Bacteroides phage DAC19	GCA_013387715.1
QIG63939.1	003195	ZNR	227	DAC20_189	Bacteroides phage DAC20	GCA_013387725.1
QIG64203.1	003195	ZNR	227	DAC22_192	Bacteroides phage DAC22	GCA_013387735.1
QIG64459.1	003195	ZNR	227	DAC23_184	Bacteroides phage DAC23	GCA_013387745.1
AUE22656.1	003196	Cluster2812_1clades	224	Ah1_00115	Aeromonas phage Ah1	GCA_002957415.1
QAX98383.1	003196	Cluster2812_1clades	224	ASfcp2_37	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52836.1	003196	Cluster2812_1clades	224	PX29p117	Aeromonas phage PX29	GCA_000920195.1
ADM80095.1	003196	Cluster2812_1clades	223	phiAS5_ORF0252	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17782.1	003196	Cluster2812_1clades	224	Aeh1ORF120c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21542.1	003197	GIT_CC	213	GAP32_094	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97157.1	003197	GIT_CC	203	E_149	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78673.1	003197	GIT_CC	221	RB43ORF151c	Escherichia virus RB43	GCA_000863505.1
AMM43661.1	003197	GIT_CC	212	CBB_96	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88613.1	003197	GIT_CC	198	BF_0088	Serratia phage BF	GCA_002619745.1
AFC21498.1	003198	Cluster2814_1clades	190	GAP32_050	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43619.1	003198	Cluster2814_1clades	203	CBB_54	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88569.1	003198	Cluster2814_1clades	219	BF_0044	Serratia phage BF	GCA_002619745.1
SOK58845.1	003198	Cluster2814_1clades	211	g037	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58307.1	003198	Cluster2814_1clades	208	g030	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCH63525.1	003199	MerR-HTH+GDResolvase	209	CP21_063	Campylobacter virus CP21	GCA_000902535.1
BAE47831.1	003199	MerR-HTH+GDResolvase	199	CST133	Clostridium phage c-st	GCA_000865225.1
BAE47845.1	003199	MerR-HTH+GDResolvase	219	CST147	Clostridium phage c-st	GCA_000865225.1
BAE47874.1	003199	MerR-HTH+GDResolvase	219	CST176	Clostridium phage c-st	GCA_000865225.1
prev15ph1000000559	003199	MerR-HTH+GDResolvase	202	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QIG63472.1	003200	Cluster2816_1clades	219	DAC16_243	Bacteroides phage DAC16	GCA_013387695.1
QIG63735.1	003200	Cluster2816_1clades	219	DAC19_248	Bacteroides phage DAC19	GCA_013387715.1
QIG63996.1	003200	Cluster2816_1clades	219	DAC20_247	Bacteroides phage DAC20	GCA_013387725.1
QIG64260.1	003200	Cluster2816_1clades	219	DAC22_250	Bacteroides phage DAC22	GCA_013387735.1
QIG64516.1	003200	Cluster2816_1clades	219	DAC23_242	Bacteroides phage DAC23	GCA_013387745.1
AJK27437.1	003201	Cluster2817_1clades	157	PTIM40_10	Cyanophage P-TIM40	GCA_001470935.1
AGH07550.1	003201	Cluster2817_1clades	162	CYVG_00106	Cyanophage S-SSM6a	GCA_002710385.1
AGH26284.1	003201	Cluster2817_1clades	157	CPMG_00184	Prochlorococcus phage MED4-213	GCA_000904535.1
QGT54738.1	003201	Cluster2817_1clades	218	b23_0123	Synechococcus phage B23	GCA_009745195.1
QGT54368.1	003201	Cluster2817_1clades	218	b3_0124	Synechococcus phage B3	GCA_009745215.1
QIG63439.1	003202	Cluster2818_1clades	218	DAC16_210	Bacteroides phage DAC16	GCA_013387695.1
QIG63702.1	003202	Cluster2818_1clades	218	DAC19_215	Bacteroides phage DAC19	GCA_013387715.1
QIG63963.1	003202	Cluster2818_1clades	218	DAC20_214	Bacteroides phage DAC20	GCA_013387725.1
QIG64227.1	003202	Cluster2818_1clades	218	DAC22_217	Bacteroides phage DAC22	GCA_013387735.1
QIG64483.1	003202	Cluster2818_1clades	218	DAC23_209	Bacteroides phage DAC23	GCA_013387745.1
QIG63460.1	003203	35exo	217	DAC16_231	Bacteroides phage DAC16	GCA_013387695.1
QIG63723.1	003203	35exo	217	DAC19_236	Bacteroides phage DAC19	GCA_013387715.1
QIG63984.1	003203	35exo	217	DAC20_235	Bacteroides phage DAC20	GCA_013387725.1
QIG64248.1	003203	35exo	217	DAC22_238	Bacteroides phage DAC22	GCA_013387735.1
QIG64504.1	003203	35exo	217	DAC23_230	Bacteroides phage DAC23	GCA_013387745.1
AUE22675.1	003204	CR-ATPase2	213	Ah1_00134	Aeromonas phage Ah1	GCA_002957415.1
QAX98401.1	003204	CR-ATPase2	213	ASfcp2_57	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52857.1	003204	CR-ATPase2	213	PX29p138	Aeromonas phage PX29	GCA_000920195.1
ADM80116.1	003204	CR-ATPase2	204	phiAS5_ORF0273	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17803.1	003204	CR-ATPase2	213	Aeh1ORF138c	Aeromonas virus Aeh1	GCA_000843245.1
AJK27657.1	003205	Redoxin	173	PTIM40_218	Cyanophage P-TIM40	GCA_001470935.1
AOO14391.1	003205	Redoxin	168	Sn110110_198	Cyanophage S-RIM14	GCA_002599065.1
AOO15039.1	003205	Redoxin	168	W1230910_194	Cyanophage S-RIM14	GCA_002599125.1
AGH07556.1	003205	Redoxin	212	CYVG_00112	Cyanophage S-SSM6a	GCA_002710385.1
AGG54398.1	003205	Redoxin	166	CYWG_00114	Cyanophage S-SSM6b	GCA_002710425.1
AMM43743.1	003206	Cluster2822_1clades	199	CBB_178	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18893.1	003206	Cluster2822_1clades	211	7t3_0372	Salmonella phage 7t3	GCA_006083215.1
AZU98151.1	003206	Cluster2822_1clades	201	CPT_Munch_207	Salmonella phage Munch	GCA_004015485.1
QIG62832.1	003206	Cluster2822_1clades	201	SEPL_219	Salmonella phage SE_PL	GCA_011067555.1
CCE26181.1	003206	Cluster2822_1clades	89	g157	Yersinia phage phiR1-37	GCA_000895615.1
QIG63434.1	003207	Cluster2823_1clades	205	DAC16_205	Bacteroides phage DAC16	GCA_013387695.1
QIG63698.1	003207	Cluster2823_1clades	211	DAC19_211	Bacteroides phage DAC19	GCA_013387715.1
QIG63959.1	003207	Cluster2823_1clades	211	DAC20_210	Bacteroides phage DAC20	GCA_013387725.1
QIG64223.1	003207	Cluster2823_1clades	205	DAC22_213	Bacteroides phage DAC22	GCA_013387735.1
QIG64479.1	003207	Cluster2823_1clades	205	DAC23_205	Bacteroides phage DAC23	GCA_013387745.1
AAQ64326.1	003208	Cluster2824_1clades	210	KVP40.0257	Vibrio phage KVP40	GCA_000843785.1
QIW90641.1	003208	Cluster2824_1clades	210	GCAPEGMB_00294	Vibrio phage V07	GCA_012361095.1
QIW91158.1	003208	Cluster2824_1clades	210	COHAPHLL_00322	Vibrio phage V09	GCA_012361135.1
QHJ74436.1	003208	Cluster2824_1clades	210	VH12019_00109	Vibrio phage VH1_2019	GCA_009931825.1
AFN37485.1	003208	Cluster2824_1clades	210	pp2_252	Vibriophage phi-pp2	GCA_002630725.1
AFC21499.1	003209	Cluster2825_1clades	205	GAP32_051	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43620.1	003209	Cluster2825_1clades	210	CBB_55	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88570.1	003209	Cluster2825_1clades	199	BF_0045	Serratia phage BF	GCA_002619745.1
SOK58846.1	003209	Cluster2825_1clades	198	g038	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58308.1	003209	Cluster2825_1clades	198	g031	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21926.1	003210	Cluster2826_1clades	209	GAP32_468	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44052.1	003210	Cluster2826_1clades	207	CBB_489	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89007.1	003210	Cluster2826_1clades	203	BF_0482	Serratia phage BF	GCA_002619745.1

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SOK59289.1	003210	Cluster2826_1clades	207	g481	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58754.1	003210	Cluster2826_1clades	207	g477	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ABY63187.1	003211	Cluster2827_1clades	206	201phi2-1p362	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32446.1	003211	Cluster2827_1clades	185	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76990.1	003211	Cluster2827_1clades	182	PHABIO_359	Pseudomonas phage Phabio	GCA_002624965.1
AEH03716.1	003211	Cluster2827_1clades	181	293	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42017.1	003211	Cluster2827_1clades	185	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGZ14493.1	003212	Cluster2828_1clades	205	HWC77_gp130	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04241.1	003212	Cluster2828_1clades	205	HWC03_gp086	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23122.1	003212	Cluster2828_1clades	203	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81028.1	003212	Cluster2828_1clades	205	Aphrodite1_0009	Vibrio phage Aphrodite1	GCA_002958015.1
BAW98211.1	003212	Cluster2828_1clades	206	FDH33_gp002	Vibrio phage pTD1	GCA_002618825.1
QIG63308.1	003213	Cluster2829_1clades	206	DAC16_75	Bacteroides phage DAC16	GCA_013387695.1
QIG63567.1	003213	Cluster2829_1clades	206	DAC19_76	Bacteroides phage DAC19	GCA_013387715.1
QIG63828.1	003213	Cluster2829_1clades	206	DAC20_75	Bacteroides phage DAC20	GCA_013387725.1
QIG64090.1	003213	Cluster2829_1clades	206	DAC22_76	Bacteroides phage DAC22	GCA_013387735.1
QIG64353.1	003213	Cluster2829_1clades	206	DAC23_75	Bacteroides phage DAC23	GCA_013387745.1
QIG63373.1	003214	Cluster2830_1clades	206	DAC16_140	Bacteroides phage DAC16	GCA_013387695.1
QIG63638.1	003214	Cluster2830_1clades	206	DAC19_147	Bacteroides phage DAC19	GCA_013387715.1
QIG63899.1	003214	Cluster2830_1clades	206	DAC20_146	Bacteroides phage DAC20	GCA_013387725.1
QIG64162.1	003214	Cluster2830_1clades	206	DAC22_148	Bacteroides phage DAC22	GCA_013387735.1
QIG64419.1	003214	Cluster2830_1clades	206	DAC23_141	Bacteroides phage DAC23	GCA_013387745.1
QIG63381.1	003215	SIG+Ferretin	206	DAC16_148	Bacteroides phage DAC16	GCA_013387695.1
QIG63645.1	003215	SIG+Ferretin	206	DAC19_154	Bacteroides phage DAC19	GCA_013387715.1
QIG63906.1	003215	SIG+Ferretin	206	DAC20_153	Bacteroides phage DAC20	GCA_013387725.1
QIG64170.1	003215	SIG+Ferretin	206	DAC22_156	Bacteroides phage DAC22	GCA_013387735.1
QIG64426.1	003215	SIG+Ferretin	206	DAC23_148	Bacteroides phage DAC23	GCA_013387745.1
AUE22669.1	003216	Cluster2832_1clades	205	Ah1_00128	Aeromonas phage Ah1	GCA_002957415.1
QAX98395.1	003216	Cluster2832_1clades	205	ASfcp2_51	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52851.1	003216	Cluster2832_1clades	205	PX29p132	Aeromonas phage PX29	GCA_000920195.1
ADM80110.1	003216	Cluster2832_1clades	204	phiAS5_ORF0267	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17798.1	003216	Cluster2832_1clades	205	Aeh1ORF133c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63427.1	003217	Cluster2833_1clades	205	DAC16_197	Bacteroides phage DAC16	GCA_013387695.1
QIG63691.1	003217	Cluster2833_1clades	205	DAC19_203	Bacteroides phage DAC19	GCA_013387715.1
QIG63952.1	003217	Cluster2833_1clades	205	DAC20_202	Bacteroides phage DAC20	GCA_013387725.1
QIG64216.1	003217	Cluster2833_1clades	205	DAC22_205	Bacteroides phage DAC22	GCA_013387735.1
QIG64472.1	003217	Cluster2833_1clades	205	DAC23_197	Bacteroides phage DAC23	GCA_013387745.1
QIG63483.1	003218	Cluster2836_1clades	201	DAC16_254	Bacteroides phage DAC16	GCA_013387695.1
QIG63745.1	003218	Cluster2836_1clades	201	DAC19_258	Bacteroides phage DAC19	GCA_013387715.1
QIG64006.1	003218	Cluster2836_1clades	201	DAC20_257	Bacteroides phage DAC20	GCA_013387725.1
QIG64270.1	003218	Cluster2836_1clades	201	DAC22_260	Bacteroides phage DAC22	GCA_013387735.1
QIG64527.1	003218	Cluster2836_1clades	201	DAC23_253	Bacteroides phage DAC23	GCA_013387745.1
QIG63457.1	003219	Cluster2838_1clades	200	DAC16_228	Bacteroides phage DAC16	GCA_013387695.1
QIG63720.1	003219	Cluster2838_1clades	200	DAC19_233	Bacteroides phage DAC19	GCA_013387715.1
QIG63981.1	003219	Cluster2838_1clades	200	DAC20_232	Bacteroides phage DAC20	GCA_013387725.1
QIG64245.1	003219	Cluster2838_1clades	200	DAC22_235	Bacteroides phage DAC22	GCA_013387735.1
QIG64501.1	003219	Cluster2838_1clades	200	DAC23_227	Bacteroides phage DAC23	GCA_013387745.1
AUE22597.1	003220	Cluster2839_1clades	190	Ah1_00056	Aeromonas phage Ah1	GCA_002957415.1
QAX98635.1	003220	Cluster2839_1clades	190	ASfcp2_302	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52775.1	003220	Cluster2839_1clades	190	PX29p056	Aeromonas phage PX29	GCA_000920195.1
ADM80031.1	003220	Cluster2839_1clades	193	phiAS5_ORF0188	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17720.1	003220	Cluster2839_1clades	199	Aeh1ORF060c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21500.1	003221	Cluster2840_1clades	198	GAP32_052	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43621.1	003221	Cluster2840_1clades	199	CBB_56	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88571.1	003221	Cluster2840_1clades	198	BF_0046	Serratia phage BF	GCA_002619745.1
SOK58847.1	003221	Cluster2840_1clades	198	g039	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58309.1	003221	Cluster2840_1clades	198	g032	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63329.1	003222	Cluster2841_1clades	138	DAC16_96	Bacteroides phage DAC16	GCA_013387695.1
QIG63591.1	003222	Cluster2841_1clades	198	DAC19_100	Bacteroides phage DAC19	GCA_013387715.1
QIG63852.1	003222	Cluster2841_1clades	198	DAC20_99	Bacteroides phage DAC20	GCA_013387725.1
QIG64115.1	003222	Cluster2841_1clades	138	DAC22_101	Bacteroides phage DAC22	GCA_013387735.1
QIG64373.1	003222	Cluster2841_1clades	138	DAC23_95	Bacteroides phage DAC23	GCA_013387745.1
AFC21966.1	003223	Cluster2842_1clades	174	GAP32_506	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44089.1	003223	Cluster2842_1clades	174	CBB_526	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89046.1	003223	Cluster2842_1clades	174	BF_0521	Serratia phage BF	GCA_002619745.1
SOK59321.1	003223	Cluster2842_1clades	182	g513	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58783.1	003223	Cluster2842_1clades	198	g506	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AAQ64323.1	003224	Cluster2843_1clades	197	KVP40.0254	Vibrio phage KVP40	GCA_000843785.1
QIW90638.1	003224	Cluster2843_1clades	176	GCAPEGMB_00291	Vibrio phage V07	GCA_012361095.1
QIW91161.1	003224	Cluster2843_1clades	176	COHAPHLL_00325	Vibrio phage V09	GCA_012361135.1
QHJ74433.1	003224	Cluster2843_1clades	176	VH12019_00106	Vibrio phage VH1_2019	GCA_009931825.1
AFN37482.1	003224	Cluster2843_1clades	176	pp2_249	Vibriophage phi-pp2	GCA_002630725.1
ANZ49849.1	003225	SIG+TM	187	MACHINA_211	Erwinia phage Machina	GCA_002758035.1
ANZ48506.1	003225	SIG+TM	197	CAITLIN_211	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48783.1	003225	SIG+TM	194	CHRISDB_221	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49293.1	003225	SIG+TM	187	HUXLEY_211	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50121.1	003225	SIG+TM	187	PARSHIK_212	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AXG67073.1	003226	TM+TM+TM	194	AD1_029	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80048.1	003226	TM+TM+TM	197	JA11_243	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66647.1	003226	TM+TM+TM	197	JA13_244	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66971.1	003226	TM+TM+TM	197	JA29_245	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67618.1	003226	TM+TM+TM	197	JA33_244	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QIG63350.1	003227	DEDD_Tnp_IS110	197	DAC16_117	Bacteroides phage DAC16	GCA_013387695.1
QIG63616.1	003227	DEDD_Tnp_IS110	197	DAC19_125	Bacteroides phage DAC19	GCA_013387715.1
QIG63877.1	003227	DEDD_Tnp_IS110	197	DAC20_124	Bacteroides phage DAC20	GCA_013387725.1
QIG64140.1	003227	DEDD_Tnp_IS110	197	DAC22_126	Bacteroides phage DAC22	GCA_013387735.1
QIG64397.1	003227	DEDD_Tnp_IS110	197	DAC23_119	Bacteroides phage DAC23	GCA_013387745.1
AXH70803.1	003228	Cluster2847_1clades	152	-	Vibrio phage BONAISH1	GCA_003441475.1
QAX96706.1	003228	Cluster2847_1clades	196	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97024.1	003228	Cluster2847_1clades	196	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96070.1	003228	Cluster2847_1clades	196	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96388.1	003228	Cluster2847_1clades	196	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63432.1	003229	Cluster2849_1clades	184	DAC16_203	Bacteroides phage DAC16	GCA_013387695.1
QIG63696.1	003229	Cluster2849_1clades	196	DAC19_209	Bacteroides phage DAC19	GCA_013387715.1
QIG63957.1	003229	Cluster2849_1clades	196	DAC20_208	Bacteroides phage DAC20	GCA_013387725.1
QIG64221.1	003229	Cluster2849_1clades	184	DAC22_211	Bacteroides phage DAC22	GCA_013387735.1
QIG64477.1	003229	Cluster2849_1clades	184	DAC23_203	Bacteroides phage DAC23	GCA_013387745.1
AUE22588.1	003230	Cluster2850_1clades	193	Ah1_00047	Aeromonas phage Ah1	GCA_002957415.1
QAX98626.1	003230	Cluster2850_1clades	193	ASfcp2_293	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52766.1	003230	Cluster2850_1clades	193	PX29p047	Aeromonas phage PX29	GCA_000920195.1
ADM80020.1	003230	Cluster2850_1clades	186	phiAS5_ORF0177	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17710.1	003230	Cluster2850_1clades	189	Aeh1ORF051c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21629.1	003231	Cluster2851_1clades	191	GAP32_179	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43751.1	003231	Cluster2851_1clades	191	CBB_186	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88709.1	003231	Cluster2851_1clades	190	BF_0184	Serratia phage BF	GCA_002619745.1
SOK58991.1	003231	Cluster2851_1clades	192	g183	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58456.1	003231	Cluster2851_1clades	192	g179	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22795.1	003232	Cluster2852_1clades	153	Ah1_00277	Aeromonas phage Ah1	GCA_002957415.1
QAX98510.1	003232	Cluster2852_1clades	189	ASfcp2_174	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52971.1	003232	Cluster2852_1clades	191	PX29p252	Aeromonas phage PX29	GCA_000920195.1
ADM79897.1	003232	Cluster2852_1clades	152	phiAS5_ORF0054	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17921.1	003232	Cluster2852_1clades	185	Aeh1ORF258c	Aeromonas virus Aeh1	GCA_000843245.1
ANZ49828.1	003233	Cluster2853_1clades	190	MACHINA_190	Erwinia phage Machina	GCA_002758035.1
ANZ48483.1	003233	Cluster2853_1clades	190	CAITLIN_188	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48762.1	003233	Cluster2853_1clades	191	CHRISDB_200	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49272.1	003233	Cluster2853_1clades	190	HUXLEY_190	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50100.1	003233	Cluster2853_1clades	190	PARSHIK_191	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AGX01922.1	003234	TM+TM	181	-	Erwinia phage PhiEaH1	GCA_000914555.1
QBO63878.1	003234	TM+TM	189	Goslar_00085	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ATA65390.1	003234	TM+TM	191	2050HW_00055	Serratia phage 2050HW	GCA_002628125.1
QDB71171.1	003234	TM+TM	191	CPT_Moabite_141	Serratia phage Moabite	GCA_006384735.1
QFP93187.1	003234	TM+TM	167	-	Serratia phage PCH45	GCA_009187865.1
AUE22590.1	003235	Cluster2855_1clades	185	Ah1_00049	Aeromonas phage Ah1	GCA_002957415.1
QAX98628.1	003235	Cluster2855_1clades	190	ASfcp2_295	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52768.1	003235	Cluster2855_1clades	190	PX29p049	Aeromonas phage PX29	GCA_000920195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADM80023.1	003235	Cluster2855_1clades	181	phiAS5_ORF0180	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17712.1	003235	Cluster2855_1clades	185	Aeh1ORF053c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22680.1	003236	Cluster2856_1clades	189	Ah1_00139	Aeromonas phage Ah1	GCA_002957415.1
QAX98406.1	003236	Cluster2856_1clades	188	ASfcp2_62	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52862.1	003236	Cluster2856_1clades	188	PX29p143	Aeromonas phage PX29	GCA_000920195.1
ADM80121.1	003236	Cluster2856_1clades	183	phiAS5_ORF0278	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17808.1	003236	Cluster2856_1clades	189	Aeh1ORF143c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21843.1	003237	Cluster2857_1clades	189	GAP32_391	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43963.1	003237	Cluster2857_1clades	103	CBB_400	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88923.1	003237	Cluster2857_1clades	103	BF_0398	Serratia phage BF	GCA_002619745.1
SOK59212.1	003237	Cluster2857_1clades	102	g404	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58678.1	003237	Cluster2857_1clades	102	g401	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QAU04298.1	003238	Cluster2858_1clades	189	HWC03_gp143	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23280.1	003238	Cluster2858_1clades	187	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81034.1	003238	Cluster2858_1clades	187	Aphrodite1_0065	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47448.1	003238	Cluster2858_1clades	187	HWC35_gp054	Vibrio phage USC-1	GCA_006864065.1
BAW98270.1	003238	Cluster2858_1clades	175	FDH33_gp061	Vibrio phage pTD1	GCA_002618825.1
ANZ49844.1	003239	Cluster2859_1clades	88	MACHINA_206	Erwinia phage Machina	GCA_002758035.1
ANZ48499.1	003239	Cluster2859_1clades	85	CAITLIN_204	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48778.1	003239	Cluster2859_1clades	188	CHRISDB_216	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49288.1	003239	Cluster2859_1clades	88	HUXLEY_206	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50116.1	003239	Cluster2859_1clades	88	PARSHIK_207	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
BBI90667.1	003240	Cluster2235_1clades	131	HYO65_gp275	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90972.1	003240	Cluster2235_1clades	131	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90978.1	003240	Cluster2235_1clades	70	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBP07665.1	003241	Cluster2861_1clades	188	DERBICUS_239	Erwinia phage Derbicus	GCA_004521655.1
QBP07666.1	003241	Cluster2861_1clades	155	DERBICUS_240	Erwinia phage Derbicus	GCA_004521655.1
ANZ49089.1	003241	Cluster2861_1clades	163	EARLPHILLIPIV_240	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49090.1	003241	Cluster2861_1clades	163	EARLPHILLIPIV_241	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50437.1	003241	Cluster2861_1clades	149	PHOBOS_247	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AFC21554.1	003242	Cluster2863_1clades	187	GAP32_106	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43672.1	003242	Cluster2863_1clades	184	CBB_107	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88625.1	003242	Cluster2863_1clades	183	BF_0100	Serratia phage BF	GCA_002619745.1
SOK58901.1	003242	Cluster2863_1clades	187	g093	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58366.1	003242	Cluster2863_1clades	187	g089	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21891.1	003243	Tox-PLA2	117	GAP32_437	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44019.1	003243	Tox-PLA2	117	CBB_456	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QHJ85919.1	003243	Tox-PLA2	187	KKIINIFJ_00007	Pseudomonas phage PN05	GCA_009931935.1
AGS82048.1	003243	Tox-PLA2	150	PaBG_00171	Pseudomonas phage PaBG	GCA_000912555.1
QAU04557.1	003243	Tox-PLA2	136	ValB1MD_274	Vibrio phage ValB1MD	GCA_004138815.1
ANS06048.1	003244	Cluster2865_1clades	147	ABCD_0009	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA65017.1	003244	Cluster2865_1clades	161	S13_220	Cronobacter phage S13	GCA_001503575.1
AON97017.1	003244	Cluster2865_1clades	143	E_008	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78530.1	003244	Cluster2865_1clades	143	RB43ORF008c	Escherichia virus RB43	GCA_000863505.1
QHJ78915.1	003244	Cluster2865_1clades	186	-	Myoviridae sp.	GCA_012593985.1
QIG63417.1	003245	Cluster2866_1clades	186	DAC16_187	Bacteroides phage DAC16	GCA_013387695.1
QIG63681.1	003245	Cluster2866_1clades	186	DAC19_193	Bacteroides phage DAC19	GCA_013387715.1
QIG63942.1	003245	Cluster2866_1clades	186	DAC20_192	Bacteroides phage DAC20	GCA_013387725.1
QIG64206.1	003245	Cluster2866_1clades	186	DAC22_195	Bacteroides phage DAC22	GCA_013387735.1
QIG64462.1	003245	Cluster2866_1clades	186	DAC23_187	Bacteroides phage DAC23	GCA_013387745.1
AFC21832.1	003246	Cluster2867_1clades	185	GAP32_380	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43953.1	003246	Cluster2867_1clades	171	CBB_390	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88914.1	003246	Cluster2867_1clades	168	BF_0389	Serratia phage BF	GCA_002619745.1
SOK59203.1	003246	Cluster2867_1clades	173	g395	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58668.1	003246	Cluster2867_1clades	173	g391	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63413.1	003247	Cluster2868_1clades	185	DAC16_183	Bacteroides phage DAC16	GCA_013387695.1
QIG63677.1	003247	Cluster2868_1clades	185	DAC19_189	Bacteroides phage DAC19	GCA_013387715.1
QIG63938.1	003247	Cluster2868_1clades	185	DAC20_188	Bacteroides phage DAC20	GCA_013387725.1
QIG64202.1	003247	Cluster2868_1clades	185	DAC22_191	Bacteroides phage DAC22	GCA_013387735.1
QIG64458.1	003247	Cluster2868_1clades	185	DAC23_183	Bacteroides phage DAC23	GCA_013387745.1
QIG63482.1	003248	Cluster2869_1clades	185	DAC16_253	Bacteroides phage DAC16	GCA_013387695.1
QIG63744.1	003248	Cluster2869_1clades	185	DAC19_257	Bacteroides phage DAC19	GCA_013387715.1
QIG64005.1	003248	Cluster2869_1clades	185	DAC20_256	Bacteroides phage DAC20	GCA_013387725.1
QIG64269.1	003248	Cluster2869_1clades	185	DAC22_259	Bacteroides phage DAC22	GCA_013387735.1
QIG64526.1	003248	Cluster2869_1clades	185	DAC23_252	Bacteroides phage DAC23	GCA_013387745.1
AUE22589.1	003249	Cluster2870_1clades	156	Ah1_00048	Aeromonas phage Ah1	GCA_002957415.1
QAX98627.1	003249	Cluster2870_1clades	173	ASfcp2_294	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52767.1	003249	Cluster2870_1clades	173	PX29p048	Aeromonas phage PX29	GCA_000920195.1
ADM80021.1	003249	Cluster2870_1clades	184	phiAS5_ORF0178	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17711.1	003249	Cluster2870_1clades	173	Aeh1ORF052c	Aeromonas virus Aeh1	GCA_000843245.1
AXH70991.1	003250	Cluster2871_1clades	164	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96833.1	003250	Cluster2871_1clades	159	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96831.1	003250	Cluster2871_1clades	184	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96196.1	003250	Cluster2871_1clades	184	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96514.1	003250	Cluster2871_1clades	184	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63400.1	003251	Cluster2873_1clades	184	DAC16_170	Bacteroides phage DAC16	GCA_013387695.1
QIG63664.1	003251	Cluster2873_1clades	184	DAC19_176	Bacteroides phage DAC19	GCA_013387715.1
QIG63925.1	003251	Cluster2873_1clades	184	DAC20_175	Bacteroides phage DAC20	GCA_013387725.1
QIG64189.1	003251	Cluster2873_1clades	184	DAC22_178	Bacteroides phage DAC22	GCA_013387735.1
QIG64445.1	003251	Cluster2873_1clades	184	DAC23_170	Bacteroides phage DAC23	GCA_013387745.1
AUE22672.1	003252	Phytase-like	182	Ah1_00131	Aeromonas phage Ah1	GCA_002957415.1
QAX98398.1	003252	Phytase-like	181	ASfcp2_54	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52854.1	003252	Phytase-like	181	PX29p135	Aeromonas phage PX29	GCA_000920195.1
ADM80113.1	003252	Phytase-like	173	phiAS5_ORF0270	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17801.1	003252	Phytase-like	182	Aeh1ORF136c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22628.1	003253	SIG+Radial_spoke_3	180	Ah1_00087	Aeromonas phage Ah1	GCA_002957415.1
QAX98358.1	003253	SIG+Radial_spoke_3	180	ASfcp2_12	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52812.1	003253	SIG+Radial_spoke_3	180	PX29p093	Aeromonas phage PX29	GCA_000920195.1
ADM80068.1	003253	SIG+Radial_spoke_3	182	phiAS5_ORF0225	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17755.1	003253	SIG+Radial_spoke_3	180	Aeh1ORF094c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21943.1	003254	C3RHD	178	GAP32_485	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44070.1	003254	C3RHD	175	CBB_507	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89027.1	003254	C3RHD	181	BF_0502	Serratia phage BF	GCA_002619745.1
SOK59307.1	003254	C3RHD	182	g499	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58772.1	003254	C3RHD	182	g495	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28738.1	003255	Cluster2877_1clades	175	AP1_0020	Aeromonas phage AP1	GCA_014183365.1
ATI17566.1	003255	Cluster2877_1clades	175	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00430.1	003255	Cluster2877_1clades	175	HWB28_gp122	Aeromonas phage AS-zj	GCA_002627665.1
QAX98006.1	003255	Cluster2877_1clades	180	ASswx1_366	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39241.1	003255	Cluster2877_1clades	180	CC2_166	Aeromonas phage CC2	GCA_000903495.1
AYD80042.1	003256	Cluster2878_1clades	159	JA11_237	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66641.1	003256	Cluster2878_1clades	159	JA13_238	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66965.1	003256	Cluster2878_1clades	159	JA29_239	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67612.1	003256	Cluster2878_1clades	159	JA33_238	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AQT28731.1	003256	Cluster2878_1clades	180	YOLOSWAG_257	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AUE22630.1	003257	Cluster2879_1clades	177	Ah1_00089	Aeromonas phage Ah1	GCA_002957415.1
QAX98360.1	003257	Cluster2879_1clades	179	ASfcp2_14	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52814.1	003257	Cluster2879_1clades	179	PX29p095	Aeromonas phage PX29	GCA_000920195.1
ADM80070.1	003257	Cluster2879_1clades	176	phiAS5_ORF0227	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17757.1	003257	Cluster2879_1clades	177	Aeh1ORF096c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22625.1	003258	Cluster2880_1clades	177	Ah1_00084	Aeromonas phage Ah1	GCA_002957415.1
QAX98352.1	003258	Cluster2880_1clades	177	ASfcp2_6	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52808.1	003258	Cluster2880_1clades	160	PX29p089	Aeromonas phage PX29	GCA_000920195.1
ADM80065.1	003258	Cluster2880_1clades	103	phiAS5_ORF0222	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17752.1	003258	Cluster2880_1clades	177	Aeh1ORF091c	Aeromonas virus Aeh1	GCA_000843245.1
AXG67100.1	003259	Cluster2884_1clades	155	AD1_056	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79856.1	003259	Cluster2884_1clades	175	JA11_051	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG67425.1	003259	Cluster2884_1clades	175	JA33_051	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AWY08336.1	003259	Cluster2884_1clades	154	Alexandra_56	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58699.1	003259	Cluster2884_1clades	174	Y3_059	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QIG63335.1	003260	Cluster2885_1clades	174	DAC16_102	Bacteroides phage DAC16	GCA_013387695.1
QIG63601.1	003260	Cluster2885_1clades	174	DAC19_110	Bacteroides phage DAC19	GCA_013387715.1
QIG63862.1	003260	Cluster2885_1clades	174	DAC20_109	Bacteroides phage DAC20	GCA_013387725.1
QIG64126.1	003260	Cluster2885_1clades	175	DAC22_112	Bacteroides phage DAC22	GCA_013387735.1
QIG64382.1	003260	Cluster2885_1clades	174	DAC23_104	Bacteroides phage DAC23	GCA_013387745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63402.1	003261	Cluster2886_1clades	174	DAC16_172	Bacteroides phage DAC16	GCA_013387695.1
QIG63666.1	003261	Cluster2886_1clades	174	DAC19_178	Bacteroides phage DAC19	GCA_013387715.1
QIG63927.1	003261	Cluster2886_1clades	174	DAC20_177	Bacteroides phage DAC20	GCA_013387725.1
QIG64191.1	003261	Cluster2886_1clades	174	DAC22_180	Bacteroides phage DAC22	GCA_013387735.1
QIG64447.1	003261	Cluster2886_1clades	174	DAC23_172	Bacteroides phage DAC23	GCA_013387745.1
AFC21501.1	003262	Cluster2887_1clades	167	GAP32_053	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43622.1	003262	Cluster2887_1clades	173	CBB_57	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88572.1	003262	Cluster2887_1clades	170	BF_0047	Serratia phage BF	GCA_002619745.1
SOK58848.1	003262	Cluster2887_1clades	174	g040	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58310.1	003262	Cluster2887_1clades	174	g033	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21561.1	003263	Cluster2888_1clades	171	GAP32_113	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43679.1	003263	Cluster2888_1clades	172	CBB_114	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88632.1	003263	Cluster2888_1clades	173	BF_0107	Serratia phage BF	GCA_002619745.1
SOK58909.1	003263	Cluster2888_1clades	172	g101	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58374.1	003263	Cluster2888_1clades	172	g097	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63395.1	003264	SIG+TM	173	DAC16_165	Bacteroides phage DAC16	GCA_013387695.1
QIG63659.1	003264	SIG+TM	173	DAC19_171	Bacteroides phage DAC19	GCA_013387715.1
QIG63920.1	003264	SIG+TM	173	DAC20_170	Bacteroides phage DAC20	GCA_013387725.1
QIG64184.1	003264	SIG+TM	173	DAC22_173	Bacteroides phage DAC22	GCA_013387735.1
QIG64440.1	003264	SIG+TM	173	DAC23_165	Bacteroides phage DAC23	GCA_013387745.1
QIG57778.1	003265	HIT	161	SEA_PAULODIABOLI_43	Microbacterium phage PauloDiaboli	GCA_011067425.1
AYD81334.1	003265	HIT	171	SEA_JUSTBECAUSE_169	Streptomyces phage JustBecause	GCA_003613775.1
QJD53737.1	003265	HIT	173	SEA_KELA_167	Streptomyces phage Kela	GCA_012934305.1
QBZ72064.1	003265	HIT	169	SEA_KRADAL_168	Streptomyces phage Kradal	GCA_004799925.1
AXH66327.1	003265	HIT	169	SEA_SATIS_168	Streptomyces phage Satis	GCA_003366315.1
QDJ96765.1	003266	Cluster2891_1clades	158	PS1_0007	Aeromonas phage PS1	GCA_007051165.2
QFR59398.1	003266	Cluster2891_1clades	158	PS2_0007	Aeromonas phage PS2	GCA_009388305.2
QBZ70852.1	003266	Cluster2891_1clades	171	pETSU_271	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71884.1	003266	Cluster2891_1clades	167	N1M2_21	Klebsiella phage N1M2	GCA_010092605.1
AEV89478.1	003266	Cluster2891_1clades	168	OBP_041	Pseudomonas phage OBP	GCA_000896635.1
QIG63489.1	003267	Cluster2892_1clades	171	DAC16_260	Bacteroides phage DAC16	GCA_013387695.1
QIG63751.1	003267	Cluster2892_1clades	163	DAC19_264	Bacteroides phage DAC19	GCA_013387715.1
QIG64012.1	003267	Cluster2892_1clades	163	DAC20_263	Bacteroides phage DAC20	GCA_013387725.1
QIG64276.1	003267	Cluster2892_1clades	163	DAC22_266	Bacteroides phage DAC22	GCA_013387735.1
QIG64533.1	003267	Cluster2892_1clades	171	DAC23_259	Bacteroides phage DAC23	GCA_013387745.1
ARB15589.1	003268	Cluster2893_1clades	165	Ccr34_gp088	Caulobacter phage Ccr34	GCA_002619525.1
AXQ69175.1	003268	Cluster2893_1clades	170	CcrBL9_gp151c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ68643.1	003268	Cluster2893_1clades	163	CcrPW_gp104c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87601.1	003268	Cluster2893_1clades	162	CcrKarma_gp084	Caulobacter virus Karma	GCA_000901575.1
AFU86914.1	003268	Cluster2893_1clades	165	CbK_gp082	Caulobacter virus phiCbK	GCA_000900535.1
AFC21598.1	003269	Cluster2894_1clades	169	GAP32_148	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43718.1	003269	Cluster2894_1clades	168	CBB_153	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88672.1	003269	Cluster2894_1clades	168	BF_0147	Serratia phage BF	GCA_002619745.1
SOK58954.1	003269	Cluster2894_1clades	166	g146	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58420.1	003269	Cluster2894_1clades	166	g143	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21621.1	003270	Cluster2895_1clades	168	GAP32_171	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43739.1	003270	Cluster2895_1clades	169	CBB_174	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88697.1	003270	Cluster2895_1clades	166	BF_0172	Serratia phage BF	GCA_002619745.1
SOK58978.1	003270	Cluster2895_1clades	167	g170	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58444.1	003270	Cluster2895_1clades	167	g167	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AJK27543.1	003271	TM	167	PTIM40_116	Cyanophage P-TIM40	GCA_001470935.1
AGH07514.1	003271	TM	167	CYVG_00070	Cyanophage S-SSM6a	GCA_002710385.1
AGG54413.1	003271	TM	167	CYWG_00129	Cyanophage S-SSM6b	GCA_002710425.1
AGH26231.1	003271	TM	167	CPMG_00130	Prochlorococcus phage MED4-213	GCA_000904535.1
ASR76280.1	003271	TM	168	PBI_BELLAMY_244	Synechococcus phage Bellamy	GCA_002627525.1
QIG63333.1	003272	Cluster2897_1clades	168	DAC16_100	Bacteroides phage DAC16	GCA_013387695.1
QIG63599.1	003272	Cluster2897_1clades	168	DAC19_108	Bacteroides phage DAC19	GCA_013387715.1
QIG63860.1	003272	Cluster2897_1clades	168	DAC20_107	Bacteroides phage DAC20	GCA_013387725.1
QIG64124.1	003272	Cluster2897_1clades	166	DAC22_110	Bacteroides phage DAC22	GCA_013387735.1
QIG64380.1	003272	Cluster2897_1clades	168	DAC23_102	Bacteroides phage DAC23	GCA_013387745.1
QIG63393.1	003273	Cluster2898_1clades	168	DAC16_163	Bacteroides phage DAC16	GCA_013387695.1
QIG63657.1	003273	Cluster2898_1clades	168	DAC19_169	Bacteroides phage DAC19	GCA_013387715.1
QIG63918.1	003273	Cluster2898_1clades	168	DAC20_168	Bacteroides phage DAC20	GCA_013387725.1
QIG64182.1	003273	Cluster2898_1clades	168	DAC22_171	Bacteroides phage DAC22	GCA_013387735.1
QIG64438.1	003273	Cluster2898_1clades	168	DAC23_163	Bacteroides phage DAC23	GCA_013387745.1
QIG63398.1	003274	Cluster2899_1clades	168	DAC16_168	Bacteroides phage DAC16	GCA_013387695.1
QIG63662.1	003274	Cluster2899_1clades	168	DAC19_174	Bacteroides phage DAC19	GCA_013387715.1
QIG63923.1	003274	Cluster2899_1clades	168	DAC20_173	Bacteroides phage DAC20	GCA_013387725.1
QIG64187.1	003274	Cluster2899_1clades	168	DAC22_176	Bacteroides phage DAC22	GCA_013387735.1
QIG64443.1	003274	Cluster2899_1clades	168	DAC23_168	Bacteroides phage DAC23	GCA_013387745.1
AUE22806.1	003275	Cluster2900_1clades	164	Ah1_00288	Aeromonas phage Ah1	GCA_002957415.1
QAX98521.1	003275	Cluster2900_1clades	164	ASfcp2_185	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52984.1	003275	Cluster2900_1clades	164	PX29p265	Aeromonas phage PX29	GCA_000920195.1
ADM79908.1	003275	Cluster2900_1clades	167	phiAS5_ORF0065	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17933.1	003275	Cluster2900_1clades	164	Aeh1ORF269c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63264.1	003276	Cluster2901_1clades	167	DAC16_31	Bacteroides phage DAC16	GCA_013387695.1
QIG63526.1	003276	Cluster2901_1clades	161	DAC19_35	Bacteroides phage DAC19	GCA_013387715.1
QIG63788.1	003276	Cluster2901_1clades	161	DAC20_35	Bacteroides phage DAC20	GCA_013387725.1
QIG64049.1	003276	Cluster2901_1clades	161	DAC22_35	Bacteroides phage DAC22	GCA_013387735.1
QIG64310.1	003276	Cluster2901_1clades	162	DAC23_32	Bacteroides phage DAC23	GCA_013387745.1
AUE22548.1	003277	Cluster2902_1clades	122	Ah1_00007	Aeromonas phage Ah1	GCA_002957415.1
QAX98588.1	003277	Cluster2902_1clades	166	ASfcp2_255	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52724.1	003277	Cluster2902_1clades	166	PX29p005	Aeromonas phage PX29	GCA_000920195.1
ADM79976.1	003277	Cluster2902_1clades	164	phiAS5_ORF0133	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17661.1	003277	Cluster2902_1clades	166	Aeh1ORF006c	Aeromonas virus Aeh1	GCA_000843245.1
ASV44355.1	003278	Cluster2903_1clades	155	PBI_SCTP2_340	Salicola phage SCTP-2	GCA_002625545.1
ASV44356.1	003278	Cluster2903_1clades	166	PBI_SCTP2_341	Salicola phage SCTP-2	GCA_002625545.1
ASV44357.1	003278	Cluster2903_1clades	155	PBI_SCTP2_342	Salicola phage SCTP-2	GCA_002625545.1
ASV44358.1	003278	Cluster2903_1clades	151	PBI_SCTP2_343	Salicola phage SCTP-2	GCA_002625545.1
ASV44359.1	003278	Cluster2903_1clades	162	PBI_SCTP2_344	Salicola phage SCTP-2	GCA_002625545.1
QIG63419.1	003279	HNH	166	DAC16_189	Bacteroides phage DAC16	GCA_013387695.1
QIG63683.1	003279	HNH	166	DAC19_195	Bacteroides phage DAC19	GCA_013387715.1
QIG63944.1	003279	HNH	166	DAC20_194	Bacteroides phage DAC20	GCA_013387725.1
QIG64208.1	003279	HNH	166	DAC22_197	Bacteroides phage DAC22	GCA_013387735.1
QIG64464.1	003279	HNH	166	DAC23_189	Bacteroides phage DAC23	GCA_013387745.1
QIG63321.1	003280	SIG+DUF1002	165	DAC16_88	Bacteroides phage DAC16	GCA_013387695.1
QIG63582.1	003280	SIG+DUF1002	165	DAC19_91	Bacteroides phage DAC19	GCA_013387715.1
QIG63843.1	003280	SIG+DUF1002	165	DAC20_90	Bacteroides phage DAC20	GCA_013387725.1
QIG64105.1	003280	SIG+DUF1002	160	DAC22_91	Bacteroides phage DAC22	GCA_013387735.1
QIG64365.1	003280	SIG+DUF1002	165	DAC23_87	Bacteroides phage DAC23	GCA_013387745.1
AXF51368.1	003281	Cluster2908_1clades	164	WELLINGTON_242	Erwinia phage Wellington	GCA_003344985.1
AFQ96681.1	003281	Cluster2908_1clades	164	G173_gp136	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48247.1	003281	Cluster2908_1clades	164	ASESINO_234	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ49594.1	003281	Cluster2908_1clades	164	KWAN_242	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50661.1	003281	Cluster2908_1clades	164	STRATTON_236	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXH70930.1	003282	SIG+TM+TM	164	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96913.1	003282	SIG+TM+TM	149	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97218.1	003282	SIG+TM+TM	149	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96277.1	003282	SIG+TM+TM	149	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96595.1	003282	SIG+TM+TM	149	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AUZ94989.1	003283	Cluster2910_1clades	141	FDI40_gp207	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGR47835.1	003283	Cluster2910_1clades	163	SmphiM12_203	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13043.1	003283	Cluster2910_1clades	163	PHIM19_138	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12684.1	003283	Cluster2910_1clades	163	PHIM7_138	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13416.1	003283	Cluster2910_1clades	163	PHIN3_153	Sinorhizobium phage phiN3	GCA_001501175.1
QMV28971.1	003284	Cluster2911_1clades	161	AP1_0264	Aeromonas phage AP1	GCA_014183365.1
ATI17323.1	003284	Cluster2911_1clades	161	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00271.1	003284	Cluster2911_1clades	161	HWB28_gp281	Aeromonas phage AS-zj	GCA_002627665.1
QAX97766.1	003284	Cluster2911_1clades	161	ASswx1_121	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39293.1	003284	Cluster2911_1clades	162	CC2_416	Aeromonas phage CC2	GCA_000903495.1
AYD80072.1	003285	Cluster2912_1clades	144	JA11_267	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66673.1	003285	Cluster2912_1clades	144	JA13_270	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66993.1	003285	Cluster2912_1clades	140	JA29_267	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67642.1	003285	Cluster2912_1clades	144	JA33_268	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AQT28743.1	003285	Cluster2912_1clades	162	YOLOSWAG_270	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21841.1	003286	Cluster2913_1clades	154	GAP32_389	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43961.1	003286	Cluster2913_1clades	154	CBB_398	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19098.1	003286	Cluster2913_1clades	162	7t3_0580	Salmonella phage 7t3	GCA_006083215.1
AZU98337.1	003286	Cluster2913_1clades	162	CPT_Munch_395	Salmonella phage Munch	GCA_004015485.1
QIG62646.1	003286	Cluster2913_1clades	162	SEPL_033	Salmonella phage SE_PL	GCA_011067555.1
QIG63326.1	003287	Cluster2914_1clades	162	DAC16_93	Bacteroides phage DAC16	GCA_013387695.1
QIG63588.1	003287	Cluster2914_1clades	161	DAC19_97	Bacteroides phage DAC19	GCA_013387715.1
QIG63849.1	003287	Cluster2914_1clades	161	DAC20_96	Bacteroides phage DAC20	GCA_013387725.1
QIG64111.1	003287	Cluster2914_1clades	161	DAC22_97	Bacteroides phage DAC22	GCA_013387735.1
QIG64370.1	003287	Cluster2914_1clades	162	DAC23_92	Bacteroides phage DAC23	GCA_013387745.1
AUE22846.1	003288	Cluster2915_1clades	157	Ah1_00328	Aeromonas phage Ah1	GCA_002957415.1
QAX98558.1	003288	Cluster2915_1clades	157	ASfcp2_224	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53023.1	003288	Cluster2915_1clades	157	PX29p304	Aeromonas phage PX29	GCA_000920195.1
ADM79947.1	003288	Cluster2915_1clades	161	phiAS5_ORF0104	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17976.1	003288	Cluster2915_1clades	157	Aeh1ORF307c	Aeromonas virus Aeh1	GCA_000843245.1
ASV44755.1	003289	TM	136	FDI40_gp678	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFU87897.1	003289	TM	161	CcrColossus_gp027	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68567.1	003289	TM	143	CcrPW_gp028	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69016.1	003289	TM	143	CcrPW_gp477	Caulobacter phage CcrPW	GCA_003443275.1
AXH72529.1	003289	TM	140	-	Myoviridae sp.	GCA_003657725.1
AFC21936.1	003290	Cluster2917_1clades	160	GAP32_478	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44062.1	003290	Cluster2917_1clades	160	CBB_499	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89017.1	003290	Cluster2917_1clades	160	BF_0492	Serratia phage BF	GCA_002619745.1
SOK59298.1	003290	Cluster2917_1clades	155	g490	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58763.1	003290	Cluster2917_1clades	155	g486	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ABY63252.1	003291	Cluster2918_1clades	146	201phi2-1p429	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32380.1	003291	Cluster2918_1clades	160	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03796.1	003291	Cluster2918_1clades	156	373	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02762.1	003291	Cluster2918_1clades	151	PSA21_236	Pseudomonas phage Psa21	GCA_004340405.1
QEM41953.1	003291	Cluster2918_1clades	160	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63389.1	003292	COX5A	160	DAC16_159	Bacteroides phage DAC16	GCA_013387695.1
QIG63653.1	003292	COX5A	160	DAC19_165	Bacteroides phage DAC19	GCA_013387715.1
QIG63914.1	003292	COX5A	160	DAC20_164	Bacteroides phage DAC20	GCA_013387725.1
QIG64178.1	003292	COX5A	160	DAC22_167	Bacteroides phage DAC22	GCA_013387735.1
QIG64433.1	003292	COX5A	160	DAC23_158	Bacteroides phage DAC23	GCA_013387745.1
QIG63441.1	003293	Cluster2921_1clades	160	DAC16_212	Bacteroides phage DAC16	GCA_013387695.1
QIG63704.1	003293	Cluster2921_1clades	160	DAC19_217	Bacteroides phage DAC19	GCA_013387715.1
QIG63965.1	003293	Cluster2921_1clades	160	DAC20_216	Bacteroides phage DAC20	GCA_013387725.1
QIG64229.1	003293	Cluster2921_1clades	160	DAC22_219	Bacteroides phage DAC22	GCA_013387735.1
QIG64485.1	003293	Cluster2921_1clades	160	DAC23_211	Bacteroides phage DAC23	GCA_013387745.1
QMV28844.1	003294	Cluster2922_1clades	160	AP1_0137	Aeromonas phage AP1	GCA_014183365.1
ATI17276.1	003294	Cluster2922_1clades	159	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00317.1	003294	Cluster2922_1clades	159	HWB28_gp235	Aeromonas phage AS-zj	GCA_002627665.1
QAX97718.1	003294	Cluster2922_1clades	159	ASswx1_72	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39184.1	003294	Cluster2922_1clades	158	CC2_040	Aeromonas phage CC2	GCA_000903495.1
QMV29029.1	003295	Cluster2923_1clades	133	AP1_0322	Aeromonas phage AP1	GCA_014183365.1
ATI17262.1	003295	Cluster2923_1clades	133	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00328.1	003295	Cluster2923_1clades	133	HWB28_gp224	Aeromonas phage AS-zj	GCA_002627665.1
QAY01432.1	003295	Cluster2923_1clades	134	ASwh1_373	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39193.1	003295	Cluster2923_1clades	159	CC2_053	Aeromonas phage CC2	GCA_000903495.1
QIG63390.1	003296	Cluster2924_1clades	159	DAC16_160	Bacteroides phage DAC16	GCA_013387695.1
QIG63654.1	003296	Cluster2924_1clades	159	DAC19_166	Bacteroides phage DAC19	GCA_013387715.1
QIG63915.1	003296	Cluster2924_1clades	159	DAC20_165	Bacteroides phage DAC20	GCA_013387725.1
QIG64179.1	003296	Cluster2924_1clades	159	DAC22_168	Bacteroides phage DAC22	GCA_013387735.1
QIG64434.1	003296	Cluster2924_1clades	159	DAC23_159	Bacteroides phage DAC23	GCA_013387745.1
QIG63408.1	003297	Cluster2925_1clades	159	DAC16_178	Bacteroides phage DAC16	GCA_013387695.1
QIG63672.1	003297	Cluster2925_1clades	159	DAC19_184	Bacteroides phage DAC19	GCA_013387715.1
QIG63933.1	003297	Cluster2925_1clades	159	DAC20_183	Bacteroides phage DAC20	GCA_013387725.1
QIG64197.1	003297	Cluster2925_1clades	159	DAC22_186	Bacteroides phage DAC22	GCA_013387735.1
QIG64453.1	003297	Cluster2925_1clades	159	DAC23_178	Bacteroides phage DAC23	GCA_013387745.1
QIG63477.1	003298	Cluster2926_1clades	159	DAC16_248	Bacteroides phage DAC16	GCA_013387695.1
QIG63740.1	003298	Cluster2926_1clades	159	DAC19_253	Bacteroides phage DAC19	GCA_013387715.1
QIG64001.1	003298	Cluster2926_1clades	159	DAC20_252	Bacteroides phage DAC20	GCA_013387725.1
QIG64265.1	003298	Cluster2926_1clades	159	DAC22_255	Bacteroides phage DAC22	GCA_013387735.1
QIG64521.1	003298	Cluster2926_1clades	159	DAC23_247	Bacteroides phage DAC23	GCA_013387745.1
AUE22684.1	003299	Cluster2927_1clades	139	Ah1_00143	Aeromonas phage Ah1	GCA_002957415.1
QAX98410.1	003299	Cluster2927_1clades	158	ASfcp2_66	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52866.1	003299	Cluster2927_1clades	158	PX29p147	Aeromonas phage PX29	GCA_000920195.1
ADM80126.1	003299	Cluster2927_1clades	152	phiAS5_ORF0283	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17812.1	003299	Cluster2927_1clades	158	Aeh1ORF147c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63448.1	003300	Cluster2928_1clades	158	DAC16_219	Bacteroides phage DAC16	GCA_013387695.1
QIG63711.1	003300	Cluster2928_1clades	158	DAC19_224	Bacteroides phage DAC19	GCA_013387715.1
QIG63972.1	003300	Cluster2928_1clades	158	DAC20_223	Bacteroides phage DAC20	GCA_013387725.1
QIG64236.1	003300	Cluster2928_1clades	158	DAC22_226	Bacteroides phage DAC22	GCA_013387735.1
QIG64492.1	003300	Cluster2928_1clades	158	DAC23_218	Bacteroides phage DAC23	GCA_013387745.1
AUE22845.1	003301	Cluster2929_1clades	149	Ah1_00327	Aeromonas phage Ah1	GCA_002957415.1
QAX98557.1	003301	Cluster2929_1clades	157	ASfcp2_223	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53022.1	003301	Cluster2929_1clades	157	PX29p303	Aeromonas phage PX29	GCA_000920195.1
ADM79946.1	003301	Cluster2929_1clades	150	phiAS5_ORF0103	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17975.1	003301	Cluster2929_1clades	149	Aeh1ORF306c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21819.1	003302	Cluster2930_1clades	157	GAP32_368	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43941.1	003302	Cluster2930_1clades	157	CBB_378	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88901.1	003302	Cluster2930_1clades	156	BF_0376	Serratia phage BF	GCA_002619745.1
SOK59189.1	003302	Cluster2930_1clades	156	g381	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58653.1	003302	Cluster2930_1clades	156	g376	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBX32504.1	003303	Cluster2931_1clades	153	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03761.1	003303	Cluster2931_1clades	156	338	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02906.1	003303	Cluster2931_1clades	153	PSA21_380	Pseudomonas phage Psa21	GCA_004340405.1
ATN94620.1	003303	Cluster2931_1clades	153	SL2_043	Pseudomonas phage SL2	GCA_002956015.1
QEM42076.1	003303	Cluster2931_1clades	153	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63406.1	003304	Cluster2932_1clades	155	DAC16_176	Bacteroides phage DAC16	GCA_013387695.1
QIG63670.1	003304	Cluster2932_1clades	155	DAC19_182	Bacteroides phage DAC19	GCA_013387715.1
QIG63931.1	003304	Cluster2932_1clades	155	DAC20_181	Bacteroides phage DAC20	GCA_013387725.1
QIG64195.1	003304	Cluster2932_1clades	155	DAC22_184	Bacteroides phage DAC22	GCA_013387735.1
QIG64451.1	003304	Cluster2932_1clades	155	DAC23_176	Bacteroides phage DAC23	GCA_013387745.1
QIG63273.1	003305	Cluster2933_1clades	121	DAC16_40	Bacteroides phage DAC16	GCA_013387695.1
QIG63534.1	003305	Cluster2933_1clades	155	DAC19_43	Bacteroides phage DAC19	GCA_013387715.1
QIG63795.1	003305	Cluster2933_1clades	155	DAC20_42	Bacteroides phage DAC20	GCA_013387725.1
QIG64056.1	003305	Cluster2933_1clades	155	DAC22_42	Bacteroides phage DAC22	GCA_013387735.1
QIG64317.1	003305	Cluster2933_1clades	155	DAC23_39	Bacteroides phage DAC23	GCA_013387745.1
AFC21830.1	003306	Cluster2934_1clades	154	GAP32_378	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43951.1	003306	Cluster2934_1clades	153	CBB_388	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88910.1	003306	Cluster2934_1clades	78	BF_0385	Serratia phage BF	GCA_002619745.1
SOK59199.1	003306	Cluster2934_1clades	79	g391	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58664.1	003306	Cluster2934_1clades	79	g387	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBX06645.1	003307	Cluster2935_1clades	154	BcepSaruman_232	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74614.1	003307	Cluster2935_1clades	154	BcepSauron_234	Burkholderia phage BcepSauron	GCA_005394215.1
BAW19141.1	003307	Cluster2935_1clades	127	FDH28_gp254	Ralstonia phage RP12	GCA_002617345.1
BAW19427.1	003307	Cluster2935_1clades	127	-	Ralstonia phage RP31	GCA_002617365.1
AKF13459.1	003307	Cluster2935_1clades	140	PHIN3_196	Sinorhizobium phage phiN3	GCA_001501175.1
QDB70413.1	003308	Cluster2936_1clades	151	CF8_0244	Aeromonas phage CF8	GCA_006384595.2
QDJ96758.1	003308	Cluster2936_1clades	154	PS1_0247	Aeromonas phage PS1	GCA_007051165.2
QFR59391.1	003308	Cluster2936_1clades	154	PS2_0249	Aeromonas phage PS2	GCA_009388305.2
QBZ70806.1	003308	Cluster2936_1clades	152	pETSU_225	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89745.1	003308	Cluster2936_1clades	153	OBP_308	Pseudomonas phage OBP	GCA_000896635.1
QIG63587.1	003309	tRNA_lig_CPD	134	DAC19_96	Bacteroides phage DAC19	GCA_013387715.1
QIG63848.1	003309	tRNA_lig_CPD	134	DAC20_95	Bacteroides phage DAC20	GCA_013387725.1
QIG64110.1	003309	tRNA_lig_CPD	134	DAC22_96	Bacteroides phage DAC22	GCA_013387735.1
prevph1000000377	003309	tRNA_lig_CPD	113	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000303	003309	tRNA_lig_CPD	155	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUE22592.1	003310	Cluster2939_1clades	152	Ah1_00051	Aeromonas phage Ah1	GCA_002957415.1
QAX98630.1	003310	Cluster2939_1clades	145	ASfcp2_297	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52770.1	003310	Cluster2939_1clades	145	PX29p051	Aeromonas phage PX29	GCA_000920195.1
ADM80025.1	003310	Cluster2939_1clades	153	phiAS5_ORF0182	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17715.1	003310	Cluster2939_1clades	153	Aeh1ORF055c	Aeromonas virus Aeh1	GCA_000843245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QMV29061.1	003311	Cluster2940_1clades	153	AP1_0354	Aeromonas phage AP1	GCA_014183365.1
ATI17616.1	003311	Cluster2940_1clades	153	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00380.1	003311	Cluster2940_1clades	153	HWB28_gp172	Aeromonas phage AS-zj	GCA_002627665.1
QAX97650.1	003311	Cluster2940_1clades	153	ASswx1_4	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39221.1	003311	Cluster2940_1clades	153	CC2_110	Aeromonas phage CC2	GCA_000903495.1
AFC21853.1	003312	Cluster2941_1clades	147	GAP32_400	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43972.1	003312	Cluster2941_1clades	143	CBB_409	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88932.1	003312	Cluster2941_1clades	153	BF_0407	Serratia phage BF	GCA_002619745.1
SOK59221.1	003312	Cluster2941_1clades	142	g413	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58687.1	003312	Cluster2941_1clades	142	g410	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63240.1	003313	DUF4494	152	DAC16_7	Bacteroides phage DAC16	GCA_013387695.1
QIG63498.1	003313	DUF4494	153	DAC19_7	Bacteroides phage DAC19	GCA_013387715.1
QIG63760.1	003313	DUF4494	153	DAC20_7	Bacteroides phage DAC20	GCA_013387725.1
QIG64021.1	003313	DUF4494	138	DAC22_7	Bacteroides phage DAC22	GCA_013387735.1
QIG64285.1	003313	DUF4494	152	DAC23_7	Bacteroides phage DAC23	GCA_013387745.1
AFO71311.1	003314	Cluster2943_1clades	143	CR5_091	Cronobacter phage CR5	GCA_000910235.1
QBP07520.1	003314	Cluster2943_1clades	143	DERBICUS_94	Erwinia phage Derbicus	GCA_004521655.1
ANZ48943.1	003314	Cluster2943_1clades	143	EARLPHILLIPIV_94	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50284.1	003314	Cluster2943_1clades	152	PHOBOS_94	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QFP93203.1	003314	Cluster2943_1clades	150	-	Serratia phage PCH45	GCA_009187865.1
AMO43156.1	003315	Cluster2944_1clades	122	R1080702_147	Cyanophage S-RIM32	GCA_001754165.1
AOO11624.1	003315	Cluster2944_1clades	152	ES420910_143	Cyanophage S-RIM44	GCA_002599165.1
AOO12089.1	003315	Cluster2944_1clades	152	Np200711_143	Cyanophage S-RIM44	GCA_002599205.1
AOO12325.1	003315	Cluster2944_1clades	152	Np420711_143	Cyanophage S-RIM44	GCA_002599225.1
AOO12790.1	003315	Cluster2944_1clades	152	Sn130910_143	Cyanophage S-RIM44	GCA_002599265.1
AXG67065.1	003316	Cluster2945_1clades	151	AD1_021	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08302.1	003316	Cluster2945_1clades	151	Alexandra_22	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58663.1	003316	Cluster2945_1clades	151	Y3_023	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28511.1	003316	Cluster2945_1clades	152	YOLOSWAG_24	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGS82055.1	003316	Cluster2945_1clades	150	PaBG_00179	Pseudomonas phage PaBG	GCA_000912555.1
QGZ14532.1	003317	Cluster2946_1clades	149	HWC77_gp169	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04202.1	003317	Cluster2946_1clades	151	HWC03_gp047	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23158.1	003317	Cluster2946_1clades	151	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47570.1	003317	Cluster2946_1clades	151	HWC35_gp176	Vibrio phage USC-1	GCA_006864065.1
BAW98384.1	003317	Cluster2946_1clades	144	FDH33_gp175	Vibrio phage pTD1	GCA_002618825.1
QIG63375.1	003318	TM	151	DAC16_142	Bacteroides phage DAC16	GCA_013387695.1
QIG63640.1	003318	TM	151	DAC19_149	Bacteroides phage DAC19	GCA_013387715.1
QIG63901.1	003318	TM	151	DAC20_148	Bacteroides phage DAC20	GCA_013387725.1
QIG64164.1	003318	TM	151	DAC22_150	Bacteroides phage DAC22	GCA_013387735.1
QIG64421.1	003318	TM	151	DAC23_143	Bacteroides phage DAC23	GCA_013387745.1
ALN97788.1	003319	Cluster2948_1clades	150	Bp8pS_109	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97790.1	003319	Cluster2948_1clades	135	Bp8pS_111	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97791.1	003319	Cluster2948_1clades	140	Bp8pS_112	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97792.1	003319	Cluster2948_1clades	136	Bp8pS_113	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97793.1	003319	Cluster2948_1clades	133	Bp8pS_114	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QIG63364.1	003320	Cluster2949_1clades	150	DAC16_131	Bacteroides phage DAC16	GCA_013387695.1
QIG63629.1	003320	Cluster2949_1clades	150	DAC19_138	Bacteroides phage DAC19	GCA_013387715.1
QIG63890.1	003320	Cluster2949_1clades	150	DAC20_137	Bacteroides phage DAC20	GCA_013387725.1
QIG64153.1	003320	Cluster2949_1clades	150	DAC22_139	Bacteroides phage DAC22	GCA_013387735.1
QIG64410.1	003320	Cluster2949_1clades	150	DAC23_132	Bacteroides phage DAC23	GCA_013387745.1
AFC21812.1	003321	LEVANB	149	GAP32_362	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43936.1	003321	LEVANB	149	CBB_373	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88895.1	003321	LEVANB	146	BF_0370	Serratia phage BF	GCA_002619745.1
SOK59181.1	003321	LEVANB	146	g373	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58647.1	003321	LEVANB	146	g370	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXQ69052.1	003322	Cluster2951_1clades	102	CcrBL9_gp028	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69568.1	003322	Cluster2951_1clades	102	CcrBL9_gp544	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87879.1	003322	Cluster2951_1clades	145	CcrColossus_gp009	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68548.1	003322	Cluster2951_1clades	148	CcrPW_gp009	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68998.1	003322	Cluster2951_1clades	148	CcrPW_gp459	Caulobacter phage CcrPW	GCA_003443275.1
AUE22862.1	003323	TM	147	Ah1_00344	Aeromonas phage Ah1	GCA_002957415.1
QAX98572.1	003323	TM	76	ASfcp2_238	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53037.1	003323	TM	81	PX29p320	Aeromonas phage PX29	GCA_000920195.1
ADM79961.1	003323	TM	112	phiAS5_ORF0118	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17990.1	003323	TM	101	Aeh1ORF321w	Aeromonas virus Aeh1	GCA_000843245.1
QGZ14523.1	003324	Cluster2954_1clades	147	HWC77_gp160	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04211.1	003324	Cluster2954_1clades	147	HWC03_gp056	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23149.1	003324	Cluster2954_1clades	147	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81060.1	003324	Cluster2954_1clades	147	Aphrodite1_0191	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47578.1	003324	Cluster2954_1clades	147	HWC35_gp184	Vibrio phage USC-1	GCA_006864065.1
AUE22857.1	003325	Cluster2955_1clades	127	Ah1_00339	Aeromonas phage Ah1	GCA_002957415.1
QAX98568.1	003325	Cluster2955_1clades	127	ASfcp2_234	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53032.1	003325	Cluster2955_1clades	143	PX29p315	Aeromonas phage PX29	GCA_000920195.1
ADM79957.1	003325	Cluster2955_1clades	123	phiAS5_ORF0114	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17986.1	003325	Cluster2955_1clades	146	Aeh1ORF317w	Aeromonas virus Aeh1	GCA_000843245.1
QIG63428.1	003326	Cluster2956_1clades	146	DAC16_199	Bacteroides phage DAC16	GCA_013387695.1
QIG63692.1	003326	Cluster2956_1clades	146	DAC19_205	Bacteroides phage DAC19	GCA_013387715.1
QIG63953.1	003326	Cluster2956_1clades	146	DAC20_204	Bacteroides phage DAC20	GCA_013387725.1
QIG64217.1	003326	Cluster2956_1clades	146	DAC22_207	Bacteroides phage DAC22	GCA_013387735.1
QIG64473.1	003326	Cluster2956_1clades	146	DAC23_199	Bacteroides phage DAC23	GCA_013387745.1
ANM44791.1	003327	TM+TM	145	KTN4_033	Pseudomonas phage KTN4	GCA_002607225.1
QBX32292.1	003327	TM+TM	145	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03552.1	003327	TM+TM	141	128	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41866.1	003327	TM+TM	145	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL82924.1	003327	TM+TM	138	PHIKZ023	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ49861.1	003328	Cluster2958_1clades	129	MACHINA_223	Erwinia phage Machina	GCA_002758035.1
ANZ48518.1	003328	Cluster2958_1clades	145	CAITLIN_223	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48795.1	003328	Cluster2958_1clades	144	CHRISDB_233	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49305.1	003328	Cluster2958_1clades	129	HUXLEY_223	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50133.1	003328	Cluster2958_1clades	129	PARSHIK_224	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AUE22867.1	003329	SIG+TM+TM+TM	140	Ah1_00349	Aeromonas phage Ah1	GCA_002957415.1
QAX98577.1	003329	SIG+TM+TM+TM	140	ASfcp2_243	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53042.1	003329	SIG+TM+TM+TM	140	PX29p325	Aeromonas phage PX29	GCA_000920195.1
ADM79965.1	003329	SIG+TM+TM+TM	144	phiAS5_ORF0122	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17995.1	003329	SIG+TM+TM+TM	140	Aeh1ORF325c	Aeromonas virus Aeh1	GCA_000843245.1
QMV28884.1	003330	SIG+TM	144	AP1_0177	Aeromonas phage AP1	GCA_014183365.1
ATI17239.1	003330	SIG+TM	144	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00348.1	003330	SIG+TM	144	HWB28_gp204	Aeromonas phage AS-zj	GCA_002627665.1
QAX97682.1	003330	SIG+TM	144	ASswx1_36	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39210.1	003330	SIG+TM	144	CC2_079	Aeromonas phage CC2	GCA_000903495.1
AUE22771.1	003331	Cluster2962_1clades	142	Ah1_00253	Aeromonas phage Ah1	GCA_002957415.1
QAX98487.1	003331	Cluster2962_1clades	142	ASfcp2_149	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52949.1	003331	Cluster2962_1clades	142	PX29p230	Aeromonas phage PX29	GCA_000920195.1
ADM79873.1	003331	Cluster2962_1clades	142	phiAS5_ORF0030	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17895.1	003331	Cluster2962_1clades	142	Aeh1ORF234c	Aeromonas virus Aeh1	GCA_000843245.1
QMV29008.1	003332	TM+TM+TM	142	AP1_0301	Aeromonas phage AP1	GCA_014183365.1
ATI17349.1	003332	TM+TM+TM	142	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00244.1	003332	TM+TM+TM	142	HWB28_gp308	Aeromonas phage AS-zj	GCA_002627665.1
QAX97794.1	003332	TM+TM+TM	142	ASswx1_149	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39160.1	003332	TM+TM+TM	142	CC2_388	Aeromonas phage CC2	GCA_000903495.1
AXF51189.1	003333	Cluster2964_1clades	135	WELLINGTON_59	Erwinia phage Wellington	GCA_003344985.1
AFQ96774.1	003333	Cluster2964_1clades	137	G173_gp229	Erwinia phage phiEaH2	GCA_000902915.1
ANZ49411.1	003333	Cluster2964_1clades	135	KWAN_59	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50486.1	003333	Cluster2964_1clades	137	STRATTON_61	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXF51095.1	003333	Cluster2964_1clades	142	MLDJOKPK_00120	Salmonella phage SPAsTU	GCA_003183805.1
AUE22694.1	003334	SIG+CreA	141	Ah1_00153	Aeromonas phage Ah1	GCA_002957415.1
QAX98419.1	003334	SIG+CreA	141	ASfcp2_75	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52874.1	003334	SIG+CreA	141	PX29p155	Aeromonas phage PX29	GCA_000920195.1
ADM80136.1	003334	SIG+CreA	141	phiAS5_ORF0293	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17822.1	003334	SIG+CreA	141	Aeh1ORF157c	Aeromonas virus Aeh1	GCA_000843245.1
ANZ49783.1	003335	Cluster2966_1clades	141	MACHINA_145	Erwinia phage Machina	GCA_002758035.1
ANZ48165.1	003335	Cluster2966_1clades	140	ASESINO_152	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48715.1	003335	Cluster2966_1clades	140	CHRISDB_153	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49227.1	003335	Cluster2966_1clades	141	HUXLEY_145	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50055.1	003335	Cluster2966_1clades	141	PARSHIK_146	Erwinia phage vB_EamM_Parshik	GCA_002758055.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21475.1	003336	Cluster2967_1clades	115	GAP32_027	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
QCW18691.1	003336	Cluster2967_1clades	77	7t3_0170	Salmonella phage 7t3	GCA_006083215.1
AZU97965.1	003336	Cluster2967_1clades	77	CPT_Munch_021	Salmonella phage Munch	GCA_004015485.1
QIG63013.1	003336	Cluster2967_1clades	77	SEPL_400	Salmonella phage SE_PL	GCA_011067555.1
AQW88549.1	003336	Cluster2967_1clades	141	BF_0024	Serratia phage BF	GCA_002619745.1
QIG63332.1	003337	Cluster2968_1clades	141	DAC16_99	Bacteroides phage DAC16	GCA_013387695.1
QIG63598.1	003337	Cluster2968_1clades	141	DAC19_107	Bacteroides phage DAC19	GCA_013387715.1
QIG63859.1	003337	Cluster2968_1clades	141	DAC20_106	Bacteroides phage DAC20	GCA_013387725.1
QIG64121.1	003337	Cluster2968_1clades	141	DAC22_107	Bacteroides phage DAC22	GCA_013387735.1
QIG64379.1	003337	Cluster2968_1clades	141	DAC23_101	Bacteroides phage DAC23	GCA_013387745.1
QIG63353.1	003338	Cluster2969_1clades	141	DAC16_120	Bacteroides phage DAC16	GCA_013387695.1
QIG63618.1	003338	Cluster2969_1clades	141	DAC19_127	Bacteroides phage DAC19	GCA_013387715.1
QIG63879.1	003338	Cluster2969_1clades	141	DAC20_126	Bacteroides phage DAC20	GCA_013387725.1
QIG64142.1	003338	Cluster2969_1clades	141	DAC22_128	Bacteroides phage DAC22	GCA_013387735.1
QIG64399.1	003338	Cluster2969_1clades	141	DAC23_121	Bacteroides phage DAC23	GCA_013387745.1
AUE22635.1	003339	SIG+C58	114	Ah1_00094	Aeromonas phage Ah1	GCA_002957415.1
QAX98364.1	003339	SIG+C58	140	ASfcp2_18	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52818.1	003339	SIG+C58	140	PX29p099	Aeromonas phage PX29	GCA_000920195.1
ADM80075.1	003339	SIG+C58	134	phiAS5_ORF0232	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17762.1	003339	SIG+C58	140	Aeh1ORF101c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22818.1	003340	SIG+TM	135	Ah1_00300	Aeromonas phage Ah1	GCA_002957415.1
QAX98533.1	003340	SIG+TM	138	ASfcp2_197	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52996.1	003340	SIG+TM	138	PX29p277	Aeromonas phage PX29	GCA_000920195.1
ADM79919.1	003340	SIG+TM	139	phiAS5_ORF0076	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17947.1	003340	SIG+TM	140	Aeh1ORF281c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21814.1	003341	Cluster2972_1clades	139	GAP32_364	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43937.1	003341	Cluster2972_1clades	138	CBB_374	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88897.1	003341	Cluster2972_1clades	138	BF_0372	Serratia phage BF	GCA_002619745.1
SOK59183.1	003341	Cluster2972_1clades	137	g375	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58649.1	003341	Cluster2972_1clades	139	g372	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BAE47705.1	003342	SIG+Y1_Tnp	133	CST007	Clostridium phage c-st	GCA_000865225.1
BAE47718.1	003342	SIG+Y1_Tnp	133	CST020	Clostridium phage c-st	GCA_000865225.1
BAE47840.1	003342	SIG+Y1_Tnp	93	CST142	Clostridium phage c-st	GCA_000865225.1
BAE47870.1	003342	SIG+Y1_Tnp	133	CST172	Clostridium phage c-st	GCA_000865225.1
BAE47880.1	003342	SIG+Y1_Tnp	139	CST182	Clostridium phage c-st	GCA_000865225.1
AMR59719.1	003343	Cluster2974_1clades	138	SEGD1_070	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85910.1	003343	Cluster2974_1clades	138	ACEC001_0720	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20782.1	003343	Cluster2974_1clades	138	-	Salmonella phage JN03	GCA_014319805.1
AWN09031.1	003343	Cluster2974_1clades	138	MLDJOKPK_00092	Salmonella phage SPAsTU	GCA_003183805.1
AEP83902.1	003343	Cluster2974_1clades	138	SPN3US_0069	Salmonella phage SPN3US	GCA_001042275.1
QBZ70790.1	003344	Cluster2975_1clades	138	pETSU_209	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70792.1	003344	Cluster2975_1clades	133	pETSU_211	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72093.1	003344	Cluster2975_1clades	128	N1M2_230	Klebsiella phage N1M2	GCA_010092605.1
QGH72095.1	003344	Cluster2975_1clades	138	N1M2_232	Klebsiella phage N1M2	GCA_010092605.1
AEV89728.1	003344	Cluster2975_1clades	130	OBP_291	Pseudomonas phage OBP	GCA_000896635.1
AUZ95064.1	003345	Cluster2976_1clades	127	FDI40_gp295	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGR47924.1	003345	Cluster2976_1clades	137	SmphiM12_292	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13126.1	003345	Cluster2976_1clades	137	PHIM19_221	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12765.1	003345	Cluster2976_1clades	137	PHIM7_220	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13495.1	003345	Cluster2976_1clades	137	PHIN3_232	Sinorhizobium phage phiN3	GCA_001501175.1
QMV28866.1	003346	Cluster2977_1clades	129	AP1_0159	Aeromonas phage AP1	GCA_014183365.1
ATI17298.1	003346	Cluster2977_1clades	130	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00296.1	003346	Cluster2977_1clades	136	HWB28_gp256	Aeromonas phage AS-zj	GCA_002627665.1
QAX97741.1	003346	Cluster2977_1clades	129	ASswx1_96	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39167.1	003346	Cluster2977_1clades	131	CC2_015	Aeromonas phage CC2	GCA_000903495.1
QGZ14388.1	003347	Cluster2978_1clades	136	HWC77_gp025	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04348.1	003347	Cluster2978_1clades	136	HWC03_gp193	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23228.1	003347	Cluster2978_1clades	135	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81067.1	003347	Cluster2978_1clades	135	Aphrodite1_0117	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47500.1	003347	Cluster2978_1clades	135	HWC35_gp106	Vibrio phage USC-1	GCA_006864065.1
QIG63423.1	003348	Cluster2979_1clades	136	DAC16_193	Bacteroides phage DAC16	GCA_013387695.1
QIG63687.1	003348	Cluster2979_1clades	136	DAC19_199	Bacteroides phage DAC19	GCA_013387715.1
QIG63948.1	003348	Cluster2979_1clades	136	DAC20_198	Bacteroides phage DAC20	GCA_013387725.1
QIG64212.1	003348	Cluster2979_1clades	136	DAC22_201	Bacteroides phage DAC22	GCA_013387735.1
QIG64468.1	003348	Cluster2979_1clades	136	DAC23_193	Bacteroides phage DAC23	GCA_013387745.1
ANM45043.1	003349	Cluster2980_1clades	113	KTN4_285	Pseudomonas phage KTN4	GCA_002607225.1
QBX32434.1	003349	Cluster2980_1clades	135	-	Pseudomonas phage PA1C	GCA_004785505.1
QJB22919.1	003349	Cluster2980_1clades	113	fnug_276	Pseudomonas phage fnug	GCA_012837215.1
QEM42004.1	003349	Cluster2980_1clades	135	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83137.1	003349	Cluster2980_1clades	135	PHIKZ236	Pseudomonas virus phiKZ	GCA_000842965.1
QIG63272.1	003350	Cluster2981_1clades	135	DAC16_39	Bacteroides phage DAC16	GCA_013387695.1
QIG63533.1	003350	Cluster2981_1clades	135	DAC19_42	Bacteroides phage DAC19	GCA_013387715.1
QIG63794.1	003350	Cluster2981_1clades	135	DAC20_41	Bacteroides phage DAC20	GCA_013387725.1
QIG64055.1	003350	Cluster2981_1clades	135	DAC22_41	Bacteroides phage DAC22	GCA_013387735.1
QIG64316.1	003350	Cluster2981_1clades	135	DAC23_38	Bacteroides phage DAC23	GCA_013387745.1
QIG63443.1	003351	Cluster2982_1clades	135	DAC16_214	Bacteroides phage DAC16	GCA_013387695.1
QIG63706.1	003351	Cluster2982_1clades	135	DAC19_219	Bacteroides phage DAC19	GCA_013387715.1
QIG63967.1	003351	Cluster2982_1clades	135	DAC20_218	Bacteroides phage DAC20	GCA_013387725.1
QIG64231.1	003351	Cluster2982_1clades	135	DAC22_221	Bacteroides phage DAC22	GCA_013387735.1
QIG64487.1	003351	Cluster2982_1clades	135	DAC23_213	Bacteroides phage DAC23	GCA_013387745.1
QIG63459.1	003352	Cluster2983_1clades	135	DAC16_230	Bacteroides phage DAC16	GCA_013387695.1
QIG63722.1	003352	Cluster2983_1clades	135	DAC19_235	Bacteroides phage DAC19	GCA_013387715.1
QIG63983.1	003352	Cluster2983_1clades	135	DAC20_234	Bacteroides phage DAC20	GCA_013387725.1
QIG64247.1	003352	Cluster2983_1clades	135	DAC22_237	Bacteroides phage DAC22	GCA_013387735.1
QIG64503.1	003352	Cluster2983_1clades	135	DAC23_229	Bacteroides phage DAC23	GCA_013387745.1
ANM44954.1	003353	Cluster2984_1clades	134	KTN4_196	Pseudomonas phage KTN4	GCA_002607225.1
AEH03606.1	003353	Cluster2984_1clades	133	183	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94760.1	003353	Cluster2984_1clades	134	SL2_183	Pseudomonas phage SL2	GCA_002956015.1
QJB22832.1	003353	Cluster2984_1clades	134	fnug_189	Pseudomonas phage fnug	GCA_012837215.1
AAL83060.2	003353	Cluster2984_1clades	134	PHIKZ159	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22673.1	003354	Cluster2985_1clades	128	Ah1_00132	Aeromonas phage Ah1	GCA_002957415.1
QAX98399.1	003354	Cluster2985_1clades	127	ASfcp2_55	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52855.1	003354	Cluster2985_1clades	127	PX29p136	Aeromonas phage PX29	GCA_000920195.1
ADM80114.1	003354	Cluster2985_1clades	134	phiAS5_ORF0271	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17802.1	003354	Cluster2985_1clades	128	Aeh1ORF137c	Aeromonas virus Aeh1	GCA_000843245.1
APU01692.1	003355	Cluster2986_1clades	134	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17599.1	003355	Cluster2986_1clades	132	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00398.1	003355	Cluster2986_1clades	132	HWB28_gp154	Aeromonas phage AS-zj	GCA_002627665.1
AFN39357.1	003355	Cluster2986_1clades	132	CC2_132	Aeromonas phage CC2	GCA_000903495.1
ADQ53330.1	003355	Cluster2986_1clades	134	65p322	Aeromonas virus 65	GCA_000893255.1
QIG63430.1	003356	Cluster2987_1clades	134	DAC16_201	Bacteroides phage DAC16	GCA_013387695.1
QIG63694.1	003356	Cluster2987_1clades	134	DAC19_207	Bacteroides phage DAC19	GCA_013387715.1
QIG63955.1	003356	Cluster2987_1clades	134	DAC20_206	Bacteroides phage DAC20	GCA_013387725.1
QIG64219.1	003356	Cluster2987_1clades	134	DAC22_209	Bacteroides phage DAC22	GCA_013387735.1
QIG64475.1	003356	Cluster2987_1clades	134	DAC23_201	Bacteroides phage DAC23	GCA_013387745.1
AMR59783.1	003357	SIG+She9_MDM33	133	SEGD1_136	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85973.1	003357	SIG+She9_MDM33	123	ACEC001_1350	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20835.1	003357	SIG+She9_MDM33	133	-	Salmonella phage JN03	GCA_014319805.1
AWN08985.1	003357	SIG+She9_MDM33	132	MLDJOKPK_00021	Salmonella phage SPAsTU	GCA_003183805.1
AEP83965.1	003357	SIG+She9_MDM33	133	SPN3US_0132	Salmonella phage SPN3US	GCA_001042275.1
QDB70453.1	003358	Cluster2989_1clades	133	CF8_0041	Aeromonas phage CF8	GCA_006384595.2
QDJ97194.1	003358	Cluster2989_1clades	129	D6_0034	Aeromonas phage D6	GCA_007051205.2
QDH47205.1	003358	Cluster2989_1clades	129	LAh10_201	Aeromonas phage LAh10	GCA_006863975.1
QDJ96796.1	003358	Cluster2989_1clades	130	PS1_0037	Aeromonas phage PS1	GCA_007051165.2
QFR59427.1	003358	Cluster2989_1clades	130	PS2_0036	Aeromonas phage PS2	GCA_009388305.2
QIG63379.1	003359	Cluster2990_1clades	133	DAC16_146	Bacteroides phage DAC16	GCA_013387695.1
QIG63643.1	003359	Cluster2990_1clades	133	DAC19_152	Bacteroides phage DAC19	GCA_013387715.1
QIG63904.1	003359	Cluster2990_1clades	133	DAC20_151	Bacteroides phage DAC20	GCA_013387725.1
QIG64167.1	003359	Cluster2990_1clades	133	DAC22_153	Bacteroides phage DAC22	GCA_013387735.1
QIG64424.1	003359	Cluster2990_1clades	133	DAC23_146	Bacteroides phage DAC23	GCA_013387745.1
AUE22767.1	003360	HIN-HTH	114	Ah1_00249	Aeromonas phage Ah1	GCA_002957415.1
QAX98483.1	003360	HIN-HTH	115	ASfcp2_145	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52945.1	003360	HIN-HTH	115	PX29p226	Aeromonas phage PX29	GCA_000920195.1
ADM79869.1	003360	HIN-HTH	132	phiAS5_ORF0026	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17891.1	003360	HIN-HTH	117	Aeh1ORF230c	Aeromonas virus Aeh1	GCA_000843245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22789.1	003361	Cluster2992_1clades	131	Ah1_00271	Aeromonas phage Ah1	GCA_002957415.1
QAX98503.1	003361	Cluster2992_1clades	131	ASfcp2_167	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52966.1	003361	Cluster2992_1clades	127	PX29p247	Aeromonas phage PX29	GCA_000920195.1
ADM79892.1	003361	Cluster2992_1clades	130	phiAS5_ORF0049	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17914.1	003361	Cluster2992_1clades	131	Aeh1ORF252c	Aeromonas virus Aeh1	GCA_000843245.1
AMO43332.1	003362	Cluster2993_1clades	131	W270710_088	Cyanophage S-RIM44	GCA_002599145.1
AOO11804.1	003362	Cluster2993_1clades	131	Np050604_088	Cyanophage S-RIM44	GCA_002599185.1
AOO12505.1	003362	Cluster2993_1clades	131	Sn080709_088	Cyanophage S-RIM44	GCA_002599245.1
AOO12971.1	003362	Cluster2993_1clades	131	W2100709_089	Cyanophage S-RIM44	GCA_002599285.1
ADO99190.1	003362	Cluster2993_1clades	131	Syn1_089	Prochlorococcus phage Syn1	GCA_000892495.1
QIG63307.1	003363	Cluster2994_1clades	131	DAC16_74	Bacteroides phage DAC16	GCA_013387695.1
QIG63566.1	003363	Cluster2994_1clades	131	DAC19_75	Bacteroides phage DAC19	GCA_013387715.1
QIG63827.1	003363	Cluster2994_1clades	131	DAC20_74	Bacteroides phage DAC20	GCA_013387725.1
QIG64089.1	003363	Cluster2994_1clades	131	DAC22_75	Bacteroides phage DAC22	GCA_013387735.1
QIG64352.1	003363	Cluster2994_1clades	131	DAC23_74	Bacteroides phage DAC23	GCA_013387745.1
AUE22666.1	003364	Cluster2995_1clades	100	Ah1_00125	Aeromonas phage Ah1	GCA_002957415.1
QAX98393.1	003364	Cluster2995_1clades	100	ASfcp2_48	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52848.1	003364	Cluster2995_1clades	130	PX29p129	Aeromonas phage PX29	GCA_000920195.1
ADM80107.1	003364	Cluster2995_1clades	96	phiAS5_ORF0264	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17795.1	003364	Cluster2995_1clades	100	Aeh1ORF130c	Aeromonas virus Aeh1	GCA_000843245.1
ANZ49720.1	003365	Cluster2996_1clades	130	MACHINA_82	Erwinia phage Machina	GCA_002758035.1
ANZ48374.1	003365	Cluster2996_1clades	101	CAITLIN_79	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48647.1	003365	Cluster2996_1clades	104	CHRISDB_85	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49165.1	003365	Cluster2996_1clades	130	HUXLEY_83	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49993.1	003365	Cluster2996_1clades	130	PARSHIK_84	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AMR59902.1	003366	Cluster2997_1clades	44	SEGD1_255	Enterobacteria phage SEGD1	GCA_002601865.1
QKN86091.1	003366	Cluster2997_1clades	129	ACEC001_2480	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20934.1	003366	Cluster2997_1clades	129	-	Salmonella phage JN03	GCA_014319805.1
AWN09103.2	003366	Cluster2997_1clades	130	MLDJOKPK_00190	Salmonella phage SPAsTU	GCA_003183805.1
AEP84083.1	003366	Cluster2997_1clades	129	SPN3US_0250	Salmonella phage SPN3US	GCA_001042275.1
AUE22714.1	003367	Cluster2998_1clades	129	Ah1_00194	Aeromonas phage Ah1	GCA_002957415.1
QAX98439.1	003367	Cluster2998_1clades	129	ASfcp2_96	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52894.1	003367	Cluster2998_1clades	129	PX29p175	Aeromonas phage PX29	GCA_000920195.1
ADM80161.1	003367	Cluster2998_1clades	129	phiAS5_ORF0318	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17847.1	003367	Cluster2998_1clades	129	Aeh1ORF181c	Aeromonas virus Aeh1	GCA_000843245.1
AMM44150.1	003368	Cluster2999_1clades	129	CBB_34	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43599.1	003368	Cluster2999_1clades	129	CBB_587	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW18697.1	003368	Cluster2999_1clades	74	7t3_0176	Salmonella phage 7t3	GCA_006083215.1
AZU97970.1	003368	Cluster2999_1clades	74	CPT_Munch_026	Salmonella phage Munch	GCA_004015485.1
QIG63008.1	003368	Cluster2999_1clades	74	SEPL_395	Salmonella phage SE_PL	GCA_011067555.1
ANS06068.1	003369	Cluster3000_1clades	128	ABCD_0177	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AFC21802.1	003369	Cluster3000_1clades	123	GAP32_352	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97190.1	003369	Cluster3000_1clades	126	E_182	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78707.1	003369	Cluster3000_1clades	128	RB43ORF185c	Escherichia virus RB43	GCA_000863505.1
AMM43923.1	003369	Cluster3000_1clades	123	CBB_360	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AUE22650.1	003370	Cluster3001_1clades	123	Ah1_00109	Aeromonas phage Ah1	GCA_002957415.1
QAX98376.1	003370	Cluster3001_1clades	123	ASfcp2_30	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52829.1	003370	Cluster3001_1clades	123	PX29p110	Aeromonas phage PX29	GCA_000920195.1
ADM80089.1	003370	Cluster3001_1clades	128	phiAS5_ORF0246	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17776.1	003370	Cluster3001_1clades	123	Aeh1ORF114c	Aeromonas virus Aeh1	GCA_000843245.1
ARV77395.1	003371	Cluster3002_1clades	121	NOXIFER_230	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32387.1	003371	Cluster3002_1clades	128	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03657.1	003371	Cluster3002_1clades	128	234	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02795.1	003371	Cluster3002_1clades	116	PSA21_269	Pseudomonas phage Psa21	GCA_004340405.1
QEM41959.1	003371	Cluster3002_1clades	128	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63361.1	003372	Cluster3003_1clades	128	DAC16_128	Bacteroides phage DAC16	GCA_013387695.1
QIG63626.1	003372	Cluster3003_1clades	128	DAC19_135	Bacteroides phage DAC19	GCA_013387715.1
QIG63887.1	003372	Cluster3003_1clades	128	DAC20_134	Bacteroides phage DAC20	GCA_013387725.1
QIG64150.1	003372	Cluster3003_1clades	128	DAC22_136	Bacteroides phage DAC22	GCA_013387735.1
QIG64407.1	003372	Cluster3003_1clades	128	DAC23_129	Bacteroides phage DAC23	GCA_013387745.1
AFC21945.1	003373	Cluster3004_1clades	127	GAP32_487	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44072.1	003373	Cluster3004_1clades	127	CBB_509	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89028.1	003373	Cluster3004_1clades	105	BF_0503	Serratia phage BF	GCA_002619745.1
SOK59308.1	003373	Cluster3004_1clades	89	g500	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58773.1	003373	Cluster3004_1clades	89	g496	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21757.1	003374	SIG+TM	124	GAP32_307	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43875.1	003374	SIG+TM	124	CBB_312	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88834.1	003374	SIG+TM	127	BF_0309	Serratia phage BF	GCA_002619745.1
SOK59118.1	003374	SIG+TM	125	g310	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58584.1	003374	SIG+TM	125	g307	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUZ94820.1	003375	Cluster3006_1clades	127	FDI40_gp008	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGR47723.1	003375	Cluster3006_1clades	120	SmphiM12_091	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12978.1	003375	Cluster3006_1clades	120	PHIM19_71	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12618.1	003375	Cluster3006_1clades	120	PHIM7_70	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13350.1	003375	Cluster3006_1clades	120	PHIN3_86	Sinorhizobium phage phiN3	GCA_001501175.1
QIG63372.1	003376	Cluster3007_1clades	127	DAC16_139	Bacteroides phage DAC16	GCA_013387695.1
QIG63637.1	003376	Cluster3007_1clades	127	DAC19_146	Bacteroides phage DAC19	GCA_013387715.1
QIG63898.1	003376	Cluster3007_1clades	127	DAC20_145	Bacteroides phage DAC20	GCA_013387725.1
QIG64161.1	003376	Cluster3007_1clades	127	DAC22_147	Bacteroides phage DAC22	GCA_013387735.1
QIG64418.1	003376	Cluster3007_1clades	127	DAC23_140	Bacteroides phage DAC23	GCA_013387745.1
AFC21846.1	003377	Cluster3008_1clades	126	GAP32_394	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43966.1	003377	Cluster3008_1clades	118	CBB_403	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88926.1	003377	Cluster3008_1clades	113	BF_0401	Serratia phage BF	GCA_002619745.1
SOK59214.1	003377	Cluster3008_1clades	117	g406	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58680.1	003377	Cluster3008_1clades	117	g403	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGC34765.1	003378	Cluster3009_1clades	126	ACQ29_gp085	Escherichia phage PBECO4	GCA_001041035.1
AXC36880.1	003378	Cluster3009_1clades	126	-	Escherichia phage UB	GCA_003341455.1
QBO61927.1	003378	Cluster3009_1clades	126	G17_00438	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13959.1	003378	Cluster3009_1clades	126	vBEcoMphAPEC6_gp335c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80364.1	003378	Cluster3009_1clades	126	PSLUR01_00387	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG63289.1	003379	Cluster3010_1clades	126	DAC16_56	Bacteroides phage DAC16	GCA_013387695.1
QIG63548.1	003379	Cluster3010_1clades	126	DAC19_57	Bacteroides phage DAC19	GCA_013387715.1
QIG63809.1	003379	Cluster3010_1clades	126	DAC20_56	Bacteroides phage DAC20	GCA_013387725.1
QIG64071.1	003379	Cluster3010_1clades	126	DAC22_57	Bacteroides phage DAC22	GCA_013387735.1
QIG64334.1	003379	Cluster3010_1clades	126	DAC23_56	Bacteroides phage DAC23	GCA_013387745.1
AUE22663.1	003380	SIG+FtsK	125	Ah1_00122	Aeromonas phage Ah1	GCA_002957415.1
QAX98389.1	003380	SIG+FtsK	125	ASfcp2_44	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52844.1	003380	SIG+FtsK	125	PX29p125	Aeromonas phage PX29	GCA_000920195.1
ADM80103.1	003380	SIG+FtsK	124	phiAS5_ORF0260	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17791.1	003380	SIG+FtsK	125	Aeh1ORF126c	Aeromonas virus Aeh1	GCA_000843245.1
AAX44474.1	003381	Cluster3012_1clades	125	PSSM2_096	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12178.1	003381	Cluster3012_1clades	125	PRTG_00020	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93593.1	003381	Cluster3012_1clades	114	AVU42_gp042	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76123.1	003381	Cluster3012_1clades	101	PBI_BELLAMY_78	Synechococcus phage Bellamy	GCA_002627525.1
QJT70063.1	003381	Cluster3012_1clades	77	SynMITS9220M01_050	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QDB70322.1	003382	Cluster3013_1clades	113	CF8_0152	Aeromonas phage CF8	GCA_006384595.2
QDJ97305.1	003382	Cluster3013_1clades	121	D6_0145	Aeromonas phage D6	GCA_007051205.2
QDH47214.1	003382	Cluster3013_1clades	121	LAh10_70	Aeromonas phage LAh10	GCA_006863975.1
QDJ96667.1	003382	Cluster3013_1clades	125	PS1_0156	Aeromonas phage PS1	GCA_007051165.2
QFR59301.1	003382	Cluster3013_1clades	125	PS2_0160	Aeromonas phage PS2	GCA_009388305.2
QIG63362.1	003383	Cluster3014_1clades	125	DAC16_129	Bacteroides phage DAC16	GCA_013387695.1
QIG63627.1	003383	Cluster3014_1clades	125	DAC19_136	Bacteroides phage DAC19	GCA_013387715.1
QIG63888.1	003383	Cluster3014_1clades	125	DAC20_135	Bacteroides phage DAC20	GCA_013387725.1
QIG64151.1	003383	Cluster3014_1clades	125	DAC22_137	Bacteroides phage DAC22	GCA_013387735.1
QIG64408.1	003383	Cluster3014_1clades	125	DAC23_130	Bacteroides phage DAC23	GCA_013387745.1
AUE22802.1	003384	Cluster3015_1clades	124	Ah1_00284	Aeromonas phage Ah1	GCA_002957415.1
QAX98517.1	003384	Cluster3015_1clades	124	ASfcp2_181	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52980.1	003384	Cluster3015_1clades	124	PX29p261	Aeromonas phage PX29	GCA_000920195.1
ADM79904.1	003384	Cluster3015_1clades	123	phiAS5_ORF0061	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17929.1	003384	Cluster3015_1clades	124	Aeh1ORF265c	Aeromonas virus Aeh1	GCA_000843245.1
QMV29078.1	003385	Cluster3016_1clades	37	AP1_0371	Aeromonas phage AP1	GCA_014183365.1
ATI17538.1	003385	Cluster3016_1clades	123	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00459.1	003385	Cluster3016_1clades	123	HWB28_gp093	Aeromonas phage AS-zj	GCA_002627665.1
QAX97979.1	003385	Cluster3016_1clades	123	ASswx1_338	Aeromonas phage Asswx_1	GCA_004146865.1
ADQ53400.1	003385	Cluster3016_1clades	124	65p393	Aeromonas virus 65	GCA_000893255.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21876.1	003386	Cluster3017_1clades	120	GAP32_423	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44006.1	003386	Cluster3017_1clades	124	CBB_443	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88965.1	003386	Cluster3017_1clades	113	BF_0440	Serratia phage BF	GCA_002619745.1
SOK59252.1	003386	Cluster3017_1clades	119	g444	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58717.1	003386	Cluster3017_1clades	119	g440	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21614.1	003387	Cluster3018_1clades	123	GAP32_164	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43733.1	003387	Cluster3018_1clades	121	CBB_168	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88688.1	003387	Cluster3018_1clades	124	BF_0163	Serratia phage BF	GCA_002619745.1
SOK58972.1	003387	Cluster3018_1clades	124	g164	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58438.1	003387	Cluster3018_1clades	124	g161	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22629.1	003388	Cluster3019_1clades	107	Ah1_00088	Aeromonas phage Ah1	GCA_002957415.1
QAX98359.1	003388	Cluster3019_1clades	124	ASfcp2_13	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52813.1	003388	Cluster3019_1clades	115	PX29p094	Aeromonas phage PX29	GCA_000920195.1
ADM80069.1	003388	Cluster3019_1clades	110	phiAS5_ORF0226	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17756.1	003388	Cluster3019_1clades	107	Aeh1ORF095c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21840.1	003389	Cluster3020_1clades	123	GAP32_388	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43960.1	003389	Cluster3020_1clades	120	CBB_397	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88922.1	003389	Cluster3020_1clades	121	BF_0397	Serratia phage BF	GCA_002619745.1
SOK59211.1	003389	Cluster3020_1clades	119	g403	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58677.1	003389	Cluster3020_1clades	119	g400	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28852.1	003390	Cluster3021_1clades	123	AP1_0145	Aeromonas phage AP1	GCA_014183365.1
ATI17287.1	003390	Cluster3021_1clades	123	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00309.1	003390	Cluster3021_1clades	123	HWB28_gp243	Aeromonas phage AS-zj	GCA_002627665.1
QAX97729.1	003390	Cluster3021_1clades	123	ASswx1_83	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39176.1	003390	Cluster3021_1clades	123	CC2_029	Aeromonas phage CC2	GCA_000903495.1
AUE22783.1	003391	Cluster3022_1clades	109	Ah1_00265	Aeromonas phage Ah1	GCA_002957415.1
QAX98498.1	003391	Cluster3022_1clades	105	ASfcp2_162	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52961.1	003391	Cluster3022_1clades	122	PX29p242	Aeromonas phage PX29	GCA_000920195.1
ADM79887.1	003391	Cluster3022_1clades	111	phiAS5_ORF0044	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17909.1	003391	Cluster3022_1clades	109	Aeh1ORF247c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21810.1	003392	Cluster3023_1clades	119	GAP32_360	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43934.1	003392	Cluster3023_1clades	119	CBB_371	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88893.1	003392	Cluster3023_1clades	122	BF_0368	Serratia phage BF	GCA_002619745.1
SOK59179.1	003392	Cluster3023_1clades	122	g371	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58645.1	003392	Cluster3023_1clades	122	g368	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ARB13823.1	003393	FTCD_C	118	Ccr10_gp293	Caulobacter phage Ccr10	GCA_002619445.1
ARB14168.1	003393	FTCD_C	118	Ccr2_gp292	Caulobacter phage Ccr2	GCA_002619465.1
ARB14862.1	003393	FTCD_C	118	Ccr29_gp306	Caulobacter phage Ccr29	GCA_002619485.1
AXQ68488.1	003393	FTCD_C	122	CcrBL10_gp284	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86776.1	003393	FTCD_C	120	CcrRogue_gp294	Caulobacter virus Rogue	GCA_000900555.1
QGY75128.1	003394	Cluster3025_1clades	122	CF8_0183	Aeromonas phage CF8	GCA_006384595.2
QDJ97351.1	003394	Cluster3025_1clades	118	D6_0192	Aeromonas phage D6	GCA_007051205.2
QDH47220.1	003394	Cluster3025_1clades	118	LAh10_110	Aeromonas phage LAh10	GCA_006863975.1
QDJ96698.1	003394	Cluster3025_1clades	120	PS1_0187	Aeromonas phage PS1	GCA_007051165.2
QFR59331.1	003394	Cluster3025_1clades	120	PS2_0189	Aeromonas phage PS2	GCA_009388305.2
ANM45095.1	003395	Cluster3026_1clades	110	KTN4_337	Pseudomonas phage KTN4	GCA_002607225.1
ATN94618.1	003395	Cluster3026_1clades	120	SL2_041	Pseudomonas phage SL2	GCA_002956015.1
QJB22971.1	003395	Cluster3026_1clades	119	fnug_328	Pseudomonas phage fnug	GCA_012837215.1
QEM42081.1	003395	Cluster3026_1clades	119	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83181.1	003395	Cluster3026_1clades	121	PHIKZ280	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45010.1	003396	Cluster3027_1clades	110	KTN4_252	Pseudomonas phage KTN4	GCA_002607225.1
AEH03669.1	003396	Cluster3027_1clades	121	246	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94704.1	003396	Cluster3027_1clades	110	SL2_127	Pseudomonas phage SL2	GCA_002956015.1
QJB22888.1	003396	Cluster3027_1clades	110	fnug_245	Pseudomonas phage fnug	GCA_012837215.1
AAL83111.1	003396	Cluster3027_1clades	110	PHIKZ210	Pseudomonas virus phiKZ	GCA_000842965.1
AFC21927.1	003397	ATPcone	119	GAP32_469	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44053.1	003397	ATPcone	119	CBB_490	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89008.1	003397	ATPcone	121	BF_0483	Serratia phage BF	GCA_002619745.1
SOK59290.1	003397	ATPcone	120	g482	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58755.1	003397	ATPcone	120	g478	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63257.1	003398	R2K	121	DAC16_24	Bacteroides phage DAC16	GCA_013387695.1
QIG63519.1	003398	R2K	121	DAC19_28	Bacteroides phage DAC19	GCA_013387715.1
QIG63781.1	003398	R2K	121	DAC20_28	Bacteroides phage DAC20	GCA_013387725.1
QIG64042.1	003398	R2K	121	DAC22_28	Bacteroides phage DAC22	GCA_013387735.1
QIG64303.1	003398	R2K	121	DAC23_25	Bacteroides phage DAC23	GCA_013387745.1
QMV28913.1	003399	Cluster3030_1clades	120	AP1_0206	Aeromonas phage AP1	GCA_014183365.1
ATI17546.1	003399	Cluster3030_1clades	120	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00451.1	003399	Cluster3030_1clades	120	HWB28_gp101	Aeromonas phage AS-zj	GCA_002627665.1
QAX97987.1	003399	Cluster3030_1clades	120	ASswx1_346	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39253.1	003399	Cluster3030_1clades	120	CC2_189	Aeromonas phage CC2	GCA_000903495.1
AMR59777.1	003400	Cluster3031_1clades	94	SEGD1_130	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85966.1	003400	Cluster3031_1clades	111	ACEC001_1280	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20830.1	003400	Cluster3031_1clades	111	-	Salmonella phage JN03	GCA_014319805.1
AWN08988.2	003400	Cluster3031_1clades	120	MLDJOKPK_00027	Salmonella phage SPAsTU	GCA_003183805.1
AEP83959.1	003400	Cluster3031_1clades	101	SPN3US_0126	Salmonella phage SPN3US	GCA_001042275.1
AUE22594.1	003401	Cluster3032_1clades	117	Ah1_00053	Aeromonas phage Ah1	GCA_002957415.1
QAX98632.1	003401	Cluster3032_1clades	117	ASfcp2_299	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52772.1	003401	Cluster3032_1clades	117	PX29p053	Aeromonas phage PX29	GCA_000920195.1
ADM80027.1	003401	Cluster3032_1clades	115	phiAS5_ORF0184	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17717.1	003401	Cluster3032_1clades	119	Aeh1ORF057c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22639.1	003402	Cluster3033_1clades	119	Ah1_00098	Aeromonas phage Ah1	GCA_002957415.1
QAX98368.1	003402	Cluster3033_1clades	116	ASfcp2_22	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52822.1	003402	Cluster3033_1clades	116	PX29p103	Aeromonas phage PX29	GCA_000920195.1
ADM80079.1	003402	Cluster3033_1clades	108	phiAS5_ORF0236	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17765.1	003402	Cluster3033_1clades	114	Aeh1ORF104c	Aeromonas virus Aeh1	GCA_000843245.1
AXG67075.1	003403	Cluster3034_1clades	112	AD1_031	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD79850.1	003403	Cluster3034_1clades	119	JA11_045	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66450.1	003403	Cluster3034_1clades	119	JA13_047	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66774.1	003403	Cluster3034_1clades	119	JA29_048	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67419.1	003403	Cluster3034_1clades	119	JA33_045	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AUE22816.1	003404	Cluster3035_1clades	116	Ah1_00298	Aeromonas phage Ah1	GCA_002957415.1
QAX98531.1	003404	Cluster3035_1clades	117	ASfcp2_195	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52994.1	003404	Cluster3035_1clades	117	PX29p275	Aeromonas phage PX29	GCA_000920195.1
ADM79917.1	003404	Cluster3035_1clades	118	phiAS5_ORF0074	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17945.1	003404	Cluster3035_1clades	116	Aeh1ORF280c	Aeromonas virus Aeh1	GCA_000843245.1
QMV28752.1	003405	Cluster3036_1clades	94	AP1_0034	Aeromonas phage AP1	GCA_014183365.1
ATI17582.1	003405	Cluster3036_1clades	118	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00415.1	003405	Cluster3036_1clades	118	HWB28_gp137	Aeromonas phage AS-zj	GCA_002627665.1
QAX98021.1	003405	Cluster3036_1clades	115	ASswx1_381	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39238.1	003405	Cluster3036_1clades	118	CC2_151	Aeromonas phage CC2	GCA_000903495.1
AFC21887.1	003406	Cluster3038_1clades	69	GAP32_433	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44015.1	003406	Cluster3038_1clades	69	CBB_452	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88974.1	003406	Cluster3038_1clades	118	BF_0449	Serratia phage BF	GCA_002619745.1
SOK59259.1	003406	Cluster3038_1clades	118	g451	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58724.1	003406	Cluster3038_1clades	118	g447	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22865.1	003407	Cluster3039_1clades	117	Ah1_00347	Aeromonas phage Ah1	GCA_002957415.1
QAX98575.1	003407	Cluster3039_1clades	101	ASfcp2_241	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53040.1	003407	Cluster3039_1clades	101	PX29p323	Aeromonas phage PX29	GCA_000920195.1
ADM79963.1	003407	Cluster3039_1clades	105	phiAS5_ORF0120	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17993.1	003407	Cluster3039_1clades	117	Aeh1gORF376c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21985.1	003408	SIG+TM+TM	117	GAP32_525	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44106.1	003408	SIG+TM+TM	116	CBB_543	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89058.1	003408	SIG+TM+TM	114	BF_0533	Serratia phage BF	GCA_002619745.1
SOK59336.1	003408	SIG+TM+TM	116	g528	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58798.1	003408	SIG+TM+TM	116	g521	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21537.1	003409	Cluster3041_1clades	112	GAP32_089	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43656.1	003409	Cluster3041_1clades	112	CBB_91	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88607.1	003409	Cluster3041_1clades	117	BF_0082	Serratia phage BF	GCA_002619745.1
SOK58884.1	003409	Cluster3041_1clades	117	g076	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58347.1	003409	Cluster3041_1clades	117	g070	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21820.1	003410	FAD-NAD-dep-oxidoreductase	110	GAP32_369	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43942.1	003410	FAD-NAD-dep-oxidoreductase	110	CBB_379	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19083.1	003410	FAD-NAD-dep-oxidoreductase	117	7t3_0564	Salmonella phage 7t3	GCA_006083215.1
AZU98324.1	003410	FAD-NAD-dep-oxidoreductase	117	CPT_Munch_381	Salmonella phage Munch	GCA_004015485.1
QIG62659.1	003410	FAD-NAD-dep-oxidoreductase	117	SEPL_046	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63241.1	003411	Cluster3043_1clades	117	DAC16_8	Bacteroides phage DAC16	GCA_013387695.1
QIG63499.1	003411	Cluster3043_1clades	117	DAC19_8	Bacteroides phage DAC19	GCA_013387715.1
QIG63761.1	003411	Cluster3043_1clades	117	DAC20_8	Bacteroides phage DAC20	GCA_013387725.1
QIG64022.1	003411	Cluster3043_1clades	117	DAC22_8	Bacteroides phage DAC22	GCA_013387735.1
QIG64286.1	003411	Cluster3043_1clades	117	DAC23_8	Bacteroides phage DAC23	GCA_013387745.1
QIG63327.1	003412	Cluster3044_1clades	117	DAC16_94	Bacteroides phage DAC16	GCA_013387695.1
QIG63589.1	003412	Cluster3044_1clades	117	DAC19_98	Bacteroides phage DAC19	GCA_013387715.1
QIG63850.1	003412	Cluster3044_1clades	117	DAC20_97	Bacteroides phage DAC20	GCA_013387725.1
QIG64113.1	003412	Cluster3044_1clades	117	DAC22_99	Bacteroides phage DAC22	GCA_013387735.1
QIG64371.1	003412	Cluster3044_1clades	117	DAC23_93	Bacteroides phage DAC23	GCA_013387745.1
AFC21855.1	003413	Cluster3045_1clades	116	GAP32_402	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43974.1	003413	Cluster3045_1clades	116	CBB_411	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88934.1	003413	Cluster3045_1clades	116	BF_0409	Serratia phage BF	GCA_002619745.1
SOK59223.1	003413	Cluster3045_1clades	116	g415	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58689.1	003413	Cluster3045_1clades	116	g412	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21902.1	003414	Cluster3046_1clades	105	GAP32_447	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44031.1	003414	Cluster3046_1clades	116	CBB_468	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88987.1	003414	Cluster3046_1clades	109	BF_0462	Serratia phage BF	GCA_002619745.1
SOK59268.1	003414	Cluster3046_1clades	109	g460	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58733.1	003414	Cluster3046_1clades	105	g456	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21988.1	003415	SIG+TM+TM	114	GAP32_527	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44108.1	003415	SIG+TM+TM	116	CBB_545	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89061.1	003415	SIG+TM+TM	110	BF_0536	Serratia phage BF	GCA_002619745.1
SOK59339.1	003415	SIG+TM+TM	111	g531	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58801.1	003415	SIG+TM+TM	111	g524	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANM45118.1	003416	N-OB	115	KTN4_360	Pseudomonas phage KTN4	GCA_002607225.1
QBX32541.1	003416	N-OB	115	-	Pseudomonas phage PA1C	GCA_004785505.1
QJB22995.1	003416	N-OB	115	fnug_352	Pseudomonas phage fnug	GCA_012837215.1
QEM42112.1	003416	N-OB	115	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83200.1	003416	N-OB	115	PHIKZ299	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22642.1	003417	SprA-related	113	Ah1_00101	Aeromonas phage Ah1	GCA_002957415.1
QAX98370.1	003417	SprA-related	113	ASfcp2_24	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52824.1	003417	SprA-related	113	PX29p105	Aeromonas phage PX29	GCA_000920195.1
ADM80082.1	003417	SprA-related	114	phiAS5_ORF0239	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17767.1	003417	SprA-related	115	Aeh1ORF106c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22626.1	003418	Cluster3050_1clades	108	Ah1_00085	Aeromonas phage Ah1	GCA_002957415.1
QAX98353.1	003418	Cluster3050_1clades	107	ASfcp2_7	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52809.1	003418	Cluster3050_1clades	115	PX29p090	Aeromonas phage PX29	GCA_000920195.1
ADM80066.1	003418	Cluster3050_1clades	107	phiAS5_ORF0223	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17753.1	003418	Cluster3050_1clades	108	Aeh1ORF092c	Aeromonas virus Aeh1	GCA_000843245.1
AMM43605.1	003419	Cluster3051_1clades	115	CBB_40	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44156.1	003419	Cluster3051_1clades	115	CBB_593	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88538.1	003419	Cluster3051_1clades	102	BF_0013	Serratia phage BF	GCA_002619745.1
AQW88554.1	003419	Cluster3051_1clades	110	BF_0029	Serratia phage BF	GCA_002619745.1
SOK58828.1	003419	Cluster3051_1clades	109	g020	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AFC21633.1	003420	Ribosomal_S30AE	111	GAP32_183	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43753.1	003420	Ribosomal_S30AE	112	CBB_188	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88711.1	003420	Ribosomal_S30AE	115	BF_0186	Serratia phage BF	GCA_002619745.1
SOK58993.1	003420	Ribosomal_S30AE	115	g185	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58458.1	003420	Ribosomal_S30AE	115	g181	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXH72627.1	003421	Cluster3053_1clades	100	-	Myoviridae sp.	GCA_003657725.1
AXH72635.1	003421	Cluster3053_1clades	112	-	Myoviridae sp.	GCA_003657725.1
AXH72628.1	003421	Cluster3053_1clades	114	-	Myoviridae sp.	GCA_003657725.1
AXH72636.1	003421	Cluster3053_1clades	114	-	Myoviridae sp.	GCA_003657725.1
AXH72629.1	003421	Cluster3053_1clades	115	-	Myoviridae sp.	GCA_003657725.1
QIG63244.1	003422	Cluster3054_1clades	115	DAC16_11	Bacteroides phage DAC16	GCA_013387695.1
QIG63505.1	003422	Cluster3054_1clades	115	DAC19_14	Bacteroides phage DAC19	GCA_013387715.1
QIG63767.1	003422	Cluster3054_1clades	115	DAC20_14	Bacteroides phage DAC20	GCA_013387725.1
QIG64028.1	003422	Cluster3054_1clades	115	DAC22_14	Bacteroides phage DAC22	GCA_013387735.1
QIG64289.1	003422	Cluster3054_1clades	115	DAC23_11	Bacteroides phage DAC23	GCA_013387745.1
QIG63357.1	003423	Cluster3055_1clades	115	DAC16_124	Bacteroides phage DAC16	GCA_013387695.1
QIG63622.1	003423	Cluster3055_1clades	115	DAC19_131	Bacteroides phage DAC19	GCA_013387715.1
QIG63883.1	003423	Cluster3055_1clades	115	DAC20_130	Bacteroides phage DAC20	GCA_013387725.1
QIG64146.1	003423	Cluster3055_1clades	115	DAC22_132	Bacteroides phage DAC22	GCA_013387735.1
QIG64403.1	003423	Cluster3055_1clades	115	DAC23_125	Bacteroides phage DAC23	GCA_013387745.1
QIG63405.1	003424	Cluster3056_1clades	115	DAC16_175	Bacteroides phage DAC16	GCA_013387695.1
QIG63669.1	003424	Cluster3056_1clades	115	DAC19_181	Bacteroides phage DAC19	GCA_013387715.1
QIG63930.1	003424	Cluster3056_1clades	115	DAC20_180	Bacteroides phage DAC20	GCA_013387725.1
QIG64194.1	003424	Cluster3056_1clades	115	DAC22_183	Bacteroides phage DAC22	GCA_013387735.1
QIG64450.1	003424	Cluster3056_1clades	115	DAC23_175	Bacteroides phage DAC23	GCA_013387745.1
AUE22603.1	003425	Cluster3057_1clades	114	Ah1_00062	Aeromonas phage Ah1	GCA_002957415.1
QAX98640.1	003425	Cluster3057_1clades	114	ASfcp2_307	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52780.1	003425	Cluster3057_1clades	114	PX29p061	Aeromonas phage PX29	GCA_000920195.1
ADM80036.1	003425	Cluster3057_1clades	113	phiAS5_ORF0193	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17725.1	003425	Cluster3057_1clades	114	Aeh1ORF065c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22693.1	003426	Cluster3058_1clades	108	Ah1_00152	Aeromonas phage Ah1	GCA_002957415.1
QAX98418.1	003426	Cluster3058_1clades	108	ASfcp2_74	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52873.1	003426	Cluster3058_1clades	108	PX29p154	Aeromonas phage PX29	GCA_000920195.1
ADM80135.1	003426	Cluster3058_1clades	114	phiAS5_ORF0292	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17821.1	003426	Cluster3058_1clades	108	Aeh1ORF156c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21484.1	003427	Cluster3059_1clades	114	GAP32_036	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44159.1	003427	Cluster3059_1clades	110	CBB_43	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43608.1	003427	Cluster3059_1clades	110	CBB_596	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88558.1	003427	Cluster3059_1clades	111	BF_0033	Serratia phage BF	GCA_002619745.1
SOK58833.1	003427	Cluster3059_1clades	113	g025	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AMM43975.1	003428	Cluster3060_1clades	111	CBB_412	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGR47915.1	003428	Cluster3060_1clades	114	SmphiM12_283	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13117.1	003428	Cluster3060_1clades	114	PHIM19_212	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12757.1	003428	Cluster3060_1clades	114	PHIM7_212	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13487.1	003428	Cluster3060_1clades	114	PHIN3_224	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67299.1	003429	Cluster3061_1clades	105	AD1_255	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG66977.1	003429	Cluster3061_1clades	114	JA29_251	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AWY08525.1	003429	Cluster3061_1clades	105	Alexandra_268	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58904.1	003429	Cluster3061_1clades	108	Y3_264	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28732.1	003429	Cluster3061_1clades	104	YOLOSWAG_259	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFQ96586.1	003430	Cluster3062_1clades	84	G173_gp041	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48147.1	003430	Cluster3062_1clades	95	ASESINO_134	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50563.1	003430	Cluster3062_1clades	113	STRATTON_138	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXF51067.1	003430	Cluster3062_1clades	110	MLDJOKPK_00037	Salmonella phage SPAsTU	GCA_003183805.1
AEP83951.1	003430	Cluster3062_1clades	110	SPN3US_0118	Salmonella phage SPN3US	GCA_001042275.1
AUE22793.1	003431	Cluster3063_1clades	113	Ah1_00275	Aeromonas phage Ah1	GCA_002957415.1
QAX98507.1	003431	Cluster3063_1clades	109	ASfcp2_171	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52969.1	003431	Cluster3063_1clades	91	PX29p250	Aeromonas phage PX29	GCA_000920195.1
ADM79895.1	003431	Cluster3063_1clades	83	phiAS5_ORF0052	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17918.1	003431	Cluster3063_1clades	112	Aeh1ORF255c	Aeromonas virus Aeh1	GCA_000843245.1
AMR59776.1	003432	Cluster3064_1clades	110	SEGD1_129	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85965.1	003432	Cluster3064_1clades	110	ACEC001_1270	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20829.1	003432	Cluster3064_1clades	110	-	Salmonella phage JN03	GCA_014319805.1
AWN08989.1	003432	Cluster3064_1clades	113	MLDJOKPK_00028	Salmonella phage SPAsTU	GCA_003183805.1
AEP83958.1	003432	Cluster3064_1clades	110	SPN3US_0125	Salmonella phage SPN3US	GCA_001042275.1
QDH83694.1	003433	S4	73	H1O15_gp267	Achromobacter phage Motura	GCA_006964305.1
QBX06781.1	003433	S4	75	BcepSaruman_368	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74751.1	003433	S4	75	BcepSauron_371	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65661.1	003433	S4	113	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65202.1	003433	S4	113	-	Xanthomonas phage XacN1	GCA_003173815.1
QIG63370.1	003434	Cluster3066_1clades	113	DAC16_137	Bacteroides phage DAC16	GCA_013387695.1
QIG63635.1	003434	Cluster3066_1clades	113	DAC19_144	Bacteroides phage DAC19	GCA_013387715.1
QIG63896.1	003434	Cluster3066_1clades	113	DAC20_143	Bacteroides phage DAC20	GCA_013387725.1
QIG64159.1	003434	Cluster3066_1clades	113	DAC22_145	Bacteroides phage DAC22	GCA_013387735.1
QIG64416.1	003434	Cluster3066_1clades	113	DAC23_138	Bacteroides phage DAC23	GCA_013387745.1
AFC21603.1	003435	DltD	93	GAP32_153	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43723.1	003435	DltD	111	CBB_158	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88677.1	003435	DltD	96	BF_0152	Serratia phage BF	GCA_002619745.1
SOK58959.1	003435	DltD	113	g151	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58425.1	003435	DltD	113	g148	Yersinia phage fHe-Yen9-04	GCA_002990485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATI17309.1	003436	Cluster3068_1clades	112	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00285.1	003436	Cluster3068_1clades	112	HWB28_gp267	Aeromonas phage AS-zj	GCA_002627665.1
QAX97752.1	003436	Cluster3068_1clades	112	ASswx1_107	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01403.1	003436	Cluster3068_1clades	112	ASwh1_344	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39161.1	003436	Cluster3068_1clades	112	CC2_002	Aeromonas phage CC2	GCA_000903495.1
ANM44783.1	003437	Cluster3070_1clades	112	KTN4_025	Pseudomonas phage KTN4	GCA_002607225.1
QBX32286.1	003437	Cluster3070_1clades	112	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94924.1	003437	Cluster3070_1clades	111	SL2_347	Pseudomonas phage SL2	GCA_002956015.1
QJB22667.1	003437	Cluster3070_1clades	112	fnug_24	Pseudomonas phage fnug	GCA_012837215.1
QEM41860.1	003437	Cluster3070_1clades	112	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63337.1	003438	Cluster3071_1clades	112	DAC16_104	Bacteroides phage DAC16	GCA_013387695.1
QIG63603.1	003438	Cluster3071_1clades	112	DAC19_112	Bacteroides phage DAC19	GCA_013387715.1
QIG63864.1	003438	Cluster3071_1clades	112	DAC20_111	Bacteroides phage DAC20	GCA_013387725.1
QIG64127.1	003438	Cluster3071_1clades	112	DAC22_113	Bacteroides phage DAC22	GCA_013387735.1
QIG64384.1	003438	Cluster3071_1clades	112	DAC23_106	Bacteroides phage DAC23	GCA_013387745.1
QIG63266.1	003439	Cluster3072_1clades	84	DAC16_33	Bacteroides phage DAC16	GCA_013387695.1
QIG63528.1	003439	Cluster3072_1clades	91	DAC19_37	Bacteroides phage DAC19	GCA_013387715.1
QIG63790.1	003439	Cluster3072_1clades	91	DAC20_37	Bacteroides phage DAC20	GCA_013387725.1
QIG64051.1	003439	Cluster3072_1clades	91	DAC22_37	Bacteroides phage DAC22	GCA_013387735.1
QIG64312.1	003439	Cluster3072_1clades	112	DAC23_34	Bacteroides phage DAC23	GCA_013387745.1
ANM44786.1	003440	Cluster3073_1clades	111	KTN4_028	Pseudomonas phage KTN4	GCA_002607225.1
AEH03550.1	003440	Cluster3073_1clades	109	126	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94920.1	003440	Cluster3073_1clades	111	SL2_343	Pseudomonas phage SL2	GCA_002956015.1
QJB22669.1	003440	Cluster3073_1clades	111	fnug_26	Pseudomonas phage fnug	GCA_012837215.1
AAL82922.1	003440	Cluster3073_1clades	111	PHIKZ021	Pseudomonas virus phiKZ	GCA_000842965.1
QMV28991.1	003441	Cluster3074_1clades	79	AP1_0284	Aeromonas phage AP1	GCA_014183365.1
ATI17516.1	003441	Cluster3074_1clades	111	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00480.1	003441	Cluster3074_1clades	111	HWB28_gp072	Aeromonas phage AS-zj	GCA_002627665.1
QAX97956.1	003441	Cluster3074_1clades	111	ASswx1_314	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39263.1	003441	Cluster3074_1clades	111	CC2_218	Aeromonas phage CC2	GCA_000903495.1
AFC21512.1	003442	SIG+TM	108	GAP32_064	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43633.1	003442	SIG+TM	106	CBB_68	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88584.1	003442	SIG+TM	111	BF_0059	Serratia phage BF	GCA_002619745.1
SOK58859.1	003442	SIG+TM	111	g051	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58321.1	003442	SIG+TM	111	g044	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22664.1	003443	Cluster3076_1clades	109	Ah1_00123	Aeromonas phage Ah1	GCA_002957415.1
QAX98390.1	003443	Cluster3076_1clades	99	ASfcp2_45	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52845.1	003443	Cluster3076_1clades	99	PX29p126	Aeromonas phage PX29	GCA_000920195.1
ADM80104.1	003443	Cluster3076_1clades	83	phiAS5_ORF0261	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17792.1	003443	Cluster3076_1clades	109	Aeh1ORF127c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21969.1	003444	SIG+TM+TM	105	GAP32_509	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44092.1	003444	SIG+TM+TM	106	CBB_529	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89050.1	003444	SIG+TM+TM	109	BF_0525	Serratia phage BF	GCA_002619745.1
SOK59325.1	003444	SIG+TM+TM	106	g517	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58787.1	003444	SIG+TM+TM	106	g510	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14576.1	003445	Cluster3078_1clades	108	HWC77_gp213	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04157.1	003445	Cluster3078_1clades	95	HWC03_gp002	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23201.1	003445	Cluster3078_1clades	77	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81085.1	003445	Cluster3078_1clades	109	Aphrodite1_0143	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47527.1	003445	Cluster3078_1clades	109	HWC35_gp133	Vibrio phage USC-1	GCA_006864065.1
AUE22711.1	003446	Cluster3079_1clades	101	Ah1_00191	Aeromonas phage Ah1	GCA_002957415.1
QAX98438.1	003446	Cluster3079_1clades	106	ASfcp2_94	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52892.1	003446	Cluster3079_1clades	108	PX29p173	Aeromonas phage PX29	GCA_000920195.1
ADM80159.1	003446	Cluster3079_1clades	101	phiAS5_ORF0316	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17845.1	003446	Cluster3079_1clades	101	Aeh1ORF179c	Aeromonas virus Aeh1	GCA_000843245.1
ABY63201.1	003447	Cluster3080_1clades	92	201phi2-1p376	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32468.1	003447	Cluster3080_1clades	96	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77004.1	003447	Cluster3080_1clades	96	PHABIO_373	Pseudomonas phage Phabio	GCA_002624965.1
AEH03736.1	003447	Cluster3080_1clades	108	313	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42040.1	003447	Cluster3080_1clades	96	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AFC21895.1	003448	Preader17	108	GAP32_440	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44024.1	003448	Preader17	108	CBB_461	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88981.1	003448	Preader17	108	BF_0456	Serratia phage BF	GCA_002619745.1
SOK59265.1	003448	Preader17	108	g457	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58729.1	003448	Preader17	108	g452	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28912.1	003449	GlobuloviralATPase	108	AP1_0205	Aeromonas phage AP1	GCA_014183365.1
ATI17583.1	003449	GlobuloviralATPase	108	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00414.1	003449	GlobuloviralATPase	108	HWB28_gp138	Aeromonas phage AS-zj	GCA_002627665.1
QAX98022.1	003449	GlobuloviralATPase	108	ASswx1_382	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39237.1	003449	GlobuloviralATPase	108	CC2_150	Aeromonas phage CC2	GCA_000903495.1
AIT14340.1	003450	Cluster3083_1clades	108	PBI_121Q_450	Escherichia phage 121Q	GCA_000926855.1
AGC34798.1	003450	Cluster3083_1clades	88	ACQ29_gp118	Escherichia phage PBECO4	GCA_001041035.1
BBM62011.1	003450	Cluster3083_1clades	108	EO157G_4220	Escherichia phage SP27	GCA_008033345.1
QBO61964.1	003450	Cluster3083_1clades	108	G17_00475	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80327.1	003450	Cluster3083_1clades	108	PSLUR01_00350	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG63259.1	003451	Cluster3084_1clades	108	DAC16_26	Bacteroides phage DAC16	GCA_013387695.1
QIG63521.1	003451	Cluster3084_1clades	108	DAC19_30	Bacteroides phage DAC19	GCA_013387715.1
QIG63783.1	003451	Cluster3084_1clades	108	DAC20_30	Bacteroides phage DAC20	GCA_013387725.1
QIG64044.1	003451	Cluster3084_1clades	108	DAC22_30	Bacteroides phage DAC22	GCA_013387735.1
QIG64305.1	003451	Cluster3084_1clades	108	DAC23_27	Bacteroides phage DAC23	GCA_013387745.1
QIG63360.1	003452	TM+TM+TM	108	DAC16_127	Bacteroides phage DAC16	GCA_013387695.1
QIG63625.1	003452	TM+TM+TM	108	DAC19_134	Bacteroides phage DAC19	GCA_013387715.1
QIG63886.1	003452	TM+TM+TM	108	DAC20_133	Bacteroides phage DAC20	GCA_013387725.1
QIG64149.1	003452	TM+TM+TM	108	DAC22_135	Bacteroides phage DAC22	GCA_013387735.1
QIG64406.1	003452	TM+TM+TM	108	DAC23_128	Bacteroides phage DAC23	GCA_013387745.1
QIG63415.1	003453	Cluster3086_1clades	108	DAC16_185	Bacteroides phage DAC16	GCA_013387695.1
QIG63679.1	003453	Cluster3086_1clades	108	DAC19_191	Bacteroides phage DAC19	GCA_013387715.1
QIG63940.1	003453	Cluster3086_1clades	108	DAC20_190	Bacteroides phage DAC20	GCA_013387725.1
QIG64204.1	003453	Cluster3086_1clades	108	DAC22_193	Bacteroides phage DAC22	GCA_013387735.1
QIG64460.1	003453	Cluster3086_1clades	108	DAC23_185	Bacteroides phage DAC23	GCA_013387745.1
QIG63444.1	003454	Cluster3087_1clades	108	DAC16_215	Bacteroides phage DAC16	GCA_013387695.1
QIG63707.1	003454	Cluster3087_1clades	108	DAC19_220	Bacteroides phage DAC19	GCA_013387715.1
QIG63968.1	003454	Cluster3087_1clades	108	DAC20_219	Bacteroides phage DAC20	GCA_013387725.1
QIG64232.1	003454	Cluster3087_1clades	108	DAC22_222	Bacteroides phage DAC22	GCA_013387735.1
QIG64488.1	003454	Cluster3087_1clades	108	DAC23_214	Bacteroides phage DAC23	GCA_013387745.1
AAX44551.1	003455	PurS	107	PSSM2_173	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12420.1	003455	PurS	107	PRTG_00269	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59482.1	003455	PurS	91	S330809_021	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59244.1	003455	PurS	91	C440309_021	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59720.1	003455	PurS	91	N231010_021	Synechococcus phage S-CAM4	GCA_002922155.1
QMV28832.1	003456	Cluster3089_1clades	107	AP1_0125	Aeromonas phage AP1	GCA_014183365.1
ATI17266.1	003456	Cluster3089_1clades	107	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00326.1	003456	Cluster3089_1clades	107	HWB28_gp226	Aeromonas phage AS-zj	GCA_002627665.1
QAX97705.1	003456	Cluster3089_1clades	107	ASswx1_59	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39191.1	003456	Cluster3089_1clades	107	CC2_051	Aeromonas phage CC2	GCA_000903495.1
AFC21509.1	003457	Cluster3090_1clades	106	GAP32_061	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43630.1	003457	Cluster3090_1clades	106	CBB_65	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88581.1	003457	Cluster3090_1clades	107	BF_0056	Serratia phage BF	GCA_002619745.1
SOK58856.1	003457	Cluster3090_1clades	107	g048	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58318.1	003457	Cluster3090_1clades	107	g041	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63328.1	003458	Cluster3091_1clades	107	DAC16_95	Bacteroides phage DAC16	GCA_013387695.1
QIG63590.1	003458	Cluster3091_1clades	104	DAC19_99	Bacteroides phage DAC19	GCA_013387715.1
QIG63851.1	003458	Cluster3091_1clades	104	DAC20_98	Bacteroides phage DAC20	GCA_013387725.1
QIG64114.1	003458	Cluster3091_1clades	79	DAC22_100	Bacteroides phage DAC22	GCA_013387735.1
QIG64372.1	003458	Cluster3091_1clades	79	DAC23_94	Bacteroides phage DAC23	GCA_013387745.1
QIG63397.1	003459	SIG+WYL	107	DAC16_167	Bacteroides phage DAC16	GCA_013387695.1
QIG63661.1	003459	SIG+WYL	107	DAC19_173	Bacteroides phage DAC19	GCA_013387715.1
QIG63922.1	003459	SIG+WYL	107	DAC20_172	Bacteroides phage DAC20	GCA_013387725.1
QIG64186.1	003459	SIG+WYL	107	DAC22_175	Bacteroides phage DAC22	GCA_013387735.1
QIG64442.1	003459	SIG+WYL	107	DAC23_167	Bacteroides phage DAC23	GCA_013387745.1
AMR59779.1	003460	Cluster3093_1clades	106	SEGD1_132	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ48433.1	003460	Cluster3093_1clades	101	CAITLIN_138	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
QKN85968.1	003460	Cluster3093_1clades	106	ACEC001_1300	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20832.1	003460	Cluster3093_1clades	106	-	Salmonella phage JN03	GCA_014319805.1
AEP83961.1	003460	Cluster3093_1clades	106	SPN3US_0128	Salmonella phage SPN3US	GCA_001042275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QMV28816.1	003461	Cluster3094_1clades	106	AP1_0109	Aeromonas phage AP1	GCA_014183365.1
ATI17610.1	003461	Cluster3094_1clades	106	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00386.1	003461	Cluster3094_1clades	106	HWB28_gp166	Aeromonas phage AS-zj	GCA_002627665.1
QAX98051.1	003461	Cluster3094_1clades	106	ASswx1_411	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39224.1	003461	Cluster3094_1clades	106	CC2_118	Aeromonas phage CC2	GCA_000903495.1
QMV28829.1	003462	Cluster3095_1clades	101	AP1_0122	Aeromonas phage AP1	GCA_014183365.1
ATI17598.1	003462	Cluster3095_1clades	101	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00399.1	003462	Cluster3095_1clades	101	HWB28_gp153	Aeromonas phage AS-zj	GCA_002627665.1
QAX98038.1	003462	Cluster3095_1clades	101	ASswx1_398	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39227.1	003462	Cluster3095_1clades	106	CC2_133	Aeromonas phage CC2	GCA_000903495.1
QGZ14465.1	003463	Imm26	106	HWC77_gp102	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04269.1	003463	Imm26	106	HWC03_gp114	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23096.1	003463	Imm26	106	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81089.1	003463	Imm26	106	Aphrodite1_0037	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47420.1	003463	Imm26	106	HWC35_gp026	Vibrio phage USC-1	GCA_006864065.1
AIR93503.1	003464	Cluster3097_1clades	105	AVU42_gp164	Prochlorococcus phage P-TIM68	GCA_001503075.1
QGT54925.1	003464	Cluster3097_1clades	75	b23_0312	Synechococcus phage B23	GCA_009745195.1
QGT54560.1	003464	Cluster3097_1clades	75	b3_0319	Synechococcus phage B3	GCA_009745215.1
QCW22949.1	003464	Cluster3097_1clades	102	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50533.1	003464	Cluster3097_1clades	102	-	Synechococcus phage S-B43	GCA_006869725.1
AGR48096.1	003465	Cluster3098_1clades	78	SmphiM12_464	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13265.1	003465	Cluster3098_1clades	78	PHIM19_360	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12905.1	003465	Cluster3098_1clades	78	PHIM7_360	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13628.1	003465	Cluster3098_1clades	72	PHIN3_365	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13629.1	003465	Cluster3098_1clades	105	PHIN3_366	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21811.1	003466	Cluster3099_1clades	61	GAP32_361	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43935.1	003466	Cluster3099_1clades	101	CBB_372	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88894.1	003466	Cluster3099_1clades	105	BF_0369	Serratia phage BF	GCA_002619745.1
SOK59180.1	003466	Cluster3099_1clades	105	g372	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58646.1	003466	Cluster3099_1clades	105	g369	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63242.1	003467	Cluster3100_1clades	105	DAC16_9	Bacteroides phage DAC16	GCA_013387695.1
QIG63500.1	003467	Cluster3100_1clades	105	DAC19_9	Bacteroides phage DAC19	GCA_013387715.1
QIG63762.1	003467	Cluster3100_1clades	105	DAC20_9	Bacteroides phage DAC20	GCA_013387725.1
QIG64023.1	003467	Cluster3100_1clades	105	DAC22_9	Bacteroides phage DAC22	GCA_013387735.1
QIG64287.1	003467	Cluster3100_1clades	105	DAC23_9	Bacteroides phage DAC23	GCA_013387745.1
QIG63243.1	003468	Cluster3101_1clades	105	DAC16_10	Bacteroides phage DAC16	GCA_013387695.1
QIG63504.1	003468	Cluster3101_1clades	105	DAC19_13	Bacteroides phage DAC19	GCA_013387715.1
QIG63766.1	003468	Cluster3101_1clades	105	DAC20_13	Bacteroides phage DAC20	GCA_013387725.1
QIG64027.1	003468	Cluster3101_1clades	105	DAC22_13	Bacteroides phage DAC22	GCA_013387735.1
QIG64288.1	003468	Cluster3101_1clades	105	DAC23_10	Bacteroides phage DAC23	GCA_013387745.1
QIG63365.1	003469	Cluster3102_1clades	105	DAC16_132	Bacteroides phage DAC16	GCA_013387695.1
QIG63630.1	003469	Cluster3102_1clades	105	DAC19_139	Bacteroides phage DAC19	GCA_013387715.1
QIG63891.1	003469	Cluster3102_1clades	105	DAC20_138	Bacteroides phage DAC20	GCA_013387725.1
QIG64154.1	003469	Cluster3102_1clades	105	DAC22_140	Bacteroides phage DAC22	GCA_013387735.1
QIG64411.1	003469	Cluster3102_1clades	105	DAC23_133	Bacteroides phage DAC23	GCA_013387745.1
AUE22631.1	003470	Cluster3103_1clades	104	Ah1_00090	Aeromonas phage Ah1	GCA_002957415.1
QAX98361.1	003470	Cluster3103_1clades	104	ASfcp2_15	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52815.1	003470	Cluster3103_1clades	104	PX29p096	Aeromonas phage PX29	GCA_000920195.1
ADM80071.1	003470	Cluster3103_1clades	99	phiAS5_ORF0228	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17758.1	003470	Cluster3103_1clades	104	Aeh1ORF097c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21916.1	003471	Cluster3104_1clades	104	GAP32_459	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44042.1	003471	Cluster3104_1clades	104	CBB_479	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88998.1	003471	Cluster3104_1clades	104	BF_0473	Serratia phage BF	GCA_002619745.1
SOK59281.1	003471	Cluster3104_1clades	101	g473	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58746.1	003471	Cluster3104_1clades	101	g469	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21797.1	003472	Cluster3105_1clades	100	GAP32_347	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43917.1	003472	Cluster3105_1clades	104	CBB_354	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88878.1	003472	Cluster3105_1clades	102	BF_0353	Serratia phage BF	GCA_002619745.1
SOK59163.1	003472	Cluster3105_1clades	103	g355	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58631.1	003472	Cluster3105_1clades	103	g354	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGG54349.1	003473	Cluster3106_1clades	56	CYWG_00065	Cyanophage S-SSM6b	GCA_002710425.1
ASR76071.1	003473	Cluster3106_1clades	56	PBI_BELLAMY_26	Synechococcus phage Bellamy	GCA_002627525.1
QCW22910.1	003473	Cluster3106_1clades	104	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50549.1	003473	Cluster3106_1clades	55	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70039.1	003473	Cluster3106_1clades	49	SynMITS9220M01_026	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUE22702.1	003474	Cluster3107_1clades	103	Ah1_00161	Aeromonas phage Ah1	GCA_002957415.1
QAX98427.1	003474	Cluster3107_1clades	103	ASfcp2_83	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52882.1	003474	Cluster3107_1clades	103	PX29p163	Aeromonas phage PX29	GCA_000920195.1
ADM80145.1	003474	Cluster3107_1clades	103	phiAS5_ORF0302	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17833.1	003474	Cluster3107_1clades	103	Aeh1ORF167c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21935.1	003475	Cluster3108_1clades	100	GAP32_477	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44061.1	003475	Cluster3108_1clades	101	CBB_498	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89016.1	003475	Cluster3108_1clades	103	BF_0491	Serratia phage BF	GCA_002619745.1
SOK59297.1	003475	Cluster3108_1clades	101	g489	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58762.1	003475	Cluster3108_1clades	101	g485	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QGZ14421.1	003476	Cluster3109_1clades	103	HWC77_gp058	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04314.1	003476	Cluster3109_1clades	103	HWC03_gp159	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23264.1	003476	Cluster3109_1clades	103	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81091.1	003476	Cluster3109_1clades	103	Aphrodite1_0081	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47464.1	003476	Cluster3109_1clades	103	HWC35_gp070	Vibrio phage USC-1	GCA_006864065.1
QIG63476.1	003477	DUF2829	103	DAC16_247	Bacteroides phage DAC16	GCA_013387695.1
QIG63739.1	003477	DUF2829	103	DAC19_252	Bacteroides phage DAC19	GCA_013387715.1
QIG64000.1	003477	DUF2829	103	DAC20_251	Bacteroides phage DAC20	GCA_013387725.1
QIG64264.1	003477	DUF2829	103	DAC22_254	Bacteroides phage DAC22	GCA_013387735.1
QIG64520.1	003477	DUF2829	103	DAC23_246	Bacteroides phage DAC23	GCA_013387745.1
AUE22671.1	003478	Cluster3111_1clades	93	Ah1_00130	Aeromonas phage Ah1	GCA_002957415.1
QAX98397.1	003478	Cluster3111_1clades	93	ASfcp2_53	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52853.1	003478	Cluster3111_1clades	93	PX29p134	Aeromonas phage PX29	GCA_000920195.1
ADM80112.1	003478	Cluster3111_1clades	102	phiAS5_ORF0269	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17800.1	003478	Cluster3111_1clades	93	Aeh1ORF135c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06099.1	003479	Cluster3112_1clades	98	ABCD_0018	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AIA64945.1	003479	Cluster3112_1clades	102	S13_146	Cronobacter phage S13	GCA_001503575.1
AON97026.1	003479	Cluster3112_1clades	101	E_017	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78539.1	003479	Cluster3112_1clades	98	RB43ORF017c	Escherichia virus RB43	GCA_000863505.1
QHJ78997.1	003479	Cluster3112_1clades	100	-	Myoviridae sp.	GCA_012593985.1
AUE22601.1	003480	SIG+RdRP_5	102	Ah1_00060	Aeromonas phage Ah1	GCA_002957415.1
QAX98638.1	003480	SIG+RdRP_5	98	ASfcp2_305	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52778.1	003480	SIG+RdRP_5	98	PX29p059	Aeromonas phage PX29	GCA_000920195.1
ADM80034.1	003480	SIG+RdRP_5	98	phiAS5_ORF0191	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17723.1	003480	SIG+RdRP_5	97	Aeh1ORF063c	Aeromonas virus Aeh1	GCA_000843245.1
QMV28872.1	003481	Cluster3114_1clades	101	AP1_0165	Aeromonas phage AP1	GCA_014183365.1
ATI17498.1	003481	Cluster3114_1clades	101	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00499.1	003481	Cluster3114_1clades	101	HWB28_gp053	Aeromonas phage AS-zj	GCA_002627665.1
QAX97937.1	003481	Cluster3114_1clades	101	ASswx1_295	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39268.1	003481	Cluster3114_1clades	101	CC2_236	Aeromonas phage CC2	GCA_000903495.1
AUE22595.1	003482	Cluster3115_1clades	101	Ah1_00054	Aeromonas phage Ah1	GCA_002957415.1
QAX98633.1	003482	Cluster3115_1clades	75	ASfcp2_300	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52773.1	003482	Cluster3115_1clades	75	PX29p054	Aeromonas phage PX29	GCA_000920195.1
ADM80028.1	003482	Cluster3115_1clades	76	phiAS5_ORF0185	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17718.1	003482	Cluster3115_1clades	75	Aeh1ORF058c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63280.1	003483	Cluster3116_1clades	101	DAC16_47	Bacteroides phage DAC16	GCA_013387695.1
QIG63542.1	003483	Cluster3116_1clades	101	DAC19_51	Bacteroides phage DAC19	GCA_013387715.1
QIG63803.1	003483	Cluster3116_1clades	101	DAC20_50	Bacteroides phage DAC20	GCA_013387725.1
QIG64064.1	003483	Cluster3116_1clades	101	DAC22_50	Bacteroides phage DAC22	GCA_013387735.1
QIG64325.1	003483	Cluster3116_1clades	101	DAC23_47	Bacteroides phage DAC23	GCA_013387745.1
AGR47656.1	003484	LuxR-HTH	100	SmphiM12_024	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12922.1	003484	LuxR-HTH	100	PHIM19_15	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12562.1	003484	LuxR-HTH	100	PHIM7_14	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13290.1	003484	LuxR-HTH	85	PHIN3_25	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13294.1	003484	LuxR-HTH	78	PHIN3_29	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21870.1	003485	Cluster3118_1clades	97	GAP32_417	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43998.1	003485	Cluster3118_1clades	97	CBB_435	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88958.1	003485	Cluster3118_1clades	100	BF_0433	Serratia phage BF	GCA_002619745.1
SOK59244.1	003485	Cluster3118_1clades	100	g436	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58710.1	003485	Cluster3118_1clades	100	g433	Yersinia phage fHe-Yen9-04	GCA_002990485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63249.1	003486	Cluster3119_1clades	100	DAC16_16	Bacteroides phage DAC16	GCA_013387695.1
QIG63511.1	003486	Cluster3119_1clades	100	DAC19_20	Bacteroides phage DAC19	GCA_013387715.1
QIG63773.1	003486	Cluster3119_1clades	100	DAC20_20	Bacteroides phage DAC20	GCA_013387725.1
QIG64034.1	003486	Cluster3119_1clades	100	DAC22_20	Bacteroides phage DAC22	GCA_013387735.1
QIG64295.1	003486	Cluster3119_1clades	100	DAC23_17	Bacteroides phage DAC23	GCA_013387745.1
QIG63355.1	003487	Cluster3120_1clades	100	DAC16_122	Bacteroides phage DAC16	GCA_013387695.1
QIG63620.1	003487	Cluster3120_1clades	100	DAC19_129	Bacteroides phage DAC19	GCA_013387715.1
QIG63881.1	003487	Cluster3120_1clades	100	DAC20_128	Bacteroides phage DAC20	GCA_013387725.1
QIG64144.1	003487	Cluster3120_1clades	100	DAC22_130	Bacteroides phage DAC22	GCA_013387735.1
QIG64401.1	003487	Cluster3120_1clades	100	DAC23_123	Bacteroides phage DAC23	GCA_013387745.1
QIG63418.1	003488	Cluster3121_1clades	100	DAC16_188	Bacteroides phage DAC16	GCA_013387695.1
QIG63682.1	003488	Cluster3121_1clades	100	DAC19_194	Bacteroides phage DAC19	GCA_013387715.1
QIG63943.1	003488	Cluster3121_1clades	100	DAC20_193	Bacteroides phage DAC20	GCA_013387725.1
QIG64207.1	003488	Cluster3121_1clades	100	DAC22_196	Bacteroides phage DAC22	GCA_013387735.1
QIG64463.1	003488	Cluster3121_1clades	100	DAC23_188	Bacteroides phage DAC23	GCA_013387745.1
APU01607.1	003489	Cluster3122_1clades	99	-	Aeromonas phage 65.2	GCA_002618145.1
AUE22604.1	003489	Cluster3122_1clades	95	Ah1_00063	Aeromonas phage Ah1	GCA_002957415.1
QAX98641.1	003489	Cluster3122_1clades	95	ASfcp2_308	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52781.1	003489	Cluster3122_1clades	95	PX29p062	Aeromonas phage PX29	GCA_000920195.1
ADQ53231.1	003489	Cluster3122_1clades	99	65p223	Aeromonas virus 65	GCA_000893255.1
AEO93364.1	003490	Cluster3123_1clades	93	G_102	Bacillus virus G	GCA_000917535.1
AEO93365.1	003490	Cluster3123_1clades	92	G_103	Bacillus virus G	GCA_000917535.1
AEO93366.1	003490	Cluster3123_1clades	94	G_104	Bacillus virus G	GCA_000917535.1
AEO93367.1	003490	Cluster3123_1clades	99	G_105	Bacillus virus G	GCA_000917535.1
AEO93368.1	003490	Cluster3123_1clades	99	G_106	Bacillus virus G	GCA_000917535.1
AFA44639.1	003491	TM	97	RaK2_00366	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44640.1	003491	TM	94	RaK2_00367	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44641.1	003491	TM	93	RaK2_00368	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44648.1	003491	TM	94	RaK2_00375	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44666.1	003491	TM	99	RaK2_00393	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AUE22566.1	003492	Phage_RpbA	98	Ah1_00025	Aeromonas phage Ah1	GCA_002957415.1
QAX98604.1	003492	Phage_RpbA	98	ASfcp2_271	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52739.1	003492	Phage_RpbA	98	PX29p020	Aeromonas phage PX29	GCA_000920195.1
ADM79992.1	003492	Phage_RpbA	94	phiAS5_ORF0149	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17677.1	003492	Phage_RpbA	98	rpbA	Aeromonas virus Aeh1	GCA_000843245.1
AFC21527.1	003493	Cluster3126_1clades	98	GAP32_079	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43647.1	003493	Cluster3126_1clades	98	CBB_82	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88596.1	003493	Cluster3126_1clades	97	BF_0071	Serratia phage BF	GCA_002619745.1
SOK58872.1	003493	Cluster3126_1clades	97	g064	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58335.1	003493	Cluster3126_1clades	97	g058	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28850.1	003494	Cluster3127_1clades	98	AP1_0143	Aeromonas phage AP1	GCA_014183365.1
ATI17285.1	003494	Cluster3127_1clades	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00311.1	003494	Cluster3127_1clades	98	HWB28_gp241	Aeromonas phage AS-zj	GCA_002627665.1
QAX97727.1	003494	Cluster3127_1clades	98	ASswx1_81	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39178.1	003494	Cluster3127_1clades	98	CC2_031	Aeromonas phage CC2	GCA_000903495.1
QMV28917.1	003495	Cluster3128_1clades	98	AP1_0210	Aeromonas phage AP1	GCA_014183365.1
ATI17550.1	003495	Cluster3128_1clades	98	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00447.1	003495	Cluster3128_1clades	98	HWB28_gp105	Aeromonas phage AS-zj	GCA_002627665.1
QAX97991.1	003495	Cluster3128_1clades	98	ASswx1_350	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39250.1	003495	Cluster3128_1clades	98	CC2_185	Aeromonas phage CC2	GCA_000903495.1
AFC21989.1	003496	TM	92	GAP32_528	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44109.1	003496	TM	98	CBB_546	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89062.1	003496	TM	97	BF_0537	Serratia phage BF	GCA_002619745.1
SOK59340.1	003496	TM	94	g532	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58802.1	003496	TM	93	g525	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANM44784.1	003497	Cluster3130_1clades	46	KTN4_026	Pseudomonas phage KTN4	GCA_002607225.1
QBX32287.1	003497	Cluster3130_1clades	94	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03539.1	003497	Cluster3130_1clades	97	115	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02681.1	003497	Cluster3130_1clades	93	PSA21_154	Pseudomonas phage Psa21	GCA_004340405.1
QEM41861.1	003497	Cluster3130_1clades	94	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AMS01145.1	003498	Cluster3131_1clades	89	AR9_g061	Bacillus phage AR9	GCA_001743835.1
ALN97814.1	003498	Cluster3131_1clades	88	Bp8pS_135	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97816.1	003498	Cluster3131_1clades	97	Bp8pS_137	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00071.1	003498	Cluster3131_1clades	91	PBI_PBS1_249	Bacillus virus PBS1	GCA_002601325.1
ASU00073.1	003498	Cluster3131_1clades	89	PBI_PBS1_251	Bacillus virus PBS1	GCA_002601325.1
QGZ14572.1	003499	Cluster3132_1clades	97	HWC77_gp209	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04161.1	003499	Cluster3132_1clades	97	HWC03_gp006	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23197.1	003499	Cluster3132_1clades	97	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47532.1	003499	Cluster3132_1clades	97	HWC35_gp138	Vibrio phage USC-1	GCA_006864065.1
BAW98348.1	003499	Cluster3132_1clades	96	FDH33_gp139	Vibrio phage pTD1	GCA_002618825.1
QIG63345.1	003500	Cluster3133_1clades	97	DAC16_112	Bacteroides phage DAC16	GCA_013387695.1
QIG63611.1	003500	Cluster3133_1clades	97	DAC19_120	Bacteroides phage DAC19	GCA_013387715.1
QIG63872.1	003500	Cluster3133_1clades	97	DAC20_119	Bacteroides phage DAC20	GCA_013387725.1
QIG64135.1	003500	Cluster3133_1clades	97	DAC22_121	Bacteroides phage DAC22	GCA_013387735.1
QIG64392.1	003500	Cluster3133_1clades	97	DAC23_114	Bacteroides phage DAC23	GCA_013387745.1
QMV28916.1	003501	Cluster3134_1clades	96	AP1_0209	Aeromonas phage AP1	GCA_014183365.1
ATI17549.1	003501	Cluster3134_1clades	96	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00448.1	003501	Cluster3134_1clades	96	HWB28_gp104	Aeromonas phage AS-zj	GCA_002627665.1
QAX97990.1	003501	Cluster3134_1clades	96	ASswx1_349	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39251.1	003501	Cluster3134_1clades	96	CC2_186	Aeromonas phage CC2	GCA_000903495.1
AGH56893.1	003502	SIG+TM	95	CPXG_00090	Cyanophage P-RSM6	GCA_000906155.1
AGH26242.1	003502	SIG+TM	96	CPMG_00141	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44667.1	003502	SIG+TM	93	PSSM2_290	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12310.1	003502	SIG+TM	93	PRTG_00157	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93548.1	003502	SIG+TM	90	AVU42_gp211	Prochlorococcus phage P-TIM68	GCA_001503075.1
QIG63339.1	003503	Cluster3137_1clades	96	DAC16_106	Bacteroides phage DAC16	GCA_013387695.1
QIG63605.1	003503	Cluster3137_1clades	96	DAC19_114	Bacteroides phage DAC19	GCA_013387715.1
QIG63866.1	003503	Cluster3137_1clades	96	DAC20_113	Bacteroides phage DAC20	GCA_013387725.1
QIG64129.1	003503	Cluster3137_1clades	96	DAC22_115	Bacteroides phage DAC22	GCA_013387735.1
QIG64386.1	003503	Cluster3137_1clades	96	DAC23_108	Bacteroides phage DAC23	GCA_013387745.1
AUE22688.1	003504	Cluster3138_1clades	89	Ah1_00147	Aeromonas phage Ah1	GCA_002957415.1
QAX98413.1	003504	Cluster3138_1clades	95	ASfcp2_69	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52868.1	003504	Cluster3138_1clades	95	PX29p149	Aeromonas phage PX29	GCA_000920195.1
ADM80130.1	003504	Cluster3138_1clades	94	phiAS5_ORF0287	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17815.1	003504	Cluster3138_1clades	95	Aeh1ORF150c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63235.1	003505	Cluster3139_1clades	95	DAC16_2	Bacteroides phage DAC16	GCA_013387695.1
QIG63493.1	003505	Cluster3139_1clades	95	DAC19_2	Bacteroides phage DAC19	GCA_013387715.1
QIG63755.1	003505	Cluster3139_1clades	95	DAC20_2	Bacteroides phage DAC20	GCA_013387725.1
QIG64016.1	003505	Cluster3139_1clades	88	DAC22_2	Bacteroides phage DAC22	GCA_013387735.1
QIG64280.1	003505	Cluster3139_1clades	95	DAC23_2	Bacteroides phage DAC23	GCA_013387745.1
AIT14316.1	003506	RHSP	78	PBI_121Q_426	Escherichia phage 121Q	GCA_000926855.1
QAY00622.1	003506	RHSP	94	Ecwhy1_347	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61990.1	003506	RHSP	94	EO157G_4010	Escherichia phage SP27	GCA_008033345.1
QBO61988.1	003506	RHSP	94	G17_00499	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80303.1	003506	RHSP	94	PSLUR01_00326	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUE22698.1	003507	Cluster3141_1clades	91	Ah1_00157	Aeromonas phage Ah1	GCA_002957415.1
QAX98422.1	003507	Cluster3141_1clades	92	ASfcp2_78	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52877.1	003507	Cluster3141_1clades	92	PX29p158	Aeromonas phage PX29	GCA_000920195.1
ADM80140.1	003507	Cluster3141_1clades	93	phiAS5_ORF0297	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17827.1	003507	Cluster3141_1clades	92	Aeh1ORF161c	Aeromonas virus Aeh1	GCA_000843245.1
QMV29033.1	003508	Cluster3143_1clades	93	AP1_0326	Aeromonas phage AP1	GCA_014183365.1
ATI17259.1	003508	Cluster3143_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00332.1	003508	Cluster3143_1clades	93	HWB28_gp220	Aeromonas phage AS-zj	GCA_002627665.1
QAX97699.1	003508	Cluster3143_1clades	93	ASswx1_53	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39197.1	003508	Cluster3143_1clades	93	CC2_057	Aeromonas phage CC2	GCA_000903495.1
QMV29020.1	003509	Cluster3144_1clades	93	AP1_0313	Aeromonas phage AP1	GCA_014183365.1
ATI17631.1	003509	Cluster3144_1clades	93	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00364.1	003509	Cluster3144_1clades	93	HWB28_gp188	Aeromonas phage AS-zj	GCA_002627665.1
QAX97666.1	003509	Cluster3144_1clades	93	ASswx1_20	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39215.1	003509	Cluster3144_1clades	93	CC2_095	Aeromonas phage CC2	GCA_000903495.1
ARB14799.1	003510	Cluster3145_1clades	93	Ccr29_gp243	Caulobacter phage Ccr29	GCA_002619485.1
ARB15139.1	003510	Cluster3145_1clades	93	Ccr32_gp221	Caulobacter phage Ccr32	GCA_002619505.1
ARB15473.1	003510	Cluster3145_1clades	93	Ccr34_gp231	Caulobacter phage Ccr34	GCA_002619525.1
AFU87755.1	003510	Cluster3145_1clades	93	CcrKarma_gp238	Caulobacter virus Karma	GCA_000901575.1
AFU87058.1	003510	Cluster3145_1clades	93	CbK_gp226	Caulobacter virus phiCbK	GCA_000900535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22833.1	003511	Cluster3146_1clades	92	Ah1_00315	Aeromonas phage Ah1	GCA_002957415.1
QAX98547.1	003511	Cluster3146_1clades	92	ASfcp2_212	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53011.1	003511	Cluster3146_1clades	92	PX29p292	Aeromonas phage PX29	GCA_000920195.1
ADM79934.1	003511	Cluster3146_1clades	90	phiAS5_ORF0091	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17962.1	003511	Cluster3146_1clades	92	Aeh1ORF293c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22868.1	003512	Cluster3147_1clades	92	Ah1_00350	Aeromonas phage Ah1	GCA_002957415.1
QAX98578.1	003512	Cluster3147_1clades	92	ASfcp2_244	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53043.1	003512	Cluster3147_1clades	92	PX29p326	Aeromonas phage PX29	GCA_000920195.1
ADM79966.1	003512	Cluster3147_1clades	91	phiAS5_ORF0123	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17996.1	003512	Cluster3147_1clades	92	Aeh1ORF326c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22677.1	003513	SIG+TM	85	Ah1_00136	Aeromonas phage Ah1	GCA_002957415.1
QAX98403.1	003513	SIG+TM	85	ASfcp2_59	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52859.1	003513	SIG+TM	85	PX29p140	Aeromonas phage PX29	GCA_000920195.1
ADM80118.1	003513	SIG+TM	92	phiAS5_ORF0275	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17805.1	003513	SIG+TM	85	Aeh1ORF140c	Aeromonas virus Aeh1	GCA_000843245.1
QMV28920.1	003514	SIG+TM	92	AP1_0213	Aeromonas phage AP1	GCA_014183365.1
ATI17553.1	003514	SIG+TM	92	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00444.1	003514	SIG+TM	92	HWB28_gp108	Aeromonas phage AS-zj	GCA_002627665.1
QAX97993.1	003514	SIG+TM	92	ASswx1_353	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39248.1	003514	SIG+TM	92	CC2_182	Aeromonas phage CC2	GCA_000903495.1
QIG63274.1	003515	Cluster3150_1clades	92	DAC16_41	Bacteroides phage DAC16	GCA_013387695.1
QIG63535.1	003515	Cluster3150_1clades	92	DAC19_44	Bacteroides phage DAC19	GCA_013387715.1
QIG63796.1	003515	Cluster3150_1clades	92	DAC20_43	Bacteroides phage DAC20	GCA_013387725.1
QIG64057.1	003515	Cluster3150_1clades	92	DAC22_43	Bacteroides phage DAC22	GCA_013387735.1
QIG64318.1	003515	Cluster3150_1clades	92	DAC23_40	Bacteroides phage DAC23	GCA_013387745.1
QIG63348.1	003516	Cluster3151_1clades	91	DAC16_115	Bacteroides phage DAC16	GCA_013387695.1
QIG63614.1	003516	Cluster3151_1clades	91	DAC19_123	Bacteroides phage DAC19	GCA_013387715.1
QIG63875.1	003516	Cluster3151_1clades	91	DAC20_122	Bacteroides phage DAC20	GCA_013387725.1
QIG64138.1	003516	Cluster3151_1clades	91	DAC22_124	Bacteroides phage DAC22	GCA_013387735.1
QIG64395.1	003516	Cluster3151_1clades	91	DAC23_117	Bacteroides phage DAC23	GCA_013387745.1
QIG63325.1	003517	Cluster3152_1clades	83	DAC16_92	Bacteroides phage DAC16	GCA_013387695.1
QIG63584.1	003517	Cluster3152_1clades	91	DAC19_93	Bacteroides phage DAC19	GCA_013387715.1
QIG63845.1	003517	Cluster3152_1clades	91	DAC20_92	Bacteroides phage DAC20	GCA_013387725.1
QIG64107.1	003517	Cluster3152_1clades	91	DAC22_93	Bacteroides phage DAC22	GCA_013387735.1
QIG64369.1	003517	Cluster3152_1clades	83	DAC23_91	Bacteroides phage DAC23	GCA_013387745.1
ASV44758.1	003518	Cluster3153_1clades	89	FDI40_gp685	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGR47979.1	003518	Cluster3153_1clades	90	SmphiM12_347	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13167.1	003518	Cluster3153_1clades	90	PHIM19_262	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12807.1	003518	Cluster3153_1clades	90	PHIM7_262	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13530.1	003518	Cluster3153_1clades	90	PHIN3_267	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21482.1	003519	Cluster3154_1clades	75	GAP32_034	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44157.1	003519	Cluster3154_1clades	72	CBB_41	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43606.1	003519	Cluster3154_1clades	72	CBB_594	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88555.1	003519	Cluster3154_1clades	90	BF_0030	Serratia phage BF	GCA_002619745.1
SOK58829.1	003519	Cluster3154_1clades	73	g021	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QMV29124.1	003520	Cluster3155_1clades	87	AP1_0421	Aeromonas phage AP1	GCA_014183365.1
ASU00362.1	003520	Cluster3155_1clades	87	HWB28_gp190	Aeromonas phage AS-zj	GCA_002627665.1
QAX97668.1	003520	Cluster3155_1clades	87	ASswx1_22	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01074.1	003520	Cluster3155_1clades	90	ASwh1_6	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39147.1	003520	Cluster3155_1clades	87	CC2_093	Aeromonas phage CC2	GCA_000903495.1
QIG63394.1	003521	Cluster3156_1clades	90	DAC16_164	Bacteroides phage DAC16	GCA_013387695.1
QIG63658.1	003521	Cluster3156_1clades	90	DAC19_170	Bacteroides phage DAC19	GCA_013387715.1
QIG63919.1	003521	Cluster3156_1clades	90	DAC20_169	Bacteroides phage DAC20	GCA_013387725.1
QIG64183.1	003521	Cluster3156_1clades	90	DAC22_172	Bacteroides phage DAC22	GCA_013387735.1
QIG64439.1	003521	Cluster3156_1clades	90	DAC23_164	Bacteroides phage DAC23	GCA_013387745.1
AUE22701.1	003522	Cluster3157_1clades	89	Ah1_00160	Aeromonas phage Ah1	GCA_002957415.1
QAX98426.1	003522	Cluster3157_1clades	89	ASfcp2_82	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52881.1	003522	Cluster3157_1clades	89	PX29p162	Aeromonas phage PX29	GCA_000920195.1
ADM80144.1	003522	Cluster3157_1clades	86	phiAS5_ORF0301	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17832.1	003522	Cluster3157_1clades	89	Aeh1ORF166c	Aeromonas virus Aeh1	GCA_000843245.1
ADM79923.1	003523	Cluster3158_2clades	89	phiAS5_ORF0080	Aeromonas phage phiAS5	GCA_000887715.1
AUE22822.1	003523	Cluster3158_2clades	85	Ah1_00304	Aeromonas phage Ah1	GCA_002957415.1
QAX98537.1	003523	Cluster3158_2clades	87	ASfcp2_201	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53000.1	003523	Cluster3158_2clades	87	PX29p281	Aeromonas phage PX29	GCA_000920195.1
AAQ17952.1	003523	Cluster3158_2clades	85	Aeh1ORF283c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21831.1	003524	Cluster3159_1clades	89	GAP32_379	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43952.1	003524	Cluster3159_1clades	89	CBB_389	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88913.1	003524	Cluster3159_1clades	76	BF_0388	Serratia phage BF	GCA_002619745.1
SOK59202.1	003524	Cluster3159_1clades	77	g394	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58667.1	003524	Cluster3159_1clades	77	g390	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28822.1	003525	AGT	89	AP1_0115	Aeromonas phage AP1	GCA_014183365.1
ATI17604.1	003525	AGT	89	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00392.1	003525	AGT	87	HWB28_gp160	Aeromonas phage AS-zj	GCA_002627665.1
QAX98045.1	003525	AGT	89	ASswx1_405	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39226.1	003525	AGT	89	CC2_125	Aeromonas phage CC2	GCA_000903495.1
QMV28906.1	003526	Cluster3161_1clades	89	AP1_0199	Aeromonas phage AP1	GCA_014183365.1
ATI17589.1	003526	Cluster3161_1clades	89	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00408.1	003526	Cluster3161_1clades	89	HWB28_gp144	Aeromonas phage AS-zj	GCA_002627665.1
QAX98028.1	003526	Cluster3161_1clades	89	ASswx1_388	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39233.1	003526	Cluster3161_1clades	89	CC2_143	Aeromonas phage CC2	GCA_000903495.1
AFC21539.1	003527	Cluster3162_1clades	82	GAP32_091	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43658.1	003527	Cluster3162_1clades	82	CBB_93	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88612.1	003527	Cluster3162_1clades	89	BF_0087	Serratia phage BF	GCA_002619745.1
SOK58889.1	003527	Cluster3162_1clades	85	g081	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58352.1	003527	Cluster3162_1clades	84	g075	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18876.1	003528	Cluster3163_1clades	74	7t3_0355	Salmonella phage 7t3	GCA_006083215.1
AZU98134.1	003528	Cluster3163_1clades	74	CPT_Munch_190	Salmonella phage Munch	GCA_004015485.1
QIG62848.1	003528	Cluster3163_1clades	74	SEPL_235	Salmonella phage SE_PL	GCA_011067555.1
ATA65495.1	003528	Cluster3163_1clades	89	2050HW_00160	Serratia phage 2050HW	GCA_002628125.1
QDB71263.1	003528	Cluster3163_1clades	88	CPT_Moabite_233	Serratia phage Moabite	GCA_006384735.1
QGZ14543.1	003529	TM+TM	87	HWC77_gp180	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04191.1	003529	TM+TM	87	HWC03_gp036	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23169.1	003529	TM+TM	87	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81097.1	003529	TM+TM	87	Aphrodite1_0173	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47560.1	003529	TM+TM	89	HWC35_gp166	Vibrio phage USC-1	GCA_006864065.1
QIG63256.1	003530	Cluster3165_1clades	89	DAC16_23	Bacteroides phage DAC16	GCA_013387695.1
QIG63518.1	003530	Cluster3165_1clades	89	DAC19_27	Bacteroides phage DAC19	GCA_013387715.1
QIG63780.1	003530	Cluster3165_1clades	89	DAC20_27	Bacteroides phage DAC20	GCA_013387725.1
QIG64041.1	003530	Cluster3165_1clades	89	DAC22_27	Bacteroides phage DAC22	GCA_013387735.1
QIG64302.1	003530	Cluster3165_1clades	89	DAC23_24	Bacteroides phage DAC23	GCA_013387745.1
AFC21972.1	003531	Cluster3166_1clades	88	GAP32_512	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44095.1	003531	Cluster3166_1clades	85	CBB_532	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89051.1	003531	Cluster3166_1clades	86	BF_0526	Serratia phage BF	GCA_002619745.1
SOK59329.1	003531	Cluster3166_1clades	86	g521	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58791.1	003531	Cluster3166_1clades	86	g514	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANM44792.1	003532	Cluster3167_1clades	88	KTN4_034	Pseudomonas phage KTN4	GCA_002607225.1
QBX32293.1	003532	Cluster3167_1clades	88	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94919.1	003532	Cluster3167_1clades	88	SL2_342	Pseudomonas phage SL2	GCA_002956015.1
QJB22671.1	003532	Cluster3167_1clades	88	fnug_28	Pseudomonas phage fnug	GCA_012837215.1
QEM41867.1	003532	Cluster3167_1clades	88	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63377.1	003533	Cluster3168_1clades	88	DAC16_144	Bacteroides phage DAC16	GCA_013387695.1
QIG63642.1	003533	Cluster3168_1clades	88	DAC19_151	Bacteroides phage DAC19	GCA_013387715.1
QIG63903.1	003533	Cluster3168_1clades	88	DAC20_150	Bacteroides phage DAC20	GCA_013387725.1
QIG64166.1	003533	Cluster3168_1clades	88	DAC22_152	Bacteroides phage DAC22	GCA_013387735.1
QIG64423.1	003533	Cluster3168_1clades	88	DAC23_145	Bacteroides phage DAC23	GCA_013387745.1
AFC21613.1	003534	Cluster3169_1clades	85	GAP32_163	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43732.1	003534	Cluster3169_1clades	84	CBB_167	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88687.1	003534	Cluster3169_1clades	85	BF_0162	Serratia phage BF	GCA_002619745.1
SOK58969.1	003534	Cluster3169_1clades	88	g161	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58435.1	003534	Cluster3169_1clades	88	g158	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CAG27179.1	003535	Cluster3170_1clades	80	PPEV_gp085	Pseudomonas phage EL	GCA_000866825.1
ANM44901.1	003535	Cluster3170_1clades	87	KTN4_143	Pseudomonas phage KTN4	GCA_002607225.1
ATN94812.1	003535	Cluster3170_1clades	87	SL2_235	Pseudomonas phage SL2	GCA_002956015.1
QJB22779.1	003535	Cluster3170_1clades	87	fnug_136	Pseudomonas phage fnug	GCA_012837215.1
AAL83014.1	003535	Cluster3170_1clades	87	PHIKZ113	Pseudomonas virus phiKZ	GCA_000842965.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22638.1	003536	Cluster3171_1clades	87	Ah1_00097	Aeromonas phage Ah1	GCA_002957415.1
QAX98367.1	003536	Cluster3171_1clades	87	ASfcp2_21	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52821.1	003536	Cluster3171_1clades	87	PX29p102	Aeromonas phage PX29	GCA_000920195.1
ADM80078.1	003536	Cluster3171_1clades	87	phiAS5_ORF0235	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17764.1	003536	Cluster3171_1clades	87	Aeh1ORF103c	Aeromonas virus Aeh1	GCA_000843245.1
ANM45057.1	003537	Cluster3172_1clades	87	KTN4_299	Pseudomonas phage KTN4	GCA_002607225.1
AEH03626.1	003537	Cluster3172_1clades	86	203	Pseudomonas phage PhiPA3	GCA_001502095.1
ATN94658.1	003537	Cluster3172_1clades	87	SL2_081	Pseudomonas phage SL2	GCA_002956015.1
QJB22932.1	003537	Cluster3172_1clades	87	fnug_289	Pseudomonas phage fnug	GCA_012837215.1
AGC26354.1	003537	Cluster3172_1clades	87	PHIKZ246.1	Pseudomonas virus phiKZ	GCA_000842965.1
QIG63290.1	003538	Cluster3173_1clades	87	DAC16_57	Bacteroides phage DAC16	GCA_013387695.1
QIG63549.1	003538	Cluster3173_1clades	87	DAC19_58	Bacteroides phage DAC19	GCA_013387715.1
QIG63810.1	003538	Cluster3173_1clades	87	DAC20_57	Bacteroides phage DAC20	GCA_013387725.1
QIG64072.1	003538	Cluster3173_1clades	87	DAC22_58	Bacteroides phage DAC22	GCA_013387735.1
QIG64335.1	003538	Cluster3173_1clades	87	DAC23_57	Bacteroides phage DAC23	GCA_013387745.1
QIG63354.1	003539	Cluster3174_1clades	87	DAC16_121	Bacteroides phage DAC16	GCA_013387695.1
QIG63619.1	003539	Cluster3174_1clades	87	DAC19_128	Bacteroides phage DAC19	GCA_013387715.1
QIG63880.1	003539	Cluster3174_1clades	87	DAC20_127	Bacteroides phage DAC20	GCA_013387725.1
QIG64143.1	003539	Cluster3174_1clades	87	DAC22_129	Bacteroides phage DAC22	GCA_013387735.1
QIG64400.1	003539	Cluster3174_1clades	87	DAC23_122	Bacteroides phage DAC23	GCA_013387745.1
AUE22682.1	003540	LPD11	84	Ah1_00141	Aeromonas phage Ah1	GCA_002957415.1
QAX98408.1	003540	LPD11	84	ASfcp2_64	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52864.1	003540	LPD11	84	PX29p145	Aeromonas phage PX29	GCA_000920195.1
ADM80123.1	003540	LPD11	84	phiAS5_ORF0280	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17810.1	003540	LPD11	85	Aeh1ORF145c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22773.1	003541	Cluster3177_1clades	54	Ah1_00255	Aeromonas phage Ah1	GCA_002957415.1
QAX98489.1	003541	Cluster3177_1clades	85	ASfcp2_151	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52951.1	003541	Cluster3177_1clades	85	PX29p232	Aeromonas phage PX29	GCA_000920195.1
ADM79875.1	003541	Cluster3177_1clades	85	phiAS5_ORF0032	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17897.1	003541	Cluster3177_1clades	85	Aeh1ORF235c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22803.1	003542	Cluster3178_1clades	85	Ah1_00285	Aeromonas phage Ah1	GCA_002957415.1
QAX98518.1	003542	Cluster3178_1clades	85	ASfcp2_182	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52981.1	003542	Cluster3178_1clades	85	PX29p262	Aeromonas phage PX29	GCA_000920195.1
ADM79905.1	003542	Cluster3178_1clades	85	phiAS5_ORF0062	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17930.1	003542	Cluster3178_1clades	85	Aeh1ORF266c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22836.1	003543	Cluster3179_1clades	85	Ah1_00318	Aeromonas phage Ah1	GCA_002957415.1
QAX98550.1	003543	Cluster3179_1clades	85	ASfcp2_215	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53014.1	003543	Cluster3179_1clades	85	PX29p295	Aeromonas phage PX29	GCA_000920195.1
ADM79937.1	003543	Cluster3179_1clades	84	phiAS5_ORF0094	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17965.1	003543	Cluster3179_1clades	85	Aeh1ORF296c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21646.1	003544	Cluster3180_1clades	83	GAP32_196	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43767.1	003544	Cluster3180_1clades	84	CBB_202	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88723.1	003544	Cluster3180_1clades	85	BF_0198	Serratia phage BF	GCA_002619745.1
SOK59005.1	003544	Cluster3180_1clades	85	g197	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58470.1	003544	Cluster3180_1clades	85	g193	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63251.1	003545	Cluster3181_1clades	85	DAC16_18	Bacteroides phage DAC16	GCA_013387695.1
QIG63513.1	003545	Cluster3181_1clades	85	DAC19_22	Bacteroides phage DAC19	GCA_013387715.1
QIG63775.1	003545	Cluster3181_1clades	85	DAC20_22	Bacteroides phage DAC20	GCA_013387725.1
QIG64036.1	003545	Cluster3181_1clades	85	DAC22_22	Bacteroides phage DAC22	GCA_013387735.1
QIG64297.1	003545	Cluster3181_1clades	85	DAC23_19	Bacteroides phage DAC23	GCA_013387745.1
AFC21827.1	003546	Cluster3182_1clades	84	GAP32_375	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43948.1	003546	Cluster3182_1clades	84	CBB_385	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88907.1	003546	Cluster3182_1clades	84	BF_0382	Serratia phage BF	GCA_002619745.1
SOK59196.1	003546	Cluster3182_1clades	84	g388	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58660.1	003546	Cluster3182_1clades	84	g383	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28754.1	003547	Cluster3183_1clades	84	AP1_0036	Aeromonas phage AP1	GCA_014183365.1
ATI17477.1	003547	Cluster3183_1clades	84	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00520.1	003547	Cluster3183_1clades	84	HWB28_gp032	Aeromonas phage AS-zj	GCA_002627665.1
QAX97917.1	003547	Cluster3183_1clades	84	ASswx1_274	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39270.1	003547	Cluster3183_1clades	84	CC2_258	Aeromonas phage CC2	GCA_000903495.1
QIG63409.1	003548	Cluster3184_1clades	84	DAC16_179	Bacteroides phage DAC16	GCA_013387695.1
QIG63673.1	003548	Cluster3184_1clades	84	DAC19_185	Bacteroides phage DAC19	GCA_013387715.1
QIG63934.1	003548	Cluster3184_1clades	84	DAC20_184	Bacteroides phage DAC20	GCA_013387725.1
QIG64198.1	003548	Cluster3184_1clades	84	DAC22_187	Bacteroides phage DAC22	GCA_013387735.1
QIG64454.1	003548	Cluster3184_1clades	84	DAC23_179	Bacteroides phage DAC23	GCA_013387745.1
AGB06878.1	003549	Cluster3185_1clades	83	CF80_gp091	Vibrio phage VH7D	GCA_000914495.1
QBX06268.1	003549	Cluster3185_1clades	83	ValB1HC_315	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60894.1	003549	Cluster3185_1clades	83	AVU32_gp053	Vibrio phage ValKK3	GCA_001501635.1
ALP47271.1	003549	Cluster3185_1clades	78	phiGrn1_0316	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54895.1	003549	Cluster3185_1clades	78	vBValMR10Z_355	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AIT14104.1	003550	SIG+TM	83	PBI_121Q_214	Escherichia phage 121Q	GCA_000926855.1
QAY00818.1	003550	SIG+TM	83	Ecwhy1_545	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61786.1	003550	SIG+TM	83	EO157G_1970	Escherichia phage SP27	GCA_008033345.1
QBO61595.1	003550	SIG+TM	83	G17_00099	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80098.1	003550	SIG+TM	83	PSLUR01_00121	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ANZ49839.1	003551	Cluster3187_1clades	83	MACHINA_201	Erwinia phage Machina	GCA_002758035.1
ANZ48495.1	003551	Cluster3187_1clades	76	CAITLIN_200	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48775.1	003551	Cluster3187_1clades	76	CHRISDB_213	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49283.1	003551	Cluster3187_1clades	83	HUXLEY_201	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50111.1	003551	Cluster3187_1clades	83	PARSHIK_202	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QIG63277.1	003552	Cluster3188_1clades	83	DAC16_44	Bacteroides phage DAC16	GCA_013387695.1
QIG63539.1	003552	Cluster3188_1clades	83	DAC19_48	Bacteroides phage DAC19	GCA_013387715.1
QIG63800.1	003552	Cluster3188_1clades	83	DAC20_47	Bacteroides phage DAC20	GCA_013387725.1
QIG64061.1	003552	Cluster3188_1clades	83	DAC22_47	Bacteroides phage DAC22	GCA_013387735.1
QIG64322.1	003552	Cluster3188_1clades	83	DAC23_44	Bacteroides phage DAC23	GCA_013387745.1
QIG63410.1	003553	Cluster3189_1clades	83	DAC16_180	Bacteroides phage DAC16	GCA_013387695.1
QIG63674.1	003553	Cluster3189_1clades	83	DAC19_186	Bacteroides phage DAC19	GCA_013387715.1
QIG63935.1	003553	Cluster3189_1clades	83	DAC20_185	Bacteroides phage DAC20	GCA_013387725.1
QIG64199.1	003553	Cluster3189_1clades	83	DAC22_188	Bacteroides phage DAC22	GCA_013387735.1
QIG64455.1	003553	Cluster3189_1clades	83	DAC23_180	Bacteroides phage DAC23	GCA_013387745.1
QIG65754.1	003554	Cluster3190_1clades	83	phiOC_p089	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47897.2	003554	Cluster3190_1clades	82	SmphiM12_265	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13097.1	003554	Cluster3190_1clades	82	PHIM19_192	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12737.1	003554	Cluster3190_1clades	82	PHIM7_192	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13467.1	003554	Cluster3190_1clades	82	PHIN3_204	Sinorhizobium phage phiN3	GCA_001501175.1
AUE22575.1	003555	Cluster3191_1clades	82	Ah1_00034	Aeromonas phage Ah1	GCA_002957415.1
QAX98611.1	003555	Cluster3191_1clades	82	ASfcp2_278	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52748.1	003555	Cluster3191_1clades	82	PX29p029	Aeromonas phage PX29	GCA_000920195.1
ADM80004.1	003555	Cluster3191_1clades	82	phiAS5_ORF0161	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17690.1	003555	Cluster3191_1clades	82	55.2	Aeromonas virus Aeh1	GCA_000843245.1
QMV28779.1	003556	Cluster3192_1clades	81	AP1_0072	Aeromonas phage AP1	GCA_014183365.1
ATI17382.1	003556	Cluster3192_1clades	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00211.1	003556	Cluster3192_1clades	82	HWB28_gp341	Aeromonas phage AS-zj	GCA_002627665.1
QAX97824.1	003556	Cluster3192_1clades	82	ASswx1_180	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39157.1	003556	Cluster3192_1clades	82	CC2_355	Aeromonas phage CC2	GCA_000903495.1
AFC21582.1	003557	Cluster3193_1clades	68	GAP32_132	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43698.1	003557	Cluster3193_1clades	68	CBB_133	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88652.1	003557	Cluster3193_1clades	82	BF_0127	Serratia phage BF	GCA_002619745.1
SOK58932.1	003557	Cluster3193_1clades	82	g124	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58397.1	003557	Cluster3193_1clades	82	g120	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD80051.1	003558	Cluster3194_1clades	82	JA11_246	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66650.1	003558	Cluster3194_1clades	82	JA13_247	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66974.1	003558	Cluster3194_1clades	82	JA29_248	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67621.1	003558	Cluster3194_1clades	82	JA33_247	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGS81902.1	003558	Cluster3194_1clades	74	PaBG_00018	Pseudomonas phage PaBG	GCA_000912555.1
QIG63386.1	003559	Cluster3195_1clades	82	DAC16_156	Bacteroides phage DAC16	GCA_013387695.1
QIG63649.1	003559	Cluster3195_1clades	81	DAC19_161	Bacteroides phage DAC19	GCA_013387715.1
QIG63910.1	003559	Cluster3195_1clades	81	DAC20_160	Bacteroides phage DAC20	GCA_013387725.1
QIG64174.1	003559	Cluster3195_1clades	81	DAC22_163	Bacteroides phage DAC22	GCA_013387735.1
QIG64430.1	003559	Cluster3195_1clades	81	DAC23_155	Bacteroides phage DAC23	GCA_013387745.1
QMV28856.1	003560	Cluster3196_1clades	81	AP1_0149	Aeromonas phage AP1	GCA_014183365.1
ATI17307.1	003560	Cluster3196_1clades	81	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00287.1	003560	Cluster3196_1clades	81	HWB28_gp265	Aeromonas phage AS-zj	GCA_002627665.1
QAX97750.1	003560	Cluster3196_1clades	81	ASswx1_105	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39162.1	003560	Cluster3196_1clades	81	CC2_004	Aeromonas phage CC2	GCA_000903495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFQ96795.1	003561	SIG+TM	81	G173_gp250	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96797.1	003561	SIG+TM	81	G173_gp252	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48096.1	003561	SIG+TM	81	ASESINO_83	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50508.1	003561	SIG+TM	81	STRATTON_83	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50510.1	003561	SIG+TM	81	STRATTON_85	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AGH07620.1	003562	Cluster3198_1clades	81	CYVG_00177	Cyanophage S-SSM6a	GCA_002710385.1
QGT54982.1	003562	Cluster3198_1clades	63	b23_0376	Synechococcus phage B23	GCA_009745195.1
QGT54617.1	003562	Cluster3198_1clades	63	b3_0382	Synechococcus phage B3	GCA_009745215.1
QCW23056.1	003562	Cluster3198_1clades	64	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50695.1	003562	Cluster3198_1clades	64	-	Synechococcus phage S-B43	GCA_006869725.1
AGH07593.1	003563	Cluster3199_1clades	66	CYVG_00149	Cyanophage S-SSM6a	GCA_002710385.1
AGH26236.1	003563	Cluster3199_1clades	81	CPMG_00135	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44544.1	003563	Cluster3199_1clades	58	PSSM2_166	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12427.1	003563	Cluster3199_1clades	58	PRTG_00277	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93572.1	003563	Cluster3199_1clades	48	AVU42_gp234	Prochlorococcus phage P-TIM68	GCA_001503075.1
AGH56808.1	003564	SIG+DUF2973	81	CPXG_00005	Cyanophage P-RSM6	GCA_000906155.1
AJK27636.1	003564	SIG+DUF2973	80	PTIM40_232	Cyanophage P-TIM40	GCA_001470935.1
AOO14406.1	003564	SIG+DUF2973	80	Sn110110_213	Cyanophage S-RIM14	GCA_002599065.1
AOO15055.1	003564	SIG+DUF2973	80	W1230910_210	Cyanophage S-RIM14	GCA_002599125.1
AGG54382.1	003564	SIG+DUF2973	77	CYWG_00098	Cyanophage S-SSM6b	GCA_002710425.1
AFC21806.1	003565	Cluster3201_1clades	80	GAP32_356	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43927.1	003565	Cluster3201_1clades	80	CBB_364	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88886.1	003565	Cluster3201_1clades	81	BF_0361	Serratia phage BF	GCA_002619745.1
SOK59173.1	003565	Cluster3201_1clades	81	g365	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58639.1	003565	Cluster3201_1clades	81	g362	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21862.1	003566	Cluster3202_1clades	66	GAP32_409	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43985.1	003566	Cluster3202_1clades	66	CBB_422	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88942.1	003566	Cluster3202_1clades	69	BF_0417	Serratia phage BF	GCA_002619745.1
SOK59231.1	003566	Cluster3202_1clades	81	g423	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58697.1	003566	Cluster3202_1clades	81	g420	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22593.1	003567	Cluster3203_1clades	72	Ah1_00052	Aeromonas phage Ah1	GCA_002957415.1
QAX98631.1	003567	Cluster3203_1clades	72	ASfcp2_298	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52771.1	003567	Cluster3203_1clades	72	PX29p052	Aeromonas phage PX29	GCA_000920195.1
ADM80026.1	003567	Cluster3203_1clades	71	phiAS5_ORF0183	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17716.1	003567	Cluster3203_1clades	80	Aeh1ORF056c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22598.1	003568	Cluster3204_1clades	80	Ah1_00057	Aeromonas phage Ah1	GCA_002957415.1
QAX98636.1	003568	Cluster3204_1clades	75	ASfcp2_303	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52776.1	003568	Cluster3204_1clades	75	PX29p057	Aeromonas phage PX29	GCA_000920195.1
ADM80032.1	003568	Cluster3204_1clades	78	phiAS5_ORF0189	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17721.1	003568	Cluster3204_1clades	80	Aeh1ORF061c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22696.1	003569	Cluster3205_1clades	80	Ah1_00155	Aeromonas phage Ah1	GCA_002957415.1
QAX98421.1	003569	Cluster3205_1clades	57	ASfcp2_77	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52876.1	003569	Cluster3205_1clades	58	PX29p157	Aeromonas phage PX29	GCA_000920195.1
ADM80138.1	003569	Cluster3205_1clades	80	phiAS5_ORF0295	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17824.1	003569	Cluster3205_1clades	80	Aeh1ORF158c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21567.1	003570	Cluster3206_1clades	78	GAP32_118A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43684.1	003570	Cluster3206_1clades	80	CBB_119	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88636.1	003570	Cluster3206_1clades	71	BF_0111	Serratia phage BF	GCA_002619745.1
SOK58915.1	003570	Cluster3206_1clades	72	g107	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58380.1	003570	Cluster3206_1clades	72	g103	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGH56924.1	003571	Cluster3207_1clades	70	CPXG_00121	Cyanophage P-RSM6	GCA_000906155.1
AJK27532.1	003571	Cluster3207_1clades	76	PTIM40_106	Cyanophage P-TIM40	GCA_001470935.1
AOO14292.1	003571	Cluster3207_1clades	80	Sn110110_098	Cyanophage S-RIM14	GCA_002599065.1
AOO14941.1	003571	Cluster3207_1clades	80	W1230910_095	Cyanophage S-RIM14	GCA_002599125.1
AGG54292.1	003571	Cluster3207_1clades	69	CYWG_00008	Cyanophage S-SSM6b	GCA_002710425.1
QMV28833.1	003572	Cluster3208_1clades	79	AP1_0126	Aeromonas phage AP1	GCA_014183365.1
ATI17267.1	003572	Cluster3208_1clades	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00325.1	003572	Cluster3208_1clades	79	HWB28_gp227	Aeromonas phage AS-zj	GCA_002627665.1
QAY01429.1	003572	Cluster3208_1clades	80	ASwh1_370	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39190.1	003572	Cluster3208_1clades	79	CC2_050	Aeromonas phage CC2	GCA_000903495.1
QIG63295.1	003573	Cluster3209_1clades	80	DAC16_62	Bacteroides phage DAC16	GCA_013387695.1
QIG63554.1	003573	Cluster3209_1clades	80	DAC19_63	Bacteroides phage DAC19	GCA_013387715.1
QIG63815.1	003573	Cluster3209_1clades	80	DAC20_62	Bacteroides phage DAC20	GCA_013387725.1
QIG64077.1	003573	Cluster3209_1clades	80	DAC22_63	Bacteroides phage DAC22	GCA_013387735.1
QIG64340.1	003573	Cluster3209_1clades	80	DAC23_62	Bacteroides phage DAC23	GCA_013387745.1
QIG63342.1	003574	SIG+TM	77	DAC16_109	Bacteroides phage DAC16	GCA_013387695.1
QIG63608.1	003574	SIG+TM	80	DAC19_117	Bacteroides phage DAC19	GCA_013387715.1
QIG63869.1	003574	SIG+TM	80	DAC20_116	Bacteroides phage DAC20	GCA_013387725.1
QIG64132.1	003574	SIG+TM	77	DAC22_118	Bacteroides phage DAC22	GCA_013387735.1
QIG64389.1	003574	SIG+TM	77	DAC23_111	Bacteroides phage DAC23	GCA_013387745.1
AAQ64336.1	003575	Cluster3211_1clades	79	KVP40.0267	Vibrio phage KVP40	GCA_000843785.1
QIW90651.1	003575	Cluster3211_1clades	79	GCAPEGMB_00304	Vibrio phage V07	GCA_012361095.1
QIW91148.1	003575	Cluster3211_1clades	79	COHAPHLL_00312	Vibrio phage V09	GCA_012361135.1
QHJ74446.1	003575	Cluster3211_1clades	79	VH12019_00119	Vibrio phage VH1_2019	GCA_009931825.1
AFN37496.1	003575	Cluster3211_1clades	79	pp2_263	Vibriophage phi-pp2	GCA_002630725.1
AIT14228.1	003576	Cluster3212_1clades	71	PBI_121Q_338	Escherichia phage 121Q	GCA_000926855.1
QAY00707.1	003576	Cluster3212_1clades	79	Ecwhy1_432	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61904.1	003576	Cluster3212_1clades	71	EO157G_3150	Escherichia phage SP27	GCA_008033345.1
AXC37000.1	003576	Cluster3212_1clades	73	-	Escherichia phage UB	GCA_003341455.1
QBO62077.1	003576	Cluster3212_1clades	71	G17_00588	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QIG63255.1	003577	Cluster3213_1clades	79	DAC16_22	Bacteroides phage DAC16	GCA_013387695.1
QIG63517.1	003577	Cluster3213_1clades	79	DAC19_26	Bacteroides phage DAC19	GCA_013387715.1
QIG63779.1	003577	Cluster3213_1clades	79	DAC20_26	Bacteroides phage DAC20	GCA_013387725.1
QIG64040.1	003577	Cluster3213_1clades	79	DAC22_26	Bacteroides phage DAC22	GCA_013387735.1
QIG64301.1	003577	Cluster3213_1clades	79	DAC23_23	Bacteroides phage DAC23	GCA_013387745.1
QIG63303.1	003578	TM+TM	79	DAC16_70	Bacteroides phage DAC16	GCA_013387695.1
QIG63562.1	003578	TM+TM	79	DAC19_71	Bacteroides phage DAC19	GCA_013387715.1
QIG63823.1	003578	TM+TM	79	DAC20_70	Bacteroides phage DAC20	GCA_013387725.1
QIG64085.1	003578	TM+TM	79	DAC22_71	Bacteroides phage DAC22	GCA_013387735.1
QIG64348.1	003578	TM+TM	79	DAC23_70	Bacteroides phage DAC23	GCA_013387745.1
QIG63363.1	003579	Cluster3215_1clades	79	DAC16_130	Bacteroides phage DAC16	GCA_013387695.1
QIG63628.1	003579	Cluster3215_1clades	79	DAC19_137	Bacteroides phage DAC19	GCA_013387715.1
QIG63889.1	003579	Cluster3215_1clades	79	DAC20_136	Bacteroides phage DAC20	GCA_013387725.1
QIG64152.1	003579	Cluster3215_1clades	79	DAC22_138	Bacteroides phage DAC22	GCA_013387735.1
QIG64409.1	003579	Cluster3215_1clades	79	DAC23_131	Bacteroides phage DAC23	GCA_013387745.1
QIG63323.1	003580	Cluster3216_1clades	75	DAC16_90	Bacteroides phage DAC16	GCA_013387695.1
QIG63585.1	003580	Cluster3216_1clades	79	DAC19_94	Bacteroides phage DAC19	GCA_013387715.1
QIG63846.1	003580	Cluster3216_1clades	79	DAC20_93	Bacteroides phage DAC20	GCA_013387725.1
QIG64108.1	003580	Cluster3216_1clades	79	DAC22_94	Bacteroides phage DAC22	GCA_013387735.1
QIG64367.1	003580	Cluster3216_1clades	75	DAC23_89	Bacteroides phage DAC23	GCA_013387745.1
AUE22834.1	003581	Cluster3217_1clades	41	Ah1_00316	Aeromonas phage Ah1	GCA_002957415.1
QAX98548.1	003581	Cluster3217_1clades	76	ASfcp2_213	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53012.1	003581	Cluster3217_1clades	76	PX29p293	Aeromonas phage PX29	GCA_000920195.1
ADM79935.1	003581	Cluster3217_1clades	75	phiAS5_ORF0092	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17963.1	003581	Cluster3217_1clades	78	Aeh1ORF294c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64332.1	003582	Cluster3218_1clades	78	KVP40.0263	Vibrio phage KVP40	GCA_000843785.1
QIW90647.1	003582	Cluster3218_1clades	78	GCAPEGMB_00300	Vibrio phage V07	GCA_012361095.1
QIW91152.1	003582	Cluster3218_1clades	78	COHAPHLL_00316	Vibrio phage V09	GCA_012361135.1
QHJ74442.1	003582	Cluster3218_1clades	78	VH12019_00115	Vibrio phage VH1_2019	GCA_009931825.1
AFN37491.1	003582	Cluster3218_1clades	78	pp2_258	Vibriophage phi-pp2	GCA_002630725.1
QMV29116.1	003583	Cluster3219_1clades	61	AP1_0413	Aeromonas phage AP1	GCA_014183365.1
ATI17249.1	003583	Cluster3219_1clades	78	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00339.1	003583	Cluster3219_1clades	64	HWB28_gp213	Aeromonas phage AS-zj	GCA_002627665.1
QAX97692.1	003583	Cluster3219_1clades	78	ASswx1_46	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39202.1	003583	Cluster3219_1clades	78	CC2_066	Aeromonas phage CC2	GCA_000903495.1
AUE22627.1	003584	Cluster3220_1clades	78	Ah1_00086	Aeromonas phage Ah1	GCA_002957415.1
QAX98354.1	003584	Cluster3220_1clades	77	ASfcp2_8	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52810.1	003584	Cluster3220_1clades	77	PX29p091	Aeromonas phage PX29	GCA_000920195.1
ADM80067.1	003584	Cluster3220_1clades	77	phiAS5_ORF0224	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17754.1	003584	Cluster3220_1clades	77	Aeh1ORF093c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63250.1	003585	Cluster3221_1clades	78	DAC16_17	Bacteroides phage DAC16	GCA_013387695.1
QIG63512.1	003585	Cluster3221_1clades	78	DAC19_21	Bacteroides phage DAC19	GCA_013387715.1
QIG63774.1	003585	Cluster3221_1clades	78	DAC20_21	Bacteroides phage DAC20	GCA_013387725.1
QIG64035.1	003585	Cluster3221_1clades	78	DAC22_21	Bacteroides phage DAC22	GCA_013387735.1
QIG64296.1	003585	Cluster3221_1clades	78	DAC23_18	Bacteroides phage DAC23	GCA_013387745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63292.1	003586	Cluster3222_1clades	78	DAC16_59	Bacteroides phage DAC16	GCA_013387695.1
QIG63551.1	003586	Cluster3222_1clades	78	DAC19_60	Bacteroides phage DAC19	GCA_013387715.1
QIG63812.1	003586	Cluster3222_1clades	78	DAC20_59	Bacteroides phage DAC20	GCA_013387725.1
QIG64074.1	003586	Cluster3222_1clades	78	DAC22_60	Bacteroides phage DAC22	GCA_013387735.1
QIG64337.1	003586	Cluster3222_1clades	78	DAC23_59	Bacteroides phage DAC23	GCA_013387745.1
AXG67137.1	003587	Cluster3223_1clades	73	AD1_093	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08372.1	003587	Cluster3223_1clades	73	Alexandra_97	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58735.1	003587	Cluster3223_1clades	73	Y3_095	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28569.1	003587	Cluster3223_1clades	73	YOLOSWAG_86	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38288.1	003587	Cluster3223_1clades	78	BN7874_119	Phage NCTB	GCA_900092385.1
AUE22657.1	003588	Cluster3224_1clades	77	Ah1_00116	Aeromonas phage Ah1	GCA_002957415.1
QAX98384.1	003588	Cluster3224_1clades	77	ASfcp2_38	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52837.1	003588	Cluster3224_1clades	77	PX29p118	Aeromonas phage PX29	GCA_000920195.1
ADM80097.1	003588	Cluster3224_1clades	76	phiAS5_ORF0254	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17784.1	003588	Cluster3224_1clades	77	Aeh1ORF121c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22699.1	003589	Cluster3225_1clades	77	Ah1_00158	Aeromonas phage Ah1	GCA_002957415.1
QAX98423.1	003589	Cluster3225_1clades	76	ASfcp2_79	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52878.1	003589	Cluster3225_1clades	76	PX29p159	Aeromonas phage PX29	GCA_000920195.1
ADM80141.1	003589	Cluster3225_1clades	77	phiAS5_ORF0298	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17828.1	003589	Cluster3225_1clades	77	Aeh1ORF162c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64237.1	003590	Cluster3226_1clades	77	KVP40.0168	Vibrio phage KVP40	GCA_000843785.1
QIW90551.1	003590	Cluster3226_1clades	77	GCAPEGMB_00204	Vibrio phage V07	GCA_012361095.1
QIW90871.1	003590	Cluster3226_1clades	77	COHAPHLL_00008	Vibrio phage V09	GCA_012361135.1
QHJ74349.1	003590	Cluster3226_1clades	64	VH12019_00022	Vibrio phage VH1_2019	GCA_009931825.1
AFN37396.1	003590	Cluster3226_1clades	77	pp2_163	Vibriophage phi-pp2	GCA_002630725.1
AUE22830.1	003591	Cluster3227_1clades	76	Ah1_00312	Aeromonas phage Ah1	GCA_002957415.1
QAX98544.1	003591	Cluster3227_1clades	77	ASfcp2_209	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53008.1	003591	Cluster3227_1clades	77	PX29p289	Aeromonas phage PX29	GCA_000920195.1
ADM79932.1	003591	Cluster3227_1clades	76	phiAS5_ORF0089	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17959.1	003591	Cluster3227_1clades	76	Aeh1ORF290c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21875.1	003592	Cluster3228_1clades	77	GAP32_422	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44003.1	003592	Cluster3228_1clades	77	CBB_440	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88962.1	003592	Cluster3228_1clades	68	BF_0437	Serratia phage BF	GCA_002619745.1
SOK59249.1	003592	Cluster3228_1clades	68	g441	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58714.1	003592	Cluster3228_1clades	68	g437	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QMV28868.1	003593	Cluster3229_1clades	77	AP1_0161	Aeromonas phage AP1	GCA_014183365.1
ATI17296.1	003593	Cluster3229_1clades	77	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00300.1	003593	Cluster3229_1clades	77	HWB28_gp252	Aeromonas phage AS-zj	GCA_002627665.1
QAX97737.1	003593	Cluster3229_1clades	77	ASswx1_92	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39170.1	003593	Cluster3229_1clades	77	CC2_019	Aeromonas phage CC2	GCA_000903495.1
AMM43993.1	003594	Cluster3230_1clades	67	CBB_430	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QCW19116.1	003594	Cluster3230_1clades	77	7t3_0599	Salmonella phage 7t3	GCA_006083215.1
AZU98353.1	003594	Cluster3230_1clades	65	CPT_Munch_412	Salmonella phage Munch	GCA_004015485.1
QIG62629.1	003594	Cluster3230_1clades	65	SEPL_016	Salmonella phage SE_PL	GCA_011067555.1
AQW88952.1	003594	Cluster3230_1clades	62	BF_0427	Serratia phage BF	GCA_002619745.1
QIG63302.1	003595	Cluster3231_1clades	77	DAC16_69	Bacteroides phage DAC16	GCA_013387695.1
QIG63561.1	003595	Cluster3231_1clades	47	DAC19_70	Bacteroides phage DAC19	GCA_013387715.1
QIG63822.1	003595	Cluster3231_1clades	47	DAC20_69	Bacteroides phage DAC20	GCA_013387725.1
QIG64084.1	003595	Cluster3231_1clades	76	DAC22_70	Bacteroides phage DAC22	GCA_013387735.1
QIG64347.1	003595	Cluster3231_1clades	76	DAC23_69	Bacteroides phage DAC23	GCA_013387745.1
QIG63320.1	003596	Cluster3232_1clades	77	DAC16_87	Bacteroides phage DAC16	GCA_013387695.1
QIG63581.1	003596	Cluster3232_1clades	77	DAC19_90	Bacteroides phage DAC19	GCA_013387715.1
QIG63842.1	003596	Cluster3232_1clades	77	DAC20_89	Bacteroides phage DAC20	GCA_013387725.1
QIG64104.1	003596	Cluster3232_1clades	77	DAC22_90	Bacteroides phage DAC22	GCA_013387735.1
QIG64364.1	003596	Cluster3232_1clades	77	DAC23_86	Bacteroides phage DAC23	GCA_013387745.1
AUE22871.1	003597	Cluster3233_1clades	71	Ah1_00353	Aeromonas phage Ah1	GCA_002957415.1
QAX98581.1	003597	Cluster3233_1clades	70	ASfcp2_247	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53046.1	003597	Cluster3233_1clades	76	PX29p329	Aeromonas phage PX29	GCA_000920195.1
ADM79969.1	003597	Cluster3233_1clades	73	phiAS5_ORF0126	Aeromonas phage phiAS5	GCA_000887715.1
AAQ18000.1	003597	Cluster3233_1clades	71	Aeh1ORF329c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21530.1	003598	Cluster3234_1clades	74	GAP32_082	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43650.1	003598	Cluster3234_1clades	74	CBB_85	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88599.1	003598	Cluster3234_1clades	76	BF_0074	Serratia phage BF	GCA_002619745.1
SOK58876.1	003598	Cluster3234_1clades	75	g068	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58339.1	003598	Cluster3234_1clades	75	g062	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBX06415.1	003599	Cluster3235_1clades	76	BcepSaruman_002	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74382.1	003599	Cluster3235_1clades	76	BcepSauron_002	Burkholderia phage BcepSauron	GCA_005394215.1
QCW18632.1	003599	Cluster3235_1clades	75	7t3_0111	Salmonella phage 7t3	GCA_006083215.1
AZU98457.1	003599	Cluster3235_1clades	75	CPT_Munch_525	Salmonella phage Munch	GCA_004015485.1
QIG63057.1	003599	Cluster3235_1clades	75	SEPL_444	Salmonella phage SE_PL	GCA_011067555.1
QIG63298.1	003600	Cluster3236_1clades	76	DAC16_65	Bacteroides phage DAC16	GCA_013387695.1
QIG63557.1	003600	Cluster3236_1clades	76	DAC19_66	Bacteroides phage DAC19	GCA_013387715.1
QIG63818.1	003600	Cluster3236_1clades	76	DAC20_65	Bacteroides phage DAC20	GCA_013387725.1
QIG64080.1	003600	Cluster3236_1clades	76	DAC22_66	Bacteroides phage DAC22	GCA_013387735.1
QIG64343.1	003600	Cluster3236_1clades	76	DAC23_65	Bacteroides phage DAC23	GCA_013387745.1
QIG63462.1	003601	Cluster3237_1clades	76	DAC16_233	Bacteroides phage DAC16	GCA_013387695.1
QIG63725.1	003601	Cluster3237_1clades	76	DAC19_238	Bacteroides phage DAC19	GCA_013387715.1
QIG63986.1	003601	Cluster3237_1clades	76	DAC20_237	Bacteroides phage DAC20	GCA_013387725.1
QIG64250.1	003601	Cluster3237_1clades	76	DAC22_240	Bacteroides phage DAC22	GCA_013387735.1
QIG64506.1	003601	Cluster3237_1clades	76	DAC23_232	Bacteroides phage DAC23	GCA_013387745.1
AUE22679.1	003602	Cluster3238_1clades	75	Ah1_00138	Aeromonas phage Ah1	GCA_002957415.1
QAX98405.1	003602	Cluster3238_1clades	75	ASfcp2_61	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52861.1	003602	Cluster3238_1clades	75	PX29p142	Aeromonas phage PX29	GCA_000920195.1
ADM80120.1	003602	Cluster3238_1clades	75	phiAS5_ORF0277	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17807.1	003602	Cluster3238_1clades	75	Aeh1ORF142c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22772.1	003603	SIG+TM	75	Ah1_00254	Aeromonas phage Ah1	GCA_002957415.1
QAX98488.1	003603	SIG+TM	58	ASfcp2_150	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52950.1	003603	SIG+TM	75	PX29p231	Aeromonas phage PX29	GCA_000920195.1
ADM79874.1	003603	SIG+TM	62	phiAS5_ORF0031	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17896.1	003603	SIG+TM	75	Aeh1gORF274c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22687.1	003604	Cluster3240_1clades	68	Ah1_00146	Aeromonas phage Ah1	GCA_002957415.1
QAX98412.1	003604	Cluster3240_1clades	67	ASfcp2_68	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52867.1	003604	Cluster3240_1clades	66	PX29p148	Aeromonas phage PX29	GCA_000920195.1
ADM80129.1	003604	Cluster3240_1clades	75	phiAS5_ORF0286	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17814.1	003604	Cluster3240_1clades	68	Aeh1ORF149c	Aeromonas virus Aeh1	GCA_000843245.1
APU01686.1	003605	Cluster3241_1clades	75	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28824.1	003605	Cluster3241_1clades	74	AP1_0117	Aeromonas phage AP1	GCA_014183365.1
QAX98043.1	003605	Cluster3241_1clades	74	ASswx1_403	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39355.1	003605	Cluster3241_1clades	75	CC2_127	Aeromonas phage CC2	GCA_000903495.1
ADQ53322.1	003605	Cluster3241_1clades	75	65p314	Aeromonas virus 65	GCA_000893255.1
QAY00724.1	003606	Cluster3242_1clades	72	Ecwhy1_449	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61887.1	003606	Cluster3242_1clades	72	EO157G_2980	Escherichia phage SP27	GCA_008033345.1
QBO62097.1	003606	Cluster3242_1clades	75	G17_00608	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14107.1	003606	Cluster3242_1clades	72	vBEcoMphAPEC6_gp484c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80197.1	003606	Cluster3242_1clades	75	PSLUR01_00220	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG63371.1	003607	Cluster3243_1clades	75	DAC16_138	Bacteroides phage DAC16	GCA_013387695.1
QIG63636.1	003607	Cluster3243_1clades	75	DAC19_145	Bacteroides phage DAC19	GCA_013387715.1
QIG63897.1	003607	Cluster3243_1clades	75	DAC20_144	Bacteroides phage DAC20	GCA_013387725.1
QIG64160.1	003607	Cluster3243_1clades	75	DAC22_146	Bacteroides phage DAC22	GCA_013387735.1
QIG64417.1	003607	Cluster3243_1clades	75	DAC23_139	Bacteroides phage DAC23	GCA_013387745.1
QIG63387.1	003608	GerA	75	DAC16_157	Bacteroides phage DAC16	GCA_013387695.1
QIG63650.1	003608	GerA	75	DAC19_162	Bacteroides phage DAC19	GCA_013387715.1
QIG63911.1	003608	GerA	75	DAC20_161	Bacteroides phage DAC20	GCA_013387725.1
QIG64175.1	003608	GerA	75	DAC22_164	Bacteroides phage DAC22	GCA_013387735.1
QIG64431.1	003608	GerA	75	DAC23_156	Bacteroides phage DAC23	GCA_013387745.1
QIG65795.1	003609	Cluster3245_1clades	75	phiOC_p130	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGR47943.1	003609	Cluster3245_1clades	74	SmphiM12_311	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13138.1	003609	Cluster3245_1clades	74	PHIM19_233	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12777.1	003609	Cluster3245_1clades	74	PHIM7_232	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13506.1	003609	Cluster3245_1clades	74	PHIN3_243	Sinorhizobium phage phiN3	GCA_001501175.1
AUE22709.1	003610	Cluster3246_1clades	74	Ah1_00189	Aeromonas phage Ah1	GCA_002957415.1
QAX98436.1	003610	Cluster3246_1clades	74	ASfcp2_92	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52890.1	003610	Cluster3246_1clades	74	PX29p171	Aeromonas phage PX29	GCA_000920195.1
ADM80157.1	003610	Cluster3246_1clades	73	phiAS5_ORF0314	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17843.1	003610	Cluster3246_1clades	74	Aeh1ORF177c	Aeromonas virus Aeh1	GCA_000843245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIT14381.1	003611	Cluster3247_1clades	74	PBI_121Q_491	Escherichia phage 121Q	GCA_000926855.1
QAY00567.1	003611	Cluster3247_1clades	73	Ecwhy1_288	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM62052.1	003611	Cluster3247_1clades	73	EO157G_4630	Escherichia phage SP27	GCA_008033345.1
QBO61921.1	003611	Cluster3247_1clades	74	G17_00432	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80370.1	003611	Cluster3247_1clades	73	PSLUR01_00393	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG63253.1	003612	Aldedh	74	DAC16_20	Bacteroides phage DAC16	GCA_013387695.1
QIG63515.1	003612	Aldedh	74	DAC19_24	Bacteroides phage DAC19	GCA_013387715.1
QIG63777.1	003612	Aldedh	74	DAC20_24	Bacteroides phage DAC20	GCA_013387725.1
QIG64038.1	003612	Aldedh	74	DAC22_24	Bacteroides phage DAC22	GCA_013387735.1
QIG64299.1	003612	Aldedh	74	DAC23_21	Bacteroides phage DAC23	GCA_013387745.1
QIG63324.1	003613	Cluster3249_1clades	74	DAC16_91	Bacteroides phage DAC16	GCA_013387695.1
QIG63586.1	003613	Cluster3249_1clades	74	DAC19_95	Bacteroides phage DAC19	GCA_013387715.1
QIG63847.1	003613	Cluster3249_1clades	74	DAC20_94	Bacteroides phage DAC20	GCA_013387725.1
QIG64109.1	003613	Cluster3249_1clades	74	DAC22_95	Bacteroides phage DAC22	GCA_013387735.1
QIG64368.1	003613	Cluster3249_1clades	74	DAC23_90	Bacteroides phage DAC23	GCA_013387745.1
QIG63349.1	003614	Cluster3250_1clades	74	DAC16_116	Bacteroides phage DAC16	GCA_013387695.1
QIG63615.1	003614	Cluster3250_1clades	74	DAC19_124	Bacteroides phage DAC19	GCA_013387715.1
QIG63876.1	003614	Cluster3250_1clades	74	DAC20_123	Bacteroides phage DAC20	GCA_013387725.1
QIG64139.1	003614	Cluster3250_1clades	74	DAC22_125	Bacteroides phage DAC22	GCA_013387735.1
QIG64396.1	003614	Cluster3250_1clades	74	DAC23_118	Bacteroides phage DAC23	GCA_013387745.1
QMV28904.1	003615	Cluster3251_1clades	73	AP1_0197	Aeromonas phage AP1	GCA_014183365.1
ATI17591.1	003615	Cluster3251_1clades	73	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00406.1	003615	Cluster3251_1clades	73	HWB28_gp146	Aeromonas phage AS-zj	GCA_002627665.1
QAX98030.1	003615	Cluster3251_1clades	73	ASswx1_390	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39232.1	003615	Cluster3251_1clades	73	CC2_141	Aeromonas phage CC2	GCA_000903495.1
QMV29104.1	003616	Cluster3252_1clades	73	AP1_0397	Aeromonas phage AP1	GCA_014183365.1
ATI17433.1	003616	Cluster3252_1clades	73	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00162.1	003616	Cluster3252_1clades	73	HWB28_gp390	Aeromonas phage AS-zj	GCA_002627665.1
QAX97873.1	003616	Cluster3252_1clades	73	ASswx1_230	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39274.1	003616	Cluster3252_1clades	73	CC2_304	Aeromonas phage CC2	GCA_000903495.1
QIG63268.1	003617	Cluster3253_1clades	73	DAC16_35	Bacteroides phage DAC16	GCA_013387695.1
QIG63530.1	003617	Cluster3253_1clades	73	DAC19_39	Bacteroides phage DAC19	GCA_013387715.1
QIG63792.1	003617	Cluster3253_1clades	73	DAC20_39	Bacteroides phage DAC20	GCA_013387725.1
QIG64053.1	003617	Cluster3253_1clades	73	DAC22_39	Bacteroides phage DAC22	GCA_013387735.1
QIG64313.1	003617	Cluster3253_1clades	73	DAC23_35	Bacteroides phage DAC23	GCA_013387745.1
QIG63287.1	003618	Cluster3254_1clades	73	DAC16_54	Bacteroides phage DAC16	GCA_013387695.1
QIG63546.1	003618	Cluster3254_1clades	73	DAC19_55	Bacteroides phage DAC19	GCA_013387715.1
QIG63807.1	003618	Cluster3254_1clades	73	DAC20_54	Bacteroides phage DAC20	GCA_013387725.1
QIG64069.1	003618	Cluster3254_1clades	73	DAC22_55	Bacteroides phage DAC22	GCA_013387735.1
QIG64332.1	003618	Cluster3254_1clades	73	DAC23_54	Bacteroides phage DAC23	GCA_013387745.1
AAQ64324.1	003619	Cluster3255_1clades	72	KVP40.0255	Vibrio phage KVP40	GCA_000843785.1
QIW90639.1	003619	Cluster3255_1clades	72	GCAPEGMB_00292	Vibrio phage V07	GCA_012361095.1
QIW91160.1	003619	Cluster3255_1clades	72	COHAPHLL_00324	Vibrio phage V09	GCA_012361135.1
QHJ74434.1	003619	Cluster3255_1clades	72	VH12019_00107	Vibrio phage VH1_2019	GCA_009931825.1
AFN37483.1	003619	Cluster3255_1clades	72	pp2_250	Vibriophage phi-pp2	GCA_002630725.1
QMV28972.1	003620	Cluster3256_1clades	72	AP1_0265	Aeromonas phage AP1	GCA_014183365.1
ATI17322.1	003620	Cluster3256_1clades	72	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00272.1	003620	Cluster3256_1clades	72	HWB28_gp280	Aeromonas phage AS-zj	GCA_002627665.1
QAX97765.1	003620	Cluster3256_1clades	72	ASswx1_120	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39294.1	003620	Cluster3256_1clades	72	CC2_417	Aeromonas phage CC2	GCA_000903495.1
AIT14269.1	003621	Cluster3257_1clades	72	PBI_121Q_379	Escherichia phage 121Q	GCA_000926855.1
QAY00668.1	003621	Cluster3257_1clades	60	Ecwhy1_393	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61944.1	003621	Cluster3257_1clades	72	EO157G_3550	Escherichia phage SP27	GCA_008033345.1
QBO62035.1	003621	Cluster3257_1clades	72	G17_00546	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14056.1	003621	Cluster3257_1clades	72	vBEcoMphAPEC6_gp433c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AFC21921.1	003622	Cluster3258_1clades	70	GAP32_463	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44047.1	003622	Cluster3258_1clades	67	CBB_484	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89001.1	003622	Cluster3258_1clades	72	BF_0476	Serratia phage BF	GCA_002619745.1
SOK59284.1	003622	Cluster3258_1clades	71	g476	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58749.1	003622	Cluster3258_1clades	71	g472	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AAQ64171.1	003623	Cluster3259_1clades	71	KVP40.0100	Vibrio phage KVP40	GCA_000843785.1
QIW90494.1	003623	Cluster3259_1clades	71	GCAPEGMB_00147	Vibrio phage V07	GCA_012361095.1
QIW90935.1	003623	Cluster3259_1clades	71	COHAPHLL_00072	Vibrio phage V09	GCA_012361135.1
QHJ74282.1	003623	Cluster3259_1clades	71	VH12019_00363	Vibrio phage VH1_2019	GCA_009931825.1
AFN37330.1	003623	Cluster3259_1clades	71	pp2_097	Vibriophage phi-pp2	GCA_002630725.1
AJK27510.1	003624	Cluster3260_1clades	45	PTIM40_83	Cyanophage P-TIM40	GCA_001470935.1
AGG54314.1	003624	Cluster3260_1clades	46	CYWG_00030	Cyanophage S-SSM6b	GCA_002710425.1
AAX44461.1	003624	Cluster3260_1clades	71	PSSM2_083	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12192.1	003624	Cluster3260_1clades	71	PRTG_00034	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93604.1	003624	Cluster3260_1clades	51	AVU42_gp059	Prochlorococcus phage P-TIM68	GCA_001503075.1
AUE22549.1	003625	Cluster3261_1clades	67	Ah1_00008	Aeromonas phage Ah1	GCA_002957415.1
QAX98589.1	003625	Cluster3261_1clades	67	ASfcp2_256	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52725.1	003625	Cluster3261_1clades	67	PX29p006	Aeromonas phage PX29	GCA_000920195.1
ADM79977.1	003625	Cluster3261_1clades	71	phiAS5_ORF0134	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17662.1	003625	Cluster3261_1clades	67	Aeh1ORF007c	Aeromonas virus Aeh1	GCA_000843245.1
AMO43327.1	003626	Cluster3262_1clades	66	W270710_083	Cyanophage S-RIM44	GCA_002599145.1
AOO11799.1	003626	Cluster3262_1clades	66	Np050604_083	Cyanophage S-RIM44	GCA_002599185.1
AOO12500.1	003626	Cluster3262_1clades	66	Sn080709_083	Cyanophage S-RIM44	GCA_002599245.1
AOO12966.1	003626	Cluster3262_1clades	66	W2100709_084	Cyanophage S-RIM44	GCA_002599285.1
ADO99183.1	003626	Cluster3262_1clades	71	Syn1_082	Prochlorococcus phage Syn1	GCA_000892495.1
QMV28903.1	003627	Cluster3263_1clades	70	AP1_0196	Aeromonas phage AP1	GCA_014183365.1
ATI17592.1	003627	Cluster3263_1clades	71	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00405.1	003627	Cluster3263_1clades	71	HWB28_gp147	Aeromonas phage AS-zj	GCA_002627665.1
QAX98031.1	003627	Cluster3263_1clades	71	ASswx1_391	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39231.1	003627	Cluster3263_1clades	65	CC2_140	Aeromonas phage CC2	GCA_000903495.1
AFC21574.1	003628	SIG+TM	68	GAP32_124A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43691.1	003628	SIG+TM	68	CBB_126	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88644.1	003628	SIG+TM	70	BF_0119	Serratia phage BF	GCA_002619745.1
SOK58924.1	003628	SIG+TM	71	g116	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58389.1	003628	SIG+TM	71	g112	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63254.1	003629	Cluster3266_1clades	70	DAC16_21	Bacteroides phage DAC16	GCA_013387695.1
QIG63516.1	003629	Cluster3266_1clades	70	DAC19_25	Bacteroides phage DAC19	GCA_013387715.1
QIG63778.1	003629	Cluster3266_1clades	70	DAC20_25	Bacteroides phage DAC20	GCA_013387725.1
QIG64039.1	003629	Cluster3266_1clades	70	DAC22_25	Bacteroides phage DAC22	GCA_013387735.1
QIG64300.1	003629	Cluster3266_1clades	70	DAC23_22	Bacteroides phage DAC23	GCA_013387745.1
QIG63296.1	003630	Cluster3267_1clades	70	DAC16_63	Bacteroides phage DAC16	GCA_013387695.1
QIG63555.1	003630	Cluster3267_1clades	70	DAC19_64	Bacteroides phage DAC19	GCA_013387715.1
QIG63816.1	003630	Cluster3267_1clades	70	DAC20_63	Bacteroides phage DAC20	GCA_013387725.1
QIG64078.1	003630	Cluster3267_1clades	70	DAC22_64	Bacteroides phage DAC22	GCA_013387735.1
QIG64341.1	003630	Cluster3267_1clades	70	DAC23_63	Bacteroides phage DAC23	GCA_013387745.1
QIG63367.1	003631	Cluster3268_1clades	70	DAC16_134	Bacteroides phage DAC16	GCA_013387695.1
QIG63632.1	003631	Cluster3268_1clades	70	DAC19_141	Bacteroides phage DAC19	GCA_013387715.1
QIG63893.1	003631	Cluster3268_1clades	70	DAC20_140	Bacteroides phage DAC20	GCA_013387725.1
QIG64156.1	003631	Cluster3268_1clades	70	DAC22_142	Bacteroides phage DAC22	GCA_013387735.1
QIG64413.1	003631	Cluster3268_1clades	70	DAC23_135	Bacteroides phage DAC23	GCA_013387745.1
AFC21800.1	003632	Cluster3269_1clades	64	GAP32_350	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43921.1	003632	Cluster3269_1clades	64	CBB_358	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88881.1	003632	Cluster3269_1clades	67	BF_0356	Serratia phage BF	GCA_002619745.1
SOK59167.1	003632	Cluster3269_1clades	70	g359	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58635.1	003632	Cluster3269_1clades	69	g358	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21533.1	003633	Cluster3270_1clades	69	GAP32_085	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43653.1	003633	Cluster3270_1clades	69	CBB_88	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88602.1	003633	Cluster3270_1clades	65	BF_0077	Serratia phage BF	GCA_002619745.1
SOK58879.1	003633	Cluster3270_1clades	60	g071	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58342.1	003633	Cluster3270_1clades	60	g065	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63334.1	003634	Cluster3271_1clades	66	DAC16_101	Bacteroides phage DAC16	GCA_013387695.1
QIG63600.1	003634	Cluster3271_1clades	69	DAC19_109	Bacteroides phage DAC19	GCA_013387715.1
QIG63861.1	003634	Cluster3271_1clades	66	DAC20_108	Bacteroides phage DAC20	GCA_013387725.1
QIG64125.1	003634	Cluster3271_1clades	66	DAC22_111	Bacteroides phage DAC22	GCA_013387735.1
QIG64381.1	003634	Cluster3271_1clades	66	DAC23_103	Bacteroides phage DAC23	GCA_013387745.1
AUE22695.1	003635	Cluster3272_1clades	67	Ah1_00154	Aeromonas phage Ah1	GCA_002957415.1
QAX98420.1	003635	Cluster3272_1clades	68	ASfcp2_76	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52875.1	003635	Cluster3272_1clades	68	PX29p156	Aeromonas phage PX29	GCA_000920195.1
ADM80137.1	003635	Cluster3272_1clades	67	phiAS5_ORF0294	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17823.1	003635	Cluster3272_1clades	67	Aeh1gORF190c	Aeromonas virus Aeh1	GCA_000843245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63475.1	003636	Cluster3273_1clades	68	DAC16_246	Bacteroides phage DAC16	GCA_013387695.1
QIG63738.1	003636	Cluster3273_1clades	68	DAC19_251	Bacteroides phage DAC19	GCA_013387715.1
QIG63999.1	003636	Cluster3273_1clades	68	DAC20_250	Bacteroides phage DAC20	GCA_013387725.1
QIG64263.1	003636	Cluster3273_1clades	68	DAC22_253	Bacteroides phage DAC22	GCA_013387735.1
QIG64519.1	003636	Cluster3273_1clades	68	DAC23_245	Bacteroides phage DAC23	GCA_013387745.1
AIR93588.1	003637	RPN13	67	AVU42_gp037	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76103.1	003637	RPN13	64	PBI_BELLAMY_58	Synechococcus phage Bellamy	GCA_002627525.1
QCW22996.1	003637	RPN13	64	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50647.1	003637	RPN13	64	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70051.1	003637	RPN13	68	SynMITS9220M01_038	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFC21795.1	003638	TCAD12	67	GAP32_345	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43915.1	003638	TCAD12	67	CBB_352	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88876.1	003638	TCAD12	66	BF_0351	Serratia phage BF	GCA_002619745.1
SOK59161.1	003638	TCAD12	66	g353	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58629.1	003638	TCAD12	66	g352	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14238.1	003639	Cluster3276_1clades	63	PBI_121Q_348	Escherichia phage 121Q	GCA_000926855.1
QAY00694.1	003639	Cluster3276_1clades	60	Ecwhy1_419	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61916.1	003639	Cluster3276_1clades	67	EO157G_3270	Escherichia phage SP27	GCA_008033345.1
QBO62066.1	003639	Cluster3276_1clades	67	G17_00577	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80227.1	003639	Cluster3276_1clades	67	PSLUR01_00250	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUE22707.1	003640	Cluster3277_2clades	66	Ah1_00181	Aeromonas phage Ah1	GCA_002957415.1
QAX98434.1	003640	Cluster3277_2clades	66	ASfcp2_90	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52888.1	003640	Cluster3277_2clades	66	PX29p169	Aeromonas phage PX29	GCA_000920195.1
ADM80153.1	003640	Cluster3277_2clades	66	phiAS5_ORF0310	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17841.1	003640	Cluster3277_2clades	66	Aeh1ORF175c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21783.1	003641	Cluster3278_1clades	66	GAP32_333	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43901.1	003641	Cluster3278_1clades	66	CBB_338	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88861.1	003641	Cluster3278_1clades	66	BF_0336	Serratia phage BF	GCA_002619745.1
SOK59145.1	003641	Cluster3278_1clades	66	g337	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58611.1	003641	Cluster3278_1clades	66	g334	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD79992.1	003642	Cluster3279_1clades	66	JA11_187	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66590.1	003642	Cluster3279_1clades	66	JA13_187	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66915.1	003642	Cluster3279_1clades	66	JA29_189	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67561.1	003642	Cluster3279_1clades	66	JA33_187	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AQT28675.1	003642	Cluster3279_1clades	66	YOLOSWAG_196	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QIG63236.1	003643	Cluster3280_1clades	66	DAC16_3	Bacteroides phage DAC16	GCA_013387695.1
QIG63494.1	003643	Cluster3280_1clades	66	DAC19_3	Bacteroides phage DAC19	GCA_013387715.1
QIG63756.1	003643	Cluster3280_1clades	66	DAC20_3	Bacteroides phage DAC20	GCA_013387725.1
QIG64017.1	003643	Cluster3280_1clades	66	DAC22_3	Bacteroides phage DAC22	GCA_013387735.1
QIG64281.1	003643	Cluster3280_1clades	66	DAC23_3	Bacteroides phage DAC23	GCA_013387745.1
QIG63396.1	003644	Cluster3281_1clades	66	DAC16_166	Bacteroides phage DAC16	GCA_013387695.1
QIG63660.1	003644	Cluster3281_1clades	66	DAC19_172	Bacteroides phage DAC19	GCA_013387715.1
QIG63921.1	003644	Cluster3281_1clades	66	DAC20_171	Bacteroides phage DAC20	GCA_013387725.1
QIG64185.1	003644	Cluster3281_1clades	66	DAC22_174	Bacteroides phage DAC22	GCA_013387735.1
QIG64441.1	003644	Cluster3281_1clades	66	DAC23_166	Bacteroides phage DAC23	GCA_013387745.1
QIG63369.1	003645	Cluster3282_1clades	64	DAC16_136	Bacteroides phage DAC16	GCA_013387695.1
QIG63634.1	003645	Cluster3282_1clades	66	DAC19_143	Bacteroides phage DAC19	GCA_013387715.1
QIG63895.1	003645	Cluster3282_1clades	56	DAC20_142	Bacteroides phage DAC20	GCA_013387725.1
QIG64158.1	003645	Cluster3282_1clades	63	DAC22_144	Bacteroides phage DAC22	GCA_013387735.1
QIG64415.1	003645	Cluster3282_1clades	63	DAC23_137	Bacteroides phage DAC23	GCA_013387745.1
AUE22670.1	003646	Cluster3283_1clades	65	Ah1_00129	Aeromonas phage Ah1	GCA_002957415.1
QAX98396.1	003646	Cluster3283_1clades	65	ASfcp2_52	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52852.1	003646	Cluster3283_1clades	65	PX29p133	Aeromonas phage PX29	GCA_000920195.1
ADM80111.1	003646	Cluster3283_1clades	65	phiAS5_ORF0268	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17799.1	003646	Cluster3283_1clades	65	Aeh1ORF134c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22747.1	003647	Cluster3284_1clades	65	Ah1_00229	Aeromonas phage Ah1	GCA_002957415.1
QAX98463.1	003647	Cluster3284_1clades	65	ASfcp2_123	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52923.1	003647	Cluster3284_1clades	65	PX29p204	Aeromonas phage PX29	GCA_000920195.1
ADM79848.1	003647	Cluster3284_1clades	65	phiAS5_ORF0005	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17873.1	003647	Cluster3284_1clades	65	Aeh1ORF210w	Aeromonas virus Aeh1	GCA_000843245.1
AUE22821.1	003648	TM	65	Ah1_00303	Aeromonas phage Ah1	GCA_002957415.1
QAX98536.1	003648	TM	64	ASfcp2_200	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52999.1	003648	TM	64	PX29p280	Aeromonas phage PX29	GCA_000920195.1
ADM79922.1	003648	TM	64	phiAS5_ORF0079	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17951.1	003648	TM	65	Aeh1hmmORF07c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21864.1	003649	SIG+TM	51	GAP32_411	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43987.1	003649	SIG+TM	65	CBB_424	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88944.1	003649	SIG+TM	63	BF_0419	Serratia phage BF	GCA_002619745.1
SOK59232.1	003649	SIG+TM	63	g424	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58698.1	003649	SIG+TM	63	g421	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63306.1	003650	Cluster3287_1clades	65	DAC16_73	Bacteroides phage DAC16	GCA_013387695.1
QIG63565.1	003650	Cluster3287_1clades	65	DAC19_74	Bacteroides phage DAC19	GCA_013387715.1
QIG63826.1	003650	Cluster3287_1clades	65	DAC20_73	Bacteroides phage DAC20	GCA_013387725.1
QIG64088.1	003650	Cluster3287_1clades	65	DAC22_74	Bacteroides phage DAC22	GCA_013387735.1
QIG64351.1	003650	Cluster3287_1clades	65	DAC23_73	Bacteroides phage DAC23	GCA_013387745.1
QMV29086.1	003651	TM	63	AP1_0379	Aeromonas phage AP1	GCA_014183365.1
ATI17346.1	003651	TM	63	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00247.1	003651	TM	63	HWB28_gp305	Aeromonas phage AS-zj	GCA_002627665.1
QAX97791.1	003651	TM	63	ASswx1_146	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39288.1	003651	TM	64	CC2_392	Aeromonas phage CC2	GCA_000903495.1
AFC21854.1	003652	Cluster3289_1clades	62	GAP32_401	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43973.1	003652	Cluster3289_1clades	64	CBB_410	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88933.1	003652	Cluster3289_1clades	63	BF_0408	Serratia phage BF	GCA_002619745.1
SOK59222.1	003652	Cluster3289_1clades	63	g414	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58688.1	003652	Cluster3289_1clades	63	g411	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22643.1	003653	Cluster3290_1clades	63	Ah1_00102	Aeromonas phage Ah1	GCA_002957415.1
QAX98371.1	003653	Cluster3290_1clades	63	ASfcp2_25	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52825.1	003653	Cluster3290_1clades	63	PX29p106	Aeromonas phage PX29	GCA_000920195.1
ADM80083.1	003653	Cluster3290_1clades	63	phiAS5_ORF0240	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17768.1	003653	Cluster3290_1clades	63	Aeh1ORF107c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22678.1	003654	SIG+TM	63	Ah1_00137	Aeromonas phage Ah1	GCA_002957415.1
QAX98404.1	003654	SIG+TM	63	ASfcp2_60	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52860.1	003654	SIG+TM	63	PX29p141	Aeromonas phage PX29	GCA_000920195.1
ADM80119.1	003654	SIG+TM	63	phiAS5_ORF0276	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17806.1	003654	SIG+TM	63	Aeh1ORF141c	Aeromonas virus Aeh1	GCA_000843245.1
QMV28880.1	003655	Cluster3292_1clades	63	AP1_0173	Aeromonas phage AP1	GCA_014183365.1
ATI17243.1	003655	Cluster3292_1clades	63	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00344.1	003655	Cluster3292_1clades	63	HWB28_gp208	Aeromonas phage AS-zj	GCA_002627665.1
QAX97686.1	003655	Cluster3292_1clades	63	ASswx1_40	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39208.1	003655	Cluster3292_1clades	63	CC2_074	Aeromonas phage CC2	GCA_000903495.1
QMV28737.1	003656	Cluster3293_1clades	52	AP1_0019	Aeromonas phage AP1	GCA_014183365.1
ATI17565.1	003656	Cluster3293_1clades	62	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00431.1	003656	Cluster3293_1clades	62	HWB28_gp121	Aeromonas phage AS-zj	GCA_002627665.1
QAX98005.1	003656	Cluster3293_1clades	62	ASswx1_365	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39242.1	003656	Cluster3293_1clades	63	CC2_167	Aeromonas phage CC2	GCA_000903495.1
QMV28871.1	003657	Cluster3294_1clades	63	AP1_0164	Aeromonas phage AP1	GCA_014183365.1
ATI17497.1	003657	Cluster3294_1clades	63	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00500.1	003657	Cluster3294_1clades	63	HWB28_gp052	Aeromonas phage AS-zj	GCA_002627665.1
QAX97936.1	003657	Cluster3294_1clades	63	ASswx1_294	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39269.1	003657	Cluster3294_1clades	63	CC2_237	Aeromonas phage CC2	GCA_000903495.1
QIG63247.1	003658	Cluster3295_1clades	63	DAC16_14	Bacteroides phage DAC16	GCA_013387695.1
QIG63509.1	003658	Cluster3295_1clades	63	DAC19_18	Bacteroides phage DAC19	GCA_013387715.1
QIG63771.1	003658	Cluster3295_1clades	63	DAC20_18	Bacteroides phage DAC20	GCA_013387725.1
QIG64032.1	003658	Cluster3295_1clades	63	DAC22_18	Bacteroides phage DAC22	GCA_013387735.1
QIG64293.1	003658	Cluster3295_1clades	63	DAC23_15	Bacteroides phage DAC23	GCA_013387745.1
QIG63343.1	003659	Cluster3296_1clades	63	DAC16_110	Bacteroides phage DAC16	GCA_013387695.1
QIG63609.1	003659	Cluster3296_1clades	63	DAC19_118	Bacteroides phage DAC19	GCA_013387715.1
QIG63870.1	003659	Cluster3296_1clades	63	DAC20_117	Bacteroides phage DAC20	GCA_013387725.1
QIG64133.1	003659	Cluster3296_1clades	63	DAC22_119	Bacteroides phage DAC22	GCA_013387735.1
QIG64390.1	003659	Cluster3296_1clades	63	DAC23_112	Bacteroides phage DAC23	GCA_013387745.1
AGH56938.1	003660	MazE_antitoxin	62	CPXG_00135	Cyanophage P-RSM6	GCA_000906155.1
AJK27518.1	003660	MazE_antitoxin	54	PTIM40_91	Cyanophage P-TIM40	GCA_001470935.1
AOO14277.1	003660	MazE_antitoxin	53	Sn110110_083	Cyanophage S-RIM14	GCA_002599065.1
AOO14926.1	003660	MazE_antitoxin	53	W1230910_080	Cyanophage S-RIM14	GCA_002599125.1
AGG54306.1	003660	MazE_antitoxin	53	CYWG_00022	Cyanophage S-SSM6b	GCA_002710425.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63262.1	003661	Cluster3298_1clades	62	DAC16_29	Bacteroides phage DAC16	GCA_013387695.1
QIG63524.1	003661	Cluster3298_1clades	62	DAC19_33	Bacteroides phage DAC19	GCA_013387715.1
QIG63786.1	003661	Cluster3298_1clades	62	DAC20_33	Bacteroides phage DAC20	GCA_013387725.1
QIG64047.1	003661	Cluster3298_1clades	62	DAC22_33	Bacteroides phage DAC22	GCA_013387735.1
QIG64308.1	003661	Cluster3298_1clades	62	DAC23_30	Bacteroides phage DAC23	GCA_013387745.1
QIG63486.1	003662	Cluster3299_1clades	62	DAC16_257	Bacteroides phage DAC16	GCA_013387695.1
QIG63748.1	003662	Cluster3299_1clades	62	DAC19_261	Bacteroides phage DAC19	GCA_013387715.1
QIG64009.1	003662	Cluster3299_1clades	62	DAC20_260	Bacteroides phage DAC20	GCA_013387725.1
QIG64273.1	003662	Cluster3299_1clades	62	DAC22_263	Bacteroides phage DAC22	GCA_013387735.1
QIG64530.1	003662	Cluster3299_1clades	62	DAC23_256	Bacteroides phage DAC23	GCA_013387745.1
AUE22653.1	003663	Cluster3300_1clades	61	Ah1_00112	Aeromonas phage Ah1	GCA_002957415.1
QAX98379.1	003663	Cluster3300_1clades	61	ASfcp2_33	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52832.1	003663	Cluster3300_1clades	61	PX29p113	Aeromonas phage PX29	GCA_000920195.1
ADM80092.1	003663	Cluster3300_1clades	61	phiAS5_ORF0249	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17779.1	003663	Cluster3300_1clades	61	Aeh1ORF117c	Aeromonas virus Aeh1	GCA_000843245.1
QMV28838.1	003664	Cluster3301_1clades	60	AP1_0131	Aeromonas phage AP1	GCA_014183365.1
ATI17271.1	003664	Cluster3301_1clades	61	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00322.1	003664	Cluster3301_1clades	61	HWB28_gp230	Aeromonas phage AS-zj	GCA_002627665.1
QAX97711.1	003664	Cluster3301_1clades	61	ASswx1_65	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39187.1	003664	Cluster3301_1clades	61	CC2_046	Aeromonas phage CC2	GCA_000903495.1
AIT14011.1	003665	Cluster3302_1clades	61	PBI_121Q_114	Escherichia phage 121Q	GCA_000926855.1
QAY00327.1	003665	Cluster3302_1clades	61	Ecwhy1_46	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35073.1	003665	Cluster3302_1clades	61	ACQ29_gp393	Escherichia phage PBECO4	GCA_001041035.1
BBM61702.1	003665	Cluster3302_1clades	61	EO157G_1130	Escherichia phage SP27	GCA_008033345.1
QDF13731.1	003665	Cluster3302_1clades	61	vBEcoMphAPEC6_gp101c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AIT14143.1	003666	Cluster3303_1clades	61	PBI_121Q_253	Escherichia phage 121Q	GCA_000926855.1
AGC34965.1	003666	Cluster3303_1clades	39	ACQ29_gp285	Escherichia phage PBECO4	GCA_001041035.1
BBM61818.1	003666	Cluster3303_1clades	61	EO157G_2290	Escherichia phage SP27	GCA_008033345.1
QBO61560.1	003666	Cluster3303_1clades	61	G17_00064	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80134.1	003666	Cluster3303_1clades	61	PSLUR01_00157	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QAX96765.1	003667	Cluster3304_1clades	61	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97084.1	003667	Cluster3304_1clades	61	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96130.1	003667	Cluster3304_1clades	61	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96448.1	003667	Cluster3304_1clades	61	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QNI20978.1	003667	Cluster3304_1clades	57	-	Vibrio phage vB_pir03	GCA_014319855.1
ADQ52741.1	003668	Gp45_2	58	PX29p022	Aeromonas phage PX29	GCA_000920195.1
ADM79993.1	003668	Gp45_2	58	phiAS5_ORF0150	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17678.1	003668	Gp45_2	58	45.2	Aeromonas virus Aeh1	GCA_000843245.1
AIA65042.1	003668	Gp45_2	60	S13_245	Cronobacter phage S13	GCA_001503575.1
QHJ78890.1	003668	Gp45_2	61	-	Myoviridae sp.	GCA_012593985.1
QIG63261.1	003669	Cluster3306_1clades	61	DAC16_28	Bacteroides phage DAC16	GCA_013387695.1
QIG63523.1	003669	Cluster3306_1clades	61	DAC19_32	Bacteroides phage DAC19	GCA_013387715.1
QIG63785.1	003669	Cluster3306_1clades	61	DAC20_32	Bacteroides phage DAC20	GCA_013387725.1
QIG64046.1	003669	Cluster3306_1clades	61	DAC22_32	Bacteroides phage DAC22	GCA_013387735.1
QIG64307.1	003669	Cluster3306_1clades	61	DAC23_29	Bacteroides phage DAC23	GCA_013387745.1
QIG63399.1	003670	Cluster3307_1clades	61	DAC16_169	Bacteroides phage DAC16	GCA_013387695.1
QIG63663.1	003670	Cluster3307_1clades	61	DAC19_175	Bacteroides phage DAC19	GCA_013387715.1
QIG63924.1	003670	Cluster3307_1clades	61	DAC20_174	Bacteroides phage DAC20	GCA_013387725.1
QIG64188.1	003670	Cluster3307_1clades	61	DAC22_177	Bacteroides phage DAC22	GCA_013387735.1
QIG64444.1	003670	Cluster3307_1clades	61	DAC23_169	Bacteroides phage DAC23	GCA_013387745.1
AFC21592.1	003671	UMP1	58	GAP32_142	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43711.1	003671	UMP1	58	CBB_146	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88665.1	003671	UMP1	59	BF_0140	Serratia phage BF	GCA_002619745.1
SOK58947.1	003671	UMP1	61	g139	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58413.1	003671	UMP1	57	g136	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMO43436.1	003672	Cluster3309_1clades	38	W270710_194	Cyanophage S-RIM44	GCA_002599145.1
AOO11908.1	003672	Cluster3309_1clades	38	Np050604_194	Cyanophage S-RIM44	GCA_002599185.1
AOO12609.1	003672	Cluster3309_1clades	38	Sn080709_194	Cyanophage S-RIM44	GCA_002599245.1
AOO13075.1	003672	Cluster3309_1clades	38	W2100709_195	Cyanophage S-RIM44	GCA_002599285.1
ADO99295.1	003672	Cluster3309_1clades	60	Syn1_196	Prochlorococcus phage Syn1	GCA_000892495.1
AUE22550.1	003673	Cluster3310_1clades	60	Ah1_00009	Aeromonas phage Ah1	GCA_002957415.1
QAX98590.1	003673	Cluster3310_1clades	57	ASfcp2_257	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52726.1	003673	Cluster3310_1clades	57	PX29p007	Aeromonas phage PX29	GCA_000920195.1
ADM79978.1	003673	Cluster3310_1clades	58	phiAS5_ORF0135	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17663.1	003673	Cluster3310_1clades	57	Aeh1ORF008c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63245.1	003674	Cluster3311_1clades	60	DAC16_12	Bacteroides phage DAC16	GCA_013387695.1
QIG63507.1	003674	Cluster3311_1clades	60	DAC19_16	Bacteroides phage DAC19	GCA_013387715.1
QIG63769.1	003674	Cluster3311_1clades	60	DAC20_16	Bacteroides phage DAC20	GCA_013387725.1
QIG64030.1	003674	Cluster3311_1clades	60	DAC22_16	Bacteroides phage DAC22	GCA_013387735.1
QIG64291.1	003674	Cluster3311_1clades	60	DAC23_13	Bacteroides phage DAC23	GCA_013387745.1
QMV28902.1	003675	Cluster3312_1clades	59	AP1_0195	Aeromonas phage AP1	GCA_014183365.1
ATI17593.1	003675	Cluster3312_1clades	59	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00404.1	003675	Cluster3312_1clades	59	HWB28_gp148	Aeromonas phage AS-zj	GCA_002627665.1
QAX98032.1	003675	Cluster3312_1clades	59	ASswx1_392	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39230.1	003675	Cluster3312_1clades	59	CC2_139	Aeromonas phage CC2	GCA_000903495.1
AIT14145.1	003676	Cluster3313_1clades	59	PBI_121Q_255	Escherichia phage 121Q	GCA_000926855.1
BBM61823.1	003676	Cluster3313_1clades	59	EO157G_2340	Escherichia phage SP27	GCA_008033345.1
QBO61558.1	003676	Cluster3313_1clades	59	G17_00062	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14168.1	003676	Cluster3313_1clades	59	vBEcoMphAPEC6_gp545c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80137.1	003676	Cluster3313_1clades	59	PSLUR01_00160	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QMV28826.1	003677	Cluster3314_1clades	58	AP1_0119	Aeromonas phage AP1	GCA_014183365.1
ATI17602.1	003677	Cluster3314_1clades	59	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00394.1	003677	Cluster3314_1clades	59	HWB28_gp158	Aeromonas phage AS-zj	GCA_002627665.1
QAX98041.1	003677	Cluster3314_1clades	58	ASswx1_401	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39151.1	003677	Cluster3314_1clades	58	CC2_129	Aeromonas phage CC2	GCA_000903495.1
QDB70395.1	003678	Cluster3315_1clades	47	CF8_0226	Aeromonas phage CF8	GCA_006384595.2
QDJ96739.1	003678	Cluster3315_1clades	56	PS1_0228	Aeromonas phage PS1	GCA_007051165.2
QFR59372.1	003678	Cluster3315_1clades	56	PS2_0230	Aeromonas phage PS2	GCA_009388305.2
QGZ14514.1	003678	Cluster3315_1clades	59	HWC77_gp151	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04220.1	003678	Cluster3315_1clades	53	HWC03_gp065	Vibrio phage 2 TSL-2019	GCA_006964105.1
QIG63311.1	003679	Cluster3316_1clades	59	DAC16_78	Bacteroides phage DAC16	GCA_013387695.1
QIG63572.1	003679	Cluster3316_1clades	59	DAC19_81	Bacteroides phage DAC19	GCA_013387715.1
QIG63833.1	003679	Cluster3316_1clades	59	DAC20_80	Bacteroides phage DAC20	GCA_013387725.1
QIG64095.1	003679	Cluster3316_1clades	59	DAC22_81	Bacteroides phage DAC22	GCA_013387735.1
QIG64355.1	003679	Cluster3316_1clades	59	DAC23_77	Bacteroides phage DAC23	GCA_013387745.1
QIG63316.1	003680	Cluster3317_1clades	59	DAC16_83	Bacteroides phage DAC16	GCA_013387695.1
QIG63577.1	003680	Cluster3317_1clades	59	DAC19_86	Bacteroides phage DAC19	GCA_013387715.1
QIG63838.1	003680	Cluster3317_1clades	59	DAC20_85	Bacteroides phage DAC20	GCA_013387725.1
QIG64100.1	003680	Cluster3317_1clades	59	DAC22_86	Bacteroides phage DAC22	GCA_013387735.1
QIG64360.1	003680	Cluster3317_1clades	59	DAC23_82	Bacteroides phage DAC23	GCA_013387745.1
QIG63265.1	003681	Cluster3318_1clades	57	DAC16_32	Bacteroides phage DAC16	GCA_013387695.1
QIG63527.1	003681	Cluster3318_1clades	59	DAC19_36	Bacteroides phage DAC19	GCA_013387715.1
QIG63789.1	003681	Cluster3318_1clades	59	DAC20_36	Bacteroides phage DAC20	GCA_013387725.1
QIG64050.1	003681	Cluster3318_1clades	59	DAC22_36	Bacteroides phage DAC22	GCA_013387735.1
QIG64311.1	003681	Cluster3318_1clades	57	DAC23_33	Bacteroides phage DAC23	GCA_013387745.1
AUE22591.1	003682	Cluster3319_1clades	57	Ah1_00050	Aeromonas phage Ah1	GCA_002957415.1
QAX98629.1	003682	Cluster3319_1clades	57	ASfcp2_296	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52769.1	003682	Cluster3319_1clades	57	PX29p050	Aeromonas phage PX29	GCA_000920195.1
ADM80024.1	003682	Cluster3319_1clades	58	phiAS5_ORF0181	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17713.1	003682	Cluster3319_1clades	57	Aeh1ORF054c	Aeromonas virus Aeh1	GCA_000843245.1
AIT14334.1	003683	Cluster3320_1clades	58	PBI_121Q_444	Escherichia phage 121Q	GCA_000926855.1
AGC34804.1	003683	Cluster3320_1clades	58	ACQ29_gp124	Escherichia phage PBECO4	GCA_001041035.1
QBO61970.1	003683	Cluster3320_1clades	58	G17_00481	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13995.1	003683	Cluster3320_1clades	58	vBEcoMphAPEC6_gp371c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80321.1	003683	Cluster3320_1clades	58	PSLUR01_00344	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14320.1	003684	Cluster3321_1clades	58	PBI_121Q_430	Escherichia phage 121Q	GCA_000926855.1
QAY00619.1	003684	Cluster3321_1clades	57	Ecwhy1_344	Escherichia phage Ecwhy_1	GCA_004146585.1
AXC36926.1	003684	Cluster3321_1clades	46	-	Escherichia phage UB	GCA_003341455.1
QBO61984.1	003684	Cluster3321_1clades	58	G17_00495	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80307.1	003684	Cluster3321_1clades	58	PSLUR01_00330	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14251.1	003685	Cluster3322_1clades	56	PBI_121Q_361	Escherichia phage 121Q	GCA_000926855.1
AGC34876.1	003685	Cluster3322_1clades	53	ACQ29_gp196	Escherichia phage PBECO4	GCA_001041035.1
BBM61929.1	003685	Cluster3322_1clades	53	EO157G_3400	Escherichia phage SP27	GCA_008033345.1
QBO62053.1	003685	Cluster3322_1clades	58	G17_00564	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80241.1	003685	Cluster3322_1clades	56	PSLUR01_00264	Escherichia phage vB_Eco_slurp01	GCA_900094095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63275.1	003686	Cluster3323_1clades	58	DAC16_42	Bacteroides phage DAC16	GCA_013387695.1
QIG63536.1	003686	Cluster3323_1clades	58	DAC19_45	Bacteroides phage DAC19	GCA_013387715.1
QIG63797.1	003686	Cluster3323_1clades	58	DAC20_44	Bacteroides phage DAC20	GCA_013387725.1
QIG64058.1	003686	Cluster3323_1clades	58	DAC22_44	Bacteroides phage DAC22	GCA_013387735.1
QIG64319.1	003686	Cluster3323_1clades	58	DAC23_41	Bacteroides phage DAC23	GCA_013387745.1
QIG63291.1	003687	Cluster3324_1clades	58	DAC16_58	Bacteroides phage DAC16	GCA_013387695.1
QIG63550.1	003687	Cluster3324_1clades	58	DAC19_59	Bacteroides phage DAC19	GCA_013387715.1
QIG63811.1	003687	Cluster3324_1clades	58	DAC20_58	Bacteroides phage DAC20	GCA_013387725.1
QIG64073.1	003687	Cluster3324_1clades	58	DAC22_59	Bacteroides phage DAC22	GCA_013387735.1
QIG64336.1	003687	Cluster3324_1clades	58	DAC23_58	Bacteroides phage DAC23	GCA_013387745.1
QIG63304.1	003688	Cluster3325_1clades	58	DAC16_71	Bacteroides phage DAC16	GCA_013387695.1
QIG63563.1	003688	Cluster3325_1clades	58	DAC19_72	Bacteroides phage DAC19	GCA_013387715.1
QIG63824.1	003688	Cluster3325_1clades	58	DAC20_71	Bacteroides phage DAC20	GCA_013387725.1
QIG64086.1	003688	Cluster3325_1clades	58	DAC22_72	Bacteroides phage DAC22	GCA_013387735.1
QIG64349.1	003688	Cluster3325_1clades	58	DAC23_71	Bacteroides phage DAC23	GCA_013387745.1
QIG63340.1	003689	Cluster3326_1clades	58	DAC16_107	Bacteroides phage DAC16	GCA_013387695.1
QIG63606.1	003689	Cluster3326_1clades	58	DAC19_115	Bacteroides phage DAC19	GCA_013387715.1
QIG63867.1	003689	Cluster3326_1clades	58	DAC20_114	Bacteroides phage DAC20	GCA_013387725.1
QIG64130.1	003689	Cluster3326_1clades	54	DAC22_116	Bacteroides phage DAC22	GCA_013387735.1
QIG64387.1	003689	Cluster3326_1clades	54	DAC23_109	Bacteroides phage DAC23	GCA_013387745.1
AAQ64258.1	003690	Cluster3327_1clades	57	KVP40.0189	Vibrio phage KVP40	GCA_000843785.1
QIW90574.1	003690	Cluster3327_1clades	57	GCAPEGMB_00227	Vibrio phage V07	GCA_012361095.1
QIW91224.1	003690	Cluster3327_1clades	57	COHAPHLL_00388	Vibrio phage V09	GCA_012361135.1
QHJ74372.1	003690	Cluster3327_1clades	57	VH12019_00045	Vibrio phage VH1_2019	GCA_009931825.1
AFN37420.1	003690	Cluster3327_1clades	57	pp2_187	Vibriophage phi-pp2	GCA_002630725.1
QBX06301.1	003691	SIG+TM	57	ValB1HC_348	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60931.1	003691	SIG+TM	57	AVU32_gp090	Vibrio phage ValKK3	GCA_001501635.1
ALP47318.1	003691	SIG+TM	57	phiGrn1_0282	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47696.1	003691	SIG+TM	57	phiST2_0041	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54544.1	003691	SIG+TM	57	vBValMR10Z_3	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ASR76311.1	003692	Cluster3329_1clades	55	PBI_BELLAMY_275	Synechococcus phage Bellamy	GCA_002627525.1
QCW23059.1	003692	Cluster3329_1clades	52	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50692.1	003692	Cluster3329_1clades	52	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70527.1	003692	Cluster3329_1clades	54	HOU04_gp128	Synechococcus phage S-T4	GCA_003443335.1
QJT70256.1	003692	Cluster3329_1clades	57	SynMITS9220M01_250	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUE22780.1	003693	DUF2685	56	Ah1_00262	Aeromonas phage Ah1	GCA_002957415.1
QAX98495.1	003693	DUF2685	56	ASfcp2_159	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52958.1	003693	DUF2685	56	PX29p239	Aeromonas phage PX29	GCA_000920195.1
ADM79884.1	003693	DUF2685	55	phiAS5_ORF0041	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17906.1	003693	DUF2685	56	Aeh1ORF244c	Aeromonas virus Aeh1	GCA_000843245.1
QIG63313.1	003694	Cluster3331_1clades	56	DAC16_80	Bacteroides phage DAC16	GCA_013387695.1
QIG63574.1	003694	Cluster3331_1clades	56	DAC19_83	Bacteroides phage DAC19	GCA_013387715.1
QIG63835.1	003694	Cluster3331_1clades	56	DAC20_82	Bacteroides phage DAC20	GCA_013387725.1
QIG64097.1	003694	Cluster3331_1clades	56	DAC22_83	Bacteroides phage DAC22	GCA_013387735.1
QIG64357.1	003694	Cluster3331_1clades	56	DAC23_79	Bacteroides phage DAC23	GCA_013387745.1
QIG63416.1	003695	Cluster3332_1clades	56	DAC16_186	Bacteroides phage DAC16	GCA_013387695.1
QIG63680.1	003695	Cluster3332_1clades	56	DAC19_192	Bacteroides phage DAC19	GCA_013387715.1
QIG63941.1	003695	Cluster3332_1clades	56	DAC20_191	Bacteroides phage DAC20	GCA_013387725.1
QIG64205.1	003695	Cluster3332_1clades	56	DAC22_194	Bacteroides phage DAC22	GCA_013387735.1
QIG64461.1	003695	Cluster3332_1clades	56	DAC23_186	Bacteroides phage DAC23	GCA_013387745.1
AAQ64241.1	003696	Cluster3333_1clades	55	KVP40.0172	Vibrio phage KVP40	GCA_000843785.1
QIW90557.1	003696	Cluster3333_1clades	55	GCAPEGMB_00210	Vibrio phage V07	GCA_012361095.1
QIW90865.1	003696	Cluster3333_1clades	55	COHAPHLL_00002	Vibrio phage V09	GCA_012361135.1
QHJ74355.1	003696	Cluster3333_1clades	55	VH12019_00028	Vibrio phage VH1_2019	GCA_009931825.1
AJT60928.1	003696	Cluster3333_1clades	55	AVU32_gp087	Vibrio phage ValKK3	GCA_001501635.1
AFC21535.1	003697	Cluster3334_1clades	55	GAP32_087	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43654.1	003697	Cluster3334_1clades	55	CBB_89	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88605.1	003697	Cluster3334_1clades	55	BF_0080	Serratia phage BF	GCA_002619745.1
SOK58882.1	003697	Cluster3334_1clades	55	g074	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58345.1	003697	Cluster3334_1clades	55	g068	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63238.1	003698	DUF4177	55	DAC16_5	Bacteroides phage DAC16	GCA_013387695.1
QIG63496.1	003698	DUF4177	55	DAC19_5	Bacteroides phage DAC19	GCA_013387715.1
QIG63758.1	003698	DUF4177	55	DAC20_5	Bacteroides phage DAC20	GCA_013387725.1
QIG64019.1	003698	DUF4177	55	DAC22_5	Bacteroides phage DAC22	GCA_013387735.1
QIG64283.1	003698	DUF4177	55	DAC23_5	Bacteroides phage DAC23	GCA_013387745.1
QIG63294.1	003699	Cluster3336_1clades	55	DAC16_61	Bacteroides phage DAC16	GCA_013387695.1
QIG63553.1	003699	Cluster3336_1clades	55	DAC19_62	Bacteroides phage DAC19	GCA_013387715.1
QIG63814.1	003699	Cluster3336_1clades	55	DAC20_61	Bacteroides phage DAC20	GCA_013387725.1
QIG64076.1	003699	Cluster3336_1clades	55	DAC22_62	Bacteroides phage DAC22	GCA_013387735.1
QIG64339.1	003699	Cluster3336_1clades	55	DAC23_61	Bacteroides phage DAC23	GCA_013387745.1
QIG63297.1	003700	Cluster3337_1clades	55	DAC16_64	Bacteroides phage DAC16	GCA_013387695.1
QIG63556.1	003700	Cluster3337_1clades	55	DAC19_65	Bacteroides phage DAC19	GCA_013387715.1
QIG63817.1	003700	Cluster3337_1clades	55	DAC20_64	Bacteroides phage DAC20	GCA_013387725.1
QIG64079.1	003700	Cluster3337_1clades	55	DAC22_65	Bacteroides phage DAC22	GCA_013387735.1
QIG64342.1	003700	Cluster3337_1clades	55	DAC23_64	Bacteroides phage DAC23	GCA_013387745.1
QIG63382.1	003701	Cluster3338_1clades	55	DAC16_149	Bacteroides phage DAC16	GCA_013387695.1
QIG63646.1	003701	Cluster3338_1clades	55	DAC19_155	Bacteroides phage DAC19	GCA_013387715.1
QIG63907.1	003701	Cluster3338_1clades	55	DAC20_154	Bacteroides phage DAC20	GCA_013387725.1
QIG64171.1	003701	Cluster3338_1clades	55	DAC22_157	Bacteroides phage DAC22	GCA_013387735.1
QIG64427.1	003701	Cluster3338_1clades	55	DAC23_149	Bacteroides phage DAC23	GCA_013387745.1
QIW90555.1	003702	SIG+TM	51	GCAPEGMB_00208	Vibrio phage V07	GCA_012361095.1
QIW90867.1	003702	SIG+TM	51	COHAPHLL_00004	Vibrio phage V09	GCA_012361135.1
QHJ74353.1	003702	SIG+TM	51	VH12019_00026	Vibrio phage VH1_2019	GCA_009931825.1
AJT60930.1	003702	SIG+TM	54	AVU32_gp089	Vibrio phage ValKK3	GCA_001501635.1
QNJ54543.1	003702	SIG+TM	54	vBValMR10Z_2	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QIG63338.1	003703	Cluster3340_1clades	53	DAC16_105	Bacteroides phage DAC16	GCA_013387695.1
QIG63604.1	003703	Cluster3340_1clades	53	DAC19_113	Bacteroides phage DAC19	GCA_013387715.1
QIG63865.1	003703	Cluster3340_1clades	53	DAC20_112	Bacteroides phage DAC20	GCA_013387725.1
QIG64128.1	003703	Cluster3340_1clades	53	DAC22_114	Bacteroides phage DAC22	GCA_013387735.1
QIG64385.1	003703	Cluster3340_1clades	53	DAC23_107	Bacteroides phage DAC23	GCA_013387745.1
QMV29083.1	003704	Cluster3341_1clades	51	AP1_0376	Aeromonas phage AP1	GCA_014183365.1
ATI17387.1	003704	Cluster3341_1clades	46	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00206.1	003704	Cluster3341_1clades	51	HWB28_gp346	Aeromonas phage AS-zj	GCA_002627665.1
QAX97829.1	003704	Cluster3341_1clades	46	ASswx1_185	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39277.1	003704	Cluster3341_1clades	51	CC2_350	Aeromonas phage CC2	GCA_000903495.1
QIW91227.1	003705	Cluster3342_1clades	51	COHAPHLL_00391	Vibrio phage V09	GCA_012361135.1
AGB06865.1	003705	Cluster3342_1clades	51	CF80_gp078	Vibrio phage VH7D	GCA_000914495.1
AJT60906.1	003705	Cluster3342_1clades	51	AVU32_gp065	Vibrio phage ValKK3	GCA_001501635.1
AGN30246.1	003705	Cluster3342_1clades	50	VPFG_00247	Vibrio phage nt-1	GCA_000910195.2
AFN37417.1	003705	Cluster3342_1clades	48	pp2_184	Vibriophage phi-pp2	GCA_002630725.1
AFC21826.1	003706	Cluster3343_1clades	49	GAP32_374A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43947.1	003706	Cluster3343_1clades	49	CBB_384	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88906.1	003706	Cluster3343_1clades	51	BF_0381	Serratia phage BF	GCA_002619745.1
SOK59195.1	003706	Cluster3343_1clades	51	g387	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58659.1	003706	Cluster3343_1clades	51	g382	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01625.1	003707	CW-binding-EndolysinC	50	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28839.1	003707	CW-binding-EndolysinC	50	AP1_0132	Aeromonas phage AP1	GCA_014183365.1
QAX97712.1	003707	CW-binding-EndolysinC	50	ASswx1_66	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39186.1	003707	CW-binding-EndolysinC	50	CC2_045	Aeromonas phage CC2	GCA_000903495.1
ADQ53250.1	003707	CW-binding-EndolysinC	50	65p242	Aeromonas virus 65	GCA_000893255.1
AFC21861.1	003708	Cluster3345_1clades	50	GAP32_408	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43984.1	003708	Cluster3345_1clades	50	CBB_421	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88941.1	003708	Cluster3345_1clades	50	BF_0416	Serratia phage BF	GCA_002619745.1
SOK59230.1	003708	Cluster3345_1clades	49	g422	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58696.1	003708	Cluster3345_1clades	49	g419	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63234.1	003709	Cluster3346_1clades	50	DAC16_1	Bacteroides phage DAC16	GCA_013387695.1
QIG63492.1	003709	Cluster3346_1clades	50	DAC19_1	Bacteroides phage DAC19	GCA_013387715.1
QIG63754.1	003709	Cluster3346_1clades	50	DAC20_1	Bacteroides phage DAC20	GCA_013387725.1
QIG64015.1	003709	Cluster3346_1clades	50	DAC22_1	Bacteroides phage DAC22	GCA_013387735.1
QIG64279.1	003709	Cluster3346_1clades	50	DAC23_1	Bacteroides phage DAC23	GCA_013387745.1
QMV28983.1	003710	Cluster3347_1clades	49	AP1_0276	Aeromonas phage AP1	GCA_014183365.1
ATI17534.1	003710	Cluster3347_1clades	49	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00462.1	003710	Cluster3347_1clades	49	HWB28_gp090	Aeromonas phage AS-zj	GCA_002627665.1
QAX97975.1	003710	Cluster3347_1clades	49	ASswx1_334	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39256.1	003710	Cluster3347_1clades	49	CC2_199	Aeromonas phage CC2	GCA_000903495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63258.1	003711	Cluster3348_1clades	49	DAC16_25	Bacteroides phage DAC16	GCA_013387695.1
QIG63520.1	003711	Cluster3348_1clades	49	DAC19_29	Bacteroides phage DAC19	GCA_013387715.1
QIG63782.1	003711	Cluster3348_1clades	49	DAC20_29	Bacteroides phage DAC20	GCA_013387725.1
QIG64043.1	003711	Cluster3348_1clades	49	DAC22_29	Bacteroides phage DAC22	GCA_013387735.1
QIG64304.1	003711	Cluster3348_1clades	49	DAC23_26	Bacteroides phage DAC23	GCA_013387745.1
QMV29022.1	003712	Cluster3349_1clades	45	AP1_0315	Aeromonas phage AP1	GCA_014183365.1
ATI17629.1	003712	Cluster3349_1clades	45	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00366.1	003712	Cluster3349_1clades	45	HWB28_gp186	Aeromonas phage AS-zj	GCA_002627665.1
QAX97664.1	003712	Cluster3349_1clades	45	ASswx1_18	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39216.1	003712	Cluster3349_1clades	47	CC2_097	Aeromonas phage CC2	GCA_000903495.1
AOO14394.1	003713	Cluster3350_1clades	47	Sn110110_201	Cyanophage S-RIM14	GCA_002599065.1
AOO15042.1	003713	Cluster3350_1clades	47	W1230910_197	Cyanophage S-RIM14	GCA_002599125.1
AOV59671.1	003713	Cluster3350_1clades	46	S330809_210	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59433.1	003713	Cluster3350_1clades	46	C440309_210	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59908.1	003713	Cluster3350_1clades	46	N231010_209	Synechococcus phage S-CAM4	GCA_002922155.1
QIG63356.1	003714	Cluster3351_1clades	47	DAC16_123	Bacteroides phage DAC16	GCA_013387695.1
QIG63621.1	003714	Cluster3351_1clades	47	DAC19_130	Bacteroides phage DAC19	GCA_013387715.1
QIG63882.1	003714	Cluster3351_1clades	47	DAC20_129	Bacteroides phage DAC20	GCA_013387725.1
QIG64145.1	003714	Cluster3351_1clades	47	DAC22_131	Bacteroides phage DAC22	GCA_013387735.1
QIG64402.1	003714	Cluster3351_1clades	47	DAC23_124	Bacteroides phage DAC23	GCA_013387745.1
AFC21850.1	003715	Cluster3352_1clades	46	GAP32_398	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43970.1	003715	Cluster3352_1clades	46	CBB_407	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88930.1	003715	Cluster3352_1clades	46	BF_0405	Serratia phage BF	GCA_002619745.1
SOK59219.1	003715	Cluster3352_1clades	46	g411	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58685.1	003715	Cluster3352_1clades	46	g408	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01782.1	003716	TM	46	-	Aeromonas phage 65.2	GCA_002618145.1
ASU00477.1	003716	TM	35	HWB28_gp075	Aeromonas phage AS-zj	GCA_002627665.1
QAX97960.1	003716	TM	35	ASswx1_318	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39260.1	003716	TM	46	CC2_213	Aeromonas phage CC2	GCA_000903495.1
ADQ53425.1	003716	TM	35	65p419	Aeromonas virus 65	GCA_000893255.1
QMV29017.1	003717	Cluster3354_1clades	45	AP1_0310	Aeromonas phage AP1	GCA_014183365.1
ATI17623.1	003717	Cluster3354_1clades	45	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00373.1	003717	Cluster3354_1clades	45	HWB28_gp179	Aeromonas phage AS-zj	GCA_002627665.1
QAX97657.1	003717	Cluster3354_1clades	45	ASswx1_11	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39218.1	003717	Cluster3354_1clades	45	CC2_103	Aeromonas phage CC2	GCA_000903495.1
QMV28781.1	003718	Cluster3355_1clades	45	AP1_0074	Aeromonas phage AP1	GCA_014183365.1
ATI17384.1	003718	Cluster3355_1clades	45	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00209.1	003718	Cluster3355_1clades	45	HWB28_gp343	Aeromonas phage AS-zj	GCA_002627665.1
QAX97826.1	003718	Cluster3355_1clades	45	ASswx1_182	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39279.1	003718	Cluster3355_1clades	44	CC2_353	Aeromonas phage CC2	GCA_000903495.1
QIG63263.1	003719	TM	32	DAC16_30	Bacteroides phage DAC16	GCA_013387695.1
QIG63525.1	003719	TM	45	DAC19_34	Bacteroides phage DAC19	GCA_013387715.1
QIG63787.1	003719	TM	45	DAC20_34	Bacteroides phage DAC20	GCA_013387725.1
QIG64048.1	003719	TM	45	DAC22_34	Bacteroides phage DAC22	GCA_013387735.1
QIG64309.1	003719	TM	32	DAC23_31	Bacteroides phage DAC23	GCA_013387745.1
QIG63278.1	003720	Cluster3357_1clades	44	DAC16_45	Bacteroides phage DAC16	GCA_013387695.1
QIG63540.1	003720	Cluster3357_1clades	44	DAC19_49	Bacteroides phage DAC19	GCA_013387715.1
QIG63801.1	003720	Cluster3357_1clades	44	DAC20_48	Bacteroides phage DAC20	GCA_013387725.1
QIG64062.1	003720	Cluster3357_1clades	44	DAC22_48	Bacteroides phage DAC22	GCA_013387735.1
QIG64323.1	003720	Cluster3357_1clades	44	DAC23_45	Bacteroides phage DAC23	GCA_013387745.1
QIG63374.1	003721	Cluster3358_1clades	44	DAC16_141	Bacteroides phage DAC16	GCA_013387695.1
QIG63639.1	003721	Cluster3358_1clades	44	DAC19_148	Bacteroides phage DAC19	GCA_013387715.1
QIG63900.1	003721	Cluster3358_1clades	44	DAC20_147	Bacteroides phage DAC20	GCA_013387725.1
QIG64163.1	003721	Cluster3358_1clades	44	DAC22_149	Bacteroides phage DAC22	GCA_013387735.1
QIG64420.1	003721	Cluster3358_1clades	44	DAC23_142	Bacteroides phage DAC23	GCA_013387745.1
QIG63424.1	003722	Cluster3359_1clades	43	DAC16_194	Bacteroides phage DAC16	GCA_013387695.1
QIG63688.1	003722	Cluster3359_1clades	43	DAC19_200	Bacteroides phage DAC19	GCA_013387715.1
QIG63949.1	003722	Cluster3359_1clades	43	DAC20_199	Bacteroides phage DAC20	GCA_013387725.1
QIG64213.1	003722	Cluster3359_1clades	43	DAC22_202	Bacteroides phage DAC22	GCA_013387735.1
QIG64469.1	003722	Cluster3359_1clades	43	DAC23_194	Bacteroides phage DAC23	GCA_013387745.1
QGZ14372.1	003723	TM	42	HWC77_gp009	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04364.1	003723	TM	42	HWC03_gp209	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23212.1	003723	TM	42	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81104.1	003723	TM	42	Aphrodite1_0133	Vibrio phage Aphrodite1	GCA_002958015.1
QDH47516.1	003723	TM	42	HWC35_gp122	Vibrio phage USC-1	GCA_006864065.1
AFC21941.1	003724	Cluster3361_1clades	39	GAP32_483	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44068.1	003724	Cluster3361_1clades	39	CBB_505	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89023.1	003724	Cluster3361_1clades	40	BF_0498	Serratia phage BF	GCA_002619745.1
SOK59304.1	003724	Cluster3361_1clades	39	g496	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58769.1	003724	Cluster3361_1clades	39	g492	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QIG63286.1	003725	Cluster3362_1clades	39	DAC16_53	Bacteroides phage DAC16	GCA_013387695.1
QIG63545.1	003725	Cluster3362_1clades	40	DAC19_54	Bacteroides phage DAC19	GCA_013387715.1
QIG63806.1	003725	Cluster3362_1clades	40	DAC20_53	Bacteroides phage DAC20	GCA_013387725.1
QIG64067.1	003725	Cluster3362_1clades	40	DAC22_53	Bacteroides phage DAC22	GCA_013387735.1
QIG64331.1	003725	Cluster3362_1clades	39	DAC23_53	Bacteroides phage DAC23	GCA_013387745.1
AIT14090.1	003726	Cluster3363_1clades	37	PBI_121Q_200	Escherichia phage 121Q	GCA_000926855.1
AGC35004.1	003726	Cluster3363_1clades	37	ACQ29_gp324	Escherichia phage PBECO4	GCA_001041035.1
QBO61609.1	003726	Cluster3363_1clades	37	G17_00113	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13667.1	003726	Cluster3363_1clades	37	vBEcoMphAPEC6_gp036c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80084.1	003726	Cluster3363_1clades	37	PSLUR01_00107	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QIG63385.1	003727	Cluster3364_1clades	36	DAC16_155	Bacteroides phage DAC16	GCA_013387695.1
QIG63648.1	003727	Cluster3364_1clades	31	DAC19_160	Bacteroides phage DAC19	GCA_013387715.1
QIG63909.1	003727	Cluster3364_1clades	31	DAC20_159	Bacteroides phage DAC20	GCA_013387725.1
QIG64173.1	003727	Cluster3364_1clades	31	DAC22_162	Bacteroides phage DAC22	GCA_013387735.1
QIG64429.1	003727	Cluster3364_1clades	36	DAC23_154	Bacteroides phage DAC23	GCA_013387745.1
QIG63301.1	003728	Cluster3365_1clades	35	DAC16_68	Bacteroides phage DAC16	GCA_013387695.1
QIG63560.1	003728	Cluster3365_1clades	35	DAC19_69	Bacteroides phage DAC19	GCA_013387715.1
QIG63821.1	003728	Cluster3365_1clades	35	DAC20_68	Bacteroides phage DAC20	GCA_013387725.1
QIG64083.1	003728	Cluster3365_1clades	35	DAC22_69	Bacteroides phage DAC22	GCA_013387735.1
QIG64346.1	003728	Cluster3365_1clades	35	DAC23_68	Bacteroides phage DAC23	GCA_013387745.1
AMO43406.1	003729	Cluster3366_1clades	28	W270710_162	Cyanophage S-RIM44	GCA_002599145.1
AOO11878.1	003729	Cluster3366_1clades	28	Np050604_162	Cyanophage S-RIM44	GCA_002599185.1
AOO12579.1	003729	Cluster3366_1clades	28	Sn080709_162	Cyanophage S-RIM44	GCA_002599245.1
AOO13045.1	003729	Cluster3366_1clades	28	W2100709_163	Cyanophage S-RIM44	GCA_002599285.1
ADO99265.1	003729	Cluster3366_1clades	28	Syn1_164	Prochlorococcus phage Syn1	GCA_000892495.1
ARB14306.1	003730	Cluster3367_1clades	24	Ccr5_gp088	Caulobacter phage Ccr5	GCA_002619545.1
AFU87608.1	003730	Cluster3367_1clades	24	CcrKarma_gp091	Caulobacter virus Karma	GCA_000901575.1
AFU87257.1	003730	Cluster3367_1clades	24	CcrMagneto_gp087	Caulobacter virus Magneto	GCA_000903095.1
AFU88404.1	003730	Cluster3367_1clades	24	CcrSwift_gp086	Caulobacter virus Swift	GCA_000899655.1
AFU86922.1	003730	Cluster3367_1clades	24	CbK_gp090	Caulobacter virus phiCbK	GCA_000900535.1
QAX96796.1	003731	Laminin_G_3	1901	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97115.1	003731	Laminin_G_3	1901	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96161.1	003731	Laminin_G_3	1901	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96479.1	003731	Laminin_G_3	1901	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AEO93682.1	003732	IG	1540	G_424	Bacillus virus G	GCA_000917535.1
AEO93683.1	003732	IG	1198	G_425	Bacillus virus G	GCA_000917535.1
AEO93684.1	003732	IG	1131	G_426	Bacillus virus G	GCA_000917535.1
AEO93685.1	003732	IG	1826	G_427	Bacillus virus G	GCA_000917535.1
AYD81223.1	003733	VirB5+TM+TM	1740	SEA_JUSTBECAUSE_54	Streptomyces phage JustBecause	GCA_003613775.1
QJD53626.1	003733	VirB5+TM+TM	1740	SEA_KELA_55	Streptomyces phage Kela	GCA_012934305.1
QBZ71958.1	003733	VirB5+TM+TM	1738	SEA_KRADAL_60	Streptomyces phage Kradal	GCA_004799925.1
AXH66221.1	003733	VirB5+TM+TM	1738	SEA_SATIS_60	Streptomyces phage Satis	GCA_003366315.1
QDH83709.1	003734	Cluster3372_1clades	911	H1O15_gp119	Achromobacter phage Motura	GCA_006964305.1
QBX06694.1	003734	Cluster3372_1clades	774	BcepSaruman_281	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74662.1	003734	Cluster3372_1clades	774	BcepSauron_282	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41630.1	003734	Cluster3372_1clades	1586	RSL1_ORF182	Ralstonia phage phiRSL1	GCA_000879455.1
AFF28263.1	003735	Cluster3375_1clades	1262	PAU_265	Sphingomonas phage PAU	GCA_000902455.1
BBI90687.1	003735	Cluster3375_1clades	1020	HYO65_gp295	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90994.1	003735	Cluster3375_1clades	1020	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39271.1	003735	Cluster3375_1clades	1478	BPT24_145	Tenacibaculum phage pT24	GCA_002611925.1
QAX96798.1	003736	Cluster3376_1clades	1455	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97117.1	003736	Cluster3376_1clades	1455	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96163.1	003736	Cluster3376_1clades	1455	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96481.1	003736	Cluster3376_1clades	1455	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BBA65520.1	003737	SIG+IG	1088	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65518.1	003737	SIG+IG	1317	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96375.1	003737	SIG+IG	996	Xoosp13_189	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96518.1	003737	SIG+IG	1439	Xoosp13_332	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDH83713.1	003738	DUF3751	949	H1O15_gp114	Achromobacter phage Motura	GCA_006964305.1
QBX06700.1	003738	DUF3751	811	BcepSaruman_287	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74668.1	003738	DUF3751	811	BcepSauron_288	Burkholderia phage BcepSauron	GCA_005394215.1
AYD81225.1	003739	Cluster3381_1clades	1105	SEA_JUSTBECAUSE_56	Streptomyces phage JustBecause	GCA_003613775.1
QJD53628.1	003739	Cluster3381_1clades	1105	SEA_KELA_57	Streptomyces phage Kela	GCA_012934305.1
QBZ71960.1	003739	Cluster3381_1clades	1108	SEA_KRADAL_62	Streptomyces phage Kradal	GCA_004799925.1
AXH66223.1	003739	Cluster3381_1clades	1108	SEA_SATIS_62	Streptomyces phage Satis	GCA_003366315.1
AGR47767.1	003740	Cluster3383_1clades	1007	SmphiM12_135	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12999.1	003740	Cluster3383_1clades	1007	PHIM19_93	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12639.1	003740	Cluster3383_1clades	1006	PHIM7_92	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13372.1	003740	Cluster3383_1clades	1006	PHIN3_107	Sinorhizobium phage phiN3	GCA_001501175.1
BBI90419.1	003741	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	391	HYO65_gp027	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90420.1	003741	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	492	HYO65_gp028	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90727.1	003741	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	883	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39243.1	003741	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	925	BPT24_118	Tenacibaculum phage pT24	GCA_002611925.1
QAX96632.1	003742	Cluster3387_1clades	911	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96950.1	003742	Cluster3387_1clades	911	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95996.1	003742	Cluster3387_1clades	911	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96314.1	003742	Cluster3387_1clades	911	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMS01296.1	003743	Cluster3388_1clades	904	AR9_g212	Bacillus phage AR9	GCA_001743835.1
ALN97947.1	003743	Cluster3388_1clades	903	Bp8pS_268	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99925.1	003743	Cluster3388_1clades	904	PBI_PBS1_103	Bacillus virus PBS1	GCA_002601325.1
CCE26230.1	003743	Cluster3388_1clades	863	g207	Yersinia phage phiR1-37	GCA_000895615.1
AMS01344.1	003744	Cluster3390_1clades	738	AR9_g260	Bacillus phage AR9	GCA_001743835.1
ALN97996.1	003744	Cluster3390_1clades	734	Bp8pS_317	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99974.1	003744	Cluster3390_1clades	738	PBI_PBS1_153	Bacillus virus PBS1	GCA_002601325.1
CCE26257.1	003744	Cluster3390_1clades	864	g234	Yersinia phage phiR1-37	GCA_000895615.1
ASU03720.1	003745	SUN	796	JOAD_195	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03718.1	003745	SUN	819	JOAD_197	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03477.1	003745	SUN	796	RISINGSUN_193	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03475.1	003745	SUN	819	RISINGSUN_195	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AGR48030.1	003746	GDSL+IG	775	SmphiM12_398	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13213.1	003746	GDSL+IG	775	PHIM19_308	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12854.1	003746	GDSL+IG	775	PHIM7_308	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13575.1	003746	GDSL+IG	775	PHIN3_312	Sinorhizobium phage phiN3	GCA_001501175.1
QBX06691.1	003747	Cluster3394_1clades	750	BcepSaruman_278	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74659.1	003747	Cluster3394_1clades	750	BcepSauron_279	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41633.1	003747	Cluster3394_1clades	735	RSL1_ORF184	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41632.1	003747	Cluster3394_1clades	762	RSL1_ORF183	Ralstonia phage phiRSL1	GCA_000879455.1
QDJ96660.1	003748	Beta-helix	755	PS1_0149	Aeromonas phage PS1	GCA_007051165.2
QDJ96679.1	003748	Beta-helix	712	PS1_0168	Aeromonas phage PS1	GCA_007051165.2
QFR59293.1	003748	Beta-helix	654	PS2_0152	Aeromonas phage PS2	GCA_009388305.2
QFR59314.1	003748	Beta-helix	712	PS2_0173	Aeromonas phage PS2	GCA_009388305.2
QBX32544.1	003749	Cdh1_DBD_1	250	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77091.1	003749	Cdh1_DBD_1	736	PHABIO_463	Pseudomonas phage Phabio	GCA_002624965.1
AEH03798.1	003749	Cdh1_DBD_1	233	375	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42115.1	003749	Cdh1_DBD_1	250	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGR48023.1	003750	Cluster3400_1clades	727	SmphiM12_391	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13208.1	003750	Cluster3400_1clades	727	PHIM19_303	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12849.1	003750	Cluster3400_1clades	727	PHIM7_303	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13570.1	003750	Cluster3400_1clades	727	PHIN3_307	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47734.1	003751	SIG+Beta-helix	703	SmphiM12_102	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12986.1	003751	SIG+Beta-helix	703	PHIM19_79	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12626.1	003751	SIG+Beta-helix	703	PHIM7_78	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13358.1	003751	SIG+Beta-helix	703	PHIN3_94	Sinorhizobium phage phiN3	GCA_001501175.1
AXH70933.1	003752	Cluster3402_1clades	701	-	Vibrio phage BONAISHI	GCA_003441475.1
QAX96834.1	003752	Cluster3402_1clades	452	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96198.1	003752	Cluster3402_1clades	652	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96516.1	003752	Cluster3402_1clades	652	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ATA65471.1	003753	Cluster3403_1clades	683	2050HW_00136	Serratia phage 2050HW	GCA_002628125.1
ATA65472.1	003753	Cluster3403_1clades	688	2050HW_00137	Serratia phage 2050HW	GCA_002628125.1
QDB71240.1	003753	Cluster3403_1clades	683	CPT_Moabite_210	Serratia phage Moabite	GCA_006384735.1
QDB71241.1	003753	Cluster3403_1clades	688	CPT_Moabite_211	Serratia phage Moabite	GCA_006384735.1
AGX01744.1	003754	Cluster3404_1clades	656	CF95_gp022	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65645.1	003754	Cluster3404_1clades	285	2050HW_00310	Serratia phage 2050HW	GCA_002628125.1
QDB71072.1	003754	Cluster3404_1clades	610	CPT_Moabite_040	Serratia phage Moabite	GCA_006384735.1
QFP93061.1	003754	Cluster3404_1clades	659	-	Serratia phage PCH45	GCA_009187865.1
AYD81494.1	003755	Cluster3406_1clades	643	SEA_JUSTBECAUSE_339	Streptomyces phage JustBecause	GCA_003613775.1
QJD53897.1	003755	Cluster3406_1clades	649	SEA_KELA_337	Streptomyces phage Kela	GCA_012934305.1
QBZ72222.1	003755	Cluster3406_1clades	513	SEA_KRADAL_336	Streptomyces phage Kradal	GCA_004799925.1
AXH66485.1	003755	Cluster3406_1clades	513	SEA_SATIS_336	Streptomyces phage Satis	GCA_003366315.1
QAX96697.1	003756	Cluster3407_1clades	634	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97015.1	003756	Cluster3407_1clades	634	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96061.1	003756	Cluster3407_1clades	634	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96379.1	003756	Cluster3407_1clades	634	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR48090.2	003757	Cluster3408_1clades	602	SmphiM12_458	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13260.1	003757	Cluster3408_1clades	602	PHIM19_355	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12900.1	003757	Cluster3408_1clades	602	PHIM7_355	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13623.1	003757	Cluster3408_1clades	602	PHIN3_360	Sinorhizobium phage phiN3	GCA_001501175.1
QAX96675.1	003758	Cluster3409_1clades	601	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96993.1	003758	Cluster3409_1clades	601	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96039.1	003758	Cluster3409_1clades	601	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96357.1	003758	Cluster3409_1clades	601	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81191.1	003759	Cluster3410_1clades	579	SEA_JUSTBECAUSE_22	Streptomyces phage JustBecause	GCA_003613775.1
QJD53593.1	003759	Cluster3410_1clades	579	SEA_KELA_22	Streptomyces phage Kela	GCA_012934305.1
QBZ71925.1	003759	Cluster3410_1clades	576	SEA_KRADAL_26	Streptomyces phage Kradal	GCA_004799925.1
AXH66187.1	003759	Cluster3410_1clades	576	SEA_SATIS_26	Streptomyces phage Satis	GCA_003366315.1
ARM70868.1	003760	SIG+Pkinase	561	phiC120_c163	Escherichia phage phiC120	GCA_002621185.1
AFF28213.1	003760	SIG+Pkinase	576	PAU_215	Sphingomonas phage PAU	GCA_000902455.1
BBI90557.1	003760	SIG+Pkinase	521	HYO65_gp165	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90865.1	003760	SIG+Pkinase	521	-	Tenacibaculum phage PTm5	GCA_009730715.1
AGR47798.1	003761	Cluster3412_1clades	567	SmphiM12_166	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13015.1	003761	Cluster3412_1clades	567	PHIM19_109	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12655.1	003761	Cluster3412_1clades	567	PHIM7_108	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13387.1	003761	Cluster3412_1clades	568	PHIN3_122	Sinorhizobium phage phiN3	GCA_001501175.1
BAW19123.1	003762	Cluster3413_1clades	553	FDH28_gp272	Ralstonia phage RP12	GCA_002617345.1
BAW19122.1	003762	Cluster3413_1clades	561	FDH28_gp273	Ralstonia phage RP12	GCA_002617345.1
BAW19408.1	003762	Cluster3413_1clades	561	-	Ralstonia phage RP31	GCA_002617365.1
BAW19409.1	003762	Cluster3413_1clades	565	-	Ralstonia phage RP31	GCA_002617365.1
AEO93508.1	003763	SIG+PBPB+OmpA	525	G_249	Bacillus virus G	GCA_000917535.1
AEO93509.1	003763	SIG+PBPB+OmpA	518	G_250	Bacillus virus G	GCA_000917535.1
prevph1000000422	003763	SIG+PBPB+OmpA	528	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000333	003763	SIG+PBPB+OmpA	528	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFF28012.1	003764	Cluster3416_1clades	466	PAU_14	Sphingomonas phage PAU	GCA_000902455.1
BBI90563.1	003764	Cluster3416_1clades	465	HYO65_gp171	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90871.1	003764	Cluster3416_1clades	465	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39365.1	003764	Cluster3416_1clades	524	BPT24_245	Tenacibaculum phage pT24	GCA_002611925.1
AGR47776.1	003765	Peptidase-M15	520	SmphiM12_144	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13004.1	003765	Peptidase-M15	520	PHIM19_98	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12644.1	003765	Peptidase-M15	520	PHIM7_97	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13376.1	003765	Peptidase-M15	520	PHIN3_111	Sinorhizobium phage phiN3	GCA_001501175.1
QAX96795.1	003766	Cluster3418_1clades	520	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97114.1	003766	Cluster3418_1clades	520	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96160.1	003766	Cluster3418_1clades	520	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96478.1	003766	Cluster3418_1clades	520	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFF28065.1	003767	Cluster3423_1clades	492	PAU_67	Sphingomonas phage PAU	GCA_000902455.1
BBI90501.1	003767	Cluster3423_1clades	497	HYO65_gp109	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90809.1	003767	Cluster3423_1clades	497	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39222.1	003767	Cluster3423_1clades	489	BPT24_097	Tenacibaculum phage pT24	GCA_002611925.1
AGX01865.1	003768	XpaC	496	CF95_gp143	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65439.1	003768	XpaC	493	2050HW_00104	Serratia phage 2050HW	GCA_002628125.1
QDB71210.1	003768	XpaC	493	CPT_Moabite_180	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFP93074.1	003768	XpaC	495	-	Serratia phage PCH45	GCA_009187865.1
QAX96807.1	003769	Cluster3425_1clades	496	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97126.1	003769	Cluster3425_1clades	496	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96172.1	003769	Cluster3425_1clades	496	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96490.1	003769	Cluster3425_1clades	496	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01948.1	003770	SIG+phiKZ_IP	458	CF95_gp226	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65356.1	003770	SIG+phiKZ_IP	484	2050HW_00021	Serratia phage 2050HW	GCA_002628125.1
QDB71143.1	003770	SIG+phiKZ_IP	484	CPT_Moabite_113	Serratia phage Moabite	GCA_006384735.1
QFP93078.1	003770	SIG+phiKZ_IP	469	-	Serratia phage PCH45	GCA_009187865.1
QAX96634.1	003771	TM	483	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96952.1	003771	TM	483	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95998.1	003771	TM	483	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96316.1	003771	TM	483	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96653.1	003772	PTSEIIB	481	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96971.1	003772	PTSEIIB	481	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96017.1	003772	PTSEIIB	481	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96335.1	003772	PTSEIIB	481	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BAW19211.1	003773	phiKZ_IP	433	FDH28_gp184	Ralstonia phage RP12	GCA_002617345.1
BAW19212.1	003773	phiKZ_IP	479	FDH28_gp183	Ralstonia phage RP12	GCA_002617345.1
BAW19497.1	003773	phiKZ_IP	433	-	Ralstonia phage RP31	GCA_002617365.1
BAW19498.1	003773	phiKZ_IP	479	-	Ralstonia phage RP31	GCA_002617365.1
AYD81274.1	003774	SIG+TM+TM+HIN-HTH	477	SEA_JUSTBECAUSE_105	Streptomyces phage JustBecause	GCA_003613775.1
QJD53677.1	003774	SIG+TM+TM+HIN-HTH	477	SEA_KELA_106	Streptomyces phage Kela	GCA_012934305.1
QBZ72005.1	003774	SIG+TM+TM+HIN-HTH	472	SEA_KRADAL_107	Streptomyces phage Kradal	GCA_004799925.1
AXH66268.1	003774	SIG+TM+TM+HIN-HTH	472	SEA_SATIS_107	Streptomyces phage Satis	GCA_003366315.1
QDH83645.1	003775	PAT1	438	H1O15_gp143	Achromobacter phage Motura	GCA_006964305.1
QBX06666.1	003775	PAT1	476	BcepSaruman_253	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74636.1	003775	PAT1	476	BcepSauron_256	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41656.1	003775	PAT1	384	RSL1_ORF207	Ralstonia phage phiRSL1	GCA_000879455.1
AMS01315.1	003776	Cluster3432_1clades	398	AR9_g231	Bacillus phage AR9	GCA_001743835.1
ALN97965.1	003776	Cluster3432_1clades	389	Bp8pS_286	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99944.1	003776	Cluster3432_1clades	398	PBI_PBS1_122	Bacillus virus PBS1	GCA_002601325.1
CCE26264.1	003776	Cluster3432_1clades	475	g241	Yersinia phage phiR1-37	GCA_000895615.1
QAX96759.1	003777	Cluster3433_1clades	474	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97078.1	003777	Cluster3433_1clades	474	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96124.1	003777	Cluster3433_1clades	474	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96442.1	003777	Cluster3433_1clades	474	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96882.1	003778	Cluster3434_1clades	469	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97187.1	003778	Cluster3434_1clades	469	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96246.1	003778	Cluster3434_1clades	469	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96564.1	003778	Cluster3434_1clades	469	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANS05994.1	003779	Phage_tail_NK	233	ABCD_0127	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AGC34683.1	003779	Phage_tail_NK	455	ACQ29_gp003	Escherichia phage PBECO4	GCA_001041035.1
AXC36803.1	003779	Phage_tail_NK	455	-	Escherichia phage UB	GCA_003341455.1
AAX78650.1	003779	Phage_tail_NK	233	RB43ORF128w	Escherichia virus RB43	GCA_000863505.1
QAX96646.1	003780	Cluster3437_1clades	442	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96964.1	003780	Cluster3437_1clades	442	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96010.1	003780	Cluster3437_1clades	442	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96328.1	003780	Cluster3437_1clades	442	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMM44944.1	003781	UDPG_MGDP_dh_N+UDPG_MGDP_dh	436	SP15_146	Bacillus phage SP-15	GCA_001754685.1
AGH07571.1	003781	UDPG_MGDP_dh_N+UDPG_MGDP_dh	383	CYVG_00127	Cyanophage S-SSM6a	GCA_002710385.1
AIR93517.1	003781	UDPG_MGDP_dh_N+UDPG_MGDP_dh	374	AVU42_gp180	Prochlorococcus phage P-TIM68	GCA_001503075.1
QHJ86049.1	003781	UDPG_MGDP_dh_N+UDPG_MGDP_dh	442	KKIINIFJ_00137	Pseudomonas phage PN05	GCA_009931935.1
AMS01249.1	003782	Cluster3439_1clades	395	AR9_g165	Bacillus phage AR9	GCA_001743835.1
ALN97906.1	003782	Cluster3439_1clades	397	Bp8pS_227	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99875.1	003782	Cluster3439_1clades	395	PBI_PBS1_53	Bacillus virus PBS1	GCA_002601325.1
CCE26152.1	003782	Cluster3439_1clades	440	g128	Yersinia phage phiR1-37	GCA_000895615.1
QAX96934.1	003783	Cluster3440_1clades	440	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97239.1	003783	Cluster3440_1clades	440	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96298.1	003783	Cluster3440_1clades	440	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96616.1	003783	Cluster3440_1clades	440	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BAS04971.1	003784	TM	436	AVU11_gp179	Ralstonia phage RSF1	GCA_001500875.1
BAS04972.1	003784	TM	438	AVU11_gp180	Ralstonia phage RSF1	GCA_001500875.1
BAQ02697.2	003784	TM	427	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02698.1	003784	TM	438	AVU38_gp170	Ralstonia phage RSL2	GCA_001503055.1
AYD81194.1	003785	Mu-like-gpT	437	SEA_JUSTBECAUSE_25	Streptomyces phage JustBecause	GCA_003613775.1
QJD53596.1	003785	Mu-like-gpT	437	SEA_KELA_25	Streptomyces phage Kela	GCA_012934305.1
QBZ71928.1	003785	Mu-like-gpT	437	SEA_KRADAL_29	Streptomyces phage Kradal	GCA_004799925.1
AXH66190.1	003785	Mu-like-gpT	437	SEA_SATIS_29	Streptomyces phage Satis	GCA_003366315.1
AFF28127.1	003786	Cluster3443_1clades	420	PAU_129	Sphingomonas phage PAU	GCA_000902455.1
BBI90638.1	003786	Cluster3443_1clades	298	HYO65_gp246	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90945.1	003786	Cluster3443_1clades	298	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39301.1	003786	Cluster3443_1clades	436	BPT24_175	Tenacibaculum phage pT24	GCA_002611925.1
AOV59653.1	003787	Cluster3444_1clades	434	S330809_192	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59654.1	003787	Cluster3444_1clades	427	S330809_193	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59415.1	003787	Cluster3444_1clades	434	C440309_192	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59416.1	003787	Cluster3444_1clades	427	C440309_193	Synechococcus phage S-CAM4	GCA_002922145.1
QDH83631.1	003788	Cluster3445_1clades	434	H1O15_gp157	Achromobacter phage Motura	GCA_006964305.1
QBX06508.1	003788	Cluster3445_1clades	278	BcepSaruman_095	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74474.1	003788	Cluster3445_1clades	278	BcepSauron_094	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41561.1	003788	Cluster3445_1clades	215	RSL1_ORF116	Ralstonia phage phiRSL1	GCA_000879455.1
AYD81309.1	003789	FTSK	432	SEA_JUSTBECAUSE_144	Streptomyces phage JustBecause	GCA_003613775.1
QJD53712.1	003789	FTSK	432	SEA_KELA_142	Streptomyces phage Kela	GCA_012934305.1
QBZ72039.1	003789	FTSK	433	SEA_KRADAL_143	Streptomyces phage Kradal	GCA_004799925.1
AXH66302.1	003789	FTSK	433	SEA_SATIS_143	Streptomyces phage Satis	GCA_003366315.1
QAX96659.1	003790	Cluster3447_1clades	431	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96977.1	003790	Cluster3447_1clades	431	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96023.1	003790	Cluster3447_1clades	431	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96341.1	003790	Cluster3447_1clades	431	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83632.1	003791	AvrE	423	H1O15_gp156	Achromobacter phage Motura	GCA_006964305.1
QBX06509.1	003791	AvrE	411	BcepSaruman_096	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74475.1	003791	AvrE	411	BcepSauron_095	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41560.1	003791	AvrE	426	RSL1_ORF115	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96645.1	003792	Cluster3450_1clades	421	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96963.1	003792	Cluster3450_1clades	421	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96009.1	003792	Cluster3450_1clades	421	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96327.1	003792	Cluster3450_1clades	421	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67357.1	003793	SIG+CP-ATPgrasp	410	AD1_313	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08581.1	003793	SIG+CP-ATPgrasp	418	Alexandra_330	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58956.1	003793	SIG+CP-ATPgrasp	411	Y3_316	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28783.1	003793	SIG+CP-ATPgrasp	359	YOLOSWAG_314	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81234.1	003794	Cluster3452_1clades	416	SEA_JUSTBECAUSE_65	Streptomyces phage JustBecause	GCA_003613775.1
QJD53637.1	003794	Cluster3452_1clades	416	SEA_KELA_66	Streptomyces phage Kela	GCA_012934305.1
QBZ71968.1	003794	Cluster3452_1clades	411	SEA_KRADAL_70	Streptomyces phage Kradal	GCA_004799925.1
AXH66231.1	003794	Cluster3452_1clades	411	SEA_SATIS_70	Streptomyces phage Satis	GCA_003366315.1
AFO71307.1	003795	Cluster3453_1clades	415	CR5_087	Cronobacter phage CR5	GCA_000910235.1
QBP07516.1	003795	Cluster3453_1clades	415	DERBICUS_90	Erwinia phage Derbicus	GCA_004521655.1
ANZ48939.1	003795	Cluster3453_1clades	415	EARLPHILLIPIV_90	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50280.1	003795	Cluster3453_1clades	415	PHOBOS_90	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QAX96896.1	003796	Cluster3454_1clades	413	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97201.1	003796	Cluster3454_1clades	413	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96260.1	003796	Cluster3454_1clades	413	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96578.1	003796	Cluster3454_1clades	413	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMS01356.1	003797	PG-binding+PG-binding+PG-binding	404	AR9_g272	Bacillus phage AR9	GCA_001743835.1
AMM44867.1	003797	PG-binding+PG-binding+PG-binding	313	SP15_068	Bacillus phage SP-15	GCA_001754685.1
ALN97698.1	003797	PG-binding+PG-binding+PG-binding	406	Bp8pS_019	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99986.1	003797	PG-binding+PG-binding+PG-binding	404	PBI_PBS1_165	Bacillus virus PBS1	GCA_002601325.1
QAX96783.1	003798	Cluster3456_1clades	406	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97102.1	003798	Cluster3456_1clades	406	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96148.1	003798	Cluster3456_1clades	406	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96466.1	003798	Cluster3456_1clades	406	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR47814.1	003799	LEVANB	405	SmphiM12_182	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13028.1	003799	LEVANB	405	PHIM19_123	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12668.1	003799	LEVANB	405	PHIM7_122	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13399.1	003799	LEVANB	405	PHIN3_136	Sinorhizobium phage phiN3	GCA_001501175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96922.1	003800	Cluster3458_1clades	404	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97227.1	003800	Cluster3458_1clades	404	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96286.1	003800	Cluster3458_1clades	404	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96604.1	003800	Cluster3458_1clades	404	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXQ69464.1	003801	Cluster3459_1clades	145	CcrBL9_gp440	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88037.1	003801	Cluster3459_1clades	402	CcrColossus_gp167	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68714.1	003801	Cluster3459_1clades	402	CcrPW_gp175c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70013.1	003801	Cluster3459_1clades	145	CcrSC_gp431	Caulobacter phage CcrSC	GCA_003443315.1
ABS83795.1	003802	LysM+LysM+LysM	368	0305phi8-36p237	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01279.1	003802	LysM+LysM+LysM	390	AR9_g195	Bacillus phage AR9	GCA_001743835.1
ALN97934.1	003802	LysM+LysM+LysM	402	Bp8pS_255	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99907.1	003802	LysM+LysM+LysM	390	PBI_PBS1_85	Bacillus virus PBS1	GCA_002601325.1
QAX96713.1	003803	Cluster3461_1clades	401	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97032.1	003803	Cluster3461_1clades	401	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96078.1	003803	Cluster3461_1clades	401	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96396.1	003803	Cluster3461_1clades	401	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44800.1	003804	Cluster3462_1clades	398	KTN4_042	Pseudomonas phage KTN4	GCA_002607225.1
ATN94911.1	003804	Cluster3462_1clades	398	SL2_334	Pseudomonas phage SL2	GCA_002956015.1
QJB22679.1	003804	Cluster3462_1clades	398	fnug_36	Pseudomonas phage fnug	GCA_012837215.1
AAL82932.1	003804	Cluster3462_1clades	398	PHIKZ031	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96895.1	003805	Cluster3463_1clades	393	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97200.1	003805	Cluster3463_1clades	393	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96259.1	003805	Cluster3463_1clades	393	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96577.1	003805	Cluster3463_1clades	393	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96684.1	003806	Cluster3465_1clades	391	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97002.1	003806	Cluster3465_1clades	391	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96048.1	003806	Cluster3465_1clades	391	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96366.1	003806	Cluster3465_1clades	391	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX32202.1	003807	Cluster3467_1clades	389	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76706.1	003807	Cluster3467_1clades	264	PHABIO_75	Pseudomonas phage Phabio	GCA_002624965.1
AEH03476.1	003807	Cluster3467_1clades	374	049	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41779.1	003807	Cluster3467_1clades	389	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AMS01137.1	003808	Cluster3468_1clades	386	AR9_g052	Bacillus phage AR9	GCA_001743835.1
ALN97807.1	003808	Cluster3468_1clades	387	Bp8pS_128	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00064.1	003808	Cluster3468_1clades	387	PBI_PBS1_242	Bacillus virus PBS1	GCA_002601325.1
CCE26228.1	003808	Cluster3468_1clades	386	g205	Yersinia phage phiR1-37	GCA_000895615.1
AYD81235.1	003809	DUF3106	387	SEA_JUSTBECAUSE_66	Streptomyces phage JustBecause	GCA_003613775.1
QJD53638.1	003809	DUF3106	387	SEA_KELA_67	Streptomyces phage Kela	GCA_012934305.1
QBZ71969.1	003809	DUF3106	386	SEA_KRADAL_71	Streptomyces phage Kradal	GCA_004799925.1
AXH66232.1	003809	DUF3106	386	SEA_SATIS_71	Streptomyces phage Satis	GCA_003366315.1
QAX96909.1	003810	SIG+TM+TM+TM+TM	383	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97214.1	003810	SIG+TM+TM+TM+TM	383	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96273.1	003810	SIG+TM+TM+TM+TM	383	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96591.1	003810	SIG+TM+TM+TM+TM	383	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD80004.1	003811	Cluster3471_1clades	362	JA11_199	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66602.1	003811	Cluster3471_1clades	379	JA13_199	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66927.1	003811	Cluster3471_1clades	379	JA29_201	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67573.1	003811	Cluster3471_1clades	362	JA33_199	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ANM45022.1	003812	Cluster3472_1clades	377	KTN4_264	Pseudomonas phage KTN4	GCA_002607225.1
ATN94692.1	003812	Cluster3472_1clades	377	SL2_115	Pseudomonas phage SL2	GCA_002956015.1
QJB22899.1	003812	Cluster3472_1clades	377	fnug_256	Pseudomonas phage fnug	GCA_012837215.1
AAL83120.1	003812	Cluster3472_1clades	377	PHIKZ219	Pseudomonas virus phiKZ	GCA_000842965.1
BBI90475.1	003813	Cluster3473_1clades	369	HYO65_gp083	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90781.1	003813	Cluster3473_1clades	157	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90782.1	003813	Cluster3473_1clades	192	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39332.1	003813	Cluster3473_1clades	372	BPT24_208	Tenacibaculum phage pT24	GCA_002611925.1
AYD81398.1	003814	Cluster3474_1clades	371	SEA_JUSTBECAUSE_243	Streptomyces phage JustBecause	GCA_003613775.1
QJD53802.1	003814	Cluster3474_1clades	371	SEA_KELA_242	Streptomyces phage Kela	GCA_012934305.1
QBZ72128.1	003814	Cluster3474_1clades	370	SEA_KRADAL_242	Streptomyces phage Kradal	GCA_004799925.1
AXH66390.1	003814	Cluster3474_1clades	370	SEA_SATIS_241	Streptomyces phage Satis	GCA_003366315.1
QBO63880.1	003815	Cluster3475_1clades	213	Goslar_00087	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ATA65397.1	003815	Cluster3475_1clades	175	2050HW_00062	Serratia phage 2050HW	GCA_002628125.1
QDB71177.1	003815	Cluster3475_1clades	175	CPT_Moabite_147	Serratia phage Moabite	GCA_006384735.1
QFP93093.1	003815	Cluster3475_1clades	370	-	Serratia phage PCH45	GCA_009187865.1
ANS05960.1	003816	T4_tail_cap	361	ABCD_0105	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97115.1	003816	T4_tail_cap	361	E_107	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70753.1	003816	T4_tail_cap	369	phiC120_c47	Escherichia phage phiC120	GCA_002621185.1
AAX78627.1	003816	T4_tail_cap	361	RB43ORF105w	Escherichia virus RB43	GCA_000863505.1
QAX96725.1	003817	SIG+TM	369	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97044.1	003817	SIG+TM	369	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96090.1	003817	SIG+TM	369	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96408.1	003817	SIG+TM	369	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96722.1	003818	Cluster3479_1clades	366	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97041.1	003818	Cluster3479_1clades	366	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96087.1	003818	Cluster3479_1clades	366	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96405.1	003818	Cluster3479_1clades	366	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81285.1	003819	SIG+LysM+PG-binding	361	SEA_JUSTBECAUSE_116	Streptomyces phage JustBecause	GCA_003613775.1
QJD53688.1	003819	SIG+LysM+PG-binding	361	SEA_KELA_117	Streptomyces phage Kela	GCA_012934305.1
QBZ72016.1	003819	SIG+LysM+PG-binding	361	SEA_KRADAL_118	Streptomyces phage Kradal	GCA_004799925.1
AXH66279.1	003819	SIG+LysM+PG-binding	361	SEA_SATIS_118	Streptomyces phage Satis	GCA_003366315.1
QAX96841.1	003820	Cluster3483_1clades	361	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97146.1	003820	Cluster3483_1clades	361	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96205.1	003820	Cluster3483_1clades	361	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96523.1	003820	Cluster3483_1clades	361	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96857.1	003821	Cluster3484_1clades	360	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97162.1	003821	Cluster3484_1clades	360	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96221.1	003821	Cluster3484_1clades	360	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96539.1	003821	Cluster3484_1clades	360	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83410.1	003822	Cluster3485_1clades	352	H1O15_gp001	Achromobacter phage Motura	GCA_006964305.1
QBX06714.1	003822	Cluster3485_1clades	360	BcepSaruman_301	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74682.1	003822	Cluster3485_1clades	360	BcepSauron_302	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41603.1	003822	Cluster3485_1clades	355	RSL1_ORF157	Ralstonia phage phiRSL1	GCA_000879455.1
AYD79903.1	003823	Cluster3486_1clades	356	JA11_098	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66502.1	003823	Cluster3486_1clades	356	JA13_099	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66827.1	003823	Cluster3486_1clades	356	JA29_101	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67472.1	003823	Cluster3486_1clades	356	JA33_098	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96846.1	003824	Cluster3487_1clades	356	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97151.1	003824	Cluster3487_1clades	356	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96210.1	003824	Cluster3487_1clades	356	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96528.1	003824	Cluster3487_1clades	356	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67307.1	003825	Cluster3488_1clades	351	AD1_263	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08533.1	003825	Cluster3488_1clades	354	Alexandra_276	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58910.1	003825	Cluster3488_1clades	346	Y3_270	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28734.1	003825	Cluster3488_1clades	279	YOLOSWAG_261	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD79985.1	003826	Cluster3489_1clades	330	JA11_180	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66583.1	003826	Cluster3489_1clades	342	JA13_180	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66908.1	003826	Cluster3489_1clades	353	JA29_182	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67554.1	003826	Cluster3489_1clades	330	JA33_180	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79887.1	003827	Cluster3491_1clades	350	JA11_082	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66486.1	003827	Cluster3491_1clades	350	JA13_083	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66811.1	003827	Cluster3491_1clades	350	JA29_085	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67456.1	003827	Cluster3491_1clades	350	JA33_082	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96839.1	003828	Cluster3492_1clades	313	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97144.1	003828	Cluster3492_1clades	349	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96203.1	003828	Cluster3492_1clades	313	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96521.1	003828	Cluster3492_1clades	313	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96866.1	003829	Cluster3493_1clades	348	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97171.1	003829	Cluster3493_1clades	348	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96230.1	003829	Cluster3493_1clades	348	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96548.1	003829	Cluster3493_1clades	348	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71348.1	003830	Cluster3494_1clades	346	CR5_128	Cronobacter phage CR5	GCA_000910235.1
QBP07556.1	003830	Cluster3494_1clades	346	DERBICUS_130	Erwinia phage Derbicus	GCA_004521655.1
ANZ48979.1	003830	Cluster3494_1clades	346	EARLPHILLIPIV_130	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50321.1	003830	Cluster3494_1clades	341	PHOBOS_131	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QBX06736.1	003831	GxC-R+GxC-R+GxC-R	271	BcepSaruman_323	Burkholderia phage BcepSaruman	GCA_004771375.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06752.1	003831	GxC-R+GxC-R+GxC-R	344	BcepSaruman_339	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74705.1	003831	GxC-R+GxC-R+GxC-R	273	BcepSauron_325	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74721.1	003831	GxC-R+GxC-R+GxC-R	344	BcepSauron_341	Burkholderia phage BcepSauron	GCA_005394215.1
AYD81349.1	003832	BirA-HTH	328	SEA_JUSTBECAUSE_184	Streptomyces phage JustBecause	GCA_003613775.1
QJD53752.1	003832	BirA-HTH	324	SEA_KELA_182	Streptomyces phage Kela	GCA_012934305.1
QBZ72078.1	003832	BirA-HTH	343	SEA_KRADAL_182	Streptomyces phage Kradal	GCA_004799925.1
AXH66341.1	003832	BirA-HTH	339	SEA_SATIS_182	Streptomyces phage Satis	GCA_003366315.1
AXQ69272.1	003833	DUF5525	291	CcrBL9_gp248c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88088.1	003833	DUF5525	336	CcrColossus_gp218	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68764.1	003833	DUF5525	210	CcrPW_gp225c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69828.1	003833	DUF5525	291	CcrSC_gp246c	Caulobacter phage CcrSC	GCA_003443315.1
QGT54962.1	003834	Cluster3499_1clades	335	b23_0356	Synechococcus phage B23	GCA_009745195.1
QGT54597.1	003834	Cluster3499_1clades	335	b3_0362	Synechococcus phage B3	GCA_009745215.1
ASR76256.1	003834	Cluster3499_1clades	323	PBI_BELLAMY_220	Synechococcus phage Bellamy	GCA_002627525.1
QJT70207.1	003834	Cluster3499_1clades	325	SynMITS9220M01_201	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXQ69039.1	003835	Cluster3500_1clades	334	CcrBL9_gp015	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69555.1	003835	Cluster3500_1clades	334	CcrBL9_gp531	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69599.1	003835	Cluster3500_1clades	332	CcrSC_gp017	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70099.1	003835	Cluster3500_1clades	332	CcrSC_gp517	Caulobacter phage CcrSC	GCA_003443315.1
QDH83483.1	003836	Cluster3501_1clades	308	H1O15_gp323	Achromobacter phage Motura	GCA_006964305.1
QBX06572.1	003836	Cluster3501_1clades	331	BcepSaruman_159	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74539.1	003836	Cluster3501_1clades	331	BcepSauron_159	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41456.1	003836	Cluster3501_1clades	315	RSL1_ORF011	Ralstonia phage phiRSL1	GCA_000879455.1
QDH83442.1	003837	Cluster3502_1clades	320	H1O15_gp034	Achromobacter phage Motura	GCA_006964305.1
QBX06652.1	003837	Cluster3502_1clades	322	BcepSaruman_239	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74620.1	003837	Cluster3502_1clades	322	BcepSauron_240	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41674.1	003837	Cluster3502_1clades	324	RSL1_ORF224	Ralstonia phage phiRSL1	GCA_000879455.1
AYD79837.1	003838	Cluster3503_1clades	319	JA11_032	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66436.1	003838	Cluster3503_1clades	319	JA13_033	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66760.1	003838	Cluster3503_1clades	321	JA29_034	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67406.1	003838	Cluster3503_1clades	319	JA33_032	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ANM44971.1	003839	Cluster3504_1clades	308	KTN4_213	Pseudomonas phage KTN4	GCA_002607225.1
ATN94743.1	003839	Cluster3504_1clades	319	SL2_166	Pseudomonas phage SL2	GCA_002956015.1
QJB22849.1	003839	Cluster3504_1clades	308	fnug_206	Pseudomonas phage fnug	GCA_012837215.1
AAL83074.2	003839	Cluster3504_1clades	319	PHIKZ173	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ69344.1	003840	Cluster3505_1clades	319	CcrBL9_gp320	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88280.1	003840	Cluster3505_1clades	285	CcrColossus_gp410	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68956.1	003840	Cluster3505_1clades	284	CcrPW_gp417c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69903.1	003840	Cluster3505_1clades	317	CcrSC_gp321	Caulobacter phage CcrSC	GCA_003443315.1
ASV44262.1	003841	BetaPropeller	315	PBI_SCTP2_247	Salicola phage SCTP-2	GCA_002625545.1
ASV44384.1	003841	BetaPropeller	127	PBI_SCTP2_369	Salicola phage SCTP-2	GCA_002625545.1
ASV44528.1	003841	BetaPropeller	155	PBI_SCTP2_513	Salicola phage SCTP-2	GCA_002625545.1
ASV44084.1	003841	BetaPropeller	318	PBI_SCTP2_69	Salicola phage SCTP-2	GCA_002625545.1
AMS01365.1	003842	Cluster3507_1clades	310	AR9_g281	Bacillus phage AR9	GCA_001743835.1
ALN97707.1	003842	Cluster3507_1clades	310	Bp8pS_028	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99995.1	003842	Cluster3507_1clades	310	PBI_PBS1_174	Bacillus virus PBS1	GCA_002601325.1
CCE26293.1	003842	Cluster3507_1clades	318	g270	Yersinia phage phiR1-37	GCA_000895615.1
AGR48021.1	003843	DUF932	317	SmphiM12_389	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13206.1	003843	DUF932	317	PHIM19_301	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12847.1	003843	DUF932	317	PHIM7_301	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13568.1	003843	DUF932	317	PHIN3_305	Sinorhizobium phage phiN3	GCA_001501175.1
QGZ14565.1	003844	Cluster3509_1clades	317	HWC77_gp202	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04168.1	003844	Cluster3509_1clades	316	HWC03_gp013	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23189.1	003844	Cluster3509_1clades	317	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47540.1	003844	Cluster3509_1clades	317	HWC35_gp146	Vibrio phage USC-1	GCA_006864065.1
QDJ96764.1	003845	Cluster3510_1clades	317	PS1_0006	Aeromonas phage PS1	GCA_007051165.2
QDJ96879.1	003845	Cluster3510_1clades	147	PS1_0120	Aeromonas phage PS1	GCA_007051165.2
QFR59397.1	003845	Cluster3510_1clades	317	PS2_0006	Aeromonas phage PS2	GCA_009388305.2
QFR59511.1	003845	Cluster3510_1clades	147	PS2_0120	Aeromonas phage PS2	GCA_009388305.2
QAX96859.1	003846	Cluster3511_1clades	316	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97164.1	003846	Cluster3511_1clades	316	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96223.1	003846	Cluster3511_1clades	316	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96541.1	003846	Cluster3511_1clades	316	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96886.1	003847	Cluster3512_1clades	316	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97191.1	003847	Cluster3512_1clades	316	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96250.1	003847	Cluster3512_1clades	316	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96568.1	003847	Cluster3512_1clades	316	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81232.1	003848	TM	315	SEA_JUSTBECAUSE_63	Streptomyces phage JustBecause	GCA_003613775.1
QJD53635.1	003848	TM	315	SEA_KELA_64	Streptomyces phage Kela	GCA_012934305.1
QBZ71966.1	003848	TM	315	SEA_KRADAL_68	Streptomyces phage Kradal	GCA_004799925.1
AXH66229.1	003848	TM	315	SEA_SATIS_68	Streptomyces phage Satis	GCA_003366315.1
QAX96803.1	003849	Cluster3514_1clades	315	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97122.1	003849	Cluster3514_1clades	315	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96168.1	003849	Cluster3514_1clades	315	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96486.1	003849	Cluster3514_1clades	315	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
prevph1000000636	003850	Cluster3515_1clades	153	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000811	003850	Cluster3515_1clades	89	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000452	003850	Cluster3515_1clades	315	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000557	003850	Cluster3515_1clades	290	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QAX98645.1	003851	Fucokinase	309	ASfcp2_312	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52785.1	003851	Fucokinase	309	PX29p066	Aeromonas phage PX29	GCA_000920195.1
ADM80040.1	003851	Fucokinase	313	phiAS5_ORF0197	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17728.1	003851	Fucokinase	309	Aeh1ORF068c	Aeromonas virus Aeh1	GCA_000843245.1
AFO71224.1	003852	Cluster3517_1clades	304	CR5_004	Cronobacter phage CR5	GCA_000910235.1
QBP07431.1	003852	Cluster3517_1clades	308	DERBICUS_4	Erwinia phage Derbicus	GCA_004521655.1
ANZ48854.1	003852	Cluster3517_1clades	304	EARLPHILLIPIV_4	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50194.1	003852	Cluster3517_1clades	310	PHOBOS_4	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD80109.1	003853	Cluster3518_1clades	308	JA11_304	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66710.1	003853	Cluster3518_1clades	308	JA13_307	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67028.1	003853	Cluster3518_1clades	309	JA29_302	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67679.1	003853	Cluster3518_1clades	308	JA33_305	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96885.1	003854	Cluster3519_1clades	309	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97190.1	003854	Cluster3519_1clades	309	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96249.1	003854	Cluster3519_1clades	309	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96567.1	003854	Cluster3519_1clades	309	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83408.1	003855	Cluster3520_1clades	287	H1O15_gp054	Achromobacter phage Motura	GCA_006964305.1
QBX06712.1	003855	Cluster3520_1clades	283	BcepSaruman_299	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74680.1	003855	Cluster3520_1clades	283	BcepSauron_300	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41604.1	003855	Cluster3520_1clades	307	RSL1_ORF158	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96884.1	003856	Cluster3521_1clades	307	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97189.1	003856	Cluster3521_1clades	307	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96248.1	003856	Cluster3521_1clades	307	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96566.1	003856	Cluster3521_1clades	307	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71394.1	003857	Cluster3522_1clades	295	CR5_174	Cronobacter phage CR5	GCA_000910235.1
QBP07605.1	003857	Cluster3522_1clades	306	DERBICUS_179	Erwinia phage Derbicus	GCA_004521655.1
ANZ49029.1	003857	Cluster3522_1clades	306	EARLPHILLIPIV_180	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50377.1	003857	Cluster3522_1clades	203	PHOBOS_187	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81216.1	003858	GT4	304	SEA_JUSTBECAUSE_47	Streptomyces phage JustBecause	GCA_003613775.1
QJD53619.1	003858	GT4	304	SEA_KELA_48	Streptomyces phage Kela	GCA_012934305.1
QBZ71952.1	003858	GT4	304	SEA_KRADAL_53	Streptomyces phage Kradal	GCA_004799925.1
AXH66214.1	003858	GT4	304	SEA_SATIS_53	Streptomyces phage Satis	GCA_003366315.1
QAX96915.1	003859	Cluster3524_1clades	304	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97220.1	003859	Cluster3524_1clades	304	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96279.1	003859	Cluster3524_1clades	304	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96597.1	003859	Cluster3524_1clades	304	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67121.1	003860	Cluster3525_1clades	300	AD1_077	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08357.1	003860	Cluster3525_1clades	303	Alexandra_80	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58720.1	003860	Cluster3525_1clades	288	Y3_080	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28554.1	003860	Cluster3525_1clades	293	YOLOSWAG_71	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81265.1	003861	TM+TM+TM+TM+TM	303	SEA_JUSTBECAUSE_96	Streptomyces phage JustBecause	GCA_003613775.1
QJD53668.1	003861	TM+TM+TM+TM+TM	303	SEA_KELA_97	Streptomyces phage Kela	GCA_012934305.1
QBZ71997.1	003861	TM+TM+TM+TM+TM	303	SEA_KRADAL_99	Streptomyces phage Kradal	GCA_004799925.1
AXH66260.1	003861	TM+TM+TM+TM+TM	303	SEA_SATIS_99	Streptomyces phage Satis	GCA_003366315.1
ANM45037.1	003862	SspB	302	KTN4_279	Pseudomonas phage KTN4	GCA_002607225.1
ATN94677.1	003862	SspB	302	SL2_100	Pseudomonas phage SL2	GCA_002956015.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QJB22913.1	003862	SspB	302	fnug_270	Pseudomonas phage fnug	GCA_012837215.1
AAL83133.1	003862	SspB	302	PHIKZ232	Pseudomonas virus phiKZ	GCA_000842965.1
AYD79878.1	003863	DISCOIDIN	302	JA11_073	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66477.1	003863	DISCOIDIN	302	JA13_074	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66802.1	003863	DISCOIDIN	302	JA29_076	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67447.1	003863	DISCOIDIN	302	JA33_073	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QDH83608.1	003864	CheC	153	H1O15_gp180	Achromobacter phage Motura	GCA_006964305.1
QBX06503.1	003864	CheC	150	BcepSaruman_090	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74470.1	003864	CheC	150	BcepSauron_090	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41570.1	003864	CheC	300	RSL1_ORF125	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96845.1	003865	Cluster3530_1clades	300	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97150.1	003865	Cluster3530_1clades	300	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96209.1	003865	Cluster3530_1clades	300	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96527.1	003865	Cluster3530_1clades	300	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71389.1	003866	Cluster3531_1clades	270	CR5_169	Cronobacter phage CR5	GCA_000910235.1
QBP07600.1	003866	Cluster3531_1clades	300	DERBICUS_174	Erwinia phage Derbicus	GCA_004521655.1
ANZ49023.1	003866	Cluster3531_1clades	278	EARLPHILLIPIV_174	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50370.1	003866	Cluster3531_1clades	273	PHOBOS_180	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AFO71225.1	003867	Cluster3532_1clades	297	CR5_005	Cronobacter phage CR5	GCA_000910235.1
QBP07432.1	003867	Cluster3532_1clades	297	DERBICUS_5	Erwinia phage Derbicus	GCA_004521655.1
ANZ48855.1	003867	Cluster3532_1clades	297	EARLPHILLIPIV_5	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50195.1	003867	Cluster3532_1clades	299	PHOBOS_5	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81177.1	003868	Peptidase_M4+Peptidase_M4_C	299	SEA_JUSTBECAUSE_8	Streptomyces phage JustBecause	GCA_003613775.1
QJD53579.1	003868	Peptidase_M4+Peptidase_M4_C	299	SEA_KELA_8	Streptomyces phage Kela	GCA_012934305.1
QBZ71908.1	003868	Peptidase_M4+Peptidase_M4_C	298	SEA_KRADAL_9	Streptomyces phage Kradal	GCA_004799925.1
AXH66170.1	003868	Peptidase_M4+Peptidase_M4_C	298	SEA_SATIS_9	Streptomyces phage Satis	GCA_003366315.1
ANM45053.1	003869	Cluster3534_1clades	298	KTN4_295	Pseudomonas phage KTN4	GCA_002607225.1
ATN94662.1	003869	Cluster3534_1clades	298	SL2_085	Pseudomonas phage SL2	GCA_002956015.1
QJB22928.1	003869	Cluster3534_1clades	298	fnug_285	Pseudomonas phage fnug	GCA_012837215.1
AAL83144.1	003869	Cluster3534_1clades	298	PHIKZ243	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71321.1	003870	ACET	295	CR5_101	Cronobacter phage CR5	GCA_000910235.1
QBP07530.1	003870	ACET	296	DERBICUS_104	Erwinia phage Derbicus	GCA_004521655.1
ANZ48953.1	003870	ACET	296	EARLPHILLIPIV_104	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50294.1	003870	ACET	278	PHOBOS_104	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AMS01235.1	003871	D6	241	AR9_g151	Bacillus phage AR9	GCA_001743835.1
ALN97895.1	003871	D6	249	Bp8pS_216	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99861.1	003871	D6	241	PBI_PBS1_39	Bacillus virus PBS1	GCA_002601325.1
CCE26201.1	003871	D6	292	g177	Yersinia phage phiR1-37	GCA_000895615.1
AXQ69203.1	003872	Glyco_transf_9	285	CcrBL9_gp179	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88001.1	003872	Glyco_transf_9	276	CcrColossus_gp131	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68677.1	003872	Glyco_transf_9	291	CcrPW_gp138	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69756.1	003872	Glyco_transf_9	285	CcrSC_gp174	Caulobacter phage CcrSC	GCA_003443315.1
AFF28186.1	003873	TM+TM+TM+TM	264	PAU_188	Sphingomonas phage PAU	GCA_000902455.1
BBI90439.1	003873	TM+TM+TM+TM	291	HYO65_gp047	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90746.1	003873	TM+TM+TM+TM	291	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39228.1	003873	TM+TM+TM+TM	287	BPT24_103	Tenacibaculum phage pT24	GCA_002611925.1
QAX96809.1	003874	Cluster3539_1clades	291	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97128.1	003874	Cluster3539_1clades	291	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96174.1	003874	Cluster3539_1clades	291	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96492.1	003874	Cluster3539_1clades	291	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45100.1	003875	Cluster3540_1clades	290	KTN4_342	Pseudomonas phage KTN4	GCA_002607225.1
ATN94613.1	003875	Cluster3540_1clades	282	SL2_036	Pseudomonas phage SL2	GCA_002956015.1
QJB22976.1	003875	Cluster3540_1clades	282	fnug_333	Pseudomonas phage fnug	GCA_012837215.1
AAL83185.1	003875	Cluster3540_1clades	278	PHIKZ284	Pseudomonas virus phiKZ	GCA_000842965.1
AMS01311.1	003876	Cluster3541_1clades	274	AR9_g227	Bacillus phage AR9	GCA_001743835.1
ALN97961.1	003876	Cluster3541_1clades	254	Bp8pS_282	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99940.1	003876	Cluster3541_1clades	274	PBI_PBS1_118	Bacillus virus PBS1	GCA_002601325.1
CCE26267.1	003876	Cluster3541_1clades	290	g244	Yersinia phage phiR1-37	GCA_000895615.1
ANM44803.1	003877	Cluster3542_1clades	289	KTN4_045	Pseudomonas phage KTN4	GCA_002607225.1
ATN94908.1	003877	Cluster3542_1clades	289	SL2_331	Pseudomonas phage SL2	GCA_002956015.1
QJB22682.1	003877	Cluster3542_1clades	289	fnug_39	Pseudomonas phage fnug	GCA_012837215.1
AAL82934.1	003877	Cluster3542_1clades	289	PHIKZ033	Pseudomonas virus phiKZ	GCA_000842965.1
AGX01897.1	003878	Cluster3544_1clades	285	CF95_gp175	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65411.1	003878	Cluster3544_1clades	289	2050HW_00076	Serratia phage 2050HW	GCA_002628125.1
QDB71190.1	003878	Cluster3544_1clades	289	CPT_Moabite_160	Serratia phage Moabite	GCA_006384735.1
QFP93116.1	003878	Cluster3544_1clades	284	-	Serratia phage PCH45	GCA_009187865.1
ARW58915.1	003879	Cluster3545_1clades	184	Y3_275	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AFH14794.1	003879	Cluster3545_1clades	227	Lu11_0258	Pseudomonas phage Lu11	GCA_000897175.1
AGS81904.2	003879	Cluster3545_1clades	288	PaBG_00020	Pseudomonas phage PaBG	GCA_000912555.1
BAG41518.1	003879	Cluster3545_1clades	113	RSL1_ORF072	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96906.1	003880	Cluster3546_1clades	288	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97211.1	003880	Cluster3546_1clades	288	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96270.1	003880	Cluster3546_1clades	288	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96588.1	003880	Cluster3546_1clades	288	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83640.1	003881	Cluster3547_1clades	239	H1O15_gp148	Achromobacter phage Motura	GCA_006964305.1
QBX06660.1	003881	Cluster3547_1clades	288	BcepSaruman_247	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74628.1	003881	Cluster3547_1clades	288	BcepSauron_248	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41662.1	003881	Cluster3547_1clades	264	RSL1_ORF213	Ralstonia phage phiRSL1	GCA_000879455.1
AYD79838.1	003882	Cluster3548_1clades	287	JA11_033	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66437.1	003882	Cluster3548_1clades	287	JA13_034	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66761.1	003882	Cluster3548_1clades	287	JA29_035	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67407.1	003882	Cluster3548_1clades	287	JA33_033	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ABY63262.1	003883	TM	286	201phi2-1p439	Pseudomonas phage 201phi2-1	GCA_000875305.1
ANM45115.1	003883	TM	152	KTN4_357	Pseudomonas phage KTN4	GCA_002607225.1
ATN94598.1	003883	TM	286	SL2_021	Pseudomonas phage SL2	GCA_002956015.1
QJB22992.1	003883	TM	152	fnug_349	Pseudomonas phage fnug	GCA_012837215.1
AXQ69200.1	003884	Cluster3550_1clades	286	CcrBL9_gp176	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87998.1	003884	Cluster3550_1clades	241	CcrColossus_gp128	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68674.1	003884	Cluster3550_1clades	256	CcrPW_gp135	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69753.1	003884	Cluster3550_1clades	286	CcrSC_gp171	Caulobacter phage CcrSC	GCA_003443315.1
AEO93467.1	003885	Cluster3551_2clades	236	G_208	Bacillus virus G	GCA_000917535.1
ASV44186.1	003885	Cluster3551_2clades	285	PBI_SCTP2_171	Salicola phage SCTP-2	GCA_002625545.1
prevph1000000168	003885	Cluster3551_2clades	258	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000130	003885	Cluster3551_2clades	258	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXQ69326.1	003886	Cluster3552_1clades	283	CcrBL9_gp302	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88128.1	003886	Cluster3552_1clades	268	CcrColossus_gp258	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68805.1	003886	Cluster3552_1clades	268	CcrPW_gp266	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69886.1	003886	Cluster3552_1clades	285	CcrSC_gp304	Caulobacter phage CcrSC	GCA_003443315.1
QAX96908.1	003887	Cluster3553_1clades	285	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97213.1	003887	Cluster3553_1clades	285	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96272.1	003887	Cluster3553_1clades	285	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96590.1	003887	Cluster3553_1clades	285	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXQ69389.1	003888	Cluster3554_1clades	256	CcrBL9_gp365	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88161.1	003888	Cluster3554_1clades	281	CcrColossus_gp291	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68837.1	003888	Cluster3554_1clades	281	CcrPW_gp298	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69949.1	003888	Cluster3554_1clades	256	CcrSC_gp367	Caulobacter phage CcrSC	GCA_003443315.1
QAX96727.1	003889	Cluster3556_1clades	281	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97046.1	003889	Cluster3556_1clades	281	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96092.1	003889	Cluster3556_1clades	281	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96410.1	003889	Cluster3556_1clades	281	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63309.1	003890	SIG+ZetaToxin	281	DAC16_76	Bacteroides phage DAC16	GCA_013387695.1
QIG63568.1	003890	SIG+ZetaToxin	281	DAC19_77	Bacteroides phage DAC19	GCA_013387715.1
QIG63829.1	003890	SIG+ZetaToxin	281	DAC20_76	Bacteroides phage DAC20	GCA_013387725.1
QIG64091.1	003890	SIG+ZetaToxin	281	DAC22_77	Bacteroides phage DAC22	GCA_013387735.1
AYD81224.1	003891	Cluster3558_1clades	280	SEA_JUSTBECAUSE_55	Streptomyces phage JustBecause	GCA_003613775.1
QJD53627.1	003891	Cluster3558_1clades	280	SEA_KELA_56	Streptomyces phage Kela	GCA_012934305.1
QBZ71959.1	003891	Cluster3558_1clades	280	SEA_KRADAL_61	Streptomyces phage Kradal	GCA_004799925.1
AXH66222.1	003891	Cluster3558_1clades	280	SEA_SATIS_61	Streptomyces phage Satis	GCA_003366315.1
AXQ69035.1	003892	Cluster3560_1clades	280	CcrBL9_gp011	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69551.1	003892	Cluster3560_1clades	280	CcrBL9_gp527	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69595.1	003892	Cluster3560_1clades	280	CcrSC_gp013	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70095.1	003892	Cluster3560_1clades	280	CcrSC_gp513	Caulobacter phage CcrSC	GCA_003443315.1
QAX96718.1	003893	Cluster3561_1clades	280	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97037.1	003893	Cluster3561_1clades	280	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96083.1	003893	Cluster3561_1clades	280	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96401.1	003893	Cluster3561_1clades	280	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AOO14233.1	003894	SIG+2OG-FeII_Oxy_5	215	Sn110110_039	Cyanophage S-RIM14	GCA_002599065.1
AOO14885.1	003894	SIG+2OG-FeII_Oxy_5	215	W1230910_039	Cyanophage S-RIM14	GCA_002599125.1
AAX44435.1	003894	SIG+2OG-FeII_Oxy_5	279	PSSM2_057	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12217.1	003894	SIG+2OG-FeII_Oxy_5	279	PRTG_00059	Prochlorococcus phage P-SSM5	GCA_002991095.1
AYD79857.1	003895	SbcC	279	JA11_052	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66456.1	003895	SbcC	279	JA13_053	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66780.1	003895	SbcC	279	JA29_054	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67426.1	003895	SbcC	279	JA33_052	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXQ69199.1	003896	RnasePH	274	CcrBL9_gp175	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87997.1	003896	RnasePH	278	CcrColossus_gp127	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68673.1	003896	RnasePH	277	CcrPW_gp134	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69752.1	003896	RnasePH	274	CcrSC_gp170	Caulobacter phage CcrSC	GCA_003443315.1
AYD80101.1	003897	Cluster3565_1clades	277	JA11_296	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66702.1	003897	Cluster3565_1clades	277	JA13_299	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67021.1	003897	Cluster3565_1clades	277	JA29_295	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67671.1	003897	Cluster3565_1clades	277	JA33_297	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79860.1	003898	Cluster3566_1clades	252	JA11_055	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66459.1	003898	Cluster3566_1clades	252	JA13_056	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66782.1	003898	Cluster3566_1clades	277	JA29_056	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67429.1	003898	Cluster3566_1clades	252	JA33_055	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBX06429.1	003899	7TMR-HDED	214	BcepSaruman_016	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74396.1	003899	7TMR-HDED	214	BcepSauron_016	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ69342.1	003899	7TMR-HDED	277	CcrBL9_gp318	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69902.1	003899	7TMR-HDED	277	CcrSC_gp320	Caulobacter phage CcrSC	GCA_003443315.1
QAX96692.1	003900	Cluster3568_1clades	277	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97010.1	003900	Cluster3568_1clades	277	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96056.1	003900	Cluster3568_1clades	277	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96374.1	003900	Cluster3568_1clades	277	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD80068.1	003901	Cluster3569_1clades	130	JA11_263	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66669.1	003901	Cluster3569_1clades	130	JA13_266	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66990.1	003901	Cluster3569_1clades	276	JA29_264	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67638.1	003901	Cluster3569_1clades	130	JA33_264	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFF28261.1	003902	Cluster3570_1clades	274	PAU_263	Sphingomonas phage PAU	GCA_000902455.1
BBI90394.1	003902	Cluster3570_1clades	276	HYO65_gp002	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90702.1	003902	Cluster3570_1clades	276	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39302.1	003902	Cluster3570_1clades	260	BPT24_177	Tenacibaculum phage pT24	GCA_002611925.1
AYD81379.1	003903	Cluster3571_1clades	275	SEA_JUSTBECAUSE_224	Streptomyces phage JustBecause	GCA_003613775.1
QJD53782.1	003903	Cluster3571_1clades	276	SEA_KELA_222	Streptomyces phage Kela	GCA_012934305.1
QBZ72107.1	003903	Cluster3571_1clades	271	SEA_KRADAL_221	Streptomyces phage Kradal	GCA_004799925.1
AXH66368.1	003903	Cluster3571_1clades	271	SEA_SATIS_219	Streptomyces phage Satis	GCA_003366315.1
AGR48097.1	003904	Cluster3572_1clades	274	SmphiM12_465	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13266.1	003904	Cluster3572_1clades	274	PHIM19_361	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12906.1	003904	Cluster3572_1clades	274	PHIM7_361	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13630.2	003904	Cluster3572_1clades	274	PHIN3_367	Sinorhizobium phage phiN3	GCA_001501175.1
QAX96855.1	003905	Cluster3573_1clades	274	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97160.1	003905	Cluster3573_1clades	274	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96219.1	003905	Cluster3573_1clades	274	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96537.1	003905	Cluster3573_1clades	274	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44808.1	003906	Dip	273	KTN4_050	Pseudomonas phage KTN4	GCA_002607225.1
ATN94903.1	003906	Dip	273	SL2_326	Pseudomonas phage SL2	GCA_002956015.1
QJB22687.1	003906	Dip	273	fnug_44	Pseudomonas phage fnug	GCA_012837215.1
AAL82938.1	003906	Dip	273	PHIKZ037	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71312.1	003907	Cluster3575_1clades	262	CR5_092	Cronobacter phage CR5	GCA_000910235.1
QBP07521.1	003907	Cluster3575_1clades	273	DERBICUS_95	Erwinia phage Derbicus	GCA_004521655.1
ANZ48944.1	003907	Cluster3575_1clades	269	EARLPHILLIPIV_95	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50285.1	003907	Cluster3575_1clades	254	PHOBOS_95	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AXQ69201.1	003908	Cluster3576_1clades	272	CcrBL9_gp177	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87999.1	003908	Cluster3576_1clades	261	CcrColossus_gp129	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68675.1	003908	Cluster3576_1clades	261	CcrPW_gp136	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69754.1	003908	Cluster3576_1clades	271	CcrSC_gp172	Caulobacter phage CcrSC	GCA_003443315.1
QDH83675.1	003909	Toast-rack	272	H1O15_gp136	Achromobacter phage Motura	GCA_006964305.1
QBX06673.1	003909	Toast-rack	266	BcepSaruman_260	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74643.1	003909	Toast-rack	266	BcepSauron_263	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41649.1	003909	Toast-rack	264	RSL1_ORF200	Ralstonia phage phiRSL1	GCA_000879455.1
ANM44807.1	003910	3Beta_HSD	270	KTN4_049	Pseudomonas phage KTN4	GCA_002607225.1
ATN94904.1	003910	3Beta_HSD	270	SL2_327	Pseudomonas phage SL2	GCA_002956015.1
QJB22686.1	003910	3Beta_HSD	271	fnug_43	Pseudomonas phage fnug	GCA_012837215.1
AAL82937.1	003910	3Beta_HSD	271	PHIKZ036	Pseudomonas virus phiKZ	GCA_000842965.1
AYD81378.1	003911	TRPR-HTH+TRPR-HTH	235	SEA_JUSTBECAUSE_223	Streptomyces phage JustBecause	GCA_003613775.1
QJD53781.1	003911	TRPR-HTH+TRPR-HTH	235	SEA_KELA_221	Streptomyces phage Kela	GCA_012934305.1
QBZ72106.1	003911	TRPR-HTH+TRPR-HTH	271	SEA_KRADAL_220	Streptomyces phage Kradal	GCA_004799925.1
AXH66367.1	003911	TRPR-HTH+TRPR-HTH	271	SEA_SATIS_218	Streptomyces phage Satis	GCA_003366315.1
AYD80076.1	003912	Cluster3580_1clades	269	JA11_271	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66677.1	003912	Cluster3580_1clades	269	JA13_274	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66997.1	003912	Cluster3580_1clades	270	JA29_271	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67646.1	003912	Cluster3580_1clades	269	JA33_272	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96854.1	003913	Cluster3581_1clades	270	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97159.1	003913	Cluster3581_1clades	270	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96218.1	003913	Cluster3581_1clades	270	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96536.1	003913	Cluster3581_1clades	270	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96865.1	003914	Cluster3582_1clades	270	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97170.1	003914	Cluster3582_1clades	270	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96229.1	003914	Cluster3582_1clades	270	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96547.1	003914	Cluster3582_1clades	270	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71408.1	003915	Cluster3583_1clades	268	CR5_188	Cronobacter phage CR5	GCA_000910235.1
QBP07620.1	003915	Cluster3583_1clades	268	DERBICUS_194	Erwinia phage Derbicus	GCA_004521655.1
ANZ49044.1	003915	Cluster3583_1clades	268	EARLPHILLIPIV_195	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50392.1	003915	Cluster3583_1clades	264	PHOBOS_202	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QAX96654.1	003916	Cluster3584_1clades	268	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96972.1	003916	Cluster3584_1clades	268	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96018.1	003916	Cluster3584_1clades	268	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96336.1	003916	Cluster3584_1clades	268	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BBI90644.1	003917	Cluster3585_1clades	175	HYO65_gp252	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90643.1	003917	Cluster3585_1clades	89	HYO65_gp251	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90950.1	003917	Cluster3585_1clades	264	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39311.1	003917	Cluster3585_1clades	267	BPT24_186	Tenacibaculum phage pT24	GCA_002611925.1
AMS01211.1	003918	Cas9_C	265	AR9_g127	Bacillus phage AR9	GCA_001743835.1
ALN97882.1	003918	Cas9_C	265	Bp8pS_203	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99836.1	003918	Cas9_C	265	PBL_PBS1_14	Bacillus virus PBS1	GCA_002601325.1
CCE26174.1	003918	Cas9_C	250	g150	Yersinia phage phiR1-37	GCA_000895615.1
ANM45060.1	003919	Cluster3588_1clades	264	KTN4_302	Pseudomonas phage KTN4	GCA_002607225.1
ATN94655.1	003919	Cluster3588_1clades	264	SL2_078	Pseudomonas phage SL2	GCA_002956015.1
QJB22935.1	003919	Cluster3588_1clades	264	fnug_292	Pseudomonas phage fnug	GCA_012837215.1
AAL83150.1	003919	Cluster3588_1clades	264	PHIKZ249	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96748.1	003920	Cluster3589_1clades	264	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97067.1	003920	Cluster3589_1clades	264	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96113.1	003920	Cluster3589_1clades	264	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96431.1	003920	Cluster3589_1clades	264	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44990.1	003921	Cluster3590_1clades	263	KTN4_232	Pseudomonas phage KTN4	GCA_002607225.1
ATN94724.1	003921	Cluster3590_1clades	263	SL2_147	Pseudomonas phage SL2	GCA_002956015.1
QJB22868.1	003921	Cluster3590_1clades	263	fnug_225	Pseudomonas phage fnug	GCA_012837215.1
AAL83092.1	003921	Cluster3590_1clades	263	PHIKZ191	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22622.1	003922	Cluster3591_1clades	259	Ah1_00081	Aeromonas phage Ah1	GCA_002957415.1
QAX98349.1	003922	Cluster3591_1clades	263	ASfcp2_3	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52805.1	003922	Cluster3591_1clades	263	PX29p086	Aeromonas phage PX29	GCA_000920195.1
AAQ17749.1	003922	Cluster3591_1clades	259	Aeh1ORF088c	Aeromonas virus Aeh1	GCA_000843245.1
AYD79872.1	003923	Cluster3592_1clades	263	JA11_067	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66471.1	003923	Cluster3592_1clades	263	JA13_068	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66796.1	003923	Cluster3592_1clades	251	JA29_070	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67441.1	003923	Cluster3592_1clades	263	JA33_067	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80056.1	003924	Cluster3593_1clades	261	JA11_251	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66655.1	003924	Cluster3593_1clades	261	JA13_252	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66980.1	003924	Cluster3593_1clades	263	JA29_254	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67626.1	003924	Cluster3593_1clades	261	JA33_252	Dickeya phage vB_DsoM_JA33	GCA_003568495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDH83683.1	003925	SIG+TM	251	H1O15_gp278	Achromobacter phage Motura	GCA_006964305.1
BAW19169.1	003925	SIG+TM	263	FDH28_gp226	Ralstonia phage RP12	GCA_002617345.1
BAW19455.1	003925	SIG+TM	263	-	Ralstonia phage RP31	GCA_002617365.1
BAG41541.1	003925	SIG+TM	259	RSL1_ORF096	Ralstonia phage phiRSL1	GCA_000879455.1
QDH83473.1	003926	Cluster3595_1clades	224	H1O15_gp333	Achromobacter phage Motura	GCA_006964305.1
QBX06585.1	003926	Cluster3595_1clades	263	BcepSaruman_172	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74550.1	003926	Cluster3595_1clades	263	BcepSauron_170	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41777.1	003926	Cluster3595_1clades	255	RSL1_ORF331	Ralstonia phage phiRSL1	GCA_000879455.1
ANM45101.1	003927	Cluster3597_1clades	261	KTN4_343	Pseudomonas phage KTN4	GCA_002607225.1
AEH03769.1	003927	Cluster3597_1clades	261	346	Pseudomonas phage PhiPA3	GCA_001502095.1
QJB22977.1	003927	Cluster3597_1clades	261	fnug_334	Pseudomonas phage fnug	GCA_012837215.1
AAL83186.1	003927	Cluster3597_1clades	261	PHIKZ285	Pseudomonas virus phiKZ	GCA_000842965.1
AFF28257.1	003928	VgrG	247	PAU_259	Sphingomonas phage PAU	GCA_000902455.1
BBI90626.1	003928	VgrG	261	HYO65_gp234	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90932.1	003928	VgrG	261	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39288.1	003928	VgrG	254	BPT24_162	Tenacibaculum phage pT24	GCA_002611925.1
AYD80102.1	003929	Cluster3599_1clades	260	JA11_297	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66703.1	003929	Cluster3599_1clades	260	JA13_300	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67022.1	003929	Cluster3599_1clades	260	JA29_296	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67672.1	003929	Cluster3599_1clades	260	JA33_298	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96874.1	003930	Cluster3600_1clades	260	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97179.1	003930	Cluster3600_1clades	260	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96238.1	003930	Cluster3600_1clades	260	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96556.1	003930	Cluster3600_1clades	260	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX06522.1	003931	Cluster3601_1clades	217	BcepSaruman_109	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74488.1	003931	Cluster3601_1clades	217	BcepSauron_108	Burkholderia phage BcepSauron	GCA_005394215.1
AFH14697.1	003931	Cluster3601_1clades	259	Lu11_0163	Pseudomonas phage Lu11	GCA_000897175.1
AGS82007.1	003931	Cluster3601_1clades	253	PaBG_00123	Pseudomonas phage PaBG	GCA_000912555.1
AYD80029.1	003932	Cluster3602_1clades	259	JA11_224	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66628.1	003932	Cluster3602_1clades	259	JA13_225	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66952.1	003932	Cluster3602_1clades	259	JA29_226	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67599.1	003932	Cluster3602_1clades	259	JA33_225	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFF28087.1	003933	Cluster3603_1clades	248	PAU_89	Sphingomonas phage PAU	GCA_000902455.1
BBI90686.1	003933	Cluster3603_1clades	230	HYO65_gp294	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90993.1	003933	Cluster3603_1clades	230	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39273.1	003933	Cluster3603_1clades	257	BPT24_147	Tenacibaculum phage pT24	GCA_002611925.1
AYD81226.1	003934	Cluster3604_1clades	256	SEA_JUSTBECAUSE_57	Streptomyces phage JustBecause	GCA_003613775.1
QJD53629.1	003934	Cluster3604_1clades	256	SEA_KELA_58	Streptomyces phage Kela	GCA_012934305.1
QBZ71961.1	003934	Cluster3604_1clades	256	SEA_KRADAL_63	Streptomyces phage Kradal	GCA_004799925.1
AXH66224.1	003934	Cluster3604_1clades	256	SEA_SATIS_63	Streptomyces phage Satis	GCA_003366315.1
AMS01323.1	003935	Cluster3605_1clades	255	AR9_g239	Bacillus phage AR9	GCA_001743835.1
ALN97974.1	003935	Cluster3605_1clades	255	Bp8pS_295	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99952.1	003935	Cluster3605_1clades	255	PBI_PBS1_130	Bacillus virus PBS1	GCA_002601325.1
CCE26299.1	003935	Cluster3605_1clades	253	g276	Yersinia phage phiR1-37	GCA_000895615.1
QGH71994.1	003936	Cluster3606_1clades	248	N1M2_131	Klebsiella phage N1M2	GCA_010092605.1
AEV89602.1	003936	Cluster3606_1clades	253	OBP_165	Pseudomonas phage OBP	GCA_000896635.1
ATA65612.1	003936	Cluster3606_1clades	254	2050HW_00277	Serratia phage 2050HW	GCA_002628125.1
QDB71041.1	003936	Cluster3606_1clades	254	CPT_Moabite_009	Serratia phage Moabite	GCA_006384735.1
QAX96878.1	003937	Cluster3607_1clades	253	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97183.1	003937	Cluster3607_1clades	253	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96242.1	003937	Cluster3607_1clades	253	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96560.1	003937	Cluster3607_1clades	253	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81493.1	003938	TM	235	SEA_JUSTBECAUSE_338	Streptomyces phage JustBecause	GCA_003613775.1
QJD53896.1	003938	TM	235	SEA_KELA_336	Streptomyces phage Kela	GCA_012934305.1
QBZ72221.1	003938	TM	253	SEA_KRADAL_335	Streptomyces phage Kradal	GCA_004799925.1
AXH66484.1	003938	TM	249	SEA_SATIS_335	Streptomyces phage Satis	GCA_003366315.1
AYD80047.1	003939	Cluster3609_1clades	252	JA11_242	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66646.1	003939	Cluster3609_1clades	252	JA13_243	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66970.1	003939	Cluster3609_1clades	252	JA29_244	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67617.1	003939	Cluster3609_1clades	252	JA33_243	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMS01107.1	003940	Mbetalac	240	AR9_g022	Bacillus phage AR9	GCA_001743835.1
ALN97821.1	003940	Mbetalac	231	Bp8pS_142	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93647.1	003940	Mbetalac	251	G_388	Bacillus virus G	GCA_000917535.1
ASU00029.1	003940	Mbetalac	240	PBI_PBS1_207	Bacillus virus PBS1	GCA_002601325.1
AYD81384.1	003941	Cluster3611_1clades	251	SEA_JUSTBECAUSE_229	Streptomyces phage JustBecause	GCA_003613775.1
QJD53788.1	003941	Cluster3611_1clades	251	SEA_KELA_228	Streptomyces phage Kela	GCA_012934305.1
QBZ72113.1	003941	Cluster3611_1clades	243	SEA_KRADAL_227	Streptomyces phage Kradal	GCA_004799925.1
AXH66375.1	003941	Cluster3611_1clades	243	SEA_SATIS_226	Streptomyces phage Satis	GCA_003366315.1
ANS05990.1	003942	T4_baseplate	247	ABCD_0107	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97117.1	003942	T4_baseplate	247	E_109	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70749.1	003942	T4_baseplate	250	phiC120_c42	Escherichia phage phiC120	GCA_002621185.1
AAX78629.1	003942	T4_baseplate	247	RB43ORF107w	Escherichia virus RB43	GCA_000863505.1
AYD79846.1	003943	Cluster3613_1clades	250	JA11_041	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66446.1	003943	Cluster3613_1clades	250	JA13_043	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66770.1	003943	Cluster3613_1clades	250	JA29_044	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67415.1	003943	Cluster3613_1clades	250	JA33_041	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80114.1	003944	Cluster3614_1clades	250	JA11_309	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66715.1	003944	Cluster3614_1clades	250	JA13_312	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67033.1	003944	Cluster3614_1clades	250	JA29_307	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67684.1	003944	Cluster3614_1clades	250	JA33_310	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXQ69473.1	003945	SIG+MNS	250	CcrBL9_gp449	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88114.1	003945	SIG+MNS	227	CcrColossus_gp244	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68792.1	003945	SIG+MNS	227	CcrPW_gp253	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70022.1	003945	SIG+MNS	250	CcrSC_gp440	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69494.1	003946	Cluster3616_1clades	250	CcrBL9_gp470	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88308.1	003946	Cluster3616_1clades	216	CcrColossus_gp438	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68980.1	003946	Cluster3616_1clades	226	CcrPW_gp441c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ70042.1	003946	Cluster3616_1clades	249	CcrSC_gp460	Caulobacter phage CcrSC	GCA_003443315.1
AFO71392.1	003947	Cluster3617_1clades	231	CR5_172	Cronobacter phage CR5	GCA_000910235.1
QBP07603.1	003947	Cluster3617_1clades	250	DERBICUS_177	Erwinia phage Derbicus	GCA_004521655.1
ANZ49026.1	003947	Cluster3617_1clades	246	EARLPHILLIPIV_177	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50374.1	003947	Cluster3617_1clades	242	PHOBOS_184	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AFU86492.1	003948	Cluster3618_1clades	248	CcrRogue_gp010	Caulobacter virus Rogue	GCA_000900555.1
AFU86823.1	003948	Cluster3618_1clades	248	CcrRogue_gp341	Caulobacter virus Rogue	GCA_000900555.1
AFU88327.1	003948	Cluster3618_1clades	232	CcrSwift_gp009	Caulobacter virus Swift	GCA_000899655.1
AFU88652.1	003948	Cluster3618_1clades	232	CcrSwift_gp334	Caulobacter virus Swift	GCA_000899655.1
AMS01209.1	003949	Cluster3619_1clades	248	AR9_g125	Bacillus phage AR9	GCA_001743835.1
ALN97880.1	003949	Cluster3619_1clades	248	Bp8pS_201	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99834.1	003949	Cluster3619_1clades	248	PBI_PBS1_12	Bacillus virus PBS1	GCA_002601325.1
CCE26172.1	003949	Cluster3619_1clades	232	g148	Yersinia phage phiR1-37	GCA_000895615.1
AYD81342.1	003950	Cluster3620_1clades	244	SEA_JUSTBECAUSE_177	Streptomyces phage JustBecause	GCA_003613775.1
QJD53745.1	003950	Cluster3620_1clades	244	SEA_KELA_175	Streptomyces phage Kela	GCA_012934305.1
QBZ72071.1	003950	Cluster3620_1clades	247	SEA_KRADAL_175	Streptomyces phage Kradal	GCA_004799925.1
AXH66334.1	003950	Cluster3620_1clades	247	SEA_SATIS_175	Streptomyces phage Satis	GCA_003366315.1
AGR47932.1	003951	Cluster3621_1clades	246	SmphiM12_300	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13132.1	003951	Cluster3621_1clades	246	PHIM19_227	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12771.1	003951	Cluster3621_1clades	246	PHIM7_226	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13500.1	003951	Cluster3621_1clades	246	PHIN3_237	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47726.1	003952	Cluster3623_1clades	244	SmphiM12_094	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12981.1	003952	Cluster3623_1clades	244	PHIM19_74	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12621.1	003952	Cluster3623_1clades	244	PHIM7_73	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13353.1	003952	Cluster3623_1clades	244	PHIN3_89	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01343.1	003953	Cluster3624_1clades	244	AR9_g259	Bacillus phage AR9	GCA_001743835.1
ALN97997.1	003953	Cluster3624_1clades	244	Bp8pS_318	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99973.1	003953	Cluster3624_1clades	244	PBI_PBS1_152	Bacillus virus PBS1	GCA_002601325.1
CCE26256.1	003953	Cluster3624_1clades	228	g233	Yersinia phage phiR1-37	GCA_000895615.1
AYD81267.1	003954	GNTR-HTH+UTRA	244	SEA_JUSTBECAUSE_98	Streptomyces phage JustBecause	GCA_003613775.1
QJD53670.1	003954	GNTR-HTH+UTRA	244	SEA_KELA_99	Streptomyces phage Kela	GCA_012934305.1
QBZ71999.1	003954	GNTR-HTH+UTRA	244	SEA_KRADAL_101	Streptomyces phage Kradal	GCA_004799925.1
AXH66262.1	003954	GNTR-HTH+UTRA	244	SEA_SATIS_101	Streptomyces phage Satis	GCA_003366315.1
AYD81323.1	003955	Cluster3626_1clades	240	SEA_JUSTBECAUSE_158	Streptomyces phage JustBecause	GCA_003613775.1
QJD53726.1	003955	Cluster3626_1clades	240	SEA_KELA_156	Streptomyces phage Kela	GCA_012934305.1
QBZ72055.1	003955	Cluster3626_1clades	244	SEA_KRADAL_159	Streptomyces phage Kradal	GCA_004799925.1
AXH66318.1	003955	Cluster3626_1clades	244	SEA_SATIS_159	Streptomyces phage Satis	GCA_003366315.1
AXH70971.1	003956	Cluster3627_1clades	244	-	Vibrio phage BONAISHI	GCA_003441475.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96830.1	003956	Cluster3627_1clades	243	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96195.1	003956	Cluster3627_1clades	243	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96513.1	003956	Cluster3627_1clades	243	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83406.1	003957	Cluster3629_1clades	235	H1O15_gp056	Achromobacter phage Motura	GCA_006964305.1
QBX06710.1	003957	Cluster3629_1clades	240	BcepSaruman_297	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74678.1	003957	Cluster3629_1clades	240	BcepSauron_298	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41607.1	003957	Cluster3629_1clades	242	RSL1_ORF160	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96870.1	003958	Cluster3630_1clades	242	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97175.1	003958	Cluster3630_1clades	242	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96234.1	003958	Cluster3630_1clades	242	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96552.1	003958	Cluster3630_1clades	242	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67272.1	003959	Cluster3631_1clades	177	AD1_228	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG66615.1	003959	Cluster3631_1clades	195	JA13_212	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AWY08611.1	003959	Cluster3631_1clades	241	Alexandra_237	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58872.1	003959	Cluster3631_1clades	176	Y3_232	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AYD79831.1	003960	Cluster3632_1clades	236	JA11_026	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66430.1	003960	Cluster3632_1clades	236	JA13_027	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66754.1	003960	Cluster3632_1clades	241	JA29_028	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67400.1	003960	Cluster3632_1clades	236	JA33_026	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXQ69381.1	003961	Cluster3633_1clades	241	CcrBL9_gp357	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88045.1	003961	Cluster3633_1clades	214	CcrColossus_gp175	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68722.1	003961	Cluster3633_1clades	213	CcrPW_gp183c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69941.1	003961	Cluster3633_1clades	241	CcrSC_gp359	Caulobacter phage CcrSC	GCA_003443315.1
QDH83598.1	003962	ISOCOT	219	H1O15_gp190	Achromobacter phage Motura	GCA_006964305.1
QBX06493.1	003962	ISOCOT	233	BcepSaruman_080	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74460.1	003962	ISOCOT	233	BcepSauron_080	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41583.1	003962	ISOCOT	241	RSL1_ORF138	Ralstonia phage phiRSL1	GCA_000879455.1
QDH83481.1	003963	Cluster3635_1clades	241	H1O15_gp325	Achromobacter phage Motura	GCA_006964305.1
QBX06574.1	003963	Cluster3635_1clades	232	BcepSaruman_161	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74541.1	003963	Cluster3635_1clades	232	BcepSauron_161	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41455.1	003963	Cluster3635_1clades	228	RSL1_ORF010	Ralstonia phage phiRSL1	GCA_000879455.1
AFU88267.1	003964	Cluster3636_1clades	240	CcrColossus_gp397	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68941.1	003964	Cluster3636_1clades	240	CcrPW_gp402	Caulobacter phage CcrPW	GCA_003443275.1
QGT54785.1	003964	Cluster3636_1clades	183	b23_0170	Synechococcus phage B23	GCA_009745195.1
QGT54415.1	003964	Cluster3636_1clades	183	b3_0171	Synechococcus phage B3	GCA_009745215.1
AYD79871.1	003965	Cluster3637_1clades	240	JA11_066	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66470.1	003965	Cluster3637_1clades	240	JA13_067	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66795.1	003965	Cluster3637_1clades	234	JA29_069	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67440.1	003965	Cluster3637_1clades	240	JA33_066	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
BAW19257.1	003966	Cluster3638_1clades	192	FDH28_gp138	Ralstonia phage RP12	GCA_002617345.1
BAW19543.1	003966	Cluster3638_1clades	192	-	Ralstonia phage RP31	GCA_002617365.1
BAS05016.1	003966	Cluster3638_1clades	240	AVU11_gp224	Ralstonia phage RSF1	GCA_001500875.1
BAQ02746.1	003966	Cluster3638_1clades	238	AVU38_gp218	Ralstonia phage RSL2	GCA_001503055.1
QAX96916.1	003967	Cluster3639_1clades	240	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97221.1	003967	Cluster3639_1clades	240	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96280.1	003967	Cluster3639_1clades	240	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96598.1	003967	Cluster3639_1clades	240	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81176.1	003968	SAM-methylase	239	SEA_JUSTBECAUSE_7	Streptomyces phage JustBecause	GCA_003613775.1
QJD53578.1	003968	SAM-methylase	240	SEA_KELA_7	Streptomyces phage Kela	GCA_012934305.1
QBZ71906.1	003968	SAM-methylase	234	SEA_KRADAL_7	Streptomyces phage Kradal	GCA_004799925.1
AXH66168.1	003968	SAM-methylase	234	SEA_SATIS_7	Streptomyces phage Satis	GCA_003366315.1
ANM44828.1	003969	Cluster3641_1clades	239	KTN4_070	Pseudomonas phage KTN4	GCA_002607225.1
ATN94884.1	003969	Cluster3641_1clades	239	SL2_307	Pseudomonas phage SL2	GCA_002956015.1
QJB22706.1	003969	Cluster3641_1clades	239	fnug_63	Pseudomonas phage fnug	GCA_012837215.1
AAL82952.1	003969	Cluster3641_1clades	239	PHIKZ051	Pseudomonas virus phiKZ	GCA_000842965.1
ASU00173.1	003970	HNH	239	HWB28_gp379	Aeromonas phage AS-zj	GCA_002627665.1
AGR47738.1	003970	HNH	190	SmphiM12_106	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12987.1	003970	HNH	190	PHIM19_80	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12627.1	003970	HNH	190	PHIM7_79	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01196.1	003971	Cluster3643_1clades	230	AR9_g112	Bacillus phage AR9	GCA_001743835.1
ALN97865.1	003971	Cluster3643_1clades	230	Bp8pS_186	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00130.1	003971	Cluster3643_1clades	230	PBI_PBS1_308	Bacillus virus PBS1	GCA_002601325.1
CCE26356.1	003971	Cluster3643_1clades	239	g333	Yersinia phage phiR1-37	GCA_000895615.1
AYD80063.1	003972	Cluster3644_1clades	238	JA11_258	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66664.1	003972	Cluster3644_1clades	238	JA13_261	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66985.1	003972	Cluster3644_1clades	238	JA29_259	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67633.1	003972	Cluster3644_1clades	238	JA33_259	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96729.1	003973	Cluster3645_1clades	238	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97048.1	003973	Cluster3645_1clades	238	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96094.1	003973	Cluster3645_1clades	238	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96412.1	003973	Cluster3645_1clades	238	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96944.1	003974	Cluster3646_1clades	238	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97249.1	003974	Cluster3646_1clades	238	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96308.1	003974	Cluster3646_1clades	238	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96626.1	003974	Cluster3646_1clades	238	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81257.1	003975	SIG+TM+TM+TM	237	SEA_JUSTBECAUSE_88	Streptomyces phage JustBecause	GCA_003613775.1
QJD53660.1	003975	SIG+TM+TM+TM	237	SEA_KELA_89	Streptomyces phage Kela	GCA_012934305.1
QBZ71989.1	003975	SIG+TM+TM+TM	237	SEA_KRADAL_91	Streptomyces phage Kradal	GCA_004799925.1
AXH66252.1	003975	SIG+TM+TM+TM	237	SEA_SATIS_91	Streptomyces phage Satis	GCA_003366315.1
AYD81203.1	003976	Cluster3648_1clades	237	SEA_JUSTBECAUSE_34	Streptomyces phage JustBecause	GCA_003613775.1
QJD53606.1	003976	Cluster3648_1clades	191	SEA_KELA_35	Streptomyces phage Kela	GCA_012934305.1
QBZ71942.1	003976	Cluster3648_1clades	191	SEA_KRADAL_43	Streptomyces phage Kradal	GCA_004799925.1
AXH66204.1	003976	Cluster3648_1clades	191	SEA_SATIS_43	Streptomyces phage Satis	GCA_003366315.1
QAX96925.1	003977	Cluster3649_1clades	237	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97230.1	003977	Cluster3649_1clades	237	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96289.1	003977	Cluster3649_1clades	237	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96607.1	003977	Cluster3649_1clades	237	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45006.1	003978	Cluster3651_1clades	236	KTN4_248	Pseudomonas phage KTN4	GCA_002607225.1
ATN94708.1	003978	Cluster3651_1clades	236	SL2_131	Pseudomonas phage SL2	GCA_002956015.1
QJB22884.1	003978	Cluster3651_1clades	236	fnug_241	Pseudomonas phage fnug	GCA_012837215.1
AAL83107.1	003978	Cluster3651_1clades	236	PHIKZ206	Pseudomonas virus phiKZ	GCA_000842965.1
AYD79870.1	003979	Cluster3652_1clades	235	JA11_065	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66469.1	003979	Cluster3652_1clades	235	JA13_066	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66794.1	003979	Cluster3652_1clades	236	JA29_068	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67439.1	003979	Cluster3652_1clades	235	JA33_065	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ANM45039.1	003980	NarQ	235	KTN4_281	Pseudomonas phage KTN4	GCA_002607225.1
ATN94675.1	003980	NarQ	235	SL2_098	Pseudomonas phage SL2	GCA_002956015.1
QJB22915.1	003980	NarQ	235	fnug_272	Pseudomonas phage fnug	GCA_012837215.1
AAL83134.1	003980	NarQ	235	PHIKZ233	Pseudomonas virus phiKZ	GCA_000842965.1
AFA44492.1	003981	Tox-HNH	235	RaK2_00219	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43983.1	003981	Tox-HNH	134	CBB_420	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK59228.1	003981	Tox-HNH	133	g420	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58694.1	003981	Tox-HNH	133	g417	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD81237.1	003982	Glyco_transf_7C	235	SEA_JUSTBECAUSE_68	Streptomyces phage JustBecause	GCA_003613775.1
QJD53640.1	003982	Glyco_transf_7C	235	SEA_KELA_69	Streptomyces phage Kela	GCA_012934305.1
QBZ71971.1	003982	Glyco_transf_7C	235	SEA_KRADAL_73	Streptomyces phage Kradal	GCA_004799925.1
AXH66234.1	003982	Glyco_transf_7C	235	SEA_SATIS_73	Streptomyces phage Satis	GCA_003366315.1
QDH83607.1	003983	SIG+BRK	228	H1O15_gp181	Achromobacter phage Motura	GCA_006964305.1
QBX06502.1	003983	SIG+BRK	235	BcepSaruman_089	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74469.1	003983	SIG+BRK	235	BcepSauron_089	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41573.1	003983	SIG+BRK	235	RSL1_ORF128	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96929.1	003984	TM+TM	235	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97234.1	003984	TM+TM	235	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96293.1	003984	TM+TM	235	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96611.1	003984	TM+TM	235	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD79835.1	003985	Cluster3659_1clades	234	JA11_030	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66434.1	003985	Cluster3659_1clades	234	JA13_031	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66758.1	003985	Cluster3659_1clades	234	JA29_032	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67404.1	003985	Cluster3659_1clades	234	JA33_030	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXG67341.1	003986	TM	234	AD1_297	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG66658.1	003986	TM	220	JA13_255	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AWY08621.1	003986	TM	230	Alexandra_316	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58944.1	003986	TM	230	Y3_304	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AYD81238.1	003987	Cluster3661_1clades	234	SEA_JUSTBECAUSE_69	Streptomyces phage JustBecause	GCA_003613775.1
QJD53641.1	003987	Cluster3661_1clades	234	SEA_KELA_70	Streptomyces phage Kela	GCA_012934305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBZ71972.1	003987	Cluster3661_1clades	232	SEA_KRADAL_74	Streptomyces phage Kradal	GCA_004799925.1
AXH66235.1	003987	Cluster3661_1clades	232	SEA_SATIS_74	Streptomyces phage Satis	GCA_003366315.1
AFU87884.1	003988	Cluster3662_1clades	233	CcrColossus_gp014	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68553.1	003988	Cluster3662_1clades	102	CcrPW_gp014	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68554.1	003988	Cluster3662_1clades	125	CcrPW_gp015	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69003.1	003988	Cluster3662_1clades	227	CcrPW_gp464	Caulobacter phage CcrPW	GCA_003443275.1
AMR59725.1	003989	PyocinS	232	SEGD1_076	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ48378.1	003989	PyocinS	232	CAITLIN_83	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48651.1	003989	PyocinS	233	CHRISDB_89	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AWN09025.1	003989	PyocinS	232	MLDJOKPK_00084	Salmonella phage SPAsTU	GCA_003183805.1
AXG67200.1	003990	Cluster3664_1clades	231	AD1_156	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08433.1	003990	Cluster3664_1clades	231	Alexandra_161	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58797.1	003990	Cluster3664_1clades	231	Y3_157	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28635.1	003990	Cluster3664_1clades	233	YOLOSWAG_155	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXG67074.1	003991	Cluster3665_1clades	232	AD1_030	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08308.1	003991	Cluster3665_1clades	228	Alexandra_28	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58672.1	003991	Cluster3665_1clades	216	Y3_032	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28513.1	003991	Cluster3665_1clades	218	YOLOSWAG_28	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QAX96642.1	003992	Cluster3666_1clades	232	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96960.1	003992	Cluster3666_1clades	232	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96006.1	003992	Cluster3666_1clades	232	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96324.1	003992	Cluster3666_1clades	232	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83447.1	003993	HSP70	186	H1O15_gp039	Achromobacter phage Motura	GCA_006964305.1
QBX06656.1	003993	HSP70	232	BcepSaruman_243	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74624.1	003993	HSP70	232	BcepSauron_244	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41667.1	003993	HSP70	137	RSL1_ORF218	Ralstonia phage phiRSL1	GCA_000879455.1
AGX01860.1	003994	SLATT	231	CF95_gp138	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65444.1	003994	SLATT	231	2050HW_00109	Serratia phage 2050HW	GCA_002628125.1
QDB71214.1	003994	SLATT	231	CPT_Moabite_184	Serratia phage Moabite	GCA_006384735.1
QFP93137.1	003994	SLATT	230	-	Serratia phage PCH45	GCA_009187865.1
AYD80009.1	003995	Cluster3669_1clades	213	JA11_204	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66607.1	003995	Cluster3669_1clades	231	JA13_204	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66932.1	003995	Cluster3669_1clades	213	JA29_206	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67579.1	003995	Cluster3669_1clades	213	JA33_205	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFA44472.1	003996	Cluster3670_1clades	175	RaK2_00199	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW19124.1	003996	Cluster3670_1clades	231	7t3_0609	Salmonella phage 7t3	GCA_006083215.1
AZU98361.1	003996	Cluster3670_1clades	231	CPT_Munch_421	Salmonella phage Munch	GCA_004015485.1
QIG62621.1	003996	Cluster3670_1clades	231	SEPL_008	Salmonella phage SE_PL	GCA_011067555.1
QDH83420.1	003997	Cluster3671_1clades	217	H1O15_gp011	Achromobacter phage Motura	GCA_006964305.1
QBX06637.1	003997	Cluster3671_1clades	216	BcepSaruman_224	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74607.1	003997	Cluster3671_1clades	231	BcepSauron_227	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41702.1	003997	Cluster3671_1clades	230	RSL1_ORF254	Ralstonia phage phiRSL1	GCA_000879455.1
BAS04876.1	003998	Cluster3672_1clades	193	AVU11_gp084	Ralstonia phage RSF1	GCA_001500875.1
BAS04875.1	003998	Cluster3672_1clades	230	AVU11_gp083	Ralstonia phage RSF1	GCA_001500875.1
BAQ02608.2	003998	Cluster3672_1clades	196	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02607.2	003998	Cluster3672_1clades	218	-	Ralstonia phage RSL2	GCA_001503055.1
AYD80036.1	003999	Cluster3673_1clades	213	JA11_231	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66635.1	003999	Cluster3673_1clades	229	JA13_232	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66959.1	003999	Cluster3673_1clades	213	JA29_233	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67606.1	003999	Cluster3673_1clades	213	JA33_232	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ANM45069.1	004000	Cluster3674_1clades	228	KTN4_311	Pseudomonas phage KTN4	GCA_002607225.1
ATN94646.1	004000	Cluster3674_1clades	228	SL2_069	Pseudomonas phage SL2	GCA_002956015.1
QJB22944.1	004000	Cluster3674_1clades	228	fnug_301	Pseudomonas phage fnug	GCA_012837215.1
AAL83158.1	004000	Cluster3674_1clades	228	PHIKZ257	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45088.1	004001	Cluster3675_1clades	228	KTN4_330	Pseudomonas phage KTN4	GCA_002607225.1
ATN94627.1	004001	Cluster3675_1clades	228	SL2_050	Pseudomonas phage SL2	GCA_002956015.1
QJB22964.1	004001	Cluster3675_1clades	228	fnug_321	Pseudomonas phage fnug	GCA_012837215.1
AAL83174.1	004001	Cluster3675_1clades	228	PHIKZ273	Pseudomonas virus phiKZ	GCA_000842965.1
QDB70443.1	004002	Cluster3676_1clades	219	CF8_0031	Aeromonas phage CF8	GCA_006384595.2
QDJ96653.1	004002	Cluster3676_1clades	82	PS1_0142	Aeromonas phage PS1	GCA_007051165.2
QDJ96654.1	004002	Cluster3676_1clades	154	PS1_0143	Aeromonas phage PS1	GCA_007051165.2
QFR59531.1	004002	Cluster3676_1clades	228	PS2_0140	Aeromonas phage PS2	GCA_009388305.2
ASU03764.1	004003	Cluster3677_1clades	227	JOAD_151	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03763.1	004003	Cluster3677_1clades	221	JOAD_152	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03520.1	004003	Cluster3677_1clades	227	RISINGSUN_150	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03519.1	004003	Cluster3677_1clades	221	RISINGSUN_151	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QAX96805.1	004004	HTH	227	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97124.1	004004	HTH	227	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96170.1	004004	HTH	227	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96488.1	004004	HTH	227	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45109.1	004005	Cluster3680_1clades	226	KTN4_351	Pseudomonas phage KTN4	GCA_002607225.1
ATN94604.1	004005	Cluster3680_1clades	226	SL2_027	Pseudomonas phage SL2	GCA_002956015.1
QJB22986.1	004005	Cluster3680_1clades	226	fnug_343	Pseudomonas phage fnug	GCA_012837215.1
AAL83192.1	004005	Cluster3680_1clades	226	PHIKZ291	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96872.1	004006	Cluster3681_1clades	224	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97177.1	004006	Cluster3681_1clades	224	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96236.1	004006	Cluster3681_1clades	224	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96554.1	004006	Cluster3681_1clades	224	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01740.1	004007	Cluster3682_1clades	198	CF95_gp018	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65652.1	004007	Cluster3682_1clades	187	2050HW_00317	Serratia phage 2050HW	GCA_002628125.1
QDB71076.1	004007	Cluster3682_1clades	187	CPT_Moabite_044	Serratia phage Moabite	GCA_006384735.1
QFP93143.1	004007	Cluster3682_1clades	224	-	Serratia phage PCH45	GCA_009187865.1
AXH72609.1	004008	Cluster3684_1clades	164	-	Myoviridae sp.	GCA_003657725.1
AXH72575.1	004008	Cluster3684_1clades	170	-	Myoviridae sp.	GCA_003657725.1
AXH72687.1	004008	Cluster3684_1clades	204	-	Myoviridae sp.	GCA_003657725.1
AXH72701.1	004008	Cluster3684_1clades	222	-	Myoviridae sp.	GCA_003657725.1
AYD80079.1	004009	Cluster3685_1clades	219	JA11_274	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66680.1	004009	Cluster3685_1clades	219	JA13_277	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67000.1	004009	Cluster3685_1clades	221	JA29_274	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67649.1	004009	Cluster3685_1clades	219	JA33_275	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96724.1	004010	TM+TM	221	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97043.1	004010	TM+TM	221	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96089.1	004010	TM+TM	221	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96407.1	004010	TM+TM	221	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFU88291.1	004011	Cluster3687_1clades	220	CcrColossus_gp421	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88292.1	004011	Cluster3687_1clades	95	CcrColossus_gp422	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68965.1	004011	Cluster3687_1clades	220	CcrPW_gp426c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68966.1	004011	Cluster3687_1clades	95	CcrPW_gp427c	Caulobacter phage CcrPW	GCA_003443275.1
AYD81269.1	004012	TM	220	SEA_JUSTBECAUSE_100	Streptomyces phage JustBecause	GCA_003613775.1
QJD53672.1	004012	TM	220	SEA_KELA_101	Streptomyces phage Kela	GCA_012934305.1
QBZ72000.1	004012	TM	215	SEA_KRADAL_102	Streptomyces phage Kradal	GCA_004799925.1
AXH66263.1	004012	TM	215	SEA_SATIS_102	Streptomyces phage Satis	GCA_003366315.1
QAX96844.1	004013	Cluster3689_1clades	220	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97149.1	004013	Cluster3689_1clades	220	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96208.1	004013	Cluster3689_1clades	220	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96526.1	004013	Cluster3689_1clades	220	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANS06005.1	004014	Phage_holin_T	214	ABCD_0265	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97284.1	004014	Phage_holin_T	214	E_276	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70803.1	004014	Phage_holin_T	219	phiC120_c97	Escherichia phage phiC120	GCA_002621185.1
AAX78805.1	004014	Phage_holin_T	196	RB43ORF283w	Escherichia virus RB43	GCA_000863505.1
AMS01161.1	004015	Cluster3691_1clades	140	AR9_g077	Bacillus phage AR9	GCA_001743835.1
ALN97892.1	004015	Cluster3691_1clades	218	Bp8pS_213	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97893.1	004015	Cluster3691_1clades	143	Bp8pS_214	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00090.1	004015	Cluster3691_1clades	140	PBI_PBS1_268	Bacillus virus PBS1	GCA_002601325.1
AXQ68927.1	004016	Cluster3692_1clades	107	CcrPW_gp388c	Caulobacter phage CcrPW	GCA_003443275.1
AFU87736.1	004016	Cluster3692_1clades	217	CcrKarma_gp219	Caulobacter virus Karma	GCA_000901575.1
AFU86695.1	004016	Cluster3692_1clades	207	CcrRogue_gp213	Caulobacter virus Rogue	GCA_000900555.1
AFU88532.1	004016	Cluster3692_1clades	216	CcrSwift_gp214	Caulobacter virus Swift	GCA_000899655.1
QAX96815.1	004017	Cluster3693_1clades	217	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97134.1	004017	Cluster3693_1clades	217	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96180.1	004017	Cluster3693_1clades	217	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96498.1	004017	Cluster3693_1clades	217	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96943.1	004018	Cluster3694_1clades	217	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97248.1	004018	Cluster3694_1clades	217	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96307.1	004018	Cluster3694_1clades	217	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96625.1	004018	Cluster3694_1clades	217	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR48107.1	004019	Cluster3695_1clades	210	SmphiM12_475	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13653.1	004019	Cluster3695_1clades	216	PHIN3_390	Sinorhizobium phage phiN3	GCA_001501175.1
QGT54754.1	004019	Cluster3695_1clades	159	b23_0139	Synechococcus phage B23	GCA_009745195.1
QGT54384.1	004019	Cluster3695_1clades	159	b3_0140	Synechococcus phage B3	GCA_009745215.1
QAX96900.1	004020	Cluster3696_1clades	216	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97205.1	004020	Cluster3696_1clades	216	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96264.1	004020	Cluster3696_1clades	216	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96582.1	004020	Cluster3696_1clades	216	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96910.1	004021	Cluster3697_1clades	216	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97215.1	004021	Cluster3697_1clades	216	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96274.1	004021	Cluster3697_1clades	216	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96592.1	004021	Cluster3697_1clades	216	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFQ96796.1	004022	Cluster3698_1clades	199	G173_gp251	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48480.1	004022	Cluster3698_1clades	206	CAITLIN_185	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48759.1	004022	Cluster3698_1clades	215	CHRISDB_197	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ50509.1	004022	Cluster3698_1clades	199	STRATTON_84	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AYD81284.1	004023	SIG+Spc7_N	207	SEA_JUSTBECAUSE_115	Streptomyces phage JustBecause	GCA_003613775.1
QJD53687.1	004023	SIG+Spc7_N	207	SEA_KELA_116	Streptomyces phage Kela	GCA_012934305.1
QBZ72015.1	004023	SIG+Spc7_N	213	SEA_KRADAL_117	Streptomyces phage Kradal	GCA_004799925.1
AXH66278.1	004023	SIG+Spc7_N	215	SEA_SATIS_117	Streptomyces phage Satis	GCA_003366315.1
QAX96842.1	004024	Cluster3700_1clades	215	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97147.1	004024	Cluster3700_1clades	215	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96206.1	004024	Cluster3700_1clades	215	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96524.1	004024	Cluster3700_1clades	215	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX32494.1	004025	Cluster3701_1clades	214	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77029.1	004025	Cluster3701_1clades	178	PHABIO_398	Pseudomonas phage Phabio	GCA_002624965.1
AEH03752.1	004025	Cluster3701_1clades	208	329	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42067.1	004025	Cluster3701_1clades	214	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QAX96860.1	004026	Cluster3704_1clades	211	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97165.1	004026	Cluster3704_1clades	211	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96224.1	004026	Cluster3704_1clades	211	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96542.1	004026	Cluster3704_1clades	211	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45114.1	004027	halocin-C858	208	KTN4_356	Pseudomonas phage KTN4	GCA_002607225.1
ATN94599.1	004027	halocin-C858	194	SL2_022	Pseudomonas phage SL2	GCA_002956015.1
QJB22991.1	004027	halocin-C858	208	fnug_348	Pseudomonas phage fnug	GCA_012837215.1
AAL83195.1	004027	halocin-C858	209	PHIKZ294	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96851.1	004028	Cluster3707_1clades	209	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97156.1	004028	Cluster3707_1clades	209	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96215.1	004028	Cluster3707_1clades	209	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96533.1	004028	Cluster3707_1clades	209	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
APU01601.1	004029	Cluster3708_1clades	192	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53225.1	004029	Cluster3708_1clades	192	65p217	Aeromonas virus 65	GCA_000893255.1
QBX06750.1	004029	Cluster3708_1clades	209	BcepSaruman_337	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74719.1	004029	Cluster3708_1clades	209	BcepSauron_339	Burkholderia phage BcepSauron	GCA_005394215.1
AYD79915.1	004030	Cluster3709_1clades	208	JA11_110	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66514.1	004030	Cluster3709_1clades	208	JA13_111	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66839.1	004030	Cluster3709_1clades	208	JA29_113	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67484.1	004030	Cluster3709_1clades	208	JA33_110	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXQ69044.1	004031	Cluster3710_1clades	208	CcrBL9_gp020	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69560.1	004031	Cluster3710_1clades	208	CcrBL9_gp536	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69604.1	004031	Cluster3710_1clades	208	CcrSC_gp022	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70104.1	004031	Cluster3710_1clades	208	CcrSC_gp522	Caulobacter phage CcrSC	GCA_003443315.1
AYD81243.1	004032	35exo	208	SEA_JUSTBECAUSE_74	Streptomyces phage JustBecause	GCA_003613775.1
QJD53646.1	004032	35exo	208	SEA_KELA_75	Streptomyces phage Kela	GCA_012934305.1
QBZ71976.1	004032	35exo	207	SEA_KRADAL_78	Streptomyces phage Kradal	GCA_004799925.1
AXH66239.1	004032	35exo	207	SEA_SATIS_78	Streptomyces phage Satis	GCA_003366315.1
AYD81419.1	004033	Cluster3712_1clades	208	SEA_JUSTBECAUSE_264	Streptomyces phage JustBecause	GCA_003613775.1
QJD53824.1	004033	Cluster3712_1clades	208	SEA_KELA_264	Streptomyces phage Kela	GCA_012934305.1
QBZ72150.1	004033	Cluster3712_1clades	198	SEA_KRADAL_264	Streptomyces phage Kradal	GCA_004799925.1
AXH66413.1	004033	Cluster3712_1clades	198	SEA_SATIS_264	Streptomyces phage Satis	GCA_003366315.1
QAX96894.1	004034	Cluster3713_1clades	208	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97199.1	004034	Cluster3713_1clades	208	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96258.1	004034	Cluster3713_1clades	208	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96576.1	004034	Cluster3713_1clades	208	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMM44004.1	004035	Cluster3714_1clades	207	CBB_441	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88963.1	004035	Cluster3714_1clades	201	BF_0438	Serratia phage BF	GCA_002619745.1
SOK59250.1	004035	Cluster3714_1clades	201	g442	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58715.1	004035	Cluster3714_1clades	201	g438	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD80097.1	004036	Cluster3715_1clades	207	JA11_292	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66698.1	004036	Cluster3715_1clades	207	JA13_295	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67017.1	004036	Cluster3715_1clades	207	JA29_291	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67667.1	004036	Cluster3715_1clades	207	JA33_293	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81482.1	004037	Cluster3716_1clades	207	SEA_JUSTBECAUSE_327	Streptomyces phage JustBecause	GCA_003613775.1
QJD53885.1	004037	Cluster3716_1clades	207	SEA_KELA_325	Streptomyces phage Kela	GCA_012934305.1
QBZ72213.1	004037	Cluster3716_1clades	207	SEA_KRADAL_327	Streptomyces phage Kradal	GCA_004799925.1
AXH66476.1	004037	Cluster3716_1clades	207	SEA_SATIS_327	Streptomyces phage Satis	GCA_003366315.1
QGZ14558.1	004038	Cluster3717_1clades	197	HWC77_gp195	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04175.1	004038	Cluster3717_1clades	197	HWC03_gp020	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23183.1	004038	Cluster3717_1clades	207	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47546.1	004038	Cluster3717_1clades	190	HWC35_gp152	Vibrio phage USC-1	GCA_006864065.1
QAX96898.1	004039	Cluster3718_1clades	206	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97203.1	004039	Cluster3718_1clades	206	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96262.1	004039	Cluster3718_1clades	206	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96580.1	004039	Cluster3718_1clades	206	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01941.1	004040	Cluster3719_1clades	205	CF95_gp220	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65365.1	004040	Cluster3719_1clades	189	2050HW_00030	Serratia phage 2050HW	GCA_002628125.1
QDB71150.1	004040	Cluster3719_1clades	189	CPT_Moabite_120	Serratia phage Moabite	GCA_006384735.1
QFP93165.1	004040	Cluster3719_1clades	196	-	Serratia phage PCH45	GCA_009187865.1
QAX96720.1	004041	Cluster3720_1clades	205	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97039.1	004041	Cluster3720_1clades	205	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96085.1	004041	Cluster3720_1clades	205	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96403.1	004041	Cluster3720_1clades	205	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81469.1	004042	SIG+ydhR	203	SEA_JUSTBECAUSE_314	Streptomyces phage JustBecause	GCA_003613775.1
QJD53872.1	004042	SIG+ydhR	203	SEA_KELA_312	Streptomyces phage Kela	GCA_012934305.1
QBZ72202.1	004042	SIG+ydhR	204	SEA_KRADAL_316	Streptomyces phage Kradal	GCA_004799925.1
AXH66465.1	004042	SIG+ydhR	204	SEA_SATIS_316	Streptomyces phage Satis	GCA_003366315.1
AYD80077.1	004043	Cluster3722_1clades	202	JA11_272	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66678.1	004043	Cluster3722_1clades	203	JA13_275	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66998.1	004043	Cluster3722_1clades	203	JA29_272	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67647.1	004043	Cluster3722_1clades	202	JA33_273	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGX01917.1	004044	TM	194	CF95_gp195	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65391.1	004044	TM	202	2050HW_00056	Serratia phage 2050HW	GCA_002628125.1
QDB71172.1	004044	TM	202	CPT_Moabite_142	Serratia phage Moabite	GCA_006384735.1
QFP93176.1	004044	TM	178	-	Serratia phage PCH45	GCA_009187865.1
AMS01096.1	004045	Cluster3724_1clades	190	AR9_g011	Bacillus phage AR9	GCA_001743835.1
ALN97729.1	004045	Cluster3724_1clades	190	Bp8pS_050	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00018.1	004045	Cluster3724_1clades	190	PBI_PBS1_196	Bacillus virus PBS1	GCA_002601325.1
CCE26070.1	004045	Cluster3724_1clades	202	g046	Yersinia phage phiR1-37	GCA_000895615.1
AFO71288.1	004046	Cluster3725_1clades	195	CR5_068	Cronobacter phage CR5	GCA_000910235.1
QBP07496.1	004046	Cluster3725_1clades	192	DERBICUS_70	Erwinia phage Derbicus	GCA_004521655.1
ANZ48920.1	004046	Cluster3725_1clades	192	EARLPHILLIPIV_70	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50261.1	004046	Cluster3725_1clades	201	PHOBOS_71	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD80098.1	004047	Cluster3726_1clades	201	JA11_293	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66699.1	004047	Cluster3726_1clades	201	JA13_296	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67018.1	004047	Cluster3726_1clades	201	JA29_292	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67668.1	004047	Cluster3726_1clades	201	JA33_294	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFC21504.1	004048	Cluster3727_1clades	178	GAP32_056	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88576.1	004048	Cluster3727_1clades	191	BF_0051	Serratia phage BF	GCA_002619745.1
SOK58851.1	004048	Cluster3727_1clades	201	g043	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58313.1	004048	Cluster3727_1clades	201	g036	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AGX01766.1	004049	Cluster3728_1clades	200	CF95_gp044	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65625.1	004049	Cluster3728_1clades	199	2050HW_00290	Serratia phage 2050HW	GCA_002628125.1
QDB71052.1	004049	Cluster3728_1clades	199	CPT_Moabite_020	Serratia phage Moabite	GCA_006384735.1
QFP93167.1	004049	Cluster3728_1clades	190	-	Serratia phage PCH45	GCA_009187865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGX01938.1	004050	Cluster3729_1clades	200	CF95_gp216	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65373.1	004050	Cluster3729_1clades	165	2050HW_00038	Serratia phage 2050HW	GCA_002628125.1
QDB71157.1	004050	Cluster3729_1clades	188	CPT_Moabite_127	Serratia phage Moabite	GCA_006384735.1
QFP93166.1	004050	Cluster3729_1clades	192	-	Serratia phage PCH45	GCA_009187865.1
AXG67253.1	004051	Cluster3730_1clades	190	AD1_209	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08483.1	004051	Cluster3730_1clades	190	Alexandra_219	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58853.1	004051	Cluster3730_1clades	190	Y3_213	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28684.1	004051	Cluster3730_1clades	200	YOLOSWAG_206	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QAX96861.1	004052	Cluster3731_1clades	200	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97166.1	004052	Cluster3731_1clades	200	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96225.1	004052	Cluster3731_1clades	200	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96543.1	004052	Cluster3731_1clades	200	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45031.1	004053	Cluster3732_1clades	199	KTN4_273	Pseudomonas phage KTN4	GCA_002607225.1
ATN94683.1	004053	Cluster3732_1clades	199	SL2_106	Pseudomonas phage SL2	GCA_002956015.1
QJB22908.1	004053	Cluster3732_1clades	199	fnug_265	Pseudomonas phage fnug	GCA_012837215.1
AAL83129.1	004053	Cluster3732_1clades	199	PHIKZ228	Pseudomonas virus phiKZ	GCA_000842965.1
APU01682.1	004054	Phage_gp49_66	199	-	Aeromonas phage 65.2	GCA_002618145.1
QAX98052.1	004054	Phage_gp49_66	98	ASswx1_412	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39350.1	004054	Phage_gp49_66	98	CC2_117	Aeromonas phage CC2	GCA_000903495.1
ADQ53318.1	004054	Phage_gp49_66	199	65p310	Aeromonas virus 65	GCA_000893255.1
AFO71301.1	004055	Cluster3734_1clades	199	CR5_081	Cronobacter phage CR5	GCA_000910235.1
QBP07510.1	004055	Cluster3734_1clades	198	DERBICUS_84	Erwinia phage Derbicus	GCA_004521655.1
ANZ48934.1	004055	Cluster3734_1clades	198	EARLPHILLIPIV_84	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50274.1	004055	Cluster3734_1clades	195	PHOBOS_84	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD79868.1	004056	Cluster3735_1clades	199	JA11_063	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66467.1	004056	Cluster3735_1clades	199	JA13_064	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66792.1	004056	Cluster3735_1clades	199	JA29_066	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67437.1	004056	Cluster3735_1clades	199	JA33_063	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96669.1	004057	Cluster3736_1clades	198	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96987.1	004057	Cluster3736_1clades	198	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96033.1	004057	Cluster3736_1clades	198	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96351.1	004057	Cluster3736_1clades	198	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01857.1	004058	Cluster3737_1clades	197	CF95_gp135	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65447.1	004058	Cluster3737_1clades	190	2050HW_00112	Serratia phage 2050HW	GCA_002628125.1
QDB71217.1	004058	Cluster3737_1clades	190	CPT_Moabite_187	Serratia phage Moabite	GCA_006384735.1
QFP93174.1	004058	Cluster3737_1clades	180	-	Serratia phage PCH45	GCA_009187865.1
AYD79852.1	004059	Cluster3738_1clades	197	JA11_047	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66452.1	004059	Cluster3738_1clades	197	JA13_049	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66776.1	004059	Cluster3738_1clades	196	JA29_050	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67421.1	004059	Cluster3738_1clades	197	JA33_047	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80034.1	004060	Cluster3739_1clades	197	JA11_229	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66633.1	004060	Cluster3739_1clades	197	JA13_230	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66957.1	004060	Cluster3739_1clades	197	JA29_231	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67604.1	004060	Cluster3739_1clades	197	JA33_230	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81463.1	004061	Cluster3740_1clades	197	SEA_JUSTBECAUSE_308	Streptomyces phage JustBecause	GCA_003613775.1
QJD53866.1	004061	Cluster3740_1clades	197	SEA_KELA_306	Streptomyces phage Kela	GCA_012934305.1
QBZ72196.1	004061	Cluster3740_1clades	194	SEA_KRADAL_310	Streptomyces phage Kradal	GCA_004799925.1
AXH66459.1	004061	Cluster3740_1clades	194	SEA_SATIS_310	Streptomyces phage Satis	GCA_003366315.1
AUE22633.1	004062	Cluster3741_1clades	195	Ah1_00092	Aeromonas phage Ah1	GCA_002957415.1
ADQ52817.1	004062	Cluster3741_1clades	195	PX29p098	Aeromonas phage PX29	GCA_000920195.1
ADM80073.1	004062	Cluster3741_1clades	194	phiAS5_ORF0230	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17760.1	004062	Cluster3741_1clades	195	Aeh1ORF099c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21496.1	004063	Cluster3742_1clades	193	GAP32_048	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43618.1	004063	Cluster3742_1clades	195	CBB_53	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88568.1	004063	Cluster3742_1clades	189	BF_0043	Serratia phage BF	GCA_002619745.1
SOK58305.1	004063	Cluster3742_1clades	194	g028	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDJ97372.1	004064	Cluster3743_1clades	188	D6_0213	Aeromonas phage D6	GCA_007051205.2
QDH47152.1	004064	Cluster3743_1clades	188	LAh10_127	Aeromonas phage LAh10	GCA_006863975.1
QDJ96716.1	004064	Cluster3743_1clades	195	PS1_0205	Aeromonas phage PS1	GCA_007051165.2
QFR59349.1	004064	Cluster3743_1clades	195	PS2_0207	Aeromonas phage PS2	GCA_009388305.2
AFO71448.1	004065	Cluster3744_1clades	190	CR5_228	Cronobacter phage CR5	GCA_000910235.1
QBP07661.1	004065	Cluster3744_1clades	194	DERBICUS_235	Erwinia phage Derbicus	GCA_004521655.1
ANZ49085.1	004065	Cluster3744_1clades	194	EARLPHILLIPIV_236	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50432.1	004065	Cluster3744_1clades	188	PHOBOS_242	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QDH83529.1	004066	Cluster3746_1clades	131	H1O15_gp259	Achromobacter phage Motura	GCA_006964305.1
ASU03757.1	004066	Cluster3746_1clades	194	JOAD_158	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03513.1	004066	Cluster3746_1clades	194	RISINGSUN_157	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QFP93217.1	004066	Cluster3746_1clades	132	-	Serratia phage PCH45	GCA_009187865.1
AYD81180.1	004067	Cluster3747_1clades	194	SEA_JUSTBECAUSE_11	Streptomyces phage JustBecause	GCA_003613775.1
QJD53582.1	004067	Cluster3747_1clades	194	SEA_KELA_11	Streptomyces phage Kela	GCA_012934305.1
QBZ71911.1	004067	Cluster3747_1clades	192	SEA_KRADAL_12	Streptomyces phage Kradal	GCA_004799925.1
AXH66173.1	004067	Cluster3747_1clades	192	SEA_SATIS_12	Streptomyces phage Satis	GCA_003366315.1
QAX96893.1	004068	Cluster3748_1clades	194	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97198.1	004068	Cluster3748_1clades	194	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96257.1	004068	Cluster3748_1clades	194	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96575.1	004068	Cluster3748_1clades	194	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96930.1	004069	TM+TM	194	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97235.1	004069	TM+TM	194	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96294.1	004069	TM+TM	194	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96612.1	004069	TM+TM	194	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR47881.1	004070	Cluster3750_1clades	193	SmphiM12_249	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13082.1	004070	Cluster3750_1clades	193	PHIM19_177	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12722.1	004070	Cluster3750_1clades	193	PHIM7_177	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13452.1	004070	Cluster3750_1clades	193	PHIN3_189	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67278.1	004071	Cluster3751_1clades	177	AD1_234	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08503.1	004071	Cluster3751_1clades	174	Alexandra_243	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58878.1	004071	Cluster3751_1clades	174	Y3_238	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28711.1	004071	Cluster3751_1clades	193	YOLOSWAG_233	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QAX96749.1	004072	TM+TM	193	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97068.1	004072	TM+TM	193	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96114.1	004072	TM+TM	193	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96432.1	004072	TM+TM	193	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR48048.2	004073	Cluster3754_1clades	192	SmphiM12_416	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13230.1	004073	Cluster3754_1clades	192	PHIM19_325	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12870.1	004073	Cluster3754_1clades	192	PHIM7_325	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13593.1	004073	Cluster3754_1clades	192	PHIN3_330	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79825.1	004074	Cluster3755_1clades	192	JA11_020	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66424.1	004074	Cluster3755_1clades	192	JA13_021	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66746.1	004074	Cluster3755_1clades	192	JA29_020	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67394.1	004074	Cluster3755_1clades	192	JA33_020	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80030.1	004075	Cluster3756_1clades	192	JA11_225	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66629.1	004075	Cluster3756_1clades	192	JA13_226	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66953.1	004075	Cluster3756_1clades	192	JA29_227	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67600.1	004075	Cluster3756_1clades	192	JA33_226	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
BAS04872.1	004076	DNAglycofused-2OGFEDO	181	AVU11_gp080	Ralstonia phage RSF1	GCA_001500875.1
BAS04874.2	004076	DNAglycofused-2OGFEDO	192	AVU11_gp082	Ralstonia phage RSF1	GCA_001500875.1
BAQ02606.2	004076	DNAglycofused-2OGFEDO	171	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02604.1	004076	DNAglycofused-2OGFEDO	182	AVU38_gp076	Ralstonia phage RSL2	GCA_001503055.1
QGZ14557.1	004077	Cluster3758_1clades	192	HWC77_gp194	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04176.1	004077	Cluster3758_1clades	192	HWC03_gp021	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23182.1	004077	Cluster3758_1clades	182	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47547.1	004077	Cluster3758_1clades	182	HWC35_gp153	Vibrio phage USC-1	GCA_006864065.1
AFO71387.1	004078	Cluster3759_1clades	188	CR5_167	Cronobacter phage CR5	GCA_000910235.1
QBP07598.1	004078	Cluster3759_1clades	192	DERBICUS_172	Erwinia phage Derbicus	GCA_004521655.1
ANZ49021.1	004078	Cluster3759_1clades	189	EARLPHILLIPIV_172	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50368.1	004078	Cluster3759_1clades	189	PHOBOS_178	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81229.1	004079	Cluster3760_1clades	186	SEA_JUSTBECAUSE_60	Streptomyces phage JustBecause	GCA_003613775.1
QJD53632.1	004079	Cluster3760_1clades	192	SEA_KELA_61	Streptomyces phage Kela	GCA_012934305.1
QBZ71964.1	004079	Cluster3760_1clades	190	SEA_KRADAL_66	Streptomyces phage Kradal	GCA_004799925.1
AXH66227.1	004079	Cluster3760_1clades	190	SEA_SATIS_66	Streptomyces phage Satis	GCA_003366315.1
ANZ49782.1	004080	Cluster3761_1clades	190	MACHINA_144	Erwinia phage Machina	GCA_002758035.1
ANZ49226.1	004080	Cluster3761_1clades	190	HUXLEY_144	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50054.1	004080	Cluster3761_1clades	190	PARSHIK_145	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50575.1	004080	Cluster3761_1clades	76	STRATTON_150	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AYD81264.1	004081	TM+TM+TM+TM	190	SEA_JUSTBECAUSE_95	Streptomyces phage JustBecause	GCA_003613775.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QJD53667.1	004081	TM+TM+TM+TM	190	SEA_KELA_96	Streptomyces phage Kela	GCA_012934305.1
QBZ71996.1	004081	TM+TM+TM+TM	190	SEA_KRADAL_98	Streptomyces phage Kradal	GCA_004799925.1
AXH66259.1	004081	TM+TM+TM+TM	190	SEA_SATIS_98	Streptomyces phage Satis	GCA_003366315.1
AXQ69028.1	004082	Cluster3763_1clades	190	CcrBL9_gp004	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69544.1	004082	Cluster3763_1clades	190	CcrBL9_gp520	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69587.1	004082	Cluster3763_1clades	190	CcrSC_gp005	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70087.1	004082	Cluster3763_1clades	190	CcrSC_gp505	Caulobacter phage CcrSC	GCA_003443315.1
QBZ70795.1	004083	SIG+Plant_NMP1	180	pETSU_214	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70796.1	004083	SIG+Plant_NMP1	189	pETSU_216	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89733.1	004083	SIG+Plant_NMP1	183	OBP_296	Pseudomonas phage OBP	GCA_000896635.1
AEV89734.1	004083	SIG+Plant_NMP1	189	OBP_297	Pseudomonas phage OBP	GCA_000896635.1
AYD81215.1	004084	Cluster3765_1clades	189	SEA_JUSTBECAUSE_46	Streptomyces phage JustBecause	GCA_003613775.1
QJD53618.1	004084	Cluster3765_1clades	189	SEA_KELA_47	Streptomyces phage Kela	GCA_012934305.1
QBZ71951.1	004084	Cluster3765_1clades	189	SEA_KRADAL_52	Streptomyces phage Kradal	GCA_004799925.1
AXH66213.1	004084	Cluster3765_1clades	189	SEA_SATIS_52	Streptomyces phage Satis	GCA_003366315.1
AXQ69026.1	004085	Cluster3766_1clades	189	CcrBL9_gp002	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69542.1	004085	Cluster3766_1clades	189	CcrBL9_gp518	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69585.1	004085	Cluster3766_1clades	187	CcrSC_gp003	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70085.1	004085	Cluster3766_1clades	187	CcrSC_gp503	Caulobacter phage CcrSC	GCA_003443315.1
AYD81464.1	004086	Cluster3767_1clades	189	SEA_JUSTBECAUSE_309	Streptomyces phage JustBecause	GCA_003613775.1
QJD53867.1	004086	Cluster3767_1clades	189	SEA_KELA_307	Streptomyces phage Kela	GCA_012934305.1
QBZ72197.1	004086	Cluster3767_1clades	121	SEA_KRADAL_311	Streptomyces phage Kradal	GCA_004799925.1
AXH66460.1	004086	Cluster3767_1clades	121	SEA_SATIS_311	Streptomyces phage Satis	GCA_003366315.1
QAX96666.1	004087	Cluster3768_1clades	189	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96984.1	004087	Cluster3768_1clades	189	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96030.1	004087	Cluster3768_1clades	189	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96348.1	004087	Cluster3768_1clades	189	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR47941.2	004088	Cluster3769_1clades	188	SmphiM12_309	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13137.1	004088	Cluster3769_1clades	188	PHIM19_232	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12776.1	004088	Cluster3769_1clades	188	PHIM7_231	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13505.1	004088	Cluster3769_1clades	188	PHIN3_242	Sinorhizobium phage phiN3	GCA_001501175.1
AFO71278.1	004089	Cluster3770_1clades	185	CR5_058	Cronobacter phage CR5	GCA_000910235.1
QBP07485.1	004089	Cluster3770_1clades	181	DERBICUS_59	Erwinia phage Derbicus	GCA_004521655.1
ANZ48909.1	004089	Cluster3770_1clades	181	EARLPHILLIPIV_59	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50250.1	004089	Cluster3770_1clades	188	PHOBOS_60	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81220.1	004090	Cluster3771_1clades	188	SEA_JUSTBECAUSE_51	Streptomyces phage JustBecause	GCA_003613775.1
QJD53623.1	004090	Cluster3771_1clades	188	SEA_KELA_52	Streptomyces phage Kela	GCA_012934305.1
QBZ71956.1	004090	Cluster3771_1clades	188	SEA_KRADAL_57	Streptomyces phage Kradal	GCA_004799925.1
AXH66218.1	004090	Cluster3771_1clades	188	SEA_SATIS_57	Streptomyces phage Satis	GCA_003366315.1
QAX96688.1	004091	SIG+TM	188	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97006.1	004091	SIG+TM	188	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96052.1	004091	SIG+TM	188	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96370.1	004091	SIG+TM	188	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFQ96801.1	004092	FamB-divDNAPol	187	G173_gp256	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48100.1	004092	FamB-divDNAPol	187	ASESINO_87	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50514.1	004092	FamB-divDNAPol	187	STRATTON_89	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXF51088.1	004092	FamB-divDNAPol	94	MLDJOKPK_00093	Salmonella phage SPAsTU	GCA_003183805.1
AIR93408.1	004093	Cluster3775_1clades	187	AVU42_gp023	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76075.1	004093	Cluster3775_1clades	179	PBI_BELLAMY_30	Synechococcus phage Bellamy	GCA_002627525.1
QCW23074.1	004093	Cluster3775_1clades	175	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70045.1	004093	Cluster3775_1clades	179	SynMITS9220M01_032	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QAX98365.1	004094	Cluster3776_1clades	186	ASfcp2_19	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52819.1	004094	Cluster3776_1clades	186	PX29p100	Aeromonas phage PX29	GCA_000920195.1
ADM80076.1	004094	Cluster3776_1clades	183	phiAS5_ORF0233	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17763.1	004094	Cluster3776_1clades	186	Aeh1ORF102c	Aeromonas virus Aeh1	GCA_000843245.1
AXG67326.1	004095	TraJ-RHH	183	AD1_282	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08553.1	004095	TraJ-RHH	184	Alexandra_297	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58926.1	004095	TraJ-RHH	186	Y3_286	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28748.1	004095	TraJ-RHH	152	YOLOSWAG_276	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFA44619.1	004096	N4ART	185	RaK2_00346	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18701.1	004096	N4ART	179	7t3_0180	Salmonella phage 7t3	GCA_006083215.1
AZU97973.1	004096	N4ART	179	CPT_Munch_029	Salmonella phage Munch	GCA_004015485.1
QIG63005.1	004096	N4ART	179	SEPL_392	Salmonella phage SE_PL	GCA_011067555.1
QAX96717.1	004097	Cluster3779_1clades	185	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97036.1	004097	Cluster3779_1clades	185	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96082.1	004097	Cluster3779_1clades	185	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96400.1	004097	Cluster3779_1clades	185	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44983.1	004098	Cluster3780_1clades	184	KTN4_225	Pseudomonas phage KTN4	GCA_002607225.1
ATN94731.1	004098	Cluster3780_1clades	164	SL2_154	Pseudomonas phage SL2	GCA_002956015.1
QJB22861.1	004098	Cluster3780_1clades	184	fnug_218	Pseudomonas phage fnug	GCA_012837215.1
AAL83086.1	004098	Cluster3780_1clades	184	PHIKZ185	Pseudomonas virus phiKZ	GCA_000842965.1
AUZ95435.1	004099	Cluster3781_1clades	79	FDI40_gp689	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72724.1	004099	Cluster3781_1clades	184	-	Myoviridae sp.	GCA_003657725.1
QCG76023.1	004099	Cluster3781_1clades	165	EST35_0141	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44451.1	004099	Cluster3781_1clades	166	PBI_SCTP2_436	Salicola phage SCTP-2	GCA_002625545.1
AXQ69384.1	004100	Ferretin	184	CcrBL9_gp360	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88126.1	004100	Ferretin	180	CcrColossus_gp256	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68803.1	004100	Ferretin	180	CcrPW_gp264	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69944.1	004100	Ferretin	184	CcrSC_gp362	Caulobacter phage CcrSC	GCA_003443315.1
QAX96816.1	004101	Cluster3783_1clades	184	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97135.1	004101	Cluster3783_1clades	184	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96181.1	004101	Cluster3783_1clades	184	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96499.1	004101	Cluster3783_1clades	184	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96899.1	004102	Cluster3784_1clades	184	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97204.1	004102	Cluster3784_1clades	184	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96263.1	004102	Cluster3784_1clades	184	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96581.1	004102	Cluster3784_1clades	184	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96905.1	004103	Cluster3785_1clades	184	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97210.1	004103	Cluster3785_1clades	184	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96269.1	004103	Cluster3785_1clades	184	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96587.1	004103	Cluster3785_1clades	184	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67056.1	004104	TM	180	AD1_012	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08293.1	004104	TM	176	Alexandra_12	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58652.1	004104	TM	171	Y3_012	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28499.1	004104	TM	183	YOLOSWAG_12	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QIG63522.1	004105	Cluster3787_1clades	183	DAC19_31	Bacteroides phage DAC19	GCA_013387715.1
QIG63784.1	004105	Cluster3787_1clades	183	DAC20_31	Bacteroides phage DAC20	GCA_013387725.1
QIG64045.1	004105	Cluster3787_1clades	183	DAC22_31	Bacteroides phage DAC22	GCA_013387735.1
QIG64306.1	004105	Cluster3787_1clades	183	DAC23_28	Bacteroides phage DAC23	GCA_013387745.1
AFO71342.1	004106	Cluster3788_1clades	182	CR5_122	Cronobacter phage CR5	GCA_000910235.1
QBP07550.1	004106	Cluster3788_1clades	182	DERBICUS_124	Erwinia phage Derbicus	GCA_004521655.1
ANZ48973.1	004106	Cluster3788_1clades	182	EARLPHILLIPIV_124	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50314.1	004106	Cluster3788_1clades	182	PHOBOS_124	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QDH83479.1	004107	Cluster3789_1clades	182	H1O15_gp327	Achromobacter phage Motura	GCA_006964305.1
QBX06578.1	004107	Cluster3789_1clades	169	BcepSaruman_165	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74544.1	004107	Cluster3789_1clades	169	BcepSauron_164	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41452.1	004107	Cluster3789_1clades	164	RSL1_ORF007	Ralstonia phage phiRSL1	GCA_000879455.1
AYD81477.1	004108	Cluster3790_1clades	148	SEA_JUSTBECAUSE_322	Streptomyces phage JustBecause	GCA_003613775.1
QJD53880.1	004108	Cluster3790_1clades	162	SEA_KELA_320	Streptomyces phage Kela	GCA_012934305.1
QBZ72211.1	004108	Cluster3790_1clades	180	SEA_KRADAL_325	Streptomyces phage Kradal	GCA_004799925.1
AXH66474.1	004108	Cluster3790_1clades	180	SEA_SATIS_325	Streptomyces phage Satis	GCA_003366315.1
AYD81430.1	004109	Cluster3791_1clades	180	SEA_JUSTBECAUSE_275	Streptomyces phage JustBecause	GCA_003613775.1
QJD53836.1	004109	Cluster3791_1clades	180	SEA_KELA_276	Streptomyces phage Kela	GCA_012934305.1
QBZ72165.1	004109	Cluster3791_1clades	179	SEA_KRADAL_279	Streptomyces phage Kradal	GCA_004799925.1
AXH66428.1	004109	Cluster3791_1clades	179	SEA_SATIS_279	Streptomyces phage Satis	GCA_003366315.1
AMS01322.1	004110	NACHT	173	AR9_g238	Bacillus phage AR9	GCA_001743835.1
ALN97969.1	004110	NACHT	171	Bp8pS_290	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99951.1	004110	NACHT	173	PBI_PBS1_129	Bacillus virus PBS1	GCA_002601325.1
CCE26080.1	004110	NACHT	180	g056	Yersinia phage phiR1-37	GCA_000895615.1
ANM45015.1	004111	Cluster3793_1clades	179	KTN4_257	Pseudomonas phage KTN4	GCA_002607225.1
ATN94699.1	004111	Cluster3793_1clades	179	SL2_122	Pseudomonas phage SL2	GCA_002956015.1
QJB22892.1	004111	Cluster3793_1clades	179	fnug_249	Pseudomonas phage fnug	GCA_012837215.1
AAL83114.2	004111	Cluster3793_1clades	179	PHIKZ213	Pseudomonas virus phiKZ	GCA_000842965.1
AYD81332.1	004112	Cluster3794_1clades	178	SEA_JUSTBECAUSE_167	Streptomyces phage JustBecause	GCA_003613775.1
QJD53735.1	004112	Cluster3794_1clades	178	SEA_KELA_165	Streptomyces phage Kela	GCA_012934305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBZ72062.1	004112	Cluster3794_1clades	179	SEA_KRADAL_166	Streptomyces phage Kradal	GCA_004799925.1
AXH66325.1	004112	Cluster3794_1clades	179	SEA_SATIS_166	Streptomyces phage Satis	GCA_003366315.1
AUZ94862.1	004113	Cluster3795_1clades	135	FDI40_gp050	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72773.1	004113	Cluster3795_1clades	179	-	Myoviridae sp.	GCA_003657725.1
QCG76115.1	004113	Cluster3795_1clades	154	EST35_0234	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44028.1	004113	Cluster3795_1clades	142	PBI_SCTP2_13	Salicola phage SCTP-2	GCA_002625545.1
AYD81353.1	004114	Cluster3796_1clades	179	SEA_JUSTBECAUSE_188	Streptomyces phage JustBecause	GCA_003613775.1
QJD53756.1	004114	Cluster3796_1clades	179	SEA_KELA_186	Streptomyces phage Kela	GCA_012934305.1
QBZ72082.1	004114	Cluster3796_1clades	178	SEA_KRADAL_186	Streptomyces phage Kradal	GCA_004799925.1
AXH66344.1	004114	Cluster3796_1clades	178	SEA_SATIS_185	Streptomyces phage Satis	GCA_003366315.1
AFO71400.1	004115	Cluster3797_1clades	149	CR5_180	Cronobacter phage CR5	GCA_000910235.1
QBP07612.1	004115	Cluster3797_1clades	179	DERBICUS_186	Erwinia phage Derbicus	GCA_004521655.1
ANZ49036.1	004115	Cluster3797_1clades	169	EARLPHILLIPIV_187	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50384.1	004115	Cluster3797_1clades	169	PHOBOS_194	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81453.1	004116	Cluster3798_1clades	172	SEA_JUSTBECAUSE_298	Streptomyces phage JustBecause	GCA_003613775.1
QJD53858.1	004116	Cluster3798_1clades	172	SEA_KELA_298	Streptomyces phage Kela	GCA_012934305.1
QBZ72189.1	004116	Cluster3798_1clades	178	SEA_KRADAL_303	Streptomyces phage Kradal	GCA_004799925.1
AXH66452.1	004116	Cluster3798_1clades	178	SEA_SATIS_303	Streptomyces phage Satis	GCA_003366315.1
QAX96933.1	004117	Cluster3799_1clades	178	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97238.1	004117	Cluster3799_1clades	178	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96297.1	004117	Cluster3799_1clades	178	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96615.1	004117	Cluster3799_1clades	178	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01763.1	004118	Cluster3800_1clades	152	CF95_gp041	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65626.1	004118	Cluster3800_1clades	146	2050HW_00291	Serratia phage 2050HW	GCA_002628125.1
QDB71053.1	004118	Cluster3800_1clades	146	CPT_Moabite_021	Serratia phage Moabite	GCA_006384735.1
QFP93178.1	004118	Cluster3800_1clades	178	-	Serratia phage PCH45	GCA_009187865.1
AFO71409.1	004119	Cluster3801_1clades	177	CR5_189	Cronobacter phage CR5	GCA_000910235.1
QBP07621.1	004119	Cluster3801_1clades	177	DERBICUS_195	Erwinia phage Derbicus	GCA_004521655.1
ANZ49045.1	004119	Cluster3801_1clades	177	EARLPHILLIPIV_196	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50393.1	004119	Cluster3801_1clades	177	PHOBOS_203	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AMS01260.1	004120	Cluster3802_1clades	177	AR9_g176	Bacillus phage AR9	GCA_001743835.1
AMS01261.1	004120	Cluster3802_1clades	164	AR9_g177	Bacillus phage AR9	GCA_001743835.1
AST99886.1	004120	Cluster3802_1clades	177	PBI_PBS1_64	Bacillus virus PBS1	GCA_002601325.1
AST99888.1	004120	Cluster3802_1clades	164	PBI_PBS1_66	Bacillus virus PBS1	GCA_002601325.1
AYD80031.1	004121	Cluster3803_1clades	177	JA11_226	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66630.1	004121	Cluster3803_1clades	177	JA13_227	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66954.1	004121	Cluster3803_1clades	177	JA29_228	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67601.1	004121	Cluster3803_1clades	177	JA33_227	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81251.1	004122	Cluster3804_1clades	176	SEA_JUSTBECAUSE_82	Streptomyces phage JustBecause	GCA_003613775.1
QJD53654.1	004122	Cluster3804_1clades	176	SEA_KELA_83	Streptomyces phage Kela	GCA_012934305.1
QBZ71983.1	004122	Cluster3804_1clades	177	SEA_KRADAL_85	Streptomyces phage Kradal	GCA_004799925.1
AXH66246.1	004122	Cluster3804_1clades	177	SEA_SATIS_85	Streptomyces phage Satis	GCA_003366315.1
AYD81392.1	004123	Cluster3805_1clades	171	SEA_JUSTBECAUSE_237	Streptomyces phage JustBecause	GCA_003613775.1
QJD53796.1	004123	Cluster3805_1clades	171	SEA_KELA_236	Streptomyces phage Kela	GCA_012934305.1
QBZ72122.1	004123	Cluster3805_1clades	177	SEA_KRADAL_236	Streptomyces phage Kradal	GCA_004799925.1
AXH66384.1	004123	Cluster3805_1clades	177	SEA_SATIS_235	Streptomyces phage Satis	GCA_003366315.1
AYD81438.1	004124	Cluster3806_1clades	159	SEA_JUSTBECAUSE_283	Streptomyces phage JustBecause	GCA_003613775.1
QJD53843.1	004124	Cluster3806_1clades	159	SEA_KELA_283	Streptomyces phage Kela	GCA_012934305.1
QBZ72173.1	004124	Cluster3806_1clades	177	SEA_KRADAL_287	Streptomyces phage Kradal	GCA_004799925.1
AXH66436.1	004124	Cluster3806_1clades	177	SEA_SATIS_287	Streptomyces phage Satis	GCA_003366315.1
AXQ69059.1	004125	Cluster3807_1clades	112	CcrBL9_gp035	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69575.1	004125	Cluster3807_1clades	112	CcrBL9_gp551	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69619.1	004125	Cluster3807_1clades	177	CcrSC_gp037	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70119.1	004125	Cluster3807_1clades	177	CcrSC_gp537	Caulobacter phage CcrSC	GCA_003443315.1
AYD81248.1	004126	NUDIX	177	SEA_JUSTBECAUSE_79	Streptomyces phage JustBecause	GCA_003613775.1
QJD53651.1	004126	NUDIX	177	SEA_KELA_80	Streptomyces phage Kela	GCA_012934305.1
QBZ71980.1	004126	NUDIX	175	SEA_KRADAL_82	Streptomyces phage Kradal	GCA_004799925.1
AXH66243.1	004126	NUDIX	175	SEA_SATIS_82	Streptomyces phage Satis	GCA_003366315.1
QAX96721.1	004127	Cluster3809_1clades	177	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97040.1	004127	Cluster3809_1clades	177	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96086.1	004127	Cluster3809_1clades	177	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96404.1	004127	Cluster3809_1clades	177	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96890.1	004128	Cluster3810_1clades	177	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97195.1	004128	Cluster3810_1clades	177	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96254.1	004128	Cluster3810_1clades	177	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96572.1	004128	Cluster3810_1clades	177	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96917.1	004129	Cluster3811_1clades	177	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97222.1	004129	Cluster3811_1clades	177	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96281.1	004129	Cluster3811_1clades	177	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96599.1	004129	Cluster3811_1clades	177	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD79861.1	004130	SIG+TM	176	JA11_056	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66460.1	004130	SIG+TM	176	JA13_057	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66783.1	004130	SIG+TM	176	JA29_057	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67430.1	004130	SIG+TM	176	JA33_056	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96873.1	004131	Tox-PLOTU	176	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97178.1	004131	Tox-PLOTU	176	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96237.1	004131	Tox-PLOTU	176	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96555.1	004131	Tox-PLOTU	176	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QGT54939.1	004132	Cluster3816_1clades	176	b23_0328	Synechococcus phage B23	GCA_009745195.1
QGT54940.1	004132	Cluster3816_1clades	94	b23_0329	Synechococcus phage B23	GCA_009745195.1
QGT54574.1	004132	Cluster3816_1clades	176	b3_0334	Synechococcus phage B3	GCA_009745215.1
QGT54575.1	004132	Cluster3816_1clades	94	b3_0335	Synechococcus phage B3	GCA_009745215.1
AFO71277.1	004133	Cluster3817_1clades	175	CR5_057	Cronobacter phage CR5	GCA_000910235.1
QBP07484.1	004133	Cluster3817_1clades	174	DERBICUS_58	Erwinia phage Derbicus	GCA_004521655.1
ANZ48908.1	004133	Cluster3817_1clades	174	EARLPHILLIPIV_58	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50249.1	004133	Cluster3817_1clades	171	PHOBOS_59	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGX01900.1	004134	SIG+TM	175	CF95_gp178	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65408.1	004134	SIG+TM	143	2050HW_00073	Serratia phage 2050HW	GCA_002628125.1
QDB71187.1	004134	SIG+TM	143	CPT_Moabite_157	Serratia phage Moabite	GCA_006384735.1
QFP93180.1	004134	SIG+TM	174	-	Serratia phage PCH45	GCA_009187865.1
AYD80093.1	004135	Cluster3819_1clades	174	JA11_288	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66694.1	004135	Cluster3819_1clades	174	JA13_291	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67013.1	004135	Cluster3819_1clades	175	JA29_287	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67663.1	004135	Cluster3819_1clades	174	JA33_289	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81388.1	004136	Cluster3820_1clades	175	SEA_JUSTBECAUSE_233	Streptomyces phage JustBecause	GCA_003613775.1
QJD53792.1	004136	Cluster3820_1clades	175	SEA_KELA_232	Streptomyces phage Kela	GCA_012934305.1
QBZ72117.1	004136	Cluster3820_1clades	175	SEA_KRADAL_231	Streptomyces phage Kradal	GCA_004799925.1
AXH66379.1	004136	Cluster3820_1clades	175	SEA_SATIS_230	Streptomyces phage Satis	GCA_003366315.1
AYD81471.1	004137	Cluster3822_1clades	175	SEA_JUSTBECAUSE_316	Streptomyces phage JustBecause	GCA_003613775.1
QJD53874.1	004137	Cluster3822_1clades	175	SEA_KELA_314	Streptomyces phage Kela	GCA_012934305.1
QBZ72203.1	004137	Cluster3822_1clades	150	SEA_KRADAL_317	Streptomyces phage Kradal	GCA_004799925.1
AXH66466.1	004137	Cluster3822_1clades	150	SEA_SATIS_317	Streptomyces phage Satis	GCA_003366315.1
APU01586.1	004138	Cluster3824_1clades	83	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01388.1	004138	Cluster3824_1clades	84	ASwh1_328	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53209.1	004138	Cluster3824_1clades	83	65p201	Aeromonas virus 65	GCA_000893255.1
QNI21177.1	004138	Cluster3824_1clades	175	-	Vibrio phage vB_pir03	GCA_014319855.1
AFO71239.1	004139	Cluster3825_1clades	156	CR5_019	Cronobacter phage CR5	GCA_000910235.1
QBP07445.1	004139	Cluster3825_1clades	174	DERBICUS_19	Erwinia phage Derbicus	GCA_004521655.1
ANZ48869.1	004139	Cluster3825_1clades	164	EARLPHILLIPIV_19	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50209.1	004139	Cluster3825_1clades	155	PHOBOS_19	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM45091.1	004140	Cluster3826_1clades	173	KTN4_333	Pseudomonas phage KTN4	GCA_002607225.1
ATN94624.1	004140	Cluster3826_1clades	173	SL2_047	Pseudomonas phage SL2	GCA_002956015.1
QJB22967.1	004140	Cluster3826_1clades	173	fnug_324	Pseudomonas phage fnug	GCA_012837215.1
AAL83177.1	004140	Cluster3826_1clades	173	PHIKZ276	Pseudomonas virus phiKZ	GCA_000842965.1
AFU87974.1	004141	Pep_deformylase	173	CcrColossus_gp104	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68651.1	004141	Pep_deformylase	173	CcrPW_gp112	Caulobacter phage CcrPW	GCA_003443275.1
AGH56898.1	004141	Pep_deformylase	146	CPXG_00095	Cyanophage P-RSM6	GCA_000906155.1
AIX30694.1	004141	Pep_deformylase	148	Syn7803US37_217	Synechococcus phage ACG-2014f	GCA_002594065.1
AGX01881.1	004142	Cluster3828_1clades	173	CF95_gp167	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65421.1	004142	Cluster3828_1clades	109	2050HW_00086	Serratia phage 2050HW	GCA_002628125.1
QDB71198.1	004142	Cluster3828_1clades	170	CPT_Moabite_168	Serratia phage Moabite	GCA_006384735.1
QFP93183.1	004142	Cluster3828_1clades	173	-	Serratia phage PCH45	GCA_009187865.1
AFO71451.1	004143	Cluster3829_1clades	150	CR5_231	Cronobacter phage CR5	GCA_000910235.1
QBP07664.1	004143	Cluster3829_1clades	173	DERBICUS_238	Erwinia phage Derbicus	GCA_004521655.1
ANZ49088.1	004143	Cluster3829_1clades	173	EARLPHILLIPIV_239	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ50435.1	004143	Cluster3829_1clades	153	PHOBOS_245	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD80022.1	004144	Cluster3830_1clades	173	JA11_217	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66621.1	004144	Cluster3830_1clades	173	JA13_218	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66945.1	004144	Cluster3830_1clades	172	JA29_219	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67592.1	004144	Cluster3830_1clades	173	JA33_218	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96941.1	004145	Cluster3831_1clades	173	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97246.1	004145	Cluster3831_1clades	173	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96305.1	004145	Cluster3831_1clades	173	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96623.1	004145	Cluster3831_1clades	173	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83643.1	004146	RE_EcoO109I	154	H1O15_gp145	Achromobacter phage Motura	GCA_006964305.1
QBX06663.1	004146	RE_EcoO109I	148	BcepSaruman_250	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74632.1	004146	RE_EcoO109I	148	BcepSauron_252	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41658.1	004146	RE_EcoO109I	172	RSL1_ORF209	Ralstonia phage phiRSL1	GCA_000879455.1
ANM45030.1	004147	Cluster3833_1clades	171	KTN4_272	Pseudomonas phage KTN4	GCA_002607225.1
ATN94684.1	004147	Cluster3833_1clades	171	SL2_107	Pseudomonas phage SL2	GCA_002956015.1
QJB22907.1	004147	Cluster3833_1clades	171	fnug_264	Pseudomonas phage fnug	GCA_012837215.1
AAL83128.1	004147	Cluster3833_1clades	171	PHIKZ227	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45108.1	004148	RRM	171	KTN4_350	Pseudomonas phage KTN4	GCA_002607225.1
ATN94606.1	004148	RRM	171	SL2_029	Pseudomonas phage SL2	GCA_002956015.1
QJB22984.1	004148	RRM	166	fnug_341	Pseudomonas phage fnug	GCA_012837215.1
AAL83191.1	004148	RRM	171	PHIKZ290	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ69034.1	004149	Cluster3836_1clades	169	CcrBL9_gp010	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69550.1	004149	Cluster3836_1clades	169	CcrBL9_gp526	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69594.1	004149	Cluster3836_1clades	171	CcrSC_gp012	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70094.1	004149	Cluster3836_1clades	171	CcrSC_gp512	Caulobacter phage CcrSC	GCA_003443315.1
AFO71388.1	004150	Cluster3837_1clades	169	CR5_168	Cronobacter phage CR5	GCA_000910235.1
QBP07599.1	004150	Cluster3837_1clades	170	DERBICUS_173	Erwinia phage Derbicus	GCA_004521655.1
ANZ49022.1	004150	Cluster3837_1clades	170	EARLPHILLIPIV_173	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50369.1	004150	Cluster3837_1clades	168	PHOBOS_179	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AXG67331.1	004151	Cluster3838_1clades	170	AD1_287	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08559.1	004151	Cluster3838_1clades	169	Alexandra_303	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58932.1	004151	Cluster3838_1clades	169	Y3_292	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28755.1	004151	Cluster3838_1clades	169	YOLOSWAG_284	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QAX96686.1	004152	Cluster3839_1clades	170	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97004.1	004152	Cluster3839_1clades	170	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96050.1	004152	Cluster3839_1clades	170	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96368.1	004152	Cluster3839_1clades	170	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96808.1	004153	Cluster3840_1clades	170	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97127.1	004153	Cluster3840_1clades	170	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96173.1	004153	Cluster3840_1clades	170	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96491.1	004153	Cluster3840_1clades	170	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96902.1	004154	Cluster3841_1clades	170	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97207.1	004154	Cluster3841_1clades	170	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96266.1	004154	Cluster3841_1clades	170	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96584.1	004154	Cluster3841_1clades	170	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGR47652.2	004155	Cluster3842_1clades	169	SmphiM12_020	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12918.1	004155	Cluster3842_1clades	169	PHIM19_11	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12558.1	004155	Cluster3842_1clades	169	PHIM7_10	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13286.1	004155	Cluster3842_1clades	169	PHIN3_21	Sinorhizobium phage phiN3	GCA_001501175.1
QAX96940.1	004156	Cluster3843_1clades	169	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97245.1	004156	Cluster3843_1clades	169	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96304.1	004156	Cluster3843_1clades	169	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96622.1	004156	Cluster3843_1clades	169	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44761.1	004157	Cas_Csy2	168	KTN4_003	Pseudomonas phage KTN4	GCA_002607225.1
ATN94582.1	004157	Cas_Csy2	168	SL2_005	Pseudomonas phage SL2	GCA_002956015.1
QJB22646.1	004157	Cas_Csy2	168	fnug_3	Pseudomonas phage fnug	GCA_012837215.1
AAL82904.1	004157	Cas_Csy2	168	PHIKZ003	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96881.1	004158	Cluster3846_1clades	168	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97186.1	004158	Cluster3846_1clades	168	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96245.1	004158	Cluster3846_1clades	168	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96563.1	004158	Cluster3846_1clades	168	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ATI17358.1	004159	Cluster3847_1clades	167	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00236.1	004159	Cluster3847_1clades	167	HWB28_gp316	Aeromonas phage AS-zj	GCA_002627665.1
QAY01347.1	004159	Cluster3847_1clades	168	ASwh1_286	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39284.1	004159	Cluster3847_1clades	167	CC2_380	Aeromonas phage CC2	GCA_000903495.1
AFO71341.1	004160	Cluster3848_1clades	167	CR5_121	Cronobacter phage CR5	GCA_000910235.1
QBP07549.1	004160	Cluster3848_1clades	167	DERBICUS_123	Erwinia phage Derbicus	GCA_004521655.1
ANZ48972.1	004160	Cluster3848_1clades	167	EARLPHILLIPIV_123	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50313.1	004160	Cluster3848_1clades	167	PHOBOS_123	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QGT54959.1	004161	GDPD	150	b23_0353	Synechococcus phage B23	GCA_009745195.1
QGT54594.1	004161	GDPD	150	b3_0359	Synechococcus phage B3	GCA_009745215.1
ASR76249.1	004161	GDPD	167	PBI_BELLAMY_213	Synechococcus phage Bellamy	GCA_002627525.1
QJT70201.1	004161	GDPD	151	SynMITS9220M01_195	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QAX96708.1	004162	Cluster3852_1clades	167	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97026.1	004162	Cluster3852_1clades	167	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96072.1	004162	Cluster3852_1clades	167	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96390.1	004162	Cluster3852_1clades	167	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96924.1	004163	Cluster3853_1clades	167	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97229.1	004163	Cluster3853_1clades	167	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96288.1	004163	Cluster3853_1clades	167	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96606.1	004163	Cluster3853_1clades	167	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
prevph1000000187	004164	Cluster3854_1clades	128	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000842	004164	Cluster3854_1clades	168	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000150	004164	Cluster3854_1clades	128	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000584	004164	Cluster3854_1clades	168	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANM45047.1	004165	Cluster3855_1clades	164	KTN4_289	Pseudomonas phage KTN4	GCA_002607225.1
ATN94668.1	004165	Cluster3855_1clades	166	SL2_091	Pseudomonas phage SL2	GCA_002956015.1
QJB22922.1	004165	Cluster3855_1clades	164	fnug_279	Pseudomonas phage fnug	GCA_012837215.1
AAL83139.1	004165	Cluster3855_1clades	166	PHIKZ238	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71223.1	004166	Cluster3856_1clades	166	CR5_003	Cronobacter phage CR5	GCA_000910235.1
QBP07430.1	004166	Cluster3856_1clades	166	DERBICUS_3	Erwinia phage Derbicus	GCA_004521655.1
ANZ48853.1	004166	Cluster3856_1clades	166	EARLPHILLIPIV_3	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50193.1	004166	Cluster3856_1clades	166	PHOBOS_3	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AFO71222.1	004167	Cluster3857_1clades	165	CR5_002	Cronobacter phage CR5	GCA_000910235.1
QBP07429.1	004167	Cluster3857_1clades	166	DERBICUS_2	Erwinia phage Derbicus	GCA_004521655.1
ANZ48852.1	004167	Cluster3857_1clades	166	EARLPHILLIPIV_2	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50192.1	004167	Cluster3857_1clades	163	PHOBOS_2	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD80062.1	004168	Cluster3858_1clades	166	JA11_257	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66663.1	004168	Cluster3858_1clades	166	JA13_260	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66984.1	004168	Cluster3858_1clades	166	JA29_258	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67632.1	004168	Cluster3858_1clades	166	JA33_258	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81410.1	004169	Cluster3859_1clades	166	SEA_JUSTBECAUSE_255	Streptomyces phage JustBecause	GCA_003613775.1
QJD53817.1	004169	Cluster3859_1clades	166	SEA_KELA_257	Streptomyces phage Kela	GCA_012934305.1
QBZ72144.1	004169	Cluster3859_1clades	166	SEA_KRADAL_258	Streptomyces phage Kradal	GCA_004799925.1
AXH66406.1	004169	Cluster3859_1clades	166	SEA_SATIS_257	Streptomyces phage Satis	GCA_003366315.1
AYD81208.1	004170	Cluster3860_1clades	166	SEA_JUSTBECAUSE_39	Streptomyces phage JustBecause	GCA_003613775.1
QJD53611.1	004170	Cluster3860_1clades	166	SEA_KELA_40	Streptomyces phage Kela	GCA_012934305.1
QBZ71945.1	004170	Cluster3860_1clades	146	SEA_KRADAL_46	Streptomyces phage Kradal	GCA_004799925.1
AXH66207.1	004170	Cluster3860_1clades	146	SEA_SATIS_46	Streptomyces phage Satis	GCA_003366315.1
AYD81362.1	004171	Cluster3861_1clades	166	SEA_JUSTBECAUSE_207	Streptomyces phage JustBecause	GCA_003613775.1
QJD53765.1	004171	Cluster3861_1clades	166	SEA_KELA_205	Streptomyces phage Kela	GCA_012934305.1
QBZ72094.1	004171	Cluster3861_1clades	164	SEA_KRADAL_208	Streptomyces phage Kradal	GCA_004799925.1
AXH66355.1	004171	Cluster3861_1clades	164	SEA_SATIS_206	Streptomyces phage Satis	GCA_003366315.1
AFO71422.1	004172	Cluster3862_1clades	151	CR5_202	Cronobacter phage CR5	GCA_000910235.1
QBP07635.1	004172	Cluster3862_1clades	166	DERBICUS_209	Erwinia phage Derbicus	GCA_004521655.1
ANZ49059.1	004172	Cluster3862_1clades	152	EARLPHILLIPIV_210	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50406.1	004172	Cluster3862_1clades	161	PHOBOS_216	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM44899.1	004173	Cluster3863_1clades	165	KTN4_141	Pseudomonas phage KTN4	GCA_002607225.1
ATN94814.1	004173	Cluster3863_1clades	165	SL2_237	Pseudomonas phage SL2	GCA_002956015.1
QJB22777.1	004173	Cluster3863_1clades	165	fnug_134	Pseudomonas phage fnug	GCA_012837215.1
AAL83012.1	004173	Cluster3863_1clades	165	PHIKZ111	Pseudomonas virus phiKZ	GCA_000842965.1
AEO93595.1	004174	KptA-ART	157	G_336	Bacillus virus G	GCA_000917535.1
AEO93789.1	004174	KptA-ART	165	G_531	Bacillus virus G	GCA_000917535.1
AEO93790.1	004174	KptA-ART	154	G_532	Bacillus virus G	GCA_000917535.1
AEO93814.1	004174	KptA-ART	143	G_568	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AYD81239.1	004175	Cluster3865_1clades	165	SEA_JUSTBECAUSE_70	Streptomyces phage JustBecause	GCA_003613775.1
QJD53642.1	004175	Cluster3865_1clades	165	SEA_KELA_71	Streptomyces phage Kela	GCA_012934305.1
QBZ71973.1	004175	Cluster3865_1clades	161	SEA_KRADAL_75	Streptomyces phage Kradal	GCA_004799925.1
AXH66236.1	004175	Cluster3865_1clades	161	SEA_SATIS_75	Streptomyces phage Satis	GCA_003366315.1
AUE22810.1	004176	Cluster3866_1clades	78	Ah1_00292	Aeromonas phage Ah1	GCA_002957415.1
AUE22811.1	004176	Cluster3866_1clades	97	Ah1_00293	Aeromonas phage Ah1	GCA_002957415.1
ADM79912.1	004176	Cluster3866_1clades	164	phiAS5_ORF0069	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17938.1	004176	Cluster3866_1clades	164	Aeh1ORF273c	Aeromonas virus Aeh1	GCA_000843245.1
AFO71221.1	004177	Cluster3867_1clades	164	CR5_001	Cronobacter phage CR5	GCA_000910235.1
QBP07428.1	004177	Cluster3867_1clades	149	DERBICUS_1	Erwinia phage Derbicus	GCA_004521655.1
ANZ48851.1	004177	Cluster3867_1clades	149	EARLPHILLIPIV_1	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50191.1	004177	Cluster3867_1clades	150	PHOBOS_1	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD80002.1	004178	Cluster3868_1clades	164	JA11_197	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66600.1	004178	Cluster3868_1clades	164	JA13_197	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66925.1	004178	Cluster3868_1clades	164	JA29_199	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67571.1	004178	Cluster3868_1clades	164	JA33_197	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96716.1	004179	Cluster3869_1clades	164	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97035.1	004179	Cluster3869_1clades	164	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96081.1	004179	Cluster3869_1clades	164	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96399.1	004179	Cluster3869_1clades	164	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXG67348.1	004180	Cluster3870_1clades	154	AD1_304	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08575.1	004180	Cluster3870_1clades	155	Alexandra_324	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58951.1	004180	Cluster3870_1clades	154	Y3_311	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28778.1	004180	Cluster3870_1clades	163	YOLOSWAG_308	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81400.1	004181	Cluster3871_1clades	163	SEA_JUSTBECAUSE_245	Streptomyces phage JustBecause	GCA_003613775.1
QJD53804.1	004181	Cluster3871_1clades	163	SEA_KELA_244	Streptomyces phage Kela	GCA_012934305.1
QBZ72130.1	004181	Cluster3871_1clades	161	SEA_KRADAL_244	Streptomyces phage Kradal	GCA_004799925.1
AXH66392.1	004181	Cluster3871_1clades	161	SEA_SATIS_243	Streptomyces phage Satis	GCA_003366315.1
QAX96774.1	004182	Cluster3872_1clades	163	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97093.1	004182	Cluster3872_1clades	163	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96139.1	004182	Cluster3872_1clades	163	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96457.1	004182	Cluster3872_1clades	163	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71310.1	004183	TM	158	CR5_090	Cronobacter phage CR5	GCA_000910235.1
QBP07519.1	004183	TM	163	DERBICUS_93	Erwinia phage Derbicus	GCA_004521655.1
ANZ48942.1	004183	TM	158	EARLPHILLIPIV_93	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50283.1	004183	TM	156	PHOBOS_93	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGR48042.1	004184	Cluster3874_1clades	162	SmphiM12_410	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13226.1	004184	Cluster3874_1clades	162	PHIM19_321	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12866.1	004184	Cluster3874_1clades	162	PHIM7_321	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13589.1	004184	Cluster3874_1clades	162	PHIN3_326	Sinorhizobium phage phiN3	GCA_001501175.1
ANZ49848.1	004185	SIG+TM	162	MACHINA_210	Erwinia phage Machina	GCA_002758035.1
ANZ48505.1	004185	SIG+TM	161	CAITLIN_210	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ49292.1	004185	SIG+TM	162	HUXLEY_210	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50120.1	004185	SIG+TM	162	PARSHIK_211	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AUE22813.1	004186	Cluster3876_1clades	162	Ah1_00295	Aeromonas phage Ah1	GCA_002957415.1
QAX98526.1	004186	Cluster3876_1clades	161	ASfcp2_190	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52989.1	004186	Cluster3876_1clades	161	PX29p270	Aeromonas phage PX29	GCA_000920195.1
AAQ17941.1	004186	Cluster3876_1clades	151	Aeh1ORF276c	Aeromonas virus Aeh1	GCA_000843245.1
AYD81193.1	004187	Cluster3877_1clades	162	SEA_JUSTBECAUSE_24	Streptomyces phage JustBecause	GCA_003613775.1
QJD53595.1	004187	Cluster3877_1clades	162	SEA_KELA_24	Streptomyces phage Kela	GCA_012934305.1
QBZ71927.1	004187	Cluster3877_1clades	162	SEA_KRADAL_28	Streptomyces phage Kradal	GCA_004799925.1
AXH66189.1	004187	Cluster3877_1clades	162	SEA_SATIS_28	Streptomyces phage Satis	GCA_003366315.1
AYD81213.1	004188	Cluster3878_1clades	162	SEA_JUSTBECAUSE_44	Streptomyces phage JustBecause	GCA_003613775.1
QJD53616.1	004188	Cluster3878_1clades	162	SEA_KELA_45	Streptomyces phage Kela	GCA_012934305.1
QBZ71949.1	004188	Cluster3878_1clades	162	SEA_KRADAL_50	Streptomyces phage Kradal	GCA_004799925.1
AXH66211.1	004188	Cluster3878_1clades	159	SEA_SATIS_50	Streptomyces phage Satis	GCA_003366315.1
ANM45050.1	004189	Cluster3879_1clades	161	KTN4_292	Pseudomonas phage KTN4	GCA_002607225.1
ATN94665.1	004189	Cluster3879_1clades	160	SL2_088	Pseudomonas phage SL2	GCA_002956015.1
QJB22925.1	004189	Cluster3879_1clades	161	fnug_282	Pseudomonas phage fnug	GCA_012837215.1
AAL83141.1	004189	Cluster3879_1clades	160	PHIKZ240	Pseudomonas virus phiKZ	GCA_000842965.1
AYD81219.1	004190	Cluster3881_1clades	161	SEA_JUSTBECAUSE_50	Streptomyces phage JustBecause	GCA_003613775.1
QJD53622.1	004190	Cluster3881_1clades	161	SEA_KELA_51	Streptomyces phage Kela	GCA_012934305.1
QBZ71955.1	004190	Cluster3881_1clades	161	SEA_KRADAL_56	Streptomyces phage Kradal	GCA_004799925.1
AXH66217.1	004190	Cluster3881_1clades	161	SEA_SATIS_56	Streptomyces phage Satis	GCA_003366315.1
AYD81403.1	004191	Cluster3882_1clades	161	SEA_JUSTBECAUSE_248	Streptomyces phage JustBecause	GCA_003613775.1
QJD53807.1	004191	Cluster3882_1clades	161	SEA_KELA_247	Streptomyces phage Kela	GCA_012934305.1
QBZ72132.1	004191	Cluster3882_1clades	160	SEA_KRADAL_246	Streptomyces phage Kradal	GCA_004799925.1
AXH66394.1	004191	Cluster3882_1clades	160	SEA_SATIS_245	Streptomyces phage Satis	GCA_003366315.1
AYD81425.1	004192	Cluster3883_1clades	161	SEA_JUSTBECAUSE_270	Streptomyces phage JustBecause	GCA_003613775.1
QJD53830.1	004192	Cluster3883_1clades	161	SEA_KELA_270	Streptomyces phage Kela	GCA_012934305.1
QBZ72157.1	004192	Cluster3883_1clades	160	SEA_KRADAL_271	Streptomyces phage Kradal	GCA_004799925.1
AXH66420.1	004192	Cluster3883_1clades	160	SEA_SATIS_271	Streptomyces phage Satis	GCA_003366315.1
AGR47931.1	004193	Cluster3884_1clades	160	SmphiM12_299	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13131.1	004193	Cluster3884_1clades	160	PHIM19_226	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12770.1	004193	Cluster3884_1clades	160	PHIM7_225	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13499.1	004193	Cluster3884_1clades	160	PHIN3_236	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81435.1	004194	Cluster3885_1clades	159	SEA_JUSTBECAUSE_280	Streptomyces phage JustBecause	GCA_003613775.1
QJD53841.1	004194	Cluster3885_1clades	159	SEA_KELA_281	Streptomyces phage Kela	GCA_012934305.1
QBZ72170.1	004194	Cluster3885_1clades	160	SEA_KRADAL_284	Streptomyces phage Kradal	GCA_004799925.1
AXH66433.1	004194	Cluster3885_1clades	160	SEA_SATIS_284	Streptomyces phage Satis	GCA_003366315.1
QAX96871.1	004195	Cluster3886_1clades	160	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97176.1	004195	Cluster3886_1clades	160	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96235.1	004195	Cluster3886_1clades	160	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96553.1	004195	Cluster3886_1clades	160	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ABY63220.1	004196	Cluster3887_1clades	159	201phi2-1p396	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32482.1	004196	Cluster3887_1clades	157	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV77024.1	004196	Cluster3887_1clades	156	PHABIO_393	Pseudomonas phage Phabio	GCA_002624965.1
QEM42054.1	004196	Cluster3887_1clades	157	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AXQ68475.1	004197	Cluster3888_1clades	158	CcrBL10_gp271	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88197.1	004197	Cluster3888_1clades	159	CcrColossus_gp327	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68874.1	004197	Cluster3888_1clades	159	CcrPW_gp335	Caulobacter phage CcrPW	GCA_003443275.1
AFU86760.1	004197	Cluster3888_1clades	155	CcrRogue_gp278	Caulobacter virus Rogue	GCA_000900555.1
AYD81447.1	004198	DEATH	153	SEA_JUSTBECAUSE_292	Streptomyces phage JustBecause	GCA_003613775.1
QJD53852.1	004198	DEATH	154	SEA_KELA_292	Streptomyces phage Kela	GCA_012934305.1
QBZ72183.1	004198	DEATH	159	SEA_KRADAL_297	Streptomyces phage Kradal	GCA_004799925.1
AXH66446.1	004198	DEATH	159	SEA_SATIS_297	Streptomyces phage Satis	GCA_003366315.1
AMS01237.1	004199	Cluster3890_1clades	99	AR9_g153	Bacillus phage AR9	GCA_001743835.1
ALN97897.1	004199	Cluster3890_1clades	98	Bp8pS_218	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99863.1	004199	Cluster3890_1clades	99	PBI_PBS1_41	Bacillus virus PBS1	GCA_002601325.1
CCE26192.1	004199	Cluster3890_1clades	159	g168	Yersinia phage phiR1-37	GCA_000895615.1
QGZ14471.1	004200	Cluster3891_1clades	159	HWC77_gp108	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04263.1	004200	Cluster3891_1clades	159	HWC03_gp108	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23101.1	004200	Cluster3891_1clades	152	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47415.1	004200	Cluster3891_1clades	152	HWC35_gp021	Vibrio phage USC-1	GCA_006864065.1
QAX96772.1	004201	Cluster3892_1clades	159	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97091.1	004201	Cluster3892_1clades	159	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96137.1	004201	Cluster3892_1clades	159	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96455.1	004201	Cluster3892_1clades	159	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96789.1	004202	SIG+DUF3584	159	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97108.1	004202	SIG+DUF3584	159	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96154.1	004202	SIG+DUF3584	159	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96472.1	004202	SIG+DUF3584	159	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96907.1	004203	Cluster3894_1clades	159	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97212.1	004203	Cluster3894_1clades	159	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96271.1	004203	Cluster3894_1clades	159	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96589.1	004203	Cluster3894_1clades	159	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71399.1	004204	Cluster3895_1clades	157	CR5_179	Cronobacter phage CR5	GCA_000910235.1
QBP07611.1	004204	Cluster3895_1clades	157	DERBICUS_185	Erwinia phage Derbicus	GCA_004521655.1
ANZ49035.1	004204	Cluster3895_1clades	157	EARLPHILLIPIV_186	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50383.1	004204	Cluster3895_1clades	158	PHOBOS_193	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD80001.1	004205	Cluster3896_1clades	155	JA11_196	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66599.1	004205	Cluster3896_1clades	155	JA13_196	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66924.1	004205	Cluster3896_1clades	158	JA29_198	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67570.1	004205	Cluster3896_1clades	155	JA33_196	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81196.1	004206	SIG+TM	130	SEA_JUSTBECAUSE_27	Streptomyces phage JustBecause	GCA_003613775.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QJD53598.1	004206	SIG+TM	130	SEA_KELA_27	Streptomyces phage Kela	GCA_012934305.1
QBZ71933.1	004206	SIG+TM	158	SEA_KRADAL_34	Streptomyces phage Kradal	GCA_004799925.1
AXH66195.1	004206	SIG+TM	158	SEA_SATIS_34	Streptomyces phage Satis	GCA_003366315.1
AYD81404.1	004207	Cluster3898_1clades	158	SEA_JUSTBECAUSE_249	Streptomyces phage JustBecause	GCA_003613775.1
QJD53808.1	004207	Cluster3898_1clades	158	SEA_KELA_248	Streptomyces phage Kela	GCA_012934305.1
QBZ72133.1	004207	Cluster3898_1clades	158	SEA_KRADAL_247	Streptomyces phage Kradal	GCA_004799925.1
AXH66395.1	004207	Cluster3898_1clades	158	SEA_SATIS_246	Streptomyces phage Satis	GCA_003366315.1
AYD81311.1	004208	Cluster3899_1clades	158	SEA_JUSTBECAUSE_146	Streptomyces phage JustBecause	GCA_003613775.1
QJD53714.1	004208	Cluster3899_1clades	156	SEA_KELA_144	Streptomyces phage Kela	GCA_012934305.1
QBZ72041.1	004208	Cluster3899_1clades	157	SEA_KRADAL_145	Streptomyces phage Kradal	GCA_004799925.1
AXH66304.1	004208	Cluster3899_1clades	157	SEA_SATIS_145	Streptomyces phage Satis	GCA_003366315.1
ANM44955.1	004209	Cluster3900_1clades	157	KTN4_197	Pseudomonas phage KTN4	GCA_002607225.1
ATN94759.1	004209	Cluster3900_1clades	157	SL2_182	Pseudomonas phage SL2	GCA_002956015.1
QJB22833.1	004209	Cluster3900_1clades	157	fnug_190	Pseudomonas phage fnug	GCA_012837215.1
AAL83061.1	004209	Cluster3900_1clades	157	PHIKZ160	Pseudomonas virus phiKZ	GCA_000842965.1
QBX32196.1	004210	Cluster3901_1clades	156	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76693.1	004210	Cluster3901_1clades	153	PHABIO_62	Pseudomonas phage Phabio	GCA_002624965.1
AEH03469.1	004210	Cluster3901_1clades	157	042	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02571.1	004210	Cluster3901_1clades	120	PSA21_41	Pseudomonas phage Psa21	GCA_004340405.1
AXQ69324.1	004211	Cluster3902_1clades	151	CcrBL9_gp300	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88120.1	004211	Cluster3902_1clades	157	CcrColossus_gp250	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68798.1	004211	Cluster3902_1clades	75	CcrPW_gp259	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69884.1	004211	Cluster3902_1clades	151	CcrSC_gp302	Caulobacter phage CcrSC	GCA_003443315.1
AYD81260.1	004212	Cluster3903_1clades	156	SEA_JUSTBECAUSE_91	Streptomyces phage JustBecause	GCA_003613775.1
QJD53663.1	004212	Cluster3903_1clades	156	SEA_KELA_92	Streptomyces phage Kela	GCA_012934305.1
QBZ71992.1	004212	Cluster3903_1clades	157	SEA_KRADAL_94	Streptomyces phage Kradal	GCA_004799925.1
AXH66255.1	004212	Cluster3903_1clades	157	SEA_SATIS_94	Streptomyces phage Satis	GCA_003366315.1
AFF28084.1	004213	Cluster3904_1clades	153	PAU_86	Sphingomonas phage PAU	GCA_000902455.1
BBI90678.1	004213	Cluster3904_1clades	153	HYO65_gp286	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90985.1	004213	Cluster3904_1clades	153	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39287.1	004213	Cluster3904_1clades	157	BPT24_161	Tenacibaculum phage pT24	GCA_002611925.1
QAX96939.1	004214	Cluster3906_1clades	157	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97244.1	004214	Cluster3906_1clades	157	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96303.1	004214	Cluster3906_1clades	157	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96621.1	004214	Cluster3906_1clades	157	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDH83480.1	004215	Tox-HNH	156	H1O15_gp326	Achromobacter phage Motura	GCA_006964305.1
QBX06576.1	004215	Tox-HNH	155	BcepSaruman_163	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74543.1	004215	Tox-HNH	157	BcepSauron_163	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41453.1	004215	Tox-HNH	155	RSL1_ORF008	Ralstonia phage phiRSL1	GCA_000879455.1
ANM45001.1	004216	Cluster3908_1clades	156	KTN4_243	Pseudomonas phage KTN4	GCA_002607225.1
ATN94713.1	004216	Cluster3908_1clades	156	SL2_136	Pseudomonas phage SL2	GCA_002956015.1
QJB22879.1	004216	Cluster3908_1clades	156	fnug_236	Pseudomonas phage fnug	GCA_012837215.1
AAL83103.1	004216	Cluster3908_1clades	156	PHIKZ202	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45023.1	004217	Cluster3909_1clades	156	KTN4_265	Pseudomonas phage KTN4	GCA_002607225.1
ATN94691.1	004217	Cluster3909_1clades	156	SL2_114	Pseudomonas phage SL2	GCA_002956015.1
QJB22900.1	004217	Cluster3909_1clades	156	fnug_257	Pseudomonas phage fnug	GCA_012837215.1
AAL83121.1	004217	Cluster3909_1clades	156	PHIKZ220	Pseudomonas virus phiKZ	GCA_000842965.1
AGR48063.1	004218	Cluster3910_1clades	156	SmphiM12_431	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13241.1	004218	Cluster3910_1clades	156	PHIM19_336	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12881.1	004218	Cluster3910_1clades	156	PHIM7_336	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13604.1	004218	Cluster3910_1clades	156	PHIN3_341	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79836.1	004219	Cluster3911_1clades	156	JA11_031	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66435.1	004219	Cluster3911_1clades	156	JA13_032	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66759.1	004219	Cluster3911_1clades	156	JA29_033	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67405.1	004219	Cluster3911_1clades	156	JA33_031	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81228.1	004220	Cluster3912_1clades	156	SEA_JUSTBECAUSE_59	Streptomyces phage JustBecause	GCA_003613775.1
QJD53631.1	004220	Cluster3912_1clades	156	SEA_KELA_60	Streptomyces phage Kela	GCA_012934305.1
QBZ71963.1	004220	Cluster3912_1clades	156	SEA_KRADAL_65	Streptomyces phage Kradal	GCA_004799925.1
AXH66226.1	004220	Cluster3912_1clades	156	SEA_SATIS_65	Streptomyces phage Satis	GCA_003366315.1
AYD81394.1	004221	Cluster3913_1clades	156	SEA_JUSTBECAUSE_239	Streptomyces phage JustBecause	GCA_003613775.1
QJD53798.1	004221	Cluster3913_1clades	156	SEA_KELA_238	Streptomyces phage Kela	GCA_012934305.1
QBZ72124.1	004221	Cluster3913_1clades	156	SEA_KRADAL_238	Streptomyces phage Kradal	GCA_004799925.1
AXH66386.1	004221	Cluster3913_1clades	156	SEA_SATIS_237	Streptomyces phage Satis	GCA_003366315.1
AYD81375.1	004222	Cluster3914_1clades	156	SEA_JUSTBECAUSE_220	Streptomyces phage JustBecause	GCA_003613775.1
QJD53778.1	004222	Cluster3914_1clades	156	SEA_KELA_218	Streptomyces phage Kela	GCA_012934305.1
QBZ72103.1	004222	Cluster3914_1clades	152	SEA_KRADAL_217	Streptomyces phage Kradal	GCA_004799925.1
AXH66364.1	004222	Cluster3914_1clades	152	SEA_SATIS_215	Streptomyces phage Satis	GCA_003366315.1
QGZ14561.1	004223	Cluster3915_1clades	156	HWC77_gp198	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04172.1	004223	Cluster3915_1clades	156	HWC03_gp017	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23186.1	004223	Cluster3915_1clades	156	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47543.1	004223	Cluster3915_1clades	156	HWC35_gp149	Vibrio phage USC-1	GCA_006864065.1
QAX96637.1	004224	Cluster3916_1clades	156	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96955.1	004224	Cluster3916_1clades	156	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96001.1	004224	Cluster3916_1clades	156	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96319.1	004224	Cluster3916_1clades	156	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96867.1	004225	Cluster3917_1clades	156	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97172.1	004225	Cluster3917_1clades	156	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96231.1	004225	Cluster3917_1clades	156	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96549.1	004225	Cluster3917_1clades	156	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45036.1	004226	Cluster3918_1clades	155	KTN4_278	Pseudomonas phage KTN4	GCA_002607225.1
ATN94678.1	004226	Cluster3918_1clades	155	SL2_101	Pseudomonas phage SL2	GCA_002956015.1
QJB22912.1	004226	Cluster3918_1clades	155	fnug_269	Pseudomonas phage fnug	GCA_012837215.1
AAL83132.1	004226	Cluster3918_1clades	155	PHIKZ231	Pseudomonas virus phiKZ	GCA_000842965.1
ABY63186.1	004227	TM	131	201phi2-1p361	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32445.1	004227	TM	149	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03714.1	004227	TM	155	291	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42016.1	004227	TM	149	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AYD79851.1	004228	Cluster3920_1clades	155	JA11_046	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66451.1	004228	Cluster3920_1clades	155	JA13_048	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66775.1	004228	Cluster3920_1clades	155	JA29_049	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67420.1	004228	Cluster3920_1clades	155	JA33_046	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79883.1	004229	Cluster3921_1clades	155	JA11_078	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66482.1	004229	Cluster3921_1clades	155	JA13_079	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66807.1	004229	Cluster3921_1clades	155	JA29_081	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67452.1	004229	Cluster3921_1clades	155	JA33_078	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79986.1	004230	Atg14	155	JA11_181	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66584.1	004230	Atg14	155	JA13_181	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66909.1	004230	Atg14	155	JA29_183	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67555.1	004230	Atg14	155	JA33_181	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AXQ69277.1	004231	Cluster3923_1clades	155	CcrBL9_gp253c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88143.1	004231	Cluster3923_1clades	81	CcrColossus_gp273	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68819.1	004231	Cluster3923_1clades	81	CcrPW_gp280	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69834.1	004231	Cluster3923_1clades	155	CcrSC_gp252c	Caulobacter phage CcrSC	GCA_003443315.1
QAX96750.1	004232	Cluster3925_1clades	155	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97069.1	004232	Cluster3925_1clades	155	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96115.1	004232	Cluster3925_1clades	155	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96433.1	004232	Cluster3925_1clades	155	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96810.1	004233	Cluster3926_1clades	155	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97129.1	004233	Cluster3926_1clades	155	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96175.1	004233	Cluster3926_1clades	155	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96493.1	004233	Cluster3926_1clades	155	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44841.1	004234	Cluster3927_1clades	150	KTN4_083	Pseudomonas phage KTN4	GCA_002607225.1
ATN94872.1	004234	Cluster3927_1clades	154	SL2_295	Pseudomonas phage SL2	GCA_002956015.1
QJB22719.1	004234	Cluster3927_1clades	150	fnug_76	Pseudomonas phage fnug	GCA_012837215.1
AAL82962.1	004234	Cluster3927_1clades	154	PHIKZ061	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45098.1	004235	Cluster3928_1clades	154	KTN4_340	Pseudomonas phage KTN4	GCA_002607225.1
ATN94615.1	004235	Cluster3928_1clades	154	SL2_038	Pseudomonas phage SL2	GCA_002956015.1
QJB22974.1	004235	Cluster3928_1clades	154	fnug_331	Pseudomonas phage fnug	GCA_012837215.1
AAL83184.1	004235	Cluster3928_1clades	154	PHIKZ283	Pseudomonas virus phiKZ	GCA_000842965.1
QBZ70830.1	004236	SIG+TM	135	pETSU_249	Edwardsiella virus pEt-SU	GCA_004800915.1
ARM70908.1	004236	SIG+TM	137	phiC120_c203	Escherichia phage phiC120	GCA_002621185.1
ABY63132.1	004236	SIG+TM	154	201phi2-1p306	Pseudomonas phage 201phi2-1	GCA_000875305.1
AEV89464.1	004236	SIG+TM	137	OBP_027	Pseudomonas phage OBP	GCA_000896635.1
AYD80003.1	004237	ORC-AAA	154	JA11_198	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66601.1	004237	ORC-AAA	154	JA13_198	Dickeya phage vB_DsoM_JA13	GCA_003568455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG66926.1	004237	ORC-AAA	73	JA29_200	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67572.1	004237	ORC-AAA	154	JA33_198	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFF28266.1	004238	Cluster3931_1clades	151	PAU_268	Sphingomonas phage PAU	GCA_000902455.1
BBI90402.1	004238	Cluster3931_1clades	154	HYO65_gp010	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90710.1	004238	Cluster3931_1clades	126	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39306.1	004238	Cluster3931_1clades	148	BPT24_181	Tenacibaculum phage pT24	GCA_002611925.1
QAX96812.1	004239	Cluster3932_1clades	154	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97131.1	004239	Cluster3932_1clades	154	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96177.1	004239	Cluster3932_1clades	154	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96495.1	004239	Cluster3932_1clades	154	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01956.1	004240	Cluster3933_1clades	148	CF95_gp234	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65346.1	004240	Cluster3933_1clades	146	2050HW_00011	Serratia phage 2050HW	GCA_002628125.1
QDB71134.1	004240	Cluster3933_1clades	146	CPT_Moabite_104	Serratia phage Moabite	GCA_006384735.1
QFP93198.1	004240	Cluster3933_1clades	154	-	Serratia phage PCH45	GCA_009187865.1
ANM45067.1	004241	Cluster3934_1clades	153	KTN4_309	Pseudomonas phage KTN4	GCA_002607225.1
ATN94648.1	004241	Cluster3934_1clades	153	SL2_071	Pseudomonas phage SL2	GCA_002956015.1
QJB22942.1	004241	Cluster3934_1clades	151	fnug_299	Pseudomonas phage fnug	GCA_012837215.1
AAL83156.2	004241	Cluster3934_1clades	153	PHIKZ255	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62911.1	004242	Cluster3935_1clades	153	201phi2-1p078	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76694.1	004242	Cluster3935_1clades	108	PHABIO_63	Pseudomonas phage Phabio	GCA_002624965.1
AEH03470.1	004242	Cluster3935_1clades	89	043	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41773.1	004242	Cluster3935_1clades	143	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGR48046.1	004243	Cluster3936_1clades	153	SmphiM12_414	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13229.1	004243	Cluster3936_1clades	153	PHIM19_324	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12869.1	004243	Cluster3936_1clades	153	PHIM7_324	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13592.1	004243	Cluster3936_1clades	153	PHIN3_329	Sinorhizobium phage phiN3	GCA_001501175.1
AFO71286.1	004244	Cluster3937_1clades	149	CR5_066	Cronobacter phage CR5	GCA_000910235.1
QBP07493.1	004244	Cluster3937_1clades	149	DERBICUS_67	Erwinia phage Derbicus	GCA_004521655.1
ANZ48917.1	004244	Cluster3937_1clades	149	EARLPHILLIPIV_67	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50258.1	004244	Cluster3937_1clades	153	PHOBOS_68	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD79855.1	004245	Cluster3938_1clades	143	JA11_050	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66455.1	004245	Cluster3938_1clades	153	JA13_052	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66779.1	004245	Cluster3938_1clades	143	JA29_053	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67424.1	004245	Cluster3938_1clades	143	JA33_050	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79867.1	004246	Cluster3939_1clades	153	JA11_062	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66466.1	004246	Cluster3939_1clades	153	JA13_063	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66791.1	004246	Cluster3939_1clades	153	JA29_065	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67436.1	004246	Cluster3939_1clades	153	JA33_062	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AGR47717.1	004247	Cluster3940_1clades	152	SmphiM12_085	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12972.1	004247	Cluster3940_1clades	152	PHIM19_65	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12612.1	004247	Cluster3940_1clades	152	PHIM7_64	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13344.1	004247	Cluster3940_1clades	152	PHIN3_80	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47754.1	004248	Cluster3941_1clades	152	SmphiM12_122	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12994.1	004248	Cluster3941_1clades	152	PHIM19_88	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12634.1	004248	Cluster3941_1clades	152	PHIM7_87	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13366.1	004248	Cluster3941_1clades	152	PHIN3_102	Sinorhizobium phage phiN3	GCA_001501175.1
AGX01858.1	004249	Cluster3942_1clades	152	CF95_gp136	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65446.1	004249	Cluster3942_1clades	151	2050HW_00111	Serratia phage 2050HW	GCA_002628125.1
QDB71216.1	004249	Cluster3942_1clades	151	CPT_Moabite_186	Serratia phage Moabite	GCA_006384735.1
QFP93202.1	004249	Cluster3942_1clades	146	-	Serratia phage PCH45	GCA_009187865.1
AFO71324.1	004250	Cluster3943_1clades	139	CR5_104	Cronobacter phage CR5	GCA_000910235.1
QBP07534.1	004250	Cluster3943_1clades	146	DERBICUS_108	Erwinia phage Derbicus	GCA_004521655.1
ANZ48957.1	004250	Cluster3943_1clades	146	EARLPHILLIPIV_108	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50299.1	004250	Cluster3943_1clades	152	PHOBOS_109	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AXG67128.1	004251	Cluster3944_1clades	151	AD1_084	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08364.1	004251	Cluster3944_1clades	151	Alexandra_88	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58727.1	004251	Cluster3944_1clades	152	Y3_087	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28559.1	004251	Cluster3944_1clades	132	YOLOSWAG_76	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD80082.1	004252	Cluster3945_1clades	152	JA11_277	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66683.1	004252	Cluster3945_1clades	152	JA13_280	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67003.1	004252	Cluster3945_1clades	152	JA29_277	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67652.1	004252	Cluster3945_1clades	152	JA33_278	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ANM45062.1	004253	Cluster3946_1clades	151	KTN4_304	Pseudomonas phage KTN4	GCA_002607225.1
ATN94653.1	004253	Cluster3946_1clades	151	SL2_076	Pseudomonas phage SL2	GCA_002956015.1
QJB22937.1	004253	Cluster3946_1clades	151	fnug_294	Pseudomonas phage fnug	GCA_012837215.1
AAL83152.1	004253	Cluster3946_1clades	151	PHIKZ251	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47841.1	004254	Cluster3947_1clades	146	SmphiM12_209	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13047.1	004254	Cluster3947_1clades	146	PHIM19_142	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12688.1	004254	Cluster3947_1clades	146	PHIM7_142	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13419.1	004254	Cluster3947_1clades	151	PHIN3_156	Sinorhizobium phage phiN3	GCA_001501175.1
AMM43954.1	004255	Cluster3948_1clades	151	CBB_391	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88915.1	004255	Cluster3948_1clades	148	BF_0390	Serratia phage BF	GCA_002619745.1
SOK59204.1	004255	Cluster3948_1clades	143	g396	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58669.1	004255	Cluster3948_1clades	143	g392	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD80094.1	004256	Cluster3949_1clades	151	JA11_289	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66695.1	004256	Cluster3949_1clades	151	JA13_292	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67014.1	004256	Cluster3949_1clades	150	JA29_288	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67664.1	004256	Cluster3949_1clades	151	JA33_290	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81185.1	004257	Cluster3950_1clades	143	SEA_JUSTBECAUSE_16	Streptomyces phage JustBecause	GCA_003613775.1
QJD53587.1	004257	Cluster3950_1clades	143	SEA_KELA_16	Streptomyces phage Kela	GCA_012934305.1
QBZ71918.1	004257	Cluster3950_1clades	151	SEA_KRADAL_19	Streptomyces phage Kradal	GCA_004799925.1
AXH66180.1	004257	Cluster3950_1clades	151	SEA_SATIS_19	Streptomyces phage Satis	GCA_003366315.1
AYD81317.1	004258	Cluster3951_1clades	151	SEA_JUSTBECAUSE_152	Streptomyces phage JustBecause	GCA_003613775.1
QJD53720.1	004258	Cluster3951_1clades	151	SEA_KELA_150	Streptomyces phage Kela	GCA_012934305.1
QBZ72048.1	004258	Cluster3951_1clades	151	SEA_KRADAL_152	Streptomyces phage Kradal	GCA_004799925.1
AXH66311.1	004258	Cluster3951_1clades	151	SEA_SATIS_152	Streptomyces phage Satis	GCA_003366315.1
AYD81331.1	004259	Cluster3952_1clades	151	SEA_JUSTBECAUSE_166	Streptomyces phage JustBecause	GCA_003613775.1
QJD53734.1	004259	Cluster3952_1clades	151	SEA_KELA_164	Streptomyces phage Kela	GCA_012934305.1
QBZ72060.1	004259	Cluster3952_1clades	146	SEA_KRADAL_164	Streptomyces phage Kradal	GCA_004799925.1
AXH66323.1	004259	Cluster3952_1clades	146	SEA_SATIS_164	Streptomyces phage Satis	GCA_003366315.1
ANM44914.1	004260	Cluster3953_1clades	150	KTN4_156	Pseudomonas phage KTN4	GCA_002607225.1
ATN94800.1	004260	Cluster3953_1clades	150	SL2_223	Pseudomonas phage SL2	GCA_002956015.1
QJB22792.1	004260	Cluster3953_1clades	150	fnug_149	Pseudomonas phage fnug	GCA_012837215.1
AAL83022.1	004260	Cluster3953_1clades	150	PHIKZ121	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45122.1	004261	Cluster3954_1clades	150	KTN4_364	Pseudomonas phage KTN4	GCA_002607225.1
ATN94589.1	004261	Cluster3954_1clades	150	SL2_012	Pseudomonas phage SL2	GCA_002956015.1
QJB22999.1	004261	Cluster3954_1clades	150	fnug_356	Pseudomonas phage fnug	GCA_012837215.1
AAL83203.1	004261	Cluster3954_1clades	150	PHIKZ302	Pseudomonas virus phiKZ	GCA_000842965.1
QBX32198.1	004262	Cluster3955_1clades	141	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76696.1	004262	Cluster3955_1clades	141	PHABIO_65	Pseudomonas phage Phabio	GCA_002624965.1
AEH03472.1	004262	Cluster3955_1clades	150	045	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41775.1	004262	Cluster3955_1clades	141	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AYD81351.1	004263	Cluster3956_1clades	150	SEA_JUSTBECAUSE_186	Streptomyces phage JustBecause	GCA_003613775.1
QJD53754.1	004263	Cluster3956_1clades	146	SEA_KELA_184	Streptomyces phage Kela	GCA_012934305.1
QBZ72080.1	004263	Cluster3956_1clades	146	SEA_KRADAL_184	Streptomyces phage Kradal	GCA_004799925.1
AXH66343.1	004263	Cluster3956_1clades	146	SEA_SATIS_184	Streptomyces phage Satis	GCA_003366315.1
QAX96664.1	004264	Cluster3958_1clades	150	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96982.1	004264	Cluster3958_1clades	150	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96028.1	004264	Cluster3958_1clades	150	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96346.1	004264	Cluster3958_1clades	150	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96775.1	004265	Cluster3959_1clades	150	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97094.1	004265	Cluster3959_1clades	150	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96140.1	004265	Cluster3959_1clades	150	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96458.1	004265	Cluster3959_1clades	150	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96912.1	004266	Cluster3960_1clades	150	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97217.1	004266	Cluster3960_1clades	150	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96276.1	004266	Cluster3960_1clades	150	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96594.1	004266	Cluster3960_1clades	150	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71287.1	004267	Cluster3961_1clades	147	CR5_067	Cronobacter phage CR5	GCA_000910235.1
QBP07495.1	004267	Cluster3961_1clades	150	DERBICUS_69	Erwinia phage Derbicus	GCA_004521655.1
ANZ48919.1	004267	Cluster3961_1clades	146	EARLPHILLIPIV_69	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50260.1	004267	Cluster3961_1clades	145	PHOBOS_70	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM44894.1	004268	Cluster3962_1clades	146	KTN4_136	Pseudomonas phage KTN4	GCA_002607225.1
ATN94819.1	004268	Cluster3962_1clades	146	SL2_242	Pseudomonas phage SL2	GCA_002956015.1
QJB22772.1	004268	Cluster3962_1clades	150	fnug_129	Pseudomonas phage fnug	GCA_012837215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGC26326.1	004268	Cluster3962_1clades	99	PHIKZ107.1	Pseudomonas virus phiKZ	GCA_000842965.1
BBI90521.1	004269	Cluster3963_2clades	124	HYO65_gp129	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90829.1	004269	Cluster3963_2clades	124	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000653	004269	Cluster3963_2clades	151	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000465	004269	Cluster3963_2clades	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44065.1	004270	SIG+TM+TM+TM	149	CBB_502	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89020.1	004270	SIG+TM+TM+TM	142	BF_0495	Serratia phage BF	GCA_002619745.1
SOK59301.1	004270	SIG+TM+TM+TM	142	g493	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58766.1	004270	SIG+TM+TM+TM	142	g489	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASR76272.1	004271	SpoIID	131	PBI_BELLAMY_236	Synechococcus phage Bellamy	GCA_002627525.1
AOV59641.1	004271	SpoIID	149	S330809_180	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59403.1	004271	SpoIID	149	C440309_180	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59879.1	004271	SpoIID	149	N231010_180	Synechococcus phage S-CAM4	GCA_002922155.1
AYD79815.1	004272	Cluster3966_1clades	149	JA11_010	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66413.1	004272	Cluster3966_1clades	149	JA13_010	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66736.1	004272	Cluster3966_1clades	149	JA29_010	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67384.1	004272	Cluster3966_1clades	149	JA33_010	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81333.1	004273	Cluster3967_1clades	106	SEA_JUSTBECAUSE_168	Streptomyces phage JustBecause	GCA_003613775.1
QJD53736.1	004273	Cluster3967_1clades	106	SEA_KELA_166	Streptomyces phage Kela	GCA_012934305.1
QBZ72063.1	004273	Cluster3967_1clades	149	SEA_KRADAL_167	Streptomyces phage Kradal	GCA_004799925.1
AXH66326.1	004273	Cluster3967_1clades	149	SEA_SATIS_167	Streptomyces phage Satis	GCA_003366315.1
QAX96868.1	004274	Cluster3968_1clades	149	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97173.1	004274	Cluster3968_1clades	149	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96232.1	004274	Cluster3968_1clades	149	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96550.1	004274	Cluster3968_1clades	149	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDB70245.1	004275	Cluster3969_1clades	149	CF8_0077	Aeromonas phage CF8	GCA_006384595.2
QBZ70606.1	004275	Cluster3969_1clades	119	pETSU_025	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71922.1	004275	Cluster3969_1clades	91	N1M2_59	Klebsiella phage N1M2	GCA_010092605.1
AEV89523.1	004275	Cluster3969_1clades	134	OBP_086	Pseudomonas phage OBP	GCA_000896635.1
QBX32507.1	004276	Cluster3970_1clades	122	-	Pseudomonas phage PA1C	GCA_004785505.1
QJB22768.1	004276	Cluster3970_1clades	148	fnug_125	Pseudomonas phage fnug	GCA_012837215.1
QEM42079.1	004276	Cluster3970_1clades	122	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83006.1	004276	Cluster3970_1clades	148	PHIKZ105	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71226.1	004277	Cluster3971_1clades	148	CR5_006	Cronobacter phage CR5	GCA_000910235.1
QBP07433.1	004277	Cluster3971_1clades	148	DERBICUS_6	Erwinia phage Derbicus	GCA_004521655.1
ANZ48856.1	004277	Cluster3971_1clades	148	EARLPHILLIPIV_6	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50196.1	004277	Cluster3971_1clades	126	PHOBOS_6	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGR47953.1	004278	NUDIX	148	SmphiM12_321	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13147.1	004278	NUDIX	148	PHIM19_242	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12786.1	004278	NUDIX	148	PHIM7_241	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13514.1	004278	NUDIX	144	PHIN3_251	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80065.1	004279	Cluster3974_1clades	112	JA11_260	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66666.1	004279	Cluster3974_1clades	112	JA13_263	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66987.1	004279	Cluster3974_1clades	148	JA29_261	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67635.1	004279	Cluster3974_1clades	112	JA33_261	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFA44475.1	004280	SF2-DUF3427A	143	RaK2_00202	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW19113.1	004280	SF2-DUF3427A	148	7t3_0596	Salmonella phage 7t3	GCA_006083215.1
AZU98350.1	004280	SF2-DUF3427A	148	CPT_Munch_409	Salmonella phage Munch	GCA_004015485.1
QIG62632.1	004280	SF2-DUF3427A	148	SEPL_019	Salmonella phage SE_PL	GCA_011067555.1
QAX96648.1	004281	Cluster3976_1clades	148	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96966.1	004281	Cluster3976_1clades	128	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96012.1	004281	Cluster3976_1clades	148	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96330.1	004281	Cluster3976_1clades	148	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96731.1	004282	Cluster3977_1clades	148	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97050.1	004282	Cluster3977_1clades	148	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96096.1	004282	Cluster3977_1clades	148	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96414.1	004282	Cluster3977_1clades	148	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BBA65680.1	004283	TM	145	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65221.1	004283	TM	145	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96250.1	004283	TM	148	Xoosp13_63	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96251.1	004283	TM	75	Xoosp13_64	Xanthomonas phage Xoo-sp13	GCA_013364725.1
APU01411.1	004284	Cluster3979_1clades	138	-	Aeromonas phage 65.2	GCA_002618145.1
ATI17486.1	004284	Cluster3979_1clades	136	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97926.1	004284	Cluster3979_1clades	136	ASswx1_283	Aeromonas phage Asswx_1	GCA_004146865.1
AAR90918.1	004284	Cluster3979_1clades	147	65p020	Aeromonas virus 65	GCA_000893255.1
ANS06053.1	004285	Cluster3980_1clades	142	ABCD_0237	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97255.1	004285	Cluster3980_1clades	147	E_247	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78773.1	004285	Cluster3980_1clades	67	RB43ORF251w	Escherichia virus RB43	GCA_000863505.1
AAX78774.1	004285	Cluster3980_1clades	73	RB43ORF252w	Escherichia virus RB43	GCA_000863505.1
AYD81369.1	004286	Cluster3981_1clades	145	SEA_JUSTBECAUSE_214	Streptomyces phage JustBecause	GCA_003613775.1
QJD53772.1	004286	Cluster3981_1clades	145	SEA_KELA_212	Streptomyces phage Kela	GCA_012934305.1
QBZ72101.1	004286	Cluster3981_1clades	147	SEA_KRADAL_215	Streptomyces phage Kradal	GCA_004799925.1
AXH66362.1	004286	Cluster3981_1clades	147	SEA_SATIS_213	Streptomyces phage Satis	GCA_003366315.1
BAW19174.1	004287	TM+TM	84	FDH28_gp221	Ralstonia phage RP12	GCA_002617345.1
BAW19460.1	004287	TM+TM	84	-	Ralstonia phage RP31	GCA_002617365.1
BAS04950.1	004287	TM+TM	147	AVU11_gp158	Ralstonia phage RSF1	GCA_001500875.1
BAQ02675.1	004287	TM+TM	147	AVU38_gp147	Ralstonia phage RSL2	GCA_001503055.1
ANM44989.1	004288	Cluster3983_1clades	146	KTN4_231	Pseudomonas phage KTN4	GCA_002607225.1
ATN94725.1	004288	Cluster3983_1clades	146	SL2_148	Pseudomonas phage SL2	GCA_002956015.1
QJB22867.1	004288	Cluster3983_1clades	146	fnug_224	Pseudomonas phage fnug	GCA_012837215.1
AAL83091.1	004288	Cluster3983_1clades	146	PHIKZ190	Pseudomonas virus phiKZ	GCA_000842965.1
AGR48010.1	004289	Cluster3984_1clades	146	SmphiM12_378	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13196.1	004289	Cluster3984_1clades	146	PHIM19_291	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12836.1	004289	Cluster3984_1clades	146	PHIM7_291	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13557.1	004289	Cluster3984_1clades	145	PHIN3_294	Sinorhizobium phage phiN3	GCA_001501175.1
AFA44601.1	004290	Cluster3985_1clades	104	RaK2_00328	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18672.1	004290	Cluster3985_1clades	146	7t3_0151	Salmonella phage 7t3	GCA_006083215.1
AZU97949.1	004290	Cluster3985_1clades	146	CPT_Munch_005	Salmonella phage Munch	GCA_004015485.1
QIG63026.1	004290	Cluster3985_1clades	146	SEPL_413	Salmonella phage SE_PL	GCA_011067555.1
QAX96746.1	004291	SuzC	146	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97065.1	004291	SuzC	146	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96111.1	004291	SuzC	146	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96429.1	004291	SuzC	146	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81383.1	004292	Cluster3987_1clades	142	SEA_JUSTBECAUSE_228	Streptomyces phage JustBecause	GCA_003613775.1
QJD53787.1	004292	Cluster3987_1clades	146	SEA_KELA_227	Streptomyces phage Kela	GCA_012934305.1
QBZ72112.1	004292	Cluster3987_1clades	140	SEA_KRADAL_226	Streptomyces phage Kradal	GCA_004799925.1
AXH66374.1	004292	Cluster3987_1clades	140	SEA_SATIS_225	Streptomyces phage Satis	GCA_003366315.1
ANM45052.1	004293	Cluster3988_1clades	145	KTN4_294	Pseudomonas phage KTN4	GCA_002607225.1
ATN94663.1	004293	Cluster3988_1clades	145	SL2_086	Pseudomonas phage SL2	GCA_002956015.1
QJB22927.1	004293	Cluster3988_1clades	145	fnug_284	Pseudomonas phage fnug	GCA_012837215.1
AAL83143.1	004293	Cluster3988_1clades	145	PHIKZ242	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71235.1	004294	Cluster3989_1clades	145	CR5_015	Cronobacter phage CR5	GCA_000910235.1
QBP07441.1	004294	Cluster3989_1clades	145	DERBICUS_15	Erwinia phage Derbicus	GCA_004521655.1
ANZ48865.1	004294	Cluster3989_1clades	145	EARLPHILLIPIV_15	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50205.1	004294	Cluster3989_1clades	145	PHOBOS_15	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGB07088.1	004295	Cluster3990_1clades	145	CF80_gp301	Vibrio phage VH7D	GCA_000914495.1
QBX06007.1	004295	Cluster3990_1clades	145	ValB1HC_053	Vibrio phage ValB1 HC	GCA_004771355.1
ALP47520.1	004295	Cluster3990_1clades	145	phiST2_0328	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54631.1	004295	Cluster3990_1clades	145	vBValMR10Z_90	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AGR47980.1	004296	Cluster3991_1clades	144	SmphiM12_348	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13168.1	004296	Cluster3991_1clades	144	PHIM19_263	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12808.1	004296	Cluster3991_1clades	144	PHIM7_263	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13531.1	004296	Cluster3991_1clades	145	PHIN3_268	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81484.1	004297	SP2	145	SEA_JUSTBECAUSE_329	Streptomyces phage JustBecause	GCA_003613775.1
QJD53887.1	004297	SP2	145	SEA_KELA_327	Streptomyces phage Kela	GCA_012934305.1
QBZ72214.1	004297	SP2	129	SEA_KRADAL_328	Streptomyces phage Kradal	GCA_004799925.1
AXH66477.1	004297	SP2	129	SEA_SATIS_328	Streptomyces phage Satis	GCA_003366315.1
QAX96806.1	004298	Cluster3993_1clades	145	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97125.1	004298	Cluster3993_1clades	145	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96171.1	004298	Cluster3993_1clades	145	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96489.1	004298	Cluster3993_1clades	145	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44822.1	004299	Cluster3994_1clades	144	KTN4_064	Pseudomonas phage KTN4	GCA_002607225.1
ATN94890.1	004299	Cluster3994_1clades	144	SL2_313	Pseudomonas phage SL2	GCA_002956015.1
QJB22700.1	004299	Cluster3994_1clades	144	fnug_57	Pseudomonas phage fnug	GCA_012837215.1
AAL82947.1	004299	Cluster3994_1clades	144	PHIKZ046	Pseudomonas virus phiKZ	GCA_000842965.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANM45071.1	004300	Cluster3995_1clades	144	KTN4_313	Pseudomonas phage KTN4	GCA_002607225.1
ATN94644.1	004300	Cluster3995_1clades	144	SL2_067	Pseudomonas phage SL2	GCA_002956015.1
QJB22946.1	004300	Cluster3995_1clades	144	fnug_303	Pseudomonas phage fnug	GCA_012837215.1
AAL83160.1	004300	Cluster3995_1clades	144	PHIKZ259	Pseudomonas virus phiKZ	GCA_000842965.1
AYD81287.1	004301	SIG+TM+TM+TM	144	SEA_JUSTBECAUSE_118	Streptomyces phage JustBecause	GCA_003613775.1
QJD53690.1	004301	SIG+TM+TM+TM	144	SEA_KELA_119	Streptomyces phage Kela	GCA_012934305.1
QBZ72018.1	004301	SIG+TM+TM+TM	144	SEA_KRADAL_120	Streptomyces phage Kradal	GCA_004799925.1
AXH66281.1	004301	SIG+TM+TM+TM	144	SEA_SATIS_120	Streptomyces phage Satis	GCA_003366315.1
AYD81412.1	004302	VirB4-FtsK	143	SEA_JUSTBECAUSE_257	Streptomyces phage JustBecause	GCA_003613775.1
QJD53819.1	004302	VirB4-FtsK	143	SEA_KELA_259	Streptomyces phage Kela	GCA_012934305.1
QBZ72146.1	004302	VirB4-FtsK	144	SEA_KRADAL_260	Streptomyces phage Kradal	GCA_004799925.1
AXH66408.1	004302	VirB4-FtsK	144	SEA_SATIS_259	Streptomyces phage Satis	GCA_003366315.1
AXQ69040.1	004303	Cluster3998_1clades	144	CcrBL9_gp016	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69556.1	004303	Cluster3998_1clades	144	CcrBL9_gp532	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69600.1	004303	Cluster3998_1clades	144	CcrSC_gp018	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70100.1	004303	Cluster3998_1clades	144	CcrSC_gp518	Caulobacter phage CcrSC	GCA_003443315.1
QAX96777.1	004304	Cluster3999_1clades	144	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97096.1	004304	Cluster3999_1clades	144	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96142.1	004304	Cluster3999_1clades	144	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96460.1	004304	Cluster3999_1clades	144	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71424.1	004305	Cluster4000_1clades	139	CR5_204	Cronobacter phage CR5	GCA_000910235.1
QBP07637.1	004305	Cluster4000_1clades	143	DERBICUS_211	Erwinia phage Derbicus	GCA_004521655.1
ANZ49061.1	004305	Cluster4000_1clades	143	EARLPHILLIPIV_212	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50408.1	004305	Cluster4000_1clades	141	PHOBOS_218	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81273.1	004306	Cluster4001_1clades	143	SEA_JUSTBECAUSE_104	Streptomyces phage JustBecause	GCA_003613775.1
QJD53676.1	004306	Cluster4001_1clades	143	SEA_KELA_105	Streptomyces phage Kela	GCA_012934305.1
QBZ72004.1	004306	Cluster4001_1clades	143	SEA_KRADAL_106	Streptomyces phage Kradal	GCA_004799925.1
AXH66267.1	004306	Cluster4001_1clades	143	SEA_SATIS_106	Streptomyces phage Satis	GCA_003366315.1
AYD81357.1	004307	Cluster4002_1clades	143	SEA_JUSTBECAUSE_192	Streptomyces phage JustBecause	GCA_003613775.1
QJD53760.1	004307	Cluster4002_1clades	143	SEA_KELA_190	Streptomyces phage Kela	GCA_012934305.1
QBZ72087.1	004307	Cluster4002_1clades	141	SEA_KRADAL_191	Streptomyces phage Kradal	GCA_004799925.1
AXH66349.1	004307	Cluster4002_1clades	141	SEA_SATIS_190	Streptomyces phage Satis	GCA_003366315.1
ANM44965.1	004308	SIG+TM	142	KTN4_207	Pseudomonas phage KTN4	GCA_002607225.1
ATN94749.1	004308	SIG+TM	142	SL2_172	Pseudomonas phage SL2	GCA_002956015.1
QJB22843.1	004308	SIG+TM	142	fnug_200	Pseudomonas phage fnug	GCA_012837215.1
AAL83068.1	004308	SIG+TM	142	PHIKZ167	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47806.1	004309	Cluster4004_1clades	142	SmphiM12_174	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13023.1	004309	Cluster4004_1clades	142	PHIM19_117	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12662.1	004309	Cluster4004_1clades	142	PHIM7_116	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13394.1	004309	Cluster4004_1clades	142	PHIN3_130	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47830.1	004310	Cluster4005_1clades	142	SmphiM12_198	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13040.1	004310	Cluster4005_1clades	142	PHIM19_135	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12681.1	004310	Cluster4005_1clades	117	PHIM7_135	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13413.1	004310	Cluster4005_1clades	119	PHIN3_150	Sinorhizobium phage phiN3	GCA_001501175.1
AGX01741.1	004311	Cluster4006_1clades	142	CF95_gp019	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65651.1	004311	Cluster4006_1clades	131	2050HW_00316	Serratia phage 2050HW	GCA_002628125.1
QDB71075.1	004311	Cluster4006_1clades	131	CPT_Moabite_043	Serratia phage Moabite	GCA_006384735.1
QFP93221.1	004311	Cluster4006_1clades	130	-	Serratia phage PCH45	GCA_009187865.1
AYD81365.1	004312	Cluster4007_1clades	138	SEA_JUSTBECAUSE_210	Streptomyces phage JustBecause	GCA_003613775.1
QJD53768.1	004312	Cluster4007_1clades	138	SEA_KELA_208	Streptomyces phage Kela	GCA_012934305.1
QBZ72097.1	004312	Cluster4007_1clades	142	SEA_KRADAL_211	Streptomyces phage Kradal	GCA_004799925.1
AXH66358.1	004312	Cluster4007_1clades	142	SEA_SATIS_209	Streptomyces phage Satis	GCA_003366315.1
ANM44837.1	004313	Cluster4008_1clades	141	KTN4_079	Pseudomonas phage KTN4	GCA_002607225.1
ATN94876.1	004313	Cluster4008_1clades	141	SL2_299	Pseudomonas phage SL2	GCA_002956015.1
QJB22715.1	004313	Cluster4008_1clades	141	fnug_72	Pseudomonas phage fnug	GCA_012837215.1
AAL82959.1	004313	Cluster4008_1clades	141	PHIKZ058	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47902.2	004314	Cluster4009_1clades	141	SmphiM12_270	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13108.1	004314	Cluster4009_1clades	141	PHIM19_203	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12748.1	004314	Cluster4009_1clades	141	PHIM7_203	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13478.1	004314	Cluster4009_1clades	141	PHIN3_215	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21905.1	004315	Cluster4010_1clades	139	GAP32_449A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88989.1	004315	Cluster4010_1clades	141	BF_0464	Serratia phage BF	GCA_002619745.1
SOK59270.1	004315	Cluster4010_1clades	141	g462	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58735.1	004315	Cluster4010_1clades	141	g458	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD80044.1	004316	Cluster4011_1clades	141	JA11_239	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66643.1	004316	Cluster4011_1clades	141	JA13_240	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66967.1	004316	Cluster4011_1clades	141	JA29_241	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67614.1	004316	Cluster4011_1clades	141	JA33_240	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ASV44738.1	004317	NUDIX	130	FDI40_gp303	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44417.1	004317	NUDIX	134	PBI_SCTP2_402	Salicola phage SCTP-2	GCA_002625545.1
BBA65435.1	004317	NUDIX	141	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96452.1	004317	NUDIX	141	Xoosp13_266	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QAX96745.1	004318	Cluster4013_1clades	141	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97064.1	004318	Cluster4013_1clades	141	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96110.1	004318	Cluster4013_1clades	141	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96428.1	004318	Cluster4013_1clades	141	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
prevph1000000128	004319	Cluster4014_1clades	142	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000834	004319	Cluster4014_1clades	126	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000096	004319	Cluster4014_1clades	142	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000577	004319	Cluster4014_1clades	126	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANM44896.1	004320	Cluster4015_1clades	140	KTN4_138	Pseudomonas phage KTN4	GCA_002607225.1
ATN94817.1	004320	Cluster4015_1clades	140	SL2_240	Pseudomonas phage SL2	GCA_002956015.1
QJB22774.1	004320	Cluster4015_1clades	140	fnug_131	Pseudomonas phage fnug	GCA_012837215.1
AAL83010.1	004320	Cluster4015_1clades	140	PHIKZ109	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71326.1	004321	Cluster4016_1clades	140	CR5_106	Cronobacter phage CR5	GCA_000910235.1
QBP07535.1	004321	Cluster4016_1clades	140	DERBICUS_109	Erwinia phage Derbicus	GCA_004521655.1
ANZ48958.1	004321	Cluster4016_1clades	140	EARLPHILLIPIV_109	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50300.1	004321	Cluster4016_1clades	139	PHOBOS_110	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81218.1	004322	HK97-gp10_like	140	SEA_JUSTBECAUSE_49	Streptomyces phage JustBecause	GCA_003613775.1
QJD53621.1	004322	HK97-gp10_like	140	SEA_KELA_50	Streptomyces phage Kela	GCA_012934305.1
QBZ71954.1	004322	HK97-gp10_like	137	SEA_KRADAL_55	Streptomyces phage Kradal	GCA_004799925.1
AXH66216.1	004322	HK97-gp10_like	137	SEA_SATIS_55	Streptomyces phage Satis	GCA_003366315.1
AYD81256.1	004323	TM	140	SEA_JUSTBECAUSE_87	Streptomyces phage JustBecause	GCA_003613775.1
QJD53659.1	004323	TM	140	SEA_KELA_88	Streptomyces phage Kela	GCA_012934305.1
QBZ71988.1	004323	TM	139	SEA_KRADAL_90	Streptomyces phage Kradal	GCA_004799925.1
AXH66251.1	004323	TM	139	SEA_SATIS_90	Streptomyces phage Satis	GCA_003366315.1
ANM45013.1	004324	Cluster4019_1clades	139	KTN4_255	Pseudomonas phage KTN4	GCA_002607225.1
ATN94701.1	004324	Cluster4019_1clades	139	SL2_124	Pseudomonas phage SL2	GCA_002956015.1
QJB22890.1	004324	Cluster4019_1clades	139	fnug_247	Pseudomonas phage fnug	GCA_012837215.1
AAL83112.1	004324	Cluster4019_1clades	139	PHIKZ211	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45077.1	004325	Cluster4020_1clades	139	KTN4_319	Pseudomonas phage KTN4	GCA_002607225.1
ATN94638.1	004325	Cluster4020_1clades	139	SL2_061	Pseudomonas phage SL2	GCA_002956015.1
QJB22952.1	004325	Cluster4020_1clades	139	fnug_309	Pseudomonas phage fnug	GCA_012837215.1
AAL83165.1	004325	Cluster4020_1clades	139	PHIKZ264	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47797.1	004326	TM+TM	139	SmphiM12_165	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13014.1	004326	TM+TM	139	PHIM19_108	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12654.1	004326	TM+TM	139	PHIM7_107	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13386.1	004326	TM+TM	139	PHIN3_121	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81247.1	004327	Cluster4022_1clades	138	SEA_JUSTBECAUSE_78	Streptomyces phage JustBecause	GCA_003613775.1
QJD53650.1	004327	Cluster4022_1clades	138	SEA_KELA_79	Streptomyces phage Kela	GCA_012934305.1
QBZ71979.1	004327	Cluster4022_1clades	139	SEA_KRADAL_81	Streptomyces phage Kradal	GCA_004799925.1
AXH66242.1	004327	Cluster4022_1clades	139	SEA_SATIS_81	Streptomyces phage Satis	GCA_003366315.1
AYD81283.1	004328	Cluster4023_1clades	138	SEA_JUSTBECAUSE_114	Streptomyces phage JustBecause	GCA_003613775.1
QJD53686.1	004328	Cluster4023_1clades	138	SEA_KELA_115	Streptomyces phage Kela	GCA_012934305.1
QBZ72013.1	004328	Cluster4023_1clades	139	SEA_KRADAL_115	Streptomyces phage Kradal	GCA_004799925.1
AXH66277.1	004328	Cluster4023_1clades	139	SEA_SATIS_116	Streptomyces phage Satis	GCA_003366315.1
AYD81490.1	004329	Cluster4024_1clades	136	SEA_JUSTBECAUSE_335	Streptomyces phage JustBecause	GCA_003613775.1
QJD53893.1	004329	Cluster4024_1clades	136	SEA_KELA_333	Streptomyces phage Kela	GCA_012934305.1
QBZ72218.1	004329	Cluster4024_1clades	139	SEA_KRADAL_332	Streptomyces phage Kradal	GCA_004799925.1
AXH66481.1	004329	Cluster4024_1clades	139	SEA_SATIS_332	Streptomyces phage Satis	GCA_003366315.1
QDH83407.1	004330	Cluster4025_1clades	123	H1O15_gp055	Achromobacter phage Motura	GCA_006964305.1
QBX06711.1	004330	Cluster4025_1clades	122	BcepSaruman_298	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74679.1	004330	Cluster4025_1clades	122	BcepSauron_299	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41606.1	004330	Cluster4025_1clades	139	RSL1_ORF159	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96797.1	004331	Cluster4026_1clades	139	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX97116.1	004331	Cluster4026_1clades	139	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96162.1	004331	Cluster4026_1clades	139	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96480.1	004331	Cluster4026_1clades	139	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96817.1	004332	Cluster4027_1clades	139	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97136.1	004332	Cluster4027_1clades	139	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96182.1	004332	Cluster4027_1clades	139	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96500.1	004332	Cluster4027_1clades	139	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71345.1	004333	Cluster4028_1clades	106	CR5_125	Cronobacter phage CR5	GCA_000910235.1
QBP07552.1	004333	Cluster4028_1clades	139	DERBICUS_126	Erwinia phage Derbicus	GCA_004521655.1
ANZ48975.1	004333	Cluster4028_1clades	106	EARLPHILLIPIV_126	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50317.1	004333	Cluster4028_1clades	99	PHOBOS_127	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QDH83575.1	004334	SIG+PC4	139	H1O15_gp213	Achromobacter phage Motura	GCA_006964305.1
QBX06516.1	004334	SIG+PC4	94	BcepSaruman_103	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74482.1	004334	SIG+PC4	94	BcepSauron_102	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41540.1	004334	SIG+PC4	111	RSL1_ORF095	Ralstonia phage phiRSL1	GCA_000879455.1
AGR47712.1	004335	Cluster4030_1clades	138	SmphiM12_080	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12967.1	004335	Cluster4030_1clades	138	PHIM19_60	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12607.1	004335	Cluster4030_1clades	138	PHIM7_59	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13340.1	004335	Cluster4030_1clades	138	PHIN3_75	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47857.1	004336	AdoMet_dc	138	SmphiM12_225	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13060.1	004336	AdoMet_dc	138	PHIM19_155	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12701.1	004336	AdoMet_dc	138	PHIM7_155	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13430.2	004336	AdoMet_dc	138	PHIN3_167	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14037.1	004337	Cluster4032_1clades	138	PBI_121Q_147	Escherichia phage 121Q	GCA_000926855.1
BBM61720.1	004337	Cluster4032_1clades	138	EO157G_1310	Escherichia phage SP27	GCA_008033345.1
QBO61662.1	004337	Cluster4032_1clades	138	G17_00166	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80032.1	004337	Cluster4032_1clades	138	PSLUR01_00055	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMM43707.1	004338	Cluster4033_1clades	105	CBB_142	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88659.1	004338	Cluster4033_1clades	138	BF_0134	Serratia phage BF	GCA_002619745.1
SOK58942.1	004338	Cluster4033_1clades	103	g134	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58408.1	004338	Cluster4033_1clades	138	g131	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD81397.1	004339	Cluster4034_1clades	136	SEA_JUSTBECAUSE_242	Streptomyces phage JustBecause	GCA_003613775.1
QJD53801.1	004339	Cluster4034_1clades	136	SEA_KELA_241	Streptomyces phage Kela	GCA_012934305.1
QBZ72127.1	004339	Cluster4034_1clades	138	SEA_KRADAL_241	Streptomyces phage Kradal	GCA_004799925.1
AXH66389.1	004339	Cluster4034_1clades	138	SEA_SATIS_240	Streptomyces phage Satis	GCA_003366315.1
QAX96901.1	004340	Cluster4035_1clades	138	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97206.1	004340	Cluster4035_1clades	138	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96265.1	004340	Cluster4035_1clades	138	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96583.1	004340	Cluster4035_1clades	138	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81446.1	004341	Cluster4036_1clades	136	SEA_JUSTBECAUSE_291	Streptomyces phage JustBecause	GCA_003613775.1
QJD53850.1	004341	Cluster4036_1clades	138	SEA_KELA_290	Streptomyces phage Kela	GCA_012934305.1
QBZ72181.1	004341	Cluster4036_1clades	132	SEA_KRADAL_295	Streptomyces phage Kradal	GCA_004799925.1
AXH66444.1	004341	Cluster4036_1clades	132	SEA_SATIS_295	Streptomyces phage Satis	GCA_003366315.1
AXG67270.1	004342	Cluster4037_1clades	109	AD1_226	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08610.1	004342	Cluster4037_1clades	136	Alexandra_235	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58870.1	004342	Cluster4037_1clades	122	Y3_230	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28702.1	004342	Cluster4037_1clades	137	YOLOSWAG_224	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD79842.1	004343	Cluster4038_1clades	137	JA11_037	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66442.1	004343	Cluster4038_1clades	137	JA13_039	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66766.1	004343	Cluster4038_1clades	137	JA29_040	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67411.1	004343	Cluster4038_1clades	137	JA33_037	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81399.1	004344	Cluster4039_1clades	135	SEA_JUSTBECAUSE_244	Streptomyces phage JustBecause	GCA_003613775.1
QJD53803.1	004344	Cluster4039_1clades	135	SEA_KELA_243	Streptomyces phage Kela	GCA_012934305.1
QBZ72129.1	004344	Cluster4039_1clades	137	SEA_KRADAL_243	Streptomyces phage Kradal	GCA_004799925.1
AXH66391.1	004344	Cluster4039_1clades	137	SEA_SATIS_242	Streptomyces phage Satis	GCA_003366315.1
AYD81259.1	004345	Cluster4040_1clades	137	SEA_JUSTBECAUSE_90	Streptomyces phage JustBecause	GCA_003613775.1
QJD53662.1	004345	Cluster4040_1clades	137	SEA_KELA_91	Streptomyces phage Kela	GCA_012934305.1
QBZ71991.1	004345	Cluster4040_1clades	114	SEA_KRADAL_93	Streptomyces phage Kradal	GCA_004799925.1
AXH66254.1	004345	Cluster4040_1clades	131	SEA_SATIS_93	Streptomyces phage Satis	GCA_003366315.1
ANM45111.1	004346	Cluster4041_1clades	136	KTN4_353	Pseudomonas phage KTN4	GCA_002607225.1
ATN94602.1	004346	Cluster4041_1clades	136	SL2_025	Pseudomonas phage SL2	GCA_002956015.1
QJB22988.1	004346	Cluster4041_1clades	136	fnug_345	Pseudomonas phage fnug	GCA_012837215.1
AAL83194.1	004346	Cluster4041_1clades	136	PHIKZ293	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47649.1	004347	WLM	136	SmphiM12_017	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12915.1	004347	WLM	136	PHIM19_8	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12555.1	004347	WLM	136	PHIM7_7	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13285.1	004347	WLM	136	PHIN3_18	Sinorhizobium phage phiN3	GCA_001501175.1
AXQ69063.1	004348	Cluster4043_1clades	124	CcrBL9_gp039	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69579.1	004348	Cluster4043_1clades	124	CcrBL9_gp555	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69623.1	004348	Cluster4043_1clades	136	CcrSC_gp041	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70123.1	004348	Cluster4043_1clades	136	CcrSC_gp541	Caulobacter phage CcrSC	GCA_003443315.1
ASR76273.1	004349	Cluster4044_1clades	131	PBI_BELLAMY_237	Synechococcus phage Bellamy	GCA_002627525.1
QCW23018.1	004349	Cluster4044_1clades	130	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50525.1	004349	Cluster4044_1clades	130	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70223.1	004349	Cluster4044_1clades	136	SynMITS9220M01_217	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ANM45058.1	004350	Cluster4045_1clades	135	KTN4_300	Pseudomonas phage KTN4	GCA_002607225.1
ATN94657.1	004350	Cluster4045_1clades	135	SL2_080	Pseudomonas phage SL2	GCA_002956015.1
QJB22933.1	004350	Cluster4045_1clades	135	fnug_290	Pseudomonas phage fnug	GCA_012837215.1
AAL83148.1	004350	Cluster4045_1clades	135	PHIKZ247	Pseudomonas virus phiKZ	GCA_000842965.1
AFU88155.1	004351	Cluster4046_1clades	135	CcrColossus_gp285	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68830.1	004351	Cluster4046_1clades	135	CcrPW_gp291	Caulobacter phage CcrPW	GCA_003443275.1
QGT54772.1	004351	Cluster4046_1clades	125	b23_0157	Synechococcus phage B23	GCA_009745195.1
QGT54402.1	004351	Cluster4046_1clades	125	b3_0158	Synechococcus phage B3	GCA_009745215.1
AGR47702.1	004352	Cluster4047_1clades	135	SmphiM12_070	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12959.1	004352	Cluster4047_1clades	135	PHIM19_52	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12599.1	004352	Cluster4047_1clades	135	PHIM7_51	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13332.1	004352	Cluster4047_1clades	135	PHIN3_67	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80100.1	004353	Cluster4048_1clades	135	JA11_295	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66701.1	004353	Cluster4048_1clades	135	JA13_298	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67020.1	004353	Cluster4048_1clades	135	JA29_294	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67670.1	004353	Cluster4048_1clades	135	JA33_296	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QDB70458.1	004354	Cluster4049_1clades	95	CF8_0045	Aeromonas phage CF8	GCA_006384595.2
QBZ70862.1	004354	Cluster4049_1clades	135	pETSU_281	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71893.1	004354	Cluster4049_1clades	100	N1M2_30	Klebsiella phage N1M2	GCA_010092605.1
AEV89488.1	004354	Cluster4049_1clades	107	OBP_051	Pseudomonas phage OBP	GCA_000896635.1
ANM44763.1	004355	Cluster4050_1clades	134	KTN4_005	Pseudomonas phage KTN4	GCA_002607225.1
ATN94580.1	004355	Cluster4050_1clades	134	SL2_003	Pseudomonas phage SL2	GCA_002956015.1
QJB22648.1	004355	Cluster4050_1clades	134	fnug_5	Pseudomonas phage fnug	GCA_012837215.1
AAL82906.1	004355	Cluster4050_1clades	134	PHIKZ005	Pseudomonas virus phiKZ	GCA_000842965.1
AYD79834.1	004356	Cluster4051_1clades	134	JA11_029	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66433.1	004356	Cluster4051_1clades	134	JA13_030	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66757.1	004356	Cluster4051_1clades	134	JA29_031	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67403.1	004356	Cluster4051_1clades	134	JA33_029	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80096.1	004357	Cluster4052_1clades	134	JA11_291	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66697.1	004357	Cluster4052_1clades	134	JA13_294	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67016.1	004357	Cluster4052_1clades	134	JA29_290	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67666.1	004357	Cluster4052_1clades	134	JA33_292	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81303.1	004358	Cluster4053_1clades	132	SEA_JUSTBECAUSE_134	Streptomyces phage JustBecause	GCA_003613775.1
QJD53706.1	004358	Cluster4053_1clades	134	SEA_KELA_135	Streptomyces phage Kela	GCA_012934305.1
QBZ72032.1	004358	Cluster4053_1clades	125	SEA_KRADAL_134	Streptomyces phage Kradal	GCA_004799925.1
AXH66295.1	004358	Cluster4053_1clades	125	SEA_SATIS_134	Streptomyces phage Satis	GCA_003366315.1
ANM45005.1	004359	Cluster4054_1clades	133	KTN4_247	Pseudomonas phage KTN4	GCA_002607225.1
ATN94709.1	004359	Cluster4054_1clades	133	SL2_132	Pseudomonas phage SL2	GCA_002956015.1
QJB22883.1	004359	Cluster4054_1clades	133	fnug_240	Pseudomonas phage fnug	GCA_012837215.1
AAL83106.1	004359	Cluster4054_1clades	133	PHIKZ205	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71423.1	004360	Cluster4055_1clades	133	CR5_203	Cronobacter phage CR5	GCA_000910235.1
QBP07636.1	004360	Cluster4055_1clades	132	DERBICUS_210	Erwinia phage Derbicus	GCA_004521655.1
ANZ49060.1	004360	Cluster4055_1clades	132	EARLPHILLIPIV_211	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50407.1	004360	Cluster4055_1clades	132	PHOBOS_217	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGR47718.1	004361	Cluster4056_1clades	133	SmphiM12_086	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12973.1	004361	Cluster4056_1clades	133	PHIM19_66	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12613.1	004361	Cluster4056_1clades	133	PHIM7_65	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13345.1	004361	Cluster4056_1clades	133	PHIN3_81	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80028.1	004362	Cluster4057_1clades	133	JA11_223	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66627.1	004362	Cluster4057_1clades	133	JA13_224	Dickeya phage vB_DsoM_JA13	GCA_003568455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXG66951.1	004362	Cluster4057_1clades	133	JA29_225	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67598.1	004362	Cluster4057_1clades	133	JA33_224	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81314.1	004363	Cluster4058_1clades	133	SEA_JUSTBECAUSE_149	Streptomyces phage JustBecause	GCA_003613775.1
QJD53717.1	004363	Cluster4058_1clades	133	SEA_KELA_147	Streptomyces phage Kela	GCA_012934305.1
QBZ72044.1	004363	Cluster4058_1clades	133	SEA_KRADAL_148	Streptomyces phage Kradal	GCA_004799925.1
AXH66307.1	004363	Cluster4058_1clades	133	SEA_SATIS_148	Streptomyces phage Satis	GCA_003366315.1
AYD81348.1	004364	Cluster4059_1clades	129	SEA_JUSTBECAUSE_183	Streptomyces phage JustBecause	GCA_003613775.1
QJD53751.1	004364	Cluster4059_1clades	129	SEA_KELA_181	Streptomyces phage Kela	GCA_012934305.1
QBZ72077.1	004364	Cluster4059_1clades	133	SEA_KRADAL_181	Streptomyces phage Kradal	GCA_004799925.1
AXH66340.1	004364	Cluster4059_1clades	133	SEA_SATIS_181	Streptomyces phage Satis	GCA_003366315.1
QAX96631.1	004365	TM	133	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96949.1	004365	TM	133	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95995.1	004365	TM	133	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96313.1	004365	TM	133	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
APU01737.1	004366	HECT	114	-	Aeromonas phage 65.2	GCA_002618145.1
ASU00435.1	004366	HECT	132	HWB28_gp117	Aeromonas phage AS-zj	GCA_002627665.1
AFN39368.1	004366	HECT	132	CC2_173	Aeromonas phage CC2	GCA_000903495.1
ADQ53379.1	004366	HECT	106	65p371	Aeromonas virus 65	GCA_000893255.1
ANM45103.1	004367	Cluster4062_1clades	132	KTN4_345	Pseudomonas phage KTN4	GCA_002607225.1
ATN94611.1	004367	Cluster4062_1clades	62	SL2_034	Pseudomonas phage SL2	GCA_002956015.1
QJB22979.1	004367	Cluster4062_1clades	132	fnug_336	Pseudomonas phage fnug	GCA_012837215.1
AGC26359.1	004367	Cluster4062_1clades	62	PHIKZ286.1	Pseudomonas virus phiKZ	GCA_000842965.1
AUZ95383.1	004368	Peptidase_M15_4	132	FDI40_gp624	Agrobacterium phage Atu_ph07	GCA_002628245.1
ANS06063.1	004368	Peptidase_M15_4	131	ABCD_0153	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97165.1	004368	Peptidase_M15_4	131	E_157	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78681.1	004368	Peptidase_M15_4	131	RB43ORF159c	Escherichia virus RB43	GCA_000863505.1
AYD81171.1	004369	Cluster4064_1clades	108	SEA_JUSTBECAUSE_2	Streptomyces phage JustBecause	GCA_003613775.1
QJD53573.1	004369	Cluster4064_1clades	108	SEA_KELA_2	Streptomyces phage Kela	GCA_012934305.1
QBZ71901.1	004369	Cluster4064_1clades	132	SEA_KRADAL_2	Streptomyces phage Kradal	GCA_004799925.1
AXH66163.1	004369	Cluster4064_1clades	132	SEA_SATIS_2	Streptomyces phage Satis	GCA_003366315.1
AXQ69061.1	004370	Cluster4065_1clades	119	CcrBL9_gp037	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69577.1	004370	Cluster4065_1clades	119	CcrBL9_gp553	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69621.1	004370	Cluster4065_1clades	132	CcrSC_gp039	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70121.1	004370	Cluster4065_1clades	132	CcrSC_gp539	Caulobacter phage CcrSC	GCA_003443315.1
AYD81492.1	004371	Cluster4066_1clades	132	SEA_JUSTBECAUSE_337	Streptomyces phage JustBecause	GCA_003613775.1
QJD53895.1	004371	Cluster4066_1clades	132	SEA_KELA_335	Streptomyces phage Kela	GCA_012934305.1
QBZ72220.1	004371	Cluster4066_1clades	113	SEA_KRADAL_334	Streptomyces phage Kradal	GCA_004799925.1
AXH66483.1	004371	Cluster4066_1clades	113	SEA_SATIS_334	Streptomyces phage Satis	GCA_003366315.1
QAX96682.1	004372	Cluster4067_1clades	132	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97000.1	004372	Cluster4067_1clades	132	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96046.1	004372	Cluster4067_1clades	132	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96364.1	004372	Cluster4067_1clades	132	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96707.1	004373	Cluster4068_1clades	132	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97025.1	004373	Cluster4068_1clades	132	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96071.1	004373	Cluster4068_1clades	132	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96389.1	004373	Cluster4068_1clades	132	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96813.1	004374	Cluster4069_1clades	132	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97132.1	004374	Cluster4069_1clades	132	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96178.1	004374	Cluster4069_1clades	132	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96496.1	004374	Cluster4069_1clades	132	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71232.1	004375	Cluster4070_1clades	131	CR5_012	Cronobacter phage CR5	GCA_000910235.1
QBP07438.1	004375	Cluster4070_1clades	132	DERBICUS_12	Erwinia phage Derbicus	GCA_004521655.1
ANZ48862.1	004375	Cluster4070_1clades	131	EARLPHILLIPIV_12	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50202.1	004375	Cluster4070_1clades	131	PHOBOS_12	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QDH83411.1	004376	Cluster4071_1clades	123	H1O15_gp002	Achromobacter phage Motura	GCA_006964305.1
QBX06715.1	004376	Cluster4071_1clades	132	BcepSaruman_302	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74683.1	004376	Cluster4071_1clades	132	BcepSauron_303	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41602.1	004376	Cluster4071_1clades	130	RSL1_ORF156	Ralstonia phage phiRSL1	GCA_000879455.1
AYD81286.1	004377	SIG+TM+TM	125	SEA_JUSTBECAUSE_117	Streptomyces phage JustBecause	GCA_003613775.1
QJD53689.1	004377	SIG+TM+TM	132	SEA_KELA_118	Streptomyces phage Kela	GCA_012934305.1
QBZ72017.1	004377	SIG+TM+TM	125	SEA_KRADAL_119	Streptomyces phage Kradal	GCA_004799925.1
AXH66280.1	004377	SIG+TM+TM	125	SEA_SATIS_119	Streptomyces phage Satis	GCA_003366315.1
ANM44963.1	004378	Cluster4073_1clades	131	KTN4_205	Pseudomonas phage KTN4	GCA_002607225.1
ATN94751.1	004378	Cluster4073_1clades	131	SL2_174	Pseudomonas phage SL2	GCA_002956015.1
QJB22841.1	004378	Cluster4073_1clades	131	fnug_198	Pseudomonas phage fnug	GCA_012837215.1
AAL83067.1	004378	Cluster4073_1clades	131	PHIKZ166	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45003.1	004379	Cluster4074_1clades	131	KTN4_245	Pseudomonas phage KTN4	GCA_002607225.1
ATN94711.1	004379	Cluster4074_1clades	131	SL2_134	Pseudomonas phage SL2	GCA_002956015.1
QJB22881.1	004379	Cluster4074_1clades	131	fnug_238	Pseudomonas phage fnug	GCA_012837215.1
AAL83105.1	004379	Cluster4074_1clades	131	PHIKZ204	Pseudomonas virus phiKZ	GCA_000842965.1
AFU87666.1	004380	Cluster4075_1clades	131	CcrKarma_gp149	Caulobacter virus Karma	GCA_000901575.1
AFU87315.1	004380	Cluster4075_1clades	131	CcrMagneto_gp145	Caulobacter virus Magneto	GCA_000903095.1
AFU88462.1	004380	Cluster4075_1clades	131	CcrSwift_gp144	Caulobacter virus Swift	GCA_000899655.1
AFU86979.1	004380	Cluster4075_1clades	131	CbK_gp147	Caulobacter virus phiCbK	GCA_000900535.1
AGR47937.1	004381	Cluster4076_1clades	131	SmphiM12_305	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13134.1	004381	Cluster4076_1clades	131	PHIM19_229	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12773.1	004381	Cluster4076_1clades	131	PHIM7_228	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13502.1	004381	Cluster4076_1clades	131	PHIN3_239	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47999.1	004382	Cluster4077_1clades	131	SmphiM12_367	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13185.1	004382	Cluster4077_1clades	131	PHIM19_280	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12825.1	004382	Cluster4077_1clades	131	PHIM7_280	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13547.1	004382	Cluster4077_1clades	131	PHIN3_284	Sinorhizobium phage phiN3	GCA_001501175.1
ANZ49774.1	004383	Cluster4078_1clades	130	MACHINA_136	Erwinia phage Machina	GCA_002758035.1
ANZ48703.1	004383	Cluster4078_1clades	131	CHRISDB_141	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49218.1	004383	Cluster4078_1clades	130	HUXLEY_136	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50046.1	004383	Cluster4078_1clades	130	PARSHIK_137	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AYD79866.1	004384	Cluster4079_1clades	131	JA11_061	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66465.1	004384	Cluster4079_1clades	131	JA13_062	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66789.1	004384	Cluster4079_1clades	131	JA29_063	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67435.1	004384	Cluster4079_1clades	131	JA33_061	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81361.1	004385	Cluster4080_1clades	131	SEA_JUSTBECAUSE_205	Streptomyces phage JustBecause	GCA_003613775.1
QJD53764.1	004385	Cluster4080_1clades	131	SEA_KELA_203	Streptomyces phage Kela	GCA_012934305.1
QBZ72091.1	004385	Cluster4080_1clades	131	SEA_KRADAL_205	Streptomyces phage Kradal	GCA_004799925.1
AXH66353.1	004385	Cluster4080_1clades	131	SEA_SATIS_204	Streptomyces phage Satis	GCA_003366315.1
AYD81436.1	004386	Cluster4081_1clades	129	SEA_JUSTBECAUSE_281	Streptomyces phage JustBecause	GCA_003613775.1
QJD53842.1	004386	Cluster4081_1clades	129	SEA_KELA_282	Streptomyces phage Kela	GCA_012934305.1
QBZ72171.1	004386	Cluster4081_1clades	131	SEA_KRADAL_285	Streptomyces phage Kradal	GCA_004799925.1
AXH66434.1	004386	Cluster4081_1clades	131	SEA_SATIS_285	Streptomyces phage Satis	GCA_003366315.1
QDH83472.1	004387	Cluster4082_1clades	96	H1O15_gp334	Achromobacter phage Motura	GCA_006964305.1
QBX06586.1	004387	Cluster4082_1clades	103	BcepSaruman_173	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74551.1	004387	Cluster4082_1clades	103	BcepSauron_171	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41776.1	004387	Cluster4082_1clades	131	RSL1_ORF330	Ralstonia phage phiRSL1	GCA_000879455.1
ANM44889.1	004388	Cluster4083_1clades	130	KTN4_131	Pseudomonas phage KTN4	GCA_002607225.1
ATN94824.1	004388	Cluster4083_1clades	130	SL2_247	Pseudomonas phage SL2	GCA_002956015.1
QJB22766.1	004388	Cluster4083_1clades	130	fnug_123	Pseudomonas phage fnug	GCA_012837215.1
AAL83004.1	004388	Cluster4083_1clades	130	PHIKZ103	Pseudomonas virus phiKZ	GCA_000842965.1
ANS06067.1	004389	Cluster4084_1clades	130	ABCD_0141	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97149.1	004389	Cluster4084_1clades	130	E_141	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78664.1	004389	Cluster4084_1clades	54	RB43ORF142c	Escherichia virus RB43	GCA_000863505.1
AAX78665.1	004389	Cluster4084_1clades	85	RB43ORF143c	Escherichia virus RB43	GCA_000863505.1
AYD81356.1	004390	Cluster4086_1clades	130	SEA_JUSTBECAUSE_191	Streptomyces phage JustBecause	GCA_003613775.1
QJD53759.1	004390	Cluster4086_1clades	130	SEA_KELA_189	Streptomyces phage Kela	GCA_012934305.1
QBZ72086.1	004390	Cluster4086_1clades	128	SEA_KRADAL_190	Streptomyces phage Kradal	GCA_004799925.1
AXH66348.1	004390	Cluster4086_1clades	128	SEA_SATIS_189	Streptomyces phage Satis	GCA_003366315.1
AYD81473.1	004391	Cluster4087_1clades	130	SEA_JUSTBECAUSE_318	Streptomyces phage JustBecause	GCA_003613775.1
QJD53876.1	004391	Cluster4087_1clades	130	SEA_KELA_316	Streptomyces phage Kela	GCA_012934305.1
QBZ72207.1	004391	Cluster4087_1clades	128	SEA_KRADAL_321	Streptomyces phage Kradal	GCA_004799925.1
AXH66470.1	004391	Cluster4087_1clades	128	SEA_SATIS_321	Streptomyces phage Satis	GCA_003366315.1
QDH83499.1	004392	Cluster4088_1clades	118	H1O15_gp307	Achromobacter phage Motura	GCA_006964305.1
QDH83496.1	004392	Cluster4088_1clades	118	H1O15_gp310	Achromobacter phage Motura	GCA_006964305.1
QDH83498.1	004392	Cluster4088_1clades	120	H1O15_gp308	Achromobacter phage Motura	GCA_006964305.1
QDH83500.1	004392	Cluster4088_1clades	130	H1O15_gp306	Achromobacter phage Motura	GCA_006964305.1
QDJ96330.1	004393	Cluster4089_1clades	116	Xoosp13_143	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96331.1	004393	Cluster4089_1clades	120	Xoosp13_144	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96333.1	004393	Cluster4089_1clades	130	Xoosp13_146	Xanthomonas phage Xoo-sp13	GCA_013364725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ96335.1	004393	Cluster4089_1clades	89	Xoosp13_148	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ANM45110.1	004394	Cluster4090_1clades	129	KTN4_352	Pseudomonas phage KTN4	GCA_002607225.1
ATN94603.1	004394	Cluster4090_1clades	129	SL2_026	Pseudomonas phage SL2	GCA_002956015.1
QJB22987.1	004394	Cluster4090_1clades	129	fnug_344	Pseudomonas phage fnug	GCA_012837215.1
AAL83193.2	004394	Cluster4090_1clades	129	PHIKZ292	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47808.1	004395	Cluster4091_1clades	129	SmphiM12_176	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13024.1	004395	Cluster4091_1clades	129	PHIM19_118	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12663.1	004395	Cluster4091_1clades	129	PHIM7_117	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13395.2	004395	Cluster4091_1clades	129	PHIN3_131	Sinorhizobium phage phiN3	GCA_001501175.1
ANM44819.1	004396	Cluster4092_1clades	129	KTN4_061	Pseudomonas phage KTN4	GCA_002607225.1
ATN94892.1	004396	Cluster4092_1clades	129	SL2_315	Pseudomonas phage SL2	GCA_002956015.1
QJB22698.1	004396	Cluster4092_1clades	129	fnug_55	Pseudomonas phage fnug	GCA_012837215.1
AAL82945.2	004396	Cluster4092_1clades	119	PHIKZ044	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96730.1	004397	Cluster4093_1clades	129	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97049.1	004397	Cluster4093_1clades	129	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96095.1	004397	Cluster4093_1clades	129	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96413.1	004397	Cluster4093_1clades	129	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96712.1	004398	TM	128	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97031.1	004398	TM	128	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96077.1	004398	TM	128	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96395.1	004398	TM	128	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96719.1	004399	Cluster4095_1clades	128	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97038.1	004399	Cluster4095_1clades	128	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96084.1	004399	Cluster4095_1clades	128	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96402.1	004399	Cluster4095_1clades	128	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96824.1	004400	Cluster4096_1clades	128	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97143.1	004400	Cluster4096_1clades	128	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96189.1	004400	Cluster4096_1clades	128	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96507.1	004400	Cluster4096_1clades	128	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44824.1	004401	Cluster4097_1clades	127	KTN4_066	Pseudomonas phage KTN4	GCA_002607225.1
ATN94888.1	004401	Cluster4097_1clades	127	SL2_311	Pseudomonas phage SL2	GCA_002956015.1
QJB22702.1	004401	Cluster4097_1clades	127	fnug_59	Pseudomonas phage fnug	GCA_012837215.1
AAL82949.1	004401	Cluster4097_1clades	127	PHIKZ048	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44836.1	004402	Cluster4098_1clades	127	KTN4_078	Pseudomonas phage KTN4	GCA_002607225.1
ATN94877.1	004402	Cluster4098_1clades	127	SL2_300	Pseudomonas phage SL2	GCA_002956015.1
QJB22714.1	004402	Cluster4098_1clades	127	fnug_71	Pseudomonas phage fnug	GCA_012837215.1
AAL82958.1	004402	Cluster4098_1clades	127	PHIKZ057	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44898.1	004403	Cluster4099_1clades	127	KTN4_140	Pseudomonas phage KTN4	GCA_002607225.1
ATN94815.1	004403	Cluster4099_1clades	127	SL2_238	Pseudomonas phage SL2	GCA_002956015.1
QJB22776.1	004403	Cluster4099_1clades	127	fnug_133	Pseudomonas phage fnug	GCA_012837215.1
AAL83011.1	004403	Cluster4099_1clades	127	PHIKZ110	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45061.1	004404	Cluster4100_1clades	127	KTN4_303	Pseudomonas phage KTN4	GCA_002607225.1
ATN94654.1	004404	Cluster4100_1clades	127	SL2_077	Pseudomonas phage SL2	GCA_002956015.1
QJB22936.1	004404	Cluster4100_1clades	127	fnug_293	Pseudomonas phage fnug	GCA_012837215.1
AAL83151.1	004404	Cluster4100_1clades	127	PHIKZ250	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47961.1	004405	Cluster4101_1clades	127	SmphiM12_329	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13152.1	004405	Cluster4101_1clades	127	PHIM19_247	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12791.1	004405	Cluster4101_1clades	127	PHIM7_246	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13515.1	004405	Cluster4101_1clades	127	PHIN3_252	Sinorhizobium phage phiN3	GCA_001501175.1
ARB13882.1	004406	Cluster4102_1clades	127	Ccr2_gp007	Caulobacter phage Ccr2	GCA_002619465.1
ARB14205.1	004406	Cluster4102_1clades	127	Ccr2_gp329	Caulobacter phage Ccr2	GCA_002619465.1
AFU86488.1	004406	Cluster4102_1clades	120	CcrRogue_gp006	Caulobacter virus Rogue	GCA_000900555.1
AFU86819.1	004406	Cluster4102_1clades	120	CcrRogue_gp337	Caulobacter virus Rogue	GCA_000900555.1
AYD81491.1	004407	Cluster4103_1clades	127	SEA_JUSTBECAUSE_336	Streptomyces phage JustBecause	GCA_003613775.1
QJD53894.1	004407	Cluster4103_1clades	127	SEA_KELA_334	Streptomyces phage Kela	GCA_012934305.1
QBZ72219.1	004407	Cluster4103_1clades	126	SEA_KRADAL_333	Streptomyces phage Kradal	GCA_004799925.1
AXH66482.1	004407	Cluster4103_1clades	126	SEA_SATIS_333	Streptomyces phage Satis	GCA_003366315.1
QAX96658.1	004408	SIG+FAM76	127	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96976.1	004408	SIG+FAM76	127	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96022.1	004408	SIG+FAM76	127	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96340.1	004408	SIG+FAM76	127	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45106.1	004409	Cluster4105_1clades	126	KTN4_348	Pseudomonas phage KTN4	GCA_002607225.1
ATN94608.1	004409	Cluster4105_1clades	126	SL2_031	Pseudomonas phage SL2	GCA_002956015.1
QJB22982.1	004409	Cluster4105_1clades	126	fnug_339	Pseudomonas phage fnug	GCA_012837215.1
AAL83189.1	004409	Cluster4105_1clades	126	PHIKZ288	Pseudomonas virus phiKZ	GCA_000842965.1
QAX98425.1	004410	Cluster4106_1clades	126	ASfcp2_81	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52880.1	004410	Cluster4106_1clades	126	PX29p161	Aeromonas phage PX29	GCA_000920195.1
ADM80142.1	004410	Cluster4106_1clades	126	phiAS5_ORF0299	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17830.1	004410	Cluster4106_1clades	125	Aeh1ORF164c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47955.1	004411	Cluster4107_1clades	126	SmphiM12_323	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47956.2	004411	Cluster4107_1clades	88	SmphiM12_324	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13149.1	004411	Cluster4107_1clades	88	PHIM19_244	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12788.1	004411	Cluster4107_1clades	88	PHIM7_243	Sinorhizobium phage phiM7	GCA_002622405.1
AGX01898.1	004412	Cluster4108_1clades	121	-	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65410.1	004412	Cluster4108_1clades	126	2050HW_00075	Serratia phage 2050HW	GCA_002628125.1
QDB71189.1	004412	Cluster4108_1clades	106	CPT_Moabite_159	Serratia phage Moabite	GCA_006384735.1
QFP93231.1	004412	Cluster4108_1clades	119	-	Serratia phage PCH45	GCA_009187865.1
AYD80106.1	004413	Cluster4109_1clades	125	JA11_301	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66707.1	004413	Cluster4109_1clades	125	JA13_304	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67025.1	004413	Cluster4109_1clades	126	JA29_299	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67676.1	004413	Cluster4109_1clades	125	JA33_302	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81409.1	004414	Cluster4110_1clades	126	SEA_JUSTBECAUSE_254	Streptomyces phage JustBecause	GCA_003613775.1
QJD53816.1	004414	Cluster4110_1clades	126	SEA_KELA_256	Streptomyces phage Kela	GCA_012934305.1
QBZ72143.1	004414	Cluster4110_1clades	121	SEA_KRADAL_257	Streptomyces phage Kradal	GCA_004799925.1
AXH66405.1	004414	Cluster4110_1clades	121	SEA_SATIS_256	Streptomyces phage Satis	GCA_003366315.1
QDH83725.1	004415	TM+TM+TM	126	H1O15_gp116	Achromobacter phage Motura	GCA_006964305.1
QBX06697.1	004415	TM+TM+TM	119	BcepSaruman_284	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74665.1	004415	TM+TM+TM	119	BcepSauron_285	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41627.1	004415	TM+TM+TM	126	RSL1_ORF179	Ralstonia phage phiRSL1	GCA_000879455.1
QAX96709.1	004416	Cluster4112_1clades	126	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97027.1	004416	Cluster4112_1clades	126	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96073.1	004416	Cluster4112_1clades	126	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96391.1	004416	Cluster4112_1clades	126	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45063.1	004417	Cluster4113_1clades	125	KTN4_305	Pseudomonas phage KTN4	GCA_002607225.1
ATN94652.1	004417	Cluster4113_1clades	125	SL2_075	Pseudomonas phage SL2	GCA_002956015.1
QJB22938.1	004417	Cluster4113_1clades	125	fnug_295	Pseudomonas phage fnug	GCA_012837215.1
AAL83153.1	004417	Cluster4113_1clades	125	PHIKZ252	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45085.1	004418	Cluster4114_1clades	125	KTN4_327	Pseudomonas phage KTN4	GCA_002607225.1
ATN94630.1	004418	Cluster4114_1clades	125	SL2_053	Pseudomonas phage SL2	GCA_002956015.1
QJB22961.1	004418	Cluster4114_1clades	125	fnug_318	Pseudomonas phage fnug	GCA_012837215.1
AAL83171.1	004418	Cluster4114_1clades	125	PHIKZ270	Pseudomonas virus phiKZ	GCA_000842965.1
AFC21829.1	004419	Cluster4115_1clades	119	GAP32_377	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43950.1	004419	Cluster4115_1clades	125	CBB_387	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88909.1	004419	Cluster4115_1clades	122	BF_0384	Serratia phage BF	GCA_002619745.1
SOK58663.1	004419	Cluster4115_1clades	119	g386	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD81434.1	004420	Cluster4116_1clades	125	SEA_JUSTBECAUSE_279	Streptomyces phage JustBecause	GCA_003613775.1
QJD53840.1	004420	Cluster4116_1clades	125	SEA_KELA_280	Streptomyces phage Kela	GCA_012934305.1
QBZ72169.1	004420	Cluster4116_1clades	125	SEA_KRADAL_283	Streptomyces phage Kradal	GCA_004799925.1
AXH66432.1	004420	Cluster4116_1clades	125	SEA_SATIS_283	Streptomyces phage Satis	GCA_003366315.1
ANM44994.1	004421	Cluster4117_1clades	124	KTN4_236	Pseudomonas phage KTN4	GCA_002607225.1
ATN94720.1	004421	Cluster4117_1clades	124	SL2_143	Pseudomonas phage SL2	GCA_002956015.1
QJB22872.1	004421	Cluster4117_1clades	124	fnug_229	Pseudomonas phage fnug	GCA_012837215.1
AAL83096.1	004421	Cluster4117_1clades	124	PHIKZ195	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45066.1	004422	Cluster4118_1clades	124	KTN4_308	Pseudomonas phage KTN4	GCA_002607225.1
ATN94649.1	004422	Cluster4118_1clades	124	SL2_072	Pseudomonas phage SL2	GCA_002956015.1
QJB22941.1	004422	Cluster4118_1clades	124	fnug_298	Pseudomonas phage fnug	GCA_012837215.1
AAL83155.1	004422	Cluster4118_1clades	124	PHIKZ254	Pseudomonas virus phiKZ	GCA_000842965.1
QBX32172.1	004423	Cluster4119_1clades	90	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76667.1	004423	Cluster4119_1clades	124	PHABIO_36	Pseudomonas phage Phabio	GCA_002624965.1
AEH03447.1	004423	Cluster4119_1clades	107	021	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41752.1	004423	Cluster4119_1clades	101	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AYD81288.1	004424	SIG+RapA-C	124	SEA_JUSTBECAUSE_119	Streptomyces phage JustBecause	GCA_003613775.1
QJD53691.1	004424	SIG+RapA-C	124	SEA_KELA_120	Streptomyces phage Kela	GCA_012934305.1
QBZ72019.1	004424	SIG+RapA-C	124	SEA_KRADAL_121	Streptomyces phage Kradal	GCA_004799925.1
AXH66282.1	004424	SIG+RapA-C	124	SEA_SATIS_121	Streptomyces phage Satis	GCA_003366315.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AYD81345.1	004425	Cluster4121_1clades	122	SEA_JUSTBECAUSE_180	Streptomyces phage JustBecause	GCA_003613775.1
QJD53748.1	004425	Cluster4121_1clades	122	SEA_KELA_178	Streptomyces phage Kela	GCA_012934305.1
QBZ72074.1	004425	Cluster4121_1clades	124	SEA_KRADAL_178	Streptomyces phage Kradal	GCA_004799925.1
AXH66337.1	004425	Cluster4121_1clades	124	SEA_SATIS_178	Streptomyces phage Satis	GCA_003366315.1
QDJ96326.1	004426	Cluster4122_1clades	60	Xoosp13_139	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96327.1	004426	Cluster4122_1clades	66	Xoosp13_140	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96328.1	004426	Cluster4122_1clades	124	Xoosp13_141	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96329.1	004426	Cluster4122_1clades	87	Xoosp13_142	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AYD81187.1	004427	Cluster4123_1clades	123	SEA_JUSTBECAUSE_18	Streptomyces phage JustBecause	GCA_003613775.1
QJD53589.1	004427	Cluster4123_1clades	123	SEA_KELA_18	Streptomyces phage Kela	GCA_012934305.1
QBZ71920.1	004427	Cluster4123_1clades	120	SEA_KRADAL_21	Streptomyces phage Kradal	GCA_004799925.1
AXH66182.1	004427	Cluster4123_1clades	120	SEA_SATIS_21	Streptomyces phage Satis	GCA_003366315.1
AIT14257.1	004428	Cluster4124_1clades	122	PBL_121Q_367	Escherichia phage 121Q	GCA_000926855.1
QBO62047.1	004428	Cluster4124_1clades	123	G17_00558	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14068.1	004428	Cluster4124_1clades	123	vBEcoMphAPEC6_gp445c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80246.1	004428	Cluster4124_1clades	122	PSLUR01_00269	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUE22823.1	004429	Cluster4125_1clades	117	Ah1_00305	Aeromonas phage Ah1	GCA_002957415.1
QAX98538.1	004429	Cluster4125_1clades	122	ASfcp2_202	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53001.1	004429	Cluster4125_1clades	122	PX29p282	Aeromonas phage PX29	GCA_000920195.1
AAQ17953.1	004429	Cluster4125_1clades	116	Aeh1ORF284c	Aeromonas virus Aeh1	GCA_000843245.1
APU01565.1	004430	Cluster4126_1clades	122	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01370.1	004430	Cluster4126_1clades	119	ASwh1_310	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01447.1	004430	Cluster4126_1clades	114	ASwh1_388	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53188.1	004430	Cluster4126_1clades	122	65p180	Aeromonas virus 65	GCA_000893255.1
AGR47810.1	004431	Cluster4127_1clades	122	SmphiM12_178	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13025.1	004431	Cluster4127_1clades	122	PHIM19_119	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12664.1	004431	Cluster4127_1clades	122	PHIM7_118	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13396.1	004431	Cluster4127_1clades	122	PHIN3_132	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81181.1	004432	Cluster4128_1clades	122	SEA_JUSTBECAUSE_12	Streptomyces phage JustBecause	GCA_003613775.1
QJD53583.1	004432	Cluster4128_1clades	122	SEA_KELA_12	Streptomyces phage Kela	GCA_012934305.1
QBZ71912.1	004432	Cluster4128_1clades	107	SEA_KRADAL_13	Streptomyces phage Kradal	GCA_004799925.1
AXH66174.1	004432	Cluster4128_1clades	107	SEA_SATIS_13	Streptomyces phage Satis	GCA_003366315.1
AYD81451.1	004433	Cluster4129_1clades	122	SEA_JUSTBECAUSE_296	Streptomyces phage JustBecause	GCA_003613775.1
QJD53856.1	004433	Cluster4129_1clades	122	SEA_KELA_296	Streptomyces phage Kela	GCA_012934305.1
QBZ72186.1	004433	Cluster4129_1clades	112	SEA_KRADAL_300	Streptomyces phage Kradal	GCA_004799925.1
AXH66449.1	004433	Cluster4129_1clades	112	SEA_SATIS_300	Streptomyces phage Satis	GCA_003366315.1
ANM44830.1	004434	Cluster4130_1clades	121	KTN4_072	Pseudomonas phage KTN4	GCA_002607225.1
ATN94882.1	004434	Cluster4130_1clades	121	SL2_305	Pseudomonas phage SL2	GCA_002956015.1
QJB22708.1	004434	Cluster4130_1clades	121	fnug_65	Pseudomonas phage fnug	GCA_012837215.1
AAL82954.1	004434	Cluster4130_1clades	121	PHIKZ053	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45086.1	004435	Cluster4131_1clades	121	KTN4_328	Pseudomonas phage KTN4	GCA_002607225.1
ATN94629.1	004435	Cluster4131_1clades	121	SL2_052	Pseudomonas phage SL2	GCA_002956015.1
QJB22962.1	004435	Cluster4131_1clades	121	fnug_319	Pseudomonas phage fnug	GCA_012837215.1
AAL83172.1	004435	Cluster4131_1clades	121	PHIKZ271	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ68412.1	004436	Cluster4132_1clades	121	CcrBL10_gp208c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88158.1	004436	Cluster4132_1clades	111	CcrColossus_gp288	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68833.1	004436	Cluster4132_1clades	111	CcrPW_gp294	Caulobacter phage CcrPW	GCA_003443275.1
AFU86699.1	004436	Cluster4132_1clades	121	CcrRogue_gp217	Caulobacter virus Rogue	GCA_000900555.1
AGR48051.1	004437	Cluster4133_1clades	121	SmphiM12_419	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13232.1	004437	Cluster4133_1clades	121	PHIM19_327	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12872.1	004437	Cluster4133_1clades	121	PHIM7_327	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13595.1	004437	Cluster4133_1clades	121	PHIN3_332	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79826.1	004438	Cluster4134_1clades	121	JA11_021	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66425.1	004438	Cluster4134_1clades	121	JA13_022	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66747.1	004438	Cluster4134_1clades	108	JA29_021	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67395.1	004438	Cluster4134_1clades	121	JA33_021	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79849.1	004439	DUF2829	121	JA11_044	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66449.1	004439	DUF2829	121	JA13_046	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66773.1	004439	DUF2829	121	JA29_047	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67418.1	004439	DUF2829	121	JA33_044	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79869.1	004440	Cluster4136_1clades	121	JA11_064	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66468.1	004440	Cluster4136_1clades	121	JA13_065	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66793.1	004440	Cluster4136_1clades	121	JA29_067	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67438.1	004440	Cluster4136_1clades	121	JA33_064	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80107.1	004441	TM	121	JA11_302	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66708.1	004441	TM	121	JA13_305	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67026.1	004441	TM	121	JA29_300	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67677.1	004441	TM	121	JA33_303	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ANM44992.1	004442	Cluster4138_1clades	120	KTN4_234	Pseudomonas phage KTN4	GCA_002607225.1
ATN94722.1	004442	Cluster4138_1clades	120	SL2_145	Pseudomonas phage SL2	GCA_002956015.1
QJB22870.1	004442	Cluster4138_1clades	120	fnug_227	Pseudomonas phage fnug	GCA_012837215.1
AAL83094.1	004442	Cluster4138_1clades	120	PHIKZ193	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44801.1	004443	Cluster4139_1clades	118	KTN4_043	Pseudomonas phage KTN4	GCA_002607225.1
ATN94910.1	004443	Cluster4139_1clades	118	SL2_333	Pseudomonas phage SL2	GCA_002956015.1
QJB22680.1	004443	Cluster4139_1clades	118	fnug_37	Pseudomonas phage fnug	GCA_012837215.1
AGC26308.1	004443	Cluster4139_1clades	120	PHIKZ031.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47891.1	004444	Cluster4140_1clades	120	SmphiM12_259	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13092.1	004444	Cluster4140_1clades	120	PHIM19_187	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12732.1	004444	Cluster4140_1clades	120	PHIM7_187	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13462.1	004444	Cluster4140_1clades	120	PHIN3_199	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47927.1	004445	Cluster4141_1clades	120	SmphiM12_295	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13128.1	004445	Cluster4141_1clades	120	PHIM19_223	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12767.1	004445	Cluster4141_1clades	120	PHIM7_222	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13497.1	004445	Cluster4141_1clades	120	PHIN3_234	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14121.1	004446	SIG+TM+TM	120	PBL_121Q_231	Escherichia phage 121Q	GCA_000926855.1
QAY00804.1	004446	SIG+TM+TM	120	Ecwhy1_531	Escherichia phage Ecwhy_1	GCA_004146585.1
QBO61580.1	004446	SIG+TM+TM	120	G17_00084	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80111.1	004446	SIG+TM+TM	120	PSLUR01_00134	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGR47683.1	004447	Cluster4143_1clades	119	SmphiM12_051	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12945.1	004447	Cluster4143_1clades	119	PHIM19_38	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12585.1	004447	Cluster4143_1clades	119	PHIM7_37	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13318.1	004447	Cluster4143_1clades	120	PHIN3_53	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67313.1	004448	SIG+TM	118	AD1_269	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08538.1	004448	SIG+TM	120	Alexandra_281	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58916.1	004448	SIG+TM	110	Y3_276	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28736.1	004448	SIG+TM	91	YOLOSWAG_263	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81336.1	004449	Cluster4145_1clades	110	SEA_JUSTBECAUSE_171	Streptomyces phage JustBecause	GCA_003613775.1
QJD53739.1	004449	Cluster4145_1clades	110	SEA_KELA_169	Streptomyces phage Kela	GCA_012934305.1
QBZ72066.1	004449	Cluster4145_1clades	120	SEA_KRADAL_170	Streptomyces phage Kradal	GCA_004799925.1
AXH66329.1	004449	Cluster4145_1clades	120	SEA_SATIS_170	Streptomyces phage Satis	GCA_003366315.1
AYD81481.1	004450	Cluster4146_1clades	102	SEA_JUSTBECAUSE_326	Streptomyces phage JustBecause	GCA_003613775.1
QJD53884.1	004450	Cluster4146_1clades	102	SEA_KELA_324	Streptomyces phage Kela	GCA_012934305.1
QBZ72212.1	004450	Cluster4146_1clades	120	SEA_KRADAL_326	Streptomyces phage Kradal	GCA_004799925.1
AXH66475.1	004450	Cluster4146_1clades	120	SEA_SATIS_326	Streptomyces phage Satis	GCA_003366315.1
QAX96703.1	004451	Cluster4147_1clades	120	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97021.1	004451	Cluster4147_1clades	120	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96067.1	004451	Cluster4147_1clades	120	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96385.1	004451	Cluster4147_1clades	120	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96754.1	004452	SIG+TM	120	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97073.1	004452	SIG+TM	120	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96119.1	004452	SIG+TM	120	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96437.1	004452	SIG+TM	120	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96856.1	004453	Cluster4149_1clades	120	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97161.1	004453	Cluster4149_1clades	120	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96220.1	004453	Cluster4149_1clades	120	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96538.1	004453	Cluster4149_1clades	120	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96858.1	004454	Cluster4150_1clades	120	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97163.1	004454	Cluster4150_1clades	120	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96222.1	004454	Cluster4150_1clades	120	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96540.1	004454	Cluster4150_1clades	120	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63506.1	004455	Cluster4151_1clades	120	DAC19_15	Bacteroides phage DAC19	GCA_013387715.1
QIG63768.1	004455	Cluster4151_1clades	120	DAC20_15	Bacteroides phage DAC20	GCA_013387725.1
QIG64029.1	004455	Cluster4151_1clades	97	DAC22_15	Bacteroides phage DAC22	GCA_013387735.1
QIG64290.1	004455	Cluster4151_1clades	120	DAC23_12	Bacteroides phage DAC23	GCA_013387745.1
ANM45090.1	004456	Cluster4152_1clades	119	KTN4_332	Pseudomonas phage KTN4	GCA_002607225.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATN94625.1	004456	Cluster4152_1clades	119	SL2_048	Pseudomonas phage SL2	GCA_002956015.1
QJB22966.1	004456	Cluster4152_1clades	119	fnug_323	Pseudomonas phage fnug	GCA_012837215.1
AAL83176.1	004456	Cluster4152_1clades	119	PHIKZ275	Pseudomonas virus phiKZ	GCA_000842965.1
ABY62910.1	004457	Cluster4153_1clades	119	201phi2-1p077	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBX32195.1	004457	Cluster4153_1clades	114	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76692.1	004457	Cluster4153_1clades	97	PHABIO_61	Pseudomonas phage Phabio	GCA_002624965.1
QEM41772.1	004457	Cluster4153_1clades	114	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGR47989.1	004458	Cluster4154_1clades	119	SmphiM12_357	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13176.1	004458	Cluster4154_1clades	119	PHIM19_271	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12816.1	004458	Cluster4154_1clades	119	PHIM7_271	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13539.1	004458	Cluster4154_1clades	119	PHIN3_276	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48061.1	004459	Cluster4155_1clades	119	SmphiM12_429	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13240.1	004459	Cluster4155_1clades	119	PHIM19_335	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12880.1	004459	Cluster4155_1clades	119	PHIM7_335	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13603.1	004459	Cluster4155_1clades	119	PHIN3_340	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01254.1	004460	HEPN-RES-NTD1	116	AR9_g170	Bacillus phage AR9	GCA_001743835.1
AMS01255.1	004460	HEPN-RES-NTD1	119	AR9_g171	Bacillus phage AR9	GCA_001743835.1
AST99880.1	004460	HEPN-RES-NTD1	116	PBI_PBS1_58	Bacillus virus PBS1	GCA_002601325.1
AST99881.1	004460	HEPN-RES-NTD1	119	PBI_PBS1_59	Bacillus virus PBS1	GCA_002601325.1
AFO71241.1	004461	Cluster4157_1clades	117	CR5_021	Cronobacter phage CR5	GCA_000910235.1
QBP07448.1	004461	Cluster4157_1clades	119	DERBICUS_22	Erwinia phage Derbicus	GCA_004521655.1
ANZ48872.1	004461	Cluster4157_1clades	119	EARLPHILLIPIV_22	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50212.1	004461	Cluster4157_1clades	117	PHOBOS_22	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AUE22660.1	004462	Cluster4158_1clades	119	Ah1_00119	Aeromonas phage Ah1	GCA_002957415.1
QAX98386.1	004462	Cluster4158_1clades	115	ASfcp2_41	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52840.1	004462	Cluster4158_1clades	115	PX29p121	Aeromonas phage PX29	GCA_000920195.1
AAQ17787.1	004462	Cluster4158_1clades	115	Aeh1ORF124c	Aeromonas virus Aeh1	GCA_000843245.1
AYD79845.1	004463	Cluster4159_1clades	119	JA11_040	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66445.1	004463	Cluster4159_1clades	118	JA13_042	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66769.1	004463	Cluster4159_1clades	119	JA29_043	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67414.1	004463	Cluster4159_1clades	119	JA33_040	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81201.1	004464	Cluster4160_1clades	113	SEA_JUSTBECAUSE_32	Streptomyces phage JustBecause	GCA_003613775.1
QJD53603.1	004464	Cluster4160_1clades	113	SEA_KELA_32	Streptomyces phage Kela	GCA_012934305.1
QBZ71939.1	004464	Cluster4160_1clades	119	SEA_KRADAL_40	Streptomyces phage Kradal	GCA_004799925.1
AXH66201.1	004464	Cluster4160_1clades	119	SEA_SATIS_40	Streptomyces phage Satis	GCA_003366315.1
AYD81452.1	004465	Cluster4161_1clades	114	SEA_JUSTBECAUSE_297	Streptomyces phage JustBecause	GCA_003613775.1
QJD53857.1	004465	Cluster4161_1clades	114	SEA_KELA_297	Streptomyces phage Kela	GCA_012934305.1
QBZ72188.1	004465	Cluster4161_1clades	119	SEA_KRADAL_302	Streptomyces phage Kradal	GCA_004799925.1
AXH66451.1	004465	Cluster4161_1clades	119	SEA_SATIS_302	Streptomyces phage Satis	GCA_003366315.1
QAX96635.1	004466	Cluster4162_1clades	119	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96953.1	004466	Cluster4162_1clades	119	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX95999.1	004466	Cluster4162_1clades	119	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96317.1	004466	Cluster4162_1clades	119	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96702.1	004467	Cluster4163_1clades	119	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97020.1	004467	Cluster4163_1clades	119	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96066.1	004467	Cluster4163_1clades	119	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96384.1	004467	Cluster4163_1clades	119	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96848.1	004468	Cluster4164_1clades	119	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97153.1	004468	Cluster4164_1clades	119	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96212.1	004468	Cluster4164_1clades	119	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96530.1	004468	Cluster4164_1clades	119	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81250.1	004469	HTH	92	SEA_JUSTBECAUSE_81	Streptomyces phage JustBecause	GCA_003613775.1
QJD53653.1	004469	HTH	119	SEA_KELA_82	Streptomyces phage Kela	GCA_012934305.1
QBZ71982.1	004469	HTH	92	SEA_KRADAL_84	Streptomyces phage Kradal	GCA_004799925.1
AXH66245.1	004469	HTH	92	SEA_SATIS_84	Streptomyces phage Satis	GCA_003366315.1
AOO14303.1	004470	TM	68	Sn110110_109	Cyanophage S-RIM14	GCA_002599065.1
AOO14952.1	004470	TM	68	W1230910_106	Cyanophage S-RIM14	GCA_002599125.1
ASR76287.1	004470	TM	65	PBI_BELLAMY_251	Synechococcus phage Bellamy	GCA_002627525.1
QJT70229.1	004470	TM	119	SynMITS9220M01_223	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ANM44895.1	004471	Cluster4167_1clades	118	KTN4_137	Pseudomonas phage KTN4	GCA_002607225.1
ATN94818.1	004471	Cluster4167_1clades	118	SL2_241	Pseudomonas phage SL2	GCA_002956015.1
QJB22773.1	004471	Cluster4167_1clades	118	fnug_130	Pseudomonas phage fnug	GCA_012837215.1
AAL83009.1	004471	Cluster4167_1clades	118	PHIKZ108	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44993.1	004472	Cluster4168_1clades	118	KTN4_235	Pseudomonas phage KTN4	GCA_002607225.1
ATN94721.1	004472	Cluster4168_1clades	118	SL2_144	Pseudomonas phage SL2	GCA_002956015.1
QJB22871.1	004472	Cluster4168_1clades	118	fnug_228	Pseudomonas phage fnug	GCA_012837215.1
AAL83095.1	004472	Cluster4168_1clades	118	PHIKZ194	Pseudomonas virus phiKZ	GCA_000842965.1
ATI17280.1	004473	Cluster4169_1clades	116	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97721.1	004473	Cluster4169_1clades	116	ASswx1_75	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01448.1	004473	Cluster4169_1clades	109	ASwh1_389	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39183.1	004473	Cluster4169_1clades	118	CC2_037	Aeromonas phage CC2	GCA_000903495.1
AXQ68453.1	004474	SIG+Replic_Relax	67	CcrBL10_gp249	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87784.1	004474	SIG+Replic_Relax	118	CcrKarma_gp267	Caulobacter virus Karma	GCA_000901575.1
AFU87431.1	004474	SIG+Replic_Relax	118	CcrMagneto_gp261	Caulobacter virus Magneto	GCA_000903095.1
AFU86740.1	004474	SIG+Replic_Relax	118	CcrRogue_gp258	Caulobacter virus Rogue	GCA_000900555.1
QAX96704.1	004475	Cluster4171_1clades	118	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97022.1	004475	Cluster4171_1clades	118	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96068.1	004475	Cluster4171_1clades	118	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96386.1	004475	Cluster4171_1clades	118	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96711.1	004476	Cluster4172_1clades	85	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97030.1	004476	Cluster4172_1clades	85	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96076.1	004476	Cluster4172_1clades	118	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96394.1	004476	Cluster4172_1clades	118	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AAQ64245.1	004477	Cluster4173_1clades	117	KVP40.0176	Vibrio phage KVP40	GCA_000843785.1
QIW90561.1	004477	Cluster4173_1clades	93	GCAPEGMB_00214	Vibrio phage V07	GCA_012361095.1
QIW91238.1	004477	Cluster4173_1clades	93	COHAPHLL_00402	Vibrio phage V09	GCA_012361135.1
QHJ74359.1	004477	Cluster4173_1clades	93	VH12019_00032	Vibrio phage VH1_2019	GCA_009931825.1
APU01618.1	004478	Cluster4174_1clades	111	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01421.1	004478	Cluster4174_1clades	111	ASwh1_362	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39314.1	004478	Cluster4174_1clades	117	CC2_013	Aeromonas phage CC2	GCA_000903495.1
ADQ53243.1	004478	Cluster4174_1clades	111	65p235	Aeromonas virus 65	GCA_000893255.1
ANM45099.1	004479	Cluster4175_1clades	117	KTN4_341	Pseudomonas phage KTN4	GCA_002607225.1
ATN94614.1	004479	Cluster4175_1clades	117	SL2_037	Pseudomonas phage SL2	GCA_002956015.1
QJB22975.1	004479	Cluster4175_1clades	117	fnug_332	Pseudomonas phage fnug	GCA_012837215.1
AGC26358.1	004479	Cluster4175_1clades	117	PHIKZ283.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47715.2	004480	Cluster4176_1clades	116	SmphiM12_083	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12970.1	004480	Cluster4176_1clades	117	PHIM19_63	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12610.2	004480	Cluster4176_1clades	117	PHIM7_62	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13342.1	004480	Cluster4176_1clades	117	PHIN3_78	Sinorhizobium phage phiN3	GCA_001501175.1
QAX96687.1	004481	Cluster4178_1clades	117	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97005.1	004481	Cluster4178_1clades	117	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96051.1	004481	Cluster4178_1clades	117	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96369.1	004481	Cluster4178_1clades	117	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96788.1	004482	Cluster4179_1clades	117	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97107.1	004482	Cluster4179_1clades	117	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96153.1	004482	Cluster4179_1clades	117	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96471.1	004482	Cluster4179_1clades	117	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX06554.1	004483	Cluster4180_1clades	117	BcepSaruman_141	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74521.1	004483	Cluster4180_1clades	117	BcepSauron_141	Burkholderia phage BcepSauron	GCA_005394215.1
AFU88269.1	004483	Cluster4180_1clades	114	CcrColossus_gp399	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68945.1	004483	Cluster4180_1clades	114	CcrPW_gp406	Caulobacter phage CcrPW	GCA_003443275.1
AGR48065.2	004484	Cluster4181_1clades	116	SmphiM12_433	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13242.1	004484	Cluster4181_1clades	116	PHIM19_337	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12882.1	004484	Cluster4181_1clades	116	PHIM7_337	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13605.1	004484	Cluster4181_1clades	116	PHIN3_342	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80050.1	004485	Cluster4182_1clades	116	JA11_245	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66649.1	004485	Cluster4182_1clades	116	JA13_246	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66973.1	004485	Cluster4182_1clades	116	JA29_247	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67620.1	004485	Cluster4182_1clades	116	JA33_246	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80103.1	004486	Cluster4183_1clades	116	JA11_298	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66704.1	004486	Cluster4183_1clades	116	JA13_301	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67023.1	004486	Cluster4183_1clades	116	JA29_297	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67673.1	004486	Cluster4183_1clades	116	JA33_299	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81211.1	004487	Cluster4184_1clades	115	SEA_JUSTBECAUSE_42	Streptomyces phage JustBecause	GCA_003613775.1
QJD53614.1	004487	Cluster4184_1clades	115	SEA_KELA_43	Streptomyces phage Kela	GCA_012934305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBZ71948.1	004487	Cluster4184_1clades	116	SEA_KRADAL_49	Streptomyces phage Kradal	GCA_004799925.1
AXH66210.1	004487	Cluster4184_1clades	116	SEA_SATIS_49	Streptomyces phage Satis	GCA_003366315.1
AXQ69050.1	004488	Cluster4185_1clades	116	CcrBL9_gp026	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69566.1	004488	Cluster4185_1clades	116	CcrBL9_gp542	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69610.1	004488	Cluster4185_1clades	116	CcrSC_gp028	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70110.1	004488	Cluster4185_1clades	116	CcrSC_gp528	Caulobacter phage CcrSC	GCA_003443315.1
AYD81197.1	004489	Cluster4186_1clades	116	SEA_JUSTBECAUSE_28	Streptomyces phage JustBecause	GCA_003613775.1
QJD53599.1	004489	Cluster4186_1clades	116	SEA_KELA_28	Streptomyces phage Kela	GCA_012934305.1
QBZ71935.1	004489	Cluster4186_1clades	115	SEA_KRADAL_36	Streptomyces phage Kradal	GCA_004799925.1
AXH66197.1	004489	Cluster4186_1clades	115	SEA_SATIS_36	Streptomyces phage Satis	GCA_003366315.1
AYD81466.1	004490	Cluster4187_1clades	116	SEA_JUSTBECAUSE_311	Streptomyces phage JustBecause	GCA_003613775.1
QJD53869.1	004490	Cluster4187_1clades	116	SEA_KELA_309	Streptomyces phage Kela	GCA_012934305.1
QBZ72199.1	004490	Cluster4187_1clades	115	SEA_KRADAL_313	Streptomyces phage Kradal	GCA_004799925.1
AXH66462.1	004490	Cluster4187_1clades	115	SEA_SATIS_313	Streptomyces phage Satis	GCA_003366315.1
QAX96935.1	004491	Cluster4188_1clades	116	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97240.1	004491	Cluster4188_1clades	116	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96299.1	004491	Cluster4188_1clades	116	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96617.1	004491	Cluster4188_1clades	116	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM45024.1	004492	Cluster4190_1clades	115	KTN4_266	Pseudomonas phage KTN4	GCA_002607225.1
ATN94690.1	004492	Cluster4190_1clades	115	SL2_113	Pseudomonas phage SL2	GCA_002956015.1
QJB22901.1	004492	Cluster4190_1clades	115	fnug_258	Pseudomonas phage fnug	GCA_012837215.1
AAL83122.1	004492	Cluster4190_1clades	115	PHIKZ221	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22775.1	004493	TM	102	Ah1_00257	Aeromonas phage Ah1	GCA_002957415.1
QAX98491.1	004493	TM	103	ASfcp2_153	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52953.1	004493	TM	115	PX29p234	Aeromonas phage PX29	GCA_000920195.1
AAQ17900.1	004493	TM	103	Aeh1ORF238c	Aeromonas virus Aeh1	GCA_000843245.1
AGH56976.1	004494	HISFOLD	115	CPXG_00173	Cyanophage P-RSM6	GCA_000906155.1
AJK27483.1	004494	HISFOLD	108	PTIM40_56	Cyanophage P-TIM40	GCA_001470935.1
AOO14248.1	004494	HISFOLD	100	Sn110110_054	Cyanophage S-RIM14	GCA_002599065.1
AOO14900.1	004494	HISFOLD	100	W1230910_054	Cyanophage S-RIM14	GCA_002599125.1
AGR48022.1	004495	SIG+TM	115	SmphiM12_390	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13207.1	004495	SIG+TM	115	PHIM19_302	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12848.1	004495	SIG+TM	115	PHIM7_302	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13569.1	004495	SIG+TM	115	PHIN3_306	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67084.1	004496	Cluster4194_1clades	115	AD1_040	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08318.1	004496	Cluster4194_1clades	114	Alexandra_38	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58682.1	004496	Cluster4194_1clades	104	Y3_042	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28521.1	004496	Cluster4194_1clades	106	YOLOSWAG_36	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ANM45014.1	004497	Cluster4195_1clades	114	KTN4_256	Pseudomonas phage KTN4	GCA_002607225.1
ATN94700.1	004497	Cluster4195_1clades	114	SL2_123	Pseudomonas phage SL2	GCA_002956015.1
QJB22891.1	004497	Cluster4195_1clades	114	fnug_248	Pseudomonas phage fnug	GCA_012837215.1
AAL83113.1	004497	Cluster4195_1clades	114	PHIKZ212	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71352.1	004498	Cluster4196_1clades	114	CR5_132	Cronobacter phage CR5	GCA_000910235.1
QBP07560.1	004498	Cluster4196_1clades	114	DERBICUS_134	Erwinia phage Derbicus	GCA_004521655.1
ANZ48983.1	004498	Cluster4196_1clades	114	EARLPHILLIPIV_134	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50325.1	004498	Cluster4196_1clades	114	PHOBOS_135	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD81443.1	004499	Cluster4197_1clades	114	SEA_JUSTBECAUSE_288	Streptomyces phage JustBecause	GCA_003613775.1
QJD53848.1	004499	Cluster4197_1clades	114	SEA_KELA_288	Streptomyces phage Kela	GCA_012934305.1
QBZ72179.1	004499	Cluster4197_1clades	114	SEA_KRADAL_293	Streptomyces phage Kradal	GCA_004799925.1
AXH66442.1	004499	Cluster4197_1clades	114	SEA_SATIS_293	Streptomyces phage Satis	GCA_003366315.1
AXQ69060.1	004500	TarH	114	CcrBL9_gp036	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69576.1	004500	TarH	114	CcrBL9_gp552	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69620.1	004500	TarH	114	CcrSC_gp038	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70120.1	004500	TarH	114	CcrSC_gp538	Caulobacter phage CcrSC	GCA_003443315.1
AYD81245.1	004501	CHTH	114	SEA_JUSTBECAUSE_76	Streptomyces phage JustBecause	GCA_003613775.1
QJD53648.1	004501	CHTH	114	SEA_KELA_77	Streptomyces phage Kela	GCA_012934305.1
QBZ71978.1	004501	CHTH	111	SEA_KRADAL_80	Streptomyces phage Kradal	GCA_004799925.1
AXH66241.1	004501	CHTH	111	SEA_SATIS_80	Streptomyces phage Satis	GCA_003366315.1
QGZ14564.1	004502	Cluster4200_1clades	114	HWC77_gp201	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04169.1	004502	Cluster4200_1clades	114	HWC03_gp014	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23188.1	004502	Cluster4200_1clades	114	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47541.1	004502	Cluster4200_1clades	114	HWC35_gp147	Vibrio phage USC-1	GCA_006864065.1
AFA44578.1	004503	Cluster4201_1clades	113	RaK2_00305	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18593.1	004503	Cluster4201_1clades	108	7t3_072	Salmonella phage 7t3	GCA_006083215.1
AZU98421.1	004503	Cluster4201_1clades	108	CPT_Munch_489	Salmonella phage Munch	GCA_004015485.1
QIG63092.1	004503	Cluster4201_1clades	108	SEPL_479	Salmonella phage SE_PL	GCA_011067555.1
AXG67268.1	004504	SIG+EAD5	111	AD1_224	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08496.1	004504	SIG+EAD5	110	Alexandra_233	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58868.1	004504	SIG+EAD5	113	Y3_228	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28700.1	004504	SIG+EAD5	103	YOLOSWAG_222	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81461.1	004505	Cluster4203_1clades	107	SEA_JUSTBECAUSE_306	Streptomyces phage JustBecause	GCA_003613775.1
QJD53864.1	004505	Cluster4203_1clades	107	SEA_KELA_304	Streptomyces phage Kela	GCA_012934305.1
QBZ72195.1	004505	Cluster4203_1clades	113	SEA_KRADAL_309	Streptomyces phage Kradal	GCA_004799925.1
AXH66458.1	004505	Cluster4203_1clades	113	SEA_SATIS_309	Streptomyces phage Satis	GCA_003366315.1
QAX96821.1	004506	Cluster4204_1clades	113	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97140.1	004506	Cluster4204_1clades	113	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96186.1	004506	Cluster4204_1clades	113	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96504.1	004506	Cluster4204_1clades	113	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBZ70689.1	004507	IAT_beta	104	pETSU_108	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70690.1	004507	IAT_beta	110	pETSU_109	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72006.1	004507	IAT_beta	113	N1M2_143	Klebsiella phage N1M2	GCA_010092605.1
AEV89617.1	004507	IAT_beta	112	OBP_180	Pseudomonas phage OBP	GCA_000896635.1
ANM44891.1	004508	Cluster4207_1clades	112	KTN4_133	Pseudomonas phage KTN4	GCA_002607225.1
ATN94822.1	004508	Cluster4207_1clades	112	SL2_245	Pseudomonas phage SL2	GCA_002956015.1
QJB22769.1	004508	Cluster4207_1clades	112	fnug_126	Pseudomonas phage fnug	GCA_012837215.1
AAL83007.1	004508	Cluster4207_1clades	112	PHIKZ106	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ68446.1	004509	Cluster4208_1clades	112	CcrBL10_gp242	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86732.1	004509	Cluster4208_1clades	112	CcrRogue_gp250	Caulobacter virus Rogue	GCA_000900555.1
BBA65153.1	004509	Cluster4208_1clades	87	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65612.1	004509	Cluster4208_1clades	87	-	Xanthomonas phage XacN1	GCA_003173815.1
AGR48019.1	004510	Cluster4209_1clades	112	SmphiM12_387	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13205.1	004510	Cluster4209_1clades	112	PHIM19_300	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12846.1	004510	Cluster4209_1clades	112	PHIM7_300	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13567.1	004510	Cluster4209_1clades	112	PHIN3_304	Sinorhizobium phage phiN3	GCA_001501175.1
ANZ49649.1	004511	Cluster4210_1clades	112	MACHINA_2	Erwinia phage Machina	GCA_002758035.1
ANZ48575.1	004511	Cluster4210_1clades	111	CHRISDB_2	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49093.1	004511	Cluster4210_1clades	112	HUXLEY_2	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49921.1	004511	Cluster4210_1clades	112	PARSHIK_2	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AFO71340.1	004512	INTEGRINBETA	111	CR5_120	Cronobacter phage CR5	GCA_000910235.1
QBP07548.1	004512	INTEGRINBETA	110	DERBICUS_122	Erwinia phage Derbicus	GCA_004521655.1
ANZ48971.1	004512	INTEGRINBETA	110	EARLPHILLIPIV_122	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50312.1	004512	INTEGRINBETA	112	PHOBOS_122	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANS06094.1	004513	Cluster4212_1clades	103	ABCD_0258	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97277.1	004513	Cluster4212_1clades	112	E_269	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70888.1	004513	Cluster4212_1clades	110	phiC120_c183	Escherichia phage phiC120	GCA_002621185.1
AAX78798.1	004513	Cluster4212_1clades	103	RB43ORF276w	Escherichia virus RB43	GCA_000863505.1
AXG67256.1	004514	Cluster4213_1clades	64	AD1_212	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08485.1	004514	Cluster4213_1clades	70	Alexandra_222	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58856.1	004514	Cluster4213_1clades	74	Y3_216	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28689.1	004514	Cluster4213_1clades	112	YOLOSWAG_211	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD79959.1	004515	Cluster4215_1clades	112	JA11_154	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66558.1	004515	Cluster4215_1clades	112	JA13_155	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66883.1	004515	Cluster4215_1clades	112	JA29_157	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67528.1	004515	Cluster4215_1clades	112	JA33_154	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81293.1	004516	Cluster4216_1clades	112	SEA_JUSTBECAUSE_124	Streptomyces phage JustBecause	GCA_003613775.1
QJD53696.1	004516	Cluster4216_1clades	110	SEA_KELA_125	Streptomyces phage Kela	GCA_012934305.1
QBZ72024.1	004516	Cluster4216_1clades	112	SEA_KRADAL_126	Streptomyces phage Kradal	GCA_004799925.1
AXH66287.1	004516	Cluster4216_1clades	112	SEA_SATIS_126	Streptomyces phage Satis	GCA_003366315.1
AYD81439.1	004517	Cluster4217_1clades	112	SEA_JUSTBECAUSE_284	Streptomyces phage JustBecause	GCA_003613775.1
QJD53844.1	004517	Cluster4217_1clades	112	SEA_KELA_284	Streptomyces phage Kela	GCA_012934305.1
QBZ72174.1	004517	Cluster4217_1clades	112	SEA_KRADAL_288	Streptomyces phage Kradal	GCA_004799925.1
AXH66437.1	004517	Cluster4217_1clades	112	SEA_SATIS_288	Streptomyces phage Satis	GCA_003366315.1
AYD81207.1	004518	Cluster4218_1clades	112	SEA_JUSTBECAUSE_38	Streptomyces phage JustBecause	GCA_003613775.1
QJD53610.1	004518	Cluster4218_1clades	112	SEA_KELA_39	Streptomyces phage Kela	GCA_012934305.1
QBZ71944.1	004518	Cluster4218_1clades	111	SEA_KRADAL_45	Streptomyces phage Kradal	GCA_004799925.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH66206.1	004518	Cluster4218_1clades	111	SEA_SATIS_45	Streptomyces phage Satis	GCA_003366315.1
QAX96822.1	004519	Cluster4219_1clades	112	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97141.1	004519	Cluster4219_1clades	112	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96187.1	004519	Cluster4219_1clades	112	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96505.1	004519	Cluster4219_1clades	112	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81329.1	004520	Cluster4220_1clades	89	SEA_JUSTBECAUSE_164	Streptomyces phage JustBecause	GCA_003613775.1
QJD53732.1	004520	Cluster4220_1clades	112	SEA_KELA_162	Streptomyces phage Kela	GCA_012934305.1
QBZ72058.1	004520	Cluster4220_1clades	89	SEA_KRADAL_162	Streptomyces phage Kradal	GCA_004799925.1
AXH66321.1	004520	Cluster4220_1clades	89	SEA_SATIS_162	Streptomyces phage Satis	GCA_003366315.1
ANM44840.1	004521	Cluster4221_1clades	111	KTN4_082	Pseudomonas phage KTN4	GCA_002607225.1
ATN94873.1	004521	Cluster4221_1clades	111	SL2_296	Pseudomonas phage SL2	GCA_002956015.1
QJB22718.1	004521	Cluster4221_1clades	111	fnug_75	Pseudomonas phage fnug	GCA_012837215.1
AAL82961.1	004521	Cluster4221_1clades	111	PHIKZ060	Pseudomonas virus phiKZ	GCA_000842965.1
AXG67090.1	004522	Cluster4222_1clades	111	AD1_046	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08324.1	004522	Cluster4222_1clades	111	Alexandra_44	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58688.1	004522	Cluster4222_1clades	111	Y3_048	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28526.1	004522	Cluster4222_1clades	111	YOLOSWAG_41	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD79839.1	004523	Cluster4223_1clades	111	JA11_034	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66438.1	004523	Cluster4223_1clades	111	JA13_035	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66762.1	004523	Cluster4223_1clades	111	JA29_036	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67408.1	004523	Cluster4223_1clades	111	JA33_034	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80014.1	004524	Cluster4224_1clades	111	JA11_209	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66612.1	004524	Cluster4224_1clades	111	JA13_209	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66937.1	004524	Cluster4224_1clades	111	JA29_211	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67584.1	004524	Cluster4224_1clades	111	JA33_210	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80041.1	004525	Cluster4225_1clades	111	JA11_236	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66640.1	004525	Cluster4225_1clades	111	JA13_237	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66964.1	004525	Cluster4225_1clades	111	JA29_238	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67611.1	004525	Cluster4225_1clades	111	JA33_237	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96670.1	004526	Cluster4226_1clades	111	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96988.1	004526	Cluster4226_1clades	111	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96034.1	004526	Cluster4226_1clades	111	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96352.1	004526	Cluster4226_1clades	111	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96728.1	004527	Cluster4227_1clades	111	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97047.1	004527	Cluster4227_1clades	111	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96093.1	004527	Cluster4227_1clades	111	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96411.1	004527	Cluster4227_1clades	111	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96819.1	004528	Cluster4228_1clades	111	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97138.1	004528	Cluster4228_1clades	111	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96184.1	004528	Cluster4228_1clades	111	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96502.1	004528	Cluster4228_1clades	111	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QGZ14427.1	004529	Cluster4229_1clades	110	HWC77_gp064	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04308.1	004529	Cluster4229_1clades	110	HWC03_gp153	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23270.1	004529	Cluster4229_1clades	111	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47458.1	004529	Cluster4229_1clades	111	HWC35_gp064	Vibrio phage USC-1	GCA_006864065.1
ANM44779.1	004530	Cluster4231_1clades	109	KTN4_021	Pseudomonas phage KTN4	GCA_002607225.1
ATN94927.1	004530	Cluster4231_1clades	109	SL2_350	Pseudomonas phage SL2	GCA_002956015.1
QJB22664.1	004530	Cluster4231_1clades	109	fnug_21	Pseudomonas phage fnug	GCA_012837215.1
AAL82919.1	004530	Cluster4231_1clades	109	PHIKZ018	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44986.1	004531	Cluster4232_1clades	109	KTN4_228	Pseudomonas phage KTN4	GCA_002607225.1
ATN94728.1	004531	Cluster4232_1clades	109	SL2_151	Pseudomonas phage SL2	GCA_002956015.1
QJB22864.1	004531	Cluster4232_1clades	109	fnug_221	Pseudomonas phage fnug	GCA_012837215.1
AAL83088.1	004531	Cluster4232_1clades	109	PHIKZ187	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45029.1	004532	Cluster4233_1clades	109	KTN4_271	Pseudomonas phage KTN4	GCA_002607225.1
ATN94685.1	004532	Cluster4233_1clades	109	SL2_108	Pseudomonas phage SL2	GCA_002956015.1
QJB22906.1	004532	Cluster4233_1clades	109	fnug_263	Pseudomonas phage fnug	GCA_012837215.1
AAL83127.1	004532	Cluster4233_1clades	109	PHIKZ226	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45051.1	004533	Cluster4234_1clades	109	KTN4_293	Pseudomonas phage KTN4	GCA_002607225.1
ATN94664.1	004533	Cluster4234_1clades	109	SL2_087	Pseudomonas phage SL2	GCA_002956015.1
QJB22926.1	004533	Cluster4234_1clades	109	fnug_283	Pseudomonas phage fnug	GCA_012837215.1
AAL83142.1	004533	Cluster4234_1clades	109	PHIKZ241	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71238.1	004534	Cluster4235_1clades	109	CR5_018	Cronobacter phage CR5	GCA_000910235.1
QBP07444.1	004534	Cluster4235_1clades	98	DERBICUS_18	Erwinia phage Derbicus	GCA_004521655.1
ANZ48868.1	004534	Cluster4235_1clades	98	EARLPHILLIPIV_18	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50208.1	004534	Cluster4235_1clades	97	PHOBOS_18	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGR47916.1	004535	Cluster4236_1clades	109	SmphiM12_284	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13118.1	004535	Cluster4236_1clades	109	PHIM19_213	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12758.1	004535	Cluster4236_1clades	109	PHIM7_213	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13488.1	004535	Cluster4236_1clades	109	PHIN3_225	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81278.1	004536	Cluster4237_1clades	109	SEA_JUSTBECAUSE_109	Streptomyces phage JustBecause	GCA_003613775.1
QJD53681.1	004536	Cluster4237_1clades	109	SEA_KELA_110	Streptomyces phage Kela	GCA_012934305.1
QBZ72008.1	004536	Cluster4237_1clades	109	SEA_KRADAL_110	Streptomyces phage Kradal	GCA_004799925.1
AXH66271.1	004536	Cluster4237_1clades	109	SEA_SATIS_110	Streptomyces phage Satis	GCA_003366315.1
AYD81258.1	004537	Cluster4238_1clades	109	SEA_JUSTBECAUSE_89	Streptomyces phage JustBecause	GCA_003613775.1
QJD53661.1	004537	Cluster4238_1clades	109	SEA_KELA_90	Streptomyces phage Kela	GCA_012934305.1
QBZ71990.1	004537	Cluster4238_1clades	108	SEA_KRADAL_92	Streptomyces phage Kradal	GCA_004799925.1
AXH66253.1	004537	Cluster4238_1clades	108	SEA_SATIS_92	Streptomyces phage Satis	GCA_003366315.1
AYD81441.1	004538	Cluster4239_1clades	109	SEA_JUSTBECAUSE_286	Streptomyces phage JustBecause	GCA_003613775.1
QJD53846.1	004538	Cluster4239_1clades	109	SEA_KELA_286	Streptomyces phage Kela	GCA_012934305.1
QBZ72176.1	004538	Cluster4239_1clades	105	SEA_KRADAL_290	Streptomyces phage Kradal	GCA_004799925.1
AXH66439.1	004538	Cluster4239_1clades	105	SEA_SATIS_290	Streptomyces phage Satis	GCA_003366315.1
QAX96662.1	004539	Cluster4240_1clades	109	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96980.1	004539	Cluster4240_1clades	109	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96026.1	004539	Cluster4240_1clades	109	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96344.1	004539	Cluster4240_1clades	109	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96876.1	004540	Cluster4241_1clades	109	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97181.1	004540	Cluster4241_1clades	109	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96240.1	004540	Cluster4241_1clades	109	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96558.1	004540	Cluster4241_1clades	109	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96914.1	004541	Cluster4242_1clades	109	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97219.1	004541	Cluster4242_1clades	109	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96278.1	004541	Cluster4242_1clades	109	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96596.1	004541	Cluster4242_1clades	109	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AAX44407.1	004542	Cluster4243_1clades	107	PSSM2_029	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12244.1	004542	Cluster4243_1clades	107	PRTG_00086	Prochlorococcus phage P-SSM5	GCA_002991095.1
QCW22907.1	004542	Cluster4243_1clades	109	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50552.1	004542	Cluster4243_1clades	109	-	Synechococcus phage S-B43	GCA_006869725.1
AGR47872.1	004543	Cluster4244_1clades	108	SmphiM12_240	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13074.1	004543	Cluster4244_1clades	108	PHIM19_169	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12714.1	004543	Cluster4244_1clades	108	PHIM7_169	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13444.1	004543	Cluster4244_1clades	108	PHIN3_181	Sinorhizobium phage phiN3	GCA_001501175.1
AXQ69049.1	004544	Cluster4245_1clades	107	CcrBL9_gp025	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69565.1	004544	Cluster4245_1clades	107	CcrBL9_gp541	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69609.1	004544	Cluster4245_1clades	108	CcrSC_gp027	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70109.1	004544	Cluster4245_1clades	108	CcrSC_gp527	Caulobacter phage CcrSC	GCA_003443315.1
AUE22790.1	004545	Cluster4246_1clades	107	Ah1_00272	Aeromonas phage Ah1	GCA_002957415.1
QAX98504.1	004545	Cluster4246_1clades	102	ASfcp2_168	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52967.1	004545	Cluster4246_1clades	102	PX29p248	Aeromonas phage PX29	GCA_000920195.1
AAQ17915.1	004545	Cluster4246_1clades	107	Aeh1ORF253c	Aeromonas virus Aeh1	GCA_000843245.1
ATI17252.1	004546	Cluster4247_1clades	107	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97693.1	004546	Cluster4247_1clades	107	ASswx1_47	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01458.1	004546	Cluster4247_1clades	107	ASwh1_399	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39201.1	004546	Cluster4247_1clades	107	CC2_065	Aeromonas phage CC2	GCA_000903495.1
AGR47732.1	004547	Cluster4248_1clades	107	SmphiM12_100	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12985.1	004547	Cluster4248_1clades	107	PHIM19_78	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12625.1	004547	Cluster4248_1clades	107	PHIM7_77	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13357.1	004547	Cluster4248_1clades	107	PHIN3_93	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47843.1	004548	Cluster4249_1clades	107	SmphiM12_211	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13049.1	004548	Cluster4249_1clades	107	PHIM19_144	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12690.1	004548	Cluster4249_1clades	107	PHIM7_144	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13421.1	004548	Cluster4249_1clades	105	PHIN3_158	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79863.1	004549	Cluster4250_1clades	107	JA11_058	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66462.1	004549	Cluster4250_1clades	107	JA13_059	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66785.1	004549	Cluster4250_1clades	107	JA29_059	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67432.1	004549	Cluster4250_1clades	107	JA33_058	Dickeya phage vB_DsoM_JA33	GCA_003568495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AYD79988.1	004550	SIG+TM+TM	107	JA11_183	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66586.1	004550	SIG+TM+TM	107	JA13_183	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66911.1	004550	SIG+TM+TM	107	JA29_185	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67557.1	004550	SIG+TM+TM	107	JA33_183	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80020.1	004551	HIN-HTH	105	JA11_215	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66619.1	004551	HIN-HTH	105	JA13_216	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66943.1	004551	HIN-HTH	107	JA29_217	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67590.1	004551	HIN-HTH	105	JA33_216	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96823.1	004552	Cluster4253_1clades	107	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97142.1	004552	Cluster4253_1clades	107	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96188.1	004552	Cluster4253_1clades	107	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96506.1	004552	Cluster4253_1clades	107	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMM43744.1	004553	Cluster4254_1clades	106	CBB_179	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88700.1	004553	Cluster4254_1clades	106	BF_0175	Serratia phage BF	GCA_002619745.1
SOK58983.1	004553	Cluster4254_1clades	107	g175	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58449.1	004553	Cluster4254_1clades	107	g172	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFO71396.1	004554	Cluster4255_1clades	106	CR5_176	Cronobacter phage CR5	GCA_000910235.1
QBP07608.1	004554	Cluster4255_1clades	105	DERBICUS_182	Erwinia phage Derbicus	GCA_004521655.1
ANZ49032.1	004554	Cluster4255_1clades	105	EARLPHILLIPIV_183	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50380.1	004554	Cluster4255_1clades	105	PHOBOS_190	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AYD79862.1	004555	Cluster4256_1clades	105	JA11_057	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66461.1	004555	Cluster4256_1clades	105	JA13_058	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66784.1	004555	Cluster4256_1clades	106	JA29_058	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67431.1	004555	Cluster4256_1clades	105	JA33_057	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81310.1	004556	Cluster4257_1clades	106	SEA_JUSTBECAUSE_145	Streptomyces phage JustBecause	GCA_003613775.1
QJD53713.1	004556	Cluster4257_1clades	106	SEA_KELA_143	Streptomyces phage Kela	GCA_012934305.1
QBZ72040.1	004556	Cluster4257_1clades	104	SEA_KRADAL_144	Streptomyces phage Kradal	GCA_004799925.1
AXH66303.1	004556	Cluster4257_1clades	104	SEA_SATIS_144	Streptomyces phage Satis	GCA_003366315.1
AYD81442.1	004557	Cluster4258_1clades	106	SEA_JUSTBECAUSE_287	Streptomyces phage JustBecause	GCA_003613775.1
QJD53847.1	004557	Cluster4258_1clades	106	SEA_KELA_287	Streptomyces phage Kela	GCA_012934305.1
QBZ72177.1	004557	Cluster4258_1clades	105	SEA_KRADAL_291	Streptomyces phage Kradal	GCA_004799925.1
AXH66440.1	004557	Cluster4258_1clades	105	SEA_SATIS_291	Streptomyces phage Satis	GCA_003366315.1
QAX96726.1	004558	Cluster4259_1clades	106	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97045.1	004558	Cluster4259_1clades	106	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96091.1	004558	Cluster4259_1clades	106	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96409.1	004558	Cluster4259_1clades	106	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96863.1	004559	SIG+TM	106	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97168.1	004559	SIG+TM	106	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96227.1	004559	SIG+TM	106	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96545.1	004559	SIG+TM	106	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96864.1	004560	Cluster4261_1clades	106	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97169.1	004560	Cluster4261_1clades	106	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96228.1	004560	Cluster4261_1clades	106	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96546.1	004560	Cluster4261_1clades	106	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44893.1	004561	Cluster4262_1clades	105	KTN4_135	Pseudomonas phage KTN4	GCA_002607225.1
ATN94820.1	004561	Cluster4262_1clades	105	SL2_243	Pseudomonas phage SL2	GCA_002956015.1
QJB22771.1	004561	Cluster4262_1clades	105	fnug_128	Pseudomonas phage fnug	GCA_012837215.1
AAL83008.1	004561	Cluster4262_1clades	105	PHIKZ107	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44813.1	004562	Cluster4263_1clades	105	KTN4_055	Pseudomonas phage KTN4	GCA_002607225.1
ATN94898.1	004562	Cluster4263_1clades	105	SL2_321	Pseudomonas phage SL2	GCA_002956015.1
QJB22692.1	004562	Cluster4263_1clades	105	fnug_49	Pseudomonas phage fnug	GCA_012837215.1
AGC26310.1	004562	Cluster4263_1clades	105	PHIKZ041.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47861.1	004563	Cluster4264_1clades	105	SmphiM12_229	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13064.1	004563	Cluster4264_1clades	105	PHIM19_159	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12705.1	004563	Cluster4264_1clades	105	PHIM7_159	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13434.1	004563	Cluster4264_1clades	105	PHIN3_171	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47869.1	004564	Cluster4265_1clades	105	SmphiM12_237	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13070.1	004564	Cluster4265_1clades	105	PHIM19_165	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12711.1	004564	Cluster4265_1clades	105	PHIM7_165	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13441.1	004564	Cluster4265_1clades	105	PHIN3_178	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81195.1	004565	Cluster4266_1clades	67	SEA_JUSTBECAUSE_26	Streptomyces phage JustBecause	GCA_003613775.1
QJD53597.1	004565	Cluster4266_1clades	67	SEA_KELA_26	Streptomyces phage Kela	GCA_012934305.1
QBZ71931.1	004565	Cluster4266_1clades	105	SEA_KRADAL_32	Streptomyces phage Kradal	GCA_004799925.1
AXH66193.1	004565	Cluster4266_1clades	105	SEA_SATIS_32	Streptomyces phage Satis	GCA_003366315.1
AGR47910.2	004566	Cluster4268_1clades	104	SmphiM12_278	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13114.1	004566	Cluster4268_1clades	104	PHIM19_209	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12754.1	004566	Cluster4268_1clades	104	PHIM7_209	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13484.1	004566	Cluster4268_1clades	104	PHIN3_221	Sinorhizobium phage phiN3	GCA_001501175.1
AUZ95041.1	004567	SIG+SHR-BD	97	FDI40_gp265	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72738.1	004567	SIG+SHR-BD	101	-	Myoviridae sp.	GCA_003657725.1
QCG76211.1	004567	SIG+SHR-BD	97	EST35_0330	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44189.1	004567	SIG+SHR-BD	104	PBI_SCTP2_174	Salicola phage SCTP-2	GCA_002625545.1
ANM45028.1	004568	Cluster4270_1clades	63	KTN4_270	Pseudomonas phage KTN4	GCA_002607225.1
ATN94686.1	004568	Cluster4270_1clades	104	SL2_109	Pseudomonas phage SL2	GCA_002956015.1
QJB22905.1	004568	Cluster4270_1clades	99	fnug_262	Pseudomonas phage fnug	GCA_012837215.1
AAL83126.2	004568	Cluster4270_1clades	99	PHIKZ225	Pseudomonas virus phiKZ	GCA_000842965.1
AYD81271.1	004569	Cluster4271_1clades	104	SEA_JUSTBECAUSE_102	Streptomyces phage JustBecause	GCA_003613775.1
QJD53674.1	004569	Cluster4271_1clades	104	SEA_KELA_103	Streptomyces phage Kela	GCA_012934305.1
QBZ72002.1	004569	Cluster4271_1clades	104	SEA_KRADAL_104	Streptomyces phage Kradal	GCA_004799925.1
AXH66265.1	004569	Cluster4271_1clades	104	SEA_SATIS_104	Streptomyces phage Satis	GCA_003366315.1
AYD81380.1	004570	Cluster4272_1clades	99	SEA_JUSTBECAUSE_225	Streptomyces phage JustBecause	GCA_003613775.1
QJD53783.1	004570	Cluster4272_1clades	99	SEA_KELA_223	Streptomyces phage Kela	GCA_012934305.1
QBZ72108.1	004570	Cluster4272_1clades	104	SEA_KRADAL_222	Streptomyces phage Kradal	GCA_004799925.1
AXH66369.1	004570	Cluster4272_1clades	104	SEA_SATIS_220	Streptomyces phage Satis	GCA_003366315.1
AYD81422.1	004571	Cluster4273_1clades	103	SEA_JUSTBECAUSE_267	Streptomyces phage JustBecause	GCA_003613775.1
QJD53827.1	004571	Cluster4273_1clades	103	SEA_KELA_267	Streptomyces phage Kela	GCA_012934305.1
QBZ72154.1	004571	Cluster4273_1clades	104	SEA_KRADAL_268	Streptomyces phage Kradal	GCA_004799925.1
AXH66417.1	004571	Cluster4273_1clades	104	SEA_SATIS_268	Streptomyces phage Satis	GCA_003366315.1
AYD81173.1	004572	Cluster4274_1clades	104	SEA_JUSTBECAUSE_4	Streptomyces phage JustBecause	GCA_003613775.1
QJD53575.1	004572	Cluster4274_1clades	104	SEA_KELA_4	Streptomyces phage Kela	GCA_012934305.1
QBZ71903.1	004572	Cluster4274_1clades	99	SEA_KRADAL_4	Streptomyces phage Kradal	GCA_004799925.1
AXH66165.1	004572	Cluster4274_1clades	99	SEA_SATIS_4	Streptomyces phage Satis	GCA_003366315.1
AYD81172.1	004573	DUF4873	103	SEA_JUSTBECAUSE_3	Streptomyces phage JustBecause	GCA_003613775.1
QJD53574.1	004573	DUF4873	104	SEA_KELA_3	Streptomyces phage Kela	GCA_012934305.1
QBZ71902.1	004573	DUF4873	103	SEA_KRADAL_3	Streptomyces phage Kradal	GCA_004799925.1
AXH66164.1	004573	DUF4873	103	SEA_SATIS_3	Streptomyces phage Satis	GCA_003366315.1
APU01417.1	004574	Cluster4276_1clades	103	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01229.1	004574	Cluster4276_1clades	103	ASwh1_164	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39302.1	004574	Cluster4276_1clades	90	CC2_254	Aeromonas phage CC2	GCA_000903495.1
AAR90912.1	004574	Cluster4276_1clades	103	65p026	Aeromonas virus 65	GCA_000893255.1
AJK27638.1	004575	TM	92	PTIM40_234	Cyanophage P-TIM40	GCA_001470935.1
AOO14409.1	004575	TM	99	Sn110110_216	Cyanophage S-RIM14	GCA_002599065.1
AOO15058.1	004575	TM	99	W1230910_213	Cyanophage S-RIM14	GCA_002599125.1
AGG54379.1	004575	TM	103	CYWG_00095	Cyanophage S-SSM6b	GCA_002710425.1
AGR47946.1	004576	Cluster4278_1clades	103	SmphiM12_314	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13141.1	004576	Cluster4278_1clades	103	PHIM19_236	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12780.1	004576	Cluster4278_1clades	103	PHIM7_235	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13509.2	004576	Cluster4278_1clades	103	PHIN3_246	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79844.1	004577	Fib_alpha	103	JA11_039	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66444.1	004577	Fib_alpha	103	JA13_041	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66768.1	004577	Fib_alpha	103	JA29_042	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67413.1	004577	Fib_alpha	103	JA33_039	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81302.1	004578	Cluster4280_1clades	102	SEA_JUSTBECAUSE_133	Streptomyces phage JustBecause	GCA_003613775.1
QJD53705.1	004578	Cluster4280_1clades	102	SEA_KELA_134	Streptomyces phage Kela	GCA_012934305.1
QBZ72031.1	004578	Cluster4280_1clades	103	SEA_KRADAL_133	Streptomyces phage Kradal	GCA_004799925.1
AXH66294.1	004578	Cluster4280_1clades	103	SEA_SATIS_133	Streptomyces phage Satis	GCA_003366315.1
QAX96814.1	004579	Cluster4281_1clades	103	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97133.1	004579	Cluster4281_1clades	103	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96179.1	004579	Cluster4281_1clades	103	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96497.1	004579	Cluster4281_1clades	103	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AAQ64340.1	004580	Cluster4282_1clades	102	KVP40.0271	Vibrio phage KVP40	GCA_000843785.1
QIW91144.1	004580	Cluster4282_1clades	102	COHAPHLL_00308	Vibrio phage V09	GCA_012361135.1
AGN30316.1	004580	Cluster4282_1clades	93	VPFG_00318	Vibrio phage nt-1	GCA_000910195.2
AFN37500.1	004580	Cluster4282_1clades	102	pp2_267	Vibriophage phi-pp2	GCA_002630725.1
APU01627.1	004581	Cluster4283_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX97695.1	004581	Cluster4283_1clades	96	ASswx1_49	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39328.1	004581	Cluster4283_1clades	96	CC2_063	Aeromonas phage CC2	GCA_000903495.1
ADQ53252.1	004581	Cluster4283_1clades	102	65p244	Aeromonas virus 65	GCA_000893255.1
AGR47884.1	004582	Cluster4284_1clades	102	SmphiM12_252	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13085.1	004582	Cluster4284_1clades	102	PHIM19_180	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12725.1	004582	Cluster4284_1clades	102	PHIM7_180	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13454.1	004582	Cluster4284_1clades	102	PHIN3_191	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67165.1	004583	Cluster4285_1clades	96	AD1_121	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08398.1	004583	Cluster4285_1clades	96	Alexandra_126	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58762.1	004583	Cluster4285_1clades	94	Y3_122	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28817.1	004583	Cluster4285_1clades	102	YOLOSWAG_118	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81408.1	004584	Cluster4286_1clades	100	SEA_JUSTBECAUSE_253	Streptomyces phage JustBecause	GCA_003613775.1
QJD53812.1	004584	Cluster4286_1clades	100	SEA_KELA_252	Streptomyces phage Kela	GCA_012934305.1
QBZ72138.1	004584	Cluster4286_1clades	102	SEA_KRADAL_252	Streptomyces phage Kradal	GCA_004799925.1
AXH66400.1	004584	Cluster4286_1clades	102	SEA_SATIS_251	Streptomyces phage Satis	GCA_003366315.1
AYD81432.1	004585	Cluster4287_1clades	102	SEA_JUSTBECAUSE_277	Streptomyces phage JustBecause	GCA_003613775.1
QJD53838.1	004585	Cluster4287_1clades	102	SEA_KELA_278	Streptomyces phage Kela	GCA_012934305.1
QBZ72167.1	004585	Cluster4287_1clades	100	SEA_KRADAL_281	Streptomyces phage Kradal	GCA_004799925.1
AXH66430.1	004585	Cluster4287_1clades	100	SEA_SATIS_281	Streptomyces phage Satis	GCA_003366315.1
QAX96771.1	004586	Cluster4288_1clades	102	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97090.1	004586	Cluster4288_1clades	102	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96136.1	004586	Cluster4288_1clades	102	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96454.1	004586	Cluster4288_1clades	102	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44981.1	004587	Cluster4289_1clades	101	KTN4_223	Pseudomonas phage KTN4	GCA_002607225.1
ATN94733.1	004587	Cluster4289_1clades	101	SL2_156	Pseudomonas phage SL2	GCA_002956015.1
QJB22859.1	004587	Cluster4289_1clades	101	fnug_216	Pseudomonas phage fnug	GCA_012837215.1
AAL83084.1	004587	Cluster4289_1clades	101	PHIKZ183	Pseudomonas virus phiKZ	GCA_000842965.1
QAX98644.1	004588	Cluster4290_1clades	84	ASfcp2_311	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52784.1	004588	Cluster4290_1clades	101	PX29p065	Aeromonas phage PX29	GCA_000920195.1
ADM80039.1	004588	Cluster4290_1clades	85	phiAS5_ORF0196	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17727.1	004588	Cluster4290_1clades	84	Aeh1ORF067c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47973.2	004589	Cluster4291_1clades	101	SmphiM12_341	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13162.1	004589	Cluster4291_1clades	101	PHIM19_257	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12802.1	004589	Cluster4291_1clades	101	PHIM7_257	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13525.1	004589	Cluster4291_1clades	101	PHIN3_262	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81183.1	004590	Cluster4292_1clades	101	SEA_JUSTBECAUSE_14	Streptomyces phage JustBecause	GCA_003613775.1
QJD53585.1	004590	Cluster4292_1clades	101	SEA_KELA_14	Streptomyces phage Kela	GCA_012934305.1
QBZ71915.1	004590	Cluster4292_1clades	101	SEA_KRADAL_16	Streptomyces phage Kradal	GCA_004799925.1
AXH66177.1	004590	Cluster4292_1clades	101	SEA_SATIS_16	Streptomyces phage Satis	GCA_003366315.1
AYD81343.1	004591	RelE-ParE	101	SEA_JUSTBECAUSE_178	Streptomyces phage JustBecause	GCA_003613775.1
QJD53746.1	004591	RelE-ParE	101	SEA_KELA_176	Streptomyces phage Kela	GCA_012934305.1
QBZ72072.1	004591	RelE-ParE	101	SEA_KRADAL_176	Streptomyces phage Kradal	GCA_004799925.1
AXH66335.1	004591	RelE-ParE	101	SEA_SATIS_176	Streptomyces phage Satis	GCA_003366315.1
AXQ69409.1	004592	Cluster4294_1clades	101	CcrBL9_gp385	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88251.1	004592	Cluster4294_1clades	89	CcrColossus_gp381	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68926.1	004592	Cluster4294_1clades	89	CcrPW_gp387c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69965.1	004592	Cluster4294_1clades	101	CcrSC_gp383	Caulobacter phage CcrSC	GCA_003443315.1
AYD81427.1	004593	Cluster4295_1clades	101	SEA_JUSTBECAUSE_272	Streptomyces phage JustBecause	GCA_003613775.1
QJD53832.1	004593	Cluster4295_1clades	101	SEA_KELA_272	Streptomyces phage Kela	GCA_012934305.1
QBZ72158.1	004593	Cluster4295_1clades	97	SEA_KRADAL_272	Streptomyces phage Kradal	GCA_004799925.1
AXH66421.1	004593	Cluster4295_1clades	97	SEA_SATIS_272	Streptomyces phage Satis	GCA_003366315.1
QAX96744.1	004594	Cluster4296_1clades	101	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97063.1	004594	Cluster4296_1clades	101	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96109.1	004594	Cluster4296_1clades	101	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96427.1	004594	Cluster4296_1clades	101	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AYD81406.1	004595	Cluster4297_1clades	93	SEA_JUSTBECAUSE_251	Streptomyces phage JustBecause	GCA_003613775.1
QJD53810.1	004595	Cluster4297_1clades	93	SEA_KELA_250	Streptomyces phage Kela	GCA_012934305.1
QBZ72136.1	004595	Cluster4297_1clades	100	SEA_KRADAL_250	Streptomyces phage Kradal	GCA_004799925.1
AXH66398.1	004595	Cluster4297_1clades	100	SEA_SATIS_249	Streptomyces phage Satis	GCA_003366315.1
ANM45092.1	004596	Cluster4298_1clades	99	KTN4_334	Pseudomonas phage KTN4	GCA_002607225.1
ATN94623.1	004596	Cluster4298_1clades	99	SL2_046	Pseudomonas phage SL2	GCA_002956015.1
QJB22968.1	004596	Cluster4298_1clades	99	fnug_325	Pseudomonas phage fnug	GCA_012837215.1
AAL83178.1	004596	Cluster4298_1clades	99	PHIKZ277	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45021.1	004597	Cluster4299_1clades	99	KTN4_263	Pseudomonas phage KTN4	GCA_002607225.1
ATN94693.1	004597	Cluster4299_1clades	99	SL2_116	Pseudomonas phage SL2	GCA_002956015.1
QJB22898.1	004597	Cluster4299_1clades	99	fnug_255	Pseudomonas phage fnug	GCA_012837215.1
AGC26346.1	004597	Cluster4299_1clades	99	PHIKZ218.1	Pseudomonas virus phiKZ	GCA_000842965.1
AMS01187.1	004598	HU-IHF	98	AR9_g103	Bacillus phage AR9	GCA_001743835.1
ALN97860.1	004598	HU-IHF	99	Bp8pS_181	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00121.1	004598	HU-IHF	98	PBI_PBS1_299	Bacillus virus PBS1	GCA_002601325.1
BAE47872.1	004598	HU-IHF	86	CST174	Clostridium phage c-st	GCA_000865225.1
AYD81261.1	004599	Cluster4302_1clades	99	SEA_JUSTBECAUSE_92	Streptomyces phage JustBecause	GCA_003613775.1
QJD53664.1	004599	Cluster4302_1clades	99	SEA_KELA_93	Streptomyces phage Kela	GCA_012934305.1
QBZ71993.1	004599	Cluster4302_1clades	97	SEA_KRADAL_95	Streptomyces phage Kradal	GCA_004799925.1
AXH66256.1	004599	Cluster4302_1clades	97	SEA_SATIS_95	Streptomyces phage Satis	GCA_003366315.1
QAX96747.1	004600	XX333	99	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97066.1	004600	XX333	99	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96112.1	004600	XX333	99	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96430.1	004600	XX333	99	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96751.1	004601	Cluster4304_1clades	99	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97070.1	004601	Cluster4304_1clades	99	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96116.1	004601	Cluster4304_1clades	99	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96434.1	004601	Cluster4304_1clades	99	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96753.1	004602	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97072.1	004602	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96118.1	004602	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96436.1	004602	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96756.1	004603	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97075.1	004603	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96121.1	004603	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96439.1	004603	SIG+TM	99	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX32530.1	004604	Cluster4307_1clades	99	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94593.1	004604	Cluster4307_1clades	96	SL2_016	Pseudomonas phage SL2	GCA_002956015.1
QEM42103.1	004604	Cluster4307_1clades	99	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AAL83196.1	004604	Cluster4307_1clades	96	PHIKZ295	Pseudomonas virus phiKZ	GCA_000842965.1
AYD81391.1	004605	Cluster4308_1clades	96	SEA_JUSTBECAUSE_236	Streptomyces phage JustBecause	GCA_003613775.1
QJD53795.1	004605	Cluster4308_1clades	99	SEA_KELA_235	Streptomyces phage Kela	GCA_012934305.1
QBZ72121.1	004605	Cluster4308_1clades	96	SEA_KRADAL_235	Streptomyces phage Kradal	GCA_004799925.1
AXH66383.1	004605	Cluster4308_1clades	96	SEA_SATIS_234	Streptomyces phage Satis	GCA_003366315.1
AGR47873.1	004606	Cluster4309_1clades	98	SmphiM12_241	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13075.1	004606	Cluster4309_1clades	98	PHIM19_170	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12715.1	004606	Cluster4309_1clades	98	PHIM7_170	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13445.1	004606	Cluster4309_1clades	98	PHIN3_182	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80089.1	004607	Cluster4310_1clades	97	JA11_284	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66690.1	004607	Cluster4310_1clades	97	JA13_287	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67010.1	004607	Cluster4310_1clades	98	JA29_284	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67659.1	004607	Cluster4310_1clades	97	JA33_285	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96671.1	004608	Cluster4311_1clades	98	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96989.1	004608	Cluster4311_1clades	98	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96035.1	004608	Cluster4311_1clades	98	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96353.1	004608	Cluster4311_1clades	98	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDB70455.1	004609	SIG+KAP-glycosylase	92	CF8_0043	Aeromonas phage CF8	GCA_006384595.2
QNH80840.1	004609	SIG+KAP-glycosylase	91	D6_0036	Aeromonas phage D6	GCA_007051205.2
QBZ70859.1	004609	SIG+KAP-glycosylase	98	pETSU_278	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89485.1	004609	SIG+KAP-glycosylase	95	OBP_048	Pseudomonas phage OBP	GCA_000896635.1
ANM45040.1	004610	Cluster4313_1clades	97	KTN4_282	Pseudomonas phage KTN4	GCA_002607225.1
ATN94674.1	004610	Cluster4313_1clades	97	SL2_097	Pseudomonas phage SL2	GCA_002956015.1
QJB22916.1	004610	Cluster4313_1clades	97	fnug_273	Pseudomonas phage fnug	GCA_012837215.1
AAL83135.1	004610	Cluster4313_1clades	97	PHIKZ234	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47775.1	004611	Cluster4314_1clades	97	SmphiM12_143	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13003.1	004611	Cluster4314_1clades	97	PHIM19_97	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12643.1	004611	Cluster4314_1clades	97	PHIM7_96	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13375.1	004611	Cluster4314_1clades	97	PHIN3_110	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47826.1	004612	Cluster4315_1clades	97	SmphiM12_194	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13037.1	004612	Cluster4315_1clades	97	PHIM19_132	Sinorhizobium phage phiM19	GCA_002605865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF12677.1	004612	Cluster4315_1clades	97	PHIM7_131	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13409.1	004612	Cluster4315_1clades	97	PHIN3_146	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80055.1	004613	Cluster4316_1clades	97	JA11_250	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66654.1	004613	Cluster4316_1clades	97	JA13_251	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66979.1	004613	Cluster4316_1clades	96	JA29_253	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67625.1	004613	Cluster4316_1clades	97	JA33_251	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80084.1	004614	Cluster4317_1clades	97	JA11_279	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66685.1	004614	Cluster4317_1clades	97	JA13_282	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67005.1	004614	Cluster4317_1clades	95	JA29_279	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67654.1	004614	Cluster4317_1clades	97	JA33_280	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD80086.1	004615	Cluster4318_1clades	96	JA11_281	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66687.1	004615	Cluster4318_1clades	96	JA13_284	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67007.1	004615	Cluster4318_1clades	97	JA29_281	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67656.1	004615	Cluster4318_1clades	96	JA33_282	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81373.1	004616	Cluster4319_1clades	96	SEA_JUSTBECAUSE_218	Streptomyces phage JustBecause	GCA_003613775.1
QJD53776.1	004616	Cluster4319_1clades	96	SEA_KELA_216	Streptomyces phage Kela	GCA_012934305.1
QBZ72102.1	004616	Cluster4319_1clades	97	SEA_KRADAL_216	Streptomyces phage Kradal	GCA_004799925.1
AXH66363.1	004616	Cluster4319_1clades	97	SEA_SATIS_214	Streptomyces phage Satis	GCA_003366315.1
AYD81358.1	004617	Cluster4320_1clades	97	SEA_JUSTBECAUSE_193	Streptomyces phage JustBecause	GCA_003613775.1
QJD53761.1	004617	Cluster4320_1clades	97	SEA_KELA_191	Streptomyces phage Kela	GCA_012934305.1
QBZ72090.1	004617	Cluster4320_1clades	96	SEA_KRADAL_194	Streptomyces phage Kradal	GCA_004799925.1
AXH66352.1	004617	Cluster4320_1clades	96	SEA_SATIS_193	Streptomyces phage Satis	GCA_003366315.1
QAX96784.1	004618	Cluster4321_1clades	97	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97103.1	004618	Cluster4321_1clades	97	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96149.1	004618	Cluster4321_1clades	97	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96467.1	004618	Cluster4321_1clades	97	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96932.1	004619	Cluster4322_1clades	97	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97237.1	004619	Cluster4322_1clades	97	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96296.1	004619	Cluster4322_1clades	97	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96614.1	004619	Cluster4322_1clades	97	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX06435.1	004620	Cluster4323_1clades	97	BcepSaruman_022	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74403.1	004620	Cluster4323_1clades	97	BcepSauron_023	Burkholderia phage BcepSauron	GCA_005394215.1
AMM44049.1	004620	Cluster4323_1clades	88	CBB_486	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89003.1	004620	Cluster4323_1clades	91	BF_0478	Serratia phage BF	GCA_002619745.1
ANM45034.1	004621	Cluster4324_1clades	96	KTN4_276	Pseudomonas phage KTN4	GCA_002607225.1
ATN94680.1	004621	Cluster4324_1clades	96	SL2_103	Pseudomonas phage SL2	GCA_002956015.1
QJB22910.1	004621	Cluster4324_1clades	96	fnug_267	Pseudomonas phage fnug	GCA_012837215.1
AGC26347.1	004621	Cluster4324_1clades	96	PHIKZ230.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47721.3	004622	Cluster4325_1clades	96	SmphiM12_089	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12976.1	004622	Cluster4325_1clades	96	PHIM19_69	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12616.1	004622	Cluster4325_1clades	96	PHIM7_68	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13348.1	004622	Cluster4325_1clades	96	PHIN3_84	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47883.1	004623	Cluster4326_1clades	96	SmphiM12_251	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13084.1	004623	Cluster4326_1clades	96	PHIM19_179	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12724.1	004623	Cluster4326_1clades	96	PHIM7_179	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13453.1	004623	Cluster4326_1clades	96	PHIN3_190	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48032.1	004624	Cluster4327_1clades	96	SmphiM12_400	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13214.1	004624	Cluster4327_1clades	96	PHIM19_309	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12855.1	004624	Cluster4327_1clades	96	PHIM7_309	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13576.1	004624	Cluster4327_1clades	96	PHIN3_313	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81244.1	004625	Cluster4328_1clades	93	SEA_JUSTBECAUSE_75	Streptomyces phage JustBecause	GCA_003613775.1
QJD53647.1	004625	Cluster4328_1clades	93	SEA_KELA_76	Streptomyces phage Kela	GCA_012934305.1
QBZ71977.1	004625	Cluster4328_1clades	96	SEA_KRADAL_79	Streptomyces phage Kradal	GCA_004799925.1
AXH66240.1	004625	Cluster4328_1clades	96	SEA_SATIS_79	Streptomyces phage Satis	GCA_003366315.1
AYD81282.1	004626	pi3KINASE	94	SEA_JUSTBECAUSE_113	Streptomyces phage JustBecause	GCA_003613775.1
QJD53685.1	004626	pi3KINASE	94	SEA_KELA_114	Streptomyces phage Kela	GCA_012934305.1
QBZ72012.1	004626	pi3KINASE	96	SEA_KRADAL_114	Streptomyces phage Kradal	GCA_004799925.1
AXH66276.1	004626	pi3KINASE	96	SEA_SATIS_115	Streptomyces phage Satis	GCA_003366315.1
ANM44903.1	004627	Cluster4330_1clades	75	KTN4_145	Pseudomonas phage KTN4	GCA_002607225.1
ATN94810.1	004627	Cluster4330_1clades	75	SL2_233	Pseudomonas phage SL2	GCA_002956015.1
QJB22781.1	004627	Cluster4330_1clades	75	fnug_138	Pseudomonas phage fnug	GCA_012837215.1
AAL83016.1	004627	Cluster4330_1clades	95	PHIKZ115	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22715.1	004628	Cluster4331_1clades	78	Ah1_00195	Aeromonas phage Ah1	GCA_002957415.1
ADQ52895.1	004628	Cluster4331_1clades	95	PX29p176	Aeromonas phage PX29	GCA_000920195.1
ADM80162.1	004628	Cluster4331_1clades	72	phiAS5_ORF0319	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17848.1	004628	Cluster4331_1clades	78	Aeh1ORF182c	Aeromonas virus Aeh1	GCA_000843245.1
AFA44599.1	004629	Cluster4332_1clades	95	RaK2_00326	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QCW18695.1	004629	Cluster4332_1clades	83	7t3_0174	Salmonella phage 7t3	GCA_006083215.1
AZU97968.1	004629	Cluster4332_1clades	83	CPT_Munch_024	Salmonella phage Munch	GCA_004015485.1
QIG63010.1	004629	Cluster4332_1clades	83	SEPL_397	Salmonella phage SE_PL	GCA_011067555.1
AFO71386.1	004630	Cluster4333_1clades	95	CR5_166	Cronobacter phage CR5	GCA_000910235.1
QBP07597.1	004630	Cluster4333_1clades	95	DERBICUS_171	Erwinia phage Derbicus	GCA_004521655.1
ANZ49020.1	004630	Cluster4333_1clades	95	EARLPHILLIPIV_171	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50367.1	004630	Cluster4333_1clades	95	PHOBOS_177	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM44814.1	004631	Cluster4334_1clades	95	KTN4_056	Pseudomonas phage KTN4	GCA_002607225.1
ATN94897.1	004631	Cluster4334_1clades	95	SL2_320	Pseudomonas phage SL2	GCA_002956015.1
QJB22693.1	004631	Cluster4334_1clades	95	fnug_50	Pseudomonas phage fnug	GCA_012837215.1
AGC26311.1	004631	Cluster4334_1clades	95	PHIKZ041.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47653.2	004632	Baculo_helicase	95	SmphiM12_021	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12919.1	004632	Baculo_helicase	95	PHIM19_12	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12559.1	004632	Baculo_helicase	95	PHIM7_11	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13287.1	004632	Baculo_helicase	95	PHIN3_22	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47695.1	004633	Cluster4336_1clades	95	SmphiM12_063	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12954.1	004633	Cluster4336_1clades	95	PHIM19_47	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12594.1	004633	Cluster4336_1clades	95	PHIM7_46	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13327.1	004633	Cluster4336_1clades	95	PHIN3_62	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47844.1	004634	Cluster4337_1clades	95	SmphiM12_212	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13050.1	004634	Cluster4337_1clades	95	PHIM19_145	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12691.1	004634	Cluster4337_1clades	95	PHIM7_145	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13423.1	004634	Cluster4337_1clades	95	PHIN3_160	Sinorhizobium phage phiN3	GCA_001501175.1
AGH07604.1	004635	Cluster4338_1clades	81	CYVG_00160	Cyanophage S-SSM6a	GCA_002710385.1
AGG54388.1	004635	Cluster4338_1clades	65	CYWG_00104	Cyanophage S-SSM6b	GCA_002710425.1
AGH26234.1	004635	Cluster4338_1clades	78	CPMG_00133	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93558.1	004635	Cluster4338_1clades	95	-	Prochlorococcus phage P-TIM68	GCA_001503075.1
ANM44781.1	004636	Cluster4339_1clades	95	KTN4_023	Pseudomonas phage KTN4	GCA_002607225.1
QBJ02683.1	004636	Cluster4339_1clades	87	PSA21_156	Pseudomonas phage Psa21	GCA_004340405.1
ATN94925.1	004636	Cluster4339_1clades	88	SL2_348	Pseudomonas phage SL2	GCA_002956015.1
QJB22666.1	004636	Cluster4339_1clades	95	fnug_23	Pseudomonas phage fnug	GCA_012837215.1
AYD79840.1	004637	Cluster4340_1clades	95	JA11_035	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66439.1	004637	Cluster4340_1clades	95	JA13_036	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66763.1	004637	Cluster4340_1clades	95	JA29_037	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67409.1	004637	Cluster4340_1clades	95	JA33_035	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81395.1	004638	Cluster4341_1clades	95	SEA_JUSTBECAUSE_240	Streptomyces phage JustBecause	GCA_003613775.1
QJD53799.1	004638	Cluster4341_1clades	95	SEA_KELA_239	Streptomyces phage Kela	GCA_012934305.1
QBZ72125.1	004638	Cluster4341_1clades	95	SEA_KRADAL_239	Streptomyces phage Kradal	GCA_004799925.1
AXH66387.1	004638	Cluster4341_1clades	95	SEA_SATIS_238	Streptomyces phage Satis	GCA_003366315.1
AXQ69057.1	004639	Cluster4342_1clades	95	CcrBL9_gp033	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69573.1	004639	Cluster4342_1clades	95	CcrBL9_gp549	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69616.1	004639	Cluster4342_1clades	95	CcrSC_gp034	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70116.1	004639	Cluster4342_1clades	95	CcrSC_gp534	Caulobacter phage CcrSC	GCA_003443315.1
AYD81198.1	004640	Cluster4343_1clades	95	SEA_JUSTBECAUSE_29	Streptomyces phage JustBecause	GCA_003613775.1
QJD53600.1	004640	Cluster4343_1clades	95	SEA_KELA_29	Streptomyces phage Kela	GCA_012934305.1
QBZ71936.1	004640	Cluster4343_1clades	94	SEA_KRADAL_37	Streptomyces phage Kradal	GCA_004799925.1
AXH66198.1	004640	Cluster4343_1clades	94	SEA_SATIS_37	Streptomyces phage Satis	GCA_003366315.1
QAX96811.1	004641	Cluster4344_1clades	95	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97130.1	004641	Cluster4344_1clades	95	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96176.1	004641	Cluster4344_1clades	95	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96494.1	004641	Cluster4344_1clades	95	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96920.1	004642	Cluster4345_1clades	95	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97225.1	004642	Cluster4345_1clades	95	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96284.1	004642	Cluster4345_1clades	95	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96602.1	004642	Cluster4345_1clades	95	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AGX01895.1	004643	Cluster4346_1clades	94	CF95_gp173	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65413.1	004643	Cluster4346_1clades	93	2050HW_00078	Serratia phage 2050HW	GCA_002628125.1
QDB71192.1	004643	Cluster4346_1clades	93	CPT_Moabite_162	Serratia phage Moabite	GCA_006384735.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFP93249.1	004643	Cluster4346_1clades	95	-	Serratia phage PCH45	GCA_009187865.1
ANM44902.1	004644	HTH	94	KTN4_144	Pseudomonas phage KTN4	GCA_002607225.1
ATN94811.1	004644	HTH	94	SL2_234	Pseudomonas phage SL2	GCA_002956015.1
QJB22780.1	004644	HTH	94	fnug_137	Pseudomonas phage fnug	GCA_012837215.1
AAL83015.1	004644	HTH	94	PHIKZ114	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22800.1	004645	Cluster4348_1clades	91	Ah1_00282	Aeromonas phage Ah1	GCA_002957415.1
QAX98515.1	004645	Cluster4348_1clades	94	ASfcp2_179	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52978.1	004645	Cluster4348_1clades	94	PX29p259	Aeromonas phage PX29	GCA_000920195.1
AAQ17927.1	004645	Cluster4348_1clades	94	Aeh1ORF263c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64239.1	004646	SIG+TM	94	KVP40.0170	Vibrio phage KVP40	GCA_000843785.1
QIW90554.1	004646	SIG+TM	63	GCAPEGMB_00207	Vibrio phage V07	GCA_012361095.1
QIW90868.1	004646	SIG+TM	63	COHAPHLL_00005	Vibrio phage V09	GCA_012361135.1
AFN37399.1	004646	SIG+TM	63	pp2_166	Vibriophage phi-pp2	GCA_002630725.1
AGR47688.1	004647	Cluster4350_1clades	94	SmphiM12_056	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12949.1	004647	Cluster4350_1clades	94	PHIM19_42	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12589.1	004647	Cluster4350_1clades	94	PHIM7_41	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13323.1	004647	Cluster4350_1clades	94	PHIN3_58	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80019.1	004648	Cluster4351_1clades	90	JA11_214	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66618.1	004648	Cluster4351_1clades	90	JA13_215	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66942.1	004648	Cluster4351_1clades	94	JA29_216	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67589.1	004648	Cluster4351_1clades	90	JA33_215	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMR59669.1	004649	Cluster4352_1clades	90	SEGD1_018	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85858.1	004649	Cluster4352_1clades	90	ACEC001_0200	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51102.1	004649	Cluster4352_1clades	90	MLDJOKPK_00148	Salmonella phage SPAsTU	GCA_003183805.1
AEP83852.1	004649	Cluster4352_1clades	93	SPN3US_0019	Salmonella phage SPN3US	GCA_001042275.1
AGR47944.1	004650	Cluster4353_1clades	93	SmphiM12_312	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13140.1	004650	Cluster4353_1clades	93	PHIM19_235	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12779.1	004650	Cluster4353_1clades	93	PHIM7_234	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13508.1	004650	Cluster4353_1clades	93	PHIN3_245	Sinorhizobium phage phiN3	GCA_001501175.1
ANS06112.1	004651	Cluster4354_1clades	93	ABCD_0082	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97094.1	004651	Cluster4354_1clades	93	E_086	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ARM70935.1	004651	Cluster4354_1clades	88	phiC120_c230	Escherichia phage phiC120	GCA_002621185.1
AAX78604.1	004651	Cluster4354_1clades	74	RB43ORF082w	Escherichia virus RB43	GCA_000863505.1
AYD79957.1	004652	Cluster4355_1clades	93	JA11_152	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66556.1	004652	Cluster4355_1clades	93	JA13_153	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66881.1	004652	Cluster4355_1clades	93	JA29_155	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67526.1	004652	Cluster4355_1clades	93	JA33_152	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81407.1	004653	Cluster4356_1clades	93	SEA_JUSTBECAUSE_252	Streptomyces phage JustBecause	GCA_003613775.1
QJD53811.1	004653	Cluster4356_1clades	93	SEA_KELA_251	Streptomyces phage Kela	GCA_012934305.1
QBZ72137.1	004653	Cluster4356_1clades	93	SEA_KRADAL_251	Streptomyces phage Kradal	GCA_004799925.1
AXH66399.1	004653	Cluster4356_1clades	93	SEA_SATIS_250	Streptomyces phage Satis	GCA_003366315.1
AYD81178.1	004654	SIG+TM	93	SEA_JUSTBECAUSE_9	Streptomyces phage JustBecause	GCA_003613775.1
QJD53580.1	004654	SIG+TM	93	SEA_KELA_9	Streptomyces phage Kela	GCA_012934305.1
QBZ71910.1	004654	SIG+TM	89	SEA_KRADAL_11	Streptomyces phage Kradal	GCA_004799925.1
AXH66172.1	004654	SIG+TM	89	SEA_SATIS_11	Streptomyces phage Satis	GCA_003366315.1
ANM45076.1	004655	Cluster4358_1clades	92	KTN4_318	Pseudomonas phage KTN4	GCA_002607225.1
ATN94639.1	004655	Cluster4358_1clades	92	SL2_062	Pseudomonas phage SL2	GCA_002956015.1
QJB22951.1	004655	Cluster4358_1clades	92	fnug_308	Pseudomonas phage fnug	GCA_012837215.1
AAL83164.1	004655	Cluster4358_1clades	92	PHIKZ263	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47707.1	004656	Cluster4359_1clades	92	SmphiM12_075	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12963.1	004656	Cluster4359_1clades	92	PHIM19_56	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12603.1	004656	Cluster4359_1clades	92	PHIM7_55	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13336.1	004656	Cluster4359_1clades	92	PHIN3_71	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47845.1	004657	Cluster4360_1clades	88	SmphiM12_213	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13051.1	004657	Cluster4360_1clades	88	PHIM19_146	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12692.1	004657	Cluster4360_1clades	88	PHIM7_146	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13424.1	004657	Cluster4360_1clades	92	PHIN3_161	Sinorhizobium phage phiN3	GCA_001501175.1
AAX44425.1	004658	Cluster4361_1clades	81	PSSM2_047	Prochlorococcus phage P-SSM2	GCA_000859585.1
AIR93576.1	004658	Cluster4361_1clades	80	AVU42_gp239	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76305.1	004658	Cluster4361_1clades	92	PBI_BELLAMY_269	Synechococcus phage Bellamy	GCA_002627525.1
QJT70252.1	004658	Cluster4361_1clades	90	SynMITS9220M01_246	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AYD81292.1	004659	Cluster4362_1clades	87	SEA_JUSTBECAUSE_123	Streptomyces phage JustBecause	GCA_003613775.1
QJD53695.1	004659	Cluster4362_1clades	87	SEA_KELA_124	Streptomyces phage Kela	GCA_012934305.1
QBZ72023.1	004659	Cluster4362_1clades	92	SEA_KRADAL_125	Streptomyces phage Kradal	GCA_004799925.1
AXH66286.1	004659	Cluster4362_1clades	92	SEA_SATIS_125	Streptomyces phage Satis	GCA_003366315.1
AYD81299.1	004660	TM+TM	79	SEA_JUSTBECAUSE_130	Streptomyces phage JustBecause	GCA_003613775.1
QJD53702.1	004660	TM+TM	79	SEA_KELA_131	Streptomyces phage Kela	GCA_012934305.1
QBZ72029.1	004660	TM+TM	92	SEA_KRADAL_131	Streptomyces phage Kradal	GCA_004799925.1
AXH66292.1	004660	TM+TM	92	SEA_SATIS_131	Streptomyces phage Satis	GCA_003366315.1
AYD81363.1	004661	Cluster4364_1clades	91	SEA_JUSTBECAUSE_208	Streptomyces phage JustBecause	GCA_003613775.1
QJD53766.1	004661	Cluster4364_1clades	91	SEA_KELA_206	Streptomyces phage Kela	GCA_012934305.1
QBZ72095.1	004661	Cluster4364_1clades	92	SEA_KRADAL_209	Streptomyces phage Kradal	GCA_004799925.1
AXH66356.1	004661	Cluster4364_1clades	92	SEA_SATIS_207	Streptomyces phage Satis	GCA_003366315.1
BBI90479.1	004662	Cluster4365_1clades	80	HYO65_gp087	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90787.1	004662	Cluster4365_1clades	80	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39192.1	004662	Cluster4365_1clades	89	BPT24_069	Tenacibaculum phage pT24	GCA_002611925.1
BAV39326.1	004662	Cluster4365_1clades	92	BPT24_202	Tenacibaculum phage pT24	GCA_002611925.1
QAX96705.1	004663	Cluster4366_1clades	92	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97023.1	004663	Cluster4366_1clades	92	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96069.1	004663	Cluster4366_1clades	92	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96387.1	004663	Cluster4366_1clades	92	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63594.1	004664	Cluster4367_1clades	92	DAC19_103	Bacteroides phage DAC19	GCA_013387715.1
QIG63855.1	004664	Cluster4367_1clades	92	DAC20_102	Bacteroides phage DAC20	GCA_013387725.1
QIG64118.1	004664	Cluster4367_1clades	88	DAC22_104	Bacteroides phage DAC22	GCA_013387735.1
QIG64376.1	004664	Cluster4367_1clades	88	DAC23_98	Bacteroides phage DAC23	GCA_013387745.1
ANM44900.1	004665	Cluster4368_1clades	91	KTN4_142	Pseudomonas phage KTN4	GCA_002607225.1
ATN94813.1	004665	Cluster4368_1clades	91	SL2_236	Pseudomonas phage SL2	GCA_002956015.1
QJB22778.1	004665	Cluster4368_1clades	91	fnug_135	Pseudomonas phage fnug	GCA_012837215.1
AAL83013.1	004665	Cluster4368_1clades	91	PHIKZ112	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47842.1	004666	Cluster4369_1clades	91	SmphiM12_210	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13048.1	004666	Cluster4369_1clades	91	PHIM19_143	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12689.1	004666	Cluster4369_1clades	91	PHIM7_143	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13420.1	004666	Cluster4369_1clades	88	PHIN3_157	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47863.1	004667	Cluster4370_1clades	91	SmphiM12_231	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13066.1	004667	Cluster4370_1clades	91	PHIM19_161	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12707.1	004667	Cluster4370_1clades	91	PHIM7_161	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13436.1	004667	Cluster4370_1clades	91	PHIN3_173	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80045.1	004668	Cluster4371_1clades	91	JA11_240	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66644.1	004668	Cluster4371_1clades	91	JA13_241	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66968.1	004668	Cluster4371_1clades	65	JA29_242	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67615.1	004668	Cluster4371_1clades	91	JA33_241	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81467.1	004669	Cluster4372_1clades	90	SEA_JUSTBECAUSE_312	Streptomyces phage JustBecause	GCA_003613775.1
QJD53870.1	004669	Cluster4372_1clades	90	SEA_KELA_310	Streptomyces phage Kela	GCA_012934305.1
QBZ72200.1	004669	Cluster4372_1clades	91	SEA_KRADAL_314	Streptomyces phage Kradal	GCA_004799925.1
AXH66463.1	004669	Cluster4372_1clades	91	SEA_SATIS_314	Streptomyces phage Satis	GCA_003366315.1
AYD81340.1	004670	HTH	86	SEA_JUSTBECAUSE_175	Streptomyces phage JustBecause	GCA_003613775.1
QJD53743.1	004670	HTH	91	SEA_KELA_173	Streptomyces phage Kela	GCA_012934305.1
QBZ72069.1	004670	HTH	85	SEA_KRADAL_173	Streptomyces phage Kradal	GCA_004799925.1
AXH66332.1	004670	HTH	85	SEA_SATIS_173	Streptomyces phage Satis	GCA_003366315.1
AUE22676.1	004671	Cluster4374_1clades	90	Ah1_00135	Aeromonas phage Ah1	GCA_002957415.1
QAX98402.1	004671	Cluster4374_1clades	87	ASfcp2_58	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52858.1	004671	Cluster4374_1clades	87	PX29p139	Aeromonas phage PX29	GCA_000920195.1
AAQ17804.1	004671	Cluster4374_1clades	90	Aeh1ORF139c	Aeromonas virus Aeh1	GCA_000843245.1
QAY00321.1	004672	Cluster4375_1clades	90	Ecwhy1_39	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35068.1	004672	Cluster4375_1clades	90	ACQ29_gp388	Escherichia phage PBECO4	GCA_001041035.1
BBM61707.1	004672	Cluster4375_1clades	90	EO157G_1180	Escherichia phage SP27	GCA_008033345.1
AXC36646.1	004672	Cluster4375_1clades	90	-	Escherichia phage UB	GCA_003341455.1
AGH07510.1	004673	Cluster4376_1clades	90	CYVG_00066	Cyanophage S-SSM6a	GCA_002710385.1
AAX44505.1	004673	Cluster4376_1clades	89	PSSM2_127	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12461.1	004673	Cluster4376_1clades	89	PRTG_00314	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ70577.1	004673	Cluster4376_1clades	88	HOU04_gp178	Synechococcus phage S-T4	GCA_003443335.1
AGH56912.1	004674	Cluster4377_1clades	83	CPXG_00109	Cyanophage P-RSM6	GCA_000906155.1
AGH07516.1	004674	Cluster4377_1clades	88	CYVG_00072	Cyanophage S-SSM6a	GCA_002710385.1
AGG54442.1	004674	Cluster4377_1clades	81	CYWG_00158	Cyanophage S-SSM6b	GCA_002710425.1
AIR93545.1	004674	Cluster4377_1clades	90	AVU42_gp209	Prochlorococcus phage P-TIM68	GCA_001503075.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AYD80052.1	004675	Cluster4378_1clades	90	JA11_247	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66651.1	004675	Cluster4378_1clades	90	JA13_248	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66975.1	004675	Cluster4378_1clades	90	JA29_249	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67622.1	004675	Cluster4378_1clades	90	JA33_248	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81209.1	004676	SIG+PFU	84	SEA_JUSTBECAUSE_40	Streptomyces phage JustBecause	GCA_003613775.1
QJD53612.1	004676	SIG+PFU	84	SEA_KELA_41	Streptomyces phage Kela	GCA_012934305.1
QBZ71946.1	004676	SIG+PFU	90	SEA_KRADAL_47	Streptomyces phage Kradal	GCA_004799925.1
AXH66208.1	004676	SIG+PFU	90	SEA_SATIS_47	Streptomyces phage Satis	GCA_003366315.1
AYD81475.1	004677	Cluster4380_1clades	90	SEA_JUSTBECAUSE_320	Streptomyces phage JustBecause	GCA_003613775.1
QJD53878.1	004677	Cluster4380_1clades	90	SEA_KELA_318	Streptomyces phage Kela	GCA_012934305.1
QBZ72208.1	004677	Cluster4380_1clades	88	SEA_KRADAL_322	Streptomyces phage Kradal	GCA_004799925.1
AXH66471.1	004677	Cluster4380_1clades	88	SEA_SATIS_322	Streptomyces phage Satis	GCA_003366315.1
AGR48004.1	004678	Cluster4381_1clades	89	SmphiM12_372	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13190.1	004678	Cluster4381_1clades	89	PHIM19_285	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12830.1	004678	Cluster4381_1clades	89	PHIM7_285	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13552.1	004678	Cluster4381_1clades	89	PHIN3_289	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48027.1	004679	Cluster4382_1clades	89	SmphiM12_395	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13210.1	004679	Cluster4382_1clades	89	PHIM19_305	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12851.1	004679	Cluster4382_1clades	89	PHIM7_305	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13572.1	004679	Cluster4382_1clades	89	PHIN3_309	Sinorhizobium phage phiN3	GCA_001501175.1
AMM43716.1	004680	Cluster4383_1clades	89	CBB_151	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88670.1	004680	Cluster4383_1clades	89	BF_0145	Serratia phage BF	GCA_002619745.1
SOK58952.1	004680	Cluster4383_1clades	88	g144	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58418.1	004680	Cluster4383_1clades	88	g141	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOO11591.1	004681	Cluster4384_1clades	89	ES420910_110	Cyanophage S-RIM44	GCA_002599165.1
AOO12056.1	004681	Cluster4384_1clades	89	Np200711_110	Cyanophage S-RIM44	GCA_002599205.1
AOO12292.1	004681	Cluster4384_1clades	89	Np420711_110	Cyanophage S-RIM44	GCA_002599225.1
AOO12757.1	004681	Cluster4384_1clades	89	Sn130910_110	Cyanophage S-RIM44	GCA_002599265.1
AYD79854.1	004682	Cluster4385_1clades	89	JA11_049	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66454.1	004682	Cluster4385_1clades	89	JA13_051	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66778.1	004682	Cluster4385_1clades	89	JA29_052	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67423.1	004682	Cluster4385_1clades	89	JA33_049	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81205.1	004683	Glyco_tranf_2_4	89	SEA_JUSTBECAUSE_36	Streptomyces phage JustBecause	GCA_003613775.1
QJD53608.1	004683	Glyco_tranf_2_4	89	SEA_KELA_37	Streptomyces phage Kela	GCA_012934305.1
QBZ71943.1	004683	Glyco_tranf_2_4	88	SEA_KRADAL_44	Streptomyces phage Kradal	GCA_004799925.1
AXH66205.1	004683	Glyco_tranf_2_4	88	SEA_SATIS_44	Streptomyces phage Satis	GCA_003366315.1
QAX96755.1	004684	Cluster4387_1clades	89	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97074.1	004684	Cluster4387_1clades	89	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96120.1	004684	Cluster4387_1clades	89	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96438.1	004684	Cluster4387_1clades	89	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44790.1	004685	Cluster4388_1clades	88	KTN4_032	Pseudomonas phage KTN4	GCA_002607225.1
QBX32291.1	004685	Cluster4388_1clades	88	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94922.1	004685	Cluster4388_1clades	88	SL2_345	Pseudomonas phage SL2	GCA_002956015.1
QEM41865.1	004685	Cluster4388_1clades	88	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANS06125.1	004686	Cluster4389_1clades	88	ABCD_0071	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97085.1	004686	Cluster4389_1clades	88	E_076	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78594.1	004686	Cluster4389_1clades	28	RB43ORF072w	Escherichia virus RB43	GCA_000863505.1
AAX78595.1	004686	Cluster4389_1clades	43	RB43ORF073w	Escherichia virus RB43	GCA_000863505.1
AXQ69047.1	004687	Cluster4390_1clades	88	CcrBL9_gp023	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69563.1	004687	Cluster4390_1clades	88	CcrBL9_gp539	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69607.1	004687	Cluster4390_1clades	88	CcrSC_gp025	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70107.1	004687	Cluster4390_1clades	88	CcrSC_gp525	Caulobacter phage CcrSC	GCA_003443315.1
AYD81416.1	004688	Cluster4391_1clades	88	SEA_JUSTBECAUSE_261	Streptomyces phage JustBecause	GCA_003613775.1
QJD53821.1	004688	Cluster4391_1clades	88	SEA_KELA_261	Streptomyces phage Kela	GCA_012934305.1
QBZ72149.1	004688	Cluster4391_1clades	87	SEA_KRADAL_263	Streptomyces phage Kradal	GCA_004799925.1
AXH66412.1	004688	Cluster4391_1clades	87	SEA_SATIS_263	Streptomyces phage Satis	GCA_003366315.1
QAX96690.1	004689	Cluster4392_1clades	88	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97008.1	004689	Cluster4392_1clades	88	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96054.1	004689	Cluster4392_1clades	88	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96372.1	004689	Cluster4392_1clades	88	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96779.1	004690	Cluster4393_1clades	88	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97098.1	004690	Cluster4393_1clades	88	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96144.1	004690	Cluster4393_1clades	88	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96462.1	004690	Cluster4393_1clades	88	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AUE22582.1	004691	Cluster4394_1clades	87	Ah1_00041	Aeromonas phage Ah1	GCA_002957415.1
QAX98617.1	004691	Cluster4394_1clades	87	ASfcp2_284	Aeromonas phage AsFcp_2	GCA_004146885.1
ADM80013.1	004691	Cluster4394_1clades	85	phiAS5_ORF0170	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17700.1	004691	Cluster4394_1clades	87	Aeh1ORF041c	Aeromonas virus Aeh1	GCA_000843245.1
QAX98646.1	004692	Cluster4395_1clades	87	ASfcp2_313	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52786.1	004692	Cluster4395_1clades	87	PX29p067	Aeromonas phage PX29	GCA_000920195.1
ADM80042.1	004692	Cluster4395_1clades	87	phiAS5_ORF0199	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17730.1	004692	Cluster4395_1clades	87	Aeh1ORF070c	Aeromonas virus Aeh1	GCA_000843245.1
AGR48015.1	004693	Cluster4396_1clades	87	SmphiM12_383	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13201.1	004693	Cluster4396_1clades	87	PHIM19_296	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12842.1	004693	Cluster4396_1clades	87	PHIM7_296	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13562.1	004693	Cluster4396_1clades	87	PHIN3_299	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48017.1	004694	Cluster4397_1clades	87	SmphiM12_385	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13203.1	004694	Cluster4397_1clades	87	PHIM19_298	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12844.1	004694	Cluster4397_1clades	87	PHIM7_298	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13564.1	004694	Cluster4397_1clades	87	PHIN3_301	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48071.1	004695	Cluster4398_1clades	87	SmphiM12_439	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13246.1	004695	Cluster4398_1clades	87	PHIM19_341	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12886.1	004695	Cluster4398_1clades	87	PHIM7_341	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13609.1	004695	Cluster4398_1clades	87	PHIN3_346	Sinorhizobium phage phiN3	GCA_001501175.1
AXG67064.1	004696	Cluster4399_1clades	87	AD1_020	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08301.1	004696	Cluster4399_1clades	87	Alexandra_21	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58662.1	004696	Cluster4399_1clades	87	Y3_022	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28508.1	004696	Cluster4399_1clades	87	YOLOSWAG_21	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD79990.1	004697	Cluster4400_1clades	83	JA11_185	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66588.1	004697	Cluster4400_1clades	83	JA13_185	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66913.1	004697	Cluster4400_1clades	87	JA29_187	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67559.1	004697	Cluster4400_1clades	83	JA33_185	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81381.1	004698	Cluster4401_1clades	87	SEA_JUSTBECAUSE_226	Streptomyces phage JustBecause	GCA_003613775.1
QJD53785.1	004698	Cluster4401_1clades	87	SEA_KELA_225	Streptomyces phage Kela	GCA_012934305.1
QBZ72110.1	004698	Cluster4401_1clades	87	SEA_KRADAL_224	Streptomyces phage Kradal	GCA_004799925.1
AXH66371.1	004698	Cluster4401_1clades	87	SEA_SATIS_222	Streptomyces phage Satis	GCA_003366315.1
QIG63547.1	004699	Cluster4402_1clades	87	DAC19_56	Bacteroides phage DAC19	GCA_013387715.1
QIG63808.1	004699	Cluster4402_1clades	87	DAC20_55	Bacteroides phage DAC20	GCA_013387725.1
QIG64070.1	004699	Cluster4402_1clades	87	DAC22_56	Bacteroides phage DAC22	GCA_013387735.1
QIG64333.1	004699	Cluster4402_1clades	87	DAC23_55	Bacteroides phage DAC23	GCA_013387745.1
AFC21490.1	004700	Cluster4403_1clades	64	GAP32_043	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88563.1	004700	Cluster4403_1clades	65	BF_0038	Serratia phage BF	GCA_002619745.1
SOK58838.1	004700	Cluster4403_1clades	65	g030	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58298.1	004700	Cluster4403_1clades	87	g021	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22864.1	004701	Cluster4404_1clades	83	Ah1_00346	Aeromonas phage Ah1	GCA_002957415.1
QAX98574.1	004701	Cluster4404_1clades	86	ASfcp2_240	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53039.1	004701	Cluster4404_1clades	83	PX29p322	Aeromonas phage PX29	GCA_000920195.1
AAQ17992.1	004701	Cluster4404_1clades	86	Aeh1ORF323c	Aeromonas virus Aeh1	GCA_000843245.1
AUE22610.1	004702	SIG+TM	85	Ah1_00069	Aeromonas phage Ah1	GCA_002957415.1
ADQ52794.1	004702	SIG+TM	86	PX29p075	Aeromonas phage PX29	GCA_000920195.1
ADM80050.1	004702	SIG+TM	86	phiAS5_ORF0207	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17737.1	004702	SIG+TM	85	Aeh1ORF077c	Aeromonas virus Aeh1	GCA_000843245.1
AGR48054.1	004703	PADR-HTH	86	SmphiM12_422	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13234.1	004703	PADR-HTH	86	PHIM19_329	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12874.1	004703	PADR-HTH	86	PHIM7_329	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13597.1	004703	PADR-HTH	86	PHIN3_334	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21961.1	004704	Cluster4407_1clades	77	GAP32_502	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44086.1	004704	Cluster4407_1clades	77	CBB_523	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89039.1	004704	Cluster4407_1clades	86	BF_0514	Serratia phage BF	GCA_002619745.1
SOK59315.1	004704	Cluster4407_1clades	85	g507	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AXG67046.1	004705	Cluster4408_1clades	80	AD1_002	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08284.1	004705	Cluster4408_1clades	80	Alexandra_2	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58642.1	004705	Cluster4408_1clades	86	Y3_002	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28489.1	004705	Cluster4408_1clades	82	YOLOSWAG_2	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AYD81316.1	004706	Cluster4409_1clades	83	SEA_JUSTBECAUSE_151	Streptomyces phage JustBecause	GCA_003613775.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QJD53719.1	004706	Cluster4409_1clades	83	SEA_KELA_149	Streptomyces phage Kela	GCA_012934305.1
QBZ72047.1	004706	Cluster4409_1clades	86	SEA_KRADAL_151	Streptomyces phage Kradal	GCA_004799925.1
AXH66310.1	004706	Cluster4409_1clades	86	SEA_SATIS_151	Streptomyces phage Satis	GCA_003366315.1
QAX96818.1	004707	Cluster4410_1clades	86	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97137.1	004707	Cluster4410_1clades	86	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96183.1	004707	Cluster4410_1clades	86	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96501.1	004707	Cluster4410_1clades	86	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63593.1	004708	Cluster4411_1clades	86	DAC19_102	Bacteroides phage DAC19	GCA_013387715.1
QIG63854.1	004708	Cluster4411_1clades	86	DAC20_101	Bacteroides phage DAC20	GCA_013387725.1
QIG64117.1	004708	Cluster4411_1clades	86	DAC22_103	Bacteroides phage DAC22	GCA_013387735.1
QIG64375.1	004708	Cluster4411_1clades	86	DAC23_97	Bacteroides phage DAC23	GCA_013387745.1
ANM44785.1	004709	Cluster4412_1clades	85	KTN4_027	Pseudomonas phage KTN4	GCA_002607225.1
AEH03542.1	004709	Cluster4412_1clades	77	118	Pseudomonas phage PhiPA3	GCA_001502095.1
QJB22668.1	004709	Cluster4412_1clades	85	fnug_25	Pseudomonas phage fnug	GCA_012837215.1
AAL82921.1	004709	Cluster4412_1clades	85	PHIKZ020	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44857.1	004710	SIG+TM	85	KTN4_099	Pseudomonas phage KTN4	GCA_002607225.1
ATN94856.1	004710	SIG+TM	85	SL2_279	Pseudomonas phage SL2	GCA_002956015.1
QJB22734.1	004710	SIG+TM	85	fnug_91	Pseudomonas phage fnug	GCA_012837215.1
AAL82977.1	004710	SIG+TM	85	PHIKZ076	Pseudomonas virus phiKZ	GCA_000842965.1
AFO71346.1	004711	Cluster4414_1clades	85	CR5_126	Cronobacter phage CR5	GCA_000910235.1
QBP07553.1	004711	Cluster4414_1clades	85	DERBICUS_127	Erwinia phage Derbicus	GCA_004521655.1
ANZ48976.1	004711	Cluster4414_1clades	85	EARLPHILLIPIV_127	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50318.1	004711	Cluster4414_1clades	85	PHOBOS_128	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM45012.1	004712	Cluster4415_1clades	85	KTN4_254	Pseudomonas phage KTN4	GCA_002607225.1
ATN94702.1	004712	Cluster4415_1clades	55	SL2_125	Pseudomonas phage SL2	GCA_002956015.1
QJB22889.1	004712	Cluster4415_1clades	85	fnug_246	Pseudomonas phage fnug	GCA_012837215.1
AGC26345.1	004712	Cluster4415_1clades	85	PHIKZ210.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47647.1	004713	Cluster4416_1clades	85	SmphiM12_015	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12913.1	004713	Cluster4416_1clades	85	PHIM19_6	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12553.1	004713	Cluster4416_1clades	85	PHIM7_5	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13283.1	004713	Cluster4416_1clades	85	PHIN3_16	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47696.1	004714	Cluster4417_1clades	85	SmphiM12_064	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12955.1	004714	Cluster4417_1clades	85	PHIM19_48	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12595.1	004714	Cluster4417_1clades	85	PHIM7_47	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13328.1	004714	Cluster4417_1clades	71	PHIN3_63	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48026.1	004715	Cluster4418_1clades	85	SmphiM12_394	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13209.1	004715	Cluster4418_1clades	85	PHIM19_304	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12850.1	004715	Cluster4418_1clades	85	PHIM7_304	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13571.1	004715	Cluster4418_1clades	85	PHIN3_308	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48028.1	004716	Cluster4419_1clades	85	SmphiM12_396	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13211.1	004716	Cluster4419_1clades	85	PHIM19_306	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12852.1	004716	Cluster4419_1clades	85	PHIM7_306	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13573.1	004716	Cluster4419_1clades	85	PHIN3_310	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48075.1	004717	Cluster4420_1clades	85	SmphiM12_443	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13250.1	004717	Cluster4420_1clades	85	PHIM19_345	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12890.1	004717	Cluster4420_1clades	85	PHIM7_345	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13613.1	004717	Cluster4420_1clades	85	PHIN3_350	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48076.1	004718	Cluster4421_1clades	85	SmphiM12_444	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13251.1	004718	Cluster4421_1clades	85	PHIM19_346	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12891.1	004718	Cluster4421_1clades	85	PHIM7_346	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13614.1	004718	Cluster4421_1clades	85	PHIN3_351	Sinorhizobium phage phiN3	GCA_001501175.1
ANM45038.1	004719	Cluster4422_1clades	85	KTN4_280	Pseudomonas phage KTN4	GCA_002607225.1
ATN94676.1	004719	Cluster4422_1clades	85	SL2_099	Pseudomonas phage SL2	GCA_002956015.1
QJB22914.1	004719	Cluster4422_1clades	85	fnug_271	Pseudomonas phage fnug	GCA_012837215.1
AGC26350.1	004719	Cluster4422_1clades	54	PHIKZ232.2	Pseudomonas virus phiKZ	GCA_000842965.1
ATI17619.1	004720	Cluster4423_1clades	85	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00377.1	004720	Cluster4423_1clades	85	HWB28_gp175	Aeromonas phage AS-zj	GCA_002627665.1
QAX97653.1	004720	Cluster4423_1clades	85	ASswx1_7	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39220.1	004720	Cluster4423_1clades	80	CC2_107	Aeromonas phage CC2	GCA_000903495.1
AIT14406.1	004721	Cluster4425_1clades	51	PBI_121Q_516	Escherichia phage 121Q	GCA_000926855.1
BBM62077.1	004721	Cluster4425_1clades	85	EO157G_4880	Escherichia phage SP27	GCA_008033345.1
QBO61896.1	004721	Cluster4425_1clades	51	G17_00407	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF13932.1	004721	Cluster4425_1clades	85	vBEcoMphAPEC6_gp307	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QAX96743.1	004722	Cluster4426_1clades	85	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97062.1	004722	Cluster4426_1clades	85	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96108.1	004722	Cluster4426_1clades	85	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96426.1	004722	Cluster4426_1clades	85	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AUE22792.1	004723	Cluster4427_1clades	84	Ah1_00274	Aeromonas phage Ah1	GCA_002957415.1
QAX98506.1	004723	Cluster4427_1clades	84	ASfcp2_170	Aeromonas phage AsFcp_2	GCA_004146885.1
ADM79894.1	004723	Cluster4427_1clades	80	phiAS5_ORF0051	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17917.1	004723	Cluster4427_1clades	84	Aeh1gORF298c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47670.1	004724	Cluster4428_1clades	84	SmphiM12_038	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12933.1	004724	Cluster4428_1clades	84	PHIM19_26	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12573.1	004724	Cluster4428_1clades	84	PHIM7_25	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13305.1	004724	Cluster4428_1clades	84	PHIN3_40	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47812.2	004725	Cluster4429_1clades	84	SmphiM12_180	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13026.1	004725	Cluster4429_1clades	84	PHIM19_121	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12666.1	004725	Cluster4429_1clades	84	PHIM7_120	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13397.1	004725	Cluster4429_1clades	84	PHIN3_134	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81313.1	004726	Cluster4430_1clades	66	SEA_JUSTBECAUSE_148	Streptomyces phage JustBecause	GCA_003613775.1
QJD53716.1	004726	Cluster4430_1clades	66	SEA_KELA_146	Streptomyces phage Kela	GCA_012934305.1
QBZ72043.1	004726	Cluster4430_1clades	84	SEA_KRADAL_147	Streptomyces phage Kradal	GCA_004799925.1
AXH66306.1	004726	Cluster4430_1clades	84	SEA_SATIS_147	Streptomyces phage Satis	GCA_003366315.1
AXQ69167.1	004727	Cluster4431_1clades	84	CcrBL9_gp143	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69722.1	004727	Cluster4431_1clades	84	CcrSC_gp140	Caulobacter phage CcrSC	GCA_003443315.1
QGT54946.1	004727	Cluster4431_1clades	80	b23_0336	Synechococcus phage B23	GCA_009745195.1
QGT54581.1	004727	Cluster4431_1clades	80	b3_0342	Synechococcus phage B3	GCA_009745215.1
AYD81390.1	004728	TM	84	SEA_JUSTBECAUSE_235	Streptomyces phage JustBecause	GCA_003613775.1
QJD53794.1	004728	TM	84	SEA_KELA_234	Streptomyces phage Kela	GCA_012934305.1
QBZ72120.1	004728	TM	81	SEA_KRADAL_234	Streptomyces phage Kradal	GCA_004799925.1
AXH66382.1	004728	TM	78	SEA_SATIS_233	Streptomyces phage Satis	GCA_003366315.1
QMV28981.1	004729	Cluster4433_1clades	83	AP1_0274	Aeromonas phage AP1	GCA_014183365.1
ATI17532.1	004729	Cluster4433_1clades	83	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00464.1	004729	Cluster4433_1clades	83	HWB28_gp088	Aeromonas phage AS-zj	GCA_002627665.1
AFN39257.1	004729	Cluster4433_1clades	83	CC2_201	Aeromonas phage CC2	GCA_000903495.1
AGR47849.1	004730	Cluster4434_1clades	83	SmphiM12_217	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13054.1	004730	Cluster4434_1clades	83	PHIM19_149	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12695.1	004730	Cluster4434_1clades	83	PHIM7_149	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13425.1	004730	Cluster4434_1clades	83	PHIN3_162	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47853.1	004731	Cluster4435_1clades	83	SmphiM12_221	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13058.1	004731	Cluster4435_1clades	83	PHIM19_153	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12699.1	004731	Cluster4435_1clades	83	PHIM7_153	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13428.1	004731	Cluster4435_1clades	83	PHIN3_165	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47907.1	004732	Cluster4436_1clades	83	SmphiM12_275	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13111.1	004732	Cluster4436_1clades	83	PHIM19_206	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12751.1	004732	Cluster4436_1clades	83	PHIM7_206	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13481.1	004732	Cluster4436_1clades	83	PHIN3_218	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47978.1	004733	Cluster4437_1clades	83	SmphiM12_346	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13166.1	004733	Cluster4437_1clades	83	PHIM19_261	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12806.1	004733	Cluster4437_1clades	83	PHIM7_261	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13529.1	004733	Cluster4437_1clades	83	PHIN3_266	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47981.1	004734	SIG+TM	83	SmphiM12_349	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13169.1	004734	SIG+TM	83	PHIM19_264	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12809.1	004734	SIG+TM	83	PHIM7_264	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13532.1	004734	SIG+TM	83	PHIN3_269	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48007.1	004735	Cluster4439_1clades	83	SmphiM12_375	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13193.1	004735	Cluster4439_1clades	83	PHIM19_288	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12833.1	004735	Cluster4439_1clades	83	PHIM7_288	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13555.1	004735	Cluster4439_1clades	83	PHIN3_292	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48053.1	004736	TM	83	SmphiM12_421	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13233.1	004736	TM	83	PHIM19_328	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12873.1	004736	TM	83	PHIM7_328	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13596.1	004736	TM	83	PHIN3_333	Sinorhizobium phage phiN3	GCA_001501175.1
QDH50598.1	004737	Cluster4441_1clades	82	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59540.1	004737	Cluster4441_1clades	83	S330809_079	Synechococcus phage S-CAM4	GCA_002366065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AOV59302.1	004737	Cluster4441_1clades	83	C440309_079	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59778.1	004737	Cluster4441_1clades	83	N231010_079	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67330.1	004738	Cluster4442_1clades	83	AD1_286	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08558.1	004738	Cluster4442_1clades	83	Alexandra_302	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58931.1	004738	Cluster4442_1clades	82	Y3_291	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28754.1	004738	Cluster4442_1clades	78	YOLOSWAG_283	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QBX06561.1	004739	Cluster4443_1clades	83	BcepSaruman_148	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06562.1	004739	Cluster4443_1clades	77	BcepSaruman_149	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74529.1	004739	Cluster4443_1clades	83	BcepSauron_149	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74530.1	004739	Cluster4443_1clades	77	BcepSauron_150	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ68466.1	004740	TM	80	CcrBL10_gp262	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88209.1	004740	TM	82	CcrColossus_gp339	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68886.1	004740	TM	82	CcrPW_gp347	Caulobacter phage CcrPW	GCA_003443275.1
AFU86752.1	004740	TM	80	CcrRogue_gp270	Caulobacter virus Rogue	GCA_000900555.1
AGH56998.1	004741	Cluster4445_1clades	82	CPXG_00195	Cyanophage P-RSM6	GCA_000906155.1
AAX44666.1	004741	Cluster4445_1clades	78	PSSM2_289	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12311.1	004741	Cluster4445_1clades	78	PRTG_00158	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93463.1	004741	Cluster4445_1clades	80	AVU42_gp124	Prochlorococcus phage P-TIM68	GCA_001503075.1
AYD80081.1	004742	Cluster4446_1clades	82	JA11_276	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66682.1	004742	Cluster4446_1clades	82	JA13_279	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67002.1	004742	Cluster4446_1clades	82	JA29_276	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67651.1	004742	Cluster4446_1clades	82	JA33_277	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81190.1	004743	Cluster4447_1clades	82	SEA_JUSTBECAUSE_21	Streptomyces phage JustBecause	GCA_003613775.1
QJD53592.1	004743	Cluster4447_1clades	82	SEA_KELA_21	Streptomyces phage Kela	GCA_012934305.1
QBZ71924.1	004743	Cluster4447_1clades	82	SEA_KRADAL_25	Streptomyces phage Kradal	GCA_004799925.1
AXH66186.1	004743	Cluster4447_1clades	82	SEA_SATIS_25	Streptomyces phage Satis	GCA_003366315.1
QAX96639.1	004744	Cluster4448_1clades	82	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96957.1	004744	Cluster4448_1clades	82	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96003.1	004744	Cluster4448_1clades	82	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96321.1	004744	Cluster4448_1clades	82	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96853.1	004745	Cluster4449_1clades	82	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97158.1	004745	Cluster4449_1clades	82	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96217.1	004745	Cluster4449_1clades	82	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96535.1	004745	Cluster4449_1clades	82	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AIR93595.1	004746	Cluster4450_1clades	58	AVU42_gp044	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76148.1	004746	Cluster4450_1clades	58	PBI_BELLAMY_103	Synechococcus phage Bellamy	GCA_002627525.1
QCW23006.1	004746	Cluster4450_1clades	58	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70086.1	004746	Cluster4450_1clades	82	SynMITS9220M01_073	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QBZ70850.1	004747	Cluster4451_1clades	81	pETSU_269	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89476.1	004747	Cluster4451_1clades	81	OBP_039	Pseudomonas phage OBP	GCA_000896635.1
ATA65559.1	004747	Cluster4451_1clades	81	2050HW_00224	Serratia phage 2050HW	GCA_002628125.1
QDB71324.1	004747	Cluster4451_1clades	81	CPT_Moabite_294	Serratia phage Moabite	GCA_006384735.1
QBZ70602.1	004748	Cluster4452_1clades	77	pETSU_021	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71918.1	004748	Cluster4452_1clades	76	N1M2_55	Klebsiella phage N1M2	GCA_010092605.1
AEV89516.1	004748	Cluster4452_1clades	76	OBP_079	Pseudomonas phage OBP	GCA_000896635.1
AEV89518.1	004748	Cluster4452_1clades	81	OBP_081	Pseudomonas phage OBP	GCA_000896635.1
QDH50608.1	004749	Cluster4453_1clades	78	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59531.1	004749	Cluster4453_1clades	81	S330809_070	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59293.1	004749	Cluster4453_1clades	81	C440309_070	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59769.1	004749	Cluster4453_1clades	81	N231010_070	Synechococcus phage S-CAM4	GCA_002922155.1
AYD81275.1	004750	Cluster4454_1clades	81	SEA_JUSTBECAUSE_106	Streptomyces phage JustBecause	GCA_003613775.1
QJD53678.1	004750	Cluster4454_1clades	81	SEA_KELA_107	Streptomyces phage Kela	GCA_012934305.1
QBZ72006.1	004750	Cluster4454_1clades	81	SEA_KRADAL_108	Streptomyces phage Kradal	GCA_004799925.1
AXH66269.1	004750	Cluster4454_1clades	81	SEA_SATIS_108	Streptomyces phage Satis	GCA_003366315.1
AYD81294.1	004751	Cluster4455_1clades	81	SEA_JUSTBECAUSE_125	Streptomyces phage JustBecause	GCA_003613775.1
QJD53697.1	004751	Cluster4455_1clades	81	SEA_KELA_126	Streptomyces phage Kela	GCA_012934305.1
QBZ72025.1	004751	Cluster4455_1clades	81	SEA_KRADAL_127	Streptomyces phage Kradal	GCA_004799925.1
AXH66288.1	004751	Cluster4455_1clades	81	SEA_SATIS_127	Streptomyces phage Satis	GCA_003366315.1
AXQ69053.1	004752	Cluster4456_1clades	80	CcrBL9_gp029c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69569.1	004752	Cluster4456_1clades	80	CcrBL9_gp545c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69613.1	004752	Cluster4456_1clades	81	CcrSC_gp031c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70113.1	004752	Cluster4456_1clades	81	CcrSC_gp531c	Caulobacter phage CcrSC	GCA_003443315.1
QAX96843.1	004753	Cluster4457_1clades	81	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97148.1	004753	Cluster4457_1clades	81	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96207.1	004753	Cluster4457_1clades	81	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96525.1	004753	Cluster4457_1clades	81	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96938.1	004754	Cluster4458_1clades	81	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97243.1	004754	Cluster4458_1clades	81	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96302.1	004754	Cluster4458_1clades	81	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96620.1	004754	Cluster4458_1clades	81	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71445.1	004755	SIG+TM	80	CR5_225	Cronobacter phage CR5	GCA_000910235.1
QBP07659.1	004755	SIG+TM	80	DERBICUS_233	Erwinia phage Derbicus	GCA_004521655.1
ANZ49083.1	004755	SIG+TM	80	EARLPHILLIPIV_234	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50430.1	004755	SIG+TM	80	PHOBOS_240	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGR47690.1	004756	Cluster4460_1clades	80	SmphiM12_058	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12950.1	004756	Cluster4460_1clades	80	PHIM19_43	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12590.1	004756	Cluster4460_1clades	80	PHIM7_42	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13324.1	004756	Cluster4460_1clades	80	PHIN3_59	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47860.1	004757	Cluster4461_1clades	80	SmphiM12_228	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13063.1	004757	Cluster4461_1clades	80	PHIM19_158	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12704.1	004757	Cluster4461_1clades	80	PHIM7_158	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13433.1	004757	Cluster4461_1clades	80	PHIN3_170	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47985.2	004758	Cluster4462_1clades	80	SmphiM12_353	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13171.1	004758	Cluster4462_1clades	80	PHIM19_266	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12811.1	004758	Cluster4462_1clades	80	PHIM7_266	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13534.1	004758	Cluster4462_1clades	80	PHIN3_271	Sinorhizobium phage phiN3	GCA_001501175.1
ANM44984.1	004759	Cluster4463_1clades	80	KTN4_226	Pseudomonas phage KTN4	GCA_002607225.1
ATN94730.1	004759	Cluster4463_1clades	80	SL2_153	Pseudomonas phage SL2	GCA_002956015.1
QJB22862.1	004759	Cluster4463_1clades	80	fnug_219	Pseudomonas phage fnug	GCA_012837215.1
AGC26342.1	004759	Cluster4463_1clades	73	PHIKZ185.1	Pseudomonas virus phiKZ	GCA_000842965.1
ASR76140.1	004760	Cluster4464_1clades	80	PBI_BELLAMY_95	Synechococcus phage Bellamy	GCA_002627525.1
AXQ70404.1	004760	Cluster4464_1clades	79	HOU04_gp005	Synechococcus phage S-T4	GCA_003443335.1
AXQ70606.1	004760	Cluster4464_1clades	79	HOU04_gp005	Synechococcus phage S-T4	GCA_003443335.1
QJT70082.1	004760	Cluster4464_1clades	60	SynMITS9220M01_069	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QMV28919.1	004761	Cluster4465_1clades	73	AP1_0212	Aeromonas phage AP1	GCA_014183365.1
ATI17552.1	004761	Cluster4465_1clades	80	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00445.1	004761	Cluster4465_1clades	73	HWB28_gp107	Aeromonas phage AS-zj	GCA_002627665.1
AFN39249.1	004761	Cluster4465_1clades	74	CC2_183	Aeromonas phage CC2	GCA_000903495.1
AYD80064.1	004762	Cluster4466_1clades	80	JA11_259	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66665.1	004762	Cluster4466_1clades	80	JA13_262	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66986.1	004762	Cluster4466_1clades	80	JA29_260	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67634.1	004762	Cluster4466_1clades	80	JA33_260	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AMO43097.1	004763	Cluster4467_1clades	54	R1080702_088	Cyanophage S-RIM32	GCA_001754165.1
ASR76142.1	004763	Cluster4467_1clades	75	PBI_BELLAMY_97	Synechococcus phage Bellamy	GCA_002627525.1
QCW22857.1	004763	Cluster4467_1clades	75	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70076.1	004763	Cluster4467_1clades	80	SynMITS9220M01_063	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ANM45064.1	004764	Cluster4468_1clades	79	KTN4_306	Pseudomonas phage KTN4	GCA_002607225.1
ATN94651.1	004764	Cluster4468_1clades	79	SL2_074	Pseudomonas phage SL2	GCA_002956015.1
QJB22939.1	004764	Cluster4468_1clades	79	fnug_296	Pseudomonas phage fnug	GCA_012837215.1
AAL83154.1	004764	Cluster4468_1clades	79	PHIKZ253	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45089.1	004765	Cluster4469_1clades	79	KTN4_331	Pseudomonas phage KTN4	GCA_002607225.1
ATN94626.1	004765	Cluster4469_1clades	79	SL2_049	Pseudomonas phage SL2	GCA_002956015.1
QJB22965.1	004765	Cluster4469_1clades	79	fnug_322	Pseudomonas phage fnug	GCA_012837215.1
AAL83175.1	004765	Cluster4469_1clades	79	PHIKZ274	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22658.1	004766	Nmad3	79	Ah1_00117	Aeromonas phage Ah1	GCA_002957415.1
ADQ52838.1	004766	Nmad3	79	PX29p119	Aeromonas phage PX29	GCA_000920195.1
ADM80098.1	004766	Nmad3	79	phiAS5_ORF0255	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17785.1	004766	Nmad3	79	Aeh1ORF122c	Aeromonas virus Aeh1	GCA_000843245.1
QMV29034.1	004767	SIG+TM	79	AP1_0327	Aeromonas phage AP1	GCA_014183365.1
ATI17258.1	004767	SIG+TM	79	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00333.1	004767	SIG+TM	79	HWB28_gp219	Aeromonas phage AS-zj	GCA_002627665.1
AFN39198.1	004767	SIG+TM	79	CC2_058	Aeromonas phage CC2	GCA_000903495.1
APU01733.1	004768	Cluster4472_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28736.1	004768	Cluster4472_1clades	79	AP1_0018	Aeromonas phage AP1	GCA_014183365.1
AFN39365.1	004768	Cluster4472_1clades	79	CC2_168	Aeromonas phage CC2	GCA_000903495.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ADQ53375.1	004768	Cluster4472_1clades	78	65p367	Aeromonas virus 65	GCA_000893255.1
AGR47645.1	004769	Cluster4473_1clades	79	SmphiM12_013	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12910.1	004769	Cluster4473_1clades	79	PHIM19_3	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12550.1	004769	Cluster4473_1clades	79	PHIM7_2	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13278.1	004769	Cluster4473_1clades	79	PHIN3_11	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47722.1	004770	Cluster4474_1clades	79	SmphiM12_090	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12977.1	004770	Cluster4474_1clades	79	PHIM19_70	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12617.1	004770	Cluster4474_1clades	79	PHIM7_69	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13349.1	004770	Cluster4474_1clades	79	PHIN3_85	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21464.1	004771	Cluster4475_1clades	77	GAP32_017	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44137.1	004771	Cluster4475_1clades	77	CBB_21	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43586.1	004771	Cluster4475_1clades	77	CBB_574	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88539.1	004771	Cluster4475_1clades	79	BF_0014	Serratia phage BF	GCA_002619745.1
QBP07361.1	004772	Cluster4476_1clades	79	REBECCA_256	Erwinia phage Rebecca	GCA_004521635.1
AUG86043.1	004772	Cluster4476_1clades	79	BOSOLAPHORUS_257	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86363.1	004772	Cluster4476_1clades	79	DESERTFOX_256	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AUG87009.1	004772	Cluster4476_1clades	79	MORTIMER_261	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AYD79833.1	004773	Cluster4477_1clades	79	JA11_028	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66432.1	004773	Cluster4477_1clades	79	JA13_029	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66756.1	004773	Cluster4477_1clades	79	JA29_030	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67402.1	004773	Cluster4477_1clades	79	JA33_028	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81355.1	004774	Cluster4478_1clades	77	SEA_JUSTBECAUSE_190	Streptomyces phage JustBecause	GCA_003613775.1
QJD53758.1	004774	Cluster4478_1clades	77	SEA_KELA_188	Streptomyces phage Kela	GCA_012934305.1
QBZ72085.1	004774	Cluster4478_1clades	79	SEA_KRADAL_189	Streptomyces phage Kradal	GCA_004799925.1
AXH66347.1	004774	Cluster4478_1clades	79	SEA_SATIS_188	Streptomyces phage Satis	GCA_003366315.1
AXQ69036.1	004775	Cluster4479_1clades	79	CcrBL9_gp012	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69552.1	004775	Cluster4479_1clades	79	CcrBL9_gp528	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69596.1	004775	Cluster4479_1clades	67	CcrSC_gp014	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70096.1	004775	Cluster4479_1clades	67	CcrSC_gp514	Caulobacter phage CcrSC	GCA_003443315.1
ANM45017.1	004776	Cluster4480_1clades	78	KTN4_259	Pseudomonas phage KTN4	GCA_002607225.1
ATN94697.1	004776	Cluster4480_1clades	78	SL2_120	Pseudomonas phage SL2	GCA_002956015.1
QJB22894.1	004776	Cluster4480_1clades	78	fnug_251	Pseudomonas phage fnug	GCA_012837215.1
AAL83116.1	004776	Cluster4480_1clades	78	PHIKZ215	Pseudomonas virus phiKZ	GCA_000842965.1
APU01521.1	004777	Cluster4481_1clades	61	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28775.1	004777	Cluster4481_1clades	64	AP1_0057	Aeromonas phage AP1	GCA_014183365.1
ASU00215.1	004777	Cluster4481_1clades	64	HWB28_gp337	Aeromonas phage AS-zj	GCA_002627665.1
AFN39281.1	004777	Cluster4481_1clades	78	CC2_360	Aeromonas phage CC2	GCA_000903495.1
AGR47887.1	004778	SIG+WYL	78	SmphiM12_255	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13089.1	004778	SIG+WYL	78	PHIM19_184	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12729.1	004778	SIG+WYL	78	PHIM7_184	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13458.1	004778	SIG+WYL	78	PHIN3_195	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47990.1	004779	Cluster4483_1clades	74	SmphiM12_358	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13177.1	004779	Cluster4483_1clades	74	PHIM19_272	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12817.1	004779	Cluster4483_1clades	78	PHIM7_272	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13540.1	004779	Cluster4483_1clades	74	PHIN3_277	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79993.1	004780	Cluster4484_1clades	78	JA11_188	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66591.1	004780	Cluster4484_1clades	78	JA13_188	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66916.1	004780	Cluster4484_1clades	77	JA29_190	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67562.1	004780	Cluster4484_1clades	78	JA33_188	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81347.1	004781	TM+TM	78	SEA_JUSTBECAUSE_182	Streptomyces phage JustBecause	GCA_003613775.1
QJD53750.1	004781	TM+TM	78	SEA_KELA_180	Streptomyces phage Kela	GCA_012934305.1
QBZ72076.1	004781	TM+TM	78	SEA_KRADAL_180	Streptomyces phage Kradal	GCA_004799925.1
AXH66339.1	004781	TM+TM	78	SEA_SATIS_180	Streptomyces phage Satis	GCA_003366315.1
ANM45075.1	004782	Cluster4486_1clades	77	KTN4_317	Pseudomonas phage KTN4	GCA_002607225.1
ATN94640.1	004782	Cluster4486_1clades	77	SL2_063	Pseudomonas phage SL2	GCA_002956015.1
QJB22950.1	004782	Cluster4486_1clades	77	fnug_307	Pseudomonas phage fnug	GCA_012837215.1
AAL83163.1	004782	Cluster4486_1clades	77	PHIKZ262	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22607.1	004783	BTD	76	Ah1_00066	Aeromonas phage Ah1	GCA_002957415.1
ADQ52790.1	004783	BTD	77	PX29p071	Aeromonas phage PX29	GCA_000920195.1
ADM80045.1	004783	BTD	72	phiAS5_ORF0202	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17733.1	004783	BTD	77	Aeh1ORF073c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47905.1	004784	Cluster4488_1clades	77	SmphiM12_273	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13110.1	004784	Cluster4488_1clades	77	PHIM19_205	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12750.1	004784	Cluster4488_1clades	77	PHIM7_205	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13480.1	004784	Cluster4488_1clades	77	PHIN3_217	Sinorhizobium phage phiN3	GCA_001501175.1
AMM43991.1	004785	Cluster4489_1clades	75	CBB_428	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88948.1	004785	Cluster4489_1clades	77	BF_0423	Serratia phage BF	GCA_002619745.1
SOK59235.1	004785	Cluster4489_1clades	77	g427	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58701.1	004785	Cluster4489_1clades	77	g424	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD81279.1	004786	Cluster4490_1clades	72	SEA_JUSTBECAUSE_110	Streptomyces phage JustBecause	GCA_003613775.1
QJD53682.1	004786	Cluster4490_1clades	72	SEA_KELA_111	Streptomyces phage Kela	GCA_012934305.1
QBZ72009.1	004786	Cluster4490_1clades	77	SEA_KRADAL_111	Streptomyces phage Kradal	GCA_004799925.1
AXH66272.1	004786	Cluster4490_1clades	77	SEA_SATIS_111	Streptomyces phage Satis	GCA_003366315.1
AFC21563.1	004787	SIG+TM	70	GAP32_115	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43681.1	004787	SIG+TM	73	CBB_116	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK58911.1	004787	SIG+TM	77	g103	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58376.1	004787	SIG+TM	77	g099	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANM45068.1	004788	Cluster4492_1clades	76	KTN4_310	Pseudomonas phage KTN4	GCA_002607225.1
ATN94647.1	004788	Cluster4492_1clades	76	SL2_070	Pseudomonas phage SL2	GCA_002956015.1
QJB22943.1	004788	Cluster4492_1clades	76	fnug_300	Pseudomonas phage fnug	GCA_012837215.1
AAL83157.1	004788	Cluster4492_1clades	76	PHIKZ256	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22662.1	004789	Cluster4493_1clades	75	Ah1_00121	Aeromonas phage Ah1	GCA_002957415.1
ADQ52843.1	004789	Cluster4493_1clades	75	PX29p124	Aeromonas phage PX29	GCA_000920195.1
ADM80102.1	004789	Cluster4493_1clades	76	phiAS5_ORF0259	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17790.1	004789	Cluster4493_1clades	75	Aeh1gORF151c	Aeromonas virus Aeh1	GCA_000843245.1
ABY63180.1	004790	Cluster4494_1clades	72	201phi2-1p354	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76826.1	004790	Cluster4494_1clades	71	PHABIO_195	Pseudomonas phage Phabio	GCA_002624965.1
ARV76827.1	004790	Cluster4494_1clades	66	PHABIO_196	Pseudomonas phage Phabio	GCA_002624965.1
AEH03705.1	004790	Cluster4494_1clades	76	282	Pseudomonas phage PhiPA3	GCA_001502095.1
ARB13809.1	004791	Cluster4495_1clades	76	Ccr10_gp279	Caulobacter phage Ccr10	GCA_002619445.1
ARB14154.1	004791	Cluster4495_1clades	76	Ccr2_gp278	Caulobacter phage Ccr2	GCA_002619465.1
ARB14848.1	004791	Cluster4495_1clades	76	Ccr29_gp292	Caulobacter phage Ccr29	GCA_002619485.1
AFU86759.1	004791	Cluster4495_1clades	76	CcrRogue_gp277	Caulobacter virus Rogue	GCA_000900555.1
AGR47865.1	004792	Cluster4496_1clades	76	SmphiM12_233	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13067.1	004792	Cluster4496_1clades	76	PHIM19_162	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12708.1	004792	Cluster4496_1clades	76	PHIM7_162	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13437.1	004792	Cluster4496_1clades	76	PHIN3_174	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48083.1	004793	Cluster4497_1clades	67	SmphiM12_451	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13255.1	004793	Cluster4497_1clades	67	PHIM19_350	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12895.1	004793	Cluster4497_1clades	67	PHIM7_350	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13618.1	004793	Cluster4497_1clades	76	PHIN3_355	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81456.1	004794	Cluster4498_1clades	68	SEA_JUSTBECAUSE_301	Streptomyces phage JustBecause	GCA_003613775.1
QJD53861.1	004794	Cluster4498_1clades	69	SEA_KELA_301	Streptomyces phage Kela	GCA_012934305.1
QBZ72191.1	004794	Cluster4498_1clades	76	SEA_KRADAL_305	Streptomyces phage Kradal	GCA_004799925.1
AXH66454.1	004794	Cluster4498_1clades	76	SEA_SATIS_305	Streptomyces phage Satis	GCA_003366315.1
AXQ69174.1	004795	Cluster4499_1clades	66	CcrBL9_gp150	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87968.1	004795	Cluster4499_1clades	73	CcrColossus_gp098	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68645.1	004795	Cluster4499_1clades	73	CcrPW_gp106	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69727.1	004795	Cluster4499_1clades	76	CcrSC_gp145	Caulobacter phage CcrSC	GCA_003443315.1
AEV89517.1	004796	Cluster4500_1clades	61	OBP_080	Pseudomonas phage OBP	GCA_000896635.1
BAW19104.1	004796	Cluster4500_1clades	76	FDH28_gp130	Ralstonia phage RP12	GCA_002617345.1
BAW19390.1	004796	Cluster4500_1clades	76	-	Ralstonia phage RP31	GCA_002617365.1
ASV44429.1	004796	Cluster4500_1clades	56	PBI_SCTP2_414	Salicola phage SCTP-2	GCA_002625545.1
QAX96931.1	004797	Cluster4501_1clades	76	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97236.1	004797	Cluster4501_1clades	76	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96295.1	004797	Cluster4501_1clades	76	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96613.1	004797	Cluster4501_1clades	76	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QMV28942.1	004798	Cluster4502_1clades	75	AP1_0235	Aeromonas phage AP1	GCA_014183365.1
ASU00255.1	004798	Cluster4502_1clades	75	HWB28_gp297	Aeromonas phage AS-zj	GCA_002627665.1
QAX97783.1	004798	Cluster4502_1clades	75	ASswx1_138	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39290.1	004798	Cluster4502_1clades	75	CC2_400	Aeromonas phage CC2	GCA_000903495.1
AGR47646.1	004799	Cluster4503_1clades	75	SmphiM12_014	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12912.1	004799	Cluster4503_1clades	75	PHIM19_5	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12552.1	004799	Cluster4503_1clades	75	PHIM7_4	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13282.1	004799	Cluster4503_1clades	75	PHIN3_15	Sinorhizobium phage phiN3	GCA_001501175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGR47805.1	004800	Cluster4504_1clades	75	SmphiM12_173	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13021.1	004800	Cluster4504_1clades	75	PHIM19_115	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12661.1	004800	Cluster4504_1clades	75	PHIM7_114	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13393.1	004800	Cluster4504_1clades	75	PHIN3_128	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81297.1	004801	Cluster4506_1clades	75	SEA_JUSTBECAUSE_128	Streptomyces phage JustBecause	GCA_003613775.1
QJD53700.1	004801	Cluster4506_1clades	75	SEA_KELA_129	Streptomyces phage Kela	GCA_012934305.1
QBZ72028.1	004801	Cluster4506_1clades	74	SEA_KRADAL_130	Streptomyces phage Kradal	GCA_004799925.1
AXH66291.1	004801	Cluster4506_1clades	74	SEA_SATIS_130	Streptomyces phage Satis	GCA_003366315.1
AUE22820.1	004802	Cluster4507_1clades	74	Ah1_00302	Aeromonas phage Ah1	GCA_002957415.1
QAX98535.1	004802	Cluster4507_1clades	74	ASfcp2_199	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52998.1	004802	Cluster4507_1clades	74	PX29p279	Aeromonas phage PX29	GCA_000920195.1
AAQ17950.1	004802	Cluster4507_1clades	74	Aeh1hmmORF06c	Aeromonas virus Aeh1	GCA_000843245.1
AFO71338.1	004803	Cluster4508_1clades	74	CR5_118	Cronobacter phage CR5	GCA_000910235.1
QBP07546.1	004803	Cluster4508_1clades	74	DERBICUS_120	Erwinia phage Derbicus	GCA_004521655.1
ANZ48969.1	004803	Cluster4508_1clades	74	EARLPHILLIPIV_120	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50310.1	004803	Cluster4508_1clades	74	PHOBOS_120	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ49919.1	004804	Cluster4509_1clades	73	MACHINA_281	Erwinia phage Machina	GCA_002758035.1
ANZ48850.1	004804	Cluster4509_1clades	74	CHRISDB_288	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49362.1	004804	Cluster4509_1clades	73	HUXLEY_280	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50190.1	004804	Cluster4509_1clades	73	PARSHIK_281	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AYD81184.1	004805	Cluster4510_1clades	74	SEA_JUSTBECAUSE_15	Streptomyces phage JustBecause	GCA_003613775.1
QJD53586.1	004805	Cluster4510_1clades	74	SEA_KELA_15	Streptomyces phage Kela	GCA_012934305.1
QBZ71917.1	004805	Cluster4510_1clades	74	SEA_KRADAL_18	Streptomyces phage Kradal	GCA_004799925.1
AXH66179.1	004805	Cluster4510_1clades	74	SEA_SATIS_18	Streptomyces phage Satis	GCA_003366315.1
AUE22646.1	004806	SIG+TM	73	Ah1_00105	Aeromonas phage Ah1	GCA_002957415.1
QAX98373.1	004806	SIG+TM	73	ASfcp2_27	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52826.1	004806	SIG+TM	73	PX29p107	Aeromonas phage PX29	GCA_000920195.1
AAQ17770.1	004806	SIG+TM	73	Aeh1ORF109c	Aeromonas virus Aeh1	GCA_000843245.1
QAX98430.1	004807	Cluster4512_1clades	73	ASfcp2_86	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52885.1	004807	Cluster4512_1clades	73	PX29p166	Aeromonas phage PX29	GCA_000920195.1
ADM80149.1	004807	Cluster4512_1clades	73	phiAS5_ORF0306	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17837.1	004807	Cluster4512_1clades	73	Aeh1ORF171c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47724.1	004808	Cluster4513_1clades	73	SmphiM12_092	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12979.1	004808	Cluster4513_1clades	73	PHIM19_72	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12619.1	004808	Cluster4513_1clades	73	PHIM7_71	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13351.1	004808	Cluster4513_1clades	73	PHIN3_87	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47730.1	004809	Cluster4514_1clades	73	SmphiM12_098	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12984.1	004809	Cluster4514_1clades	73	PHIM19_77	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12624.1	004809	Cluster4514_1clades	73	PHIM7_76	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13356.1	004809	Cluster4514_1clades	73	PHIN3_92	Sinorhizobium phage phiN3	GCA_001501175.1
AYD79918.1	004810	Cluster4515_1clades	73	JA11_113	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66517.1	004810	Cluster4515_1clades	73	JA13_114	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66842.1	004810	Cluster4515_1clades	73	JA29_116	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67487.1	004810	Cluster4515_1clades	73	JA33_113	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD79853.1	004811	SIG+TM	70	JA11_048	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66453.1	004811	SIG+TM	70	JA13_050	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66777.1	004811	SIG+TM	73	JA29_051	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67422.1	004811	SIG+TM	70	JA33_048	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81255.1	004812	Cluster4517_1clades	73	SEA_JUSTBECAUSE_86	Streptomyces phage JustBecause	GCA_003613775.1
QJD53658.1	004812	Cluster4517_1clades	73	SEA_KELA_87	Streptomyces phage Kela	GCA_012934305.1
QBZ71987.1	004812	Cluster4517_1clades	72	SEA_KRADAL_89	Streptomyces phage Kradal	GCA_004799925.1
AXH66250.1	004812	Cluster4517_1clades	72	SEA_SATIS_89	Streptomyces phage Satis	GCA_003366315.1
QAX96889.1	004813	Cluster4518_1clades	73	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97194.1	004813	Cluster4518_1clades	73	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96253.1	004813	Cluster4518_1clades	73	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96571.1	004813	Cluster4518_1clades	73	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AXQ68236.1	004814	HTH	72	CcrBL10_gp032	Caulobacter phage CcrBL10	GCA_003443255.1
AFU88294.1	004814	HTH	72	CcrColossus_gp424	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68968.1	004814	HTH	72	CcrPW_gp429c	Caulobacter phage CcrPW	GCA_003443275.1
AFU86518.1	004814	HTH	72	CcrRogue_gp036	Caulobacter virus Rogue	GCA_000900555.1
AGR47858.1	004815	Cluster4520_1clades	72	SmphiM12_226	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13061.1	004815	Cluster4520_1clades	72	PHIM19_156	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12702.1	004815	Cluster4520_1clades	72	PHIM7_156	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13431.1	004815	Cluster4520_1clades	72	PHIN3_168	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47870.1	004816	Cluster4521_1clades	72	SmphiM12_238	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13072.1	004816	Cluster4521_1clades	72	PHIM19_167	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12712.1	004816	Cluster4521_1clades	72	PHIM7_167	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13442.1	004816	Cluster4521_1clades	72	PHIN3_179	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48077.2	004817	Cluster4522_1clades	72	SmphiM12_445	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13252.1	004817	Cluster4522_1clades	72	PHIM19_347	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12892.1	004817	Cluster4522_1clades	72	PHIM7_347	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13615.2	004817	Cluster4522_1clades	72	PHIN3_352	Sinorhizobium phage phiN3	GCA_001501175.1
QBX06825.1	004818	SIG+TM	64	BcepSaruman_412	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74794.1	004818	SIG+TM	64	BcepSauron_414	Burkholderia phage BcepSauron	GCA_005394215.1
AIA65027.1	004818	SIG+TM	72	S13_230	Cronobacter phage S13	GCA_001503575.1
QHJ78920.1	004818	SIG+TM	62	-	Myoviridae sp.	GCA_012593985.1
AYD80046.1	004819	Cluster4524_1clades	72	JA11_241	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66645.1	004819	Cluster4524_1clades	72	JA13_242	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66969.1	004819	Cluster4524_1clades	72	JA29_243	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67616.1	004819	Cluster4524_1clades	72	JA33_242	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81341.1	004820	Cluster4525_1clades	71	SEA_JUSTBECAUSE_176	Streptomyces phage JustBecause	GCA_003613775.1
QJD53744.1	004820	Cluster4525_1clades	71	SEA_KELA_174	Streptomyces phage Kela	GCA_012934305.1
QBZ72070.1	004820	Cluster4525_1clades	72	SEA_KRADAL_174	Streptomyces phage Kradal	GCA_004799925.1
AXH66333.1	004820	Cluster4525_1clades	72	SEA_SATIS_174	Streptomyces phage Satis	GCA_003366315.1
ANM45020.1	004821	Cluster4526_1clades	71	KTN4_262	Pseudomonas phage KTN4	GCA_002607225.1
ATN94694.1	004821	Cluster4526_1clades	71	SL2_117	Pseudomonas phage SL2	GCA_002956015.1
QJB22897.1	004821	Cluster4526_1clades	71	fnug_254	Pseudomonas phage fnug	GCA_012837215.1
AAL83119.1	004821	Cluster4526_1clades	71	PHIKZ218	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47655.1	004822	Cluster4527_1clades	71	SmphiM12_023	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12921.1	004822	Cluster4527_1clades	71	PHIM19_14	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12561.1	004822	Cluster4527_1clades	71	PHIM7_13	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13289.1	004822	Cluster4527_1clades	71	PHIN3_24	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47693.1	004823	Cluster4528_1clades	71	SmphiM12_061	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12953.1	004823	Cluster4528_1clades	71	PHIM19_46	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12593.1	004823	Cluster4528_1clades	71	PHIM7_45	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13326.1	004823	Cluster4528_1clades	71	PHIN3_61	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47988.1	004824	Cluster4529_1clades	71	SmphiM12_356	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13175.1	004824	Cluster4529_1clades	71	PHIM19_270	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12815.1	004824	Cluster4529_1clades	71	PHIM7_270	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13538.1	004824	Cluster4529_1clades	71	PHIN3_275	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48006.1	004825	Cluster4530_1clades	71	SmphiM12_374	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13192.1	004825	Cluster4530_1clades	71	PHIM19_287	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12832.1	004825	Cluster4530_1clades	71	PHIM7_287	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13554.1	004825	Cluster4530_1clades	71	PHIN3_291	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48073.1	004826	Cluster4531_1clades	71	SmphiM12_441	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13248.1	004826	Cluster4531_1clades	71	PHIM19_343	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12888.1	004826	Cluster4531_1clades	71	PHIM7_343	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13611.1	004826	Cluster4531_1clades	71	PHIN3_348	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47993.1	004827	Cluster4532_1clades	61	SmphiM12_361	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13180.2	004827	Cluster4532_1clades	71	PHIM19_275	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12819.1	004827	Cluster4532_1clades	71	PHIM7_274	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13542.1	004827	Cluster4532_1clades	71	PHIN3_279	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21948.1	004828	Cluster4533_1clades	49	GAP32_489	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44075.1	004828	Cluster4533_1clades	49	CBB_512	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89031.1	004828	Cluster4533_1clades	71	BF_0506	Serratia phage BF	GCA_002619745.1
SOK59310.1	004828	Cluster4533_1clades	49	g502	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AYD81445.1	004829	Cluster4534_1clades	69	SEA_JUSTBECAUSE_290	Streptomyces phage JustBecause	GCA_003613775.1
QJD53849.1	004829	Cluster4534_1clades	69	SEA_KELA_289	Streptomyces phage Kela	GCA_012934305.1
QBZ72180.1	004829	Cluster4534_1clades	71	SEA_KRADAL_294	Streptomyces phage Kradal	GCA_004799925.1
AXH66443.1	004829	Cluster4534_1clades	71	SEA_SATIS_294	Streptomyces phage Satis	GCA_003366315.1
AXQ69058.1	004830	Cluster4535_1clades	71	CcrBL9_gp034	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69574.1	004830	Cluster4535_1clades	71	CcrBL9_gp550	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69617.1	004830	Cluster4535_1clades	71	CcrSC_gp035	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70117.1	004830	Cluster4535_1clades	71	CcrSC_gp535	Caulobacter phage CcrSC	GCA_003443315.1
ANM45084.1	004831	Cluster4536_1clades	70	KTN4_326	Pseudomonas phage KTN4	GCA_002607225.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATN94631.1	004831	Cluster4536_1clades	70	SL2_054	Pseudomonas phage SL2	GCA_002956015.1
QJB22960.1	004831	Cluster4536_1clades	70	fnug_317	Pseudomonas phage fnug	GCA_012837215.1
AAL83170.1	004831	Cluster4536_1clades	70	PHIKZ269	Pseudomonas virus phiKZ	GCA_000842965.1
AUE22764.1	004832	Cluster4537_1clades	70	Ah1_00246	Aeromonas phage Ah1	GCA_002957415.1
QAX98479.1	004832	Cluster4537_1clades	68	ASfcp2_141	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52941.1	004832	Cluster4537_1clades	68	PX29p222	Aeromonas phage PX29	GCA_000920195.1
AAQ17887.1	004832	Cluster4537_1clades	70	Aeh1ORF226w	Aeromonas virus Aeh1	GCA_000843245.1
QBX32402.1	004833	Cluster4538_1clades	53	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03667.1	004833	Cluster4538_1clades	70	244	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02803.1	004833	Cluster4538_1clades	55	PSA21_277	Pseudomonas phage Psa21	GCA_004340405.1
QEM41972.1	004833	Cluster4538_1clades	53	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AXQ68442.1	004834	Cluster4539_1clades	70	CcrBL10_gp238	Caulobacter phage CcrBL10	GCA_003443255.1
AFU87772.1	004834	Cluster4539_1clades	70	CcrKarma_gp255	Caulobacter virus Karma	GCA_000901575.1
AFU87419.1	004834	Cluster4539_1clades	70	CcrMagneto_gp249	Caulobacter virus Magneto	GCA_000903095.1
AFU86728.1	004834	Cluster4539_1clades	70	CcrRogue_gp246	Caulobacter virus Rogue	GCA_000900555.1
AGR47654.1	004835	Cluster4540_1clades	70	SmphiM12_022	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12920.1	004835	Cluster4540_1clades	70	PHIM19_13	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12560.1	004835	Cluster4540_1clades	70	PHIM7_12	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13288.1	004835	Cluster4540_1clades	70	PHIN3_23	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47852.1	004836	Cluster4541_1clades	70	SmphiM12_220	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13057.1	004836	Cluster4541_1clades	70	PHIM19_152	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12698.1	004836	Cluster4541_1clades	70	PHIM7_152	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13427.1	004836	Cluster4541_1clades	70	PHIN3_164	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47885.1	004837	TM	70	SmphiM12_253	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13087.1	004837	TM	70	PHIM19_182	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12727.1	004837	TM	70	PHIM7_182	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13456.1	004837	TM	70	PHIN3_193	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47940.1	004838	Cluster4543_1clades	70	SmphiM12_308	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13136.1	004838	Cluster4543_1clades	70	PHIM19_231	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12775.1	004838	Cluster4543_1clades	70	PHIM7_230	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13504.1	004838	Cluster4543_1clades	70	PHIN3_241	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48072.1	004839	Cluster4544_1clades	70	SmphiM12_440	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13247.1	004839	Cluster4544_1clades	70	PHIM19_342	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12887.1	004839	Cluster4544_1clades	70	PHIM7_342	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13610.1	004839	Cluster4544_1clades	70	PHIN3_347	Sinorhizobium phage phiN3	GCA_001501175.1
APU01667.1	004840	Cluster4545_1clades	70	-	Aeromonas phage 65.2	GCA_002618145.1
QMV28834.1	004840	Cluster4545_1clades	69	AP1_0127	Aeromonas phage AP1	GCA_014183365.1
QAX97707.1	004840	Cluster4545_1clades	69	ASswx1_61	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01430.1	004840	Cluster4545_1clades	69	ASwh1_371	Aeromonas phage Aswh_1	GCA_004146945.1
AYD81270.1	004841	TM	68	SEA_JUSTBECAUSE_101	Streptomyces phage JustBecause	GCA_003613775.1
QJD53673.1	004841	TM	68	SEA_KELA_102	Streptomyces phage Kela	GCA_012934305.1
QBZ72001.1	004841	TM	70	SEA_KRADAL_103	Streptomyces phage Kradal	GCA_004799925.1
AXH66264.1	004841	TM	70	SEA_SATIS_103	Streptomyces phage Satis	GCA_003366315.1
AXQ69042.1	004842	Cluster4547_1clades	70	CcrBL9_gp018	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69558.1	004842	Cluster4547_1clades	70	CcrBL9_gp534	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69602.1	004842	Cluster4547_1clades	70	CcrSC_gp020	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70102.1	004842	Cluster4547_1clades	70	CcrSC_gp520	Caulobacter phage CcrSC	GCA_003443315.1
QAX96850.1	004843	Cluster4548_1clades	70	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97155.1	004843	Cluster4548_1clades	70	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96214.1	004843	Cluster4548_1clades	70	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96532.1	004843	Cluster4548_1clades	70	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAY00787.1	004844	Cluster4549_1clades	70	Ecwhy1_514	Escherichia phage Ecwhy_1	GCA_004146585.1
QBO61561.1	004844	Cluster4549_1clades	69	G17_00065	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14170.1	004844	Cluster4549_1clades	69	vBEcoMphAPEC6_gp547c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80133.1	004844	Cluster4549_1clades	69	PSLUR01_00156	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AUE22817.1	004845	Cluster4550_1clades	64	Ah1_00299	Aeromonas phage Ah1	GCA_002957415.1
QAX98532.1	004845	Cluster4550_1clades	69	ASfcp2_196	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52995.1	004845	Cluster4550_1clades	69	PX29p276	Aeromonas phage PX29	GCA_000920195.1
AAQ17946.1	004845	Cluster4550_1clades	64	Aeh1gORF330c	Aeromonas virus Aeh1	GCA_000843245.1
AFO71351.1	004846	Cluster4551_1clades	69	CR5_131	Cronobacter phage CR5	GCA_000910235.1
QBP07559.1	004846	Cluster4551_1clades	69	DERBICUS_133	Erwinia phage Derbicus	GCA_004521655.1
ANZ48982.1	004846	Cluster4551_1clades	69	EARLPHILLIPIV_133	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50324.1	004846	Cluster4551_1clades	69	PHOBOS_134	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AGR47816.1	004847	Cluster4552_1clades	69	SmphiM12_184	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13031.1	004847	Cluster4552_1clades	69	PHIM19_126	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12671.1	004847	Cluster4552_1clades	69	PHIM7_125	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13402.1	004847	Cluster4552_1clades	69	PHIN3_139	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48001.1	004848	SLATT	69	SmphiM12_369	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13187.1	004848	SLATT	69	PHIM19_282	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12827.1	004848	SLATT	69	PHIM7_282	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13549.1	004848	SLATT	69	PHIN3_286	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48056.2	004849	Cluster4554_1clades	69	SmphiM12_424	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13235.1	004849	Cluster4554_1clades	69	PHIM19_330	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12875.1	004849	Cluster4554_1clades	69	PHIM7_330	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13598.1	004849	Cluster4554_1clades	69	PHIN3_335	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48060.1	004850	Cluster4555_1clades	69	SmphiM12_428	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13238.1	004850	Cluster4555_1clades	69	PHIM19_333	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12878.1	004850	Cluster4555_1clades	69	PHIM7_333	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13601.1	004850	Cluster4555_1clades	69	PHIN3_338	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21534.1	004851	Cluster4556_1clades	67	GAP32_086	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88604.1	004851	Cluster4556_1clades	69	BF_0079	Serratia phage BF	GCA_002619745.1
SOK58881.1	004851	Cluster4556_1clades	64	g073	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58344.1	004851	Cluster4556_1clades	64	g067	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXQ69041.1	004852	Cluster4558_1clades	69	CcrBL9_gp017	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69557.1	004852	Cluster4558_1clades	69	CcrBL9_gp533	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69601.1	004852	Cluster4558_1clades	69	CcrSC_gp019	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70101.1	004852	Cluster4558_1clades	69	CcrSC_gp519	Caulobacter phage CcrSC	GCA_003443315.1
QAX96862.1	004853	Cluster4559_1clades	69	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97167.1	004853	Cluster4559_1clades	69	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96226.1	004853	Cluster4559_1clades	69	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96544.1	004853	Cluster4559_1clades	69	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ARB15189.1	004854	Cluster4560_1clades	68	Ccr32_gp271	Caulobacter phage Ccr32	GCA_002619505.1
ARB15523.1	004854	Cluster4560_1clades	68	Ccr34_gp281	Caulobacter phage Ccr34	GCA_002619525.1
AFU87455.1	004854	Cluster4560_1clades	68	CcrMagneto_gp285	Caulobacter virus Magneto	GCA_000903095.1
AFU87108.1	004854	Cluster4560_1clades	68	CbK_gp276	Caulobacter virus phiCbK	GCA_000900535.1
ANM44964.1	004855	Cluster4561_1clades	68	KTN4_206	Pseudomonas phage KTN4	GCA_002607225.1
ATN94750.1	004855	Cluster4561_1clades	68	SL2_173	Pseudomonas phage SL2	GCA_002956015.1
QJB22842.1	004855	Cluster4561_1clades	68	fnug_199	Pseudomonas phage fnug	GCA_012837215.1
AGC26340.1	004855	Cluster4561_1clades	68	PHIKZ166.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47672.1	004856	Cluster4562_1clades	68	SmphiM12_040	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12935.1	004856	Cluster4562_1clades	68	PHIM19_28	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12575.1	004856	Cluster4562_1clades	68	PHIM7_27	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13307.1	004856	Cluster4562_1clades	68	PHIN3_42	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48000.2	004857	Cluster4563_1clades	68	SmphiM12_368	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13186.1	004857	Cluster4563_1clades	68	PHIM19_281	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12826.1	004857	Cluster4563_1clades	68	PHIM7_281	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13548.2	004857	Cluster4563_1clades	68	PHIN3_285	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48008.1	004858	Cluster4564_1clades	68	SmphiM12_377	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13195.1	004858	Cluster4564_1clades	68	PHIM19_290	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12835.1	004858	Cluster4564_1clades	68	PHIM7_290	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13556.1	004858	Cluster4564_1clades	68	PHIN3_293	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80095.1	004859	Cluster4565_1clades	68	JA11_290	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66696.1	004859	Cluster4565_1clades	68	JA13_293	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67015.1	004859	Cluster4565_1clades	68	JA29_289	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67665.1	004859	Cluster4565_1clades	68	JA33_291	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81330.1	004860	Cluster4566_1clades	64	SEA_JUSTBECAUSE_165	Streptomyces phage JustBecause	GCA_003613775.1
QJD53733.1	004860	Cluster4566_1clades	64	SEA_KELA_163	Streptomyces phage Kela	GCA_012934305.1
QBZ72059.1	004860	Cluster4566_1clades	68	SEA_KRADAL_163	Streptomyces phage Kradal	GCA_004799925.1
AXH66322.1	004860	Cluster4566_1clades	68	SEA_SATIS_163	Streptomyces phage Satis	GCA_003366315.1
AYD81367.1	004861	S1COLD	68	SEA_JUSTBECAUSE_212	Streptomyces phage JustBecause	GCA_003613775.1
QJD53770.1	004861	S1COLD	68	SEA_KELA_210	Streptomyces phage Kela	GCA_012934305.1
QBZ72099.1	004861	S1COLD	68	SEA_KRADAL_213	Streptomyces phage Kradal	GCA_004799925.1
AXH66360.1	004861	S1COLD	68	SEA_SATIS_211	Streptomyces phage Satis	GCA_003366315.1
QAX96723.1	004862	Cluster4568_1clades	68	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97042.1	004862	Cluster4568_1clades	68	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAX96088.1	004862	Cluster4568_1clades	68	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96406.1	004862	Cluster4568_1clades	68	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QAX96869.1	004863	SIG+TM	68	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97174.1	004863	SIG+TM	68	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96233.1	004863	SIG+TM	68	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96551.1	004863	SIG+TM	68	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44804.1	004864	Cluster4570_1clades	67	KTN4_046	Pseudomonas phage KTN4	GCA_002607225.1
ATN94907.1	004864	Cluster4570_1clades	67	SL2_330	Pseudomonas phage SL2	GCA_002956015.1
QJB22683.1	004864	Cluster4570_1clades	67	fnug_40	Pseudomonas phage fnug	GCA_012837215.1
AGC26309.1	004864	Cluster4570_1clades	67	PHIKZ033.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47720.1	004865	Cluster4571_1clades	67	SmphiM12_088	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12975.1	004865	Cluster4571_1clades	67	PHIM19_68	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12615.1	004865	Cluster4571_1clades	67	PHIM7_67	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13347.1	004865	Cluster4571_1clades	67	PHIN3_83	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47760.1	004866	Cluster4572_1clades	67	SmphiM12_128	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12996.1	004866	Cluster4572_1clades	67	PHIM19_90	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12636.1	004866	Cluster4572_1clades	67	PHIM7_89	Sinorhizobium phage phiM7	GCA_002622405.1
AKZ65596.1	004866	Cluster4572_1clades	67	PHIN3_104	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81254.1	004867	Cluster4573_1clades	67	SEA_JUSTBECAUSE_85	Streptomyces phage JustBecause	GCA_003613775.1
QJD53657.1	004867	Cluster4573_1clades	67	SEA_KELA_86	Streptomyces phage Kela	GCA_012934305.1
QBZ71986.1	004867	Cluster4573_1clades	67	SEA_KRADAL_88	Streptomyces phage Kradal	GCA_004799925.1
AXH66249.1	004867	Cluster4573_1clades	67	SEA_SATIS_88	Streptomyces phage Satis	GCA_003366315.1
AYD81396.1	004868	Cluster4574_1clades	66	SEA_JUSTBECAUSE_241	Streptomyces phage JustBecause	GCA_003613775.1
QJD53800.1	004868	Cluster4574_1clades	66	SEA_KELA_240	Streptomyces phage Kela	GCA_012934305.1
QBZ72126.1	004868	Cluster4574_1clades	67	SEA_KRADAL_240	Streptomyces phage Kradal	GCA_004799925.1
AXH66388.1	004868	Cluster4574_1clades	67	SEA_SATIS_239	Streptomyces phage Satis	GCA_003366315.1
AYD81276.1	004869	Cluster4575_1clades	67	SEA_JUSTBECAUSE_107	Streptomyces phage JustBecause	GCA_003613775.1
QJD53679.1	004869	Cluster4575_1clades	67	SEA_KELA_108	Streptomyces phage Kela	GCA_012934305.1
QBZ72007.1	004869	Cluster4575_1clades	64	SEA_KRADAL_109	Streptomyces phage Kradal	GCA_004799925.1
AXH66270.1	004869	Cluster4575_1clades	64	SEA_SATIS_109	Streptomyces phage Satis	GCA_003366315.1
ASR76160.1	004870	Cluster4576_1clades	59	PBI_BELLAMY_115	Synechococcus phage Bellamy	GCA_002627525.1
QCW23002.1	004870	Cluster4576_1clades	67	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50654.1	004870	Cluster4576_1clades	67	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70100.1	004870	Cluster4576_1clades	60	SynMITS9220M01_087	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFC21565.1	004871	SIG+TM	66	GAP32_117	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88634.1	004871	SIG+TM	66	BF_0109	Serratia phage BF	GCA_002619745.1
SOK58913.1	004871	SIG+TM	66	g105	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58378.1	004871	SIG+TM	66	g101	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANM45041.1	004872	Cluster4578_1clades	66	KTN4_283	Pseudomonas phage KTN4	GCA_002607225.1
ATN94673.1	004872	Cluster4578_1clades	66	SL2_096	Pseudomonas phage SL2	GCA_002956015.1
QJB22917.1	004872	Cluster4578_1clades	66	fnug_274	Pseudomonas phage fnug	GCA_012837215.1
AGC26351.1	004872	Cluster4578_1clades	66	PHIKZ234.1	Pseudomonas virus phiKZ	GCA_000842965.1
AJK27613.1	004873	Cluster4579_1clades	46	PTIM40_198	Cyanophage P-TIM40	GCA_001470935.1
AGH07597.1	004873	Cluster4579_1clades	66	CYVG_00153	Cyanophage S-SSM6a	GCA_002710385.1
AGG54418.1	004873	Cluster4579_1clades	47	CYWG_00134	Cyanophage S-SSM6b	GCA_002710425.1
AIR93631.1	004873	Cluster4579_1clades	47	AVU42_gp240	Prochlorococcus phage P-TIM68	GCA_001503075.1
AGR47850.2	004874	UBA	66	SmphiM12_218	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13055.1	004874	UBA	66	PHIM19_150	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12696.1	004874	UBA	66	PHIM7_150	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13426.1	004874	UBA	59	PHIN3_163	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47975.1	004875	Cluster4581_1clades	66	SmphiM12_343	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13164.1	004875	Cluster4581_1clades	66	PHIM19_259	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12804.1	004875	Cluster4581_1clades	66	PHIM7_259	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13527.1	004875	Cluster4581_1clades	66	PHIN3_264	Sinorhizobium phage phiN3	GCA_001501175.1
AMR59838.1	004876	Cluster4582_1clades	63	SEGD1_191	Enterobacteria phage SEGD1	GCA_002601865.1
QKN86028.1	004876	Cluster4582_1clades	63	ACEC001_1870	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09151.1	004876	Cluster4582_1clades	66	MLDJOKPK_00253	Salmonella phage SPAsTU	GCA_003183805.1
AEP84020.1	004876	Cluster4582_1clades	63	SPN3US_0187	Salmonella phage SPN3US	GCA_001042275.1
AYD80039.1	004877	Cluster4583_1clades	48	JA11_234	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66638.1	004877	Cluster4583_1clades	62	JA13_235	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66962.1	004877	Cluster4583_1clades	66	JA29_236	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67609.1	004877	Cluster4583_1clades	48	JA33_235	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81296.1	004878	Cluster4584_1clades	66	SEA_JUSTBECAUSE_127	Streptomyces phage JustBecause	GCA_003613775.1
QJD53699.1	004878	Cluster4584_1clades	66	SEA_KELA_128	Streptomyces phage Kela	GCA_012934305.1
QBZ72027.1	004878	Cluster4584_1clades	66	SEA_KRADAL_129	Streptomyces phage Kradal	GCA_004799925.1
AXH66290.1	004878	Cluster4584_1clades	66	SEA_SATIS_129	Streptomyces phage Satis	GCA_003366315.1
AYD81372.1	004879	Cluster4585_1clades	66	SEA_JUSTBECAUSE_217	Streptomyces phage JustBecause	GCA_003613775.1
QJD53775.1	004879	Cluster4585_1clades	66	SEA_KELA_215	Streptomyces phage Kela	GCA_012934305.1
QBZ72104.1	004879	Cluster4585_1clades	66	SEA_KRADAL_218	Streptomyces phage Kradal	GCA_004799925.1
AXH66365.1	004879	Cluster4585_1clades	66	SEA_SATIS_216	Streptomyces phage Satis	GCA_003366315.1
ARM70775.1	004880	Cluster4586_1clades	63	phiC120_c69	Escherichia phage phiC120	GCA_002621185.1
QCW18877.1	004880	Cluster4586_1clades	66	7t3_0356	Salmonella phage 7t3	GCA_006083215.1
AZU98135.1	004880	Cluster4586_1clades	66	CPT_Munch_191	Salmonella phage Munch	GCA_004015485.1
QIG62847.1	004880	Cluster4586_1clades	66	SEPL_234	Salmonella phage SE_PL	GCA_011067555.1
AFC21912.1	004881	Cluster4587_1clades	57	GAP32_455	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44036.1	004881	Cluster4587_1clades	41	CBB_473	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK59277.1	004881	Cluster4587_1clades	66	g469	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58742.1	004881	Cluster4587_1clades	56	g465	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AJK27493.1	004882	Cluster4588_1clades	61	PTIM40_66	Cyanophage P-TIM40	GCA_001470935.1
AGH07708.1	004882	Cluster4588_1clades	65	CYVG_00265	Cyanophage S-SSM6a	GCA_002710385.1
AAX44481.1	004882	Cluster4588_1clades	60	PSSM2_103	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12167.1	004882	Cluster4588_1clades	60	PRTG_00009	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGR47917.1	004883	Cluster4589_1clades	65	SmphiM12_285	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13119.1	004883	Cluster4589_1clades	65	PHIM19_214	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12759.1	004883	Cluster4589_1clades	65	PHIM7_214	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13489.1	004883	Cluster4589_1clades	65	PHIN3_226	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48070.1	004884	Cluster4590_1clades	65	SmphiM12_438	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13245.1	004884	Cluster4590_1clades	65	PHIM19_340	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12885.1	004884	Cluster4590_1clades	65	PHIM7_340	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13608.1	004884	Cluster4590_1clades	65	PHIN3_345	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48074.2	004885	Cluster4591_1clades	65	SmphiM12_442	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13249.1	004885	Cluster4591_1clades	65	PHIM19_344	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12889.1	004885	Cluster4591_1clades	65	PHIM7_344	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13612.1	004885	Cluster4591_1clades	65	PHIN3_349	Sinorhizobium phage phiN3	GCA_001501175.1
AIF27785.1	004886	Cluster4592_1clades	65	SmphiM12_501	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13121.1	004886	Cluster4592_1clades	65	PHIM19_216	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12761.1	004886	Cluster4592_1clades	65	PHIM7_216	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13491.1	004886	Cluster4592_1clades	65	PHIN3_228	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81420.1	004887	Cluster4593_1clades	64	SEA_JUSTBECAUSE_265	Streptomyces phage JustBecause	GCA_003613775.1
QJD53825.1	004887	Cluster4593_1clades	64	SEA_KELA_265	Streptomyces phage Kela	GCA_012934305.1
QBZ72151.1	004887	Cluster4593_1clades	65	SEA_KRADAL_265	Streptomyces phage Kradal	GCA_004799925.1
AXH66414.1	004887	Cluster4593_1clades	65	SEA_SATIS_265	Streptomyces phage Satis	GCA_003366315.1
AYD81186.1	004888	Cluster4594_1clades	65	SEA_JUSTBECAUSE_17	Streptomyces phage JustBecause	GCA_003613775.1
QJD53588.1	004888	Cluster4594_1clades	65	SEA_KELA_17	Streptomyces phage Kela	GCA_012934305.1
QBZ71919.1	004888	Cluster4594_1clades	64	SEA_KRADAL_20	Streptomyces phage Kradal	GCA_004799925.1
AXH66181.1	004888	Cluster4594_1clades	64	SEA_SATIS_20	Streptomyces phage Satis	GCA_003366315.1
QAX96752.1	004889	Cluster4595_1clades	65	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97071.1	004889	Cluster4595_1clades	65	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96117.1	004889	Cluster4595_1clades	65	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96435.1	004889	Cluster4595_1clades	65	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AAQ64384.1	004890	Cluster4596_1clades	64	KVP40.0314	Vibrio phage KVP40	GCA_000843785.1
QIW90699.1	004890	Cluster4596_1clades	62	GCAPEGMB_00366	Vibrio phage V07	GCA_012361095.1
QIW91099.1	004890	Cluster4596_1clades	62	COHAPHLL_00249	Vibrio phage V09	GCA_012361135.1
AFN37546.1	004890	Cluster4596_1clades	62	pp2_313	Vibriophage phi-pp2	GCA_002630725.1
AUE22615.1	004891	Cluster4597_1clades	62	Ah1_00074	Aeromonas phage Ah1	GCA_002957415.1
ADQ52799.1	004891	Cluster4597_1clades	64	PX29p080	Aeromonas phage PX29	GCA_000920195.1
ADM80056.1	004891	Cluster4597_1clades	63	phiAS5_ORF0213	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17742.1	004891	Cluster4597_1clades	62	Aeh1ORF081c	Aeromonas virus Aeh1	GCA_000843245.1
ASU00299.1	004892	Cluster4598_1clades	64	HWB28_gp253	Aeromonas phage AS-zj	GCA_002627665.1
QAX97738.1	004892	Cluster4598_1clades	64	ASswx1_93	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01418.1	004892	Cluster4598_1clades	64	ASwh1_359	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39169.1	004892	Cluster4598_1clades	64	CC2_018	Aeromonas phage CC2	GCA_000903495.1
AGR47708.1	004893	Cluster4599_1clades	64	SmphiM12_076	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12964.1	004893	Cluster4599_1clades	64	PHIM19_57	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12604.1	004893	Cluster4599_1clades	64	PHIM7_56	Sinorhizobium phage phiM7	GCA_002622405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF13337.1	004893	Cluster4599_1clades	64	PHIN3_72	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47709.1	004894	Cluster4600_1clades	64	SmphiM12_077	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12965.1	004894	Cluster4600_1clades	64	PHIM19_58	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12605.1	004894	Cluster4600_1clades	64	PHIM7_57	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13338.1	004894	Cluster4600_1clades	64	PHIN3_73	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47827.1	004895	C58	64	SmphiM12_195	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13038.1	004895	C58	64	PHIM19_133	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12678.1	004895	C58	64	PHIM7_132	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13410.1	004895	C58	64	PHIN3_147	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47964.1	004896	Cluster4602_1clades	64	SmphiM12_332	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13156.1	004896	Cluster4602_1clades	64	PHIM19_251	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12795.1	004896	Cluster4602_1clades	64	PHIM7_250	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13518.1	004896	Cluster4602_1clades	64	PHIN3_255	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14142.1	004897	Cluster4603_1clades	64	PBI_121Q_252	Escherichia phage 121Q	GCA_000926855.1
BBM61817.1	004897	Cluster4603_1clades	64	EO157G_2280	Escherichia phage SP27	GCA_008033345.1
QBO61562.1	004897	Cluster4603_1clades	64	G17_00066	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80132.1	004897	Cluster4603_1clades	64	PSLUR01_00155	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AFC21477.1	004898	Cluster4604_1clades	63	GAP32_029	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44556.1	004898	Cluster4604_1clades	60	RaK2_00283	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AMM43600.1	004898	Cluster4604_1clades	63	CBB_35	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44151.1	004898	Cluster4604_1clades	63	CBB_588	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFQ96662.1	004899	Cluster4605_1clades	63	G173_gp117	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48228.1	004899	Cluster4605_1clades	63	ASESINO_215	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50641.1	004899	Cluster4605_1clades	63	STRATTON_216	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXF51123.1	004899	Cluster4605_1clades	63	MLDJOKPK_00245	Salmonella phage SPAsTU	GCA_003183805.1
ANM44858.1	004900	SIG+TM	63	KTN4_100	Pseudomonas phage KTN4	GCA_002607225.1
ATN94855.1	004900	SIG+TM	63	SL2_278	Pseudomonas phage SL2	GCA_002956015.1
QJB22735.1	004900	SIG+TM	63	fnug_92	Pseudomonas phage fnug	GCA_012837215.1
AGC26319.1	004900	SIG+TM	63	PHIKZ076.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47648.2	004901	Cluster4607_1clades	63	SmphiM12_016	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12914.1	004901	Cluster4607_1clades	63	PHIM19_7	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12554.1	004901	Cluster4607_1clades	63	PHIM7_6	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13284.2	004901	Cluster4607_1clades	63	PHIN3_17	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47661.1	004902	Cluster4608_1clades	63	SmphiM12_029	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12927.1	004902	Cluster4608_1clades	63	PHIM19_20	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12567.1	004902	Cluster4608_1clades	63	PHIM7_19	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13299.1	004902	Cluster4608_1clades	63	PHIN3_34	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47716.1	004903	Cluster4609_1clades	63	SmphiM12_084	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12971.1	004903	Cluster4609_1clades	63	PHIM19_64	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12611.1	004903	Cluster4609_1clades	63	PHIM7_63	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13343.1	004903	Cluster4609_1clades	42	PHIN3_79	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47800.1	004904	Cluster4610_1clades	63	SmphiM12_168	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13016.1	004904	Cluster4610_1clades	63	PHIM19_110	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12656.1	004904	Cluster4610_1clades	63	PHIM7_109	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13388.1	004904	Cluster4610_1clades	63	PHIN3_123	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47947.2	004905	Cluster4611_1clades	63	SmphiM12_315	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13142.1	004905	Cluster4611_1clades	63	PHIM19_237	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12781.1	004905	Cluster4611_1clades	63	PHIM7_236	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13510.1	004905	Cluster4611_1clades	63	PHIN3_247	Sinorhizobium phage phiN3	GCA_001501175.1
ANM45019.1	004906	Cluster4612_1clades	63	KTN4_261	Pseudomonas phage KTN4	GCA_002607225.1
ATN94695.1	004906	Cluster4612_1clades	63	SL2_118	Pseudomonas phage SL2	GCA_002956015.1
QJB22896.1	004906	Cluster4612_1clades	63	fnug_253	Pseudomonas phage fnug	GCA_012837215.1
AAL83118.2	004906	Cluster4612_1clades	53	PHIKZ217	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ49717.1	004907	Cluster4613_1clades	59	MACHINA_79	Erwinia phage Machina	GCA_002758035.1
ANZ48571.1	004907	Cluster4613_1clades	63	CAITLIN_276	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ49162.1	004907	Cluster4613_1clades	59	HUXLEY_80	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49990.1	004907	Cluster4613_1clades	59	PARSHIK_81	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AFO71329.1	004908	Cluster4614_1clades	59	CR5_109	Cronobacter phage CR5	GCA_000910235.1
QBP07538.1	004908	Cluster4614_1clades	59	DERBICUS_112	Erwinia phage Derbicus	GCA_004521655.1
ANZ48961.1	004908	Cluster4614_1clades	59	EARLPHILLIPIV_112	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50303.1	004908	Cluster4614_1clades	63	PHOBOS_113	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AXG67350.1	004909	Amidinotransf	63	AD1_306	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08577.1	004909	Amidinotransf	63	Alexandra_326	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58953.1	004909	Amidinotransf	63	Y3_313	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28779.1	004909	Amidinotransf	62	YOLOSWAG_309	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXQ69048.1	004910	Cluster4616_1clades	63	CcrBL9_gp024	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69564.1	004910	Cluster4616_1clades	63	CcrBL9_gp540	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69608.1	004910	Cluster4616_1clades	63	CcrSC_gp026	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70108.1	004910	Cluster4616_1clades	63	CcrSC_gp526	Caulobacter phage CcrSC	GCA_003443315.1
AYD81214.1	004911	Cluster4617_1clades	63	SEA_JUSTBECAUSE_45	Streptomyces phage JustBecause	GCA_003613775.1
QJD53617.1	004911	Cluster4617_1clades	63	SEA_KELA_46	Streptomyces phage Kela	GCA_012934305.1
QBZ71950.1	004911	Cluster4617_1clades	62	SEA_KRADAL_51	Streptomyces phage Kradal	GCA_004799925.1
AXH66212.1	004911	Cluster4617_1clades	62	SEA_SATIS_51	Streptomyces phage Satis	GCA_003366315.1
QCW22844.1	004912	Cluster4618_1clades	52	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23050.1	004912	Cluster4618_1clades	55	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50511.1	004912	Cluster4618_1clades	52	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50701.1	004912	Cluster4618_1clades	63	-	Synechococcus phage S-B43	GCA_006869725.1
QIG63336.1	004913	Cluster4619_1clades	63	DAC16_103	Bacteroides phage DAC16	GCA_013387695.1
QIG63602.1	004913	Cluster4619_1clades	63	DAC19_111	Bacteroides phage DAC19	GCA_013387715.1
QIG63863.1	004913	Cluster4619_1clades	63	DAC20_110	Bacteroides phage DAC20	GCA_013387725.1
QIG64383.1	004913	Cluster4619_1clades	63	DAC23_105	Bacteroides phage DAC23	GCA_013387745.1
QAX98433.1	004914	Cluster4620_1clades	46	ASfcp2_89	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52887.1	004914	Cluster4620_1clades	59	PX29p168	Aeromonas phage PX29	GCA_000920195.1
ADM80152.1	004914	Cluster4620_1clades	62	phiAS5_ORF0309	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17840.1	004914	Cluster4620_1clades	52	Aeh1ORF174c	Aeromonas virus Aeh1	GCA_000843245.1
AFO71323.1	004915	Cluster4621_1clades	62	CR5_103	Cronobacter phage CR5	GCA_000910235.1
QBP07533.1	004915	Cluster4621_1clades	62	DERBICUS_107	Erwinia phage Derbicus	GCA_004521655.1
ANZ48956.1	004915	Cluster4621_1clades	62	EARLPHILLIPIV_107	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50298.1	004915	Cluster4621_1clades	62	PHOBOS_108	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AXQ68508.1	004916	Cluster4622_1clades	62	CcrBL10_gp304	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69502.1	004916	Cluster4622_1clades	57	CcrBL9_gp478	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70052.1	004916	Cluster4622_1clades	57	CcrSC_gp470	Caulobacter phage CcrSC	GCA_003443315.1
AFU86796.1	004916	Cluster4622_1clades	62	CcrRogue_gp314	Caulobacter virus Rogue	GCA_000900555.1
AGR47878.1	004917	Cluster4623_1clades	62	SmphiM12_246	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13079.1	004917	Cluster4623_1clades	62	PHIM19_174	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12719.1	004917	Cluster4623_1clades	62	PHIM7_174	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13449.1	004917	Cluster4623_1clades	62	PHIN3_186	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48037.2	004918	Cluster4624_1clades	62	SmphiM12_405	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13220.1	004918	Cluster4624_1clades	62	PHIM19_315	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12861.1	004918	Cluster4624_1clades	62	PHIM7_315	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13583.1	004918	Cluster4624_1clades	62	PHIN3_320	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47895.1	004919	Cluster4625_1clades	56	SmphiM12_263	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13095.1	004919	Cluster4625_1clades	56	PHIM19_190	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12735.1	004919	Cluster4625_1clades	56	PHIM7_190	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13465.1	004919	Cluster4625_1clades	62	PHIN3_202	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81227.1	004920	Cluster4626_1clades	53	SEA_JUSTBECAUSE_58	Streptomyces phage JustBecause	GCA_003613775.1
QJD53630.1	004920	Cluster4626_1clades	53	SEA_KELA_59	Streptomyces phage Kela	GCA_012934305.1
QBZ71962.1	004920	Cluster4626_1clades	62	SEA_KRADAL_64	Streptomyces phage Kradal	GCA_004799925.1
AXH66225.1	004920	Cluster4626_1clades	62	SEA_SATIS_64	Streptomyces phage Satis	GCA_003366315.1
QAX96923.1	004921	Cluster4627_1clades	62	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97228.1	004921	Cluster4627_1clades	62	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96287.1	004921	Cluster4627_1clades	62	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96605.1	004921	Cluster4627_1clades	62	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QGT54833.1	004922	Cluster4628_1clades	62	b23_0218	Synechococcus phage B23	GCA_009745195.1
QGT54834.1	004922	Cluster4628_1clades	61	b23_0219	Synechococcus phage B23	GCA_009745195.1
QGT54463.1	004922	Cluster4628_1clades	62	b3_0220	Synechococcus phage B3	GCA_009745215.1
QGT54464.1	004922	Cluster4628_1clades	61	b3_0221	Synechococcus phage B3	GCA_009745215.1
AGR47813.2	004923	Cluster4629_1clades	61	SmphiM12_181	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13027.1	004923	Cluster4629_1clades	61	PHIM19_122	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12667.1	004923	Cluster4629_1clades	61	PHIM7_121	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13398.1	004923	Cluster4629_1clades	61	PHIN3_135	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47909.1	004924	Cluster4630_1clades	61	SmphiM12_277	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13113.1	004924	Cluster4630_1clades	61	PHIM19_208	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12753.1	004924	Cluster4630_1clades	61	PHIM7_208	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13483.1	004924	Cluster4630_1clades	61	PHIN3_220	Sinorhizobium phage phiN3	GCA_001501175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGR47963.1	004925	Cluster4631_1clades	61	SmphiM12_331	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13153.1	004925	Cluster4631_1clades	61	PHIM19_248	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12792.1	004925	Cluster4631_1clades	61	PHIM7_247	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13516.1	004925	Cluster4631_1clades	61	PHIN3_253	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47974.2	004926	Cluster4632_1clades	61	SmphiM12_342	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13163.1	004926	Cluster4632_1clades	61	PHIM19_258	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12803.1	004926	Cluster4632_1clades	61	PHIM7_258	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13526.1	004926	Cluster4632_1clades	61	PHIN3_263	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48093.1	004927	Cluster4633_1clades	61	SmphiM12_461	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13262.1	004927	Cluster4633_1clades	61	PHIM19_357	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12902.1	004927	Cluster4633_1clades	61	PHIM7_357	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13624.1	004927	Cluster4633_1clades	60	PHIN3_361	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14152.1	004928	Cluster4634_1clades	61	PBI_121Q_262	Escherichia phage 121Q	GCA_000926855.1
BBM61827.1	004928	Cluster4634_1clades	61	EO157G_2380	Escherichia phage SP27	GCA_008033345.1
QDF14164.1	004928	Cluster4634_1clades	61	vBEcoMphAPEC6_gp541c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80141.1	004928	Cluster4634_1clades	61	PSLUR01_00164	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AIT14153.1	004929	Cluster4635_1clades	61	PBI_121Q_263	Escherichia phage 121Q	GCA_000926855.1
BBM61828.1	004929	Cluster4635_1clades	61	EO157G_2390	Escherichia phage SP27	GCA_008033345.1
QBO61551.1	004929	Cluster4635_1clades	61	G17_00055	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80142.1	004929	Cluster4635_1clades	61	PSLUR01_00165	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ASR76182.1	004930	Cluster4636_1clades	61	PBI_BELLAMY_137	Synechococcus phage Bellamy	GCA_002627525.1
QCW22893.1	004930	Cluster4636_1clades	61	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50659.1	004930	Cluster4636_1clades	61	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70124.1	004930	Cluster4636_1clades	61	SynMITS9220M01_111	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AYD81335.1	004931	SIG+TM	61	SEA_JUSTBECAUSE_170	Streptomyces phage JustBecause	GCA_003613775.1
QJD53738.1	004931	SIG+TM	61	SEA_KELA_168	Streptomyces phage Kela	GCA_012934305.1
QBZ72065.1	004931	SIG+TM	61	SEA_KRADAL_169	Streptomyces phage Kradal	GCA_004799925.1
AXH66328.1	004931	SIG+TM	61	SEA_SATIS_169	Streptomyces phage Satis	GCA_003366315.1
AYD81253.1	004932	Cluster4638_1clades	61	SEA_JUSTBECAUSE_84	Streptomyces phage JustBecause	GCA_003613775.1
QJD53656.1	004932	Cluster4638_1clades	61	SEA_KELA_85	Streptomyces phage Kela	GCA_012934305.1
QBZ71985.1	004932	Cluster4638_1clades	60	SEA_KRADAL_87	Streptomyces phage Kradal	GCA_004799925.1
AXH66248.1	004932	Cluster4638_1clades	60	SEA_SATIS_87	Streptomyces phage Satis	GCA_003366315.1
AFO71395.1	004933	Cluster4639_1clades	60	CR5_175	Cronobacter phage CR5	GCA_000910235.1
QBP07606.1	004933	Cluster4639_1clades	60	DERBICUS_180	Erwinia phage Derbicus	GCA_004521655.1
ANZ49030.1	004933	Cluster4639_1clades	60	EARLPHILLIPIV_181	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50378.1	004933	Cluster4639_1clades	58	PHOBOS_188	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM44799.1	004934	Cluster4640_1clades	60	KTN4_041	Pseudomonas phage KTN4	GCA_002607225.1
ATN94912.1	004934	Cluster4640_1clades	60	SL2_335	Pseudomonas phage SL2	GCA_002956015.1
QJB22678.1	004934	Cluster4640_1clades	60	fnug_35	Pseudomonas phage fnug	GCA_012837215.1
AGC26307.1	004934	Cluster4640_1clades	60	PHIKZ030.1	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44838.1	004935	Cluster4641_1clades	60	KTN4_080	Pseudomonas phage KTN4	GCA_002607225.1
ATN94875.1	004935	Cluster4641_1clades	60	SL2_298	Pseudomonas phage SL2	GCA_002956015.1
QJB22716.1	004935	Cluster4641_1clades	60	fnug_73	Pseudomonas phage fnug	GCA_012837215.1
AGC26316.1	004935	Cluster4641_1clades	60	PHIKZ058.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47719.1	004936	Cluster4642_1clades	60	SmphiM12_087	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12974.1	004936	Cluster4642_1clades	60	PHIM19_67	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12614.1	004936	Cluster4642_1clades	60	PHIM7_66	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13346.1	004936	Cluster4642_1clades	60	PHIN3_82	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47822.1	004937	Cluster4643_1clades	60	SmphiM12_190	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13035.1	004937	Cluster4643_1clades	60	PHIM19_130	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12675.1	004937	Cluster4643_1clades	60	PHIM7_129	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13407.1	004937	Cluster4643_1clades	60	PHIN3_144	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47948.1	004938	Cluster4644_1clades	60	SmphiM12_316	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13143.1	004938	Cluster4644_1clades	60	PHIM19_238	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12782.1	004938	Cluster4644_1clades	60	PHIM7_237	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13511.1	004938	Cluster4644_1clades	60	PHIN3_248	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81170.1	004939	Cluster4645_1clades	56	SEA_JUSTBECAUSE_1	Streptomyces phage JustBecause	GCA_003613775.1
QJD53572.1	004939	Cluster4645_1clades	56	SEA_KELA_1	Streptomyces phage Kela	GCA_012934305.1
QBZ71900.1	004939	Cluster4645_1clades	60	SEA_KRADAL_1	Streptomyces phage Kradal	GCA_004799925.1
AXH66162.1	004939	Cluster4645_1clades	60	SEA_SATIS_1	Streptomyces phage Satis	GCA_003366315.1
AGR47815.1	004940	Cluster4646_1clades	59	SmphiM12_183	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13030.1	004940	Cluster4646_1clades	59	PHIM19_125	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12670.1	004940	Cluster4646_1clades	59	PHIM7_124	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13401.1	004940	Cluster4646_1clades	59	PHIN3_138	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47968.1	004941	Cluster4647_1clades	59	SmphiM12_336	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13159.1	004941	Cluster4647_1clades	59	PHIM19_254	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12798.1	004941	Cluster4647_1clades	59	PHIM7_253	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13521.1	004941	Cluster4647_1clades	59	PHIN3_258	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47692.1	004942	Cluster4648_1clades	58	SmphiM12_060	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12952.1	004942	Cluster4648_1clades	58	PHIM19_45	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12592.1	004942	Cluster4648_1clades	58	PHIM7_44	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13325.1	004942	Cluster4648_1clades	59	PHIN3_60	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80080.1	004943	Cluster4649_1clades	59	JA11_275	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66681.1	004943	Cluster4649_1clades	59	JA13_278	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67001.1	004943	Cluster4649_1clades	59	JA29_275	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67650.1	004943	Cluster4649_1clades	59	JA33_276	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QAX96693.1	004944	Cluster4650_1clades	59	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97011.1	004944	Cluster4650_1clades	59	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96057.1	004944	Cluster4650_1clades	59	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96375.1	004944	Cluster4650_1clades	59	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QMV28836.1	004945	Cluster4651_1clades	58	AP1_0129	Aeromonas phage AP1	GCA_014183365.1
ATI17269.1	004945	Cluster4651_1clades	58	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97709.1	004945	Cluster4651_1clades	58	ASswx1_63	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39188.1	004945	Cluster4651_1clades	58	CC2_048	Aeromonas phage CC2	GCA_000903495.1
ANM44827.1	004946	IMPDH	58	KTN4_069	Pseudomonas phage KTN4	GCA_002607225.1
ATN94885.1	004946	IMPDH	58	SL2_308	Pseudomonas phage SL2	GCA_002956015.1
QJB22705.1	004946	IMPDH	58	fnug_62	Pseudomonas phage fnug	GCA_012837215.1
AGC26314.1	004946	IMPDH	58	PHIKZ050.1	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45004.1	004947	Cluster4653_1clades	58	KTN4_246	Pseudomonas phage KTN4	GCA_002607225.1
ATN94710.1	004947	Cluster4653_1clades	58	SL2_133	Pseudomonas phage SL2	GCA_002956015.1
QJB22882.1	004947	Cluster4653_1clades	58	fnug_239	Pseudomonas phage fnug	GCA_012837215.1
AGC26343.1	004947	Cluster4653_1clades	58	PHIKZ204.1	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45112.1	004948	Cluster4654_1clades	58	KTN4_354	Pseudomonas phage KTN4	GCA_002607225.1
ATN94601.1	004948	Cluster4654_1clades	58	SL2_024	Pseudomonas phage SL2	GCA_002956015.1
QJB22989.1	004948	Cluster4654_1clades	58	fnug_346	Pseudomonas phage fnug	GCA_012837215.1
AGC26362.1	004948	Cluster4654_1clades	58	PHIKZ293.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGH07493.1	004949	Cluster4655_1clades	58	CYVG_00049	Cyanophage S-SSM6a	GCA_002710385.1
AGG54417.1	004949	Cluster4655_1clades	55	CYWG_00133	Cyanophage S-SSM6b	GCA_002710425.1
AGH26102.1	004949	Cluster4655_1clades	55	CPMG_00001	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26317.1	004949	Cluster4655_1clades	55	CPMG_00218	Prochlorococcus phage MED4-213	GCA_000904535.1
AGR47925.2	004950	Cluster4656_1clades	58	SmphiM12_293	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13127.1	004950	Cluster4656_1clades	58	PHIM19_222	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12766.1	004950	Cluster4656_1clades	58	PHIM7_221	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13496.1	004950	Cluster4656_1clades	58	PHIN3_233	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48036.1	004951	Cluster4657_1clades	58	SmphiM12_404	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13219.1	004951	Cluster4657_1clades	58	PHIM19_314	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12860.1	004951	Cluster4657_1clades	58	PHIM7_314	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13582.1	004951	Cluster4657_1clades	58	PHIN3_319	Sinorhizobium phage phiN3	GCA_001501175.1
AYD80099.1	004952	Cluster4658_1clades	58	JA11_294	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66700.1	004952	Cluster4658_1clades	58	JA13_297	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67019.1	004952	Cluster4658_1clades	58	JA29_293	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67669.1	004952	Cluster4658_1clades	58	JA33_295	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81389.1	004953	Cluster4659_1clades	58	SEA_JUSTBECAUSE_234	Streptomyces phage JustBecause	GCA_003613775.1
QJD53793.1	004953	Cluster4659_1clades	58	SEA_KELA_233	Streptomyces phage Kela	GCA_012934305.1
QBZ72118.1	004953	Cluster4659_1clades	38	SEA_KRADAL_232	Streptomyces phage Kradal	GCA_004799925.1
AXH66380.1	004953	Cluster4659_1clades	38	SEA_SATIS_231	Streptomyces phage Satis	GCA_003366315.1
ADM80038.1	004954	SIG+TM	57	phiAS5_ORF0195	Aeromonas phage phiAS5	GCA_000887715.1
QCW18689.1	004954	SIG+TM	57	7t3_0168	Salmonella phage 7t3	GCA_006083215.1
AZU97963.1	004954	SIG+TM	58	CPT_Munch_019	Salmonella phage Munch	GCA_004015485.1
QIG63015.1	004954	SIG+TM	57	SEPL_402	Salmonella phage SE_PL	GCA_011067555.1
QAX96760.1	004955	Cluster4661_1clades	58	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97079.1	004955	Cluster4661_1clades	58	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96125.1	004955	Cluster4661_1clades	58	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96443.1	004955	Cluster4661_1clades	58	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFO71285.1	004956	Cluster4662_1clades	57	CR5_065	Cronobacter phage CR5	GCA_000910235.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBP07492.1	004956	Cluster4662_1clades	57	DERBICUS_66	Erwinia phage Derbicus	GCA_004521655.1
ANZ48916.1	004956	Cluster4662_1clades	57	EARLPHILLIPIV_66	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50257.1	004956	Cluster4662_1clades	57	PHOBOS_67	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANM45035.1	004957	Cluster4663_1clades	57	KTN4_277	Pseudomonas phage KTN4	GCA_002607225.1
ATN94679.1	004957	Cluster4663_1clades	57	SL2_102	Pseudomonas phage SL2	GCA_002956015.1
QJB22911.1	004957	Cluster4663_1clades	57	fnug_268	Pseudomonas phage fnug	GCA_012837215.1
AGC26348.1	004957	Cluster4663_1clades	57	PHIKZ230.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47658.2	004958	Cluster4664_1clades	57	SmphiM12_026	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12924.1	004958	Cluster4664_1clades	57	PHIM19_17	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12564.1	004958	Cluster4664_1clades	57	PHIM7_16	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13296.1	004958	Cluster4664_1clades	55	PHIN3_31	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48057.2	004959	Cluster4665_1clades	57	SmphiM12_425	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13236.1	004959	Cluster4665_1clades	57	PHIM19_331	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12876.1	004959	Cluster4665_1clades	57	PHIM7_331	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13599.1	004959	Cluster4665_1clades	57	PHIN3_336	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81295.1	004960	Cluster4666_1clades	57	SEA_JUSTBECAUSE_126	Streptomyces phage JustBecause	GCA_003613775.1
QJD53698.1	004960	Cluster4666_1clades	57	SEA_KELA_127	Streptomyces phage Kela	GCA_012934305.1
QBZ72026.1	004960	Cluster4666_1clades	57	SEA_KRADAL_128	Streptomyces phage Kradal	GCA_004799925.1
AXH66289.1	004960	Cluster4666_1clades	57	SEA_SATIS_128	Streptomyces phage Satis	GCA_003366315.1
AJK27497.1	004961	Cluster4667_1clades	54	PTIM40_70	Cyanophage P-TIM40	GCA_001470935.1
AGG54334.1	004961	Cluster4667_1clades	56	CYWG_00050	Cyanophage S-SSM6b	GCA_002710425.1
AAX44457.1	004961	Cluster4667_1clades	55	PSSM2_079	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12196.1	004961	Cluster4667_1clades	55	PRTG_00038	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGR47657.1	004962	Cluster4668_1clades	56	SmphiM12_025	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12923.1	004962	Cluster4668_1clades	56	PHIM19_16	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12563.1	004962	Cluster4668_1clades	56	PHIM7_15	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13295.1	004962	Cluster4668_1clades	56	PHIN3_30	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47704.1	004963	Cluster4669_1clades	56	SmphiM12_072	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12960.1	004963	Cluster4669_1clades	56	PHIM19_53	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12600.1	004963	Cluster4669_1clades	56	PHIM7_52	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13333.1	004963	Cluster4669_1clades	56	PHIN3_68	Sinorhizobium phage phiN3	GCA_001501175.1
AXQ69064.1	004964	Cluster4670_1clades	56	CcrBL9_gp040	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69580.1	004964	Cluster4670_1clades	56	CcrBL9_gp556	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69624.1	004964	Cluster4670_1clades	56	CcrSC_gp042	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70124.1	004964	Cluster4670_1clades	56	CcrSC_gp542	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69066.1	004965	Cluster4671_1clades	56	CcrBL9_gp042	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69582.1	004965	Cluster4671_1clades	56	CcrBL9_gp558	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69626.1	004965	Cluster4671_1clades	56	CcrSC_gp044	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70126.1	004965	Cluster4671_1clades	56	CcrSC_gp544	Caulobacter phage CcrSC	GCA_003443315.1
QIG63595.1	004966	Cluster4672_1clades	56	DAC19_104	Bacteroides phage DAC19	GCA_013387715.1
QIG63856.1	004966	Cluster4672_1clades	56	DAC20_103	Bacteroides phage DAC20	GCA_013387725.1
QIG64119.1	004966	Cluster4672_1clades	50	DAC22_105	Bacteroides phage DAC22	GCA_013387735.1
QIG64377.1	004966	Cluster4672_1clades	50	DAC23_99	Bacteroides phage DAC23	GCA_013387745.1
AGR48040.1	004967	SIG+TM	55	SmphiM12_408	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13224.1	004967	SIG+TM	55	PHIM19_319	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12864.1	004967	SIG+TM	55	PHIM7_319	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13587.1	004967	SIG+TM	55	PHIN3_324	Sinorhizobium phage phiN3	GCA_001501175.1
AOO14258.1	004968	Cluster4674_1clades	55	Sn110110_064	Cyanophage S-RIM14	GCA_002599065.1
AMO43084.1	004968	Cluster4674_1clades	55	R1080702_075	Cyanophage S-RIM32	GCA_001754165.1
ASR76137.1	004968	Cluster4674_1clades	49	PBI_BELLAMY_92	Synechococcus phage Bellamy	GCA_002627525.1
QJT70074.1	004968	Cluster4674_1clades	55	SynMITS9220M01_061	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUE22757.1	004969	Cluster4675_1clades	53	Ah1_00239	Aeromonas phage Ah1	GCA_002957415.1
ADQ52935.1	004969	Cluster4675_1clades	53	PX29p216	Aeromonas phage PX29	GCA_000920195.1
ADM79858.1	004969	Cluster4675_1clades	54	phiAS5_ORF0015	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17882.1	004969	Cluster4675_1clades	53	Aeh1ORF220w	Aeromonas virus Aeh1	GCA_000843245.1
AGR47837.2	004970	HEPN	54	SmphiM12_205	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13044.1	004970	HEPN	54	PHIM19_139	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12685.1	004970	HEPN	54	PHIM7_139	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13417.1	004970	HEPN	53	PHIN3_154	Sinorhizobium phage phiN3	GCA_001501175.1
AMM43958.1	004971	Cluster4677_1clades	53	CBB_395	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88920.1	004971	Cluster4677_1clades	54	BF_0395	Serratia phage BF	GCA_002619745.1
SOK59209.1	004971	Cluster4677_1clades	53	g401	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58675.1	004971	Cluster4677_1clades	53	g398	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD80018.1	004972	Cluster4678_1clades	54	JA11_213	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66617.1	004972	Cluster4678_1clades	54	JA13_214	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66941.1	004972	Cluster4678_1clades	54	JA29_215	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67588.1	004972	Cluster4678_1clades	54	JA33_214	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81188.1	004973	Cluster4679_1clades	54	SEA_JUSTBECAUSE_19	Streptomyces phage JustBecause	GCA_003613775.1
QJD53590.1	004973	Cluster4679_1clades	54	SEA_KELA_19	Streptomyces phage Kela	GCA_012934305.1
QBZ71921.1	004973	Cluster4679_1clades	54	SEA_KRADAL_22	Streptomyces phage Kradal	GCA_004799925.1
AXH66183.1	004973	Cluster4679_1clades	54	SEA_SATIS_22	Streptomyces phage Satis	GCA_003366315.1
AYD81210.1	004974	Cluster4680_1clades	54	SEA_JUSTBECAUSE_41	Streptomyces phage JustBecause	GCA_003613775.1
QJD53613.1	004974	Cluster4680_1clades	54	SEA_KELA_42	Streptomyces phage Kela	GCA_012934305.1
QBZ71947.1	004974	Cluster4680_1clades	54	SEA_KRADAL_48	Streptomyces phage Kradal	GCA_004799925.1
AXH66209.1	004974	Cluster4680_1clades	54	SEA_SATIS_48	Streptomyces phage Satis	GCA_003366315.1
AYD81393.1	004975	Cluster4681_1clades	54	SEA_JUSTBECAUSE_238	Streptomyces phage JustBecause	GCA_003613775.1
QJD53797.1	004975	Cluster4681_1clades	54	SEA_KELA_237	Streptomyces phage Kela	GCA_012934305.1
QBZ72123.1	004975	Cluster4681_1clades	54	SEA_KRADAL_237	Streptomyces phage Kradal	GCA_004799925.1
AXH66385.1	004975	Cluster4681_1clades	54	SEA_SATIS_236	Streptomyces phage Satis	GCA_003366315.1
AXQ69065.1	004976	Cluster4682_1clades	54	CcrBL9_gp041	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69581.1	004976	Cluster4682_1clades	54	CcrBL9_gp557	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69625.1	004976	Cluster4682_1clades	54	CcrSC_gp043	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70125.1	004976	Cluster4682_1clades	54	CcrSC_gp543	Caulobacter phage CcrSC	GCA_003443315.1
QAX96689.1	004977	Cluster4683_1clades	54	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97007.1	004977	Cluster4683_1clades	54	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96053.1	004977	Cluster4683_1clades	54	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96371.1	004977	Cluster4683_1clades	54	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44892.1	004978	Cluster4684_1clades	53	KTN4_134	Pseudomonas phage KTN4	GCA_002607225.1
ATN94821.1	004978	Cluster4684_1clades	53	SL2_244	Pseudomonas phage SL2	GCA_002956015.1
QJB22770.1	004978	Cluster4684_1clades	53	fnug_127	Pseudomonas phage fnug	GCA_012837215.1
AGC26325.1	004978	Cluster4684_1clades	53	PHIKZ106.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR48029.1	004979	Cluster4685_1clades	53	SmphiM12_397	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13212.1	004979	Cluster4685_1clades	53	PHIM19_307	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12853.1	004979	Cluster4685_1clades	53	PHIM7_307	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13574.1	004979	Cluster4685_1clades	53	PHIN3_311	Sinorhizobium phage phiN3	GCA_001501175.1
ANM44904.1	004980	Cluster4686_1clades	51	KTN4_146	Pseudomonas phage KTN4	GCA_002607225.1
ATN94809.1	004980	Cluster4686_1clades	53	SL2_232	Pseudomonas phage SL2	GCA_002956015.1
QJB22782.1	004980	Cluster4686_1clades	53	fnug_139	Pseudomonas phage fnug	GCA_012837215.1
AGC26328.1	004980	Cluster4686_1clades	51	PHIKZ115.1	Pseudomonas virus phiKZ	GCA_000842965.1
AIT14168.1	004981	Cluster4687_1clades	50	PBI_121Q_278	Escherichia phage 121Q	GCA_000926855.1
QBO61537.1	004981	Cluster4687_1clades	50	G17_00041	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62143.1	004981	Cluster4687_1clades	50	G17_00654	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AZU97956.1	004981	Cluster4687_1clades	53	CPT_Munch_012	Salmonella phage Munch	GCA_004015485.1
QAY00695.1	004982	Cluster4688_1clades	50	Ecwhy1_420	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61915.1	004982	Cluster4688_1clades	53	EO157G_3260	Escherichia phage SP27	GCA_008033345.1
QBO62067.1	004982	Cluster4688_1clades	53	G17_00578	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80226.1	004982	Cluster4688_1clades	53	PSLUR01_00249	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AGR47679.1	004983	Cluster4689_1clades	52	SmphiM12_047	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12941.1	004983	Cluster4689_1clades	52	PHIM19_34	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12581.1	004983	Cluster4689_1clades	52	PHIM7_33	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13316.1	004983	Cluster4689_1clades	52	PHIN3_51	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47803.1	004984	SIG+DUF1127	52	SmphiM12_171	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13019.1	004984	SIG+DUF1127	52	PHIM19_113	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12659.1	004984	SIG+DUF1127	52	PHIM7_112	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13391.1	004984	SIG+DUF1127	52	PHIN3_126	Sinorhizobium phage phiN3	GCA_001501175.1
AMM44144.1	004985	Cluster4691_1clades	52	CBB_28	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43593.1	004985	Cluster4691_1clades	52	CBB_581	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88546.1	004985	Cluster4691_1clades	51	BF_0021	Serratia phage BF	GCA_002619745.1
SOK58821.1	004985	Cluster4691_1clades	51	g013	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QDH50607.1	004986	Cluster4693_1clades	52	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59532.1	004986	Cluster4693_1clades	51	S330809_071	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59294.1	004986	Cluster4693_1clades	51	C440309_071	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59770.1	004986	Cluster4693_1clades	51	N231010_071	Synechococcus phage S-CAM4	GCA_002922155.1
QBX06282.1	004987	Cluster4694_1clades	51	ValB1HC_329	Vibrio phage ValB1 HC	GCA_004771355.1
AJT60909.1	004987	Cluster4694_1clades	51	AVU32_gp068	Vibrio phage ValKK3	GCA_001501635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN30243.1	004987	Cluster4694_1clades	51	VPFG_00244	Vibrio phage nt-1	GCA_000910195.2
QNJ54909.1	004987	Cluster4694_1clades	51	vBValMR10Z_369	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AYD79841.1	004988	Cluster4695_1clades	51	JA11_036	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66441.1	004988	Cluster4695_1clades	51	JA13_038	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66765.1	004988	Cluster4695_1clades	51	JA29_039	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67410.1	004988	Cluster4695_1clades	51	JA33_036	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
ARB14704.1	004989	Cluster4696_1clades	43	Ccr29_gp148	Caulobacter phage Ccr29	GCA_002619485.1
ARB15059.1	004989	Cluster4696_1clades	43	Ccr32_gp141	Caulobacter phage Ccr32	GCA_002619505.1
ARB15393.1	004989	Cluster4696_1clades	43	Ccr34_gp151	Caulobacter phage Ccr34	GCA_002619525.1
AXQ68341.1	004989	Cluster4696_1clades	51	CcrBL10_gp137c	Caulobacter phage CcrBL10	GCA_003443255.1
AUE22832.1	004990	Cluster4697_1clades	49	Ah1_00314	Aeromonas phage Ah1	GCA_002957415.1
QAX98546.1	004990	Cluster4697_1clades	49	ASfcp2_211	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53010.1	004990	Cluster4697_1clades	49	PX29p291	Aeromonas phage PX29	GCA_000920195.1
AAQ17961.1	004990	Cluster4697_1clades	50	Aeh1ORF292c	Aeromonas virus Aeh1	GCA_000843245.1
ANM45082.1	004991	Cluster4698_1clades	50	KTN4_324	Pseudomonas phage KTN4	GCA_002607225.1
ATN94633.1	004991	Cluster4698_1clades	50	SL2_056	Pseudomonas phage SL2	GCA_002956015.1
QJB22957.1	004991	Cluster4698_1clades	50	fnug_314	Pseudomonas phage fnug	GCA_012837215.1
AGC26357.1	004991	Cluster4698_1clades	50	PHIKZ267.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47662.1	004992	Cluster4699_1clades	50	SmphiM12_030	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12928.1	004992	Cluster4699_1clades	50	PHIM19_21	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12568.1	004992	Cluster4699_1clades	50	PHIM7_20	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13300.1	004992	Cluster4699_1clades	35	PHIN3_35	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47879.1	004993	Cluster4700_1clades	49	SmphiM12_247	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13080.1	004993	Cluster4700_1clades	49	PHIM19_175	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12720.1	004993	Cluster4700_1clades	49	PHIM7_175	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13450.1	004993	Cluster4700_1clades	49	PHIN3_187	Sinorhizobium phage phiN3	GCA_001501175.1
AGR47880.1	004994	Cluster4701_1clades	49	SmphiM12_248	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13081.1	004994	Cluster4701_1clades	49	PHIM19_176	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12721.1	004994	Cluster4701_1clades	49	PHIM7_176	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13451.1	004994	Cluster4701_1clades	49	PHIN3_188	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81174.1	004995	Cluster4702_1clades	45	SEA_JUSTBECAUSE_5	Streptomyces phage JustBecause	GCA_003613775.1
QJD53576.1	004995	Cluster4702_1clades	45	SEA_KELA_5	Streptomyces phage Kela	GCA_012934305.1
QBZ71904.1	004995	Cluster4702_1clades	49	SEA_KRADAL_5	Streptomyces phage Kradal	GCA_004799925.1
AXH66166.1	004995	Cluster4702_1clades	49	SEA_SATIS_5	Streptomyces phage Satis	GCA_003366315.1
QKN85912.1	004996	Cluster4703_1clades	48	ACEC001_0740	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AXF51087.1	004996	Cluster4703_1clades	48	MLDJOKPK_00090	Salmonella phage SPAsTU	GCA_003183805.1
AEP83904.1	004996	Cluster4703_1clades	48	SPN3US_0071	Salmonella phage SPN3US	GCA_001042275.1
AEP83905.1	004996	Cluster4703_1clades	48	SPN3US_0072	Salmonella phage SPN3US	GCA_001042275.1
QAX96762.1	004997	Cluster4704_1clades	48	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97081.1	004997	Cluster4704_1clades	48	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96127.1	004997	Cluster4704_1clades	48	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96445.1	004997	Cluster4704_1clades	48	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANM44777.1	004998	Cluster4705_1clades	47	KTN4_019	Pseudomonas phage KTN4	GCA_002607225.1
ATN94929.1	004998	Cluster4705_1clades	47	SL2_352	Pseudomonas phage SL2	GCA_002956015.1
QJB22662.1	004998	Cluster4705_1clades	47	fnug_19	Pseudomonas phage fnug	GCA_012837215.1
AGC26304.1	004998	Cluster4705_1clades	47	PHIKZ016.1	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44859.1	004999	Cluster4706_1clades	47	KTN4_101	Pseudomonas phage KTN4	GCA_002607225.1
ATN94854.1	004999	Cluster4706_1clades	47	SL2_277	Pseudomonas phage SL2	GCA_002956015.1
QJB22737.1	004999	Cluster4706_1clades	47	fnug_94	Pseudomonas phage fnug	GCA_012837215.1
AGC26321.1	004999	Cluster4706_1clades	47	PHIKZ076.3	Pseudomonas virus phiKZ	GCA_000842965.1
ANM44906.1	005000	Cluster4707_1clades	47	KTN4_148	Pseudomonas phage KTN4	GCA_002607225.1
ATN94807.1	005000	Cluster4707_1clades	47	SL2_230	Pseudomonas phage SL2	GCA_002956015.1
QJB22784.1	005000	Cluster4707_1clades	47	fnug_141	Pseudomonas phage fnug	GCA_012837215.1
AGC26330.1	005000	Cluster4707_1clades	47	PHIKZ115.3	Pseudomonas virus phiKZ	GCA_000842965.1
AJK27454.1	005001	Cluster4708_1clades	43	PTIM40_27	Cyanophage P-TIM40	GCA_001470935.1
AMO43200.1	005001	Cluster4708_1clades	43	R1080702_191	Cyanophage S-RIM32	GCA_001754165.1
AAX44630.1	005001	Cluster4708_1clades	44	PSSM2_253	Prochlorococcus phage P-SSM2	GCA_000859585.1
AIR93506.1	005001	Cluster4708_1clades	47	AVU42_gp169	Prochlorococcus phage P-TIM68	GCA_001503075.1
AYD79822.1	005002	TM	47	JA11_017	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66421.1	005002	TM	47	JA13_018	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66743.1	005002	TM	47	JA29_017	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67391.1	005002	TM	47	JA33_017	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFC21627.1	005003	Cluster4710_1clades	46	GAP32_177	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43749.1	005003	Cluster4710_1clades	46	CBB_184	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88707.1	005003	Cluster4710_1clades	46	BF_0182	Serratia phage BF	GCA_002619745.1
SOK58989.1	005003	Cluster4710_1clades	46	g181	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AGR47995.1	005004	Cluster4711_1clades	46	SmphiM12_363	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13182.1	005004	Cluster4711_1clades	46	PHIM19_277	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12821.1	005004	Cluster4711_1clades	46	PHIM7_276	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13544.1	005004	Cluster4711_1clades	46	PHIN3_281	Sinorhizobium phage phiN3	GCA_001501175.1
AXQ69037.1	005005	Cluster4712_1clades	46	CcrBL9_gp013	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69553.1	005005	Cluster4712_1clades	46	CcrBL9_gp529	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69597.1	005005	Cluster4712_1clades	46	CcrSC_gp015	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70097.1	005005	Cluster4712_1clades	46	CcrSC_gp515	Caulobacter phage CcrSC	GCA_003443315.1
ANM45113.1	005006	TM	45	KTN4_355	Pseudomonas phage KTN4	GCA_002607225.1
ATN94600.1	005006	TM	45	SL2_023	Pseudomonas phage SL2	GCA_002956015.1
QJB22990.1	005006	TM	45	fnug_347	Pseudomonas phage fnug	GCA_012837215.1
AGC26363.1	005006	TM	45	PHIKZ293.2	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96742.1	005007	Cluster4714_1clades	45	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97061.1	005007	Cluster4714_1clades	45	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96107.1	005007	Cluster4714_1clades	45	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96425.1	005007	Cluster4714_1clades	45	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMM43742.1	005008	SIG+TM	44	CBB_177	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88701.1	005008	SIG+TM	44	BF_0176	Serratia phage BF	GCA_002619745.1
SOK58981.1	005008	SIG+TM	44	g173	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58447.1	005008	SIG+TM	44	g170	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMR59841.1	005009	SIG+TM	43	SEGD1_194	Enterobacteria phage SEGD1	GCA_002601865.1
QKN86030.1	005009	SIG+TM	43	ACEC001_1890	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AWN09148.1	005009	SIG+TM	43	MLDJOKPK_00250	Salmonella phage SPAsTU	GCA_003183805.1
AEP84022.1	005009	SIG+TM	43	SPN3US_0189	Salmonella phage SPN3US	GCA_001042275.1
ARB13651.1	005010	Cluster4717_1clades	43	Ccr10_gp122c	Caulobacter phage Ccr10	GCA_002619445.1
ARB13996.1	005010	Cluster4717_1clades	43	Ccr2_gp121c	Caulobacter phage Ccr2	GCA_002619465.1
ARB14684.1	005010	Cluster4717_1clades	43	Ccr29_gp128	Caulobacter phage Ccr29	GCA_002619485.1
ARB15371.1	005010	Cluster4717_1clades	43	Ccr34_gp129	Caulobacter phage Ccr34	GCA_002619525.1
AGR48069.2	005011	Cluster4718_1clades	42	SmphiM12_437	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13244.1	005011	Cluster4718_1clades	42	PHIM19_339	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12884.1	005011	Cluster4718_1clades	42	PHIM7_339	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13607.1	005011	Cluster4718_1clades	42	PHIN3_344	Sinorhizobium phage phiN3	GCA_001501175.1
AYD81252.1	005012	Cluster4719_1clades	41	SEA_JUSTBECAUSE_83	Streptomyces phage JustBecause	GCA_003613775.1
QJD53655.1	005012	Cluster4719_1clades	41	SEA_KELA_84	Streptomyces phage Kela	GCA_012934305.1
QBZ71984.1	005012	Cluster4719_1clades	42	SEA_KRADAL_86	Streptomyces phage Kradal	GCA_004799925.1
AXH66247.1	005012	Cluster4719_1clades	42	SEA_SATIS_86	Streptomyces phage Satis	GCA_003366315.1
ANM44888.1	005013	Cluster4720_1clades	41	KTN4_130	Pseudomonas phage KTN4	GCA_002607225.1
ATN94825.1	005013	Cluster4720_1clades	41	SL2_248	Pseudomonas phage SL2	GCA_002956015.1
QJB22765.1	005013	Cluster4720_1clades	41	fnug_122	Pseudomonas phage fnug	GCA_012837215.1
AGC26324.1	005013	Cluster4720_1clades	41	PHIKZ102.1	Pseudomonas virus phiKZ	GCA_000842965.1
ANM45049.1	005014	Cluster4721_1clades	40	KTN4_291	Pseudomonas phage KTN4	GCA_002607225.1
ATN94666.1	005014	Cluster4721_1clades	40	SL2_089	Pseudomonas phage SL2	GCA_002956015.1
QJB22924.1	005014	Cluster4721_1clades	40	fnug_281	Pseudomonas phage fnug	GCA_012837215.1
AGC26353.1	005014	Cluster4721_1clades	40	PHIKZ238.2	Pseudomonas virus phiKZ	GCA_000842965.1
QAX96732.1	005015	Cluster4722_1clades	40	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX97051.1	005015	Cluster4722_1clades	40	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96097.1	005015	Cluster4722_1clades	40	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96415.1	005015	Cluster4722_1clades	40	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QIG63537.1	005016	Cluster4723_1clades	39	DAC19_46	Bacteroides phage DAC19	GCA_013387715.1
QIG63798.1	005016	Cluster4723_1clades	39	DAC20_45	Bacteroides phage DAC20	GCA_013387725.1
QIG64059.1	005016	Cluster4723_1clades	39	DAC22_45	Bacteroides phage DAC22	GCA_013387735.1
QIG64320.1	005016	Cluster4723_1clades	39	DAC23_42	Bacteroides phage DAC23	GCA_013387745.1
AYD81315.1	005017	Cluster4724_1clades	38	SEA_JUSTBECAUSE_150	Streptomyces phage JustBecause	GCA_003613775.1
QJD53718.1	005017	Cluster4724_1clades	38	SEA_KELA_148	Streptomyces phage Kela	GCA_012934305.1
QBZ72045.1	005017	Cluster4724_1clades	38	SEA_KRADAL_149	Streptomyces phage Kradal	GCA_004799925.1
AXH66308.1	005017	Cluster4724_1clades	38	SEA_SATIS_149	Streptomyces phage Satis	GCA_003366315.1
AIF27782.1	005018	Cluster4725_1clades	37	SmphiM12_081	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12968.1	005018	Cluster4725_1clades	37	PHIM19_61	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12608.1	005018	Cluster4725_1clades	37	PHIM7_60	Sinorhizobium phage phiM7	GCA_002622405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKZ65593.1	005018	Cluster4725_1clades	37	PHIN3_76	Sinorhizobium phage phiN3	GCA_001501175.1
QBX06095.1	005019	SIG+TM	36	ValB1HC_141	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61109.1	005019	SIG+TM	36	AVU32_gp268	Vibrio phage ValKK3	GCA_001501635.1
AIE13789.1	005019	SIG+TM	36	VPFG_p14	Vibrio phage nt-1	GCA_000910195.2
QNJ54721.1	005019	SIG+TM	36	vBValMR10Z_180	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ANM45065.1	005020	TM	35	KTN4_307	Pseudomonas phage KTN4	GCA_002607225.1
ATN94650.1	005020	TM	35	SL2_073	Pseudomonas phage SL2	GCA_002956015.1
QJB22940.1	005020	TM	35	fnug_297	Pseudomonas phage fnug	GCA_012837215.1
AGC26355.1	005020	TM	35	PHIKZ253.1	Pseudomonas virus phiKZ	GCA_000842965.1
AYD80075.1	005021	Cluster4728_1clades	33	JA11_270	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66676.1	005021	Cluster4728_1clades	33	JA13_273	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66996.1	005021	Cluster4728_1clades	33	JA29_270	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67645.1	005021	Cluster4728_1clades	33	JA33_271	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFU86485.1	005022	Cluster4729_1clades	32	CcrRogue_gp003	Caulobacter virus Rogue	GCA_000900555.1
AFU86816.1	005022	Cluster4729_1clades	32	CcrRogue_gp334	Caulobacter virus Rogue	GCA_000900555.1
AFU88321.1	005022	Cluster4729_1clades	32	CcrSwift_gp003	Caulobacter virus Swift	GCA_000899655.1
AFU88646.1	005022	Cluster4729_1clades	32	CcrSwift_gp328	Caulobacter virus Swift	GCA_000899655.1
AOO11650.1	005023	Cluster4730_1clades	27	ES420910_169	Cyanophage S-RIM44	GCA_002599165.1
AOO12116.1	005023	Cluster4730_1clades	27	Np200711_170	Cyanophage S-RIM44	GCA_002599205.1
AOO12351.1	005023	Cluster4730_1clades	27	Np420711_169	Cyanophage S-RIM44	GCA_002599225.1
AOO12816.1	005023	Cluster4730_1clades	27	Sn130910_169	Cyanophage S-RIM44	GCA_002599265.1
QBZ70714.1	005024	NPCBM	5119	pETSU_133	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72025.1	005024	NPCBM	3375	N1M2_162	Klebsiella phage N1M2	GCA_010092605.1
AEV89644.1	005024	NPCBM	4079	OBP_207	Pseudomonas phage OBP	GCA_000896635.1
AMS01359.1	005025	IG	1438	AR9_g275	Bacillus phage AR9	GCA_001743835.1
ALN97701.1	005025	IG	1436	Bp8pS_022	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99989.1	005025	IG	1438	PBI_PBS1_168	Bacillus virus PBS1	GCA_002601325.1
AGN12477.1	005026	Cluster4735_1clades	1182	PRTG_00330	Prochlorococcus phage P-SSM5	GCA_002991095.1
QGT54872.1	005026	Cluster4735_1clades	1081	b23_0258	Synechococcus phage B23	GCA_009745195.1
QGT54507.1	005026	Cluster4735_1clades	1081	b3_0265	Synechococcus phage B3	GCA_009745215.1
ASU03814.1	005027	Cluster4736_1clades	1109	JOAD_101	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03569.1	005027	Cluster4736_1clades	1109	RISINGSUN_101	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27210.1	005027	Cluster4736_1clades	956	PPEV_gp116	Pseudomonas phage EL	GCA_000866825.1
ADM79996.1	005028	Cluster4737_1clades	564	phiAS5_ORF0153	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17682.1	005028	Cluster4737_1clades	964	Aeh1ORF025c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17683.1	005028	Cluster4737_1clades	1069	Aeh1ORF026c	Aeromonas virus Aeh1	GCA_000843245.1
AOO14279.1	005029	Cluster4738_1clades	1033	Sn110110_085	Cyanophage S-RIM14	GCA_002599065.1
AOO14928.1	005029	Cluster4738_1clades	1033	W1230910_082	Cyanophage S-RIM14	GCA_002599125.1
AGG54304.1	005029	Cluster4738_1clades	981	CYWG_00020	Cyanophage S-SSM6b	GCA_002710425.1
BBI90569.1	005030	Astro_capsid_p	1013	HYO65_gp177	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90877.1	005030	Astro_capsid_p	1016	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39366.1	005030	Astro_capsid_p	903	BPT24_246	Tenacibaculum phage pT24	GCA_002611925.1
BBI90485.1	005031	SNF	790	HYO65_gp093	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90793.1	005031	SNF	770	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25548.1	005031	SNF	1001	BPT24_034	Tenacibaculum phage pT24	GCA_002611925.1
AMS01362.1	005032	Cluster4741_1clades	943	AR9_g278	Bacillus phage AR9	GCA_001743835.1
ALN97704.1	005032	Cluster4741_1clades	912	Bp8pS_025	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99992.1	005032	Cluster4741_1clades	943	PBI_PBS1_171	Bacillus virus PBS1	GCA_002601325.1
AIR93399.1	005033	SIG+PTSEIIA1	659	AVU42_gp013	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22918.1	005033	SIG+PTSEIIA1	939	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70028.1	005033	SIG+PTSEIIA1	785	SynMITS9220M01_012	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AFA44802.1	005034	Tail_spike_N+End_N_terminal	895	RaK2_00531	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44803.1	005034	Tail_spike_N+End_N_terminal	806	RaK2_00532	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44804.1	005034	Tail_spike_N+End_N_terminal	767	RaK2_00533	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AOV59470.1	005035	EIIBC-GUT-C	865	S330809_009	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59232.1	005035	EIIBC-GUT-C	865	C440309_009	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59708.1	005035	EIIBC-GUT-C	865	N231010_009	Synechococcus phage S-CAM4	GCA_002922155.1
AMS01143.1	005036	Cluster4746_1clades	859	AR9_g058	Bacillus phage AR9	GCA_001743835.1
ALN97813.1	005036	Cluster4746_1clades	754	Bp8pS_134	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00070.1	005036	Cluster4746_1clades	859	PBI_PBS1_248	Bacillus virus PBS1	GCA_002601325.1
AMS01364.1	005037	Cluster4747_1clades	850	AR9_g280	Bacillus phage AR9	GCA_001743835.1
ALN97706.1	005037	Cluster4747_1clades	850	Bp8pS_027	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99994.1	005037	Cluster4747_1clades	850	PBI_PBS1_173	Bacillus virus PBS1	GCA_002601325.1
ASU03829.1	005038	Cluster4749_1clades	846	JOAD_86	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03584.1	005038	Cluster4749_1clades	846	RISINGSUN_86	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27175.1	005038	Cluster4749_1clades	779	PPEV_gp081	Pseudomonas phage EL	GCA_000866825.1
QDB70329.1	005039	Cluster4750_1clades	760	CF8_0159	Aeromonas phage CF8	GCA_006384595.2
QDJ96769.1	005039	Cluster4750_1clades	822	PS1_0011	Aeromonas phage PS1	GCA_007051165.2
QFR59402.1	005039	Cluster4750_1clades	822	PS2_0011	Aeromonas phage PS2	GCA_009388305.2
QCG76047.1	005040	Cluster4751_1clades	511	EST35_0165	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76048.1	005040	Cluster4751_1clades	532	EST35_0166	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76049.1	005040	Cluster4751_1clades	787	EST35_0167	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AAX44412.1	005041	Cluster4752_1clades	673	PSSM2_034	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12239.1	005041	Cluster4752_1clades	673	PRTG_00081	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ70430.1	005041	Cluster4752_1clades	784	HOU04_gp031	Synechococcus phage S-T4	GCA_003443335.1
AMS01363.1	005042	Cluster4753_1clades	777	AR9_g279	Bacillus phage AR9	GCA_001743835.1
ALN97705.1	005042	Cluster4753_1clades	775	Bp8pS_026	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99993.1	005042	Cluster4753_1clades	777	PBI_PBS1_172	Bacillus virus PBS1	GCA_002601325.1
AOV59649.1	005043	Cluster4754_1clades	768	S330809_188	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59411.1	005043	Cluster4754_1clades	768	C440309_188	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59887.1	005043	Cluster4754_1clades	768	N231010_188	Synechococcus phage S-CAM4	GCA_002922155.1
AMS01277.1	005044	Cluster4757_1clades	653	AR9_g193	Bacillus phage AR9	GCA_001743835.1
ALN97932.1	005044	Cluster4757_1clades	644	Bp8pS_253	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99905.1	005044	Cluster4757_1clades	653	PBI_PBS1_83	Bacillus virus PBS1	GCA_002601325.1
QBX06668.1	005045	DUF5585	627	BcepSaruman_255	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74638.1	005045	DUF5585	627	BcepSauron_258	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41654.1	005045	DUF5585	622	RSL1_ORF205	Ralstonia phage phiRSL1	GCA_000879455.1
AFF28086.1	005046	T4_neck-protein	566	PAU_88	Sphingomonas phage PAU	GCA_000902455.1
BBI90684.1	005046	T4_neck-protein	619	HYO65_gp292	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90991.1	005046	T4_neck-protein	619	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAX96837.1	005047	IONCHANNEL+TM+HAMP+MA	610	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96201.1	005047	IONCHANNEL+TM+HAMP+MA	610	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96519.1	005047	IONCHANNEL+TM+HAMP+MA	610	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMS01360.1	005048	SIG+IG	599	AR9_g276	Bacillus phage AR9	GCA_001743835.1
ALN97702.1	005048	SIG+IG	596	Bp8pS_023	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99990.1	005048	SIG+IG	599	PBI_PBS1_169	Bacillus virus PBS1	GCA_002601325.1
prevph1000000285	005049	Cluster4762_1clades	282	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000286	005049	Cluster4762_1clades	220	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000224	005049	Cluster4762_1clades	595	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS05939.1	005050	DUF5401	575	ABCD_0104	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97114.1	005050	DUF5401	580	E_106	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78625.1	005050	DUF5401	457	RB43ORF103w	Escherichia virus RB43	GCA_000863505.1
AGH26130.1	005051	Cluster4765_1clades	561	CPMG_00029	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44496.1	005051	Cluster4765_1clades	527	PSSM2_118	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12470.1	005051	Cluster4765_1clades	527	PRTG_00323	Prochlorococcus phage P-SSM5	GCA_002991095.1
QDH83614.1	005052	Cluster4766_1clades	254	H1O15_gp174	Achromobacter phage Motura	GCA_006964305.1
QDH83613.1	005052	Cluster4766_1clades	378	H1O15_gp175	Achromobacter phage Motura	GCA_006964305.1
QDH83611.1	005052	Cluster4766_1clades	556	H1O15_gp177	Achromobacter phage Motura	GCA_006964305.1
AXG67345.1	005053	Cluster4767_1clades	533	AD1_301	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08572.1	005053	Cluster4767_1clades	538	Alexandra_321	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58948.1	005053	Cluster4767_1clades	432	Y3_308	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67311.1	005054	RADICAL-SAM	495	AD1_267	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08536.1	005054	RADICAL-SAM	531	Alexandra_279	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58914.1	005054	RADICAL-SAM	447	Y3_274	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AAX44394.1	005055	TM+TM	529	PSSM2_016	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12255.1	005055	TM+TM	529	PRTG_00099	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ70441.1	005055	TM+TM	485	HOU04_gp042	Synechococcus phage S-T4	GCA_003443335.1
QCW22878.1	005056	Cluster4770_1clades	519	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50479.1	005056	Cluster4770_1clades	519	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70584.1	005056	Cluster4770_1clades	527	HOU04_gp185	Synechococcus phage S-T4	GCA_003443335.1
ASU03680.1	005057	Ntox14	504	JOAD_235	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03437.1	005057	Ntox14	504	RISINGSUN_233	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27284.1	005057	Ntox14	516	PPEV_gp190	Pseudomonas phage EL	GCA_000866825.1
ASU03856.1	005058	Cluster4772_1clades	512	JOAD_59	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03611.1	005058	Cluster4772_1clades	512	RISINGSUN_59	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
CAG27148.1	005058	Cluster4772_1clades	505	PPEV_gp054	Pseudomonas phage EL	GCA_000866825.1
QAX96825.1	005059	Cluster4773_1clades	506	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96190.1	005059	Cluster4773_1clades	506	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96508.1	005059	Cluster4773_1clades	506	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBZ70695.1	005060	Cluster4774_1clades	500	pETSU_114	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72010.1	005060	Cluster4774_1clades	459	N1M2_147	Klebsiella phage N1M2	GCA_010092605.1
AEV89620.1	005060	Cluster4774_1clades	478	OBP_183	Pseudomonas phage OBP	GCA_000896635.1
QBX06669.1	005061	TM+TM	457	BcepSaruman_256	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74639.1	005061	TM+TM	492	BcepSauron_259	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41653.1	005061	TM+TM	447	RSL1_ORF204	Ralstonia phage phiRSL1	GCA_000879455.1
prev15ph1000000010	005062	Cluster4777_1clades	487	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000108	005062	Cluster4777_1clades	479	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000223	005062	Cluster4777_1clades	419	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AOO14368.1	005063	Cluster4778_1clades	465	Sn110110_174	Cyanophage S-RIM14	GCA_002599065.1
AOO15016.1	005063	Cluster4778_1clades	465	W1230910_170	Cyanophage S-RIM14	GCA_002599125.1
AGG54434.1	005063	Cluster4778_1clades	463	CYWG_00150	Cyanophage S-SSM6b	GCA_002710425.1
AGG54405.1	005064	G6PD_N+G6PD_C	460	CYWG_00121	Cyanophage S-SSM6b	GCA_002710425.1
ASR76284.1	005064	G6PD_N+G6PD_C	443	PBI_BELLAMY_248	Synechococcus phage Bellamy	GCA_002627525.1
QJT70186.1	005064	G6PD_N+G6PD_C	447	SynMITS9220M01_178	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AEO93613.1	005065	Cluster4780_2clades	203	G_354	Bacillus virus G	GCA_000917535.1
prevph1000000783	005065	Cluster4780_2clades	242	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000534	005065	Cluster4780_2clades	448	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANZ49781.1	005066	SIG+FamB-divDNAPol	446	MACHINA_143	Erwinia phage Machina	GCA_002758035.1
ANZ49225.1	005066	SIG+FamB-divDNAPol	446	HUXLEY_143	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50053.1	005066	SIG+FamB-divDNAPol	446	PARSHIK_144	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QBX06641.1	005067	Cluster4782_1clades	432	BcepSaruman_228	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74611.1	005067	Cluster4782_1clades	432	BcepSauron_231	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41697.1	005067	Cluster4782_1clades	365	RSL1_ORF249	Ralstonia phage phiRSL1	GCA_000879455.1
AIX30702.1	005068	DegT_DnrJ_EryC1	397	Syn7803US37_225	Synechococcus phage ACG-2014f	GCA_002594065.1
QCW22972.1	005068	DegT_DnrJ_EryC1	431	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50558.1	005068	DegT_DnrJ_EryC1	431	-	Synechococcus phage S-B43	GCA_006869725.1
BBI90422.1	005069	Cluster4785_1clades	334	HYO65_gp030	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90729.1	005069	Cluster4785_1clades	334	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39249.1	005069	Cluster4785_1clades	424	BPT24_124	Tenacibaculum phage pT24	GCA_002611925.1
QAX96832.1	005070	Beta-helix	421	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96197.1	005070	Beta-helix	421	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96515.1	005070	Beta-helix	421	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AMS01298.1	005071	halocin-C858	420	AR9_g214	Bacillus phage AR9	GCA_001743835.1
ALN97949.1	005071	halocin-C858	415	Bp8pS_270	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99927.1	005071	halocin-C858	420	PBI_PBS1_105	Bacillus virus PBS1	GCA_002601325.1
AMS01335.1	005072	Cluster4788_1clades	416	AR9_g251	Bacillus phage AR9	GCA_001743835.1
ALN97688.1	005072	Cluster4788_1clades	416	Bp8pS_009	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99965.1	005072	Cluster4788_1clades	416	PBI_PBS1_144	Bacillus virus PBS1	GCA_002601325.1
prevph1000000698	005073	SIG+SidE	124	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000708	005073	SIG+SidE	345	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000709	005073	SIG+SidE	417	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AMS01302.1	005074	Cluster4790_1clades	396	AR9_g218	Bacillus phage AR9	GCA_001743835.1
ALN97953.1	005074	Cluster4790_1clades	408	Bp8pS_274	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99931.1	005074	Cluster4790_1clades	396	PBI_PBS1_109	Bacillus virus PBS1	GCA_002601325.1
AXG67277.1	005075	Cluster4791_1clades	242	AD1_233	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08502.1	005075	Cluster4791_1clades	403	Alexandra_242	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58877.1	005075	Cluster4791_1clades	227	Y3_237	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ASU03701.1	005076	Cluster4792_1clades	400	JOAD_214	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03458.1	005076	Cluster4792_1clades	400	RISINGSUN_212	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27261.1	005076	Cluster4792_1clades	388	PPEV_gp167	Pseudomonas phage EL	GCA_000866825.1
AYD81272.1	005077	TM+TM+TM+TM	396	SEA_JUSTBECAUSE_103	Streptomyces phage JustBecause	GCA_003613775.1
QJD53675.1	005077	TM+TM+TM+TM	396	SEA_KELA_104	Streptomyces phage Kela	GCA_012934305.1
AXH66266.1	005077	TM+TM+TM+TM	369	SEA_SATIS_105	Streptomyces phage Satis	GCA_003366315.1
BBI90474.1	005078	Cluster4795_1clades	396	HYO65_gp082	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90780.1	005078	Cluster4795_1clades	396	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39331.1	005078	Cluster4795_1clades	207	BPT24_207	Tenacibaculum phage pT24	GCA_002611925.1
QDH83706.1	005079	Cluster4796_1clades	392	H1O15_gp122	Achromobacter phage Motura	GCA_006964305.1
QBX06692.1	005079	Cluster4796_1clades	380	BcepSaruman_279	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74660.1	005079	Cluster4796_1clades	380	BcepSauron_280	Burkholderia phage BcepSauron	GCA_005394215.1
QDH83688.1	005080	SpermGS-ATPgrasp	375	H1O15_gp273	Achromobacter phage Motura	GCA_006964305.1
QIG65901.1	005080	SpermGS-ATPgrasp	386	phiOC_p240	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BAG41498.1	005080	SpermGS-ATPgrasp	373	gsp	Ralstonia phage phiRSL1	GCA_000879455.1
ABY63023.1	005081	TM	381	201phi2-1p193	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76813.1	005081	TM	385	PHABIO_182	Pseudomonas phage Phabio	GCA_002624965.1
ARV76814.1	005081	TM	364	PHABIO_183	Pseudomonas phage Phabio	GCA_002624965.1
ANS05956.1	005082	SPASM	384	ABCD_0162	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97175.1	005082	SPASM	383	E_167	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78691.1	005082	SPASM	340	RB43ORF169c	Escherichia virus RB43	GCA_000863505.1
AGX01926.1	005083	Cluster4800_1clades	200	CF95_gp204	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65387.1	005083	Cluster4800_1clades	382	2050HW_00052	Serratia phage 2050HW	GCA_002628125.1
QDB71168.1	005083	Cluster4800_1clades	382	CPT_Moabite_138	Serratia phage Moabite	GCA_006384735.1
ASU03831.1	005084	SHS2	381	JOAD_84	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03586.1	005084	SHS2	381	RISINGSUN_84	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27173.1	005084	SHS2	378	PPEV_gp079	Pseudomonas phage EL	GCA_000866825.1
AGH07488.1	005085	DUF4338	380	CYVG_00044	Cyanophage S-SSM6a	GCA_002710385.1
AXQ70552.1	005085	DUF4338	370	HOU04_gp153	Synechococcus phage S-T4	GCA_003443335.1
QJT70149.1	005085	DUF4338	352	SynMITS9220M01_136	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMS01304.1	005086	Cluster4803_1clades	377	AR9_g220	Bacillus phage AR9	GCA_001743835.1
ALN97954.1	005086	Cluster4803_1clades	372	Bp8pS_275	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99933.1	005086	Cluster4803_1clades	377	PBI_PBS1_111	Bacillus virus PBS1	GCA_002601325.1
AXH72890.1	005087	CTP_transf_like	374	-	Myoviridae sp.	GCA_003657725.1
prevph1000000184	005087	CTP_transf_like	164	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000147	005087	CTP_transf_like	164	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMS01300.1	005088	Cluster4805_1clades	372	AR9_g216	Bacillus phage AR9	GCA_001743835.1
ALN97951.1	005088	Cluster4805_1clades	368	Bp8pS_272	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99929.1	005088	Cluster4805_1clades	372	PBI_PBS1_107	Bacillus virus PBS1	GCA_002601325.1
AUZ94951.1	005089	Cluster4806_1clades	263	FDI40_gp169	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04865.2	005089	Cluster4806_1clades	357	AVU11_gp073	Ralstonia phage RSF1	GCA_001500875.1
BAQ02598.2	005089	Cluster4806_1clades	372	-	Ralstonia phage RSL2	GCA_001503055.1
ASV44210.1	005090	SIG+TM+TM+TM	365	PBI_SCTP2_195	Salicola phage SCTP-2	GCA_002625545.1
BBA65390.1	005090	SIG+TM+TM+TM	281	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96418.1	005090	SIG+TM+TM+TM	269	Xoosp13_232	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AUZ94950.1	005091	Radical_SAM	365	FDI40_gp168	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04867.1	005091	Radical_SAM	340	AVU11_gp075	Ralstonia phage RSF1	GCA_001500875.1
BAQ02600.1	005091	Radical_SAM	340	AVU38_gp072	Ralstonia phage RSL2	GCA_001503055.1
AFO71385.1	005092	Cluster4809_1clades	364	CR5_165	Cronobacter phage CR5	GCA_000910235.1
QBP07596.1	005092	Cluster4809_1clades	356	DERBICUS_170	Erwinia phage Derbicus	GCA_004521655.1
ANZ49019.1	005092	Cluster4809_1clades	356	EARLPHILLIPIV_170	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
AMS01142.1	005093	Cluster4810_1clades	347	AR9_g057	Bacillus phage AR9	GCA_001743835.1
ALN97812.1	005093	Cluster4810_1clades	339	Bp8pS_133	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00069.1	005093	Cluster4810_1clades	363	PBI_PBS1_247	Bacillus virus PBS1	GCA_002601325.1
AUZ94947.1	005094	RADICAL-SAM	360	FDI40_gp165	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04871.2	005094	RADICAL-SAM	362	AVU11_gp079	Ralstonia phage RSF1	GCA_001500875.1
BAQ02603.1	005094	RADICAL-SAM	358	AVU38_gp075	Ralstonia phage RSL2	GCA_001503055.1
AOV59474.1	005095	DUF2345	354	S330809_013	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59236.1	005095	DUF2345	354	C440309_013	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59712.1	005095	DUF2345	306	N231010_013	Synechococcus phage S-CAM4	GCA_002922155.1
AUZ94953.1	005096	RADICAL-SAM	352	FDI40_gp171	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04862.1	005096	RADICAL-SAM	354	AVU11_gp070	Ralstonia phage RSF1	GCA_001500875.1
BAQ02595.1	005096	RADICAL-SAM	354	AVU38_gp067	Ralstonia phage RSL2	GCA_001503055.1
AMS01146.1	005097	Cluster4815_1clades	336	AR9_g062	Bacillus phage AR9	GCA_001743835.1
ALN97817.1	005097	Cluster4815_1clades	347	Bp8pS_138	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00074.1	005097	Cluster4815_1clades	336	PBI_PBS1_252	Bacillus virus PBS1	GCA_002601325.1
AMS01299.1	005098	TM	344	AR9_g215	Bacillus phage AR9	GCA_001743835.1
ALN97950.1	005098	TM	347	Bp8pS_271	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99928.1	005098	TM	344	PBI_PBS1_106	Bacillus virus PBS1	GCA_002601325.1
AFF28167.1	005099	BACTERIALFRINGE	308	PAU_169	Sphingomonas phage PAU	GCA_000902455.1
AFF28168.1	005099	BACTERIALFRINGE	326	PAU_170	Sphingomonas phage PAU	GCA_000902455.1
AFF28169.1	005099	BACTERIALFRINGE	345	PAU_171	Sphingomonas phage PAU	GCA_000902455.1
AMS01245.1	005100	Cluster4819_1clades	341	AR9_g161	Bacillus phage AR9	GCA_001743835.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALN97902.1	005100	Cluster4819_1clades	344	Bp8pS_223	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99871.1	005100	Cluster4819_1clades	341	PBI_PBS1_49	Bacillus virus PBS1	GCA_002601325.1
QGZ14563.1	005101	Cluster4820_1clades	339	HWC77_gp200	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04170.1	005101	Cluster4820_1clades	339	HWC03_gp015	Vibrio phage 2 TSL-2019	GCA_006964105.1
AUR80984.1	005101	Cluster4820_1clades	339	Aphrodite1_0155	Vibrio phage Aphrodite1	GCA_002958015.1
AXG67115.1	005102	Tox-CNF	332	AD1_071	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08351.1	005102	Tox-CNF	309	Alexandra_73	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58714.1	005102	Tox-CNF	273	Y3_074	Erwinia phage vB_EamM_Y3	GCA_002955045.1
prevph1000000167	005103	Cluster4824_1clades	147	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000129	005103	Cluster4824_1clades	331	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000364	005103	Cluster4824_1clades	331	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMS01165.1	005104	SIG+TM	316	AR9_g081	Bacillus phage AR9	GCA_001743835.1
ALN97831.1	005104	SIG+TM	326	Bp8pS_152	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00096.1	005104	SIG+TM	316	PBI_PBS1_274	Bacillus virus PBS1	GCA_002601325.1
ANS05969.1	005105	Cluster4827_1clades	326	ABCD_0250	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97268.1	005105	Cluster4827_1clades	260	E_260	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78790.1	005105	Cluster4827_1clades	205	RB43ORF268w	Escherichia virus RB43	GCA_000863505.1
AOV59650.1	005106	Cluster4828_1clades	324	S330809_189	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59412.1	005106	Cluster4828_1clades	324	C440309_189	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59888.1	005106	Cluster4828_1clades	324	N231010_189	Synechococcus phage S-CAM4	GCA_002922155.1
BBI90531.1	005107	Cluster4829_1clades	324	HYO65_gp139	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90839.1	005107	Cluster4829_1clades	324	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39172.1	005107	Cluster4829_1clades	180	BPT24_049	Tenacibaculum phage pT24	GCA_002611925.1
AXG67132.1	005108	Cluster4830_1clades	164	AD1_088	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67133.1	005108	Cluster4830_1clades	316	AD1_089	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AQT28566.1	005108	Cluster4830_1clades	323	YOLOSWAG_83	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
BAS05002.1	005109	Cluster4831_1clades	217	AVU11_gp210	Ralstonia phage RSF1	GCA_001500875.1
BAQ02731.1	005109	Cluster4831_1clades	218	AVU38_gp203	Ralstonia phage RSL2	GCA_001503055.1
BAQ02732.2	005109	Cluster4831_1clades	322	-	Ralstonia phage RSL2	GCA_001503055.1
prevph1000000289	005110	Cluster4832_1clades	145	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000291	005110	Cluster4832_1clades	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000226	005110	Cluster4832_1clades	322	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS05970.1	005111	Cluster4833_1clades	319	ABCD_0173	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97186.1	005111	Cluster4833_1clades	102	E_178	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78703.1	005111	Cluster4833_1clades	41	RB43ORF181c	Escherichia virus RB43	GCA_000863505.1
BBI90472.1	005112	Cluster4834_1clades	101	HYO65_gp080	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90471.1	005112	Cluster4834_1clades	166	HYO65_gp079	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90778.1	005112	Cluster4834_1clades	319	-	Tenacibaculum phage PTm5	GCA_009730715.1
AAX44382.1	005113	Cluster4835_1clades	305	PSSM2_004	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44383.1	005113	Cluster4835_1clades	318	PSSM2_005	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12265.1	005113	Cluster4835_1clades	305	PRTG_00111	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOV59508.1	005114	Cluster4836_1clades	317	S330809_047	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59270.1	005114	Cluster4836_1clades	317	C440309_047	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59746.1	005114	Cluster4836_1clades	317	N231010_047	Synechococcus phage S-CAM4	GCA_002922155.1
AMS01286.1	005115	Cluster4837_1clades	316	AR9_g202	Bacillus phage AR9	GCA_001743835.1
ALN97940.1	005115	Cluster4837_1clades	198	Bp8pS_261	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99914.1	005115	Cluster4837_1clades	316	PBI_PBS1_92	Bacillus virus PBS1	GCA_002601325.1
ANS05972.1	005116	Cluster4838_1clades	308	ABCD_0255	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97274.1	005116	Cluster4838_1clades	316	E_266	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78795.1	005116	Cluster4838_1clades	308	RB43ORF273w	Escherichia virus RB43	GCA_000863505.1
QAX96829.1	005117	Cluster4839_1clades	313	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96194.1	005117	Cluster4839_1clades	313	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96512.1	005117	Cluster4839_1clades	313	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
BBI90492.1	005118	Cluster4840_1clades	308	HYO65_gp100	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90800.1	005118	Cluster4840_1clades	308	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25547.1	005118	Cluster4840_1clades	312	BPT24_030	Tenacibaculum phage pT24	GCA_002611925.1
QCW18568.1	005119	Cluster4841_1clades	310	7t3_047	Salmonella phage 7t3	GCA_006083215.1
AZU98397.1	005119	Cluster4841_1clades	310	CPT_Munch_465	Salmonella phage Munch	GCA_004015485.1
QIG63116.1	005119	Cluster4841_1clades	310	SEPL_503	Salmonella phage SE_PL	GCA_011067555.1
AMS01253.1	005120	Cluster4842_1clades	307	AR9_g169	Bacillus phage AR9	GCA_001743835.1
ALN97925.1	005120	Cluster4842_1clades	306	Bp8pS_246	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99879.1	005120	Cluster4842_1clades	307	PBI_PBS1_57	Bacillus virus PBS1	GCA_002601325.1
ANS05977.1	005121	Cluster4843_1clades	298	ABCD_0229	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97246.1	005121	Cluster4843_1clades	289	E_238	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78764.1	005121	Cluster4843_1clades	306	RB43ORF242w	Escherichia virus RB43	GCA_000863505.1
AEO93385.1	005122	Cluster4844_1clades	306	G_123	Bacillus virus G	GCA_000917535.1
AEO93403.1	005122	Cluster4844_1clades	279	G_141	Bacillus virus G	GCA_000917535.1
AEO93492.1	005122	Cluster4844_1clades	225	G_233	Bacillus virus G	GCA_000917535.1
QDH83559.1	005123	Cluster4846_1clades	302	H1O15_gp229	Achromobacter phage Motura	GCA_006964305.1
BBA65619.1	005123	Cluster4846_1clades	224	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65160.1	005123	Cluster4846_1clades	224	-	Xanthomonas phage XacN1	GCA_003173815.1
AUZ94946.1	005124	RADICAL-SAM	237	FDI40_gp164	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04873.2	005124	RADICAL-SAM	286	AVU11_agp18	Ralstonia phage RSF1	GCA_001500875.1
BAQ02605.2	005124	RADICAL-SAM	301	-	Ralstonia phage RSL2	GCA_001503055.1
QDH83561.1	005125	Cluster4848_1clades	203	H1O15_gp227	Achromobacter phage Motura	GCA_006964305.1
AXQ68381.1	005125	Cluster4848_1clades	299	CcrBL10_gp177c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86664.1	005125	Cluster4848_1clades	299	CcrRogue_gp182	Caulobacter virus Rogue	GCA_000900555.1
AXG67089.1	005126	Cluster4850_1clades	296	AD1_045	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08323.1	005126	Cluster4850_1clades	296	Alexandra_43	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58687.1	005126	Cluster4850_1clades	293	Y3_047	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AMM44946.1	005127	BACTERIALFRINGE	294	SP15_148	Bacillus phage SP-15	GCA_001754685.1
AEO93568.1	005127	BACTERIALFRINGE	246	G_309	Bacillus virus G	GCA_000917535.1
AFF28185.1	005127	BACTERIALFRINGE	293	PAU_187	Sphingomonas phage PAU	GCA_000902455.1
QCW18758.1	005128	Cluster4853_1clades	237	7t3_0237	Salmonella phage 7t3	GCA_006083215.1
AZU98027.1	005128	Cluster4853_1clades	291	CPT_Munch_083	Salmonella phage Munch	GCA_004015485.1
QIG62953.1	005128	Cluster4853_1clades	237	SEPL_340	Salmonella phage SE_PL	GCA_011067555.1
BBA65724.1	005129	Cluster4854_1clades	275	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65265.1	005129	Cluster4854_1clades	275	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96304.1	005129	Cluster4854_1clades	291	Xoosp13_117	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ABY62990.1	005130	Cluster4855_1clades	290	201phi2-1p160	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63277.1	005130	Cluster4855_1clades	281	201phi2-1p454	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBJ02938.1	005130	Cluster4855_1clades	283	PSA21_420	Pseudomonas phage Psa21	GCA_004340405.1
AEO93630.1	005131	Cluster4856_1clades	280	G_371	Bacillus virus G	GCA_000917535.1
AEO93631.1	005131	Cluster4856_1clades	290	G_372	Bacillus virus G	GCA_000917535.1
AEO93632.1	005131	Cluster4856_1clades	285	G_373	Bacillus virus G	GCA_000917535.1
AQW88580.1	005132	Cluster4857_1clades	289	BF_0055	Serratia phage BF	GCA_002619745.1
SOK58855.1	005132	Cluster4857_1clades	287	g047	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58317.1	005132	Cluster4857_1clades	287	g040	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASU03863.1	005133	CRP-HTH	284	JOAD_52	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03618.1	005133	CRP-HTH	284	RISINGSUN_52	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27140.1	005133	CRP-HTH	289	PPEV_gp046	Pseudomonas phage EL	GCA_000866825.1
QCW18603.1	005134	Cluster4859_1clades	288	7t3_082	Salmonella phage 7t3	GCA_006083215.1
AZU98428.1	005134	Cluster4859_1clades	288	CPT_Munch_496	Salmonella phage Munch	GCA_004015485.1
QIG63085.1	005134	Cluster4859_1clades	288	SEPL_472	Salmonella phage SE_PL	GCA_011067555.1
AOV59500.1	005135	Cluster4860_1clades	287	S330809_039	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59262.1	005135	Cluster4860_1clades	287	C440309_039	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59738.1	005135	Cluster4860_1clades	287	N231010_039	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67362.1	005136	Cluster4861_1clades	276	AD1_318	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08623.1	005136	Cluster4861_1clades	287	Alexandra_335	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58961.1	005136	Cluster4861_1clades	282	Y3_321	Erwinia phage vB_EamM_Y3	GCA_002955045.1
CCH63627.1	005137	Cluster4862_1clades	172	CP21_165	Campylobacter virus CP21	GCA_000902535.1
CCH63628.1	005137	Cluster4862_1clades	284	CP21_166	Campylobacter virus CP21	GCA_000902535.1
CCH63654.1	005137	Cluster4862_1clades	141	CP21_192	Campylobacter virus CP21	GCA_000902535.1
QBZ70720.1	005138	Cluster4863_1clades	158	pETSU_139	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72030.1	005138	Cluster4863_1clades	284	N1M2_167	Klebsiella phage N1M2	GCA_010092605.1
AEV89652.1	005138	Cluster4863_1clades	155	OBP_215	Pseudomonas phage OBP	GCA_000896635.1
AFU87894.1	005139	Cluster4864_1clades	282	CcrColossus_gp024	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68564.1	005139	Cluster4864_1clades	282	CcrPW_gp025	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69013.1	005139	Cluster4864_1clades	282	CcrPW_gp474	Caulobacter phage CcrPW	GCA_003443275.1
AFQ96807.1	005140	Cluster4865_1clades	280	G173_gp262	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48105.1	005140	Cluster4865_1clades	269	ASESINO_92	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50519.1	005140	Cluster4865_1clades	277	STRATTON_94	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXG67287.1	005141	Cluster4866_1clades	255	AD1_243	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08615.1	005141	Cluster4866_1clades	279	Alexandra_252	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58887.1	005141	Cluster4866_1clades	253	Y3_247	Erwinia phage vB_EamM_Y3	GCA_002955045.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBI90490.1	005142	Cluster4867_1clades	278	HYO65_gp098	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90798.1	005142	Cluster4867_1clades	278	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25559.1	005142	Cluster4867_1clades	271	BPT24_154	Tenacibaculum phage pT24	GCA_002611925.1
AEO93376.1	005143	SIG+MACRODOMAIN	276	G_114	Bacillus virus G	GCA_000917535.1
prevph1000000325	005143	SIG+MACRODOMAIN	278	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000254	005143	SIG+MACRODOMAIN	278	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93502.1	005144	TM+TM+TM+TM+TM	249	G_243	Bacillus virus G	GCA_000917535.1
prevph1000000426	005144	TM+TM+TM+TM+TM	278	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000337	005144	TM+TM+TM+TM+TM	278	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMS01295.1	005145	Cluster4870_1clades	276	AR9_g211	Bacillus phage AR9	GCA_001743835.1
ALN97946.1	005145	Cluster4870_1clades	272	Bp8pS_267	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99924.1	005145	Cluster4870_1clades	276	PBI_PBS1_102	Bacillus virus PBS1	GCA_002601325.1
QDB70432.1	005146	Cluster4871_1clades	267	CF8_0020	Aeromonas phage CF8	GCA_006384595.2
QDJ97321.1	005146	Cluster4871_1clades	273	D6_0161	Aeromonas phage D6	GCA_007051205.2
QDH47102.1	005146	Cluster4871_1clades	273	LAh10_82	Aeromonas phage LAh10	GCA_006863975.1
QBX32526.1	005147	Cluster4872_1clades	177	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03781.1	005147	Cluster4872_1clades	272	358	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42099.1	005147	Cluster4872_1clades	177	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BBI90580.1	005148	Cluster4873_1clades	246	HYO65_gp188	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90888.1	005148	Cluster4873_1clades	246	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39251.1	005148	Cluster4873_1clades	271	BPT24_126	Tenacibaculum phage pT24	GCA_002611925.1
AMS01180.1	005149	Cluster4874_1clades	268	AR9_g096	Bacillus phage AR9	GCA_001743835.1
ALN97853.1	005149	Cluster4874_1clades	270	Bp8pS_174	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00114.1	005149	Cluster4874_1clades	268	PBI_PBS1_292	Bacillus virus PBS1	GCA_002601325.1
AEO93853.1	005150	Cluster4875_1clades	185	G_608	Bacillus virus G	GCA_000917535.1
AEO93895.1	005150	Cluster4875_1clades	269	G_652	Bacillus virus G	GCA_000917535.1
AEO93908.1	005150	Cluster4875_1clades	147	G_665	Bacillus virus G	GCA_000917535.1
AFF28174.1	005151	Cluster4876_1clades	269	PAU_176	Sphingomonas phage PAU	GCA_000902455.1
BBI90434.1	005151	Cluster4876_1clades	245	HYO65_gp042	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90741.1	005151	Cluster4876_1clades	245	-	Tenacibaculum phage PTm5	GCA_009730715.1
AUZ94891.1	005152	Cluster4877_1clades	259	FDI40_gp084	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95213.1	005152	Cluster4877_1clades	265	FDI40_gp454	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95210.1	005152	Cluster4877_1clades	269	FDI40_gp451	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFC21860.1	005153	Cluster4878_1clades	267	GAP32_407	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21930.1	005153	Cluster4878_1clades	246	GAP32_472	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW89010.1	005153	Cluster4878_1clades	246	BF_0485	Serratia phage BF	GCA_002619745.1
QCG76039.1	005154	DUF4318	232	EST35_0157	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44499.1	005154	DUF4318	266	PBI_SCTP2_484	Salicola phage SCTP-2	GCA_002625545.1
QDJ96317.1	005154	DUF4318	221	Xoosp13_130	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AND75194.1	005155	Cluster4880_1clades	161	ME3_33	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83701.1	005155	Cluster4880_1clades	218	0305phi8-36p143	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83702.1	005155	Cluster4880_1clades	265	0305phi8-36p144	Bacillus phage 0305phi8-36	GCA_000871045.1
QBX32425.1	005156	SspB	265	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03693.1	005156	SspB	262	270	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41996.1	005156	SspB	265	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANZ49750.1	005157	Cluster4882_1clades	262	MACHINA_112	Erwinia phage Machina	GCA_002758035.1
ANZ49194.1	005157	Cluster4882_1clades	262	HUXLEY_112	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50022.1	005157	Cluster4882_1clades	262	PARSHIK_113	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QJD53784.1	005158	HTH	262	SEA_KELA_224	Streptomyces phage Kela	GCA_012934305.1
QBZ72109.1	005158	HTH	262	SEA_KRADAL_223	Streptomyces phage Kradal	GCA_004799925.1
AXH66370.1	005158	HTH	262	SEA_SATIS_221	Streptomyces phage Satis	GCA_003366315.1
QBX32395.1	005159	Cluster4885_1clades	156	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32394.1	005159	Cluster4885_1clades	98	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41965.1	005159	Cluster4885_1clades	260	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AJK27603.1	005160	MTHFR	259	PTIM40_181	Cyanophage P-TIM40	GCA_001470935.1
AAX44570.1	005160	MTHFR	225	PSSM2_192	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12403.1	005160	MTHFR	225	PRTG_00250	Prochlorococcus phage P-SSM5	GCA_002991095.1
prevph1000000402	005161	Cluster4887_1clades	109	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000403	005161	Cluster4887_1clades	92	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000320	005161	Cluster4887_1clades	260	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBI90590.1	005162	TM	74	HYO65_gp198	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90898.1	005162	TM	225	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39223.1	005162	TM	258	BPT24_098	Tenacibaculum phage pT24	GCA_002611925.1
AMS01228.1	005163	KAP-glycosylase	257	AR9_g144	Bacillus phage AR9	GCA_001743835.1
ALN97890.1	005163	KAP-glycosylase	242	Bp8pS_211	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99852.1	005163	KAP-glycosylase	257	PBI_PBS1_30	Bacillus virus PBS1	GCA_002601325.1
AMS01207.1	005164	Cluster4890_1clades	256	AR9_g123	Bacillus phage AR9	GCA_001743835.1
ALN97878.1	005164	Cluster4890_1clades	256	Bp8pS_199	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99832.1	005164	Cluster4890_1clades	256	PBI_PBS1_10	Bacillus virus PBS1	GCA_002601325.1
AMS01213.1	005165	Cluster4891_1clades	238	AR9_g129	Bacillus phage AR9	GCA_001743835.1
ALN97884.1	005165	Cluster4891_1clades	255	Bp8pS_205	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99838.1	005165	Cluster4891_1clades	255	PBI_PBS1_16	Bacillus virus PBS1	GCA_002601325.1
AMS01284.1	005166	Cluster4892_1clades	255	AR9_g200	Bacillus phage AR9	GCA_001743835.1
ALN97937.1	005166	Cluster4892_1clades	220	Bp8pS_258	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99912.1	005166	Cluster4892_1clades	255	PBI_PBS1_90	Bacillus virus PBS1	GCA_002601325.1
BBA65677.1	005167	C3RHD	250	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65218.1	005167	C3RHD	250	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96246.1	005167	C3RHD	254	Xoosp13_59	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXG67063.1	005168	Cluster4894_1clades	206	AD1_019	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08599.1	005168	Cluster4894_1clades	253	Alexandra_20	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58661.1	005168	Cluster4894_1clades	202	Y3_021	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18762.1	005169	Cluster4895_1clades	253	7t3_0241	Salmonella phage 7t3	GCA_006083215.1
AZU98031.1	005169	Cluster4895_1clades	253	CPT_Munch_087	Salmonella phage Munch	GCA_004015485.1
QIG62949.1	005169	Cluster4895_1clades	253	SEPL_336	Salmonella phage SE_PL	GCA_011067555.1
ANZ49725.1	005170	Cluster4897_1clades	250	MACHINA_87	Erwinia phage Machina	GCA_002758035.1
ANZ49170.1	005170	Cluster4897_1clades	250	HUXLEY_88	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49998.1	005170	Cluster4897_1clades	250	PARSHIK_89	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
BBA65189.1	005171	Cluster4898_1clades	247	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65648.1	005171	Cluster4898_1clades	247	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96218.1	005171	Cluster4898_1clades	250	Xoosp13_31	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06696.1	005172	TM	154	BcepSaruman_283	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74664.1	005172	TM	154	BcepSauron_284	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41628.2	005172	TM	249	-	Ralstonia phage phiRSL1	GCA_000879455.1
AKF13104.1	005173	Cluster4900_1clades	248	PHIM19_199	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12744.1	005173	Cluster4900_1clades	248	PHIM7_199	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13474.1	005173	Cluster4900_1clades	248	PHIN3_211	Sinorhizobium phage phiN3	GCA_001501175.1
AGH07564.1	005174	Epimerase	247	CYVG_00120	Cyanophage S-SSM6a	GCA_002710385.1
AIR93533.1	005174	Epimerase	244	AVU42_gp196	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76190.1	005174	Epimerase	238	PBI_BELLAMY_145	Synechococcus phage Bellamy	GCA_002627525.1
QBX32524.1	005175	Cluster4903_1clades	225	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03778.1	005175	Cluster4903_1clades	244	355	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42097.1	005175	Cluster4903_1clades	225	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANS05993.1	005176	HAUS2	244	ABCD_0256	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97275.1	005176	HAUS2	244	E_267	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78796.1	005176	HAUS2	237	RB43ORF274w	Escherichia virus RB43	GCA_000863505.1
BBA65266.1	005177	SIG+PTSEIIA1	244	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65725.1	005177	SIG+PTSEIIA1	244	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96305.1	005177	SIG+PTSEIIA1	240	Xoosp13_118	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QAY01371.1	005178	Cluster4907_1clades	101	ASwh1_311	Aeromonas phage Aswh_1	GCA_004146945.1
AXQ69405.1	005178	Cluster4907_1clades	243	CcrBL9_gp381	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69962.1	005178	Cluster4907_1clades	242	CcrSC_gp380	Caulobacter phage CcrSC	GCA_003443315.1
QBX06688.1	005179	SIG+DUF3175	161	BcepSaruman_275	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74656.1	005179	SIG+DUF3175	161	BcepSauron_276	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41635.1	005179	SIG+DUF3175	243	RSL1_ORF186	Ralstonia phage phiRSL1	GCA_000879455.1
AXG67113.1	005180	Cluster4909_1clades	241	AD1_069	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08349.1	005180	Cluster4909_1clades	242	Alexandra_71	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58712.1	005180	Cluster4909_1clades	218	Y3_072	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BBI90494.1	005181	Cluster4910_1clades	178	HYO65_gp102	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90802.1	005181	Cluster4910_1clades	178	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39321.1	005181	Cluster4910_1clades	242	BPT24_197	Tenacibaculum phage pT24	GCA_002611925.1
BBA65239.1	005182	SIG+TM+TM	242	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65698.1	005182	SIG+TM+TM	242	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96279.1	005182	SIG+TM+TM	236	Xoosp13_92	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90540.1	005183	Cluster4912_1clades	242	HYO65_gp148	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90848.1	005183	Cluster4912_1clades	242	-	Tenacibaculum phage PTm5	GCA_009730715.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAX25549.1	005183	Cluster4912_1clades	240	BPT24_039	Tenacibaculum phage pT24	GCA_002611925.1
AXG67166.1	005184	Cluster4913_1clades	241	AD1_122	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08399.1	005184	Cluster4913_1clades	241	Alexandra_127	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58763.1	005184	Cluster4913_1clades	231	Y3_123	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AEO93937.1	005185	Thymidylate_kin	240	G_694	Bacillus virus G	GCA_000917535.1
AXH70972.1	005185	Thymidylate_kin	220	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21228.1	005185	Thymidylate_kin	240	-	Vibrio phage vB_pir03	GCA_014319855.1
AXG67285.1	005186	Cluster4915_1clades	233	AD1_241	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08509.1	005186	Cluster4915_1clades	240	Alexandra_250	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58885.1	005186	Cluster4915_1clades	239	Y3_245	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AFU88235.1	005187	Cluster4916_1clades	239	CcrColossus_gp365	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68911.1	005187	Cluster4916_1clades	239	CcrPW_gp372c	Caulobacter phage CcrPW	GCA_003443275.1
AFU86764.1	005187	Cluster4916_1clades	239	CcrRogue_gp282	Caulobacter virus Rogue	GCA_000900555.1
AYD80058.1	005188	Cluster4917_1clades	239	JA11_253	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66657.1	005188	Cluster4917_1clades	239	JA13_254	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67628.1	005188	Cluster4917_1clades	239	JA33_254	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QMP24040.1	005189	Cluster4918_1clades	239	-	Proteus phage 10	GCA_014071245.1
ABY62867.1	005189	Cluster4918_1clades	228	201phi2-1p034	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77084.1	005189	Cluster4918_1clades	173	PHABIO_456	Pseudomonas phage Phabio	GCA_002624965.1
AGH56909.1	005190	Fe_bilin_red	222	CPXG_00106	Cyanophage P-RSM6	GCA_000906155.1
AJK27586.1	005190	Fe_bilin_red	232	PTIM40_159	Cyanophage P-TIM40	GCA_001470935.1
AGG54437.1	005190	Fe_bilin_red	238	CYWG_00153	Cyanophage S-SSM6b	GCA_002710425.1
AMS01226.1	005191	Cluster4920_1clades	228	AR9_g142	Bacillus phage AR9	GCA_001743835.1
ALN97888.1	005191	Cluster4920_1clades	237	Bp8pS_209	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99851.1	005191	Cluster4920_1clades	228	PBI_PBS1_29	Bacillus virus PBS1	GCA_002601325.1
AUZ95006.1	005192	Cluster4921_1clades	197	FDI40_gp224	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65779.1	005192	Cluster4921_1clades	197	phiOC_p114	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AKF13646.1	005192	Cluster4921_1clades	236	PHIN3_383	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01371.1	005193	Cluster4922_1clades	224	AR9_g287	Bacillus phage AR9	GCA_001743835.1
ALN97709.1	005193	Cluster4922_1clades	236	Bp8pS_030	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00002.1	005193	Cluster4922_1clades	214	PBI_PBS1_180	Bacillus virus PBS1	GCA_002601325.1
AMS01208.1	005194	DUF1633	236	AR9_g124	Bacillus phage AR9	GCA_001743835.1
ALN97879.1	005194	DUF1633	219	Bp8pS_200	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99833.1	005194	DUF1633	236	PBI_PBS1_11	Bacillus virus PBS1	GCA_002601325.1
AOV59565.1	005195	Cluster4924_1clades	236	S330809_104	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59327.1	005195	Cluster4924_1clades	236	C440309_104	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59803.1	005195	Cluster4924_1clades	236	N231010_104	Synechococcus phage S-CAM4	GCA_002922155.1
ALY07229.1	005196	GxC-R	207	VmeM32_00243	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07230.1	005196	GxC-R	191	VmeM32_00244	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07231.1	005196	GxC-R	234	VmeM32_00245	Vibrio phage vB_VmeM-32	GCA_002608825.1
AFQ96568.1	005197	Cluster4927_1clades	232	G173_gp023	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48128.1	005197	Cluster4927_1clades	234	ASESINO_115	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50543.1	005197	Cluster4927_1clades	234	STRATTON_118	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QBZ70863.1	005198	IWS1	234	pETSU_282	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71895.1	005198	IWS1	204	N1M2_32	Klebsiella phage N1M2	GCA_010092605.1
AEV89490.1	005198	IWS1	208	OBP_053	Pseudomonas phage OBP	GCA_000896635.1
QCG75921.1	005199	Cluster4929_1clades	234	EST35_0038	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75968.1	005199	Cluster4929_1clades	156	EST35_0086	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75980.1	005199	Cluster4929_1clades	153	EST35_0098	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AXG67114.1	005200	Cluster4930_1clades	233	AD1_070	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08350.1	005200	Cluster4930_1clades	229	Alexandra_72	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58713.1	005200	Cluster4930_1clades	231	Y3_073	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67349.1	005201	Cluster4931_1clades	231	AD1_305	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08576.1	005201	Cluster4931_1clades	221	Alexandra_325	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58952.1	005201	Cluster4931_1clades	210	Y3_312	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QBZ70828.1	005202	Cluster4932_1clades	219	pETSU_247	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71868.1	005202	Cluster4932_1clades	231	N1M2_5	Klebsiella phage N1M2	GCA_010092605.1
AEV89459.1	005202	Cluster4932_1clades	222	OBP_022	Pseudomonas phage OBP	GCA_000896635.1
QBX32421.1	005203	Ribonuc_P_40	166	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03690.1	005203	Ribonuc_P_40	230	267	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41992.1	005203	Ribonuc_P_40	166	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AMS01144.1	005204	Cluster4934_1clades	199	AR9_g060	Bacillus phage AR9	GCA_001743835.1
ALN97815.1	005204	Cluster4934_1clades	229	Bp8pS_136	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00072.1	005204	Cluster4934_1clades	199	PBI_PBS1_250	Bacillus virus PBS1	GCA_002601325.1
QCW18796.1	005205	Cluster4935_1clades	229	7t3_0275	Salmonella phage 7t3	GCA_006083215.1
AZU98061.1	005205	Cluster4935_1clades	229	CPT_Munch_117	Salmonella phage Munch	GCA_004015485.1
QIG62921.1	005205	Cluster4935_1clades	229	SEPL_308	Salmonella phage SE_PL	GCA_011067555.1
ASU03732.1	005206	Cluster4936_1clades	205	JOAD_183	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03488.1	005206	Cluster4936_1clades	205	RISINGSUN_182	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27239.1	005206	Cluster4936_1clades	229	PPEV_gp145	Pseudomonas phage EL	GCA_000866825.1
BBA65713.1	005207	Cluster4937_1clades	228	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65254.1	005207	Cluster4937_1clades	228	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96293.1	005207	Cluster4937_1clades	227	Xoosp13_106	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65502.1	005208	Cluster4938_2clades	207	-	Xanthomonas phage XacN1	GCA_003173815.1
prevph1000000179	005208	Cluster4938_2clades	228	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000142	005208	Cluster4938_2clades	228	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ARW58667.1	005209	Cluster4939_1clades	130	Y3_027	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28510.1	005209	Cluster4939_1clades	140	YOLOSWAG_23	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AGS82106.1	005209	Cluster4939_1clades	226	PaBG_00232	Pseudomonas phage PaBG	GCA_000912555.1
BBI90697.1	005210	Cluster4940_1clades	142	HYO65_gp305	Tenacibaculum phage PTm1	GCA_009730695.1
BBI91003.1	005210	Cluster4940_1clades	154	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39344.1	005210	Cluster4940_1clades	225	BPT24_220	Tenacibaculum phage pT24	GCA_002611925.1
ANS05995.1	005211	Cluster4941_1clades	224	ABCD_0010	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97018.1	005211	Cluster4941_1clades	199	E_009	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78531.1	005211	Cluster4941_1clades	222	RB43ORF009c	Escherichia virus RB43	GCA_000863505.1
prevph1000000479	005212	Cluster4943_1clades	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000480	005212	Cluster4943_1clades	84	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000362	005212	Cluster4943_1clades	223	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ARV77447.1	005213	Cluster4944_1clades	221	NOXIFER_282	Pseudomonas phage Noxifer	GCA_002625005.1
BAS04951.1	005213	Cluster4944_1clades	200	AVU11_gp159	Ralstonia phage RSF1	GCA_001500875.1
BAQ02676.2	005213	Cluster4944_1clades	182	-	Ralstonia phage RSL2	GCA_001503055.1
QCW18738.1	005214	Cluster4945_1clades	220	7t3_0217	Salmonella phage 7t3	GCA_006083215.1
AZU98008.1	005214	Cluster4945_1clades	220	CPT_Munch_064	Salmonella phage Munch	GCA_004015485.1
QIG62972.1	005214	Cluster4945_1clades	220	SEPL_359	Salmonella phage SE_PL	GCA_011067555.1
BBI90410.1	005215	Cluster4946_1clades	122	HYO65_gp018	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90409.1	005215	Cluster4946_1clades	98	HYO65_gp017	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90718.1	005215	Cluster4946_1clades	220	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIR93418.1	005216	Cluster4947_1clades	204	AVU42_gp045	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW23008.1	005216	Cluster4947_1clades	220	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70066.1	005216	Cluster4947_1clades	201	SynMITS9220M01_053	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMM44099.1	005217	Imm11	219	CBB_536	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44100.1	005217	Imm11	215	CBB_537	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QFP93148.1	005217	Imm11	217	-	Serratia phage PCH45	GCA_009187865.1
BBI90647.1	005218	TM	219	HYO65_gp255	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90953.1	005218	TM	217	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39313.1	005218	TM	193	BPT24_188	Tenacibaculum phage pT24	GCA_002611925.1
AFQ96784.1	005219	Cluster4950_1clades	218	G173_gp239	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48085.1	005219	Cluster4950_1clades	218	ASESINO_72	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50496.1	005219	Cluster4950_1clades	218	STRATTON_71	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANS06002.1	005220	Cluster4951_1clades	216	ABCD_0113	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97123.1	005220	Cluster4951_1clades	217	E_115	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78635.1	005220	Cluster4951_1clades	117	RB43ORF113c	Escherichia virus RB43	GCA_000863505.1
AXG67111.1	005221	Cluster4952_1clades	216	AD1_067	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08347.1	005221	Cluster4952_1clades	212	Alexandra_67	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58709.1	005221	Cluster4952_1clades	205	Y3_069	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AAX44582.1	005222	Cluster4953_1clades	215	PSSM2_205	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12390.1	005222	Cluster4953_1clades	87	PRTG_00237	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12391.1	005222	Cluster4953_1clades	66	PRTG_00238	Prochlorococcus phage P-SSM5	GCA_002991095.1
QAY01191.1	005223	Cluster4954_1clades	210	ASwh1_126	Aeromonas phage Aswh_1	GCA_004146945.1
AGR48113.2	005223	Cluster4954_1clades	215	SmphiM12_481	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13657.1	005223	Cluster4954_1clades	214	PHIN3_394	Sinorhizobium phage phiN3	GCA_001501175.1
QCW18744.1	005224	Cluster4955_1clades	215	7t3_0223	Salmonella phage 7t3	GCA_006083215.1
AZU98013.1	005224	Cluster4955_1clades	215	CPT_Munch_069	Salmonella phage Munch	GCA_004015485.1
QIG62967.1	005224	Cluster4955_1clades	215	SEPL_354	Salmonella phage SE_PL	GCA_011067555.1
ANZ49915.1	005225	Cluster4956_1clades	214	MACHINA_277	Erwinia phage Machina	GCA_002758035.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ49358.1	005225	Cluster4956_1clades	214	HUXLEY_276	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50186.1	005225	Cluster4956_1clades	214	PARSHIK_277	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QCW18748.1	005226	Cluster4957_1clades	214	7t3_0227	Salmonella phage 7t3	GCA_006083215.1
AZU98017.1	005226	Cluster4957_1clades	214	CPT_Munch_073	Salmonella phage Munch	GCA_004015485.1
QIG62963.1	005226	Cluster4957_1clades	214	SEPL_350	Salmonella phage SE_PL	GCA_011067555.1
ANZ49824.1	005227	Cluster4958_1clades	212	MACHINA_186	Erwinia phage Machina	GCA_002758035.1
ANZ49268.1	005227	Cluster4958_1clades	212	HUXLEY_186	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50096.1	005227	Cluster4958_1clades	212	PARSHIK_187	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AUE22634.1	005228	Cluster4959_1clades	212	Ah1_00093	Aeromonas phage Ah1	GCA_002957415.1
ADM80074.1	005228	Cluster4959_1clades	209	phiAS5_ORF0231	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17761.1	005228	Cluster4959_1clades	177	Aeh1ORF100c	Aeromonas virus Aeh1	GCA_000843245.1
QDB70407.1	005229	Cluster4960_1clades	212	CF8_0238	Aeromonas phage CF8	GCA_006384595.2
QDJ96755.1	005229	Cluster4960_1clades	210	PS1_0244	Aeromonas phage PS1	GCA_007051165.2
QFR59388.1	005229	Cluster4960_1clades	210	PS2_0246	Aeromonas phage PS2	GCA_009388305.2
ANZ49709.1	005230	Cluster4961_1clades	210	MACHINA_71	Erwinia phage Machina	GCA_002758035.1
ANZ49154.1	005230	Cluster4961_1clades	210	HUXLEY_72	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49982.1	005230	Cluster4961_1clades	210	PARSHIK_73	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QCW18751.1	005231	Cluster4962_1clades	210	7t3_0230	Salmonella phage 7t3	GCA_006083215.1
AZU98020.1	005231	Cluster4962_1clades	210	CPT_Munch_076	Salmonella phage Munch	GCA_004015485.1
QIG62960.1	005231	Cluster4962_1clades	207	SEPL_347	Salmonella phage SE_PL	GCA_011067555.1
QDB70460.1	005232	Cluster4963_1clades	206	CF8_0047	Aeromonas phage CF8	GCA_006384595.2
QDJ96802.1	005232	Cluster4963_1clades	210	PS1_0043	Aeromonas phage PS1	GCA_007051165.2
QFR59433.1	005232	Cluster4963_1clades	210	PS2_0042	Aeromonas phage PS2	GCA_009388305.2
AXQ70620.1	005233	Cluster4964_1clades	175	HOU04_gp019	Synechococcus phage S-T4	GCA_003443335.1
AXQ70418.1	005233	Cluster4964_1clades	175	HOU04_gp019	Synechococcus phage S-T4	GCA_003443335.1
QJT70069.1	005233	Cluster4964_1clades	210	SynMITS9220M01_056	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BAV39387.1	005234	Cluster4965_2clades	209	BPT24_270	Tenacibaculum phage pT24	GCA_002611925.1
prevph1000000854	005234	Cluster4965_2clades	200	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000592	005234	Cluster4965_2clades	200	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70437.1	005235	Cluster4966_1clades	202	CF8_0025	Aeromonas phage CF8	GCA_006384595.2
QDJ96792.1	005235	Cluster4966_1clades	209	PS1_0033	Aeromonas phage PS1	GCA_007051165.2
QFR59423.1	005235	Cluster4966_1clades	209	PS2_0032	Aeromonas phage PS2	GCA_009388305.2
ANS06008.1	005236	Cluster4967_1clades	205	ABCD_0117	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97128.1	005236	Cluster4967_1clades	208	E_120	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78640.1	005236	Cluster4967_1clades	205	RB43ORF118c	Escherichia virus RB43	GCA_000863505.1
QCW18776.1	005237	Cluster4968_1clades	208	7t3_0255	Salmonella phage 7t3	GCA_006083215.1
AZU98041.1	005237	Cluster4968_1clades	208	CPT_Munch_097	Salmonella phage Munch	GCA_004015485.1
QIG62939.1	005237	Cluster4968_1clades	208	SEPL_326	Salmonella phage SE_PL	GCA_011067555.1
AFC21497.1	005238	Cluster4969_1clades	207	GAP32_049	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
SOK58844.1	005238	Cluster4969_1clades	207	g036	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58306.1	005238	Cluster4969_1clades	207	g029	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMS01148.1	005239	Cluster4970_1clades	207	AR9_g064	Bacillus phage AR9	GCA_001743835.1
ALN97820.1	005239	Cluster4970_1clades	194	Bp8pS_141	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00076.1	005239	Cluster4970_1clades	207	PBI_PBS1_254	Bacillus virus PBS1	GCA_002601325.1
QCW18856.1	005240	Cluster4972_1clades	206	7t3_0335	Salmonella phage 7t3	GCA_006083215.1
AZU98117.1	005240	Cluster4972_1clades	206	CPT_Munch_173	Salmonella phage Munch	GCA_004015485.1
QIG62865.1	005240	Cluster4972_1clades	206	SEPL_252	Salmonella phage SE_PL	GCA_011067555.1
QBX06836.1	005241	SlG+TM+TM+TM	206	BcepSaruman_423	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74805.1	005241	SlG+TM+TM+TM	206	BcepSauron_425	Burkholderia phage BcepSauron	GCA_005394215.1
AXH72512.1	005241	SlG+TM+TM+TM	189	-	Myoviridae sp.	GCA_003657725.1
QCW18737.1	005242	Cluster4974_1clades	205	7t3_0216	Salmonella phage 7t3	GCA_006083215.1
AZU98007.1	005242	Cluster4974_1clades	205	CPT_Munch_063	Salmonella phage Munch	GCA_004015485.1
QIG62973.1	005242	Cluster4974_1clades	205	SEPL_360	Salmonella phage SE_PL	GCA_011067555.1
AMM44859.1	005243	Cluster4975_1clades	198	SP15_060	Bacillus phage SP-15	GCA_001754685.1
AEO93621.1	005243	Cluster4975_1clades	197	G_362	Bacillus virus G	GCA_000917535.1
BAE47814.1	005243	Cluster4975_1clades	205	CST116	Clostridium phage c-st	GCA_000865225.1
AXG67292.1	005244	Cluster4976_1clades	204	AD1_248	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08516.1	005244	Cluster4976_1clades	202	Alexandra_259	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08517.1	005244	Cluster4976_1clades	194	Alexandra_260	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QCW18599.1	005245	ApbE	204	7t3_078	Salmonella phage 7t3	GCA_006083215.1
AZU98427.1	005245	ApbE	204	CPT_Munch_495	Salmonella phage Munch	GCA_004015485.1
QIG63086.1	005245	ApbE	204	SEPL_473	Salmonella phage SE_PL	GCA_011067555.1
AGR47958.1	005246	Cluster4978_1clades	203	SmphiM12_326	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13150.1	005246	Cluster4978_1clades	203	PHIM19_245	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12789.1	005246	Cluster4978_1clades	203	PHIM7_244	Sinorhizobium phage phiM7	GCA_002622405.1
QCW18543.1	005247	Cluster4979_1clades	82	7t3_013	Salmonella phage 7t3	GCA_006083215.1
AZU98375.1	005247	Cluster4979_1clades	203	CPT_Munch_436	Salmonella phage Munch	GCA_004015485.1
QIG63138.1	005247	Cluster4979_1clades	82	SEPL_525	Salmonella phage SE_PL	GCA_011067555.1
AYD80057.1	005248	SlG+TM+TM	202	JA11_252	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66656.1	005248	SlG+TM+TM	202	JA13_253	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67627.1	005248	SlG+TM+TM	202	JA33_253	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QCW18741.1	005249	Cluster4981_1clades	202	7t3_0220	Salmonella phage 7t3	GCA_006083215.1
AZU98010.1	005249	Cluster4981_1clades	202	CPT_Munch_066	Salmonella phage Munch	GCA_004015485.1
QIG62970.1	005249	Cluster4981_1clades	202	SEPL_357	Salmonella phage SE_PL	GCA_011067555.1
ANZ49825.1	005250	Cluster4982_1clades	201	MACHINA_187	Erwinia phage Machina	GCA_002758035.1
ANZ49269.1	005250	Cluster4982_1clades	201	HUXLEY_187	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50097.1	005250	Cluster4982_1clades	201	PARSHIK_188	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AFC21502.1	005251	Cluster4983_1clades	183	GAP32_054	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43623.1	005251	Cluster4983_1clades	200	CBB_58	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88573.1	005251	Cluster4983_1clades	195	BF_0048	Serratia phage BF	GCA_002619745.1
BBI90604.1	005252	Cluster4984_1clades	188	HYO65_gp212	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90911.1	005252	Cluster4984_1clades	188	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39336.1	005252	Cluster4984_1clades	200	BPT24_212	Tenacibaculum phage pT24	GCA_002611925.1
AMM44858.1	005253	Cluster4986_1clades	154	SP15_059	Bacillus phage SP-15	GCA_001754685.1
AEO93620.1	005253	Cluster4986_1clades	153	G_361	Bacillus virus G	GCA_000917535.1
BAE47815.1	005253	Cluster4986_1clades	199	CST117	Clostridium phage c-st	GCA_000865225.1
BBI90642.1	005254	Cluster4987_1clades	190	HYO65_gp250	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90949.1	005254	Cluster4987_1clades	190	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39310.1	005254	Cluster4987_1clades	199	BPT24_185	Tenacibaculum phage pT24	GCA_002611925.1
QCW18731.1	005255	Cluster4988_1clades	198	7t3_0210	Salmonella phage 7t3	GCA_006083215.1
AZU98001.1	005255	Cluster4988_1clades	198	CPT_Munch_057	Salmonella phage Munch	GCA_004015485.1
QIG62978.1	005255	Cluster4988_1clades	198	SEPL_365	Salmonella phage SE_PL	GCA_011067555.1
QIG63544.1	005256	SbcC+GspA-ATPase	198	DAC19_53	Bacteroides phage DAC19	GCA_013387715.1
QIG63805.1	005256	SbcC+GspA-ATPase	198	DAC20_52	Bacteroides phage DAC20	GCA_013387725.1
QIG64066.1	005256	SbcC+GspA-ATPase	198	DAC22_52	Bacteroides phage DAC22	GCA_013387735.1
AAX44456.1	005257	Cluster4990_1clades	197	PSSM2_078	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12197.1	005257	Cluster4990_1clades	189	PRTG_00039	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93421.1	005257	Cluster4990_1clades	176	AVU42_gp051	Prochlorococcus phage P-TIM68	GCA_001503075.1
QBZ70758.1	005258	Cluster4991_1clades	193	pETSU_177	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72065.1	005258	Cluster4991_1clades	191	N1M2_202	Klebsiella phage N1M2	GCA_010092605.1
AEV89694.1	005258	Cluster4991_1clades	197	OBP_257	Pseudomonas phage OBP	GCA_000896635.1
AMS01215.1	005259	35exo	197	AR9_g131	Bacillus phage AR9	GCA_001743835.1
AEO93390.1	005259	35exo	194	G_128	Bacillus virus G	GCA_000917535.1
AST99840.1	005259	35exo	197	PBI_PBS1_18	Bacillus virus PBS1	GCA_002601325.1
QCW18747.1	005260	Cluster4993_1clades	197	7t3_0226	Salmonella phage 7t3	GCA_006083215.1
AZU98016.1	005260	Cluster4993_1clades	197	CPT_Munch_072	Salmonella phage Munch	GCA_004015485.1
QIG62964.1	005260	Cluster4993_1clades	197	SEPL_351	Salmonella phage SE_PL	GCA_011067555.1
QBX32505.1	005261	Cluster4994_1clades	197	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03758.1	005261	Cluster4994_1clades	173	335	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42077.1	005261	Cluster4994_1clades	197	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANS06010.1	005262	Cluster4995_1clades	196	ABCD_0012	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97020.1	005262	Cluster4995_1clades	196	E_011	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78533.1	005262	Cluster4995_1clades	196	RB43ORF011c	Escherichia virus RB43	GCA_000863505.1
ANS06011.1	005263	Cluster4996_1clades	196	ABCD_0169	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97182.1	005263	Cluster4996_1clades	196	E_174	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78699.1	005263	Cluster4996_1clades	196	RB43ORF177c	Escherichia virus RB43	GCA_000863505.1
QCW18749.1	005264	Cluster4998_1clades	195	7t3_0228	Salmonella phage 7t3	GCA_006083215.1
AZU98018.1	005264	Cluster4998_1clades	195	CPT_Munch_074	Salmonella phage Munch	GCA_004015485.1
QIG62962.1	005264	Cluster4998_1clades	183	SEPL_349	Salmonella phage SE_PL	GCA_011067555.1
QBX32462.1	005265	Cluster4999_1clades	164	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03727.1	005265	Cluster4999_1clades	194	304	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42034.1	005265	Cluster4999_1clades	164	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGX01786.1	005266	Tox-ART-HYD2	194	CF95_gp064	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65518.1	005266	Tox-ART-HYD2	184	2050HW_00183	Serratia phage 2050HW	GCA_002628125.1
QDB71285.1	005266	Tox-ART-HYD2	184	CPT_Moabite_255	Serratia phage Moabite	GCA_006384735.1

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ANZ49762.1	005267	Cluster5001_1clades	194	MACHINA_124	Erwinia phage Machina	GCA_002758035.1
ANZ49206.1	005267	Cluster5001_1clades	194	HUXLEY_124	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50034.1	005267	Cluster5001_1clades	194	PARSHIK_125	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AUZ94954.1	005268	DSBH	194	FDI40_gp172	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04861.1	005268	DSBH	178	AVU11_gp069	Ralstonia phage RSF1	GCA_001500875.1
BAQ02594.1	005268	DSBH	162	AVU38_gp066	Ralstonia phage RSL2	GCA_001503055.1
QCW18780.1	005269	Cluster5003_1clades	194	7t3_0259	Salmonella phage 7t3	GCA_006083215.1
AZU98045.1	005269	Cluster5003_1clades	194	CPT_Munch_101	Salmonella phage Munch	GCA_004015485.1
QIG62935.1	005269	Cluster5003_1clades	194	SEPL_322	Salmonella phage SE_PL	GCA_011067555.1
QCW19066.1	005270	Cluster5004_1clades	194	7t3_0546	Salmonella phage 7t3	GCA_006083215.1
AZU98312.1	005270	Cluster5004_1clades	194	CPT_Munch_368	Salmonella phage Munch	GCA_004015485.1
QIG62672.1	005270	Cluster5004_1clades	194	SEPL_059	Salmonella phage SE_PL	GCA_011067555.1
QKE54522.1	005271	Cluster5005_1clades	194	ACSA002_2060	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65686.1	005271	Cluster5005_1clades	80	2050HW_00351	Serratia phage 2050HW	GCA_002628125.1
QDB71111.1	005271	Cluster5005_1clades	169	CPT_Moabite_081	Serratia phage Moabite	GCA_006384735.1
AMS01276.1	005272	SIG+IG	193	AR9_g192	Bacillus phage AR9	GCA_001743835.1
ALN97931.1	005272	SIG+IG	185	Bp8pS_252	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99904.1	005272	SIG+IG	193	PBI_PBS1_82	Bacillus virus PBS1	GCA_002601325.1
ANS06015.1	005273	Cluster5007_1clades	193	ABCD_0134	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97142.1	005273	Cluster5007_1clades	185	E_134	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78656.1	005273	Cluster5007_1clades	127	RB43ORF134c	Escherichia virus RB43	GCA_000863505.1
QCW18752.1	005274	Cluster5008_1clades	193	7t3_0231	Salmonella phage 7t3	GCA_006083215.1
AZU98021.1	005274	Cluster5008_1clades	193	CPT_Munch_077	Salmonella phage Munch	GCA_004015485.1
QIG62959.1	005274	Cluster5008_1clades	193	SEPL_346	Salmonella phage SE_PL	GCA_011067555.1
BBA65681.1	005275	OGFr_N	193	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65222.1	005275	OGFr_N	193	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96252.1	005275	OGFr_N	190	Xoosp13_65	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ANS06016.1	005276	SIG+Phage_hub_GP28	191	ABCD_0103	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97113.1	005276	SIG+Phage_hub_GP28	192	E_105	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78624.1	005276	SIG+Phage_hub_GP28	191	RB43ORF102w	Escherichia virus RB43	GCA_000863505.1
ASU03689.1	005277	Cluster5011_1clades	192	JOAD_226	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03446.1	005277	Cluster5011_1clades	192	RISINGSUN_224	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27273.1	005277	Cluster5011_1clades	192	PPEV_gp179	Pseudomonas phage EL	GCA_000866825.1
AXG67344.1	005278	Cluster5012_1clades	191	AD1_300	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08571.1	005278	Cluster5012_1clades	192	Alexandra_319	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58947.1	005278	Cluster5012_1clades	180	Y3_307	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AFF28184.1	005279	dTDP_sugar_isom	190	PAU_186	Sphingomonas phage PAU	GCA_000902455.1
QCW22978.1	005279	dTDP_sugar_isom	178	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50514.1	005279	dTDP_sugar_isom	178	-	Synechococcus phage S-B43	GCA_006869725.1
AXG67093.1	005280	Cluster5014_1clades	179	AD1_049	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08328.1	005280	Cluster5014_1clades	188	Alexandra_48	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58691.1	005280	Cluster5014_1clades	190	Y3_051	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18900.1	005281	Cluster5015_1clades	190	7t3_0379	Salmonella phage 7t3	GCA_006083215.1
AZU98157.1	005281	Cluster5015_1clades	190	CPT_Munch_213	Salmonella phage Munch	GCA_004015485.1
QIG62827.1	005281	Cluster5015_1clades	190	SEPL_214	Salmonella phage SE_PL	GCA_011067555.1
BBI90655.1	005282	Cluster5016_1clades	186	HYO65_gp263	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90960.1	005282	Cluster5016_1clades	186	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39314.1	005282	Cluster5016_1clades	190	BPT24_189	Tenacibaculum phage pT24	GCA_002611925.1
AAX44541.1	005283	Cluster5017_1clades	189	PSSM2_163	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12430.1	005283	Cluster5017_1clades	189	PRTG_00280	Prochlorococcus phage P-SSM5	GCA_002991095.1
ASR76100.1	005283	Cluster5017_1clades	180	PBI_BELLAMY_55	Synechococcus phage Bellamy	GCA_002627525.1
AQW88574.1	005284	Cluster5018_1clades	189	BF_0049	Serratia phage BF	GCA_002619745.1
SOK58849.1	005284	Cluster5018_1clades	184	g041	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58311.1	005284	Cluster5018_1clades	184	g034	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18793.1	005285	Cluster5019_1clades	189	7t3_0272	Salmonella phage 7t3	GCA_006083215.1
AZU98058.1	005285	Cluster5019_1clades	189	CPT_Munch_114	Salmonella phage Munch	GCA_004015485.1
QIG62924.1	005285	Cluster5019_1clades	189	SEPL_311	Salmonella phage SE_PL	GCA_011067555.1
ANZ49764.1	005286	Cluster5020_1clades	188	MACHINA_126	Erwinia phage Machina	GCA_002758035.1
ANZ49208.1	005286	Cluster5020_1clades	182	HUXLEY_126	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50036.1	005286	Cluster5020_1clades	182	PARSHIK_127	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AQW88784.1	005287	Cluster5021_1clades	188	BF_0259	Serratia phage BF	GCA_002619745.1
SOK59065.1	005287	Cluster5021_1clades	188	g257	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58531.1	005287	Cluster5021_1clades	188	g254	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67316.1	005288	Cluster5022_1clades	142	AD1_272	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08544.1	005288	Cluster5022_1clades	188	Alexandra_288	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58921.1	005288	Cluster5022_1clades	119	Y3_281	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AMO43237.1	005289	Cluster5023_1clades	96	R1080702_232	Cyanophage S-RIM32	GCA_001754165.1
QCW22838.1	005289	Cluster5023_1clades	188	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50504.1	005289	Cluster5023_1clades	188	-	Synechococcus phage S-B43	GCA_006869725.1
AGX01839.1	005290	Cluster5024_1clades	187	CF95_gp117	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65582.1	005290	Cluster5024_1clades	175	2050HW_00247	Serratia phage 2050HW	GCA_002628125.1
QDB71347.1	005290	Cluster5024_1clades	175	CPT_Moabite_317	Serratia phage Moabite	GCA_006384735.1
ANS06019.1	005291	Cluster5025_1clades	187	ABCD_0149	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97160.1	005291	Cluster5025_1clades	185	E_152	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78676.1	005291	Cluster5025_1clades	186	RB43ORF154c	Escherichia virus RB43	GCA_000863505.1
ANZ49827.1	005292	Cluster5026_1clades	187	MACHINA_189	Erwinia phage Machina	GCA_002758035.1
ANZ49271.1	005292	Cluster5026_1clades	187	HUXLEY_189	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50099.1	005292	Cluster5026_1clades	187	PARSHIK_190	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QCW18729.1	005293	Cluster5027_1clades	187	7t3_0208	Salmonella phage 7t3	GCA_006083215.1
AZU97999.1	005293	Cluster5027_1clades	187	CPT_Munch_055	Salmonella phage Munch	GCA_004015485.1
QIG62980.1	005293	Cluster5027_1clades	187	SEPL_367	Salmonella phage SE_PL	GCA_011067555.1
AHI60238.1	005294	Cluster5028_1clades	186	Ea357_087	Erwinia phage Ea35-70	GCA_000914635.1
ANH52189.1	005294	Cluster5028_1clades	162	DM_91	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86839.1	005294	Cluster5028_1clades	186	MORTIMER_90	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AXG67335.1	005295	Cluster5030_1clades	184	AD1_291	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08563.1	005295	Cluster5030_1clades	183	Alexandra_307	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58936.1	005295	Cluster5030_1clades	186	Y3_296	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18736.1	005296	Cluster5031_1clades	186	7t3_0215	Salmonella phage 7t3	GCA_006083215.1
AZU98006.1	005296	Cluster5031_1clades	186	CPT_Munch_062	Salmonella phage Munch	GCA_004015485.1
QIG62974.1	005296	Cluster5031_1clades	186	SEPL_361	Salmonella phage SE_PL	GCA_011067555.1
QCW18740.1	005297	Cluster5032_1clades	186	7t3_0219	Salmonella phage 7t3	GCA_006083215.1
AZU98009.1	005297	Cluster5032_1clades	186	CPT_Munch_065	Salmonella phage Munch	GCA_004015485.1
QIG62971.1	005297	Cluster5032_1clades	186	SEPL_358	Salmonella phage SE_PL	GCA_011067555.1
ANS06021.1	005298	SIG+T4_baseplate	185	ABCD_0108	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97118.1	005298	SIG+T4_baseplate	185	E_110	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78630.1	005298	SIG+T4_baseplate	185	RB43ORF108w	Escherichia virus RB43	GCA_000863505.1
QCW18743.1	005299	Cluster5035_1clades	184	7t3_0222	Salmonella phage 7t3	GCA_006083215.1
AZU98012.1	005299	Cluster5035_1clades	184	CPT_Munch_068	Salmonella phage Munch	GCA_004015485.1
QIG62968.1	005299	Cluster5035_1clades	184	SEPL_355	Salmonella phage SE_PL	GCA_011067555.1
QCW19067.1	005300	Cluster5036_1clades	184	7t3_0547	Salmonella phage 7t3	GCA_006083215.1
AZU98313.1	005300	Cluster5036_1clades	184	CPT_Munch_369	Salmonella phage Munch	GCA_004015485.1
QIG62671.1	005300	Cluster5036_1clades	184	SEPL_058	Salmonella phage SE_PL	GCA_011067555.1
AFQ96727.1	005301	Portal	182	G173_gp182	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48299.1	005301	Portal	183	ASESINO_286	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50710.1	005301	Portal	182	STRATTON_285	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
BAS04853.2	005302	Cluster5038_1clades	167	AVU11_gp061	Ralstonia phage RSF1	GCA_001500875.1
BAS04854.2	005302	Cluster5038_1clades	167	AVU11_agp16	Ralstonia phage RSF1	GCA_001500875.1
BAQ02588.1	005302	Cluster5038_1clades	183	AVU38_gp060	Ralstonia phage RSL2	GCA_001503055.1
ADK66271.1	005303	Cluster5039_1clades	168	PSSM2_100.1	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12173.1	005303	Cluster5039_1clades	168	PRTG_00015	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93420.1	005303	Cluster5039_1clades	181	AVU42_gp050	Prochlorococcus phage P-TIM68	GCA_001503075.1
AXQ69134.1	005304	DUF3268	181	CcrBL9_gp110	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69688.1	005304	DUF3268	180	CcrSC_gp106	Caulobacter phage CcrSC	GCA_003443315.1
QIW90784.1	005304	DUF3268	157	GCAPEGMB_00466	Vibrio phage V07	GCA_012361095.1
AEO93606.1	005305	Cluster5041_1clades	180	G_347	Bacillus virus G	GCA_000917535.1
AEO93309.1	005305	Cluster5041_1clades	171	G_38	Bacillus virus G	GCA_000917535.1
AEO93918.1	005305	Cluster5041_1clades	175	G_675	Bacillus virus G	GCA_000917535.1
AGH56918.1	005306	Cluster5042_1clades	180	CPXG_00115	Cyanophage P-RSM6	GCA_000906155.1
AJK27539.1	005306	Cluster5042_1clades	179	PTIM40_112	Cyanophage P-TIM40	GCA_001470935.1
AGG54286.1	005306	Cluster5042_1clades	177	CYWG_00002	Cyanophage S-SSM6b	GCA_002710425.1
ALN97846.1	005307	Cluster5043_1clades	180	Bp8pS_167	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97847.1	005307	Cluster5043_1clades	179	Bp8pS_168	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97848.1	005307	Cluster5043_1clades	171	Bp8pS_169	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QCW18815.1	005308	Cluster5044_1clades	180	7t3_0294	Salmonella phage 7t3	GCA_006083215.1
AZU98079.1	005308	Cluster5044_1clades	180	CPT_Munch_135	Salmonella phage Munch	GCA_004015485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG62903.1	005308	Cluster5044_1clades	180	SEPL_290	Salmonella phage SE_PL	GCA_011067555.1
ALN97741.1	005309	Cluster5045_1clades	168	Bp8pS_062	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97742.1	005309	Cluster5045_1clades	159	Bp8pS_063	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97743.1	005309	Cluster5045_1clades	179	Bp8pS_064	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AMS01357.1	005310	Cluster5046_1clades	179	AR9_g273	Bacillus phage AR9	GCA_001743835.1
ALN97699.1	005310	Cluster5046_1clades	178	Bp8pS_020	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99987.1	005310	Cluster5046_1clades	179	PBI_PBS1_166	Bacillus virus PBS1	GCA_002601325.1
ANS06024.1	005311	Cluster5047_1clades	179	ABCD_0185	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97199.1	005311	Cluster5047_1clades	179	E_191	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78717.1	005311	Cluster5047_1clades	172	RB43ORF195c	Escherichia virus RB43	GCA_000863505.1
APU01642.1	005312	TM	179	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53268.1	005312	TM	79	65p260	Aeromonas virus 65	GCA_000893255.1
ADQ53269.1	005312	TM	131	65p261	Aeromonas virus 65	GCA_000893255.1
AXG67303.1	005313	Cluster5049_1clades	179	AD1_259	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08528.1	005313	Cluster5049_1clades	169	Alexandra_271	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58907.1	005313	Cluster5049_1clades	169	Y3_267	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18733.1	005314	Cluster5050_1clades	179	7t3_0212	Salmonella phage 7t3	GCA_006083215.1
AZU98003.1	005314	Cluster5050_1clades	179	CPT_Munch_059	Salmonella phage Munch	GCA_004015485.1
QIG62977.1	005314	Cluster5050_1clades	179	SEPL_364	Salmonella phage SE_PL	GCA_011067555.1
QCW18742.1	005315	Cluster5051_1clades	179	7t3_0221	Salmonella phage 7t3	GCA_006083215.1
AZU98011.1	005315	Cluster5051_1clades	179	CPT_Munch_067	Salmonella phage Munch	GCA_004015485.1
QIG62969.1	005315	Cluster5051_1clades	179	SEPL_356	Salmonella phage SE_PL	GCA_011067555.1
QCW18781.1	005316	Cluster5052_1clades	179	7t3_0260	Salmonella phage 7t3	GCA_006083215.1
AZU98046.1	005316	Cluster5052_1clades	179	CPT_Munch_102	Salmonella phage Munch	GCA_004015485.1
QIG62934.1	005316	Cluster5052_1clades	179	SEPL_321	Salmonella phage SE_PL	GCA_011067555.1
BBI90659.1	005317	Cluster5053_1clades	176	HYO65_gp267	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90964.1	005317	Cluster5053_1clades	176	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39286.1	005317	Cluster5053_1clades	179	BPT24_160	Tenacibaculum phage pT24	GCA_002611925.1
QBX32303.1	005318	Cluster5054_1clades	179	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03565.1	005318	Cluster5054_1clades	169	142	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41876.1	005318	Cluster5054_1clades	179	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW18984.1	005319	Caudo_TAP	179	7t3_0463	Salmonella phage 7t3	GCA_006083215.1
AZU98232.1	005319	Caudo_TAP	178	CPT_Munch_288	Salmonella phage Munch	GCA_004015485.1
QIG62752.1	005319	Caudo_TAP	179	SEPL_139	Salmonella phage SE_PL	GCA_011067555.1
QBZ70756.1	005320	Cluster5056_1clades	172	pETSU_175	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72063.1	005320	Cluster5056_1clades	163	N1M2_200	Klebsiella phage N1M2	GCA_010092605.1
AEV89692.1	005320	Cluster5056_1clades	178	OBP_255	Pseudomonas phage OBP	GCA_000896635.1
AMS01183.1	005321	Cluster5057_1clades	178	AR9_g099	Bacillus phage AR9	GCA_001743835.1
ALN97855.1	005321	Cluster5057_1clades	153	Bp8pS_176	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00117.1	005321	Cluster5057_1clades	178	PBI_PBS1_295	Bacillus virus PBS1	GCA_002601325.1
AMS01358.1	005322	DUF2203	178	AR9_g274	Bacillus phage AR9	GCA_001743835.1
ALN97700.1	005322	DUF2203	174	Bp8pS_021	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99988.1	005322	DUF2203	178	PBI_PBS1_167	Bacillus virus PBS1	GCA_002601325.1
AXG67255.1	005323	Cluster5059_1clades	144	AD1_211	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08609.1	005323	Cluster5059_1clades	178	Alexandra_221	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58855.1	005323	Cluster5059_1clades	158	Y3_215	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18746.1	005324	Cluster5060_1clades	178	7t3_0225	Salmonella phage 7t3	GCA_006083215.1
AZU98015.1	005324	Cluster5060_1clades	178	CPT_Munch_071	Salmonella phage Munch	GCA_004015485.1
QIG62965.1	005324	Cluster5060_1clades	178	SEPL_352	Salmonella phage SE_PL	GCA_011067555.1
AOO14250.1	005325	Cluster5061_1clades	165	Sn110110_056	Cyanophage S-RIM14	GCA_002599065.1
AOO14902.1	005325	Cluster5061_1clades	165	W1230910_056	Cyanophage S-RIM14	GCA_002599125.1
AGG54335.1	005325	Cluster5061_1clades	177	CYWG_00051	Cyanophage S-SSM6b	GCA_002710425.1
AFQ96663.1	005326	Cluster5062_1clades	146	G173_gp118	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48229.1	005326	Cluster5062_1clades	146	ASESINO_216	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50642.1	005326	Cluster5062_1clades	177	STRATTON_217	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AOV59507.1	005327	Cluster5063_1clades	177	S330809_046	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59269.1	005327	Cluster5063_1clades	177	C440309_046	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59745.1	005327	Cluster5063_1clades	150	N231010_046	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18730.1	005328	Cluster5064_1clades	177	7t3_0209	Salmonella phage 7t3	GCA_006083215.1
AZU98000.1	005328	Cluster5064_1clades	177	CPT_Munch_056	Salmonella phage Munch	GCA_004015485.1
QIG62979.1	005328	Cluster5064_1clades	177	SEPL_366	Salmonella phage SE_PL	GCA_011067555.1
SBV38343.1	005329	Cluster5065_1clades	177	BN7874_174	Phage NCTB	GCA_900092385.1
AFH14733.1	005329	Cluster5065_1clades	141	Lu11_0196	Pseudomonas phage Lu11	GCA_000897175.1
AGS81971.1	005329	Cluster5065_1clades	156	PaBG_00086	Pseudomonas phage PaBG	GCA_000912555.1
AMS01340.1	005330	Cluster5066_1clades	166	AR9_g256	Bacillus phage AR9	GCA_001743835.1
ALN97994.1	005330	Cluster5066_1clades	176	Bp8pS_315	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99970.1	005330	Cluster5066_1clades	166	PBI_PBS1_149	Bacillus virus PBS1	GCA_002601325.1
AFQ96584.1	005331	SIG+WYL-C	131	G173_gp039	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48144.1	005331	SIG+WYL-C	175	ASESINO_131	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50559.1	005331	SIG+WYL-C	176	STRATTON_134	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AYD80105.1	005332	Cluster5068_1clades	176	JA11_300	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66706.1	005332	Cluster5068_1clades	176	JA13_303	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67675.1	005332	Cluster5068_1clades	176	JA33_301	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AFH14836.1	005333	Cluster5070_1clades	175	Lu11_0298	Pseudomonas phage Lu11	GCA_000897175.1
QBX32459.1	005333	Cluster5070_1clades	149	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42031.1	005333	Cluster5070_1clades	149	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ANZ49763.1	005334	Cluster5071_1clades	175	MACHINA_125	Erwinia phage Machina	GCA_002758035.1
ANZ49207.1	005334	Cluster5071_1clades	175	HUXLEY_125	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50035.1	005334	Cluster5071_1clades	175	PARSHIK_126	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ARM70913.1	005335	Cluster5072_1clades	175	phiC120_c208	Escherichia phage phiC120	GCA_002621185.1
SOK58841.1	005335	Cluster5072_1clades	159	g033	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58301.1	005335	Cluster5072_1clades	159	g024	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67291.1	005336	Cluster5073_1clades	167	AD1_247	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08515.1	005336	Cluster5073_1clades	168	Alexandra_258	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58894.1	005336	Cluster5073_1clades	175	Y3_254	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BBI90428.1	005337	Cluster5074_1clades	175	HYO65_gp036	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90735.1	005337	Cluster5074_1clades	175	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39240.1	005337	Cluster5074_1clades	126	BPT24_115	Tenacibaculum phage pT24	GCA_002611925.1
QDB70336.1	005338	CITB-HTH	175	CF8_0166	Aeromonas phage CF8	GCA_006384595.2
QDJ96689.1	005338	CITB-HTH	167	PS1_0178	Aeromonas phage PS1	GCA_007051165.2
QFR59322.1	005338	CITB-HTH	161	PS2_0180	Aeromonas phage PS2	GCA_009388305.2
AFC21925.1	005339	Cluster5076_1clades	167	GAP32_467	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
SOK59288.1	005339	Cluster5076_1clades	175	g480	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58753.1	005339	Cluster5076_1clades	171	g476	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06032.1	005340	GP38	174	ABCD_0264	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97283.1	005340	GP38	172	E_275	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78804.1	005340	GP38	174	RB43ORF282w	Escherichia virus RB43	GCA_000863505.1
QCW18735.1	005341	Cluster5078_1clades	174	7t3_0214	Salmonella phage 7t3	GCA_006083215.1
AZU98005.1	005341	Cluster5078_1clades	174	CPT_Munch_061	Salmonella phage Munch	GCA_004015485.1
QIG62975.1	005341	Cluster5078_1clades	174	SEPL_362	Salmonella phage SE_PL	GCA_011067555.1
QCW18779.1	005342	Cluster5079_1clades	174	7t3_0258	Salmonella phage 7t3	GCA_006083215.1
AZU98044.1	005342	Cluster5079_1clades	174	CPT_Munch_100	Salmonella phage Munch	GCA_004015485.1
QIG62936.1	005342	Cluster5079_1clades	174	SEPL_323	Salmonella phage SE_PL	GCA_011067555.1
AXG67246.1	005343	Cluster5080_1clades	173	AD1_202	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08476.1	005343	Cluster5080_1clades	94	Alexandra_212	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28676.1	005343	Cluster5080_1clades	86	YOLOSWAG_197	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QCW18720.1	005344	Cluster5081_1clades	173	7t3_0199	Salmonella phage 7t3	GCA_006083215.1
AZU97992.1	005344	Cluster5081_1clades	173	CPT_Munch_048	Salmonella phage Munch	GCA_004015485.1
QIG62987.1	005344	Cluster5081_1clades	173	SEPL_374	Salmonella phage SE_PL	GCA_011067555.1
QCW18807.1	005345	Cluster5082_1clades	173	7t3_0286	Salmonella phage 7t3	GCA_006083215.1
AZU98072.1	005345	Cluster5082_1clades	173	CPT_Munch_128	Salmonella phage Munch	GCA_004015485.1
QIG62910.1	005345	Cluster5082_1clades	173	SEPL_297	Salmonella phage SE_PL	GCA_011067555.1
BBA65672.1	005346	Cluster5083_1clades	173	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65213.1	005346	Cluster5083_1clades	173	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96240.1	005346	Cluster5083_1clades	164	Xoosp13_53	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AMS01247.1	005347	Cluster5085_1clades	172	AR9_g163	Bacillus phage AR9	GCA_001743835.1
ALN97904.1	005347	Cluster5085_1clades	155	Bp8pS_225	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99873.1	005347	Cluster5085_1clades	152	PBI_PBS1_51	Bacillus virus PBS1	GCA_002601325.1
AXG67076.1	005348	Cluster5086_1clades	159	AD1_032	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08309.1	005348	Cluster5086_1clades	158	Alexandra_29	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58673.1	005348	Cluster5086_1clades	171	Y3_033	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ASU03719.1	005349	SIG+DUF4376	171	JOAD_196	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03476.1	005349	SIG+DUF4376	171	RISINGSUN_194	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QIG66004.1	005349	SIG+DUF4376	170	phiOC_p362	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AXG67107.1	005350	Cluster5088_1clades	171	AD1_063	Dickeya phage vB_DsoM_AD1	GCA_003568515.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AWY08343.1	005350	Cluster5088_1clades	170	Alexandra_63	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58705.1	005350	Cluster5088_1clades	170	Y3_065	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QJD53815.1	005351	Cluster5089_1clades	169	SEA_KELA_255	Streptomyces phage Kela	GCA_012934305.1
QBZ72142.1	005351	Cluster5089_1clades	171	SEA_KRADAL_256	Streptomyces phage Kradal	GCA_004799925.1
AXH66404.1	005351	Cluster5089_1clades	171	SEA_SATIS_255	Streptomyces phage Satis	GCA_003366315.1
QCW18566.1	005352	Cluster5090_1clades	138	7t3_045	Salmonella phage 7t3	GCA_006083215.1
AZU98395.1	005352	Cluster5090_1clades	171	CPT_Munch_463	Salmonella phage Munch	GCA_004015485.1
QIG63118.1	005352	Cluster5090_1clades	171	SEPL_505	Salmonella phage SE_PL	GCA_011067555.1
ANS06034.1	005353	Cluster5091_1clades	170	ABCD_0120	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97131.1	005353	Cluster5091_1clades	170	E_123	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78643.1	005353	Cluster5091_1clades	160	RB43ORF121c	Escherichia virus RB43	GCA_000863505.1
AQW88868.1	005354	Cluster5092_1clades	170	BF_0343	Serratia phage BF	GCA_002619745.1
SOK59152.1	005354	Cluster5092_1clades	162	g344	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58618.1	005354	Cluster5092_1clades	162	g341	Yersinia phage fHe-Yen9-04	GCA_002990485.1
BBI90606.1	005355	Cluster5094_1clades	88	HYO65_gp214	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90912.1	005355	Cluster5094_1clades	167	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39164.1	005355	Cluster5094_1clades	170	BPT24_042	Tenacibaculum phage pT24	GCA_002611925.1
AFQ96594.1	005356	Cluster5095_1clades	169	G173_gp049	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48159.1	005356	Cluster5095_1clades	169	ASESINO_146	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50571.1	005356	Cluster5095_1clades	169	STRATTON_146	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QCW18835.1	005357	Cluster5096_1clades	169	7t3_0314	Salmonella phage 7t3	GCA_006083215.1
AZU98098.1	005357	Cluster5096_1clades	169	CPT_Munch_154	Salmonella phage Munch	GCA_004015485.1
QIG62884.1	005357	Cluster5096_1clades	169	SEPL_271	Salmonella phage SE_PL	GCA_011067555.1
AMS01293.1	005358	KAP-glycosylase	168	AR9_g209	Bacillus phage AR9	GCA_001743835.1
ALN97945.1	005358	KAP-glycosylase	163	Bp8pS_266	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99922.1	005358	KAP-glycosylase	168	PBI_PBS1_100	Bacillus virus PBS1	GCA_002601325.1
QCW18745.1	005359	Cluster5098_1clades	168	7t3_0224	Salmonella phage 7t3	GCA_006083215.1
AZU98014.1	005359	Cluster5098_1clades	168	CPT_Munch_070	Salmonella phage Munch	GCA_004015485.1
QIG62966.1	005359	Cluster5098_1clades	168	SEPL_353	Salmonella phage SE_PL	GCA_011067555.1
QCW18539.1	005360	Cluster5099_1clades	168	7t3_06	Salmonella phage 7t3	GCA_006083215.1
AZU98372.1	005360	Cluster5099_1clades	168	CPT_Munch_432	Salmonella phage Munch	GCA_004015485.1
QIG63141.1	005360	Cluster5099_1clades	168	SEPL_528	Salmonella phage SE_PL	GCA_011067555.1
AUE22640.1	005361	Cluster5101_1clades	159	Ah1_00099	Aeromonas phage Ah1	GCA_002957415.1
ADM80080.1	005361	Cluster5101_1clades	159	phiAS5_ORF0237	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17766.1	005361	Cluster5101_1clades	167	Aeh1ORF105c	Aeromonas virus Aeh1	GCA_000843245.1
QCW18734.1	005362	Cluster5102_1clades	167	7t3_0213	Salmonella phage 7t3	GCA_006083215.1
AZU98004.1	005362	Cluster5102_1clades	167	CPT_Munch_060	Salmonella phage Munch	GCA_004015485.1
QIG62976.1	005362	Cluster5102_1clades	167	SEPL_363	Salmonella phage SE_PL	GCA_011067555.1
QCW18890.1	005363	Cluster5103_1clades	167	7t3_0369	Salmonella phage 7t3	GCA_006083215.1
AZU98148.1	005363	Cluster5103_1clades	167	CPT_Munch_204	Salmonella phage Munch	GCA_004015485.1
QIG62835.1	005363	Cluster5103_1clades	167	SEPL_222	Salmonella phage SE_PL	GCA_011067555.1
QCW19106.1	005364	Cluster5104_1clades	167	7t3_0589	Salmonella phage 7t3	GCA_006083215.1
AZU98344.1	005364	Cluster5104_1clades	167	CPT_Munch_403	Salmonella phage Munch	GCA_004015485.1
QIG62639.1	005364	Cluster5104_1clades	167	SEPL_026	Salmonella phage SE_PL	GCA_011067555.1
BBI90399.1	005365	Cluster5105_1clades	167	HYO65_gp007	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90706.1	005365	Cluster5105_1clades	167	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39262.1	005365	Cluster5105_1clades	163	BPT24_137	Tenacibaculum phage pT24	GCA_002611925.1
ATA65524.1	005366	DUF1653	58	2050HW_00189	Serratia phage 2050HW	GCA_002628125.1
ATA65525.1	005366	DUF1653	112	2050HW_00190	Serratia phage 2050HW	GCA_002628125.1
QDB71290.1	005366	DUF1653	167	CPT_Moabite_260	Serratia phage Moabite	GCA_006384735.1
ANS06037.1	005367	Cluster5107_1clades	166	ABCD_0226	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97243.1	005367	Cluster5107_1clades	166	E_235	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78761.1	005367	Cluster5107_1clades	166	RB43ORF239w	Escherichia virus RB43	GCA_000863505.1
AXG67366.1	005368	Cluster5108_1clades	166	AD1_322	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08589.1	005368	Cluster5108_1clades	164	Alexandra_340	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58965.1	005368	Cluster5108_1clades	165	Y3_325	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18881.1	005369	Cluster5109_1clades	166	7t3_0360	Salmonella phage 7t3	GCA_006083215.1
AZU98139.1	005369	Cluster5109_1clades	166	CPT_Munch_195	Salmonella phage Munch	GCA_004015485.1
QIG62843.1	005369	Cluster5109_1clades	166	SEPL_230	Salmonella phage SE_PL	GCA_011067555.1
QDB70444.1	005370	Cluster5110_1clades	166	CF8_0032	Aeromonas phage CF8	GCA_006384595.2
QDJ96789.1	005370	Cluster5110_1clades	161	PS1_0030	Aeromonas phage PS1	GCA_007051165.2
QFR59420.1	005370	Cluster5110_1clades	161	PS2_0029	Aeromonas phage PS2	GCA_009388305.2
ANS06044.1	005371	Cluster5111_1clades	159	ABCD_0110	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97120.1	005371	Cluster5111_1clades	165	E_112	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78632.1	005371	Cluster5111_1clades	165	RB43ORF110c	Escherichia virus RB43	GCA_000863505.1
SBV38285.1	005372	TM+TM	82	BN7874_116	Phage NCTB	GCA_900092385.1
AFH14789.1	005372	TM+TM	165	Lu11_0253	Pseudomonas phage Lu11	GCA_000897175.1
AGS82147.1	005372	TM+TM	126	PaBG_00274	Pseudomonas phage PaBG	GCA_000912555.1
AXG67105.1	005373	Cluster5113_1clades	160	AD1_061	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08341.1	005373	Cluster5113_1clades	165	Alexandra_61	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58702.1	005373	Cluster5113_1clades	136	Y3_062	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18548.1	005374	BC2332-ART	165	7t3_023	Salmonella phage 7t3	GCA_006083215.1
AZU98377.1	005374	BC2332-ART	165	CPT_Munch_443	Salmonella phage Munch	GCA_004015485.1
QIG63135.1	005374	BC2332-ART	165	SEPL_522	Salmonella phage SE_PL	GCA_011067555.1
QBZ70755.1	005375	Cluster5115_1clades	158	pETSU_174	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72062.1	005375	Cluster5115_1clades	163	N1M2_199	Klebsiella phage N1M2	GCA_010092605.1
AEV89691.1	005375	Cluster5115_1clades	164	OBP_254	Pseudomonas phage OBP	GCA_000896635.1
ASU03845.1	005376	Cluster5116_1clades	164	JOAD_70	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03600.1	005376	Cluster5116_1clades	164	RISINGSUN_70	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27159.1	005376	Cluster5116_1clades	161	PPEV_gp065	Pseudomonas phage EL	GCA_000866825.1
QCW18857.1	005377	Cluster5117_1clades	164	7t3_0336	Salmonella phage 7t3	GCA_006083215.1
AZU98118.1	005377	Cluster5117_1clades	164	CPT_Munch_174	Salmonella phage Munch	GCA_004015485.1
QIG62864.1	005377	Cluster5117_1clades	164	SEPL_251	Salmonella phage SE_PL	GCA_011067555.1
AFU87893.1	005378	Cluster5118_1clades	163	CcrColossus_gp023	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68563.1	005378	Cluster5118_1clades	163	CcrPW_gp024	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69012.1	005378	Cluster5118_1clades	163	CcrPW_gp473	Caulobacter phage CcrPW	GCA_003443275.1
AXG67209.1	005379	Cluster5119_1clades	163	AD1_165	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08440.1	005379	Cluster5119_1clades	158	Alexandra_170	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58805.1	005379	Cluster5119_1clades	141	Y3_165	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18558.1	005380	Cluster5120_1clades	163	7t3_035	Salmonella phage 7t3	GCA_006083215.1
AZU98387.1	005380	Cluster5120_1clades	163	CPT_Munch_454	Salmonella phage Munch	GCA_004015485.1
QIG63125.1	005380	Cluster5120_1clades	163	SEPL_512	Salmonella phage SE_PL	GCA_011067555.1
QBX06512.1	005381	Cluster5121_1clades	71	BcepSaruman_099	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74478.1	005381	Cluster5121_1clades	71	BcepSauron_098	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41556.1	005381	Cluster5121_1clades	163	RSL1_ORF112	Ralstonia phage phiRSL1	GCA_000879455.1
QAX98424.1	005382	Cluster5122_1clades	162	ASfcp2_80	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52879.1	005382	Cluster5122_1clades	162	PX29p160	Aeromonas phage PX29	GCA_000920195.1
AAQ17829.1	005382	Cluster5122_1clades	162	Aeh1ORF163c	Aeromonas virus Aeh1	GCA_000843245.1
AFO71331.1	005383	Cluster5123_1clades	162	CR5_111	Cronobacter phage CR5	GCA_000910235.1
QBP07540.1	005383	Cluster5123_1clades	162	DERBICUS_114	Erwinia phage Derbicus	GCA_004521655.1
ANZ48963.1	005383	Cluster5123_1clades	162	EARLPHILLIPIV_114	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
AXG67080.1	005384	SWIB	162	AD1_036	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08313.1	005384	SWIB	160	Alexandra_33	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58677.1	005384	SWIB	159	Y3_037	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AFU87890.1	005385	Cluster5125_1clades	146	CcrColossus_gp020	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68561.1	005385	Cluster5125_1clades	162	CcrPW_gp022	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69010.1	005385	Cluster5125_1clades	162	CcrPW_gp471	Caulobacter phage CcrPW	GCA_003443275.1
QCW19104.1	005386	Cluster5126_1clades	162	7t3_0587	Salmonella phage 7t3	GCA_006083215.1
AZU98342.1	005386	Cluster5126_1clades	162	CPT_Munch_401	Salmonella phage Munch	GCA_004015485.1
QIG62641.1	005386	Cluster5126_1clades	162	SEPL_028	Salmonella phage SE_PL	GCA_011067555.1
QBZ70843.1	005387	Cluster5127_1clades	144	pETSU_262	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71875.1	005387	Cluster5127_1clades	162	N1M2_12	Klebsiella phage N1M2	GCA_010092605.1
AEV89471.1	005387	Cluster5127_1clades	157	OBP_034	Pseudomonas phage OBP	GCA_000896635.1
AFU88231.1	005388	Cluster5128_1clades	161	CcrColossus_gp361	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68908.1	005388	Cluster5128_1clades	161	CcrPW_gp369	Caulobacter phage CcrPW	GCA_003443275.1
QIG65746.1	005388	Cluster5128_1clades	157	phiOC_p081	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QCW18728.1	005389	Cluster5129_1clades	161	7t3_0207	Salmonella phage 7t3	GCA_006083215.1
AZU97998.1	005389	Cluster5129_1clades	161	CPT_Munch_054	Salmonella phage Munch	GCA_004015485.1
QIG62981.1	005389	Cluster5129_1clades	161	SEPL_368	Salmonella phage SE_PL	GCA_011067555.1
QCW18561.1	005390	Cluster5130_1clades	161	7t3_038	Salmonella phage 7t3	GCA_006083215.1
AZU98391.1	005390	Cluster5130_1clades	161	CPT_Munch_458	Salmonella phage Munch	GCA_004015485.1
QIG63122.1	005390	Cluster5130_1clades	161	SEPL_509	Salmonella phage SE_PL	GCA_011067555.1
AXG67351.1	005391	Cluster5131_1clades	160	AD1_307	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08578.1	005391	Cluster5131_1clades	123	Alexandra_327	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58954.1	005391	Cluster5131_1clades	112	Y3_314	Erwinia phage vB_EamM_Y3	GCA_002955045.1

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QCW18559.1	005392	Cluster5132_1clades	160	7t3_036	Salmonella phage 7t3	GCA_006083215.1
AZU98388.1	005392	Cluster5132_1clades	160	CPT_Munch_455	Salmonella phage Munch	GCA_004015485.1
QIG63124.1	005392	Cluster5132_1clades	160	SEPL_511	Salmonella phage SE_PL	GCA_011067555.1
AMS01088.1	005393	Cluster5133_1clades	159	AR9_g003	Bacillus phage AR9	GCA_001743835.1
ALN97689.1	005393	Cluster5133_1clades	159	Bp8pS_010	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00010.1	005393	Cluster5133_1clades	159	PBI_PBS1_188	Bacillus virus PBS1	GCA_002601325.1
AMS01282.1	005394	Cluster5134_1clades	159	AR9_g198	Bacillus phage AR9	GCA_001743835.1
ALN97935.1	005394	Cluster5134_1clades	157	Bp8pS_256	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99910.1	005394	Cluster5134_1clades	159	PBI_PBS1_88	Bacillus virus PBS1	GCA_002601325.1
ANZ49864.1	005395	Cluster5135_1clades	159	MACHINA_226	Erwinia phage Machina	GCA_002758035.1
ANZ49308.1	005395	Cluster5135_1clades	159	HUXLEY_226	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50136.1	005395	Cluster5135_1clades	159	PARSHIK_227	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AQW88869.1	005396	Cluster5136_1clades	158	BF_0344	Serratia phage BF	GCA_002619745.1
SOK59153.1	005396	Cluster5136_1clades	147	g345	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58619.1	005396	Cluster5136_1clades	147	g342	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AQW88936.1	005397	Cluster5137_1clades	149	BF_0411	Serratia phage BF	GCA_002619745.1
SOK59225.1	005397	Cluster5137_1clades	158	g417	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58691.1	005397	Cluster5137_1clades	158	g414	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06045.1	005398	Cluster5138_1clades	155	ABCD_0115	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97126.1	005398	Cluster5138_1clades	157	E_118	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78638.1	005398	Cluster5138_1clades	155	RB43ORF116c	Escherichia virus RB43	GCA_000863505.1
QCW18582.1	005399	SIG+TM	157	7t3_061	Salmonella phage 7t3	GCA_006083215.1
AZU98410.1	005399	SIG+TM	157	CPT_Munch_478	Salmonella phage Munch	GCA_004015485.1
QIG63103.1	005399	SIG+TM	157	SEPL_490	Salmonella phage SE_PL	GCA_011067555.1
AGX01906.1	005400	Cluster5140_1clades	156	CF95_gp184	Erwinia phage PhiEaH1	GCA_000914555.1
BAS04896.2	005400	Cluster5140_1clades	125	AVU11_agp24	Ralstonia phage RSF1	GCA_001500875.1
BAQ02622.1	005400	Cluster5140_1clades	132	AVU38_gp094	Ralstonia phage RSL2	GCA_001503055.1
ANS06046.1	005401	Cluster5141_1clades	155	ABCD_0152	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97164.1	005401	Cluster5141_1clades	156	E_156	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78680.1	005401	Cluster5141_1clades	130	RB43ORF158c	Escherichia virus RB43	GCA_000863505.1
AUZ95044.1	005402	ENOYCOADEHYD	156	FDI40_gp269	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72737.1	005402	ENOYCOADEHYD	153	-	Myoviridae sp.	GCA_003657725.1
QCG76207.1	005402	ENOYCOADEHYD	152	EST35_0326	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBI90584.1	005403	Cluster5143_1clades	130	HYO65_gp192	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90892.1	005403	Cluster5143_1clades	130	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39352.1	005403	Cluster5143_1clades	156	BPT24_232	Tenacibaculum phage pT24	GCA_002611925.1
QBX32372.1	005404	Cluster5144_1clades	156	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03639.1	005404	Cluster5144_1clades	154	216	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41945.1	005404	Cluster5144_1clades	156	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBZ70822.1	005405	Cluster5145_1clades	156	pETSU_241	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72120.1	005405	Cluster5145_1clades	118	N1M2_260	Klebsiella phage N1M2	GCA_010092605.1
AEV89454.1	005405	Cluster5145_1clades	119	OBP_017	Pseudomonas phage OBP	GCA_000896635.1
AGX01762.1	005406	Cluster5146_1clades	155	CF95_gp040	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65627.1	005406	Cluster5146_1clades	153	2050HW_00292	Serratia phage 2050HW	GCA_002628125.1
QDB71054.1	005406	Cluster5146_1clades	153	CPT_Moabite_022	Serratia phage Moabite	GCA_006384735.1
QBX06639.1	005407	Cluster5147_1clades	128	BcepSaruman_226	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74609.1	005407	Cluster5147_1clades	128	BcepSauron_229	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41699.1	005407	Cluster5147_1clades	155	RSL1_ORF251	Ralstonia phage phiRSL1	GCA_000879455.1
QDB70439.1	005408	Cluster5148_1clades	150	CF8_0027	Aeromonas phage CF8	GCA_006384595.2
QDJ96675.1	005408	Cluster5148_1clades	155	PS1_0164	Aeromonas phage PS1	GCA_007051165.2
QFR59309.1	005408	Cluster5148_1clades	155	PS2_0168	Aeromonas phage PS2	GCA_009388305.2
AIX30692.1	005409	TM	131	Syn7803US37_215	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54944.1	005409	TM	155	b23_0333	Synechococcus phage B23	GCA_009745195.1
QGT54579.1	005409	TM	155	b3_0339	Synechococcus phage B3	GCA_009745215.1
ANZ49829.1	005410	Cluster5150_1clades	154	MACHINA_191	Erwinia phage Machina	GCA_002758035.1
ANZ49273.1	005410	Cluster5150_1clades	154	HUXLEY_191	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50101.1	005410	Cluster5150_1clades	154	PARSHIK_192	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AQW88651.1	005411	Cluster5151_1clades	154	BF_0126	Serratia phage BF	GCA_002619745.1
SOK58931.1	005411	Cluster5151_1clades	154	g123	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58396.1	005411	Cluster5151_1clades	50	g119	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW19090.1	005412	Cluster5152_1clades	154	7t3_0572	Salmonella phage 7t3	GCA_006083215.1
AZU98329.1	005412	Cluster5152_1clades	141	CPT_Munch_387	Salmonella phage Munch	GCA_004015485.1
QIG62654.1	005412	Cluster5152_1clades	141	SEPL_041	Salmonella phage SE_PL	GCA_011067555.1
ASU03819.1	005413	Cluster5153_1clades	138	JOAD_96	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03574.1	005413	Cluster5153_1clades	138	RISINGSUN_96	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27205.1	005413	Cluster5153_1clades	153	PPEV_gp111	Pseudomonas phage EL	GCA_000866825.1
QCW18562.1	005414	Cluster5154_1clades	153	7t3_039	Salmonella phage 7t3	GCA_006083215.1
AZU98392.1	005414	Cluster5154_1clades	148	CPT_Munch_459	Salmonella phage Munch	GCA_004015485.1
QIG63121.1	005414	Cluster5154_1clades	148	SEPL_508	Salmonella phage SE_PL	GCA_011067555.1
ANM44821.1	005415	Cluster5155_1clades	84	KTN4_063	Pseudomonas phage KTN4	GCA_002607225.1
QJB22699.1	005415	Cluster5155_1clades	152	fnug_56	Pseudomonas phage fnug	GCA_012837215.1
AAL82946.1	005415	Cluster5155_1clades	152	PHIKZ045	Pseudomonas virus phiKZ	GCA_000842965.1
QBX32503.1	005416	Phytase-like	151	-	Pseudomonas phage PA1C	GCA_004785505.1
ATN94621.1	005416	Phytase-like	152	SL2_044	Pseudomonas phage SL2	GCA_002956015.1
QEM42075.1	005416	Phytase-like	151	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW19091.1	005417	Cluster5157_1clades	152	7t3_0573	Salmonella phage 7t3	GCA_006083215.1
AZU98330.1	005417	Cluster5157_1clades	152	CPT_Munch_388	Salmonella phage Munch	GCA_004015485.1
QIG62653.1	005417	Cluster5157_1clades	152	SEPL_040	Salmonella phage SE_PL	GCA_011067555.1
BBA65584.1	005418	Cluster5158_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65585.1	005418	Cluster5158_1clades	151	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65582.1	005418	Cluster5158_1clades	152	-	Xanthomonas phage XacN1	GCA_003173815.1
QBZ70799.1	005419	Cluster5159_1clades	145	pETSU_218	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72100.1	005419	Cluster5159_1clades	152	N1M2_237	Klebsiella phage N1M2	GCA_010092605.1
AEV89737.1	005419	Cluster5159_1clades	135	OBP_300	Pseudomonas phage OBP	GCA_000896635.1
AMS01324.1	005420	Cluster5160_1clades	151	AR9_g240	Bacillus phage AR9	GCA_001743835.1
ALN97975.1	005420	Cluster5160_1clades	148	Bp8pS_296	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99953.1	005420	Cluster5160_1clades	151	PBI_PBS1_131	Bacillus virus PBS1	GCA_002601325.1
QCW18887.1	005421	Cluster5161_1clades	151	7t3_0366	Salmonella phage 7t3	GCA_006083215.1
AZU98145.1	005421	Cluster5161_1clades	151	CPT_Munch_201	Salmonella phage Munch	GCA_004015485.1
QIG62838.1	005421	Cluster5161_1clades	151	SEPL_225	Salmonella phage SE_PL	GCA_011067555.1
QCW19108.1	005422	Cluster5162_1clades	149	7t3_0591	Salmonella phage 7t3	GCA_006083215.1
AZU98346.1	005422	Cluster5162_1clades	151	CPT_Munch_405	Salmonella phage Munch	GCA_004015485.1
QIG62637.1	005422	Cluster5162_1clades	149	SEPL_024	Salmonella phage SE_PL	GCA_011067555.1
AFU87969.1	005423	Cluster5163_1clades	150	CcrColossus_gp099	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68646.1	005423	Cluster5163_1clades	150	CcrPW_gp107c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69798.1	005423	Cluster5163_1clades	142	CcrSC_gp216c	Caulobacter phage CcrSC	GCA_003443315.1
ANM44820.1	005424	Cluster5164_1clades	150	KTN4_062	Pseudomonas phage KTN4	GCA_002607225.1
ATN94891.1	005424	Cluster5164_1clades	100	SL2_314	Pseudomonas phage SL2	GCA_002956015.1
AGC26313.1	005424	Cluster5164_1clades	88	PHIKZ044.1	Pseudomonas virus phiKZ	GCA_000842965.1
ATA65522.1	005425	APATPase	72	2050HW_00187	Serratia phage 2050HW	GCA_002628125.1
ATA65523.1	005425	APATPase	66	2050HW_00188	Serratia phage 2050HW	GCA_002628125.1
QDB71289.1	005425	APATPase	150	CPT_Moabite_259	Serratia phage Moabite	GCA_006384735.1
AMS01100.1	005426	Cluster5166_1clades	149	AR9_g015	Bacillus phage AR9	GCA_001743835.1
ALN97739.1	005426	Cluster5166_1clades	146	Bp8pS_060	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00022.1	005426	Cluster5166_1clades	149	PBI_PBS1_200	Bacillus virus PBS1	GCA_002601325.1
AYD80073.1	005427	Cluster5167_1clades	149	JA11_268	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66674.1	005427	Cluster5167_1clades	149	JA13_271	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67643.1	005427	Cluster5167_1clades	149	JA33_269	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AIA64942.1	005428	Cluster5168_1clades	122	S13_143	Cronobacter phage S13	GCA_001503575.1
QHJ79000.1	005428	Cluster5168_1clades	115	-	Myoviridae sp.	GCA_012593985.1
QHJ78999.1	005428	Cluster5168_1clades	149	-	Myoviridae sp.	GCA_012593985.1
ANS06050.1	005429	Cluster5169_1clades	144	ABCD_0158	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97170.1	005429	Cluster5169_1clades	146	E_162	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78686.1	005429	Cluster5169_1clades	148	RB43ORF164c	Escherichia virus RB43	GCA_000863505.1
AFC21923.1	005430	Cluster5170_1clades	128	GAP32_465	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44050.1	005430	Cluster5170_1clades	148	CBB_487	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89005.1	005430	Cluster5170_1clades	103	BF_0480	Serratia phage BF	GCA_002619745.1
BBI90502.1	005431	FemAB	133	HYO65_gp110	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90810.1	005431	FemAB	133	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39319.1	005431	FemAB	148	BPT24_195	Tenacibaculum phage pT24	GCA_002611925.1
AFU87886.1	005432	Cluster5172_1clades	147	CcrColossus_gp016	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68557.1	005432	Cluster5172_1clades	66	CcrPW_gp018	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69006.1	005432	Cluster5172_1clades	66	CcrPW_gp467	Caulobacter phage CcrPW	GCA_003443275.1
QCW18754.1	005433	Cluster5173_1clades	147	7t3_0233	Salmonella phage 7t3	GCA_006083215.1
AZU98023.1	005433	Cluster5173_1clades	147	CPT_Munch_079	Salmonella phage Munch	GCA_004015485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG62957.1	005433	Cluster5173_1clades	147	SEPL_344	Salmonella phage SE_PL	GCA_011067555.1
QCW18584.1	005434	SIG+TM	147	7t3_063	Salmonella phage 7t3	GCA_006083215.1
AZU98412.1	005434	SIG+TM	147	CPT_Munch_480	Salmonella phage Munch	GCA_004015485.1
QIG63101.1	005434	SIG+TM	147	SEPL_488	Salmonella phage SE_PL	GCA_011067555.1
QAX96826.1	005435	Cluster5175_1clades	147	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96191.1	005435	Cluster5175_1clades	147	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96509.1	005435	Cluster5175_1clades	147	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QDB70344.1	005436	Cluster5176_1clades	147	CF8_0175	Aeromonas phage CF8	GCA_006384595.2
QDJ96694.1	005436	Cluster5176_1clades	145	PS1_0183	Aeromonas phage PS1	GCA_007051165.2
QFR59327.1	005436	Cluster5176_1clades	145	PS2_0185	Aeromonas phage PS2	GCA_009388305.2
ANS06070.1	005437	SIG+Phage_T4_Ndd	126	ABCD_0272	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97292.1	005437	SIG+Phage_T4_Ndd	145	E_284	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78813.1	005437	SIG+Phage_T4_Ndd	146	RB43ORF291c	Escherichia virus RB43	GCA_000863505.1
AMS01166.1	005438	SIG+TM+TM	136	AR9_g082	Bacillus phage AR9	GCA_001743835.1
ALN97832.1	005438	SIG+TM+TM	146	Bp8pS_153	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00097.1	005438	SIG+TM+TM	133	PBI_PBS1_275	Bacillus virus PBS1	GCA_002601325.1
QCW18842.1	005439	Cluster5179_1clades	146	7t3_0321	Salmonella phage 7t3	GCA_006083215.1
AZU98104.1	005439	Cluster5179_1clades	146	CPT_Munch_160	Salmonella phage Munch	GCA_004015485.1
QIG62878.1	005439	Cluster5179_1clades	146	SEPL_265	Salmonella phage SE_PL	GCA_011067555.1
CAG27214.1	005440	Cluster5180_1clades	146	PPEV_gp120	Pseudomonas phage EL	GCA_000866825.1
BAW19074.1	005440	Cluster5180_1clades	141	FDH28_gp100	Ralstonia phage RP12	GCA_002617345.1
BAW19359.1	005440	Cluster5180_1clades	141	-	Ralstonia phage RP31	GCA_002617365.1
QAX96838.1	005441	SIG+YadA_anchor	146	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96202.1	005441	SIG+YadA_anchor	146	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96520.1	005441	SIG+YadA_anchor	146	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QBX32355.1	005442	TM	146	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03619.1	005442	TM	142	196	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41929.1	005442	TM	146	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AQW88911.1	005443	Cluster5183_1clades	143	BF_0386	Serratia phage BF	GCA_002619745.1
SOK59200.1	005443	Cluster5183_1clades	142	g392	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58665.1	005443	Cluster5183_1clades	146	g388	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ADQ52755.1	005444	Cluster5184_1clades	145	PX29p036	Aeromonas phage PX29	GCA_000920195.1
ADM80011.1	005444	Cluster5184_1clades	130	phiAS5_ORF0168	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17698.1	005444	Cluster5184_1clades	131	Aeh1ORF039c	Aeromonas virus Aeh1	GCA_000843245.1
AGR47677.1	005445	Cluster5185_1clades	145	SmphiM12_045	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12939.1	005445	Cluster5185_1clades	145	PHIM19_32	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12579.1	005445	Cluster5185_1clades	145	PHIM7_31	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01160.1	005446	Cluster5186_1clades	144	AR9_g076	Bacillus phage AR9	GCA_001743835.1
ALN97826.1	005446	Cluster5186_1clades	145	Bp8pS_147	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00089.1	005446	Cluster5186_1clades	144	PBI_PBS1_267	Bacillus virus PBS1	GCA_002601325.1
ANM45079.1	005447	Cluster5187_1clades	145	KTN4_321	Pseudomonas phage KTN4	GCA_002607225.1
ATN94636.1	005447	Cluster5187_1clades	145	SL2_059	Pseudomonas phage SL2	GCA_002956015.1
QJB22954.1	005447	Cluster5187_1clades	145	fnug_311	Pseudomonas phage fnug	GCA_012837215.1
QBX32476.1	005448	Cluster5188_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03737.1	005448	Cluster5188_1clades	144	314	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42048.1	005448	Cluster5188_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AMS01175.1	005449	Cluster5189_1clades	135	AR9_g091	Bacillus phage AR9	GCA_001743835.1
AMM45025.1	005449	Cluster5189_1clades	144	SP15_224	Bacillus phage SP-15	GCA_001754685.1
ASU00108.1	005449	Cluster5189_1clades	135	PBI_PBS1_286	Bacillus virus PBS1	GCA_002601325.1
AGX01770.1	005450	Cluster5190_1clades	124	CF95_gp048	Erwinia phage PhiEaH1	GCA_000914555.1
ATA65611.1	005450	Cluster5190_1clades	144	2050HW_00276	Serratia phage 2050HW	GCA_002628125.1
QDB71040.1	005450	Cluster5190_1clades	144	CPT_Moabite_008	Serratia phage Moabite	GCA_006384735.1
AXG67346.1	005451	AFOR_C	144	AD1_302	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08573.1	005451	AFOR_C	139	Alexandra_322	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58949.1	005451	AFOR_C	143	Y3_309	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW19080.1	005452	TPR	144	7t3_0560	Salmonella phage 7t3	GCA_006083215.1
AZU98322.1	005452	TPR	144	CPT_Munch_378	Salmonella phage Munch	GCA_004015485.1
QIG62661.1	005452	TPR	144	SEPL_048	Salmonella phage SE_PL	GCA_011067555.1
QBX06790.1	005453	Imm-ComJ	119	BcepSaruman_377	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74760.1	005453	Imm-ComJ	144	BcepSauron_380	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ96320.1	005453	Imm-ComJ	107	Xoosp13_133	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AUZ94842.1	005454	Cluster5194_1clades	143	FDI40_gp030	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72781.1	005454	Cluster5194_1clades	143	-	Myoviridae sp.	GCA_003657725.1
QCG76123.1	005454	Cluster5194_1clades	144	EST35_0242	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QBZ70647.1	005455	Cluster5195_1clades	143	pETSU_066	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71964.1	005455	Cluster5195_1clades	142	N1M2_101	Klebsiella phage N1M2	GCA_010092605.1
AEV89565.1	005455	Cluster5195_1clades	75	OBP_128	Pseudomonas phage OBP	GCA_000896635.1
AIA64919.1	005456	Cluster5196_1clades	77	S13_120	Cronobacter phage S13	GCA_001503575.1
AIA64920.1	005456	Cluster5196_1clades	89	S13_121	Cronobacter phage S13	GCA_001503575.1
QHJ79024.1	005456	Cluster5196_1clades	143	-	Myoviridae sp.	GCA_012593985.1
AUE22824.1	005457	Cluster5197_1clades	142	Ah1_00306	Aeromonas phage Ah1	GCA_002957415.1
ADM79925.1	005457	Cluster5197_1clades	141	phiAS5_ORF0082	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17954.1	005457	Cluster5197_1clades	142	Aeh1ORF285c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06052.1	005458	Cluster5198_1clades	142	ABCD_0078	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97091.1	005458	Cluster5198_1clades	139	E_083	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78600.1	005458	Cluster5198_1clades	142	RB43ORF078w	Escherichia virus RB43	GCA_000863505.1
AXH72693.1	005459	GxC-R	113	-	Myoviridae sp.	GCA_003657725.1
AXH72673.1	005459	GxC-R	117	-	Myoviridae sp.	GCA_003657725.1
AXH72680.1	005459	GxC-R	142	-	Myoviridae sp.	GCA_003657725.1
QCW18820.1	005460	Cluster5200_1clades	142	7t3_0299	Salmonella phage 7t3	GCA_006083215.1
AZU98084.1	005460	Cluster5200_1clades	142	CPT_Munch_140	Salmonella phage Munch	GCA_004015485.1
QIG62898.1	005460	Cluster5200_1clades	132	SEPL_285	Salmonella phage SE_PL	GCA_011067555.1
QCW18864.1	005461	Cluster5201_1clades	142	7t3_0343	Salmonella phage 7t3	GCA_006083215.1
AZU98125.1	005461	Cluster5201_1clades	142	CPT_Munch_181	Salmonella phage Munch	GCA_004015485.1
QIG62857.1	005461	Cluster5201_1clades	142	SEPL_244	Salmonella phage SE_PL	GCA_011067555.1
QIG63502.1	005462	Peptidase_C37	142	DAC19_11	Bacteroides phage DAC19	GCA_013387715.1
QIG63764.1	005462	Peptidase_C37	142	DAC20_11	Bacteroides phage DAC20	GCA_013387725.1
QIG64025.1	005462	Peptidase_C37	142	DAC22_11	Bacteroides phage DAC22	GCA_013387735.1
QKN85970.1	005463	Cluster5203_1clades	141	ACEC001_1320	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20834.1	005463	Cluster5203_1clades	141	-	Salmonella phage JN03	GCA_014319805.1
AEP83963.1	005463	Cluster5203_1clades	141	SPN3US_0130	Salmonella phage SPN3US	GCA_001042275.1
AXG67099.1	005464	Cluster5204_1clades	102	AD1_055	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08334.1	005464	Cluster5204_1clades	141	Alexandra_54	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58698.1	005464	Cluster5204_1clades	94	Y3_058	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18802.1	005465	Cluster5205_1clades	136	7t3_0281	Salmonella phage 7t3	GCA_006083215.1
AZU98067.1	005465	Cluster5205_1clades	141	CPT_Munch_123	Salmonella phage Munch	GCA_004015485.1
QIG62915.1	005465	Cluster5205_1clades	141	SEPL_302	Salmonella phage SE_PL	GCA_011067555.1
QCW18874.1	005466	Cluster5206_1clades	141	7t3_0353	Salmonella phage 7t3	GCA_006083215.1
AZU98132.1	005466	Cluster5206_1clades	141	CPT_Munch_188	Salmonella phage Munch	GCA_004015485.1
QIG62850.1	005466	Cluster5206_1clades	49	SEPL_237	Salmonella phage SE_PL	GCA_011067555.1
QCW18597.1	005467	Cluster5207_1clades	141	7t3_076	Salmonella phage 7t3	GCA_006083215.1
AZU98425.1	005467	Cluster5207_1clades	141	CPT_Munch_493	Salmonella phage Munch	GCA_004015485.1
QIG63088.1	005467	Cluster5207_1clades	141	SEPL_475	Salmonella phage SE_PL	GCA_011067555.1
QBX06653.1	005468	Cluster5208_1clades	116	BcepSaruman_240	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74621.1	005468	Cluster5208_1clades	116	BcepSauron_241	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41673.1	005468	Cluster5208_1clades	141	RSL1_ORF223	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44723.1	005469	Cluster5209_1clades	140	FDI40_gp149	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04877.2	005469	Cluster5209_1clades	141	AVU11_gp085	Ralstonia phage RSF1	GCA_001500875.1
BAQ02609.1	005469	Cluster5209_1clades	139	AVU38_gp081	Ralstonia phage RSL2	GCA_001503055.1
BBA65721.1	005470	Cluster5210_1clades	141	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65262.1	005470	Cluster5210_1clades	141	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96301.1	005470	Cluster5210_1clades	133	Xoosp13_114	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QCW18549.1	005471	Cluster5211_1clades	141	7t3_024	Salmonella phage 7t3	GCA_006083215.1
AZU98378.1	005471	Cluster5211_1clades	135	CPT_Munch_444	Salmonella phage Munch	GCA_004015485.1
QIG63134.1	005471	Cluster5211_1clades	135	SEPL_521	Salmonella phage SE_PL	GCA_011067555.1
AQW88606.1	005472	Cluster5212_1clades	133	BF_0081	Serratia phage BF	GCA_002619745.1
SOK58883.1	005472	Cluster5212_1clades	141	g075	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58346.1	005472	Cluster5212_1clades	141	g069	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFU87901.1	005473	Cluster5213_1clades	140	CcrColossus_gp031	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68571.1	005473	Cluster5213_1clades	126	CcrPW_gp032	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69020.1	005473	Cluster5213_1clades	126	CcrPW_gp481	Caulobacter phage CcrPW	GCA_003443275.1
QCW18817.1	005474	Cluster5214_1clades	140	7t3_0296	Salmonella phage 7t3	GCA_006083215.1
AZU98081.1	005474	Cluster5214_1clades	140	CPT_Munch_137	Salmonella phage Munch	GCA_004015485.1
QIG62901.1	005474	Cluster5214_1clades	140	SEPL_288	Salmonella phage SE_PL	GCA_011067555.1
QCW18565.1	005475	Cluster5215_1clades	140	7t3_044	Salmonella phage 7t3	GCA_006083215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AZU98394.1	005475	Cluster5215_1clades	140	CPT_Munch_462	Salmonella phage Munch	GCA_004015485.1
QIG63119.1	005475	Cluster5215_1clades	140	SEPL_506	Salmonella phage SE_PL	GCA_011067555.1
QBX06854.1	005476	Cluster5216_1clades	140	BcepSaruman_441	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06858.1	005476	Cluster5216_1clades	120	BcepSaruman_445	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74823.1	005476	Cluster5216_1clades	140	BcepSauron_443	Burkholderia phage BcepSauron	GCA_005394215.1
AGR48016.1	005477	Cluster5217_1clades	139	SmphiM12_384	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13202.1	005477	Cluster5217_1clades	139	PHIM19_297	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12843.1	005477	Cluster5217_1clades	139	PHIM7_297	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01331.1	005478	SIG+Phage_holin_6_1	139	AR9_g247	Bacillus phage AR9	GCA_001743835.1
ALN97978.1	005478	SIG+Phage_holin_6_1	136	Bp8pS_299	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99960.1	005478	SIG+Phage_holin_6_1	139	PBI_PBS1_139	Bacillus virus PBS1	GCA_002601325.1
ANZ49779.1	005479	Cluster5219_1clades	139	MACHINA_141	Erwinia phage Machina	GCA_002758035.1
ANZ49223.1	005479	Cluster5219_1clades	139	HUXLEY_141	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50051.1	005479	Cluster5219_1clades	139	PARSHIK_142	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ49780.1	005480	Cluster5220_1clades	139	MACHINA_142	Erwinia phage Machina	GCA_002758035.1
ANZ49224.1	005480	Cluster5220_1clades	139	HUXLEY_142	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50052.1	005480	Cluster5220_1clades	139	PARSHIK_143	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QDJ96190.1	005481	Cluster5221_1clades	139	Xoosp13_3	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96194.1	005481	Cluster5221_1clades	106	Xoosp13_7	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96196.1	005481	Cluster5221_1clades	136	Xoosp13_9	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ANS06055.1	005482	TM+TM	138	ABCD_0273	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97293.1	005482	TM+TM	137	E_285	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78814.1	005482	TM+TM	138	RB43ORF292c	Escherichia virus RB43	GCA_000863505.1
QBX32415.1	005483	Cluster5223_1clades	130	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03684.1	005483	Cluster5223_1clades	138	261	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41986.1	005483	Cluster5223_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBZ70824.1	005484	Cluster5224_1clades	103	pETSU_243	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71865.1	005484	Cluster5224_1clades	138	N1M2_2	Klebsiella phage N1M2	GCA_010092605.1
AEV89456.1	005484	Cluster5224_1clades	138	OBP_019	Pseudomonas phage OBP	GCA_000896635.1
ANS06060.1	005485	Cluster5225_1clades	134	ABCD_0170	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97183.1	005485	Cluster5225_1clades	138	E_175	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78700.1	005485	Cluster5225_1clades	134	RB43ORF178c	Escherichia virus RB43	GCA_000863505.1
AXG67077.1	005486	Cluster5226_1clades	136	AD1_033	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08310.1	005486	Cluster5226_1clades	136	Alexandra_30	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58674.1	005486	Cluster5226_1clades	138	Y3_034	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18569.1	005487	Cluster5227_1clades	138	7t3_048	Salmonella phage 7t3	GCA_006083215.1
AZU98398.1	005487	Cluster5227_1clades	138	CPT_Munch_466	Salmonella phage Munch	GCA_004015485.1
QIG63115.1	005487	Cluster5227_1clades	138	SEPL_502	Salmonella phage SE_PL	GCA_011067555.1
ANS06056.1	005488	Cluster5228_1clades	137	ABCD_0132	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97141.1	005488	Cluster5228_1clades	128	E_133	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78654.1	005488	Cluster5228_1clades	126	RB43ORF132c	Escherichia virus RB43	GCA_000863505.1
ANZ49917.1	005489	Cluster5229_1clades	137	MACHINA_279	Erwinia phage Machina	GCA_002758035.1
ANZ49360.1	005489	Cluster5229_1clades	137	HUXLEY_278	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50188.1	005489	Cluster5229_1clades	131	PARSHIK_279	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AXG67094.1	005490	Cluster5230_1clades	136	AD1_050	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08330.1	005490	Cluster5230_1clades	137	Alexandra_50	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58694.1	005490	Cluster5230_1clades	133	Y3_054	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67310.1	005491	MCM_bind	137	AD1_266	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08535.1	005491	MCM_bind	133	Alexandra_278	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58913.1	005491	MCM_bind	132	Y3_273	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW19034.1	005492	SIG+TM	137	7t3_0514	Salmonella phage 7t3	GCA_006083215.1
AZU98281.1	005492	SIG+TM	137	CPT_Munch_337	Salmonella phage Munch	GCA_004015485.1
QIG62703.1	005492	SIG+TM	137	SEPL_090	Salmonella phage SE_PL	GCA_011067555.1
QCW18585.1	005493	SIG+TM+TM	137	7t3_064	Salmonella phage 7t3	GCA_006083215.1
AZU98413.1	005493	SIG+TM+TM	137	CPT_Munch_481	Salmonella phage Munch	GCA_004015485.1
QIG63100.1	005493	SIG+TM+TM	137	SEPL_487	Salmonella phage SE_PL	GCA_011067555.1
AFC21959.1	005494	Cluster5235_1clades	136	GAP32_500	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44084.1	005494	Cluster5235_1clades	131	CBB_521	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89038.1	005494	Cluster5235_1clades	129	BF_0513	Serratia phage BF	GCA_002619745.1
QCW18692.1	005495	Cluster5236_1clades	136	7t3_0171	Salmonella phage 7t3	GCA_006083215.1
AZU97966.1	005495	Cluster5236_1clades	136	CPT_Munch_022	Salmonella phage Munch	GCA_004015485.1
QIG63012.1	005495	Cluster5236_1clades	136	SEPL_399	Salmonella phage SE_PL	GCA_011067555.1
QCW18904.1	005496	Cluster5237_1clades	136	7t3_0383	Salmonella phage 7t3	GCA_006083215.1
AZU98161.1	005496	Cluster5237_1clades	136	CPT_Munch_217	Salmonella phage Munch	GCA_004015485.1
QIG62823.1	005496	Cluster5237_1clades	136	SEPL_210	Salmonella phage SE_PL	GCA_011067555.1
QCW19105.1	005497	Cluster5238_1clades	110	7t3_0588	Salmonella phage 7t3	GCA_006083215.1
AZU98343.1	005497	Cluster5238_1clades	136	CPT_Munch_402	Salmonella phage Munch	GCA_004015485.1
QIG62640.1	005497	Cluster5238_1clades	110	SEPL_027	Salmonella phage SE_PL	GCA_011067555.1
QBX06499.1	005498	Cluster5239_1clades	136	BcepSaruman_086	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74466.1	005498	Cluster5239_1clades	136	BcepSauron_086	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41576.1	005498	Cluster5239_1clades	132	RSL1_ORF131	Ralstonia phage phiRSL1	GCA_000879455.1
ATA65489.1	005499	Cluster5240_1clades	53	2050HW_00154	Serratia phage 2050HW	GCA_002628125.1
ATA65490.1	005499	Cluster5240_1clades	88	2050HW_00155	Serratia phage 2050HW	GCA_002628125.1
QDB71259.1	005499	Cluster5240_1clades	136	CPT_Moabite_229	Serratia phage Moabite	GCA_006384735.1
BBA65716.1	005500	Cluster5241_1clades	126	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65257.1	005500	Cluster5241_1clades	126	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96296.1	005500	Cluster5241_1clades	136	Xoosp13_109	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBZ70798.1	005501	Cluster5242_1clades	134	pETSU_217	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72099.1	005501	Cluster5242_1clades	136	N1M2_236	Klebsiella phage N1M2	GCA_010092605.1
AEV89736.1	005501	Cluster5242_1clades	130	OBP_299	Pseudomonas phage OBP	GCA_000896635.1
AFQ96590.1	005502	Cluster5243_1clades	135	G173_gp045	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48155.1	005502	Cluster5243_1clades	135	ASESINO_142	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50567.1	005502	Cluster5243_1clades	135	STRATTON_142	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ASR76077.1	005503	TM	133	PBI_BELLAMY_32	Synechococcus phage Bellamy	GCA_002627525.1
ASR76082.1	005503	TM	135	PBI_BELLAMY_37	Synechococcus phage Bellamy	GCA_002627525.1
ASR76088.1	005503	TM	120	PBI_BELLAMY_43	Synechococcus phage Bellamy	GCA_002627525.1
AXH72691.1	005504	Cluster5245_1clades	107	-	Myoviridae sp.	GCA_003657725.1
AXH72677.1	005504	Cluster5245_1clades	132	-	Myoviridae sp.	GCA_003657725.1
AXH72658.1	005504	Cluster5245_1clades	135	-	Myoviridae sp.	GCA_003657725.1
QCW18905.1	005505	Cluster5246_1clades	135	7t3_0384	Salmonella phage 7t3	GCA_006083215.1
AZU98162.1	005505	Cluster5246_1clades	135	CPT_Munch_218	Salmonella phage Munch	GCA_004015485.1
QIG62822.1	005505	Cluster5246_1clades	135	SEPL_209	Salmonella phage SE_PL	GCA_011067555.1
BBA65206.1	005506	Cluster5247_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65665.1	005506	Cluster5247_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96236.1	005506	Cluster5247_1clades	107	Xoosp13_49	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDB70423.1	005507	TM+TM	135	CF8_0010	Aeromonas phage CF8	GCA_006384595.2
QDJ96678.1	005507	TM+TM	133	PS1_0167	Aeromonas phage PS1	GCA_007051165.2
QFR59312.1	005507	TM+TM	133	PS2_0171	Aeromonas phage PS2	GCA_009388305.2
QMV28825.1	005508	Cluster5249_1clades	131	AP1_0118	Aeromonas phage AP1	GCA_014183365.1
QAX98042.1	005508	Cluster5249_1clades	131	ASswx1_402	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39150.1	005508	Cluster5249_1clades	134	CC2_128	Aeromonas phage CC2	GCA_000903495.1
AGH07729.1	005509	Cluster5250_1clades	134	CYVG_00286	Cyanophage S-SSM6a	GCA_002710385.1
AAX44677.1	005509	Cluster5250_1clades	119	PSSM2_300	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12299.1	005509	Cluster5250_1clades	119	PRTG_00146	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGR48014.1	005510	Cluster5251_1clades	134	SmphiM12_382	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13200.1	005510	Cluster5251_1clades	134	PHIM19_295	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12841.1	005510	Cluster5251_1clades	134	PHIM7_295	Sinorhizobium phage phiM7	GCA_002622405.1
ANS06062.1	005511	Cluster5252_1clades	133	ABCD_0147	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97158.1	005511	Cluster5252_1clades	134	E_150	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78674.1	005511	Cluster5252_1clades	133	RB43ORF152c	Escherichia virus RB43	GCA_000863505.1
AOV59619.1	005512	Cluster5253_1clades	134	S330809_158	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59381.1	005512	Cluster5253_1clades	134	C440309_158	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59857.1	005512	Cluster5253_1clades	134	N231010_158	Synechococcus phage S-CAM4	GCA_002922155.1
QBX06681.1	005513	Cluster5254_1clades	129	BcepSaruman_268	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74651.1	005513	Cluster5254_1clades	129	BcepSauron_271	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41642.1	005513	Cluster5254_1clades	134	RSL1_ORF193	Ralstonia phage phiRSL1	GCA_000879455.1
BBA65683.1	005514	Cluster5255_1clades	134	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65224.1	005514	Cluster5255_1clades	134	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96254.1	005514	Cluster5255_1clades	115	Xoosp13_67	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBZ70857.1	005515	Cluster5256_1clades	131	pETSU_276	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71889.1	005515	Cluster5256_1clades	134	N1M2_26	Klebsiella phage N1M2	GCA_010092605.1
AEV89483.1	005515	Cluster5256_1clades	131	OBP_046	Pseudomonas phage OBP	GCA_000896635.1
APU01725.1	005516	Cluster5257_1clades	133	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01132.1	005516	Cluster5257_1clades	129	ASwh1_66	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53365.1	005516	Cluster5257_1clades	133	65p357	Aeromonas virus 65	GCA_000893255.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQW88935.1	005517	Cluster5258_1clades	133	BF_0410	Serratia phage BF	GCA_002619745.1
SOK59224.1	005517	Cluster5258_1clades	130	g416	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58690.1	005517	Cluster5258_1clades	130	g413	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW19111.1	005518	Cluster5259_1clades	133	7t3_0594	Salmonella phage 7t3	GCA_006083215.1
AZU98348.1	005518	Cluster5259_1clades	133	CPT_Munch_407	Salmonella phage Munch	GCA_004015485.1
QIG62634.1	005518	Cluster5259_1clades	133	SEPL_021	Salmonella phage SE_PL	GCA_011067555.1
QGZ14544.1	005519	EAD2	133	HWC77_gp181	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04190.1	005519	EAD2	133	HWC03_gp035	Vibrio phage 2 TSL-2019	GCA_006964105.1
BAW98375.1	005519	EAD2	133	FDH33_gp166	Vibrio phage pTD1	GCA_002618825.1
AFU87875.1	005520	DUF2967	132	CcrColossus_gp005	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68545.1	005520	DUF2967	132	CcrPW_gp006	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68995.1	005520	DUF2967	132	CcrPW_gp456	Caulobacter phage CcrPW	GCA_003443275.1
AMS01278.1	005521	Cluster5262_1clades	125	AR9_g194	Bacillus phage AR9	GCA_001743835.1
ALN97933.1	005521	Cluster5262_1clades	132	Bp8pS_254	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99906.1	005521	Cluster5262_1clades	125	PBI_PBS1_84	Bacillus virus PBS1	GCA_002601325.1
ANS06064.1	005522	Cluster5263_1clades	131	ABCD_0154	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97166.1	005522	Cluster5263_1clades	132	E_158	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78682.1	005522	Cluster5263_1clades	131	RB43ORF160c	Escherichia virus RB43	GCA_000863505.1
QCW18575.1	005523	Cluster5264_1clades	132	7t3_054	Salmonella phage 7t3	GCA_006083215.1
AZU98404.1	005523	Cluster5264_1clades	132	CPT_Munch_472	Salmonella phage Munch	GCA_004015485.1
QIG63109.1	005523	Cluster5264_1clades	132	SEPL_496	Salmonella phage SE_PL	GCA_011067555.1
QBX32440.1	005524	Cluster5265_1clades	132	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03711.1	005524	Cluster5265_1clades	119	288	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42011.1	005524	Cluster5265_1clades	132	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32428.1	005525	Cluster5266_1clades	74	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03695.1	005525	Cluster5266_1clades	131	272	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41999.1	005525	Cluster5266_1clades	88	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDH83519.1	005526	SIG+TM+TM	118	H1O15_gp287	Achromobacter phage Motura	GCA_006964305.1
AFH14847.1	005526	SIG+TM+TM	124	Lu11_0309	Pseudomonas phage Lu11	GCA_000897175.1
AGS81908.1	005526	SIG+TM+TM	131	PaBG_00024	Pseudomonas phage PaBG	GCA_000912555.1
QBX06505.1	005527	Cluster5268_1clades	131	BcepSaruman_092	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74471.1	005527	Cluster5268_1clades	131	BcepSauron_091	Burkholderia phage BcepSauron	GCA_005394215.1
BAH72944.1	005527	Cluster5268_1clades	119	RSL1_ORF120	Ralstonia phage phiRSL1	GCA_000879455.1
QDB70484.1	005528	gp45-clamp	127	CF8_0073	Aeromonas phage CF8	GCA_006384595.2
QDJ96831.1	005528	gp45-clamp	131	PS1_0072	Aeromonas phage PS1	GCA_007051165.2
QFR59461.1	005528	gp45-clamp	131	PS2_0070	Aeromonas phage PS2	GCA_009388305.2
AQW88702.1	005529	Cluster5270_1clades	110	BF_0177	Serratia phage BF	GCA_002619745.1
SOK58982.1	005529	Cluster5270_1clades	131	g174	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58448.1	005529	Cluster5270_1clades	131	g171	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06065.1	005530	Cluster5271_1clades	130	ABCD_0031	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97041.1	005530	Cluster5271_1clades	127	E_032	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78553.1	005530	Cluster5271_1clades	130	RB43ORF031c	Escherichia virus RB43	GCA_000863505.1
AMO43069.1	005531	Cluster5272_1clades	130	R1080702_060	Cyanophage S-RIM32	GCA_001754165.1
QGT54732.1	005531	Cluster5272_1clades	74	b23_0117	Synechococcus phage B23	GCA_009745195.1
QGT54362.1	005531	Cluster5272_1clades	74	b3_0118	Synechococcus phage B3	GCA_009745215.1
QCW19089.1	005532	Cluster5273_1clades	130	7t3_0571	Salmonella phage 7t3	GCA_006083215.1
AZU98328.1	005532	Cluster5273_1clades	130	CPT_Munch_386	Salmonella phage Munch	GCA_004015485.1
QIG62655.1	005532	Cluster5273_1clades	130	SEPL_042	Salmonella phage SE_PL	GCA_011067555.1
QBX06596.1	005533	Cluster5274_1clades	130	BcepSaruman_183	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74561.1	005533	Cluster5274_1clades	130	BcepSauron_181	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41486.1	005533	Cluster5274_1clades	110	RSL1_ORF041	Ralstonia phage phiRSL1	GCA_000879455.1
QDB70342.1	005534	Cluster5275_1clades	130	CF8_0173	Aeromonas phage CF8	GCA_006384595.2
QDJ96692.1	005534	Cluster5275_1clades	127	PS1_0181	Aeromonas phage PS1	GCA_007051165.2
QFR59325.1	005534	Cluster5275_1clades	127	PS2_0183	Aeromonas phage PS2	GCA_009388305.2
AUZ95057.1	005535	TM+TM	127	FDI40_gp285	Agrobacterium phage Atu_ph07	GCA_002628245.1
SBV38204.1	005535	TM+TM	130	BN7874_035	Phage NCTB	GCA_900092385.1
QCG76187.1	005535	TM+TM	108	EST35_0306	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AXG67262.1	005536	Cluster5277_1clades	121	AD1_218	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08491.1	005536	Cluster5277_1clades	121	Alexandra_228	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58863.1	005536	Cluster5277_1clades	129	Y3_223	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18788.1	005537	Cluster5278_1clades	129	7t3_0267	Salmonella phage 7t3	GCA_006083215.1
AZU98053.1	005537	Cluster5278_1clades	129	CPT_Munch_109	Salmonella phage Munch	GCA_004015485.1
QIG62928.1	005537	Cluster5278_1clades	129	SEPL_315	Salmonella phage SE_PL	GCA_011067555.1
QCW19107.1	005538	Cluster5279_1clades	129	7t3_0590	Salmonella phage 7t3	GCA_006083215.1
AZU98345.1	005538	Cluster5279_1clades	129	CPT_Munch_404	Salmonella phage Munch	GCA_004015485.1
QIG62638.1	005538	Cluster5279_1clades	129	SEPL_025	Salmonella phage SE_PL	GCA_011067555.1
AQW88988.1	005539	Cluster5280_1clades	119	BF_0463	Serratia phage BF	GCA_002619745.1
SOK59269.1	005539	Cluster5280_1clades	119	g461	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58734.1	005539	Cluster5280_1clades	129	g457	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBZ70853.1	005540	Cluster5281_1clades	109	pETSU_272	Edwardsiella virus pEt-SU	GCA_004809015.1
QGH71885.1	005540	Cluster5281_1clades	77	N1M2_22	Klebsiella phage N1M2	GCA_010092605.1
AEV89479.1	005540	Cluster5281_1clades	128	OBP_042	Pseudomonas phage OBP	GCA_000896635.1
AXG67110.1	005541	Cluster5282_1clades	127	AD1_066	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08346.1	005541	Cluster5282_1clades	127	Alexandra_66	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58708.1	005541	Cluster5282_1clades	128	Y3_068	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AEH03642.1	005542	Cluster5283_1clades	127	219	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03643.1	005542	Cluster5283_1clades	111	220	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03644.1	005542	Cluster5283_1clades	118	221	Pseudomonas phage PhiPA3	GCA_001502095.1
AQW88712.1	005543	Cluster5284_1clades	127	BF_0187	Serratia phage BF	GCA_002619745.1
SOK58994.1	005543	Cluster5284_1clades	126	g186	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58459.1	005543	Cluster5284_1clades	126	g182	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67112.1	005544	Cluster5285_1clades	115	AD1_068	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08616.1	005544	Cluster5285_1clades	127	Alexandra_70	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58711.1	005544	Cluster5285_1clades	112	Y3_071	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18846.1	005545	SIG+HEPN-Toprim-NTD1	127	7t3_0325	Salmonella phage 7t3	GCA_006083215.1
AZU98108.1	005545	SIG+HEPN-Toprim-NTD1	127	CPT_Munch_164	Salmonella phage Munch	GCA_004015485.1
QIG62874.1	005545	SIG+HEPN-Toprim-NTD1	127	SEPL_261	Salmonella phage SE_PL	GCA_011067555.1
QCW19099.1	005546	Cluster5287_1clades	127	7t3_0581	Salmonella phage 7t3	GCA_006083215.1
AZU98338.1	005546	Cluster5287_1clades	127	CPT_Munch_396	Salmonella phage Munch	GCA_004015485.1
QIG62645.1	005546	Cluster5287_1clades	127	SEPL_032	Salmonella phage SE_PL	GCA_011067555.1
APU01700.1	005547	Cluster5288_1clades	125	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53339.1	005547	Cluster5288_1clades	125	65p331	Aeromonas virus 65	GCA_000893255.1
QAU04496.1	005547	Cluster5288_1clades	127	ValB1MD_143	Vibrio phage ValB1MD	GCA_004138815.1
QDB70446.1	005548	Cluster5289_1clades	127	CF8_0034	Aeromonas phage CF8	GCA_006384595.2
QDJ96791.1	005548	Cluster5289_1clades	122	PS1_0032	Aeromonas phage PS1	GCA_007051165.2
QFR59422.1	005548	Cluster5289_1clades	122	PS2_0031	Aeromonas phage PS2	GCA_009388305.2
QDB70314.1	005549	Cluster5290_1clades	126	CF8_0146	Aeromonas phage CF8	GCA_006384595.2
QDJ97298.1	005549	Cluster5290_1clades	127	D6_0138	Aeromonas phage D6	GCA_007051205.2
QDH47207.1	005549	Cluster5290_1clades	127	LAh10_63	Aeromonas phage LAh10	GCA_006863975.1
AGH07707.1	005550	Cluster5291_1clades	107	CYVG_00264	Cyanophage S-SSM6a	GCA_002710385.1
AAX44599.1	005550	Cluster5291_1clades	126	PSSM2_222	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12371.1	005550	Cluster5291_1clades	126	PRTG_00218	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU87876.1	005551	Cluster5292_1clades	126	CcrColossus_gp006	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68546.1	005551	Cluster5292_1clades	48	CcrPW_gp007	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68996.1	005551	Cluster5292_1clades	48	CcrPW_gp457	Caulobacter phage CcrPW	GCA_003443275.1
AGR47644.1	005552	Cluster5293_1clades	126	SmphiM12_012	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12909.1	005552	Cluster5293_1clades	126	PHIM19_2	Sinorhizobium phage phiM19	GCA_002605865.1
AKF13277.1	005552	Cluster5293_1clades	124	PHIN3_10	Sinorhizobium phage phiN3	GCA_001501175.1
ANS06077.1	005553	Cluster5294_1clades	114	ABCD_0160	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97173.1	005553	Cluster5294_1clades	126	E_165	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78688.1	005553	Cluster5294_1clades	108	RB43ORF166c	Escherichia virus RB43	GCA_000863505.1
AQW88977.1	005554	Cluster5295_1clades	126	BF_0452	Serratia phage BF	GCA_002619745.1
SOK59261.1	005554	Cluster5295_1clades	126	g453	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58726.1	005554	Cluster5295_1clades	126	g449	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67085.1	005555	TM	112	AD1_041	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08319.1	005555	TM	126	Alexandra_39	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58683.1	005555	TM	111	Y3_043	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW22992.1	005556	Cluster5297_1clades	122	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50643.1	005556	Cluster5297_1clades	122	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70463.1	005556	Cluster5297_1clades	126	HOU04_gp064	Synechococcus phage S-T4	GCA_003443335.1
AYD81457.1	005557	Cluster5298_1clades	126	SEA_JUSTBECAUSE_302	Streptomyces phage JustBecause	GCA_003613775.1
QBZ72193.1	005557	Cluster5298_1clades	125	SEA_KRADAL_307	Streptomyces phage Kradal	GCA_004799925.1
AXH66456.1	005557	Cluster5298_1clades	125	SEA_SATIS_307	Streptomyces phage Satis	GCA_003366315.1
QCW18681.1	005558	Cluster5299_1clades	126	7t3_0160	Salmonella phage 7t3	GCA_006083215.1
AZU97955.1	005558	Cluster5299_1clades	126	CPT_Munch_011	Salmonella phage Munch	GCA_004015485.1

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QIG63021.1	005558	Cluster5299_1clades	126	SEPL_408	Salmonella phage SE_PL	GCA_011067555.1
QCW18839.1	005559	Cluster5300_1clades	126	7t3_0318	Salmonella phage 7t3	GCA_006083215.1
AZU98101.1	005559	Cluster5300_1clades	126	CPT_Munch_157	Salmonella phage Munch	GCA_004015485.1
QIG62881.1	005559	Cluster5300_1clades	126	SEPL_268	Salmonella phage SE_PL	GCA_011067555.1
QCW19079.1	005560	Cluster5301_1clades	126	7t3_0559	Salmonella phage 7t3	GCA_006083215.1
AZU98321.1	005560	Cluster5301_1clades	126	CPT_Munch_377	Salmonella phage Munch	GCA_004015485.1
QIG62662.1	005560	Cluster5301_1clades	126	SEPL_049	Salmonella phage SE_PL	GCA_011067555.1
QCW18617.1	005561	Cluster5302_1clades	126	7t3_096	Salmonella phage 7t3	GCA_006083215.1
AZU98442.1	005561	Cluster5302_1clades	126	CPT_Munch_510	Salmonella phage Munch	GCA_004015485.1
QIG63071.1	005561	Cluster5302_1clades	126	SEPL_458	Salmonella phage SE_PL	GCA_011067555.1
ANS06071.1	005562	Cluster5303_1clades	125	ABCD_0101	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97111.1	005562	Cluster5303_1clades	124	E_103	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78622.1	005562	Cluster5303_1clades	125	RB43ORF100w	Escherichia virus RB43	GCA_000863505.1
AIT14274.1	005563	Cluster5304_1clades	125	PBI_121Q_384	Escherichia phage 121Q	GCA_000926855.1
QBO62030.1	005563	Cluster5304_1clades	125	G17_00541	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14051.1	005563	Cluster5304_1clades	125	vBEcoMphAPEC6_gp428c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AWY08557.1	005564	Cluster5305_1clades	125	Alexandra_301	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58930.1	005564	Cluster5305_1clades	97	Y3_290	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28753.1	005564	Cluster5305_1clades	125	YOLOSWAG_282	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQW88619.1	005565	Cluster5306_1clades	125	BF_0094	Serratia phage BF	GCA_002619745.1
SOK58895.1	005565	Cluster5306_1clades	125	g087	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58360.1	005565	Cluster5306_1clades	125	g083	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QDB70345.1	005566	Cluster5307_1clades	125	CF8_0176	Aeromonas phage CF8	GCA_006384595.2
QDJ96695.1	005566	Cluster5307_1clades	125	PS1_0184	Aeromonas phage PS1	GCA_007051165.2
QFR59328.1	005566	Cluster5307_1clades	125	PS2_0186	Aeromonas phage PS2	GCA_009388305.2
QBX32351.1	005567	Cluster5308_1clades	118	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03616.1	005567	Cluster5308_1clades	124	193	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41925.1	005567	Cluster5308_1clades	118	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGR47952.1	005568	Cluster5309_1clades	124	SmphiM12_320	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13146.1	005568	Cluster5309_1clades	124	PHIM19_241	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12785.1	005568	Cluster5309_1clades	124	PHIM7_240	Sinorhizobium phage phiM7	GCA_002622405.1
AIA64924.1	005569	Phage_T4_Gp30_7	124	S13_125	Cronobacter phage S13	GCA_001503575.1
ARM70764.1	005569	Phage_T4_Gp30_7	121	phiC120_c58	Escherichia phage phiC120	GCA_002621185.1
QHJ79014.1	005569	Phage_T4_Gp30_7	118	-	Myoviridae sp.	GCA_012593985.1
AOV59640.1	005570	Cluster5311_1clades	124	S330809_179	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59402.1	005570	Cluster5311_1clades	124	C440309_179	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59878.1	005570	Cluster5311_1clades	124	N231010_179	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67109.1	005571	Cluster5312_1clades	124	AD1_065	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08345.1	005571	Cluster5312_1clades	124	Alexandra_65	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58707.1	005571	Cluster5312_1clades	116	Y3_067	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ASU03861.1	005572	Cluster5313_1clades	114	JOAD_54	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03616.1	005572	Cluster5313_1clades	114	RISINGSUN_54	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27142.1	005572	Cluster5313_1clades	124	PPEV_gp048	Pseudomonas phage EL	GCA_000866825.1
QGZ14470.1	005573	Cluster5314_1clades	124	HWC77_gp107	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04264.1	005573	Cluster5314_1clades	124	HWC03_gp109	Vibrio phage 2 TSL-2019	GCA_006964105.1
BAW98235.1	005573	Cluster5314_1clades	123	FDH33_gp026	Vibrio phage pTD1	GCA_002618825.1
QCW22836.1	005574	SET	124	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50502.1	005574	SET	124	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70091.1	005574	SET	64	SynMITS9220M01_078	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QBX06480.1	005575	Cluster5316_1clades	123	BcepSaruman_067	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74447.1	005575	Cluster5316_1clades	123	BcepSauron_067	Burkholderia phage BcepSauron	GCA_005394215.1
QHJ86166.1	005575	Cluster5316_1clades	124	KKIINIFJ_00256	Pseudomonas phage PN05	GCA_009931935.1
AXG67294.1	005576	Cluster5317_1clades	122	AD1_250	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08519.1	005576	Cluster5317_1clades	123	Alexandra_262	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58897.1	005576	Cluster5317_1clades	119	Y3_257	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67323.1	005577	Cluster5318_1clades	123	AD1_279	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08550.1	005577	Cluster5318_1clades	120	Alexandra_294	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58923.1	005577	Cluster5318_1clades	121	Y3_283	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BBI90564.1	005578	Cluster5319_1clades	123	HYO65_gp172	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90872.1	005578	Cluster5319_1clades	123	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAX25562.1	005578	Cluster5319_1clades	116	BPT24_244	Tenacibaculum phage pT24	GCA_002611925.1
APU01788.1	005579	Cluster5320_1clades	122	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01188.1	005579	Cluster5320_1clades	122	ASwh1_123	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53431.1	005579	Cluster5320_1clades	122	65p425	Aeromonas virus 65	GCA_000893255.1
ANZ49859.1	005580	Cluster5321_1clades	122	MACHINA_221	Erwinia phage Machina	GCA_002758035.1
ANZ49303.1	005580	Cluster5321_1clades	122	HUXLEY_221	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50131.1	005580	Cluster5321_1clades	122	PARSHIK_222	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QDH83510.1	005581	Cluster5322_1clades	117	H1O15_gp296	Achromobacter phage Motura	GCA_006964305.1
ATN94578.1	005581	Cluster5322_1clades	122	SL2_001	Pseudomonas phage SL2	GCA_002956015.1
QJB22655.1	005581	Cluster5322_1clades	116	fnug_12	Pseudomonas phage fnug	GCA_012837215.1
QCW18823.1	005582	INTEGRINBETA	122	7t3_0302	Salmonella phage 7t3	GCA_006083215.1
AZU98087.1	005582	INTEGRINBETA	122	CPT_Munch_143	Salmonella phage Munch	GCA_004015485.1
QIG62895.1	005582	INTEGRINBETA	122	SEPL_282	Salmonella phage SE_PL	GCA_011067555.1
QCW18843.1	005583	FXSXX	120	7t3_0322	Salmonella phage 7t3	GCA_006083215.1
AZU98105.1	005583	FXSXX	121	CPT_Munch_161	Salmonella phage Munch	GCA_004015485.1
QIG62877.1	005583	FXSXX	120	SEPL_264	Salmonella phage SE_PL	GCA_011067555.1
QCW18892.1	005584	Cluster5325_1clades	121	7t3_0371	Salmonella phage 7t3	GCA_006083215.1
AZU98150.1	005584	Cluster5325_1clades	121	CPT_Munch_206	Salmonella phage Munch	GCA_004015485.1
QIG62833.1	005584	Cluster5325_1clades	121	SEPL_220	Salmonella phage SE_PL	GCA_011067555.1
QCW18574.1	005585	Cluster5326_1clades	121	7t3_053	Salmonella phage 7t3	GCA_006083215.1
AZU98403.1	005585	Cluster5326_1clades	121	CPT_Munch_471	Salmonella phage Munch	GCA_004015485.1
QIG63110.1	005585	Cluster5326_1clades	121	SEPL_497	Salmonella phage SE_PL	GCA_011067555.1
BBA65676.1	005586	Cluster5327_1clades	121	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65217.1	005586	Cluster5327_1clades	121	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96245.1	005586	Cluster5327_1clades	120	Xoosp13_58	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX32162.1	005587	Cluster5329_1clades	121	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03442.1	005587	Cluster5329_1clades	115	016	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41743.1	005587	Cluster5329_1clades	121	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65341.1	005588	Cluster5330_1clades	109	2050HW_00006	Serratia phage 2050HW	GCA_002628125.1
QDB71129.1	005588	Cluster5330_1clades	109	CPT_Moabite_099	Serratia phage Moabite	GCA_006384735.1
QFP93228.1	005588	Cluster5330_1clades	121	-	Serratia phage PCH45	GCA_009187865.1
AGH07584.1	005589	SIG+LPD31	120	CYVG_00140	Cyanophage S-SSM6a	GCA_002710385.1
AGH26243.1	005589	SIG+LPD31	92	CPMG_00142	Prochlorococcus phage MED4-213	GCA_000904535.1
AIX30724.1	005589	SIG+LPD31	81	Syn7803US37_247	Synechococcus phage ACG-2014f	GCA_002594065.1
BBA65718.1	005590	Cluster5332_1clades	120	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65259.1	005590	Cluster5332_1clades	120	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96299.1	005590	Cluster5332_1clades	120	Xoosp13_112	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QCW19100.1	005591	Cluster5333_1clades	119	7t3_0582	Salmonella phage 7t3	GCA_006083215.1
AZU98339.1	005591	Cluster5333_1clades	119	CPT_Munch_397	Salmonella phage Munch	GCA_004015485.1
QIG62644.1	005591	Cluster5333_1clades	119	SEPL_031	Salmonella phage SE_PL	GCA_011067555.1
QCW18637.1	005592	SIG+TM+TM	119	7t3_0116	Salmonella phage 7t3	GCA_006083215.1
AZU98462.1	005592	SIG+TM+TM	119	CPT_Munch_530	Salmonella phage Munch	GCA_004015485.1
QIG63052.1	005592	SIG+TM+TM	119	SEPL_439	Salmonella phage SE_PL	GCA_011067555.1
QBX32496.1	005593	Cluster5335_1clades	119	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03753.1	005593	Cluster5335_1clades	116	330	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM42069.1	005593	Cluster5335_1clades	119	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBZ70705.1	005594	Cluster5336_1clades	119	pETSU_124	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72018.1	005594	Cluster5336_1clades	115	N1M2_155	Klebsiella phage N1M2	GCA_010092605.1
AEV89632.1	005594	Cluster5336_1clades	116	OBP_195	Pseudomonas phage OBP	GCA_000896635.1
QCW18587.1	005595	Cluster5337_1clades	118	7t3_066	Salmonella phage 7t3	GCA_006083215.1
AZU98415.1	005595	Cluster5337_1clades	118	CPT_Munch_483	Salmonella phage Munch	GCA_004015485.1
QIG63098.1	005595	Cluster5337_1clades	118	SEPL_485	Salmonella phage SE_PL	GCA_011067555.1
AIT14027.1	005596	Cluster5338_1clades	106	PBI_121Q_136	Escherichia phage 121Q	GCA_000926855.1
AFA44498.1	005596	Cluster5338_1clades	106	RaK2_00225	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QHJ78872.1	005596	Cluster5338_1clades	118	-	Myoviridae sp.	GCA_012593985.1
AGR47867.1	005597	EsaC	117	SmphiM12_235	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13068.1	005597	EsaC	117	PHIM19_163	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12709.1	005597	EsaC	117	PHIM7_163	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01138.1	005598	Cluster5340_1clades	113	AR9_g053	Bacillus phage AR9	GCA_001743835.1
ALN97808.1	005598	Cluster5340_1clades	117	Bp8pS_129	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00065.1	005598	Cluster5340_1clades	113	PBI_PBS1_243	Bacillus virus PBS1	GCA_002601325.1
AMS01283.1	005599	Cluster5341_1clades	117	AR9_g199	Bacillus phage AR9	GCA_001743835.1
ALN97936.1	005599	Cluster5341_1clades	84	Bp8pS_257	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99911.1	005599	Cluster5341_1clades	117	PBI_PBS1_89	Bacillus virus PBS1	GCA_002601325.1
APU01716.1	005600	Cluster5342_1clades	117	-	Aeromonas phage 65.2	GCA_002618145.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QAY01123.1	005600	Cluster5342_1clades	115	ASwh1_56	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53356.1	005600	Cluster5342_1clades	97	65p348	Aeromonas virus 65	GCA_000893255.1
AFC21526.1	005601	Cluster5343_1clades	97	GAP32_078	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43646.1	005601	Cluster5343_1clades	99	CBB_81	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BBA65456.1	005601	Cluster5343_1clades	117	-	Xanthomonas phage XacN1	GCA_003173815.1
QDB70343.1	005602	Cluster5344_1clades	117	CF8_0174	Aeromonas phage CF8	GCA_006384595.2
QDJ96693.1	005602	Cluster5344_1clades	116	PS1_0182	Aeromonas phage PS1	GCA_007051165.2
QFR59326.1	005602	Cluster5344_1clades	116	PS2_0184	Aeromonas phage PS2	GCA_009388305.2
APU01397.1	005603	Cluster5345_1clades	116	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01209.1	005603	Cluster5345_1clades	116	ASwh1_144	Aeromonas phage Aswh_1	GCA_004146945.1
AAR90933.1	005603	Cluster5345_1clades	116	65p006	Aeromonas virus 65	GCA_000893255.1
APU01587.1	005604	Cluster5346_1clades	116	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01395.1	005604	Cluster5346_1clades	116	ASwh1_336	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53210.1	005604	Cluster5346_1clades	116	65p202	Aeromonas virus 65	GCA_000893255.1
QBZ70742.1	005605	Cluster5347_1clades	108	pETSU_161	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72050.1	005605	Cluster5347_1clades	116	N1M2_187	Klebsiella phage N1M2	GCA_010092605.1
AEV89674.1	005605	Cluster5347_1clades	116	OBP_237	Pseudomonas phage OBP	GCA_000896635.1
AFC21470.1	005606	Cluster5348_1clades	100	GAP32_022	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43591.1	005606	Cluster5348_1clades	116	CBB_26	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44142.1	005606	Cluster5348_1clades	116	CBB_579	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BBI90505.1	005607	Cluster5350_1clades	71	HYO65_gp113	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90813.1	005607	Cluster5350_1clades	71	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39195.1	005607	Cluster5350_1clades	116	BPT24_072	Tenacibaculum phage pT24	GCA_002611925.1
ANS06076.1	005608	PFL-like	115	ABCD_0159	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97172.1	005608	PFL-like	107	E_164	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78687.1	005608	PFL-like	115	RB43ORF165c	Escherichia virus RB43	GCA_000863505.1
AEO93398.1	005609	TM	115	G_136	Bacillus virus G	GCA_000917535.1
AFU87926.1	005609	TM	100	CcrColossus_gp056	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68598.1	005609	TM	100	CcrPW_gp059	Caulobacter phage CcrPW	GCA_003443275.1
ANS06091.1	005610	Cluster5353_1clades	105	ABCD_0223	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97240.1	005610	Cluster5353_1clades	115	E_232	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78757.1	005610	Cluster5353_1clades	105	RB43ORF235w	Escherichia virus RB43	GCA_000863505.1
AYD80054.1	005611	Cluster5354_1clades	115	JA11_249	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66653.1	005611	Cluster5354_1clades	115	JA13_250	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67624.1	005611	Cluster5354_1clades	115	JA33_250	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AYD81460.1	005612	Cluster5355_1clades	115	SEA_JUSTBECAUSE_305	Streptomyces phage JustBecause	GCA_003613775.1
QBZ72194.1	005612	Cluster5355_1clades	108	SEA_KRADAL_308	Streptomyces phage Kradal	GCA_004799925.1
AXH66457.1	005612	Cluster5355_1clades	108	SEA_SATIS_308	Streptomyces phage Satis	GCA_003366315.1
QDB70483.1	005613	Cluster5356_1clades	111	CF8_0072	Aeromonas phage CF8	GCA_006384595.2
QDJ96830.1	005613	Cluster5356_1clades	115	PS1_0071	Aeromonas phage PS1	GCA_007051165.2
QFR59460.1	005613	Cluster5356_1clades	115	PS2_0069	Aeromonas phage PS2	GCA_009388305.2
QBX32464.1	005614	Cluster5357_1clades	114	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42036.1	005614	Cluster5357_1clades	114	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26356.1	005614	Cluster5357_1clades	114	PHIKZ260.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47868.1	005615	Cluster5358_1clades	114	SmphiM12_236	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13069.1	005615	Cluster5358_1clades	114	PHIM19_164	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12710.1	005615	Cluster5358_1clades	114	PHIM7_164	Sinorhizobium phage phiM7	GCA_002622405.1
ANS06080.1	005616	Cluster5359_1clades	112	ABCD_0233	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97251.1	005616	Cluster5359_1clades	114	E_243	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78769.1	005616	Cluster5359_1clades	112	RB43ORF247w	Escherichia virus RB43	GCA_000863505.1
AXG67252.1	005617	Cluster5360_1clades	114	AD1_208	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08482.1	005617	Cluster5360_1clades	114	Alexandra_218	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58852.1	005617	Cluster5360_1clades	110	Y3_212	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QKE54520.1	005618	Cluster5361_1clades	114	ACSA002_2053	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QGT54782.1	005618	Cluster5361_1clades	50	b23_0167	Synechococcus phage B23	GCA_009745195.1
QGT54412.1	005618	Cluster5361_1clades	50	b3_0168	Synechococcus phage B3	GCA_009745215.1
AFO71391.1	005619	SIG+TM+TM	113	CR5_171	Cronobacter phage CR5	GCA_000910235.1
QBP07602.1	005619	SIG+TM+TM	112	DERBICUS_176	Erwinia phage Derbicus	GCA_004521655.1
ANZ49025.1	005619	SIG+TM+TM	112	EARLPHILLIPIV_176	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
AGH26159.1	005620	Cluster5363_1clades	113	CPMG_00058	Prochlorococcus phage MED4-213	GCA_000904535.1
ADK66272.1	005620	Cluster5363_1clades	76	PSSM2_100.2	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12172.1	005620	Cluster5363_1clades	76	PRTG_00014	Prochlorococcus phage P-SSM5	GCA_002991095.1
AQW89025.1	005621	Cluster5364_1clades	113	BF_0500	Serratia phage BF	GCA_002619745.1
SOK59306.1	005621	Cluster5364_1clades	113	g498	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58771.1	005621	Cluster5364_1clades	113	g494	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67239.1	005622	SIG+TM+TM+TM	113	AD1_195	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08469.1	005622	SIG+TM+TM+TM	113	Alexandra_205	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58838.1	005622	SIG+TM+TM+TM	111	Y3_198	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QDH83609.1	005623	SIG+HNH	113	H1O15_gp179	Achromobacter phage Motura	GCA_006964305.1
QBX06504.1	005623	SIG+HNH	105	BcepSaruman_091	Burkholderia phage BcepSaruman	GCA_004771375.1
BAG41567.1	005623	SIG+HNH	105	RSL1_ORF122	Ralstonia phage phiRSL1	GCA_000879455.1
ANS06083.1	005624	TM	109	ABCD_0175	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97188.1	005624	TM	109	E_180	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78705.1	005624	TM	112	RB43ORF183c	Escherichia virus RB43	GCA_000863505.1
AEO93736.1	005625	Cluster5368_1clades	109	G_478	Bacillus virus G	GCA_000917535.1
AEO93737.1	005625	Cluster5368_1clades	112	G_479	Bacillus virus G	GCA_000917535.1
AEO93738.1	005625	Cluster5368_1clades	100	G_480	Bacillus virus G	GCA_000917535.1
AMS01246.1	005626	Cluster5369_1clades	112	AR9_g162	Bacillus phage AR9	GCA_001743835.1
ALN97903.1	005626	Cluster5369_1clades	110	Bp8pS_224	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99872.1	005626	Cluster5369_1clades	112	PBI_PBS1_50	Bacillus virus PBS1	GCA_002601325.1
ANS06078.1	005627	Cluster5370_1clades	112	ABCD_0119	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97130.1	005627	Cluster5370_1clades	112	E_122	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78642.1	005627	Cluster5370_1clades	64	RB43ORF120c	Escherichia virus RB43	GCA_000863505.1
ANS06079.1	005628	DnaJ_CXXCXGXG	112	ABCD_0182	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97196.1	005628	DnaJ_CXXCXGXG	112	E_188	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78713.1	005628	DnaJ_CXXCXGXG	106	RB43ORF191c	Escherichia virus RB43	GCA_000863505.1
AXG67236.1	005629	Cluster5372_1clades	111	AD1_192	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08466.1	005629	Cluster5372_1clades	112	Alexandra_202	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58836.1	005629	Cluster5372_1clades	110	Y3_196	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18708.1	005630	Cluster5373_1clades	112	7t3_0187	Salmonella phage 7t3	GCA_006083215.1
AZU97980.1	005630	Cluster5373_1clades	112	CPT_Munch_036	Salmonella phage Munch	GCA_004015485.1
QIG62998.1	005630	Cluster5373_1clades	112	SEPL_385	Salmonella phage SE_PL	GCA_011067555.1
QCW18837.1	005631	Cluster5374_1clades	112	7t3_0316	Salmonella phage 7t3	GCA_006083215.1
AZU98100.1	005631	Cluster5374_1clades	112	CPT_Munch_156	Salmonella phage Munch	GCA_004015485.1
QIG62882.1	005631	Cluster5374_1clades	112	SEPL_269	Salmonella phage SE_PL	GCA_011067555.1
QCW19112.1	005632	Cluster5375_1clades	111	7t3_0595	Salmonella phage 7t3	GCA_006083215.1
AZU98349.1	005632	Cluster5375_1clades	112	CPT_Munch_408	Salmonella phage Munch	GCA_004015485.1
QIG62633.1	005632	Cluster5375_1clades	112	SEPL_020	Salmonella phage SE_PL	GCA_011067555.1
QCW18640.1	005633	SIG+TM+TM	112	7t3_0119	Salmonella phage 7t3	GCA_006083215.1
AZU98465.1	005633	SIG+TM+TM	112	CPT_Munch_533	Salmonella phage Munch	GCA_004015485.1
QIG63049.1	005633	SIG+TM+TM	112	SEPL_436	Salmonella phage SE_PL	GCA_011067555.1
APU01714.1	005634	Cluster5377_1clades	108	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01120.1	005634	Cluster5377_1clades	112	ASwh1_53	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53354.1	005634	Cluster5377_1clades	108	65p346	Aeromonas virus 65	GCA_000893255.1
BBA65199.1	005635	Cluster5378_1clades	76	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65658.1	005635	Cluster5378_1clades	76	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96232.1	005635	Cluster5378_1clades	112	Xoosp13_45	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AMR59816.1	005636	SIG+TM	92	SEGD1_169	Enterobacteria phage SEGD1	GCA_002601865.1
QNI20864.1	005636	SIG+TM	111	-	Salmonella phage JN03	GCA_014319805.1
AEP83999.1	005636	SIG+TM	111	SPN3US_0166	Salmonella phage SPN3US	GCA_001042275.1
QGZ14505.1	005637	MU-HTH	111	HWC77_gp142	Photobacterium phage PDCC-1	GCA_009800445.1
AGS82150.1	005637	MU-HTH	106	PaBG_00277	Pseudomonas phage PaBG	GCA_000912555.1
QAU04229.1	005637	MU-HTH	111	HWC03_gp074	Vibrio phage 2 TSL-2019	GCA_006964105.1
AOO14310.1	005638	Cluster5381_1clades	109	Sn110110_116	Cyanophage S-RIM14	GCA_002599065.1
AOO14959.1	005638	Cluster5381_1clades	109	W1230910_113	Cyanophage S-RIM14	GCA_002599125.1
AGG54493.1	005638	Cluster5381_1clades	110	CYWG_00209	Cyanophage S-SSM6b	GCA_002710425.1
AMS01313.1	005639	Cluster5382_1clades	110	AR9_g229	Bacillus phage AR9	GCA_001743835.1
ALN97963.1	005639	Cluster5382_1clades	100	Bp8pS_284	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99942.1	005639	Cluster5382_1clades	110	PBI_PBS1_120	Bacillus virus PBS1	GCA_002601325.1
ANM44767.1	005640	Cluster5383_1clades	110	KTN4_009	Pseudomonas phage KTN4	GCA_002607225.1
QJB22652.1	005640	Cluster5383_1clades	110	fnug_9	Pseudomonas phage fnug	GCA_012837215.1
AAL82910.2	005640	Cluster5383_1clades	63	PHIKZ009	Pseudomonas virus phiKZ	GCA_000842965.1
AOV59648.1	005641	Cluster5384_1clades	110	S330809_187	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59410.1	005641	Cluster5384_1clades	110	C440309_187	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59886.1	005641	Cluster5384_1clades	110	N231010_187	Synechococcus phage S-CAM4	GCA_002922155.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW18622.1	005642	Cluster5385_1clades	110	7t3_0101	Salmonella phage 7t3	GCA_006083215.1
AZU98447.1	005642	Cluster5385_1clades	110	CPT_Munch_515	Salmonella phage Munch	GCA_004015485.1
QIG63066.1	005642	Cluster5385_1clades	110	SEPL_453	Salmonella phage SE_PL	GCA_011067555.1
QBX06575.1	005643	Cluster5386_1clades	110	BcepSaruman_162	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74542.1	005643	Cluster5386_1clades	110	BcepSauron_162	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41454.1	005643	Cluster5386_1clades	105	RSL1_ORF009	Ralstonia phage phiRSL1	GCA_000879455.1
QBX32417.1	005644	Cluster5387_1clades	110	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03686.1	005644	Cluster5387_1clades	106	263	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41988.1	005644	Cluster5387_1clades	110	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AUE22837.1	005645	Cluster5388_1clades	109	Ah1_00319	Aeromonas phage Ah1	GCA_002957415.1
ADM79939.1	005645	Cluster5388_1clades	109	phiAS5_ORF0096	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17967.1	005645	Cluster5388_1clades	109	Aeh1ORF298c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06084.1	005646	Cluster5389_1clades	109	ABCD_0269	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97289.1	005646	Cluster5389_1clades	109	E_281	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78809.1	005646	Cluster5389_1clades	109	RB43ORF287c	Escherichia virus RB43	GCA_000863505.1
ANS06082.1	005647	Cluster5390_1clades	109	ABCD_0146	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97156.1	005647	Cluster5390_1clades	106	E_148	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78672.1	005647	Cluster5390_1clades	107	RB43ORF150c	Escherichia virus RB43	GCA_000863505.1
ANZ49672.1	005648	Cluster5391_1clades	109	MACHINA_34	Erwinia phage Machina	GCA_002758035.1
ANZ49117.1	005648	Cluster5391_1clades	109	HUXLEY_35	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49945.1	005648	Cluster5391_1clades	109	PARSHIK_36	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QJD53813.1	005649	Cluster5392_1clades	109	SEA_KELA_253	Streptomyces phage Kela	GCA_012934305.1
QBZ72140.1	005649	Cluster5392_1clades	109	SEA_KRADAL_254	Streptomyces phage Kradal	GCA_004799925.1
AXH66402.1	005649	Cluster5392_1clades	109	SEA_SATIS_253	Streptomyces phage Satis	GCA_003366315.1
QCW18567.1	005650	Cluster5393_1clades	109	7t3_046	Salmonella phage 7t3	GCA_006083215.1
AZU98396.1	005650	Cluster5393_1clades	109	CPT_Munch_464	Salmonella phage Munch	GCA_004015485.1
QIG63117.1	005650	Cluster5393_1clades	109	SEPL_504	Salmonella phage SE_PL	GCA_011067555.1
QCW18592.1	005651	Cluster5394_1clades	109	7t3_071	Salmonella phage 7t3	GCA_006083215.1
AZU98420.1	005651	Cluster5394_1clades	109	CPT_Munch_488	Salmonella phage Munch	GCA_004015485.1
QIG63093.1	005651	Cluster5394_1clades	109	SEPL_480	Salmonella phage SE_PL	GCA_011067555.1
QCW18621.1	005652	SIG+TM+TM	109	7t3_0100	Salmonella phage 7t3	GCA_006083215.1
AZU98446.1	005652	SIG+TM+TM	109	CPT_Munch_514	Salmonella phage Munch	GCA_004015485.1
QIG63067.1	005652	SIG+TM+TM	109	SEPL_454	Salmonella phage SE_PL	GCA_011067555.1
QCW18638.1	005653	SIG+TM+TM	109	7t3_0117	Salmonella phage 7t3	GCA_006083215.1
AZU98463.1	005653	SIG+TM+TM	109	CPT_Munch_531	Salmonella phage Munch	GCA_004015485.1
QIG63051.1	005653	SIG+TM+TM	109	SEPL_438	Salmonella phage SE_PL	GCA_011067555.1
ANS06087.1	005654	Cluster5397_1clades	108	ABCD_0232	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97250.1	005654	Cluster5397_1clades	108	E_242	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78768.1	005654	Cluster5397_1clades	108	RB43ORF246w	Escherichia virus RB43	GCA_000863505.1
ADM79882.1	005655	Cluster5398_1clades	104	phiAS5_ORF0039	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17904.1	005655	Cluster5398_1clades	104	Aeh1ORF242c	Aeromonas virus Aeh1	GCA_000843245.1
ALY07178.1	005655	Cluster5398_1clades	108	VmeM32_00192	Vibrio phage vB_VmeM-32	GCA_002608825.1
ANZ49729.1	005656	Cluster5399_1clades	108	MACHINA_91	Erwinia phage Machina	GCA_002758035.1
ANZ49174.1	005656	Cluster5399_1clades	108	HUXLEY_92	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50002.1	005656	Cluster5399_1clades	108	PARSHIK_93	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AIT14112.1	005657	Cluster5400_1clades	93	PBI_121Q_222	Escherichia phage 121Q	GCA_000926855.1
AGC34985.1	005657	Cluster5400_1clades	60	ACQ29_gp305	Escherichia phage PBECO4	GCA_001041035.1
AXC36564.1	005657	Cluster5400_1clades	108	-	Escherichia phage UB	GCA_003341455.1
BBA65629.1	005658	Cluster5401_1clades	108	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65170.1	005658	Cluster5401_1clades	108	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96203.1	005658	Cluster5401_1clades	102	Xoosp13_16	Xanthomonas phage Xoo-sp13	GCA_013364725.1
APU01784.1	005659	Cluster5402_1clades	105	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01185.1	005659	Cluster5402_1clades	108	ASwh1_120	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53427.1	005659	Cluster5402_1clades	105	65p421	Aeromonas virus 65	GCA_000893255.1
QBZ70819.1	005660	DUF2829	96	pETSU_239	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72118.1	005660	DUF2829	79	N1M2_258	Klebsiella phage N1M2	GCA_010092605.1
AEV89451.1	005660	DUF2829	107	OBP_014	Pseudomonas phage OBP	GCA_000896635.1
ANS06088.1	005661	Cluster5404_1clades	107	ABCD_0098	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78619.1	005661	Cluster5404_1clades	59	RB43ORF097w	Escherichia virus RB43	GCA_000863505.1
AAX78620.1	005661	Cluster5404_1clades	63	RB43ORF098w	Escherichia virus RB43	GCA_000863505.1
QCW18573.1	005662	Cluster5405_1clades	107	7t3_052	Salmonella phage 7t3	GCA_006083215.1
AZU98402.1	005662	Cluster5405_1clades	107	CPT_Munch_470	Salmonella phage Munch	GCA_004015485.1
QIG63111.1	005662	Cluster5405_1clades	107	SEPL_498	Salmonella phage SE_PL	GCA_011067555.1
ANS06089.1	005663	Cluster5406_1clades	106	ABCD_0039	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97049.1	005663	Cluster5406_1clades	105	E_040	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78561.1	005663	Cluster5406_1clades	106	RB43ORF039c	Escherichia virus RB43	GCA_000863505.1
ANS06090.1	005664	Cluster5407_1clades	106	ABCD_0155	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97167.1	005664	Cluster5407_1clades	106	E_159	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78683.1	005664	Cluster5407_1clades	106	RB43ORF161c	Escherichia virus RB43	GCA_000863505.1
QBZ70847.1	005665	Cluster5408_1clades	106	pETSU_266	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71879.1	005665	Cluster5408_1clades	106	N1M2_16	Klebsiella phage N1M2	GCA_010092605.1
AEV89473.1	005665	Cluster5408_1clades	106	OBP_036	Pseudomonas phage OBP	GCA_000896635.1
AXG67242.1	005666	Cluster5409_1clades	106	AD1_198	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08472.1	005666	Cluster5409_1clades	106	Alexandra_208	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58841.1	005666	Cluster5409_1clades	102	Y3_201	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ATA65615.1	005667	Cluster5410_1clades	58	2050HW_00280	Serratia phage 2050HW	GCA_002628125.1
ATA65616.1	005667	Cluster5410_1clades	50	2050HW_00281	Serratia phage 2050HW	GCA_002628125.1
QDB71044.1	005667	Cluster5410_1clades	106	CPT_Moabite_012	Serratia phage Moabite	GCA_006384735.1
QBZ70600.1	005668	Cluster5411_1clades	101	pETSU_019	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71917.1	005668	Cluster5411_1clades	100	N1M2_54	Klebsiella phage N1M2	GCA_010092605.1
AEV89514.1	005668	Cluster5411_1clades	105	OBP_077	Pseudomonas phage OBP	GCA_000896635.1
AJK27624.1	005669	Cluster5412_1clades	91	PTIM40_212	Cyanophage P-TIM40	GCA_001470935.1
AOO14389.1	005669	Cluster5412_1clades	105	Sn110110_196	Cyanophage S-RIM14	GCA_002599065.1
AOO15037.1	005669	Cluster5412_1clades	105	W1230910_192	Cyanophage S-RIM14	GCA_002599125.1
AOV59509.1	005670	Cluster5413_1clades	105	S330809_048	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59271.1	005670	Cluster5413_1clades	105	C440309_048	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59747.1	005670	Cluster5413_1clades	105	N231010_048	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67290.1	005671	Cluster5414_1clades	79	AD1_246	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08514.1	005671	Cluster5414_1clades	105	Alexandra_257	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58892.1	005671	Cluster5414_1clades	83	Y3_252	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67298.1	005672	Cluster5415_1clades	105	AD1_254	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08523.1	005672	Cluster5415_1clades	105	Alexandra_266	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58902.1	005672	Cluster5415_1clades	104	Y3_262	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18706.1	005673	Cluster5416_1clades	105	7t3_0185	Salmonella phage 7t3	GCA_006083215.1
AZU97978.1	005673	Cluster5416_1clades	105	CPT_Munch_034	Salmonella phage Munch	GCA_004015485.1
QIG63000.1	005673	Cluster5416_1clades	105	SEPL_387	Salmonella phage SE_PL	GCA_011067555.1
QCW18623.1	005674	Cluster5417_1clades	105	7t3_0102	Salmonella phage 7t3	GCA_006083215.1
AZU98448.1	005674	Cluster5417_1clades	105	CPT_Munch_516	Salmonella phage Munch	GCA_004015485.1
QIG63065.1	005674	Cluster5417_1clades	105	SEPL_452	Salmonella phage SE_PL	GCA_011067555.1
QCW18636.1	005675	SIG+TM+TM	105	7t3_0115	Salmonella phage 7t3	GCA_006083215.1
AZU98461.1	005675	SIG+TM+TM	105	CPT_Munch_529	Salmonella phage Munch	GCA_004015485.1
QIG63053.1	005675	SIG+TM+TM	105	SEPL_440	Salmonella phage SE_PL	GCA_011067555.1
QCW22877.1	005676	Cluster5419_1clades	105	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50480.1	005676	Cluster5419_1clades	105	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70585.1	005676	Cluster5419_1clades	104	HOU04_gp186	Synechococcus phage S-T4	GCA_003443335.1
AFC21813.1	005677	Cluster5420_1clades	99	GAP32_363	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88896.1	005677	Cluster5420_1clades	103	BF_0371	Serratia phage BF	GCA_002619745.1
SOK59182.1	005677	Cluster5420_1clades	105	g374	Yersinia phage fHe-Yen9-03	GCA_002990515.1
QAX98647.1	005678	Cluster5421_1clades	101	ASfcp2_314	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52787.1	005678	Cluster5421_1clades	101	PX29p068	Aeromonas phage PX29	GCA_000920195.1
AAQ17731.1	005678	Cluster5421_1clades	104	Aeh1ORF071c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06166.1	005679	Cluster5422_1clades	68	ABCD_0034	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97044.1	005679	Cluster5422_1clades	69	E_035	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78556.1	005679	Cluster5422_1clades	104	RB43ORF034c	Escherichia virus RB43	GCA_000863505.1
ALN97856.1	005680	Cluster5423_1clades	92	Bp8pS_177	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97857.1	005680	Cluster5423_1clades	103	Bp8pS_178	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97858.1	005680	Cluster5423_1clades	104	Bp8pS_179	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ANS06095.1	005681	Cluster5424_1clades	102	ABCD_0024	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97032.1	005681	Cluster5424_1clades	104	E_023	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78545.1	005681	Cluster5424_1clades	102	RB43ORF023c	Escherichia virus RB43	GCA_000863505.1
AYD81437.1	005682	Cluster5425_1clades	104	SEA_JUSTBECAUSE_282	Streptomyces phage JustBecause	GCA_003613775.1
QBZ72172.1	005682	Cluster5425_1clades	104	SEA_KRADAL_286	Streptomyces phage Kradal	GCA_004799925.1
AXH66435.1	005682	Cluster5425_1clades	104	SEA_SATIS_286	Streptomyces phage Satis	GCA_003366315.1
QCW18540.1	005683	Cluster5426_1clades	104	7t3_07	Salmonella phage 7t3	GCA_006083215.1
AZU98373.1	005683	Cluster5426_1clades	104	CPT_Munch_433	Salmonella phage Munch	GCA_004015485.1

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QIG63140.1	005683	Cluster5426_1clades	104	SEPL_527	Salmonella phage SE_PL	GCA_011067555.1
QCW19128.1	005684	Cluster5427_1clades	104	7t3_0613	Salmonella phage 7t3	GCA_006083215.1
AZU98365.1	005684	Cluster5427_1clades	86	CPT_Munch_425	Salmonella phage Munch	GCA_004015485.1
QIG62617.1	005684	Cluster5427_1clades	86	SEPL_004	Salmonella phage SE_PL	GCA_011067555.1
QDB70281.1	005685	Cluster5428_1clades	104	CF8_0113	Aeromonas phage CF8	GCA_006384595.2
QDJ96872.1	005685	Cluster5428_1clades	104	PS1_0113	Aeromonas phage PS1	GCA_007051165.2
QFR59504.1	005685	Cluster5428_1clades	104	PS2_0113	Aeromonas phage PS2	GCA_009388305.2
AQW88956.1	005686	Cluster5429_1clades	99	BF_0431	Serratia phage BF	GCA_002619745.1
SOK59242.1	005686	Cluster5429_1clades	104	g434	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58708.1	005686	Cluster5429_1clades	104	g431	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06093.1	005687	Cluster5430_1clades	103	ABCD_0023	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97031.1	005687	Cluster5430_1clades	103	E_022	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78544.1	005687	Cluster5430_1clades	103	RB43ORF022c	Escherichia virus RB43	GCA_000863505.1
QBX32362.1	005688	Cluster5431_1clades	103	-	Pseudomonas phage PA1C	GCA_004785505.1
AEH03627.1	005688	Cluster5431_1clades	103	204	Pseudomonas phage PhiPA3	GCA_001502095.1
QEM41936.1	005688	Cluster5431_1clades	103	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AQW88890.1	005689	Cluster5432_1clades	103	BF_0365	Serratia phage BF	GCA_002619745.1
SOK59176.1	005689	Cluster5432_1clades	103	g368	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58642.1	005689	Cluster5432_1clades	103	g365	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AQW88946.1	005690	Cluster5433_1clades	103	BF_0421	Serratia phage BF	GCA_002619745.1
SOK59234.1	005690	Cluster5433_1clades	100	g426	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58700.1	005690	Cluster5433_1clades	100	g423	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18596.1	005691	Cluster5434_1clades	103	7t3_075	Salmonella phage 7t3	GCA_006083215.1
AZU98424.1	005691	Cluster5434_1clades	103	CPT_Munch_492	Salmonella phage Munch	GCA_004015485.1
QIG63089.1	005691	Cluster5434_1clades	103	SEPL_476	Salmonella phage SE_PL	GCA_011067555.1
QAX96835.1	005692	Cluster5435_1clades	103	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96199.1	005692	Cluster5435_1clades	103	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96517.1	005692	Cluster5435_1clades	103	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
ANS06096.1	005693	DUF1778	102	ABCD_0100	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97110.1	005693	DUF1778	94	E_102	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78621.1	005693	DUF1778	102	RB43ORF099w	Escherichia virus RB43	GCA_000863505.1
ANS06097.1	005694	Cluster5437_1clades	102	ABCD_0241	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97260.1	005694	Cluster5437_1clades	102	E_252	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78778.1	005694	Cluster5437_1clades	102	RB43ORF256w	Escherichia virus RB43	GCA_000863505.1
ARB14497.1	005695	Cluster5438_1clades	63	Ccr5_gp277	Caulobacter phage Ccr5	GCA_002619545.1
AFU87807.1	005695	Cluster5438_1clades	102	CcrKarma_gp290	Caulobacter virus Karma	GCA_000901575.1
AFU88599.1	005695	Cluster5438_1clades	102	CcrSwift_gp281	Caulobacter virus Swift	GCA_000899655.1
APU01729.1	005696	Cluster5439_1clades	98	-	Aeromonas phage 65.2	GCA_002618145.1
AFN39206.1	005696	Cluster5439_1clades	101	CC2_072	Aeromonas phage CC2	GCA_000903495.1
ADQ53370.1	005696	Cluster5439_1clades	98	65p362	Aeromonas virus 65	GCA_000893255.1
ANM44908.1	005697	Cluster5440_1clades	101	KTN4_150	Pseudomonas phage KTN4	GCA_002607225.1
ATN94805.1	005697	Cluster5440_1clades	101	SL2_228	Pseudomonas phage SL2	GCA_002956015.1
QJB22786.1	005697	Cluster5440_1clades	101	fnug_143	Pseudomonas phage fnug	GCA_012837215.1
AQW88891.1	005698	Cluster5441_1clades	101	BF_0366	Serratia phage BF	GCA_002619745.1
SOK59177.1	005698	Cluster5441_1clades	101	g369	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58643.1	005698	Cluster5441_1clades	101	g366	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18690.1	005699	Cluster5442_1clades	101	7t3_0169	Salmonella phage 7t3	GCA_006083215.1
AZU97964.1	005699	Cluster5442_1clades	101	CPT_Munch_020	Salmonella phage Munch	GCA_004015485.1
QIG63014.1	005699	Cluster5442_1clades	101	SEPL_401	Salmonella phage SE_PL	GCA_011067555.1
ANS06101.1	005700	Cluster5443_1clades	97	ABCD_0181	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97194.1	005700	Cluster5443_1clades	100	E_186	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78711.1	005700	Cluster5443_1clades	97	RB43ORF189c	Escherichia virus RB43	GCA_000863505.1
AXG67332.1	005701	Cluster5444_1clades	95	AD1_288	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08560.1	005701	Cluster5444_1clades	100	Alexandra_304	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58933.1	005701	Cluster5444_1clades	100	Y3_293	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67328.1	005702	Cluster5446_1clades	100	AD1_284	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08555.1	005702	Cluster5446_1clades	100	Alexandra_299	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58928.1	005702	Cluster5446_1clades	97	Y3_288	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QBX06560.1	005703	Cluster5447_1clades	94	BcepSaruman_147	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74527.1	005703	Cluster5447_1clades	94	BcepSauron_147	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41496.1	005703	Cluster5447_1clades	100	RSL1_ORF050	Ralstonia phage phiRSL1	GCA_000879455.1
BBA65666.1	005704	Cluster5448_1clades	100	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65207.1	005704	Cluster5448_1clades	100	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96237.1	005704	Cluster5448_1clades	99	Xoosp13_50	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGZ14472.1	005705	TM+TM	100	HWC77_gp109	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04262.1	005705	TM+TM	100	HWC03_gp107	Vibrio phage 2 TSL-2019	GCA_006964105.1
AUR81103.1	005705	TM+TM	42	Aphrodite1_0030	Vibrio phage Aphrodite1	GCA_002958015.1
AFU87899.1	005706	Cluster5450_1clades	99	CcrColossus_gp029	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68569.1	005706	Cluster5450_1clades	99	CcrPW_gp030	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69018.1	005706	Cluster5450_1clades	99	CcrPW_gp479	Caulobacter phage CcrPW	GCA_003443275.1
ANS06106.1	005707	Cluster5451_1clades	94	ABCD_0011	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97019.1	005707	Cluster5451_1clades	99	E_010	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78532.1	005707	Cluster5451_1clades	94	RB43ORF010c	Escherichia virus RB43	GCA_000863505.1
QCW18778.1	005708	Cluster5453_1clades	99	7t3_0257	Salmonella phage 7t3	GCA_006083215.1
AZU98043.1	005708	Cluster5453_1clades	99	CPT_Munch_099	Salmonella phage Munch	GCA_004015485.1
QIG62937.1	005708	Cluster5453_1clades	99	SEPL_324	Salmonella phage SE_PL	GCA_011067555.1
BBA65163.1	005709	Cluster5454_1clades	99	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65622.1	005709	Cluster5454_1clades	99	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96216.1	005709	Cluster5454_1clades	97	Xoosp13_29	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65223.1	005710	Cluster5455_1clades	99	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65682.1	005710	Cluster5455_1clades	99	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96253.1	005710	Cluster5455_1clades	95	Xoosp13_66	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ANM45033.1	005711	Cluster5456_1clades	98	KTN4_275	Pseudomonas phage KTN4	GCA_002607225.1
ATN94681.1	005711	Cluster5456_1clades	98	SL2_104	Pseudomonas phage SL2	GCA_002956015.1
AAL83131.2	005711	Cluster5456_1clades	98	PHIKZ230	Pseudomonas virus phiKZ	GCA_000842965.1
AGH07684.1	005712	Cluster5457_1clades	78	CYVG_00241	Cyanophage S-SSM6a	GCA_002710385.1
AGH26157.1	005712	Cluster5457_1clades	84	CPMG_00056	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93605.1	005712	Cluster5457_1clades	98	AVU42_gp060	Prochlorococcus phage P-TIM68	GCA_001503075.1
ANS06100.1	005713	Cluster5458_1clades	98	ABCD_0161	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97174.1	005713	Cluster5458_1clades	97	E_166	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78689.1	005713	Cluster5458_1clades	97	RB43ORF167c	Escherichia virus RB43	GCA_000863505.1
ANZ49656.1	005714	Cluster5459_1clades	98	MACHINA_16	Erwinia phage Machina	GCA_002758035.1
ANZ49101.1	005714	Cluster5459_1clades	98	HUXLEY_17	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49929.1	005714	Cluster5459_1clades	98	PARSHIK_18	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QCW18604.1	005715	SIG+TM	98	7t3_083	Salmonella phage 7t3	GCA_006083215.1
AZU98429.1	005715	SIG+TM	98	CPT_Munch_497	Salmonella phage Munch	GCA_004015485.1
QIG63084.1	005715	SIG+TM	98	SEPL_471	Salmonella phage SE_PL	GCA_011067555.1
ANM45121.1	005716	Cluster5461_1clades	97	KTN4_363	Pseudomonas phage KTN4	GCA_002607225.1
QJB22998.1	005716	Cluster5461_1clades	97	fnug_355	Pseudomonas phage fnug	GCA_012837215.1
AAL83202.1	005716	Cluster5461_1clades	97	PHIKZ301	Pseudomonas virus phiKZ	GCA_000842965.1
AFQ96648.1	005717	Cluster5462_1clades	79	G173_gp103	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50625.1	005717	Cluster5462_1clades	97	STRATTON_200	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXF51127.1	005717	Cluster5462_1clades	79	MLDJOKPK_00261	Salmonella phage SPAsTU	GCA_003183805.1
AOV59542.1	005718	Cluster5463_1clades	97	S330809_082	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59304.1	005718	Cluster5463_1clades	97	C440309_082	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59780.1	005718	Cluster5463_1clades	97	N231010_082	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18598.1	005719	Cluster5464_1clades	97	7t3_077	Salmonella phage 7t3	GCA_006083215.1
AZU98426.1	005719	Cluster5464_1clades	97	CPT_Munch_494	Salmonella phage Munch	GCA_004015485.1
QIG63087.1	005719	Cluster5464_1clades	97	SEPL_474	Salmonella phage SE_PL	GCA_011067555.1
AFO71284.1	005720	SIG+TM	91	CR5_064	Cronobacter phage CR5	GCA_000910235.1
QBP07491.1	005720	SIG+TM	97	DERBICUS_65	Erwinia phage Derbicus	GCA_004521655.1
ANZ48915.1	005720	SIG+TM	92	EARLPHILLIPIV_65	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
BBA65276.1	005721	Cluster5466_1clades	87	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65735.1	005721	Cluster5466_1clades	87	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96316.1	005721	Cluster5466_1clades	97	Xoosp13_129	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AAX44605.1	005722	NifU	96	PSSM2_228	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12365.1	005722	NifU	96	PRTG_00212	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93439.1	005722	NifU	93	AVU42_gp100	Prochlorococcus phage P-TIM68	GCA_001503075.1
ANS06103.1	005723	Cluster5468_1clades	96	ABCD_0114	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97124.1	005723	Cluster5468_1clades	96	E_116	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78637.1	005723	Cluster5468_1clades	96	RB43ORF115c	Escherichia virus RB43	GCA_000863505.1
AFQ96592.1	005724	Cluster5469_1clades	96	G173_gp047	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48157.1	005724	Cluster5469_1clades	96	ASESINO_144	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50569.1	005724	Cluster5469_1clades	96	STRATTON_144	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AKF13173.1	005725	Cluster5470_1clades	74	PHIM19_268	Sinorhizobium phage phiM19	GCA_002605865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF12813.1	005725	Cluster5470_1clades	74	PHIM7_268	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13536.1	005725	Cluster5470_1clades	96	PHIN3_273	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01256.1	005726	Cluster5471_1clades	96	AR9_g172	Bacillus phage AR9	GCA_001743835.1
ALN97759.1	005726	Cluster5471_1clades	75	Bp8pS_080	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99882.1	005726	Cluster5471_1clades	96	PBI_PBS1_60	Bacillus virus PBS1	GCA_002601325.1
ANS06117.1	005727	Cluster5472_1clades	91	ABCD_0054	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97065.1	005727	Cluster5472_1clades	96	E_056	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78576.1	005727	Cluster5472_1clades	91	RB43ORF054w	Escherichia virus RB43	GCA_000863505.1
AOO14260.1	005728	Cluster5473_1clades	96	Sn110110_066	Cyanophage S-RIM14	GCA_002599065.1
AOO12964.1	005728	Cluster5473_1clades	89	W2100709_082	Cyanophage S-RIM44	GCA_002599285.1
QDH50508.1	005728	Cluster5473_1clades	88	-	Synechococcus phage S-B43	GCA_006869725.1
ASV44133.1	005729	FURR-HTH	96	PBI_SCTP2_118	Salicola phage SCTP-2	GCA_002625545.1
ASV44261.1	005729	FURR-HTH	93	PBI_SCTP2_246	Salicola phage SCTP-2	GCA_002625545.1
ASV44527.1	005729	FURR-HTH	93	PBI_SCTP2_512	Salicola phage SCTP-2	GCA_002625545.1
QCW18614.1	005730	Cluster5475_1clades	96	7t3_093	Salmonella phage 7t3	GCA_006083215.1
AZU98439.1	005730	Cluster5475_1clades	96	CPT_Munch_507	Salmonella phage Munch	GCA_004015485.1
QIG63074.1	005730	Cluster5475_1clades	96	SEPL_461	Salmonella phage SE_PL	GCA_011067555.1
QAX96836.1	005731	Cluster5476_1clades	96	-	Vibrio phage vB_VmeM-Yong MS31	GCA_009769835.1
QAX96200.1	005731	Cluster5476_1clades	96	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96518.1	005731	Cluster5476_1clades	96	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
QCW18550.1	005732	Cluster5477_1clades	96	7t3_025	Salmonella phage 7t3	GCA_006083215.1
AZU98379.1	005732	Cluster5477_1clades	86	CPT_Munch_445	Salmonella phage Munch	GCA_004015485.1
QIG63133.1	005732	Cluster5477_1clades	86	SEPL_520	Salmonella phage SE_PL	GCA_011067555.1
ANS06104.1	005733	Cluster5478_1clades	95	ABCD_0026	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97034.1	005733	Cluster5478_1clades	95	E_025	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78547.1	005733	Cluster5478_1clades	95	RB43ORF025c	Escherichia virus RB43	GCA_000863505.1
ANS06114.1	005734	Cluster5479_1clades	92	ABCD_0124	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97135.1	005734	Cluster5479_1clades	92	E_127	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78647.1	005734	Cluster5479_1clades	95	RB43ORF125c	Escherichia virus RB43	GCA_000863505.1
ANS06105.1	005735	Cluster5480_1clades	95	ABCD_0267	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97286.1	005735	Cluster5480_1clades	60	E_278	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78807.1	005735	Cluster5480_1clades	95	RB43ORF285c	Escherichia virus RB43	GCA_000863505.1
QGH71934.1	005736	Cluster5481_1clades	92	N1M2_71	Klebsiella phage N1M2	GCA_010092605.1
AEV89444.1	005736	Cluster5481_1clades	95	OBP_007	Pseudomonas phage OBP	GCA_000896635.1
AEV89535.1	005736	Cluster5481_1clades	84	OBP_098	Pseudomonas phage OBP	GCA_000896635.1
AOV59560.1	005737	Cluster5482_1clades	95	S330809_099	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59322.1	005737	Cluster5482_1clades	95	C440309_099	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59798.1	005737	Cluster5482_1clades	95	N231010_099	Synechococcus phage S-CAM4	GCA_002922155.1
APU01683.1	005738	Cluster5483_1clades	90	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01095.1	005738	Cluster5483_1clades	95	ASwh1_27	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53319.1	005738	Cluster5483_1clades	59	65p311	Aeromonas virus 65	GCA_000893255.1
QBZ70746.1	005739	Cluster5484_1clades	95	pETSU_165	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72053.1	005739	Cluster5484_1clades	84	N1M2_190	Klebsiella phage N1M2	GCA_010092605.1
AEV89679.1	005739	Cluster5484_1clades	69	OBP_242	Pseudomonas phage OBP	GCA_000896635.1
AGH07677.1	005740	Cluster5485_1clades	85	CYVG_00234	Cyanophage S-SSM6a	GCA_002710385.1
AAX44455.1	005740	Cluster5485_1clades	94	PSSM2_077	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12199.1	005740	Cluster5485_1clades	94	PRTG_00041	Prochlorococcus phage P-SSM5	GCA_002991095.1
ANS06107.1	005741	Phage_RpbA	94	ABCD_0044	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97054.1	005741	Phage_RpbA	94	E_045	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78566.1	005741	Phage_RpbA	94	RB43ORF044c	Escherichia virus RB43	GCA_000863505.1
ANS06108.1	005742	Cluster5487_1clades	94	ABCD_0140	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97148.1	005742	Cluster5487_1clades	94	E_140	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78663.1	005742	Cluster5487_1clades	94	RB43ORF141c	Escherichia virus RB43	GCA_000863505.1
AFC21455.1	005743	Cluster5488_1clades	94	GAP32_008	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44121.1	005743	Cluster5488_1clades	94	CBB_5	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43570.1	005743	Cluster5488_1clades	94	CBB_558	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AGH07706.1	005744	Cluster5489_1clades	94	CYVG_00263	Cyanophage S-SSM6a	GCA_002710385.1
AGG54406.1	005744	Cluster5489_1clades	87	CYWG_00122	Cyanophage S-SSM6b	GCA_002710425.1
AGH26178.1	005744	Cluster5489_1clades	87	CPMG_00077	Prochlorococcus phage MED4-213	GCA_000904535.1
AGR47960.1	005745	TM	94	SmphiM12_328	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13151.1	005745	TM	94	PHIM19_246	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12790.1	005745	TM	94	PHIM7_245	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01336.1	005746	Cluster5491_1clades	94	AR9_g252	Bacillus phage AR9	GCA_001743835.1
ALN97687.1	005746	Cluster5491_1clades	83	Bp8pS_008	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99966.1	005746	Cluster5491_1clades	94	PBI_PBS1_145	Bacillus virus PBS1	GCA_002601325.1
ANS06109.1	005747	Cluster5492_1clades	94	ABCD_0251	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97269.1	005747	Cluster5492_1clades	94	E_261	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78791.1	005747	Cluster5492_1clades	93	RB43ORF269w	Escherichia virus RB43	GCA_000863505.1
ANS06182.1	005748	Cluster5493_1clades	54	ABCD_0079	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97090.1	005748	Cluster5493_1clades	94	E_082	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78601.1	005748	Cluster5493_1clades	93	RB43ORF079w	Escherichia virus RB43	GCA_000863505.1
QBX06614.1	005749	Cluster5494_1clades	92	BcepSaruman_201	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74580.1	005749	Cluster5494_1clades	92	BcepSauron_200	Burkholderia phage BcepSauron	GCA_005394215.1
ATA65508.1	005749	Cluster5494_1clades	94	2050HW_00173	Serratia phage 2050HW	GCA_002628125.1
AYD81415.1	005750	Cluster5495_1clades	94	SEA_JUSTBECAUSE_260	Streptomyces phage JustBecause	GCA_003613775.1
QBZ72148.1	005750	Cluster5495_1clades	94	SEA_KRADAL_262	Streptomyces phage Kradal	GCA_004799925.1
AXH66411.1	005750	Cluster5495_1clades	94	SEA_SATIS_262	Streptomyces phage Satis	GCA_003366315.1
ANS06111.1	005751	Cluster5497_1clades	93	ABCD_0059	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97070.1	005751	Cluster5497_1clades	75	E_061	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78582.1	005751	Cluster5497_1clades	93	RB43ORF060w	Escherichia virus RB43	GCA_000863505.1
AFC21871.1	005752	Cluster5498_1clades	92	GAP32_418	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43999.1	005752	Cluster5498_1clades	93	CBB_436	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88959.1	005752	Cluster5498_1clades	90	BF_0434	Serratia phage BF	GCA_002619745.1
ANS06113.1	005753	Cluster5499_1clades	93	ABCD_0123	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97134.1	005753	Cluster5499_1clades	90	E_126	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78645.1	005753	Cluster5499_1clades	51	RB43ORF123c	Escherichia virus RB43	GCA_000863505.1
AOO14263.1	005754	Cluster5500_1clades	93	Sn110110_069	Cyanophage S-RIM14	GCA_002599065.1
AOO14912.1	005754	Cluster5500_1clades	93	W1230910_066	Cyanophage S-RIM14	GCA_002599125.1
AGG54327.1	005754	Cluster5500_1clades	79	CYWG_00043	Cyanophage S-SSM6b	GCA_002710425.1
AXG67274.1	005755	Cluster5501_1clades	93	AD1_230	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08499.1	005755	Cluster5501_1clades	93	Alexandra_239	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58874.1	005755	Cluster5501_1clades	74	Y3_234	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QBZ70751.1	005756	TM	91	pETSU_170	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72058.1	005756	TM	93	N1M2_195	Klebsiella phage N1M2	GCA_010092605.1
AEV89685.1	005756	TM	92	OBP_248	Pseudomonas phage OBP	GCA_000896635.1
AGH07602.1	005757	Cluster5503_1clades	92	CYVG_00158	Cyanophage S-SSM6a	GCA_002710385.1
QCW22849.1	005757	Cluster5503_1clades	66	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50708.1	005757	Cluster5503_1clades	66	-	Synechococcus phage S-B43	GCA_006869725.1
AGR47831.2	005758	Cluster5504_1clades	92	SmphiM12_199	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13041.1	005758	Cluster5504_1clades	92	PHIM19_136	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12682.1	005758	Cluster5504_1clades	92	PHIM7_136	Sinorhizobium phage phiM7	GCA_002622405.1
ANS06126.1	005759	TM	88	ABCD_0092	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97104.1	005759	TM	92	E_096	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78613.1	005759	TM	45	RB43ORF091w	Escherichia virus RB43	GCA_000863505.1
QCW18880.1	005760	Cluster5506_1clades	92	7t3_0359	Salmonella phage 7t3	GCA_006083215.1
AZU98138.1	005760	Cluster5506_1clades	92	CPT_Munch_194	Salmonella phage Munch	GCA_004015485.1
QIG62844.1	005760	Cluster5506_1clades	92	SEPL_231	Salmonella phage SE_PL	GCA_011067555.1
QGT54781.1	005761	Cluster5507_1clades	85	b23_0166	Synechococcus phage B23	GCA_009745195.1
QGT54411.1	005761	Cluster5507_1clades	85	b3_0167	Synechococcus phage B3	GCA_009745215.1
BBA65433.1	005761	Cluster5507_1clades	92	-	Xanthomonas phage XacN1	GCA_003173815.1
AUE22606.1	005762	Cluster5508_1clades	91	Ah1_00065	Aeromonas phage Ah1	GCA_002957415.1
QAX98643.1	005762	Cluster5508_1clades	91	ASfcp2_310	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52783.1	005762	Cluster5508_1clades	91	PX29p064	Aeromonas phage PX29	GCA_000920195.1
AJT61171.1	005763	Cluster5509_1clades	91	AVU32_gp330	Vibrio phage ValKK3	GCA_001501635.1
ALP47229.1	005763	Cluster5509_1clades	91	phiGrn1_0050	Vibrio phage phi-Grn1	GCA_002757115.1
QNJ54783.1	005763	Cluster5509_1clades	91	vBValMR10Z_243	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ANS06118.1	005764	Cluster5510_1clades	91	ABCD_0266	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97285.1	005764	Cluster5510_1clades	91	E_277	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78806.1	005764	Cluster5510_1clades	67	RB43ORF284c	Escherichia virus RB43	GCA_000863505.1
ANZ49777.1	005765	Mitofilin	91	MACHINA_139	Erwinia phage Machina	GCA_002758035.1
ANZ49221.1	005765	Mitofilin	91	HUXLEY_139	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50049.1	005765	Mitofilin	91	PARSHIK_140	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANS06177.1	005766	Cluster5512_1clades	60	ABCD_0060	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97071.1	005766	Cluster5512_1clades	91	E_062	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78583.1	005766	Cluster5512_1clades	60	RB43ORF061w	Escherichia virus RB43	GCA_000863505.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW18594.1	005767	Cluster5513_1clades	91	7t3_073	Salmonella phage 7t3	GCA_006083215.1
AZU98422.1	005767	Cluster5513_1clades	91	CPT_Munch_490	Salmonella phage Munch	GCA_004015485.1
QIG63091.1	005767	Cluster5513_1clades	91	SEPL_478	Salmonella phage SE_PL	GCA_011067555.1
BBA65182.1	005768	Cluster5514_1clades	91	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65641.1	005768	Cluster5514_1clades	91	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96211.1	005768	Cluster5514_1clades	90	Xoosp13_24	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ANS06132.1	005769	Cluster5515_1clades	86	ABCD_0164	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97177.1	005769	Cluster5515_1clades	86	E_169	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78693.1	005769	Cluster5515_1clades	90	RB43ORF171c	Escherichia virus RB43	GCA_000863505.1
ANS06139.1	005770	Cluster5516_1clades	84	ABCD_0187	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97201.1	005770	Cluster5516_1clades	88	E_193	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78719.1	005770	Cluster5516_1clades	90	RB43ORF197c	Escherichia virus RB43	GCA_000863505.1
ABY63195.1	005771	Cluster5517_1clades	90	201phi2-1p370	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76998.1	005771	Cluster5517_1clades	81	PHABIO_367	Pseudomonas phage Phabio	GCA_002624965.1
AEH03730.1	005771	Cluster5517_1clades	82	307	Pseudomonas phage PhiPA3	GCA_001502095.1
AOO14364.1	005772	Cluster5518_1clades	79	Sn110110_170	Cyanophage S-RIM14	GCA_002599065.1
AGH07520.1	005772	Cluster5518_1clades	90	CYVG_00076	Cyanophage S-SSM6a	GCA_002710385.1
ASR76290.1	005772	Cluster5518_1clades	80	PBI_BELLAMY_254	Synechococcus phage Bellamy	GCA_002627525.1
ANS06122.1	005773	Cluster5519_1clades	89	ABCD_0097	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97108.1	005773	Cluster5519_1clades	90	E_100	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78618.1	005773	Cluster5519_1clades	89	RB43ORF096w	Escherichia virus RB43	GCA_000863505.1
BBI90480.1	005774	Cluster5520_1clades	75	HYO65_gp088	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90788.1	005774	Cluster5520_1clades	88	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39414.1	005774	Cluster5520_1clades	90	BPT24_296	Tenacibaculum phage pT24	GCA_002611925.1
ANS06121.1	005775	Cluster5521_1clades	89	ABCD_0072	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97086.1	005775	Cluster5521_1clades	86	E_077	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78596.1	005775	Cluster5521_1clades	89	RB43ORF074w	Escherichia virus RB43	GCA_000863505.1
ANS06123.1	005776	Cluster5522_1clades	89	ABCD_0135	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97143.1	005776	Cluster5522_1clades	89	E_135	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78658.1	005776	Cluster5522_1clades	89	RB43ORF136c	Escherichia virus RB43	GCA_000863505.1
ANS06124.1	005777	Cluster5523_1clades	89	ABCD_0238	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97256.1	005777	Cluster5523_1clades	83	E_248	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78775.1	005777	Cluster5523_1clades	85	RB43ORF253w	Escherichia virus RB43	GCA_000863505.1
AOV59573.1	005778	Cluster5524_1clades	89	S330809_112	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59335.1	005778	Cluster5524_1clades	89	C440309_112	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59811.1	005778	Cluster5524_1clades	89	N231010_112	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59687.1	005779	Cluster5525_1clades	89	S330809_226	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59449.1	005779	Cluster5525_1clades	89	C440309_226	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59924.1	005779	Cluster5525_1clades	89	N231010_225	Synechococcus phage S-CAM4	GCA_002922155.1
QAY01101.1	005780	Late_protein_L1	86	ASwh1_33	Aeromonas phage Aswh_1	GCA_004146945.1
AQW88980.1	005780	Late_protein_L1	89	BF_0455	Serratia phage BF	GCA_002619745.1
SOK59263.1	005780	Late_protein_L1	88	g455	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AXG67293.1	005781	Cluster5527_1clades	86	AD1_249	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08518.1	005781	Cluster5527_1clades	86	Alexandra_261	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58895.1	005781	Cluster5527_1clades	89	Y3_255	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67295.1	005782	CopG_antitoxin	81	AD1_251	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08520.1	005782	CopG_antitoxin	81	Alexandra_263	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58898.1	005782	CopG_antitoxin	89	Y3_258	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18789.1	005783	D6	89	7t3_0268	Salmonella phage 7t3	GCA_006083215.1
AZU98054.1	005783	D6	89	CPT_Munch_110	Salmonella phage Munch	GCA_004015485.1
QIG62927.1	005783	D6	89	SEPL_314	Salmonella phage SE_PL	GCA_011067555.1
QBX06602.1	005784	Cluster5530_1clades	89	BcepSaruman_189	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74567.1	005784	Cluster5530_1clades	89	BcepSauron_187	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41743.1	005784	Cluster5530_1clades	77	RSL1_ORF297	Ralstonia phage phiRSL1	GCA_000879455.1
QIG63331.1	005785	Cluster5531_1clades	89	DAC16_98	Bacteroides phage DAC16	GCA_013387695.1
QIG63597.1	005785	Cluster5531_1clades	89	DAC19_106	Bacteroides phage DAC19	GCA_013387715.1
QIG63858.1	005785	Cluster5531_1clades	89	DAC20_105	Bacteroides phage DAC20	GCA_013387725.1
AMR59729.1	005786	Cluster5532_1clades	88	SEGD1_080	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85919.1	005786	Cluster5532_1clades	88	ACEC001_0810	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AEP83912.1	005786	Cluster5532_1clades	88	SPN3US_0079	Salmonella phage SPN3US	GCA_001042275.1
AFU87878.1	005787	Cluster5533_1clades	88	CcrColossus_gp008	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68547.1	005787	Cluster5533_1clades	88	CcrPW_gp008	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68997.1	005787	Cluster5533_1clades	88	CcrPW_gp458	Caulobacter phage CcrPW	GCA_003443275.1
ANS06133.1	005788	Cluster5534_1clades	86	ABCD_0180	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97193.1	005788	Cluster5534_1clades	88	E_185	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78710.1	005788	Cluster5534_1clades	75	RB43ORF188c	Escherichia virus RB43	GCA_000863505.1
AOO14244.1	005789	Cluster5535_1clades	88	Sn110110_050	Cyanophage S-RIM14	GCA_002599065.1
AOO14896.1	005789	Cluster5535_1clades	88	W1230910_050	Cyanophage S-RIM14	GCA_002599125.1
AGG54341.1	005789	Cluster5535_1clades	87	CYWG_00057	Cyanophage S-SSM6b	GCA_002710425.1
QIG63503.1	005790	Cluster5536_1clades	88	DAC19_12	Bacteroides phage DAC19	GCA_013387715.1
QIG63765.1	005790	Cluster5536_1clades	88	DAC20_12	Bacteroides phage DAC20	GCA_013387725.1
QIG64026.1	005790	Cluster5536_1clades	88	DAC22_12	Bacteroides phage DAC22	GCA_013387735.1
AQW88545.1	005791	SIG+TM	81	BF_0020	Serratia phage BF	GCA_002619745.1
SOK58820.1	005791	SIG+TM	88	g012	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58288.1	005791	SIG+TM	88	g011	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06130.1	005792	Cluster5538_1clades	87	ABCD_0156	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97168.1	005792	Cluster5538_1clades	87	E_160	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78684.1	005792	Cluster5538_1clades	87	RB43ORF162c	Escherichia virus RB43	GCA_000863505.1
AMS01108.1	005793	Cluster5539_1clades	87	AR9_g023	Bacillus phage AR9	GCA_001743835.1
ALN97751.1	005793	Cluster5539_1clades	82	Bp8pS_072	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00030.1	005793	Cluster5539_1clades	87	PBI_PBS1_208	Bacillus virus PBS1	GCA_002601325.1
ANS06128.1	005794	Cluster5540_1clades	87	ABCD_0068	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97081.1	005794	Cluster5540_1clades	81	E_072	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78591.1	005794	Cluster5540_1clades	70	RB43ORF069w	Escherichia virus RB43	GCA_000863505.1
ANS06129.1	005795	Cluster5541_1clades	87	ABCD_0128	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97138.1	005795	Cluster5541_1clades	86	E_130	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78651.1	005795	Cluster5541_1clades	73	RB43ORF129c	Escherichia virus RB43	GCA_000863505.1
AQW88985.1	005796	Cluster5542_1clades	87	BF_0460	Serratia phage BF	GCA_002619745.1
SOK59266.1	005796	Cluster5542_1clades	87	g458	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58730.1	005796	Cluster5542_1clades	86	g453	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67329.1	005797	Cluster5543_1clades	87	AD1_285	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08556.1	005797	Cluster5543_1clades	87	Alexandra_300	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58929.1	005797	Cluster5543_1clades	87	Y3_289	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18712.1	005798	Cluster5544_1clades	87	7t3_0191	Salmonella phage 7t3	GCA_006083215.1
AZU97985.1	005798	Cluster5544_1clades	87	CPT_Munch_041	Salmonella phage Munch	GCA_004015485.1
QIG62994.1	005798	Cluster5544_1clades	87	SEPL_381	Salmonella phage SE_PL	GCA_011067555.1
ANM44768.1	005799	Cluster5545_1clades	86	KTN4_010	Pseudomonas phage KTN4	GCA_002607225.1
QJB22653.1	005799	Cluster5545_1clades	86	fnug_10	Pseudomonas phage fnug	GCA_012837215.1
AAL82911.1	005799	Cluster5545_1clades	86	PHIKZ010	Pseudomonas virus phiKZ	GCA_000842965.1
AIR93574.1	005800	Cluster5546_1clades	86	AVU42_gp236	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76301.1	005800	Cluster5546_1clades	68	PBI_BELLAMY_265	Synechococcus phage Bellamy	GCA_002627525.1
QJT70248.1	005800	Cluster5546_1clades	68	SynMITS9220M01_242	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMS01169.1	005801	Cluster5547_1clades	85	AR9_g085	Bacillus phage AR9	GCA_001743835.1
ALN97841.1	005801	Cluster5547_1clades	86	Bp8pS_162	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ASU00101.1	005801	Cluster5547_1clades	85	PBI_PBS1_279	Bacillus virus PBS1	GCA_002601325.1
ANS06158.1	005802	Cluster5548_1clades	73	ABCD_0172	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97185.1	005802	Cluster5548_1clades	86	E_177	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78702.1	005802	Cluster5548_1clades	67	RB43ORF180c	Escherichia virus RB43	GCA_000863505.1
AGH07536.1	005803	TM	81	CYVG_00092	Cyanophage S-SSM6a	GCA_002710385.1
AAX44613.1	005803	TM	85	PSSM2_236	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12358.1	005803	TM	85	PRTG_00205	Prochlorococcus phage P-SSM5	GCA_002991095.1
ANS06134.1	005804	Cluster5550_1clades	85	ABCD_0033	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97043.1	005804	Cluster5550_1clades	84	E_034	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78555.1	005804	Cluster5550_1clades	85	RB43ORF033c	Escherichia virus RB43	GCA_000863505.1
ANS06136.1	005805	Cluster5551_1clades	85	ABCD_0271	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97291.1	005805	Cluster5551_1clades	82	E_283	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78812.1	005805	Cluster5551_1clades	85	RB43ORF290c	Escherichia virus RB43	GCA_000863505.1
AUE22831.1	005806	Cluster5552_1clades	85	Ah1_00313	Aeromonas phage Ah1	GCA_002957415.1
QAX98545.1	005806	Cluster5552_1clades	85	ASfcp2_210	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53009.1	005806	Cluster5552_1clades	85	PX29p290	Aeromonas phage PX29	GCA_000920195.1
AGR48018.1	005807	Cluster5553_1clades	85	SmphiM12_386	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13204.1	005807	Cluster5553_1clades	85	PHIM19_299	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12845.1	005807	Cluster5553_1clades	85	PHIM7_299	Sinorhizobium phage phiM7	GCA_002622405.1
AFC21585.1	005808	Cluster5554_1clades	64	GAP32_135	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43703.1	005808	Cluster5554_1clades	85	CBB_138	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58938.1	005808	Cluster5554_1clades	51	g130	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AOV59522.1	005809	Cluster5555_1clades	85	S330809_061	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59284.1	005809	Cluster5555_1clades	85	C440309_061	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59760.1	005809	Cluster5555_1clades	85	N231010_061	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59620.1	005810	Cluster5556_1clades	85	S330809_159	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59382.1	005810	Cluster5556_1clades	85	C440309_159	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59858.1	005810	Cluster5556_1clades	85	N231010_159	Synechococcus phage S-CAM4	GCA_002922155.1
BBA65200.1	005811	Cluster5557_1clades	85	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65659.1	005811	Cluster5557_1clades	85	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96233.1	005811	Cluster5557_1clades	82	Xoosp13_46	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AUE22689.1	005812	Cluster5558_1clades	84	Ah1_00148	Aeromonas phage Ah1	GCA_002957415.1
ADM80131.1	005812	Cluster5558_1clades	83	phiAS5_ORF0288	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17816.1	005812	Cluster5558_1clades	84	Aeh1ORF151c	Aeromonas virus Aeh1	GCA_000843245.1
AIT14331.1	005813	Cluster5559_1clades	84	PBI_121Q_441	Escherichia phage 121Q	GCA_000926855.1
QBO61973.1	005813	Cluster5559_1clades	84	G17_00484	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80318.1	005813	Cluster5559_1clades	84	PSLUR01_00341	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AYD79858.1	005814	Cluster5560_1clades	84	JA11_053	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66457.1	005814	Cluster5560_1clades	84	JA13_054	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67427.1	005814	Cluster5560_1clades	84	JA33_053	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QCW18791.1	005815	SIG+TM	66	7t3_0270	Salmonella phage 7t3	GCA_006083215.1
AZU98056.1	005815	SIG+TM	84	CPT_Munch_112	Salmonella phage Munch	GCA_004015485.1
QIG62926.1	005815	SIG+TM	84	SEPL_313	Salmonella phage SE_PL	GCA_011067555.1
ADQ52972.1	005816	SIG+TM	68	PX29p253	Aeromonas phage PX29	GCA_000920195.1
ADM79898.1	005816	SIG+TM	70	phiAS5_ORF0055	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17922.1	005816	SIG+TM	83	Aeh1hmmORF03c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06141.1	005817	Cluster5563_1clades	83	ABCD_0075	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97089.1	005817	Cluster5563_1clades	83	E_080	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78599.1	005817	Cluster5563_1clades	83	RB43ORF077w	Escherichia virus RB43	GCA_000863505.1
AFC21471.1	005818	SIG+TM	81	GAP32_023	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43592.1	005818	SIG+TM	83	CBB_27	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44143.1	005818	SIG+TM	83	CBB_580	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88614.1	005819	Cluster5565_1clades	83	BF_0089	Serratia phage BF	GCA_002619745.1
SOK58890.1	005819	Cluster5565_1clades	83	g082	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58353.1	005819	Cluster5565_1clades	83	g076	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXQ69080.1	005820	Cluster5566_1clades	83	CcrBL9_gp056c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69081.1	005820	Cluster5566_1clades	82	CcrBL9_gp057c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69639.1	005820	Cluster5566_1clades	79	CcrSC_gp057c	Caulobacter phage CcrSC	GCA_003443315.1
QBX06659.1	005821	zf-TFIIB	79	BcepSaruman_246	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74627.1	005821	zf-TFIIB	79	BcepSauron_247	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41663.1	005821	zf-TFIIB	83	RSL1_ORF214	Ralstonia phage phiRSL1	GCA_000879455.1
AKF13154.1	005822	Cluster5568_1clades	82	PHIM19_249	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12793.1	005822	Cluster5568_1clades	82	PHIM7_248	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13517.1	005822	Cluster5568_1clades	82	PHIN3_254	Sinorhizobium phage phiN3	GCA_001501175.1
ANS06157.1	005823	Cluster5569_1clades	73	ABCD_0093	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97105.1	005823	Cluster5569_1clades	82	E_097	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78614.1	005823	Cluster5569_1clades	65	RB43ORF092w	Escherichia virus RB43	GCA_000863505.1
AIT14233.1	005824	Cluster5570_1clades	81	PBI_121Q_343	Escherichia phage 121Q	GCA_000926855.1
QBO62071.1	005824	Cluster5570_1clades	81	G17_00582	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QDF14087.1	005824	Cluster5570_1clades	81	vBEcoMphAPEC6_gp464c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AOV59631.1	005825	Cluster5571_1clades	81	S330809_170	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59393.1	005825	Cluster5571_1clades	81	C440309_170	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59869.1	005825	Cluster5571_1clades	81	N231010_170	Synechococcus phage S-CAM4	GCA_002922155.1
AYD79864.1	005826	SIG+RelB	81	JA11_059	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66787.1	005826	SIG+RelB	81	JA29_061	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67433.1	005826	SIG+RelB	81	JA33_059	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
AIT14171.1	005827	Cluster5573_1clades	70	PBI_121Q_281	Escherichia phage 121Q	GCA_000926855.1
QAY00765.1	005827	Cluster5573_1clades	70	Ecwhy1_491	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34945.1	005827	Cluster5573_1clades	80	ACQ29_gp265	Escherichia phage PBECO4	GCA_001041035.1
ANM44789.1	005828	Cluster5574_1clades	80	KTN4_031	Pseudomonas phage KTN4	GCA_002607225.1
QBX32290.1	005828	Cluster5574_1clades	80	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41864.1	005828	Cluster5574_1clades	80	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW19114.1	005829	Cluster5575_1clades	80	7t3_0597	Salmonella phage 7t3	GCA_006083215.1
AZU98351.1	005829	Cluster5575_1clades	80	CPT_Munch_410	Salmonella phage Munch	GCA_004015485.1
QIG62631.1	005829	Cluster5575_1clades	80	SEPL_018	Salmonella phage SE_PL	GCA_011067555.1
QBX06157.1	005830	Cluster5576_1clades	80	ValB1HC_203	Vibrio phage ValB1 HC	GCA_004771355.1
ALP47710.1	005830	Cluster5576_1clades	46	phiST2_0182	Vibrio phage phi-ST2	GCA_002757135.1
QNJ54782.1	005830	Cluster5576_1clades	80	vBValMR10Z_242	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
QCW18771.1	005831	Cluster5577_1clades	80	7t3_0250	Salmonella phage 7t3	GCA_006083215.1
AZU98037.1	005831	Cluster5577_1clades	43	CPT_Munch_093	Salmonella phage Munch	GCA_004015485.1
QIG62943.1	005831	Cluster5577_1clades	80	SEPL_330	Salmonella phage SE_PL	GCA_011067555.1
AFC21956.1	005832	Cluster5578_1clades	79	GAP32_497	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44565.1	005832	Cluster5578_1clades	77	RaK2_00292	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
SOK59313.1	005832	Cluster5578_1clades	79	g505	Yersinia phage fHe-Yen9-03	GCA_002990515.1
ASU00298.1	005833	Cluster5579_1clades	79	HWB28_gp254	Aeromonas phage AS-zj	GCA_002627665.1
QAX97739.1	005833	Cluster5579_1clades	79	ASswx1_94	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39168.1	005833	Cluster5579_1clades	79	CC2_017	Aeromonas phage CC2	GCA_000903495.1
ANS06155.1	005834	Cluster5580_1clades	75	ABCD_0179	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97192.1	005834	Cluster5580_1clades	79	E_184	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78709.1	005834	Cluster5580_1clades	78	RB43ORF187c	Escherichia virus RB43	GCA_000863505.1
AOV59678.1	005835	Cluster5581_1clades	79	S330809_217	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59440.1	005835	Cluster5581_1clades	79	C440309_217	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59915.1	005835	Cluster5581_1clades	79	N231010_216	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18818.1	005836	SIG+TM	79	7t3_0297	Salmonella phage 7t3	GCA_006083215.1
AZU98082.1	005836	SIG+TM	79	CPT_Munch_138	Salmonella phage Munch	GCA_004015485.1
QIG62900.1	005836	SIG+TM	79	SEPL_287	Salmonella phage SE_PL	GCA_011067555.1
QCW18551.1	005837	Cluster5583_1clades	79	7t3_026	Salmonella phage 7t3	GCA_006083215.1
AZU98380.1	005837	Cluster5583_1clades	79	CPT_Munch_446	Salmonella phage Munch	GCA_004015485.1
QIG63132.1	005837	Cluster5583_1clades	79	SEPL_519	Salmonella phage SE_PL	GCA_011067555.1
AOO14259.1	005838	Cluster5584_1clades	64	Sn110110_065	Cyanophage S-RIM14	GCA_002599065.1
QCW22850.1	005838	Cluster5584_1clades	79	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50709.1	005838	Cluster5584_1clades	79	-	Synechococcus phage S-B43	GCA_006869725.1
AQW88887.1	005839	SIG+TM	78	BF_0362	Serratia phage BF	GCA_002619745.1
SOK59174.1	005839	SIG+TM	79	g366	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58640.1	005839	SIG+TM	79	g363	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFC21896.1	005840	Cluster5586_1clades	78	GAP32_441	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44025.1	005840	Cluster5586_1clades	78	CBB_462	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88982.1	005840	Cluster5586_1clades	75	BF_0457	Serratia phage BF	GCA_002619745.1
AFU87883.1	005841	Cluster5587_1clades	78	CcrColossus_gp013	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68552.1	005841	Cluster5587_1clades	63	CcrPW_gp013	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69002.1	005841	Cluster5587_1clades	63	CcrPW_gp463	Caulobacter phage CcrPW	GCA_003443275.1
ANM44909.1	005842	Cluster5588_1clades	78	KTN4_151	Pseudomonas phage KTN4	GCA_002607225.1
QJB22787.1	005842	Cluster5588_1clades	78	fnug_144	Pseudomonas phage fnug	GCA_012837215.1
AGC26333.1	005842	Cluster5588_1clades	78	PHIKZ117.3	Pseudomonas virus phiKZ	GCA_000842965.1
ANZ48383.1	005843	Cluster5589_1clades	78	CAITLIN_88	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48655.1	005843	Cluster5589_1clades	74	CHRISDB_93	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51083.1	005843	Cluster5589_1clades	76	MLDJOKPK_00080	Salmonella phage SPAsTU	GCA_003183805.1
ANS06149.1	005844	Cluster5590_1clades	77	ABCD_0004	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97012.1	005844	Cluster5590_1clades	78	E_003	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78524.1	005844	Cluster5590_1clades	77	RB43ORF002c	Escherichia virus RB43	GCA_000863505.1
AOV59520.1	005845	Cluster5591_1clades	78	S330809_059	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59282.1	005845	Cluster5591_1clades	78	C440309_059	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59758.1	005845	Cluster5591_1clades	78	N231010_059	Synechococcus phage S-CAM4	GCA_002922155.1
AQW89049.1	005846	SIG+TM+TM	78	BF_0524	Serratia phage BF	GCA_002619745.1
SOK59324.1	005846	SIG+TM+TM	76	g516	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58786.1	005846	SIG+TM+TM	76	g509	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18688.1	005847	Cluster5593_1clades	78	7t3_0167	Salmonella phage 7t3	GCA_006083215.1
AZU97962.1	005847	Cluster5593_1clades	78	CPT_Munch_018	Salmonella phage Munch	GCA_004015485.1
QIG63016.1	005847	Cluster5593_1clades	78	SEPL_403	Salmonella phage SE_PL	GCA_011067555.1
QCW18704.1	005848	Cluster5594_1clades	78	7t3_0183	Salmonella phage 7t3	GCA_006083215.1
AZU97976.1	005848	Cluster5594_1clades	78	CPT_Munch_032	Salmonella phage Munch	GCA_004015485.1
QIG63002.1	005848	Cluster5594_1clades	78	SEPL_389	Salmonella phage SE_PL	GCA_011067555.1
ADQ52800.1	005849	Cluster5595_1clades	77	PX29p081	Aeromonas phage PX29	GCA_000920195.1
ADM80055.1	005849	Cluster5595_1clades	57	phiAS5_ORF0212	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17743.1	005849	Cluster5595_1clades	65	Aeh1ORF082c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21858.1	005850	DUF2318	69	GAP32_405	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMM43982.1	005850	DUF2318	77	CBB_419	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88940.1	005850	DUF2318	65	BF_0415	Serratia phage BF	GCA_002619745.1
ANS06150.1	005851	Cluster5597_1clades	77	ABCD_0111	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97121.1	005851	Cluster5597_1clades	76	E_113	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78633.1	005851	Cluster5597_1clades	76	RB43ORF111c	Escherichia virus RB43	GCA_000863505.1
AOO14381.1	005852	SIG+TM	77	Sn110110_187	Cyanophage S-RIM14	GCA_002599065.1
AOO15029.1	005852	SIG+TM	77	W1230910_183	Cyanophage S-RIM14	GCA_002599125.1
ASR76230.1	005852	SIG+TM	56	PBI_BELLAMY_192	Synechococcus phage Bellamy	GCA_002627525.1
AOV59527.1	005853	MazE_antitoxin	77	S330809_066	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59289.1	005853	MazE_antitoxin	77	C440309_066	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59765.1	005853	MazE_antitoxin	77	N231010_066	Synechococcus phage S-CAM4	GCA_002922155.1
ATI17518.1	005854	Cluster5600_1clades	77	-	Aeromonas phage AS-szw	GCA_002743635.1
QAY01177.1	005854	Cluster5600_1clades	60	ASwh1_111	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39261.1	005854	Cluster5600_1clades	76	CC2_215	Aeromonas phage CC2	GCA_000903495.1
QCW18668.1	005855	Cluster5601_1clades	77	7t3_0147	Salmonella phage 7t3	GCA_006083215.1
AZU97945.1	005855	Cluster5601_1clades	77	CPT_Munch_001	Salmonella phage Munch	GCA_004015485.1
QIG63030.1	005855	Cluster5601_1clades	77	SEPL_417	Salmonella phage SE_PL	GCA_011067555.1
ANS06151.1	005856	SIG+TM	76	ABCD_0032	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97042.1	005856	SIG+TM	76	E_033	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78554.1	005856	SIG+TM	76	RB43ORF032c	Escherichia virus RB43	GCA_000863505.1
AFU87898.1	005857	KAP-NTPase	76	CcrColossus_gp028	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68568.1	005857	KAP-NTPase	76	CcrPW_gp029	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69017.1	005857	KAP-NTPase	76	CcrPW_gp478	Caulobacter phage CcrPW	GCA_003443275.1
ANS06168.1	005858	Cluster5604_1clades	68	ABCD_0085	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97097.1	005858	Cluster5604_1clades	76	E_089	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78607.1	005858	Cluster5604_1clades	40	RB43ORF085w	Escherichia virus RB43	GCA_000863505.1
AOV59692.1	005859	Cluster5605_1clades	76	S330809_231	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59454.1	005859	Cluster5605_1clades	76	C440309_231	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59929.1	005859	Cluster5605_1clades	75	N231010_230	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18698.1	005860	Cluster5606_1clades	76	7t3_0177	Salmonella phage 7t3	GCA_006083215.1
AZU97971.1	005860	Cluster5606_1clades	76	CPT_Munch_027	Salmonella phage Munch	GCA_004015485.1
QIG63007.1	005860	Cluster5606_1clades	76	SEPL_394	Salmonella phage SE_PL	GCA_011067555.1
QCW18828.1	005861	Cluster5607_1clades	76	7t3_0307	Salmonella phage 7t3	GCA_006083215.1
AZU98092.1	005861	Cluster5607_1clades	76	CPT_Munch_148	Salmonella phage Munch	GCA_004015485.1
QIG62890.1	005861	Cluster5607_1clades	49	SEPL_277	Salmonella phage SE_PL	GCA_011067555.1
QCW19129.1	005862	Cluster5608_1clades	76	7t3_0614	Salmonella phage 7t3	GCA_006083215.1
AZU98366.1	005862	Cluster5608_1clades	76	CPT_Munch_426	Salmonella phage Munch	GCA_004015485.1
QIG62616.1	005862	Cluster5608_1clades	76	SEPL_003	Salmonella phage SE_PL	GCA_011067555.1
QCW18620.1	005863	newSTAND	76	7t3_099	Salmonella phage 7t3	GCA_006083215.1
AZU98445.1	005863	newSTAND	76	CPT_Munch_513	Salmonella phage Munch	GCA_004015485.1
QIG63068.1	005863	newSTAND	76	SEPL_455	Salmonella phage SE_PL	GCA_011067555.1
QAY00768.1	005864	Cluster5610_1clades	76	Ecwhy1_494	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61842.1	005864	Cluster5610_1clades	76	EO157G_2530	Escherichia phage SP27	GCA_008033345.1
QDF14152.1	005864	Cluster5610_1clades	76	vBEcoMphAPEC6_gp529c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QCW22932.1	005865	Cluster5611_1clades	76	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50617.1	005865	Cluster5611_1clades	76	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70165.1	005865	Cluster5611_1clades	62	SynMITS9220M01_152	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJD53834.1	005866	Cluster5612_1clades	76	SEA_KELA_274	Streptomyces phage Kela	GCA_012934305.1
QBZ72163.1	005866	Cluster5612_1clades	69	SEA_KRADAL_277	Streptomyces phage Kradal	GCA_004799925.1
AXH66426.1	005866	Cluster5612_1clades	69	SEA_SATIS_277	Streptomyces phage Satis	GCA_003366315.1
AAX44495.1	005867	Cluster5613_1clades	75	PSSM2_117	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12471.1	005867	Cluster5613_1clades	75	PRTG_00324	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ70591.1	005867	Cluster5613_1clades	72	HOU04_gp192	Synechococcus phage S-T4	GCA_003443335.1
ANS06153.1	005868	Cluster5614_1clades	75	ABCD_0051	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97062.1	005868	Cluster5614_1clades	75	E_053	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78573.1	005868	Cluster5614_1clades	75	RB43ORF051w	Escherichia virus RB43	GCA_000863505.1
ANS06154.1	005869	Cluster5615_1clades	75	ABCD_0086	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97098.1	005869	Cluster5615_1clades	75	E_090	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78608.1	005869	Cluster5615_1clades	75	RB43ORF086w	Escherichia virus RB43	GCA_000863505.1
AFC21538.1	005870	SIG+TM	75	GAP32_090	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43657.1	005870	SIG+TM	75	CBB_92	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88608.1	005870	SIG+TM	69	BF_0083	Serratia phage BF	GCA_002619745.1
ATI17264.1	005871	Cluster5617_1clades	75	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97703.1	005871	Cluster5617_1clades	75	ASswx1_57	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01435.1	005871	Cluster5617_1clades	75	ASwh1_376	Aeromonas phage Aswh_1	GCA_004146945.1
QCW18785.1	005872	Cluster5618_1clades	75	7t3_0264	Salmonella phage 7t3	GCA_006083215.1
AZU98050.1	005872	Cluster5618_1clades	75	CPT_Munch_106	Salmonella phage Munch	GCA_004015485.1
QIG62930.1	005872	Cluster5618_1clades	75	SEPL_317	Salmonella phage SE_PL	GCA_011067555.1
QCW18792.1	005873	Cluster5619_1clades	75	7t3_0271	Salmonella phage 7t3	GCA_006083215.1
AZU98057.1	005873	Cluster5619_1clades	75	CPT_Munch_113	Salmonella phage Munch	GCA_004015485.1
QIG62925.1	005873	Cluster5619_1clades	75	SEPL_312	Salmonella phage SE_PL	GCA_011067555.1
APU01771.1	005874	Cluster5620_1clades	74	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01172.1	005874	Cluster5620_1clades	75	ASwh1_106	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53414.1	005874	Cluster5620_1clades	74	65p407	Aeromonas virus 65	GCA_000893255.1
ASR76116.1	005875	Cluster5621_1clades	49	PBI_BELLAMY_71	Synechococcus phage Bellamy	GCA_002627525.1
QDH50649.1	005875	Cluster5621_1clades	75	-	Synechococcus phage S-B43	GCA_006869725.1
QJT70057.1	005875	Cluster5621_1clades	61	SynMITS9220M01_044	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AQW88954.1	005876	SIG+TM	71	BF_0429	Serratia phage BF	GCA_002619745.1
SOK59239.1	005876	SIG+TM	75	g431	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58705.1	005876	SIG+TM	75	g428	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AUE22697.1	005877	Cluster5623_1clades	74	Ah1_00156	Aeromonas phage Ah1	GCA_002957415.1
ADM80139.1	005877	Cluster5623_1clades	73	phiAS5_ORF0296	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17826.1	005877	Cluster5623_1clades	74	Aeh1ORF160c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06156.1	005878	Cluster5624_1clades	74	ABCD_0015	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97024.1	005878	Cluster5624_1clades	67	E_015	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78536.1	005878	Cluster5624_1clades	74	RB43ORF014c	Escherichia virus RB43	GCA_000863505.1
AUE22624.1	005879	Cluster5625_1clades	74	Ah1_00083	Aeromonas phage Ah1	GCA_002957415.1
QAX98351.1	005879	Cluster5625_1clades	74	ASfcp2_5	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52807.1	005879	Cluster5625_1clades	74	PX29p088	Aeromonas phage PX29	GCA_000920195.1
AOO14198.1	005880	Cluster5626_1clades	66	Sn110110_004	Cyanophage S-RIM14	GCA_002599065.1
AOO14850.1	005880	Cluster5626_1clades	66	W1230910_004	Cyanophage S-RIM14	GCA_002599125.1
AGH07534.1	005880	Cluster5626_1clades	74	CYVG_00090	Cyanophage S-SSM6a	GCA_002710385.1
AGH07698.1	005881	Cluster5627_1clades	72	CYVG_00255	Cyanophage S-SSM6a	GCA_002710385.1
AGG54316.1	005881	Cluster5627_1clades	72	CYWG_00032	Cyanophage S-SSM6b	GCA_002710425.1
AIR93611.1	005881	Cluster5627_1clades	74	AVU42_gp066	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIT14125.1	005882	RCC1_2	74	PBI_121Q_235	Escherichia phage 121Q	GCA_000926855.1
AXC36555.1	005882	RCC1_2	74	-	Escherichia phage UB	GCA_003341455.1
SCA80115.1	005882	RCC1_2	74	PSLUR01_00138	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18702.1	005883	Cluster5629_1clades	74	7t3_0181	Salmonella phage 7t3	GCA_006083215.1
AZU97974.1	005883	Cluster5629_1clades	74	CPT_Munch_030	Salmonella phage Munch	GCA_004015485.1
QIG63004.1	005883	Cluster5629_1clades	74	SEPL_391	Salmonella phage SE_PL	GCA_011067555.1
AIX30506.1	005884	Cluster5630_1clades	73	Syn7803US37_29	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76127.1	005884	Cluster5630_1clades	71	PBI_BELLAMY_82	Synechococcus phage Bellamy	GCA_002627525.1
QJT70065.1	005884	Cluster5630_1clades	55	SynMITS9220M01_052	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QCW18886.1	005885	Cluster5631_1clades	73	7t3_0365	Salmonella phage 7t3	GCA_006083215.1
AZU98144.1	005885	Cluster5631_1clades	73	CPT_Munch_200	Salmonella phage Munch	GCA_004015485.1
QIG62839.1	005885	Cluster5631_1clades	73	SEPL_226	Salmonella phage SE_PL	GCA_011067555.1
AIR93513.1	005886	Cluster5632_1clades	72	AVU42_gp176	Prochlorococcus phage P-TIM68	GCA_001503075.1
ASR76235.1	005886	Cluster5632_1clades	66	PBI_BELLAMY_199	Synechococcus phage Bellamy	GCA_002627525.1
QJT70192.1	005886	Cluster5632_1clades	68	SynMITS9220M01_186	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AIT14383.1	005887	Cluster5633_1clades	72	PBI_121Q_493	Escherichia phage 121Q	GCA_000926855.1
QAY00565.1	005887	Cluster5633_1clades	72	Ecwhy1_286	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM62054.1	005887	Cluster5633_1clades	72	EO157G_4650	Escherichia phage SP27	GCA_008033345.1
ANZ49916.1	005888	Cluster5634_1clades	66	MACHINA_278	Erwinia phage Machina	GCA_002758035.1
ANZ49359.1	005888	Cluster5634_1clades	66	HUXLEY_277	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50187.1	005888	Cluster5634_1clades	72	PARSHIK_278	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOO14273.1	005889	Cluster5635_1clades	72	Sn110110_079	Cyanophage S-RIM14	GCA_002599065.1
AOO14922.1	005889	Cluster5635_1clades	72	W1230910_076	Cyanophage S-RIM14	GCA_002599125.1
AGG54309.1	005889	Cluster5635_1clades	67	CYWG_00025	Cyanophage S-SSM6b	GCA_002710425.1
AOO14276.1	005890	Cluster5636_1clades	72	Sn110110_082	Cyanophage S-RIM14	GCA_002599065.1
AOO14925.1	005890	Cluster5636_1clades	72	W1230910_079	Cyanophage S-RIM14	GCA_002599125.1
AGG54307.1	005890	Cluster5636_1clades	69	CYWG_00023	Cyanophage S-SSM6b	GCA_002710425.1
AQW88950.1	005891	Cluster5637_1clades	72	BF_0425	Serratia phage BF	GCA_002619745.1
SOK59236.1	005891	Cluster5637_1clades	72	g428	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58702.1	005891	Cluster5637_1clades	72	g425	Yersinia phage fHe-Yen9-04	GCA_002990485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUE22703.1	005892	Cluster5638_1clades	68	Ah1_00162	Aeromonas phage Ah1	GCA_002957415.1
ADM80146.1	005892	Cluster5638_1clades	71	phiAS5_ORF0303	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17834.1	005892	Cluster5638_1clades	71	Aeh1ORF168c	Aeromonas virus Aeh1	GCA_000843245.1
AFU87896.1	005893	Cluster5639_1clades	71	CcrColossus_gp026	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68566.1	005893	Cluster5639_1clades	71	CcrPW_gp027	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69015.1	005893	Cluster5639_1clades	71	CcrPW_gp476	Caulobacter phage CcrPW	GCA_003443275.1
AMS01251.1	005894	Cluster5640_1clades	71	AR9_g167	Bacillus phage AR9	GCA_001743835.1
ALN97907.1	005894	Cluster5640_1clades	70	Bp8pS_228	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AST99877.1	005894	Cluster5640_1clades	71	PBI_PBS1_55	Bacillus virus PBS1	GCA_002601325.1
ANS06162.1	005895	Cluster5641_1clades	70	ABCD_0112	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97122.1	005895	Cluster5641_1clades	71	E_114	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78634.1	005895	Cluster5641_1clades	70	RB43ORF112c	Escherichia virus RB43	GCA_000863505.1
AQW88706.1	005896	Cluster5642_1clades	71	BF_0181	Serratia phage BF	GCA_002619745.1
SOK58988.1	005896	Cluster5642_1clades	71	g180	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58454.1	005896	Cluster5642_1clades	71	g177	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ASR76149.1	005897	Cluster5643_1clades	71	PBI_BELLAMY_104	Synechococcus phage Bellamy	GCA_002627525.1
QCW22840.1	005897	Cluster5643_1clades	70	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70088.1	005897	Cluster5643_1clades	66	SynMITS9220M01_075	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QCW18714.1	005898	Cluster5644_1clades	71	7t3_0193	Salmonella phage 7t3	GCA_006083215.1
AZU97987.1	005898	Cluster5644_1clades	71	CPT_Munch_043	Salmonella phage Munch	GCA_004015485.1
QIG62992.1	005898	Cluster5644_1clades	71	SEPL_379	Salmonella phage SE_PL	GCA_011067555.1
QCW19125.1	005899	SIG+TM	71	7t3_0610	Salmonella phage 7t3	GCA_006083215.1
AZU98362.1	005899	SIG+TM	71	CPT_Munch_422	Salmonella phage Munch	GCA_004015485.1
QIG62620.1	005899	SIG+TM	71	SEPL_007	Salmonella phage SE_PL	GCA_011067555.1
BBA65647.1	005900	Cluster5646_1clades	71	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65188.1	005900	Cluster5646_1clades	71	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96221.1	005900	Cluster5646_1clades	71	Xoosp13_34	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ABY63021.1	005901	Cluster5647_1clades	69	201phi2-1p191	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76805.1	005901	Cluster5647_1clades	70	PHABIO_174	Pseudomonas phage Phabio	GCA_002624965.1
QJB22670.1	005901	Cluster5647_1clades	71	fnug_27	Pseudomonas phage fnug	GCA_012837215.1
ANM44766.1	005902	Cluster5648_1clades	70	KTN4_008	Pseudomonas phage KTN4	GCA_002607225.1
QJB22651.1	005902	Cluster5648_1clades	69	fnug_8	Pseudomonas phage fnug	GCA_012837215.1
AAL82909.1	005902	Cluster5648_1clades	70	PHIKZ008	Pseudomonas virus phiKZ	GCA_000842965.1
AFU87895.1	005903	Cluster5649_1clades	70	CcrColossus_gp025	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68565.1	005903	Cluster5649_1clades	70	CcrPW_gp026	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69014.1	005903	Cluster5649_1clades	70	CcrPW_gp475	Caulobacter phage CcrPW	GCA_003443275.1
AFU87903.1	005904	Cluster5650_1clades	70	CcrColossus_gp033	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68573.1	005904	Cluster5650_1clades	70	CcrPW_gp034	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69022.1	005904	Cluster5650_1clades	70	CcrPW_gp483	Caulobacter phage CcrPW	GCA_003443275.1
AFU87905.1	005905	TM	70	CcrColossus_gp035	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68575.1	005905	TM	70	CcrPW_gp036	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69024.1	005905	TM	70	CcrPW_gp485	Caulobacter phage CcrPW	GCA_003443275.1
ANS06163.1	005906	Cluster5652_1clades	70	ABCD_0143	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97153.1	005906	Cluster5652_1clades	70	E_145	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78667.1	005906	Cluster5652_1clades	69	RB43ORF145c	Escherichia virus RB43	GCA_000863505.1
AXG67245.1	005907	Cluster5653_1clades	70	AD1_201	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08475.1	005907	Cluster5653_1clades	69	Alexandra_211	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58844.1	005907	Cluster5653_1clades	69	Y3_204	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW19118.1	005908	Cluster5654_1clades	70	7t3_0601	Salmonella phage 7t3	GCA_006083215.1
AZU98355.1	005908	Cluster5654_1clades	70	CPT_Munch_414	Salmonella phage Munch	GCA_004015485.1
QIG62627.1	005908	Cluster5654_1clades	70	SEPL_014	Salmonella phage SE_PL	GCA_011067555.1
QCW18610.1	005909	Cluster5655_1clades	70	7t3_089	Salmonella phage 7t3	GCA_006083215.1
AZU98435.1	005909	Cluster5655_1clades	70	CPT_Munch_503	Salmonella phage Munch	GCA_004015485.1
QIG63078.1	005909	Cluster5655_1clades	70	SEPL_465	Salmonella phage SE_PL	GCA_011067555.1
AGH07619.1	005910	NUDIX	56	CYVG_00176	Cyanophage S-SSM6a	GCA_002710385.1
AAX44433.1	005910	NUDIX	69	PSSM2_055	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12219.1	005910	NUDIX	68	PRTG_00061	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01779.1	005911	Cluster5657_1clades	69	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01179.1	005911	Cluster5657_1clades	67	ASwh1_114	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53422.1	005911	Cluster5657_1clades	69	65p415	Aeromonas virus 65	GCA_000893255.1
AMR59767.1	005912	Cluster5658_1clades	69	SEGD1_120	Enterobacteria phage SEGD1	GCA_002601865.1
QKN85957.1	005912	Cluster5658_1clades	69	ACEC001_1190	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AEP83949.1	005912	Cluster5658_1clades	69	SPN3US_0116	Salmonella phage SPN3US	GCA_001042275.1
AFU87904.1	005913	Cluster5659_1clades	69	CcrColossus_gp034	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68574.1	005913	Cluster5659_1clades	67	CcrPW_gp035	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69023.1	005913	Cluster5659_1clades	67	CcrPW_gp484	Caulobacter phage CcrPW	GCA_003443275.1
AGB06906.1	005914	Cluster5660_1clades	69	CF80_gp119	Vibrio phage VH7D	GCA_000914495.1
AIE13774.1	005914	Cluster5660_1clades	43	-	Vibrio phage nt-1	GCA_000910195.2
QNJ54865.1	005914	Cluster5660_1clades	69	vBValMR10Z_325	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
ANS06164.1	005915	Cluster5661_1clades	69	ABCD_0016	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97025.1	005915	Cluster5661_1clades	53	E_016	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78537.1	005915	Cluster5661_1clades	53	RB43ORF015c	Escherichia virus RB43	GCA_000863505.1
ANS06165.1	005916	Cluster5662_1clades	68	ABCD_0019	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97027.1	005916	Cluster5662_1clades	69	E_018	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78540.1	005916	Cluster5662_1clades	68	RB43ORF018c	Escherichia virus RB43	GCA_000863505.1
AFC21898.1	005917	Cluster5663_1clades	67	GAP32_443	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44027.1	005917	Cluster5663_1clades	67	CBB_464	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88984.1	005917	Cluster5663_1clades	69	BF_0459	Serratia phage BF	GCA_002619745.1
QCW18679.1	005918	Cluster5664_1clades	69	7t3_0158	Salmonella phage 7t3	GCA_006083215.1
AZU97953.1	005918	Cluster5664_1clades	69	CPT_Munch_009	Salmonella phage Munch	GCA_004015485.1
QIG63023.1	005918	Cluster5664_1clades	69	SEPL_410	Salmonella phage SE_PL	GCA_011067555.1
QCW18581.1	005919	Cluster5665_1clades	69	7t3_060	Salmonella phage 7t3	GCA_006083215.1
AZU98409.1	005919	Cluster5665_1clades	69	CPT_Munch_477	Salmonella phage Munch	GCA_004015485.1
QIG63104.1	005919	Cluster5665_1clades	69	SEPL_491	Salmonella phage SE_PL	GCA_011067555.1
QGZ14540.1	005920	Cluster5666_1clades	68	HWC77_gp177	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04194.1	005920	Cluster5666_1clades	68	HWC03_gp039	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23166.1	005920	Cluster5666_1clades	69	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AKF13239.1	005921	Cluster5667_1clades	65	PHIM19_334	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12879.1	005921	Cluster5667_1clades	65	PHIM7_334	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13602.1	005921	Cluster5667_1clades	68	PHIN3_339	Sinorhizobium phage phiN3	GCA_001501175.1
ANS06169.1	005922	Cluster5668_1clades	67	ABCD_0163	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97176.1	005922	Cluster5668_1clades	68	E_168	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78692.1	005922	Cluster5668_1clades	62	RB43ORF170c	Escherichia virus RB43	GCA_000863505.1
AOO14268.1	005923	Cluster5669_1clades	68	Sn110110_074	Cyanophage S-RIM14	GCA_002599065.1
AOO14917.1	005923	Cluster5669_1clades	68	W1230910_071	Cyanophage S-RIM14	GCA_002599125.1
AGG54323.1	005923	Cluster5669_1clades	66	CYWG_00039	Cyanophage S-SSM6b	GCA_002710425.1
QCW18626.1	005924	Cluster5670_1clades	68	7t3_0105	Salmonella phage 7t3	GCA_006083215.1
AZU98451.1	005924	Cluster5670_1clades	68	CPT_Munch_519	Salmonella phage Munch	GCA_004015485.1
QIG63062.1	005924	Cluster5670_1clades	68	SEPL_449	Salmonella phage SE_PL	GCA_011067555.1
AFC21929.1	005925	Cluster5671_1clades	67	GAP32_471	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW89009.1	005925	Cluster5671_1clades	67	BF_0484	Serratia phage BF	GCA_002619745.1
SOK58756.1	005925	Cluster5671_1clades	67	g479	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14140.1	005926	Cluster5672_1clades	67	PBI_121Q_250	Escherichia phage 121Q	GCA_000926855.1
QBO61564.1	005926	Cluster5672_1clades	67	G17_00068	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80130.1	005926	Cluster5672_1clades	67	PSLUR01_00153	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AOV59691.1	005927	Cluster5673_1clades	67	S330809_230	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59453.1	005927	Cluster5673_1clades	67	C440309_230	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59928.1	005927	Cluster5673_1clades	67	N231010_229	Synechococcus phage S-CAM4	GCA_002922155.1
AQW88912.1	005928	Cluster5674_1clades	67	BF_0387	Serratia phage BF	GCA_002619745.1
SOK59201.1	005928	Cluster5674_1clades	60	g393	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58666.1	005928	Cluster5674_1clades	60	g389	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67325.1	005929	Cluster5675_1clades	67	AD1_281	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08552.1	005929	Cluster5675_1clades	67	Alexandra_296	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58925.1	005929	Cluster5675_1clades	65	Y3_285	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW18624.1	005930	Cluster5676_1clades	67	7t3_0103	Salmonella phage 7t3	GCA_006083215.1
AZU98449.1	005930	Cluster5676_1clades	67	CPT_Munch_517	Salmonella phage Munch	GCA_004015485.1
QIG63064.1	005930	Cluster5676_1clades	67	SEPL_451	Salmonella phage SE_PL	GCA_011067555.1
QCW18616.1	005931	SIG+TM	67	7t3_095	Salmonella phage 7t3	GCA_006083215.1
AZU98441.1	005931	SIG+TM	43	CPT_Munch_509	Salmonella phage Munch	GCA_004015485.1
QIG63072.1	005931	SIG+TM	67	SEPL_459	Salmonella phage SE_PL	GCA_011067555.1
AUE22620.1	005932	Cluster5678_1clades	66	Ah1_00079	Aeromonas phage Ah1	GCA_002957415.1
ADM80060.1	005932	Cluster5678_1clades	66	phiAS5_ORF0217	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17747.1	005932	Cluster5678_1clades	66	Aeh1ORF086c	Aeromonas virus Aeh1	GCA_000843245.1
AFQ96656.1	005933	Cluster5679_1clades	66	G173_gp111	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48221.1	005933	Cluster5679_1clades	66	ASESINO_208	Erwinia phage vB_EamM_Asesino	GCA_001744335.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ50633.1	005933	Cluster5679_1clades	66	STRATTON_208	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
QBP07607.1	005934	Cluster5680_1clades	66	DERBICUS_181	Erwinia phage Derbicus	GCA_004521655.1
ANZ49031.1	005934	Cluster5680_1clades	66	EARLPHILLIPIV_182	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50379.1	005934	Cluster5680_1clades	65	PHOBOS_189	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AQW89004.1	005935	Cluster5681_1clades	66	BF_0479	Serratia phage BF	GCA_002619745.1
SOK59286.1	005935	Cluster5681_1clades	66	g478	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58751.1	005935	Cluster5681_1clades	66	g474	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AXG67244.1	005936	Cluster5682_1clades	66	AD1_200	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08474.1	005936	Cluster5682_1clades	66	Alexandra_210	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58843.1	005936	Cluster5682_1clades	66	Y3_203	Erwinia phage vB_EamM_Y3	GCA_002955045.1
BBA65264.1	005937	Cluster5683_1clades	66	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65723.1	005937	Cluster5683_1clades	66	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96303.1	005937	Cluster5683_1clades	65	Xoosp13_116	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QCW19110.1	005938	Cluster5684_1clades	66	7t3_0593	Salmonella phage 7t3	GCA_006083215.1
AZU98347.1	005938	Cluster5684_1clades	65	CPT_Munch_406	Salmonella phage Munch	GCA_004015485.1
QIG62635.1	005938	Cluster5684_1clades	66	SEPL_022	Salmonella phage SE_PL	GCA_011067555.1
ANS06171.1	005939	Cluster5685_1clades	65	ABCD_0150	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97162.1	005939	Cluster5685_1clades	64	E_154	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78678.1	005939	Cluster5685_1clades	65	RB43ORF156c	Escherichia virus RB43	GCA_000863505.1
AFC21847.1	005940	Cluster5686_1clades	65	GAP32_395	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43968.1	005940	Cluster5686_1clades	65	CBB_405	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88927.1	005940	Cluster5686_1clades	65	BF_0402	Serratia phage BF	GCA_002619745.1
AFU87900.1	005941	Cluster5687_1clades	65	CcrColossus_gp030	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68570.1	005941	Cluster5687_1clades	65	CcrPW_gp031	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69019.1	005941	Cluster5687_1clades	65	CcrPW_gp480	Caulobacter phage CcrPW	GCA_003443275.1
AFC21474.1	005942	Cluster5688_1clades	64	GAP32_026	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43595.1	005942	Cluster5688_1clades	65	CBB_30	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44146.1	005942	Cluster5688_1clades	65	CBB_583	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ANZ49838.1	005943	Cluster5689_1clades	65	MACHINA_200	Erwinia phage Machina	GCA_002758035.1
ANZ49282.1	005943	Cluster5689_1clades	65	HUXLEY_200	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50110.1	005943	Cluster5689_1clades	65	PARSHIK_201	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOV59505.1	005944	Cluster5690_1clades	65	S330809_044	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59267.1	005944	Cluster5690_1clades	65	C440309_044	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59743.1	005944	Cluster5690_1clades	65	N231010_044	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67250.1	005945	Cluster5691_1clades	65	AD1_206	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08480.1	005945	Cluster5691_1clades	65	Alexandra_216	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58850.1	005945	Cluster5691_1clades	65	Y3_210	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXQ69068.1	005946	Cluster5692_1clades	65	CcrBL9_gp044	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69628.1	005946	Cluster5692_1clades	65	CcrSC_gp046	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70128.1	005946	Cluster5692_1clades	65	CcrSC_gp546	Caulobacter phage CcrSC	GCA_003443315.1
AUZ95393.1	005947	Cluster5693_1clades	58	FDI40_gp634	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69432.1	005947	Cluster5693_1clades	65	CcrBL9_gp408	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69984.1	005947	Cluster5693_1clades	65	CcrSC_gp402	Caulobacter phage CcrSC	GCA_003443315.1
BBA65722.1	005948	Cluster5694_1clades	65	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65263.1	005948	Cluster5694_1clades	65	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96302.1	005948	Cluster5694_1clades	64	Xoosp13_115	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBM62036.1	005949	SIG+TM	64	EO157G_4470	Escherichia phage SP27	GCA_008033345.1
QBO61939.1	005949	SIG+TM	65	G17_00450	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80352.1	005949	SIG+TM	63	PSLUR01_00375	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAQ64205.1	005950	Cluster5696_1clades	64	KVP40.0134	Vibrio phage KVP40	GCA_000843785.1
AGN30182.1	005950	Cluster5696_1clades	64	VPFG_00182	Vibrio phage nt-1	GCA_000910195.2
AFN37365.1	005950	Cluster5696_1clades	64	pp2_132	Vibriophage phi-pp2	GCA_002630725.1
AAX44431.1	005951	Cluster5697_1clades	64	PSSM2_053	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12220.1	005951	Cluster5697_1clades	64	PRTG_00062	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93597.1	005951	Cluster5697_1clades	60	AVU42_gp047	Prochlorococcus phage P-TIM68	GCA_001503075.1
AFU87902.1	005952	Cluster5698_1clades	64	CcrColossus_gp032	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68572.1	005952	Cluster5698_1clades	64	CcrPW_gp033	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69021.1	005952	Cluster5698_1clades	64	CcrPW_gp482	Caulobacter phage CcrPW	GCA_003443275.1
AIT14108.1	005953	SIG+TM	64	PBI_121Q_218	Escherichia phage 121Q	GCA_000926855.1
BBM61790.1	005953	SIG+TM	64	EO157G_2010	Escherichia phage SP27	GCA_008033345.1
QBO61591.1	005953	SIG+TM	64	G17_00095	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AKF12969.1	005954	Cluster5700_1clades	64	PHIM19_62	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12609.1	005954	Cluster5700_1clades	64	PHIM7_61	Sinorhizobium phage phiM7	GCA_002622405.1
AKZ65594.1	005954	Cluster5700_1clades	64	PHIN3_77	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13172.1	005955	Cluster5701_1clades	64	PHIM19_267	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12812.1	005955	Cluster5701_1clades	64	PHIM7_267	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13535.1	005955	Cluster5701_1clades	64	PHIN3_272	Sinorhizobium phage phiN3	GCA_001501175.1
ANS06172.1	005956	Cluster5702_1clades	64	ABCD_0252	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97270.1	005956	Cluster5702_1clades	63	E_262	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78792.1	005956	Cluster5702_1clades	63	RB43ORF270w	Escherichia virus RB43	GCA_000863505.1
ANZ49654.1	005957	Cluster5703_1clades	64	MACHINA_9	Erwinia phage Machina	GCA_002758035.1
ANZ49098.1	005957	Cluster5703_1clades	64	HUXLEY_9	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49927.1	005957	Cluster5703_1clades	64	PARSHIK_9	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOV59672.1	005958	Cluster5704_1clades	64	S330809_211	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59434.1	005958	Cluster5704_1clades	57	C440309_211	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59909.1	005958	Cluster5704_1clades	57	N231010_210	Synechococcus phage S-CAM4	GCA_002922155.1
AQW89015.1	005959	SMAD	64	BF_0490	Serratia phage BF	GCA_002619745.1
SOK59296.1	005959	SMAD	64	g488	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58761.1	005959	SMAD	64	g484	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AYD81382.1	005960	Cluster5706_1clades	64	SEA_JUSTBECAUSE_227	Streptomyces phage JustBecause	GCA_003613775.1
QJD53786.1	005960	Cluster5706_1clades	64	SEA_KELA_226	Streptomyces phage Kela	GCA_012934305.1
AXH66372.1	005960	Cluster5706_1clades	64	SEA_SATIS_223	Streptomyces phage Satis	GCA_003366315.1
ANS06173.1	005961	MED14	63	ABCD_0056	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97068.1	005961	MED14	63	E_059	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78578.1	005961	MED14	63	RB43ORF056w	Escherichia virus RB43	GCA_000863505.1
ANS06174.1	005962	Cluster5708_1clades	63	ABCD_0116	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97127.1	005962	Cluster5708_1clades	63	E_119	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78639.1	005962	Cluster5708_1clades	63	RB43ORF117c	Escherichia virus RB43	GCA_000863505.1
ANS06179.1	005963	DUF2685	59	ABCD_0219	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97235.1	005963	DUF2685	60	E_227	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78752.1	005963	DUF2685	63	RB43ORF230w	Escherichia virus RB43	GCA_000863505.1
AFC21952.1	005964	Cluster5710_1clades	63	GAP32_493	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44078.1	005964	Cluster5710_1clades	63	CBB_515	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW89035.1	005964	Cluster5710_1clades	59	BF_0510	Serratia phage BF	GCA_002619745.1
QMV29031.1	005965	Cluster5711_1clades	63	AP1_0324	Aeromonas phage AP1	GCA_014183365.1
ASU00330.1	005965	Cluster5711_1clades	63	HWB28_gp222	Aeromonas phage AS-zj	GCA_002627665.1
AFN39195.1	005965	Cluster5711_1clades	63	CC2_055	Aeromonas phage CC2	GCA_000903495.1
AGR47848.2	005966	Cluster5712_1clades	63	SmphiM12_216	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13053.1	005966	Cluster5712_1clades	63	PHIM19_148	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12694.1	005966	Cluster5712_1clades	63	PHIM7_148	Sinorhizobium phage phiM7	GCA_002622405.1
AFO71446.1	005967	Cluster5713_1clades	62	CR5_226	Cronobacter phage CR5	GCA_000910235.1
QBP07660.1	005967	Cluster5713_1clades	63	DERBICUS_234	Erwinia phage Derbicus	GCA_004521655.1
ANZ49084.1	005967	Cluster5713_1clades	63	EARLPHILLIPIV_235	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49900.1	005968	Cluster5714_1clades	63	MACHINA_262	Erwinia phage Machina	GCA_002758035.1
ANZ49343.1	005968	Cluster5714_1clades	63	HUXLEY_261	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50171.1	005968	Cluster5714_1clades	63	PARSHIK_262	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
QCW18895.1	005969	Cluster5716_1clades	63	7t3_0374	Salmonella phage 7t3	GCA_006083215.1
AZU98153.1	005969	Cluster5716_1clades	63	CPT_Munch_209	Salmonella phage Munch	GCA_004015485.1
QIG62830.1	005969	Cluster5716_1clades	63	SEPL_217	Salmonella phage SE_PL	GCA_011067555.1
QCW19076.1	005970	Cluster5717_1clades	63	7t3_0556	Salmonella phage 7t3	GCA_006083215.1
AZU98319.1	005970	Cluster5717_1clades	63	CPT_Munch_375	Salmonella phage Munch	GCA_004015485.1
QIG62665.1	005970	Cluster5717_1clades	63	SEPL_052	Salmonella phage SE_PL	GCA_011067555.1
QAX98650.1	005971	SIG+TM	62	ASfcp2_318	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52792.1	005971	SIG+TM	62	PX29p073	Aeromonas phage PX29	GCA_000920195.1
ADM80047.1	005971	SIG+TM	62	phiAS5_ORF0204	Aeromonas phage phiAS5	GCA_000887715.1
QAY00772.1	005972	Cluster5719_1clades	62	Ecwhy1_498	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34950.1	005972	Cluster5719_1clades	62	ACQ29_gp270	Escherichia phage PBECO4	GCA_001041035.1
AXC37052.1	005972	Cluster5719_1clades	62	-	Escherichia phage UB	GCA_003341455.1
AGR47847.2	005973	Cluster5720_1clades	62	SmphiM12_215	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13052.1	005973	Cluster5720_1clades	62	PHIM19_147	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12693.1	005973	Cluster5720_1clades	62	PHIM7_147	Sinorhizobium phage phiM7	GCA_002622405.1
QCW19096.1	005974	Cluster5721_1clades	62	7t3_0578	Salmonella phage 7t3	GCA_006083215.1
AZU98335.1	005974	Cluster5721_1clades	62	CPT_Munch_393	Salmonella phage Munch	GCA_004015485.1
QIG62648.1	005974	Cluster5721_1clades	62	SEPL_035	Salmonella phage SE_PL	GCA_011067555.1
QAY00785.1	005975	Cluster5722_1clades	62	Ecwhy1_512	Escherichia phage Ecwhy_1	GCA_004146585.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBM61822.1	005975	Cluster5722_1clades	62	EO157G_2330	Escherichia phage SP27	GCA_008033345.1
SCA80135.1	005975	Cluster5722_1clades	62	PSLUR01_00158	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QBP07532.1	005976	SIG+TM	62	DERBICUS_106	Erwinia phage Derbicus	GCA_004521655.1
ANZ48955.1	005976	SIG+TM	51	EARLPHILLIPIV_106	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50297.1	005976	SIG+TM	52	PHOBOS_107	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AIX30683.1	005977	TM	42	Syn7803US37_206	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76283.1	005977	TM	42	PBI_BELLAMY_247	Synechococcus phage Bellamy	GCA_002627525.1
QCW23033.1	005977	TM	62	-	Synechococcus phage S-B05	GCA_006083695.1
ANS06175.1	005978	Cluster5725_1clades	61	ABCD_0136	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97144.1	005978	Cluster5725_1clades	61	E_136	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78659.1	005978	Cluster5725_1clades	61	RB43ORF137c	Escherichia virus RB43	GCA_000863505.1
ATN94592.1	005979	Cluster5726_1clades	61	SL2_015	Pseudomonas phage SL2	GCA_002956015.1
QEM42104.1	005979	Cluster5726_1clades	61	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26366.1	005979	Cluster5726_1clades	61	PHIKZ295.1	Pseudomonas virus phiKZ	GCA_000842965.1
AXQ69067.1	005980	Cluster5727_1clades	61	CcrBL9_gp043	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69627.1	005980	Cluster5727_1clades	61	CcrSC_gp045	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70127.1	005980	Cluster5727_1clades	61	CcrSC_gp545	Caulobacter phage CcrSC	GCA_003443315.1
QCW19087.1	005981	SIG+TM	61	7t3_0569	Salmonella phage 7t3	GCA_006083215.1
AZU98326.1	005981	SIG+TM	61	CPT_Munch_384	Salmonella phage Munch	GCA_004015485.1
QIG62657.1	005981	SIG+TM	61	SEPL_044	Salmonella phage SE_PL	GCA_011067555.1
AGR48043.1	005982	Cluster5729_1clades	60	SmphiM12_411	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13227.1	005982	Cluster5729_1clades	60	PHIM19_322	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12867.1	005982	Cluster5729_1clades	60	PHIM7_322	Sinorhizobium phage phiM7	GCA_002622405.1
AKF12916.1	005983	Cluster5730_1clades	60	PHIM19_9	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12556.1	005983	Cluster5730_1clades	60	PHIM7_8	Sinorhizobium phage phiM7	GCA_002622405.1
AKZ65591.1	005983	Cluster5730_1clades	60	PHIN3_19	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13223.1	005984	TM	60	PHIM19_318	Sinorhizobium phage phiM19	GCA_002605865.1
AKZ65590.1	005984	TM	60	PHIM7_318	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13586.1	005984	TM	60	PHIN3_323	Sinorhizobium phage phiN3	GCA_001501175.1
ANS06176.1	005985	Ruc-ZnR	60	ABCD_0008	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97016.1	005985	Ruc-ZnR	54	E_007	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78529.1	005985	Ruc-ZnR	53	RB43ORF007c	Escherichia virus RB43	GCA_000863505.1
AOV59593.1	005986	Cluster5733_1clades	60	S330809_132	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59355.1	005986	Cluster5733_1clades	60	C440309_132	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59831.1	005986	Cluster5733_1clades	60	N231010_132	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18722.1	005987	Cluster5734_1clades	60	7t3_0201	Salmonella phage 7t3	GCA_006083215.1
AZU97994.1	005987	Cluster5734_1clades	60	CPT_Munch_050	Salmonella phage Munch	GCA_004015485.1
QIG62985.1	005987	Cluster5734_1clades	60	SEPL_372	Salmonella phage SE_PL	GCA_011067555.1
QCW18884.1	005988	Cluster5735_1clades	60	7t3_0363	Salmonella phage 7t3	GCA_006083215.1
AZU98142.1	005988	Cluster5735_1clades	60	CPT_Munch_198	Salmonella phage Munch	GCA_004015485.1
QIG62841.1	005988	Cluster5735_1clades	60	SEPL_228	Salmonella phage SE_PL	GCA_011067555.1
QCW19028.1	005989	Cluster5736_1clades	60	7t3_0508	Salmonella phage 7t3	GCA_006083215.1
AZU98275.1	005989	Cluster5736_1clades	60	CPT_Munch_331	Salmonella phage Munch	GCA_004015485.1
QIG62709.1	005989	Cluster5736_1clades	60	SEPL_096	Salmonella phage SE_PL	GCA_011067555.1
QCW19119.1	005990	SIG+DUF2076	60	7t3_0602	Salmonella phage 7t3	GCA_006083215.1
AZU98356.1	005990	SIG+DUF2076	60	CPT_Munch_415	Salmonella phage Munch	GCA_004015485.1
QIG62626.1	005990	SIG+DUF2076	60	SEPL_013	Salmonella phage SE_PL	GCA_011067555.1
AJK27553.1	005991	Cluster5738_1clades	59	PTIM40_126	Cyanophage P-TIM40	GCA_001470935.1
AGG54407.1	005991	Cluster5738_1clades	56	CYWG_00123	Cyanophage S-SSM6b	GCA_002710425.1
AIR93472.1	005991	Cluster5738_1clades	57	AVU42_gp135	Prochlorococcus phage P-TIM68	GCA_001503075.1
AKF13139.1	005992	Cluster5739_1clades	59	PHIM19_234	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12778.1	005992	Cluster5739_1clades	59	PHIM7_233	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13507.1	005992	Cluster5739_1clades	59	PHIN3_244	Sinorhizobium phage phiN3	GCA_001501175.1
AOV59511.1	005993	Cluster5740_1clades	37	S330809_050	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59273.1	005993	Cluster5740_1clades	37	C440309_050	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59749.1	005993	Cluster5740_1clades	59	N231010_050	Synechococcus phage S-CAM4	GCA_002922155.1
AMM43581.1	005994	Cluster5741_1clades	55	CBB_16	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44132.1	005994	Cluster5741_1clades	55	CBB_569	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88548.1	005994	Cluster5741_1clades	59	BF_0023	Serratia phage BF	GCA_002619745.1
QCW18721.1	005995	Cluster5742_1clades	59	7t3_0200	Salmonella phage 7t3	GCA_006083215.1
AZU97993.1	005995	Cluster5742_1clades	59	CPT_Munch_049	Salmonella phage Munch	GCA_004015485.1
QIG62986.1	005995	Cluster5742_1clades	59	SEPL_373	Salmonella phage SE_PL	GCA_011067555.1
BBA65220.1	005996	DHDPS	59	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65679.1	005996	DHDPS	59	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96248.1	005996	DHDPS	59	Xoosp13_61	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QAY00783.1	005997	Cluster5744_1clades	57	Ecwhy1_510	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61825.1	005997	Cluster5744_1clades	59	EO157G_2360	Escherichia phage SP27	GCA_008033345.1
SCA80139.1	005997	Cluster5744_1clades	59	PSLUR01_00162	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
ADQ52788.1	005998	Cluster5745_1clades	58	PX29p069	Aeromonas phage PX29	GCA_000920195.1
ADM80044.1	005998	Cluster5745_1clades	56	phiAS5_ORF0201	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17732.1	005998	Cluster5745_1clades	57	Aeh1ORF072c	Aeromonas virus Aeh1	GCA_000843245.1
AFC21468.1	005999	Cluster5746_1clades	58	GAP32_020	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43589.1	005999	Cluster5746_1clades	58	CBB_24	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44140.1	005999	Cluster5746_1clades	47	CBB_577	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AKF13125.1	006000	SIG+TM	58	PHIM19_220	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12764.1	006000	SIG+TM	34	PHIM7_219	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13494.1	006000	SIG+TM	34	PHIN3_231	Sinorhizobium phage phiN3	GCA_001501175.1
ANZ49771.1	006001	SIG+TM	58	MACHINA_133	Erwinia phage Machina	GCA_002758035.1
ANZ49215.1	006001	SIG+TM	58	HUXLEY_133	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50043.1	006001	SIG+TM	58	PARSHIK_134	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOV59622.1	006002	Cluster5749_1clades	51	S330809_161	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59384.1	006002	Cluster5749_1clades	51	C440309_161	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59860.1	006002	Cluster5749_1clades	58	N231010_161	Synechococcus phage S-CAM4	GCA_002922155.1
ASU03681.1	006003	Cluster5750_1clades	58	JOAD_234	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03438.1	006003	Cluster5750_1clades	58	RISINGSUN_232	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CAG27283.1	006003	Cluster5750_1clades	58	PPEV_gp189	Pseudomonas phage EL	GCA_000866825.1
ANM44772.1	006004	Cluster5751_1clades	57	KTN4_014	Pseudomonas phage KTN4	GCA_002607225.1
QBX32279.1	006004	Cluster5751_1clades	58	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41853.1	006004	Cluster5751_1clades	58	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AUE22794.1	006005	Cluster5752_1clades	57	Ah1_00276	Aeromonas phage Ah1	GCA_002957415.1
QAX98509.1	006005	Cluster5752_1clades	57	ASfcp2_173	Aeromonas phage AsFcp_2	GCA_004146885.1
AAQ17920.1	006005	Cluster5752_1clades	57	Aeh1ORF257c	Aeromonas virus Aeh1	GCA_000843245.1
ANZ49836.1	006006	Cluster5753_1clades	57	MACHINA_198	Erwinia phage Machina	GCA_002758035.1
ANZ49280.1	006006	Cluster5753_1clades	57	HUXLEY_198	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50108.1	006006	Cluster5753_1clades	57	PARSHIK_199	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANS06181.1	006007	Cluster5754_1clades	55	ABCD_0231	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97248.1	006007	Cluster5754_1clades	57	E_240	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78767.1	006007	Cluster5754_1clades	55	RB43ORF245w	Escherichia virus RB43	GCA_000863505.1
AOV59683.1	006008	Cluster5755_1clades	57	S330809_222	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59445.1	006008	Cluster5755_1clades	57	C440309_222	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59920.1	006008	Cluster5755_1clades	57	N231010_221	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18552.1	006009	Cluster5756_1clades	57	7t3_027	Salmonella phage 7t3	GCA_006083215.1
AZU98381.1	006009	Cluster5756_1clades	57	CPT_Munch_447	Salmonella phage Munch	GCA_004015485.1
QIG63131.1	006009	Cluster5756_1clades	57	SEPL_518	Salmonella phage SE_PL	GCA_011067555.1
BBA65656.1	006010	Cluster5757_1clades	54	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65197.1	006010	Cluster5757_1clades	54	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96227.1	006010	Cluster5757_1clades	57	Xoosp13_40	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QAX98380.1	006011	Cluster5758_1clades	56	ASfcp2_34	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52833.1	006011	Cluster5758_1clades	56	PX29p114	Aeromonas phage PX29	GCA_000920195.1
AAQ17780.1	006011	Cluster5758_1clades	56	Aeh1ORF118c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64164.1	006012	Cluster5759_1clades	56	KVP40.0093	Vibrio phage KVP40	GCA_000843785.1
QBX05995.1	006012	Cluster5759_1clades	56	ValB1HC_041	Vibrio phage ValB1 HC	GCA_004771355.1
AJT61008.1	006012	Cluster5759_1clades	56	AVU32_gp167	Vibrio phage ValKK3	GCA_001501635.1
AUE22586.1	006013	Cluster5760_1clades	56	Ah1_00045	Aeromonas phage Ah1	GCA_002957415.1
QAX98623.1	006013	Cluster5760_1clades	56	ASfcp2_290	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52763.1	006013	Cluster5760_1clades	56	PX29p044	Aeromonas phage PX29	GCA_000920195.1
AOV59543.1	006014	Cluster5761_1clades	56	S330809_081	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59305.1	006014	Cluster5761_1clades	56	C440309_081	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59781.1	006014	Cluster5761_1clades	56	N231010_081	Synechococcus phage S-CAM4	GCA_002922155.1
ARV77375.1	006015	Cluster5762_1clades	56	NOXIFER_206	Pseudomonas phage Noxifer	GCA_002625005.1
QBX32535.1	006015	Cluster5762_1clades	56	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42109.1	006015	Cluster5762_1clades	56	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW18671.1	006016	Cluster5763_1clades	56	7t3_0150	Salmonella phage 7t3	GCA_006083215.1
AZU97948.1	006016	Cluster5763_1clades	56	CPT_Munch_004	Salmonella phage Munch	GCA_004015485.1
QIG63027.1	006016	Cluster5763_1clades	56	SEPL_414	Salmonella phage SE_PL	GCA_011067555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCW18775.1	006017	Cluster5764_1clades	56	7t3_0254	Salmonella phage 7t3	GCA_006083215.1
AZU98040.1	006017	Cluster5764_1clades	56	CPT_Munch_096	Salmonella phage Munch	GCA_004015485.1
QIG62940.1	006017	Cluster5764_1clades	56	SEPL_327	Salmonella phage SE_PL	GCA_011067555.1
QCW18629.1	006018	Cluster5765_1clades	56	7t3_0108	Salmonella phage 7t3	GCA_006083215.1
AZU98454.1	006018	Cluster5765_1clades	56	CPT_Munch_522	Salmonella phage Munch	GCA_004015485.1
QIG63060.1	006018	Cluster5765_1clades	56	SEPL_447	Salmonella phage SE_PL	GCA_011067555.1
QCW18631.1	006019	Cluster5766_1clades	56	7t3_0110	Salmonella phage 7t3	GCA_006083215.1
AZU98456.1	006019	Cluster5766_1clades	56	CPT_Munch_524	Salmonella phage Munch	GCA_004015485.1
QIG63058.1	006019	Cluster5766_1clades	56	SEPL_445	Salmonella phage SE_PL	GCA_011067555.1
AIR93459.1	006020	Cluster5767_1clades	55	AVU42_gp120	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCW22901.1	006020	Cluster5767_1clades	56	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50586.1	006020	Cluster5767_1clades	56	-	Synechococcus phage S-B43	GCA_006869725.1
BBA65272.1	006021	Cluster5768_1clades	53	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65731.1	006021	Cluster5768_1clades	53	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96312.1	006021	Cluster5768_1clades	56	Xoosp13_125	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QIG63583.1	006022	Cluster5769_1clades	56	DAC19_92	Bacteroides phage DAC19	GCA_013387715.1
QIG63844.1	006022	Cluster5769_1clades	56	DAC20_91	Bacteroides phage DAC20	GCA_013387725.1
QIG64106.1	006022	Cluster5769_1clades	56	DAC22_92	Bacteroides phage DAC22	GCA_013387735.1
AKF13197.2	006023	Cluster5770_1clades	55	PHIM19_292	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12837.1	006023	Cluster5770_1clades	55	PHIM7_292	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13558.2	006023	Cluster5770_1clades	55	PHIN3_295	Sinorhizobium phage phiN3	GCA_001501175.1
AQW88594.1	006024	Cluster5771_1clades	55	BF_0069	Serratia phage BF	GCA_002619745.1
SOK58870.1	006024	Cluster5771_1clades	52	g062	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58333.1	006024	Cluster5771_1clades	52	g056	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18694.1	006025	Cluster5772_1clades	55	7t3_0173	Salmonella phage 7t3	GCA_006083215.1
AZU97967.1	006025	Cluster5772_1clades	53	CPT_Munch_023	Salmonella phage Munch	GCA_004015485.1
QIG63011.1	006025	Cluster5772_1clades	55	SEPL_398	Salmonella phage SE_PL	GCA_011067555.1
AUE22641.1	006026	Cluster5773_1clades	54	Ah1_00100	Aeromonas phage Ah1	GCA_002957415.1
QAX98369.1	006026	Cluster5773_1clades	54	ASfcp2_23	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52823.1	006026	Cluster5773_1clades	54	PX29p104	Aeromonas phage PX29	GCA_000920195.1
ATI17281.1	006027	SIG+TM	53	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97722.1	006027	SIG+TM	53	ASswx1_76	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39182.1	006027	SIG+TM	54	CC2_036	Aeromonas phage CC2	GCA_000903495.1
AGH56942.1	006028	Cluster5775_1clades	54	CPXG_00139	Cyanophage P-RSM6	GCA_000906155.1
AGH07610.1	006028	Cluster5775_1clades	54	CYVG_00167	Cyanophage S-SSM6a	GCA_002710385.1
ASR76114.1	006028	Cluster5775_1clades	46	PBI_BELLAMY_69	Synechococcus phage Bellamy	GCA_002627525.1
AOV59481.1	006029	Cluster5776_1clades	54	S330809_020	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59243.1	006029	Cluster5776_1clades	54	C440309_020	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59719.1	006029	Cluster5776_1clades	54	N231010_020	Synechococcus phage S-CAM4	GCA_002922155.1
AXG67081.1	006030	Cluster5777_1clades	54	AD1_037	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08314.1	006030	Cluster5777_1clades	54	Alexandra_34	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58678.1	006030	Cluster5777_1clades	51	Y3_038	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QCW19130.1	006031	Cluster5778_1clades	54	7t3_0615	Salmonella phage 7t3	GCA_006083215.1
AZU98367.1	006031	Cluster5778_1clades	54	CPT_Munch_427	Salmonella phage Munch	GCA_004015485.1
QIG62615.1	006031	Cluster5778_1clades	54	SEPL_002	Salmonella phage SE_PL	GCA_011067555.1
QCW18608.1	006032	Cluster5779_1clades	54	7t3_087	Salmonella phage 7t3	GCA_006083215.1
AZU98433.1	006032	Cluster5779_1clades	54	CPT_Munch_501	Salmonella phage Munch	GCA_004015485.1
QIG63080.1	006032	Cluster5779_1clades	54	SEPL_467	Salmonella phage SE_PL	GCA_011067555.1
QCW19115.1	006033	Cluster5780_1clades	53	7t3_0598	Salmonella phage 7t3	GCA_006083215.1
AZU98352.1	006033	Cluster5780_1clades	53	CPT_Munch_411	Salmonella phage Munch	GCA_004015485.1
QIG62630.1	006033	Cluster5780_1clades	53	SEPL_017	Salmonella phage SE_PL	GCA_011067555.1
QAU04315.1	006034	Cluster5781_1clades	53	HWC03_gp160	Vibrio phage 2 TSL-2019	GCA_006964105.1
QCW23263.1	006034	Cluster5781_1clades	53	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47465.1	006034	Cluster5781_1clades	53	HWC35_gp071	Vibrio phage USC-1	GCA_006864065.1
AFC21466.1	006035	TM	36	GAP32_018A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43587.1	006035	TM	52	CBB_22	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44138.1	006035	TM	52	CBB_575	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AOV59516.1	006036	Cluster5783_1clades	52	S330809_055	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59278.1	006036	Cluster5783_1clades	52	C440309_055	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59754.1	006036	Cluster5783_1clades	52	N231010_055	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59506.1	006037	Cluster5784_1clades	45	S330809_045	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59268.1	006037	Cluster5784_1clades	45	C440309_045	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59744.1	006037	Cluster5784_1clades	52	N231010_045	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18891.1	006038	Cluster5785_1clades	52	7t3_0370	Salmonella phage 7t3	GCA_006083215.1
AZU98149.1	006038	Cluster5785_1clades	52	CPT_Munch_205	Salmonella phage Munch	GCA_004015485.1
QIG62834.1	006038	Cluster5785_1clades	52	SEPL_221	Salmonella phage SE_PL	GCA_011067555.1
QMV29028.1	006039	Cluster5786_1clades	52	AP1_0321	Aeromonas phage AP1	GCA_014183365.1
ATI17263.1	006039	Cluster5786_1clades	45	-	Aeromonas phage AS-szw	GCA_002743635.1
QAY01431.1	006039	Cluster5786_1clades	52	ASwh1_372	Aeromonas phage Aswh_1	GCA_004146945.1
AAQ64215.1	006040	Cluster5787_1clades	51	KVP40.0145	Vibrio phage KVP40	GCA_000843785.1
QHJ74326.1	006040	Cluster5787_1clades	51	VH12019_00407	Vibrio phage VH1_2019	GCA_009931825.1
ALP47709.1	006040	Cluster5787_1clades	51	phiST2_0011	Vibrio phage phi-ST2	GCA_002757135.1
AFC21859.1	006041	Cluster5788_1clades	51	GAP32_406	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
SOK59227.1	006041	Cluster5788_1clades	49	g419	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58693.1	006041	Cluster5788_1clades	49	g416	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AOV59526.1	006042	Cluster5789_1clades	51	S330809_065	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59288.1	006042	Cluster5789_1clades	51	C440309_065	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59764.1	006042	Cluster5789_1clades	51	N231010_065	Synechococcus phage S-CAM4	GCA_002922155.1
QCW19120.1	006043	Cluster5790_1clades	51	7t3_0603	Salmonella phage 7t3	GCA_006083215.1
AZU98357.1	006043	Cluster5790_1clades	51	CPT_Munch_416	Salmonella phage Munch	GCA_004015485.1
QIG62625.1	006043	Cluster5790_1clades	51	SEPL_012	Salmonella phage SE_PL	GCA_011067555.1
QCW18634.1	006044	Cluster5791_1clades	51	7t3_0113	Salmonella phage 7t3	GCA_006083215.1
AZU98459.1	006044	Cluster5791_1clades	50	CPT_Munch_527	Salmonella phage Munch	GCA_004015485.1
QIG63055.1	006044	Cluster5791_1clades	51	SEPL_442	Salmonella phage SE_PL	GCA_011067555.1
ANS06183.1	006045	Cluster5792_1clades	50	ABCD_0088	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97102.1	006045	Cluster5792_1clades	50	E_094	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78610.1	006045	Cluster5792_1clades	50	RB43ORF088w	Escherichia virus RB43	GCA_000863505.1
AGR47682.1	006046	Cluster5793_1clades	50	SmphiM12_050	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12944.1	006046	Cluster5793_1clades	50	PHIM19_37	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12584.1	006046	Cluster5793_1clades	50	PHIM7_36	Sinorhizobium phage phiM7	GCA_002622405.1
AQW88964.1	006047	Cluster5794_1clades	50	BF_0439	Serratia phage BF	GCA_002619745.1
SOK59251.1	006047	Cluster5794_1clades	50	g443	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58716.1	006047	Cluster5794_1clades	50	g439	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QCW18556.1	006048	Cluster5795_1clades	50	7t3_031	Salmonella phage 7t3	GCA_006083215.1
AZU98385.1	006048	Cluster5795_1clades	50	CPT_Munch_451	Salmonella phage Munch	GCA_004015485.1
QIG63127.1	006048	Cluster5795_1clades	50	SEPL_514	Salmonella phage SE_PL	GCA_011067555.1
QBX06667.1	006049	Cluster5796_1clades	50	BcepSaruman_254	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74637.1	006049	Cluster5796_1clades	50	BcepSauron_257	Burkholderia phage BcepSauron	GCA_005394215.1
BAG41655.1	006049	Cluster5796_1clades	50	RSL1_ORF206	Ralstonia phage phiRSL1	GCA_000879455.1
ANS06186.1	006050	Cluster5797_1clades	48	ABCD_0166	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97178.1	006050	Cluster5797_1clades	48	E_170	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78696.1	006050	Cluster5797_1clades	49	RB43ORF174c	Escherichia virus RB43	GCA_000863505.1
AFC21575.1	006051	Cluster5798_1clades	49	GAP32_125	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43692.1	006051	Cluster5798_1clades	49	CBB_127	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88645.1	006051	Cluster5798_1clades	45	BF_0120	Serratia phage BF	GCA_002619745.1
ATN94605.1	006052	Cluster5799_1clades	49	SL2_028	Pseudomonas phage SL2	GCA_002956015.1
QJB22985.1	006052	Cluster5799_1clades	49	fnug_342	Pseudomonas phage fnug	GCA_012837215.1
AGC26361.1	006052	Cluster5799_1clades	49	PHIKZ290.1	Pseudomonas virus phiKZ	GCA_000842965.1
AJK27491.1	006053	TM	43	PTIM40_64	Cyanophage P-TIM40	GCA_001470935.1
AGH07676.1	006053	TM	49	CYVG_00233	Cyanophage S-SSM6a	GCA_002710385.1
AAX44654.1	006053	TM	42	PSSM2_277	Prochlorococcus phage P-SSM2	GCA_000859585.1
AOV59594.1	006054	Cluster5801_1clades	49	S330809_133	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59356.1	006054	Cluster5801_1clades	49	C440309_133	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59832.1	006054	Cluster5801_1clades	49	N231010_133	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18703.1	006055	Cluster5802_1clades	49	7t3_0182	Salmonella phage 7t3	GCA_006083215.1
AZU97975.1	006055	Cluster5802_1clades	49	CPT_Munch_031	Salmonella phage Munch	GCA_004015485.1
QIG63003.1	006055	Cluster5802_1clades	49	SEPL_390	Salmonella phage SE_PL	GCA_011067555.1
ANS06185.1	006056	Cluster5803_1clades	48	ABCD_0145	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97155.1	006056	Cluster5803_1clades	48	E_147	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78671.1	006056	Cluster5803_1clades	48	RB43ORF149c	Escherichia virus RB43	GCA_000863505.1
AFC21884.1	006057	Cluster5804_1clades	48	GAP32_431	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44013.1	006057	Cluster5804_1clades	48	CBB_450	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88971.1	006057	Cluster5804_1clades	47	BF_0446	Serratia phage BF	GCA_002619745.1
AGR48009.1	006058	Cluster5805_1clades	48	SmphiM12_376	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13194.1	006058	Cluster5805_1clades	48	PHIM19_289	Sinorhizobium phage phiM19	GCA_002605865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF12834.1	006058	Cluster5805_1clades	48	PHIM7_289	Sinorhizobium phage phiM7	GCA_002622405.1
QBP07604.1	006059	Cluster5806_1clades	48	DERBICUS_178	Erwinia phage Derbicus	GCA_004521655.1
ANZ49027.1	006059	Cluster5806_1clades	48	EARLPHILLIPIV_178	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50375.1	006059	Cluster5806_1clades	46	PHOBOS_185	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
QAY00507.1	006060	Cluster5807_1clades	48	Ecwhy1_228	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM62114.1	006060	Cluster5807_1clades	41	EO157G_5250	Escherichia phage SP27	GCA_008033345.1
QDF13901.1	006060	Cluster5807_1clades	41	vBEcoMphAPEC6_gp276c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
ANS06187.1	006061	Cluster5808_1clades	47	ABCD_0020	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97028.1	006061	Cluster5808_1clades	47	E_019	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78541.1	006061	Cluster5808_1clades	47	RB43ORF019c	Escherichia virus RB43	GCA_000863505.1
ANZ49721.1	006062	Cluster5809_1clades	47	MACHINA_83	Erwinia phage Machina	GCA_002758035.1
ANZ49166.1	006062	Cluster5809_1clades	47	HUXLEY_84	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49994.1	006062	Cluster5809_1clades	47	PARSHIK_85	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOV59611.1	006063	Cluster5810_1clades	47	S330809_150	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59373.1	006063	Cluster5810_1clades	47	C440309_150	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59849.1	006063	Cluster5810_1clades	47	N231010_150	Synechococcus phage S-CAM4	GCA_002922155.1
AYD80091.1	006064	Cluster5811_1clades	47	JA11_286	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66692.1	006064	Cluster5811_1clades	47	JA13_289	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG67661.1	006064	Cluster5811_1clades	47	JA33_287	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QCW18906.1	006065	Cluster5812_1clades	47	7t3_0385	Salmonella phage 7t3	GCA_006083215.1
AZU98163.1	006065	Cluster5812_1clades	47	CPT_Munch_219	Salmonella phage Munch	GCA_004015485.1
QIG62821.1	006065	Cluster5812_1clades	47	SEPL_208	Salmonella phage SE_PL	GCA_011067555.1
QAX98388.1	006066	Cluster5813_1clades	46	ASfcp2_43	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52842.1	006066	Cluster5813_1clades	46	PX29p123	Aeromonas phage PX29	GCA_000920195.1
AAQ17789.1	006066	Cluster5813_1clades	46	Aeh1hmmORF02c	Aeromonas virus Aeh1	GCA_000843245.1
ANS06188.1	006067	SIG+TM	46	ABCD_0183	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97197.1	006067	SIG+TM	46	E_189	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78714.1	006067	SIG+TM	46	RB43ORF192c	Escherichia virus RB43	GCA_000863505.1
ANS06189.1	006068	Cluster5815_1clades	46	ABCD_0184	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97198.1	006068	Cluster5815_1clades	46	E_190	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78716.1	006068	Cluster5815_1clades	46	RB43ORF194c	Escherichia virus RB43	GCA_000863505.1
AOV59533.1	006069	Cluster5816_1clades	42	S330809_072	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59295.1	006069	Cluster5816_1clades	46	C440309_072	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59771.1	006069	Cluster5816_1clades	46	N231010_072	Synechococcus phage S-CAM4	GCA_002922155.1
QCW18707.1	006070	Cluster5817_1clades	46	7t3_0186	Salmonella phage 7t3	GCA_006083215.1
AZU97979.1	006070	Cluster5817_1clades	46	CPT_Munch_035	Salmonella phage Munch	GCA_004015485.1
QIG62999.1	006070	Cluster5817_1clades	46	SEPL_386	Salmonella phage SE_PL	GCA_011067555.1
QBX32283.1	006071	Cluster5818_1clades	46	-	Pseudomonas phage PA1C	GCA_004785505.1
QBJ02882.1	006071	Cluster5818_1clades	46	PSA21_356	Pseudomonas phage Psa21	GCA_004340405.1
QEM41856.1	006071	Cluster5818_1clades	46	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AKF13199.1	006072	TM	34	PHIM19_294	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12840.1	006072	TM	34	PHIM7_294	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13560.1	006072	TM	45	PHIN3_297	Sinorhizobium phage phiN3	GCA_001501175.1
QBP07494.1	006073	Cluster5820_1clades	45	DERBICUS_68	Erwinia phage Derbicus	GCA_004521655.1
ANZ48918.1	006073	Cluster5820_1clades	45	EARLPHILLIPIV_68	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ50259.1	006073	Cluster5820_1clades	45	PHOBOS_69	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AOV59486.1	006074	Cluster5821_1clades	45	S330809_025	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59248.1	006074	Cluster5821_1clades	45	C440309_025	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59724.1	006074	Cluster5821_1clades	45	N231010_025	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59524.1	006075	Cluster5822_1clades	45	S330809_063	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59286.1	006075	Cluster5822_1clades	45	C440309_063	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59762.1	006075	Cluster5822_1clades	45	N231010_063	Synechococcus phage S-CAM4	GCA_002922155.1
ANS06190.1	006076	Cluster5823_1clades	44	ABCD_0270	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97290.1	006076	Cluster5823_1clades	44	E_282	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78810.1	006076	Cluster5823_1clades	44	RB43ORF288c	Escherichia virus RB43	GCA_000863505.1
QCW18669.1	006077	Cluster5824_1clades	43	7t3_0148	Salmonella phage 7t3	GCA_006083215.1
AZU97946.1	006077	Cluster5824_1clades	43	CPT_Munch_002	Salmonella phage Munch	GCA_004015485.1
QIG63029.1	006077	Cluster5824_1clades	43	SEPL_416	Salmonella phage SE_PL	GCA_011067555.1
AIX30515.1	006078	Cluster5825_1clades	42	Syn7803US37_38	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54697.1	006078	Cluster5825_1clades	41	b23_0082	Synechococcus phage B23	GCA_009745195.1
QGT54327.1	006078	Cluster5825_1clades	41	b3_0083	Synechococcus phage B3	GCA_009745215.1
ANM45011.1	006079	Cluster5826_1clades	41	KTN4_253	Pseudomonas phage KTN4	GCA_002607225.1
ATN94703.1	006079	Cluster5826_1clades	41	SL2_126	Pseudomonas phage SL2	GCA_002956015.1
AGC26344.1	006079	Cluster5826_1clades	41	PHIKZ210.1	Pseudomonas virus phiKZ	GCA_000842965.1
AHI60237.1	006080	Cluster5827_1clades	40	Ea357_086	Erwinia phage Ea35-70	GCA_000914635.1
ANH52188.1	006080	Cluster5827_1clades	40	DM_90	Erwinia phage vB_EamM_Deimos-Minion	GCA_002624325.1
AUG86838.1	006080	Cluster5827_1clades	40	MORTIMER_89	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AKF12911.1	006081	Cluster5828_1clades	40	PHIM19_4	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12551.1	006081	Cluster5828_1clades	40	PHIM7_3	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13281.1	006081	Cluster5828_1clades	40	PHIN3_14	Sinorhizobium phage phiN3	GCA_001501175.1
AKN19828.1	006082	Cluster5829_1clades	40	PHIM19_120	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12665.1	006082	Cluster5829_1clades	40	PHIM7_119	Sinorhizobium phage phiM7	GCA_002622405.1
AKZ65598.1	006082	Cluster5829_1clades	40	PHIN3_133	Sinorhizobium phage phiN3	GCA_001501175.1
QMV28928.1	006083	Cluster5830_1clades	39	AP1_0221	Aeromonas phage AP1	GCA_014183365.1
ASU00536.1	006083	Cluster5830_1clades	39	HWB28_gp016	Aeromonas phage AS-zj	GCA_002627665.1
AFN39271.1	006083	Cluster5830_1clades	39	CC2_274	Aeromonas phage CC2	GCA_000903495.1
AIF27786.1	006084	Cluster5831_1clades	39	SmphiM12_325	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13148.1	006084	Cluster5831_1clades	39	PHIM19_243	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12787.1	006084	Cluster5831_1clades	39	PHIM7_242	Sinorhizobium phage phiM7	GCA_002622405.1
AOV59577.1	006085	Cluster5832_1clades	39	S330809_116	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59339.1	006085	Cluster5832_1clades	39	C440309_116	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59815.1	006085	Cluster5832_1clades	39	N231010_116	Synechococcus phage S-CAM4	GCA_002922155.1
QAX97029.1	006086	Cluster5833_1clades	39	-	Vibrio phage vB_VmeM-Yong MS32	GCA_009769855.1
QAX96075.1	006086	Cluster5833_1clades	39	-	Vibrio phage vB_VmeM-Yong XC31	GCA_009769875.1
QAX96393.1	006086	Cluster5833_1clades	39	-	Vibrio phage vB_VmeM-Yong XC32	GCA_009769895.1
AFQ96621.1	006087	Cluster5834_1clades	38	G173_gp076	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48185.1	006087	Cluster5834_1clades	34	ASESINO_172	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50598.1	006087	Cluster5834_1clades	35	STRATTON_173	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AKF13029.1	006088	Cluster5835_1clades	38	PHIM19_124	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12669.1	006088	Cluster5835_1clades	38	PHIM7_123	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13400.1	006088	Cluster5835_1clades	38	PHIN3_137	Sinorhizobium phage phiN3	GCA_001501175.1
ANZ49806.1	006089	TM	38	MACHINA_168	Erwinia phage Machina	GCA_002758035.1
ANZ49250.1	006089	TM	38	HUXLEY_168	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50078.1	006089	TM	38	PARSHIK_169	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AOV59541.1	006090	Cluster5837_1clades	38	S330809_080	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59303.1	006090	Cluster5837_1clades	38	C440309_080	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59779.1	006090	Cluster5837_1clades	38	N231010_080	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59581.1	006091	Cluster5838_1clades	37	S330809_120	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59343.1	006091	Cluster5838_1clades	37	C440309_120	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59819.1	006091	Cluster5838_1clades	37	N231010_120	Synechococcus phage S-CAM4	GCA_002922155.1
AOV59661.1	006092	TM	37	S330809_200	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59423.1	006092	TM	37	C440309_200	Synechococcus phage S-CAM4	GCA_002922145.1
AOV59898.1	006092	TM	37	N231010_199	Synechococcus phage S-CAM4	GCA_002922155.1
BBA65171.1	006093	Cluster5840_1clades	37	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65630.1	006093	Cluster5840_1clades	37	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96204.1	006093	Cluster5840_1clades	37	Xoosp13_17	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AKF13218.1	006094	Cluster5841_1clades	35	PHIM19_313	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12859.1	006094	Cluster5841_1clades	35	PHIM7_313	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13581.1	006094	Cluster5841_1clades	35	PHIN3_318	Sinorhizobium phage phiN3	GCA_001501175.1
ANZ49837.1	006095	Cluster5842_1clades	35	MACHINA_199	Erwinia phage Machina	GCA_002758035.1
ANZ49281.1	006095	Cluster5842_1clades	35	HUXLEY_199	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ50109.1	006095	Cluster5842_1clades	35	PARSHIK_200	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
AKF13062.1	006096	Cluster5843_1clades	33	PHIM19_157	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12703.1	006096	Cluster5843_1clades	33	PHIM7_157	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13432.1	006096	Cluster5843_1clades	33	PHIN3_169	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13086.1	006097	Cluster5844_1clades	33	PHIM19_181	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12726.1	006097	Cluster5844_1clades	33	PHIM7_181	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13455.1	006097	Cluster5844_1clades	33	PHIN3_192	Sinorhizobium phage phiN3	GCA_001501175.1
AKF12917.1	006098	Cluster5845_1clades	32	PHIM19_10	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12557.1	006098	Cluster5845_1clades	31	PHIM7_9	Sinorhizobium phage phiM7	GCA_002622405.1
AKZ65592.1	006098	Cluster5845_1clades	32	PHIN3_20	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13022.1	006099	Cluster5846_1clades	32	PHIM19_116	Sinorhizobium phage phiM19	GCA_002605865.1
AKZ65588.1	006099	Cluster5846_1clades	32	PHIM7_115	Sinorhizobium phage phiM7	GCA_002622405.1
AKZ65597.1	006099	Cluster5846_1clades	32	PHIN3_129	Sinorhizobium phage phiN3	GCA_001501175.1
AKF12980.1	006100	Cluster5847_1clades	31	PHIM19_73	Sinorhizobium phage phiM19	GCA_002605865.1

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AKF12620.1	006100	Cluster5847_1clades	31	PHIM7_72	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13352.1	006100	Cluster5847_1clades	31	PHIN3_88	Sinorhizobium phage phiN3	GCA_001501175.1
QMV29045.1	006101	Cluster5848_1clades	31	AP1_0338	Aeromonas phage AP1	GCA_014183365.1
ATI17315.1	006101	Cluster5848_1clades	31	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97758.1	006101	Cluster5848_1clades	31	ASswx1_113	Aeromonas phage Asswx_1	GCA_004146865.1
AIT14188.1	006102	Cluster5849_1clades	30	PBI_121Q_298	Escherichia phage 121Q	GCA_000926855.1
QBO61518.1	006102	Cluster5849_1clades	30	G17_00022	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62124.1	006102	Cluster5849_1clades	30	G17_00635	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AFU87639.1	006103	Cluster5850_1clades	27	CcrKarma_gp122	Caulobacter virus Karma	GCA_000901575.1
AFU87288.1	006103	Cluster5850_1clades	27	CcrMagneto_gp118	Caulobacter virus Magneto	GCA_000903095.1
AFU88435.1	006103	Cluster5850_1clades	27	CcrSwift_gp117	Caulobacter virus Swift	GCA_000899655.1
BBA65473.1	006104	FN3	3313	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96482.1	006104	FN3	3245	Xoosp13_296	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90616.1	006105	Cluster7503_1clades	39	HYO65_gp224	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90922.1	006105	Cluster7503_1clades	39	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBA65532.1	006106	BetaPropeller+BetaPropeller	2823	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96529.1	006106	BetaPropeller+BetaPropeller	1796	Xoosp13_343	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ97325.1	006107	Cluster5853_1clades	2794	D6_0166	Aeromonas phage D6	GCA_007051205.2
QDH47007.1	006107	Cluster5853_1clades	2794	LAh10_87	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000715	006108	SidE	823	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000484	006108	SidE	2605	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBZ72050.1	006109	Beta-helix	2111	SEA_KRADAL_154	Streptomyces phage Kradal	GCA_004799925.1
AXH66313.1	006109	Beta-helix	2111	SEA_SATIS_154	Streptomyces phage Satis	GCA_003366315.1
AYD81319.1	006110	Beta-helix	1778	SEA_JUSTBECAUSE_154	Streptomyces phage JustBecause	GCA_003613775.1
QJD53722.1	006110	Beta-helix	1778	SEA_KELA_152	Streptomyces phage Kela	GCA_012934305.1
prevph1000000081	006111	DNA_pol_phi	1152	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000064	006111	DNA_pol_phi	1688	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AJK27632.1	006112	DUF4114	1458	PTIM40_226	Cyanophage P-TIM40	GCA_001470935.1
AGH56814.1	006112	DUF4114	1269	CPXG_00011	Cyanophage P-RSM6	GCA_000906155.1
AAX44678.1	006113	Cluster5864_1clades	1326	PSSM2_301	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12298.1	006113	Cluster5864_1clades	1326	PRTG_00145	Prochlorococcus phage P-SSM5	GCA_002991095.1
BBI90398.1	006114	Cluster5865_1clades	1314	HYO65_gp006	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90705.1	006114	Cluster5865_1clades	1314	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54937.1	006115	TMs	1294	b23_0324	Synechococcus phage B23	GCA_009745195.1
QGT54572.1	006115	TMs	1230	b3_0331	Synechococcus phage B3	GCA_009745215.1
AUZ95088.1	006116	Peptidase-S8+IG	1251	FDI40_gp329	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72796.1	006116	Peptidase-S8+IG	714	-	Myoviridae sp.	GCA_003657725.1
AGH56936.1	006117	Cluster5868_1clades	1240	CPXG_00133	Cyanophage P-RSM6	GCA_000906155.1
AJK27520.1	006117	Cluster5868_1clades	1231	PTIM40_93	Cyanophage P-TIM40	GCA_001470935.1
AFH14764.1	006118	Cluster5869_1clades	1052	Lu11_0227	Pseudomonas phage Lu11	GCA_000897175.1
AGS82115.1	006118	Cluster5869_1clades	1216	PaBG_00241	Pseudomonas phage PaBG	GCA_000912555.1
CCH63641.1	006119	Cluster5870_1clades	1214	CP21_179	Campylobacter virus CP21	GCA_000902535.1
QAU04565.1	006119	Cluster5870_1clades	662	ValB1MD_285	Vibrio phage ValB1MD	GCA_004138815.1
AAX44413.1	006120	Cluster5871_1clades	1147	PSSM2_035	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12238.1	006120	Cluster5871_1clades	1147	PRTG_00080	Prochlorococcus phage P-SSM5	GCA_002991095.1
QNH80847.1	006121	Cluster5873_1clades	976	D6_0167	Aeromonas phage D6	GCA_007051205.2
QDH47017.1	006121	Cluster5873_1clades	1077	LAh10_88	Aeromonas phage LAh10	GCA_006863975.1
QCG76183.1	006122	Phage_fiber	1006	EST35_0302	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AXH71039.1	006123	Cluster5875_1clades	488	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI20948.1	006123	Cluster5875_1clades	1008	-	Vibrio phage vB_pir03	GCA_014319855.1
AAX44661.1	006124	Cluster5876_1clades	1001	PSSM2_284	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12314.1	006124	Cluster5876_1clades	1001	PRTG_00161	Prochlorococcus phage P-SSM5	GCA_002991095.1
BBA65416.1	006125	FN3	977	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96439.1	006125	FN3	978	Xoosp13_253	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65469.1	006126	VgrG+DUF2345	926	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96478.1	006126	VgrG+DUF2345	978	Xoosp13_292	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGG54360.1	006127	TM+TM+TM	974	CYWG_00076	Cyanophage S-SSM6b	GCA_002710425.1
ASR76060.1	006127	TM+TM+TM	798	PBI_BELLAMY_13	Synechococcus phage Bellamy	GCA_002627525.1
BBA65450.1	006128	TM+TM+TM	918	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96465.1	006128	TM+TM+TM	907	Xoosp13_279	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AOO14401.1	006129	Cluster5882_1clades	915	Sn110110_208	Cyanophage S-RIM14	GCA_002599065.1
AOO15050.1	006129	Cluster5882_1clades	915	W1230910_205	Cyanophage S-RIM14	GCA_002599125.1
CCH63657.1	006130	SF2-DUF3427A	304	CP21_195	Campylobacter virus CP21	GCA_000902535.1
QAU04529.1	006130	SF2-DUF3427A	896	ValB1MD_212	Vibrio phage ValB1MD	GCA_004138815.1
prevph1000000700	006131	Apolipoprotein	243	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000477	006131	Apolipoprotein	852	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QNH80839.1	006132	Cluster5887_1clades	636	D6_0031	Aeromonas phage D6	GCA_007051205.2
QDH47022.1	006132	Cluster5887_1clades	800	LAh10_198	Aeromonas phage LAh10	GCA_006863975.1
QDJ96676.1	006133	Cluster5888_1clades	769	PS1_0165	Aeromonas phage PS1	GCA_007051165.2
QFR59310.1	006133	Cluster5888_1clades	769	PS2_0169	Aeromonas phage PS2	GCA_009388305.2
ATA65355.1	006134	Cluster5891_1clades	757	2050HW_00020	Serratia phage 2050HW	GCA_002628125.1
QDB71142.1	006134	Cluster5891_1clades	757	CPT_Moabite_112	Serratia phage Moabite	GCA_006384735.1
AAX44397.1	006135	DUF1351	752	PSSM2_019	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12253.1	006135	DUF1351	752	PRTG_00096	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93561.1	006136	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	741	psaA	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93562.1	006136	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	737	psaB	Prochlorococcus phage P-TIM68	GCA_001503075.1
ATA65377.1	006137	CheC	727	2050HW_00042	Serratia phage 2050HW	GCA_002628125.1
QDB71161.1	006137	CheC	727	CPT_Moabite_131	Serratia phage Moabite	GCA_006384735.1
AXQ69413.1	006138	Cluster5896_1clades	719	CcrBL9_gp389	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69970.1	006138	Cluster5896_1clades	722	CcrSC_gp388	Caulobacter phage CcrSC	GCA_003443315.1
BAW19065.1	006139	Cluster5897_1clades	706	FDH28_gp091	Ralstonia phage RP12	GCA_002617345.1
BAW19350.1	006139	Cluster5897_1clades	706	-	Ralstonia phage RP31	GCA_002617365.1
BBA65544.1	006140	ROT	695	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96539.1	006140	ROT	702	Xoosp13_353	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BAW19262.1	006141	Cluster5899_1clades	691	FDH28_gp133	Ralstonia phage RP12	GCA_002617345.1
BAW19549.1	006141	Cluster5899_1clades	693	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000033	006142	SIG+PLUG+OmpA-beta-barrel	685	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000025	006142	SIG+PLUG+OmpA-beta-barrel	685	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAS05021.2	006143	Atrophin-1	681	AVU11_gp229	Ralstonia phage RSF1	GCA_001500875.1
BAQ02751.1	006143	Atrophin-1	648	AVU38_gp223	Ralstonia phage RSL2	GCA_001503055.1
AUZ95438.1	006144	Cluster5903_1clades	663	FDI40_gp698	Agrobacterium phage Atu_ph07	GCA_002628245.1
QCG76016.1	006144	Cluster5903_1clades	674	EST35_0134	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
prevph1000000514	006145	Cluster5904_1clades	598	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000388	006145	Cluster5904_1clades	672	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBX06684.1	006146	Cluster5905_1clades	668	BcepSaruman_271	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74654.1	006146	Cluster5905_1clades	668	BcepSauron_274	Burkholderia phage BcepSauron	GCA_005394215.1
AAX44503.1	006147	Cluster5906_1clades	663	PSSM2_125	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12463.1	006147	Cluster5906_1clades	663	PRTG_00316	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXH70812.1	006148	Cluster5907_1clades	655	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21050.1	006148	Cluster5907_1clades	645	-	Vibrio phage vB_pir03	GCA_014319855.1
AND75180.1	006149	SIG+Portal	530	ME3_19	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83680.1	006149	SIG+Portal	648	0306phi8-36p122	Bacillus phage 0305phi8-36	GCA_000871045.1
ASV44139.1	006150	COOHNH2ligase	647	PBI_SCTP2_124	Salicola phage SCTP-2	GCA_002625545.1
ASV44140.1	006150	COOHNH2ligase	606	PBI_SCTP2_125	Salicola phage SCTP-2	GCA_002625545.1
BBI90524.1	006151	Cluster5911_1clades	642	HYO65_gp132	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90832.1	006151	Cluster5911_1clades	642	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000499	006152	Cluster5912_1clades	639	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000379	006152	Cluster5912_1clades	639	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXH72857.1	006153	A18	634	-	Myoviridae sp.	GCA_003657725.1
ASV44098.1	006153	A18	606	PBI_SCTP2_83	Salicola phage SCTP-2	GCA_002625545.1
BBI90682.1	006154	Cluster5914_1clades	629	HYO65_gp290	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90989.1	006154	Cluster5914_1clades	629	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06682.1	006155	Cluster5915_1clades	629	BcepSaruman_269	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74652.1	006155	Cluster5915_1clades	629	BcepSauron_272	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65468.1	006156	Cluster5916_1clades	615	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96477.1	006156	Cluster5916_1clades	626	Xoosp13_291	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06835.1	006157	Cluster5917_1clades	617	BcepSaruman_422	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74804.1	006157	Cluster5917_1clades	617	BcepSauron_424	Burkholderia phage BcepSauron	GCA_005394215.1
AXH70909.1	006158	Cluster5918_1clades	605	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70970.1	006158	Cluster5918_1clades	611	-	Vibrio phage BONAISHI	GCA_003441475.1
QBX06726.1	006159	DUF2855	611	BcepSaruman_313	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74694.1	006159	DUF2855	611	BcepSauron_314	Burkholderia phage BcepSauron	GCA_005394215.1
AIA64964.1	006160	TM+TM	610	S13_165	Cronobacter phage S13	GCA_001503575.1
QHJ78970.1	006160	TM+TM	609	-	Myoviridae sp.	GCA_012593985.1
BAW19139.1	006161	Cluster5921_1clades	609	FDH28_gp256	Ralstonia phage RP12	GCA_002617345.1

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BAW19425.1	006161	Cluster5921_1clades	609	-	Ralstonia phage RP31	GCA_002617365.1
CCH63645.1	006162	Cluster5922_1clades	230	CP21_183	Campylobacter virus CP21	GCA_000902535.1
QAU04566.1	006162	Cluster5922_1clades	607	ValB1MD_286	Vibrio phage ValB1MD	GCA_004138815.1
ATA65461.1	006163	Cluster5923_1clades	605	2050HW_00126	Serratia phage 2050HW	GCA_002628125.1
QDB71230.1	006163	Cluster5923_1clades	605	CPT_Moabite_200	Serratia phage Moabite	GCA_006384735.1
BAW18979.1	006164	Cluster5924_1clades	605	FDH28_gp005	Ralstonia phage RP12	GCA_002617345.1
BAW19267.1	006164	Cluster5924_1clades	605	-	Ralstonia phage RP31	GCA_002617365.1
BAS04978.1	006165	TM	576	AVU11_gp186	Ralstonia phage RSF1	GCA_001500875.1
BAQ02704.1	006165	TM	596	AVU38_gp176	Ralstonia phage RSL2	GCA_001503055.1
AMS01280.1	006166	Beta-helix	590	AR9_g196	Bacillus phage AR9	GCA_001743835.1
AST99908.1	006166	Beta-helix	590	PBI_PBS1_86	Bacillus virus PBS1	GCA_002601325.1
ABS83700.1	006167	CW-binding-EndolysinC+CW-binding-EndolysinC	558	0305phi8-36p142	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83767.1	006167	CW-binding-EndolysinC+CW-binding-EndolysinC	585	0305phi8-36p209	Bacillus phage 0305phi8-36	GCA_000871045.1
QBX06488.1	006168	Cluster5928_1clades	576	BcepSaruman_075	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74455.1	006168	Cluster5928_1clades	576	BcepSauron_075	Burkholderia phage BcepSauron	GCA_005394215.1
AAX44588.1	006169	Cluster5929_1clades	573	PSSM2_211	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12383.1	006169	Cluster5929_1clades	573	PRTG_00230	Prochlorococcus phage P-SSM5	GCA_002991095.1
prevph1000000638	006170	FTHFS	574	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000454	006170	FTHFS	574	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19252.1	006171	Cluster5931_1clades	567	FDH28_gp143	Ralstonia phage RP12	GCA_002617345.1
BAW19538.1	006171	Cluster5931_1clades	567	-	Ralstonia phage RP31	GCA_002617365.1
BBA65230.1	006172	Cluster5933_1clades	553	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65689.1	006172	Cluster5933_1clades	553	-	Xanthomonas phage XacN1	GCA_003173815.1
prevph1000000067	006173	SF2-DUF3427A	554	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000053	006173	SF2-DUF3427A	554	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19126.1	006174	CarboxypepD-reg-IG	552	FDH28_gp269	Ralstonia phage RP12	GCA_002617345.1
BAW19412.1	006174	CarboxypepD-reg-IG	552	-	Ralstonia phage RP31	GCA_002617365.1
AMS01167.1	006175	PVC-AAA	548	AR9_g083	Bacillus phage AR9	GCA_001743835.1
ASU00098.1	006175	PVC-AAA	548	PBI_PBS1_276	Bacillus virus PBS1	GCA_002601325.1
QBX32205.1	006176	Cluster5938_1clades	541	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41782.1	006176	Cluster5938_1clades	541	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54734.1	006177	SIG+IG	541	b23_0119	Synechococcus phage B23	GCA_009745195.1
QGT54364.1	006177	SIG+IG	541	b3_0120	Synechococcus phage B3	GCA_009745215.1
BAW19050.1	006178	RADICAL-SAM	537	FDH28_gp076	Ralstonia phage RP12	GCA_002617345.1
BAW19335.1	006178	RADICAL-SAM	537	-	Ralstonia phage RP31	GCA_002617365.1
QBX06734.1	006179	Cluster5941_1clades	517	BcepSaruman_321	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74703.1	006179	Cluster5941_1clades	537	BcepSauron_323	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54888.1	006180	Cluster5942_1clades	535	b23_0275	Synechococcus phage B23	GCA_009745195.1
QGT54523.1	006180	Cluster5942_1clades	535	b3_0282	Synechococcus phage B3	GCA_009745215.1
QBZ72051.1	006181	Collagen	532	SEA_KRADAL_155	Streptomyces phage Kradal	GCA_004799925.1
AXH66314.1	006181	Collagen	532	SEA_SATIS_155	Streptomyces phage Satis	GCA_003366315.1
prevph1000000438	006182	Cluster5944_1clades	531	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000350	006182	Cluster5944_1clades	531	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBI90510.1	006183	Cluster5945_1clades	526	HYO65_gp118	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90818.1	006183	Cluster5945_1clades	526	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54664.1	006184	PcfJ	525	b23_0036	Synechococcus phage B23	GCA_009745195.1
QGT54294.1	006184	PcfJ	526	b3_0036	Synechococcus phage B3	GCA_009745215.1
AXH70890.1	006185	Cluster5947_1clades	372	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70891.1	006185	Cluster5947_1clades	525	-	Vibrio phage BONAISHI	GCA_003441475.1
QDJ97318.1	006186	Tox-HNH-DHNNK+TM+TM+TM+TM	524	D6_0158	Aeromonas phage D6	GCA_007051205.2
QDH47042.1	006186	Tox-HNH-DHNNK+TM+TM+TM+TM	524	LAh10_80	Aeromonas phage LAh10	GCA_006863975.1
BAW19209.1	006187	Cluster5951_1clades	518	FDH28_gp186	Ralstonia phage RP12	GCA_002617345.1
BAW19495.1	006187	Cluster5951_1clades	518	-	Ralstonia phage RP31	GCA_002617365.1
AAX44395.1	006188	SIG+Tail-fiber	516	PSSM2_017	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12254.1	006188	SIG+Tail-fiber	517	PRTG_00098	Prochlorococcus phage P-SSM5	GCA_002991095.1
prevph1000000287	006189	Cluster5953_1clades	355	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000225	006189	Cluster5953_1clades	515	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDJ96794.1	006190	Cluster5954_1clades	510	PS1_0035	Aeromonas phage PS1	GCA_007051165.2
QFR59425.1	006190	Cluster5954_1clades	510	PS2_0034	Aeromonas phage PS2	GCA_009388305.2
ASU03804.1	006191	Cluster5955_1clades	506	JOAD_111	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03559.1	006191	Cluster5955_1clades	506	RISINGSUN_111	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
BBI90577.1	006192	Cluster5956_1clades	459	HYO65_gp185	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90885.1	006192	Cluster5956_1clades	506	-	Tenacibaculum phage PTm5	GCA_009730715.1
AAX44692.1	006193	Cluster5957_1clades	504	PSSM2_315	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12284.1	006193	Cluster5957_1clades	504	PRTG_00131	Prochlorococcus phage P-SSM5	GCA_002991095.1
CCH63618.1	006194	CTP_transf_like	503	CP21_156	Campylobacter virus CP21	GCA_000902535.1
QAU04508.1	006194	CTP_transf_like	484	ValB1MD_166	Vibrio phage ValB1MD	GCA_004138815.1
SOK59169.1	000000	CTP_transf_like	52	g361	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AUZ95019.1	000000	CTP_transf_like	208	FDI40_gp237	Agrobacterium phage Atu_ph07	GCA_002628245.1
prevph1000000818	006195	Cluster5960_1clades	502	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000561	006195	Cluster5960_1clades	502	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXH70769.1	006196	Cluster5961_1clades	477	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI20985.1	006196	Cluster5961_1clades	498	-	Vibrio phage vB_pir03	GCA_014319855.1
AXH70906.1	006197	Cluster5962_1clades	494	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70905.1	006197	Cluster5962_1clades	496	-	Vibrio phage BONAISHI	GCA_003441475.1
BAW19013.1	006198	Cluster5963_1clades	492	FDH28_gp039	Ralstonia phage RP12	GCA_002617345.1
BAW19299.1	006198	Cluster5963_1clades	492	-	Ralstonia phage RP31	GCA_002617365.1
ABS83681.1	006199	CCDC158	489	0306phi8-36p123	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83808.1	006199	CCDC158	257	0305phi8-36p123*	Bacillus phage 0305phi8-36	GCA_000871045.1
AUZ95335.1	006200	Cluster5966_1clades	484	FDI40_gp576	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95333.1	006200	Cluster5966_1clades	486	FDI40_gp574	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04937.1	006201	Cluster5967_1clades	481	AVU11_gp145	Ralstonia phage RSF1	GCA_001500875.1
BAQ02661.2	006201	Cluster5967_1clades	482	-	Ralstonia phage RSL2	GCA_001503055.1
AXQ69510.1	006202	Cluster5968_1clades	249	CcrBL9_gp486	Caulobacter phage CcrBL9	GCA_003443295.1
QCG76086.1	006202	Cluster5968_1clades	482	EST35_0205	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QDH83686.1	006203	BetaPropeller	436	H1O15_gp275	Achromobacter phage Motura	GCA_006964305.1
BAG41554.1	006203	BetaPropeller	480	hss	Ralstonia phage phiRSL1	GCA_000879455.1
BAW19221.1	006204	Cluster5971_1clades	478	FDH28_gp174	Ralstonia phage RP12	GCA_002617345.1
BAW19507.1	006204	Cluster5971_1clades	478	-	Ralstonia phage RP31	GCA_002617365.1
QIW90785.1	000000	SIG+DUF669	306	GCAPEGMB_00467	Vibrio phage V07	GCA_012361095.1
ASV44483.1	006205	Cluster5973_1clades	477	PBI_SCTP2_468	Salicola phage SCTP-2	GCA_002625545.1
AFF28161.1	006205	Cluster5973_1clades	416	PAU_163	Sphingomonas phage PAU	GCA_000902455.1
BAW19213.1	006206	Cluster5974_1clades	474	FDH28_gp182	Ralstonia phage RP12	GCA_002617345.1
BAW19499.1	006206	Cluster5974_1clades	474	-	Ralstonia phage RP31	GCA_002617365.1
AAX44589.1	006207	Cluster5975_1clades	470	PSSM2_212	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12382.1	006207	Cluster5975_1clades	470	PRTG_00229	Prochlorococcus phage P-SSM5	GCA_002991095.1
AEO93565.1	006208	SIG+AGT	469	G_306	Bacillus virus G	GCA_000917535.1
AEO93572.1	006208	SIG+AGT	460	G_313	Bacillus virus G	GCA_000917535.1
BBA65495.1	006209	Cluster5977_1clades	468	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96503.1	006209	Cluster5977_1clades	467	Xoosp13_317	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06581.1	006210	Cluster5978_1clades	467	BcepSaruman_168	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74547.1	006210	Cluster5978_1clades	467	BcepSauron_167	Burkholderia phage BcepSauron	GCA_005394215.1
AMO43129.1	006211	Cluster5979_1clades	463	R1080702_120	Cyanophage S-RIM32	GCA_001754165.1
ASV44176.1	006211	Cluster5979_1clades	399	PBI_SCTP2_161	Salicola phage SCTP-2	GCA_002625545.1
AAX44416.1	006212	Cluster5980_1clades	462	PSSM2_038	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12235.1	006212	Cluster5980_1clades	462	PRTG_00077	Prochlorococcus phage P-SSM5	GCA_002991095.1
prevph1000000614	006213	Cluster5981_1clades	461	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000433	006213	Cluster5981_1clades	461	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000720	006214	Cluster5982_1clades	200	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000487	006214	Cluster5982_1clades	461	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14692.1	006215	Ntox2	431	Lu11_0158	Pseudomonas phage Lu11	GCA_000897175.1
AGS82012.1	006215	Ntox2	459	PaBG_00128	Pseudomonas phage PaBG	GCA_000912555.1
BBA65482.1	006216	GlcNAc	457	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96490.1	006216	GlcNAc	450	Xoosp13_304	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBZ70679.1	006217	Cluster5985_1clades	454	pETSU_098	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89600.1	006217	Cluster5985_1clades	411	OBP_163	Pseudomonas phage OBP	GCA_000896635.1
BAS04944.1	006218	DUF3363	413	AVU11_gp152	Ralstonia phage RSF1	GCA_001500875.1
BAQ02668.1	006218	DUF3363	452	AVU38_gp140	Ralstonia phage RSL2	GCA_001503055.1
QDJ96664.1	006219	Cluster5987_1clades	451	PS1_0153	Aeromonas phage PS1	GCA_007051165.2
QFR59298.1	006219	Cluster5987_1clades	451	PS2_0157	Aeromonas phage PS2	GCA_009388305.2
prev15ph1000000383	006220	Cluster5989_1clades	452	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000560	006220	Cluster5989_1clades	450	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAE47804.1	006221	SIG+TM+Mbetalac+ADA-DBD	388	CST106	Clostridium phage c-st	GCA_000865225.1
BAE47805.1	006221	SIG+TM+Mbetalac+ADA-DBD	450	CST107	Clostridium phage c-st	GCA_000865225.1
prevph1000000279	006222	Cluster5991_1clades	277	-	Prevotella_phage_Lak-B8	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prev15ph1000000222	006222	Cluster5991_1clades	451	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03705.1	006223	Cluster5992_1clades	449	JOAD_210	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03462.1	006223	Cluster5992_1clades	449	RISINGSUN_208	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AUZ95136.1	006224	Cluster5994_1clades	436	FDI40_gp377	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44476.1	006224	Cluster5994_1clades	446	PBI_SCTP2_461	Salicola phage SCTP-2	GCA_002625545.1
AXQ69118.1	006225	CCDC158	444	CcrBL9_gp094	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69672.1	006225	CCDC158	444	CcrSC_gp090	Caulobacter phage CcrSC	GCA_003443315.1
BAW19222.1	006226	Cluster5996_1clades	444	FDH28_gp173	Ralstonia phage RP12	GCA_002617345.1
BAW19508.1	006226	Cluster5996_1clades	444	-	Ralstonia phage RP31	GCA_002617365.1
BAW19214.1	006227	Cluster6000_1clades	442	FDH28_gp181	Ralstonia phage RP12	GCA_002617345.1
BAW19500.1	006227	Cluster6000_1clades	434	-	Ralstonia phage RP31	GCA_002617365.1
BBI90634.1	006228	Cluster6001_1clades	442	HYO65_gp242	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90941.1	006228	Cluster6001_1clades	442	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIA64892.1	006229	SidE	403	S13_093	Cronobacter phage S13	GCA_001503575.1
QHJ79047.1	006229	SidE	442	-	Myoviridae sp.	GCA_012593985.1
BBA65521.1	006230	TylF	438	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96519.1	006230	TylF	441	Xoosp13_333	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBO63849.1	006231	Cluster6004_1clades	429	Goslar_00056	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63850.1	006231	Cluster6004_1clades	438	Goslar_00057	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
BAW19162.1	006232	Cluster6006_1clades	434	FDH28_gp233	Ralstonia phage RP12	GCA_002617345.1
BAW19448.1	006232	Cluster6006_1clades	434	-	Ralstonia phage RP31	GCA_002617365.1
AGH07505.1	006233	Cluster6007_1clades	419	CYVG_00061	Cyanophage S-SSM6a	GCA_002710385.1
ASR76212.1	006233	Cluster6007_1clades	432	PBI_BELLAMY_169	Synechococcus phage Bellamy	GCA_002627525.1
BAS04958.1	006234	Imm41	417	AVU11_gp166	Ralstonia phage RSF1	GCA_001500875.1
BAQ02683.1	006234	Imm41	430	AVU38_gp155	Ralstonia phage RSL2	GCA_001503055.1
BAS04824.1	006235	SIG+CarboxypepD-reg-IG	430	AVU11_gp032	Ralstonia phage RSF1	GCA_001500875.1
BAQ02557.1	006235	SIG+CarboxypepD-reg-IG	429	AVU38_gp029	Ralstonia phage RSL2	GCA_001503055.1
BBI90645.1	006236	Cluster6010_1clades	428	HYO65_gp253	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90951.1	006236	Cluster6010_1clades	428	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAS04931.1	006237	Cluster6013_1clades	420	AVU11_gp139	Ralstonia phage RSF1	GCA_001500875.1
BAQ02655.1	006237	Cluster6013_1clades	380	AVU38_gp127	Ralstonia phage RSL2	GCA_001503055.1
AFU88310.1	006238	Cluster6015_1clades	419	CcrColossus_gp440	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68981.1	006238	Cluster6015_1clades	419	CcrPW_gp442	Caulobacter phage CcrPW	GCA_003443275.1
BAW19053.1	006239	RADICAL-SAM	419	FDH28_gp079	Ralstonia phage RP12	GCA_002617345.1
BAW19338.1	006239	RADICAL-SAM	419	-	Ralstonia phage RP31	GCA_002617365.1
QGT54930.1	006240	Cluster6018_1clades	419	b23_0317	Synechococcus phage B23	GCA_009745195.1
QGT54565.1	006240	Cluster6018_1clades	419	b3_0324	Synechococcus phage B3	GCA_009745215.1
prevph1000000789	006241	TM	319	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000537	006241	TM	418	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDJ97262.1	006242	Cluster6021_1clades	392	D6_0102	Aeromonas phage D6	GCA_007051205.2
QDH47062.1	006242	Cluster6021_1clades	414	LAh10_34	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000087	006243	Cluster6022_1clades	341	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000066	006243	Cluster6022_1clades	413	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93273.1	006244	Peptidase_M16+Peptidase_M16_C	410	G_2	Bacillus virus G	GCA_000917535.1
AXH72868.1	006244	Peptidase_M16+Peptidase_M16_C	410	-	Myoviridae sp.	GCA_003657725.1
BAS04836.1	006245	Cluster6024_1clades	374	AVU11_gp044	Ralstonia phage RSF1	GCA_001500875.1
BAQ02569.1	006245	Cluster6024_1clades	410	AVU38_gp041	Ralstonia phage RSL2	GCA_001503055.1
BAS04932.2	006246	Cluster6025_1clades	391	AVU11_gp140	Ralstonia phage RSF1	GCA_001500875.1
BAQ02657.2	006246	Cluster6025_1clades	409	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19020.1	006247	Cluster6026_1clades	409	FDH28_gp046	Ralstonia phage RP12	GCA_002617345.1
BAW19306.1	006247	Cluster6026_1clades	409	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000548	006248	SIG+BZIP	194	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AFH14712.1	006249	Cluster6028_1clades	404	Lu11_0176	Pseudomonas phage Lu11	GCA_000897175.1
AGS81999.1	006249	Cluster6028_1clades	335	PaBG_00115	Pseudomonas phage PaBG	GCA_000912555.1
AXG67333.1	006250	Cluster6029_1clades	390	AD1_289	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08561.1	006250	Cluster6029_1clades	404	Alexandra_305	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AUZ95081.1	006251	SIG+IG	393	FDI40_gp320	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGN30308.1	006251	SIG+IG	402	VPFG_00309	Vibrio phage nt-1	GCA_000910195.2
AXQ69337.1	006252	Cluster6031_1clades	159	CcrBL9_gp313	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69897.1	006252	Cluster6031_1clades	401	CcrSC_gp315	Caulobacter phage CcrSC	GCA_003443315.1
ATA65357.1	006253	phiKZ_IP	400	2050HW_00022	Serratia phage 2050HW	GCA_002628125.1
QDB71144.1	006253	phiKZ_IP	400	CPT_Moabite_114	Serratia phage Moabite	GCA_006384735.1
BAW19210.1	006254	Cluster6033_1clades	399	FDH28_gp185	Ralstonia phage RP12	GCA_002617345.1
BAW19496.1	006254	Cluster6033_1clades	390	-	Ralstonia phage RP31	GCA_002617365.1
AND75183.1	006255	Phage_capsid	398	ME3_22	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ABS83683.1	006255	Phage_capsid	393	0306phi8-36p125	Bacillus phage 0305phi8-36	GCA_000871045.1
prevph1000000835	006256	Cluster6035_1clades	132	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000578	006256	Cluster6035_1clades	396	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65358.1	006257	Cluster6036_1clades	393	2050HW_00023	Serratia phage 2050HW	GCA_002628125.1
QDB71145.1	006257	Cluster6036_1clades	393	CPT_Moabite_115	Serratia phage Moabite	GCA_006384735.1
QBX06848.1	006258	HKD	393	BcepSaruman_435	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74817.1	006258	HKD	393	BcepSauron_437	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97300.1	006259	Cluster6038_1clades	382	D6_0140	Aeromonas phage D6	GCA_007051205.2
QDH47064.1	006259	Cluster6038_1clades	393	LAh10_64	Aeromonas phage LAh10	GCA_006863975.1
AFF28177.1	006260	Cluster6039_1clades	391	PAU_179	Sphingomonas phage PAU	GCA_000902455.1
AFF28178.1	006260	Cluster6039_1clades	385	PAU_180	Sphingomonas phage PAU	GCA_000902455.1
CCH63537.1	006261	ACET	388	CP21_075	Campylobacter virus CP21	GCA_000902535.1
ASV44240.1	006261	ACET	341	PBI_SCTP2_225	Salicola phage SCTP-2	GCA_002625545.1
prevph1000000775	006262	Cluster6041_1clades	389	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000528	006262	Cluster6041_1clades	389	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
CCH63476.1	006263	Cluster6042_1clades	386	CP21_014	Campylobacter virus CP21	GCA_000902535.1
QAU04506.1	006263	Cluster6042_1clades	384	ValB1MD_161	Vibrio phage ValB1MD	GCA_004138815.1
prevph1000000052	006264	Cluster6043_1clades	158	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000040	006264	Cluster6043_1clades	386	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03846.1	006265	Cluster6044_1clades	384	JOAD_69	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03601.1	006265	Cluster6044_1clades	384	RISINGSUN_69	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
prevph1000000417	006266	Aldolase_II	385	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000328	006266	Aldolase_II	385	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19052.1	006267	Cluster6046_1clades	382	FDH28_gp078	Ralstonia phage RP12	GCA_002617345.1
BAW19337.1	006267	Cluster6046_1clades	382	-	Ralstonia phage RP31	GCA_002617365.1
ATA65678.1	006268	Cluster6047_1clades	276	2050HW_00343	Serratia phage 2050HW	GCA_002628125.1
QDB71099.1	006268	Cluster6047_1clades	382	CPT_Moabite_067	Serratia phage Moabite	GCA_006384735.1
AAX44640.1	006269	Glycos_transf_1	380	PSSM2_263	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12331.1	006269	Glycos_transf_1	380	PRTG_00178	Prochlorococcus phage P-SSM5	GCA_002991095.1
SOK58940.1	006270	Cluster6049_1clades	378	g132	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58406.1	006270	Cluster6049_1clades	378	g129	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000433	006271	PCRF+RF-1	379	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000345	006271	PCRF+RF-1	379	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93622.1	006272	SUN	377	G_363	Bacillus virus G	GCA_000917535.1
AEO93624.1	006272	SUN	238	G_365	Bacillus virus G	GCA_000917535.1
ALY07226.1	006273	Cluster6053_1clades	376	VmeM32_00240	Vibrio phage vB_VmeM-32	GCA_002608825.1
QDJ96242.1	006273	Cluster6053_1clades	187	Xoosp13_55	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BAW19184.1	006274	Cluster6054_1clades	376	FDH28_gp211	Ralstonia phage RP12	GCA_002617345.1
BAW19470.1	006274	Cluster6054_1clades	376	-	Ralstonia phage RP31	GCA_002617365.1
CCH63651.1	006275	RADICAL-SAM	288	CP21_189	Campylobacter virus CP21	GCA_000902535.1
QJT70216.1	006275	RADICAL-SAM	374	SynMITS9220M01_210	Synechococcus phage SynMITS9220M01	GCA_013187275.1
prevph1000000023	006276	Cluster6056_1clades	131	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000020	006276	Cluster6056_1clades	375	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDH83680.1	006277	Cluster6057_1clades	359	H1O15_gp131	Achromobacter phage Motura	GCA_006964305.1
BAG41645.1	006277	Cluster6057_1clades	372	RSL1_ORF196	Ralstonia phage phiRSL1	GCA_000879455.1
prevph1000000100	006278	Cluster6058_1clades	366	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000071	006278	Cluster6058_1clades	373	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDJ97301.1	006279	Cluster6061_1clades	369	D6_0141	Aeromonas phage D6	GCA_007051205.2
QDH47071.1	006279	Cluster6061_1clades	369	LAh10_65	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000251	006280	S1	370	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000199	006280	S1	370	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93441.1	006281	Cluster6063_1clades	115	G_181	Bacillus virus G	GCA_000917535.1
AEO93442.1	006281	Cluster6063_1clades	367	G_182	Bacillus virus G	GCA_000917535.1
BAS04866.2	006282	Cluster6064_1clades	367	AVU11_agp17	Ralstonia phage RSF1	GCA_001500875.1
BAQ02599.1	006282	Cluster6064_1clades	319	AVU38_gp071	Ralstonia phage RSL2	GCA_001503055.1
AFU88259.1	006283	CR-ATPase9	365	CcrColossus_gp389	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68933.1	006283	CR-ATPase9	331	CcrPW_gp394	Caulobacter phage CcrPW	GCA_003443275.1
prevph1000000526	006284	Cluster6066_1clades	366	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000400	006284	Cluster6066_1clades	366	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXH72901.1	006285	Glycos_transf_1	358	-	Myoviridae sp.	GCA_003657725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAG41706.1	006285	Glycos_transf_1	363	RSL1_ORF258	Ralstonia phage phiRSL1	GCA_000879455.1
AXQ69306.1	006286	Cluster6068_1clades	355	CcrBL9_gp282	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69865.1	006286	Cluster6068_1clades	362	CcrSC_gp283	Caulobacter phage CcrSC	GCA_003443315.1
prevph1000000639	006287	TPR	362	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000455	006287	TPR	362	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19051.1	006288	RADICAL-SAM	360	FDH28_gp077	Ralstonia phage RP12	GCA_002617345.1
BAW19336.1	006288	RADICAL-SAM	360	-	Ralstonia phage RP31	GCA_002617365.1
BAW19163.1	006289	Cluster6071_1clades	360	FDH28_gp232	Ralstonia phage RP12	GCA_002617345.1
BAW19449.1	006289	Cluster6071_1clades	360	-	Ralstonia phage RP31	GCA_002617365.1
ATA65361.1	006290	Cluster6072_1clades	358	2050HW_00026	Serratia phage 2050HW	GCA_002628125.1
QDB71147.1	006290	Cluster6072_1clades	358	CPT_Moabite_117	Serratia phage Moabite	GCA_006384735.1
QDJ97417.2	006291	Cluster6073_1clades	358	D6_0243	Aeromonas phage D6	GCA_007051205.2
QDH47076.1	006291	Cluster6073_1clades	358	LAh10_156	Aeromonas phage LAh10	GCA_006863975.1
BBI90407.1	006292	Cluster6074_1clades	357	HYO65_gp015	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90716.1	006292	Cluster6074_1clades	357	-	Tenacibaculum phage PTm5	GCA_009730715.1
ATA65551.1	006293	Cluster6075_1clades	356	2050HW_00216	Serratia phage 2050HW	GCA_002628125.1
QDB71316.1	006293	Cluster6075_1clades	356	CPT_Moabite_286	Serratia phage Moabite	GCA_006384735.1
BAS04864.1	006294	Cluster6076_1clades	356	AVU11_gp072	Ralstonia phage RSF1	GCA_001500875.1
BAQ02597.1	006294	Cluster6076_1clades	355	AVU38_gp069	Ralstonia phage RSL2	GCA_001503055.1
QDJ97338.1	006295	Cluster6077_1clades	355	D6_0179	Aeromonas phage D6	GCA_007051205.2
QDH47077.1	006295	Cluster6077_1clades	355	LAh10_98	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000420	006296	TM+TM+PspA	356	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000331	006296	TM+TM+PspA	356	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000515	006297	Cluster6079_1clades	356	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000389	006297	Cluster6079_1clades	356	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01533.1	006298	Cluster6080_1clades	354	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53155.1	006298	Cluster6080_1clades	354	65p147	Aeromonas virus 65	GCA_000893255.1
QDJ97401.1	006299	Cluster6081_1clades	352	D6_0242	Aeromonas phage D6	GCA_007051205.2
QDH47078.1	006299	Cluster6081_1clades	352	LAh10_155	Aeromonas phage LAh10	GCA_006863975.1
AXG67061.1	006300	DUF1611_N+DUF1611	351	AD1_017	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08299.1	006300	DUF1611_N+DUF1611	351	Alexandra_18	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BBA65462.1	006301	DUF2229	351	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96471.1	006301	DUF2229	349	Xoosp13_285	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AFU87918.1	006302	Herpes_UL32	350	CcrColossus_gp048	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68590.1	006302	Herpes_UL32	324	CcrPW_gp051	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69402.1	006303	TM+TM+TM	349	CcrBL9_gp378	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69959.1	006303	TM+TM+TM	349	CcrSC_gp377	Caulobacter phage CcrSC	GCA_003443315.1
QKE54509.1	006304	Cluster6086_1clades	349	ACSA002_1950	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54511.1	006304	Cluster6086_1clades	344	ACSA002_1970	Salmonella phage vB_SalM_SA002	GCA_014131285.1
prevph1000000742	006305	Cluster6087_1clades	350	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000494	006305	Cluster6087_1clades	350	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXG67134.1	006306	Cluster6088_1clades	347	AD1_090	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AQT28564.1	006306	Cluster6088_1clades	348	YOLOSWAG_81	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXQ69419.1	006307	TM+TM+TM+TM+TM+TM+TM+TM+TM	348	CcrBL9_gp395	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69974.1	006307	TM+TM+TM+TM+TM+TM+TM+TM+TM	348	CcrSC_gp392	Caulobacter phage CcrSC	GCA_003443315.1
ASR76251.1	006308	SIG+GHMP_kinases_N+GHMP_kinases_C	338	PBI_BELLAMY_215	Synechococcus phage Bellamy	GCA_002627525.1
QJT70202.1	006308	SIG+GHMP_kinases_N+GHMP_kinases_C	348	SynMITS9220M01_196	Synechococcus phage SynMITS9220M01	GCA_013187275.1
prevph1000000238	006309	SIG+TM+TM+TM+CBS	349	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000188	006309	SIG+TM+TM+TM+CBS	349	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000302	006310	SIG+OmpA-beta-barrel+OmpA	348	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000234	006310	SIG+OmpA-beta-barrel+OmpA	348	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000103	006311	Cluster6094_1clades	114	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000074	006311	Cluster6094_1clades	347	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65375.1	006312	Cluster6095_1clades	345	2050HW_00040	Serratia phage 2050HW	GCA_002628125.1
QDB71159.1	006312	Cluster6095_1clades	345	CPT_Moabite_129	Serratia phage Moabite	GCA_006384735.1
QBX06683.1	006313	Cluster6096_1clades	345	BcepSaruman_270	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74653.1	006313	Cluster6096_1clades	345	BcepSauron_273	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65486.1	006314	Cluster6097_1clades	309	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96493.1	006314	Cluster6097_1clades	345	Xoosp13_307	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ASU03792.1	006315	Cluster6099_1clades	344	JOAD_123	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03548.1	006315	Cluster6099_1clades	344	RISINGSUN_122	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASV44067.1	006316	Cluster6100_1clades	344	PBI_SCTP2_52	Salicola phage SCTP-2	GCA_002625545.1
ASV44068.1	006316	Cluster6100_1clades	321	PBI_SCTP2_53	Salicola phage SCTP-2	GCA_002625545.1
ASU03771.1	006317	Cluster6102_1clades	343	JOAD_144	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03527.1	006317	Cluster6102_1clades	343	RISINGSUN_143	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ABS83805.1	006318	CCDC158	341	0305phi8-36p105	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83663.1	006318	CCDC158	341	0305phi8-36p105R	Bacillus phage 0305phi8-36	GCA_000871045.1
prevph1000000156	006319	MYND	342	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000117	006319	MYND	342	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXF51214.1	006320	Cluster6105_1clades	340	WELLINGTON_84	Erwinia phage Wellington	GCA_003344985.1
ANZ49436.1	006320	Cluster6105_1clades	340	KWAN_84	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
prevph1000000144	006321	Cluster6106_1clades	341	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000111	006321	Cluster6106_1clades	341	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000254	006322	Cluster6107_1clades	221	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000201	006322	Cluster6107_1clades	341	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBI90442.1	006323	Cluster6108_1clades	339	HYO65_gp050	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90750.1	006323	Cluster6108_1clades	329	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90662.1	006324	Cluster6109_1clades	339	HYO65_gp270	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90967.1	006324	Cluster6109_1clades	339	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54908.1	006325	CheC	339	b23_0295	Synechococcus phage B23	GCA_009745195.1
QGT54543.1	006325	CheC	339	b3_0302	Synechococcus phage B3	GCA_009745215.1
AQT27991.1	006326	Cluster6111_1clades	327	pVa21_049	Vibrio phage pVa-21	GCA_002619305.1
AQT27992.1	006326	Cluster6111_1clades	338	pVa21_050	Vibrio phage pVa-21	GCA_002619305.1
ASR76095.1	006327	Cluster6112_1clades	307	PBI_BELLAMY_50	Synechococcus phage Bellamy	GCA_002627525.1
ASR76098.1	006327	Cluster6112_1clades	337	PBI_BELLAMY_53	Synechococcus phage Bellamy	GCA_002627525.1
AWY08368.1	006328	Cluster6113_1clades	337	Alexandra_92	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58731.1	006328	Cluster6113_1clades	335	Y3_091	Erwinia phage vB_EamM_Y3	GCA_002955045.1
QDJ97356.1	006329	Cluster6114_1clades	333	D6_0197	Aeromonas phage D6	GCA_007051205.2
QDH47079.1	006329	Cluster6114_1clades	337	LAh10_115	Aeromonas phage LAh10	GCA_006863975.1
ATA65347.1	006330	Cluster6115_1clades	196	2050HW_00012	Serratia phage 2050HW	GCA_002628125.1
QDB71135.1	006330	Cluster6115_1clades	336	CPT_Moabite_105	Serratia phage Moabite	GCA_006384735.1
QDJ97317.1	006331	Cluster6116_1clades	336	D6_0157	Aeromonas phage D6	GCA_007051205.2
QDH47081.1	006331	Cluster6116_1clades	336	LAh10_79	Aeromonas phage LAh10	GCA_006863975.1
BBI90671.1	006332	Cluster6117_1clades	335	HYO65_gp279	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90976.1	006332	Cluster6117_1clades	335	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06448.1	006333	Cluster6118_1clades	335	BcepSaruman_035	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74416.1	006333	Cluster6118_1clades	334	BcepSauron_036	Burkholderia phage BcepSauron	GCA_005394215.1
prevph1000000036	006334	Cluster6119_1clades	336	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000028	006334	Cluster6119_1clades	336	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMS01164.1	006335	Cluster6120_1clades	334	AR9_g080	Bacillus phage AR9	GCA_001743835.1
ASU00095.1	006335	Cluster6120_1clades	334	PBI_PBS1_273	Bacillus virus PBS1	GCA_002601325.1
QBX32166.1	006336	Cluster6121_1clades	334	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41747.1	006336	Cluster6121_1clades	320	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAW19079.1	006337	Cluster6122_1clades	332	FDH28_gp105	Ralstonia phage RP12	GCA_002617345.1
BAW19364.1	006337	Cluster6122_1clades	332	-	Ralstonia phage RP31	GCA_002617365.1
AFH14641.1	006338	Cluster6124_1clades	298	Lu11_0109	Pseudomonas phage Lu11	GCA_000897175.1
AGS82068.2	006338	Cluster6124_1clades	331	PaBG_00192	Pseudomonas phage PaBG	GCA_000912555.1
QNI21188.1	006339	Cluster6125_1clades	161	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21196.1	006339	Cluster6125_1clades	331	-	Vibrio phage vB_pir03	GCA_014319855.1
prevph1000000166	006340	Cluster6126_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000128	006340	Cluster6126_1clades	332	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44400.1	006341	Cluster6127_1clades	330	PSSM2_022	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12251.1	006341	Cluster6127_1clades	330	PRTG_00093	Prochlorococcus phage P-SSM5	GCA_002991095.1
ATA65608.1	006342	Cluster6128_1clades	330	2050HW_00273	Serratia phage 2050HW	GCA_002628125.1
QDB71034.1	006342	Cluster6128_1clades	330	CPT_Moabite_002	Serratia phage Moabite	GCA_006384735.1
BBI90503.1	006343	PAPS_reduct	330	HYO65_gp111	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90811.1	006343	PAPS_reduct	330	-	Tenacibaculum phage PTm5	GCA_009730715.1
AFU88177.1	006344	Cluster6131_1clades	325	CcrColossus_gp307	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68854.1	006344	Cluster6131_1clades	326	CcrPW_gp315	Caulobacter phage CcrPW	GCA_003443275.1
AGH07568.1	006345	SIG+Glyco_transf_10	325	CYVG_00124	Cyanophage S-SSM6a	GCA_002710385.1
AXQ70517.1	006345	SIG+Glyco_transf_10	267	HOU04_gp118	Synechococcus phage S-T4	GCA_003443335.1
ATA65579.1	006346	Cluster6133_1clades	315	2050HW_00244	Serratia phage 2050HW	GCA_002628125.1
QDB71344.1	006346	Cluster6133_1clades	324	CPT_Moabite_314	Serratia phage Moabite	GCA_006384735.1
AMS01202.1	006347	TM	323	AR9_g118	Bacillus phage AR9	GCA_001743835.1
AST99826.1	006347	TM	323	PBI_PBS1_4	Bacillus virus PBS1	GCA_002601325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AYD81454.1	006348	Cluster6135_1clades	323	SEA_JUSTBECAUSE_299	Streptomyces phage JustBecause	GCA_003613775.1
QJD53859.1	006348	Cluster6135_1clades	323	SEA_KELA_299	Streptomyces phage Kela	GCA_012934305.1
BAS04935.2	006349	Cluster6136_1clades	293	AVU11_agp32	Ralstonia phage RSF1	GCA_001500875.1
BAQ02660.2	006349	Cluster6136_1clades	323	-	Ralstonia phage RSL2	GCA_001503055.1
BBI90641.1	006350	Cluster6137_1clades	323	HYO65_gp249	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90948.1	006350	Cluster6137_1clades	323	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ97403.1	006351	Cluster6138_1clades	323	D6_0244	Aeromonas phage D6	GCA_007051205.2
QDH47083.1	006351	Cluster6138_1clades	323	LAh10_157	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000592	006352	Cluster6139_1clades	113	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000418	006352	Cluster6139_1clades	324	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000796	006353	SIG+TM+TM	324	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000544	006353	SIG+TM+TM	324	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000839	006354	Cluster6141_1clades	323	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000581	006354	Cluster6141_1clades	323	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65514.1	006355	Cluster6142_1clades	198	2050HW_00179	Serratia phage 2050HW	GCA_002628125.1
QDB71281.1	006355	Cluster6142_1clades	321	CPT_Moabite_251	Serratia phage Moabite	GCA_006384735.1
ANZ48428.1	006356	Cluster6144_1clades	318	CAITLIN_133	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48701.1	006356	Cluster6144_1clades	284	CHRISDB_139	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
BBA65527.1	006357	Rota_VP2	290	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96525.1	006357	Rota_VP2	317	Xoosp13_339	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXH70903.1	006358	DUF4457	309	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70901.1	006358	DUF4457	315	-	Vibrio phage BONAISHI	GCA_003441475.1
AXQ69120.1	006359	DivIC	315	CcrBL9_gp096	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69674.1	006359	DivIC	315	CcrSC_gp092	Caulobacter phage CcrSC	GCA_003443315.1
ASU03728.1	006360	Cluster6148_1clades	314	JOAD_187	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03485.1	006360	Cluster6148_1clades	311	RISINGSUN_185	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AAX44568.1	006361	AICARFT_IMPCHas	313	PSSM2_190	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12405.1	006361	AICARFT_IMPCHas	313	PRTG_00252	Prochlorococcus phage P-SSM5	GCA_002991095.1
QBX06523.1	006362	KELCH	313	BcepSaruman_110	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74489.1	006362	KELCH	313	BcepSauron_109	Burkholderia phage BcepSauron	GCA_005394215.1
prevph1000000002	006363	Cluster6151_1clades	314	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000002	006363	Cluster6151_1clades	314	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000015	006364	Cluster6152_1clades	314	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000014	006364	Cluster6152_1clades	314	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAS04846.1	006365	Cluster6153_1clades	312	AVU11_gp054	Ralstonia phage RSF1	GCA_001500875.1
BAQ02579.1	006365	Cluster6153_1clades	293	AVU38_gp051	Ralstonia phage RSL2	GCA_001503055.1
QGT54960.1	006366	Cluster6154_1clades	312	b23_0354	Synechococcus phage B23	GCA_009745195.1
QGT54595.1	006366	Cluster6154_1clades	312	b3_0360	Synechococcus phage B3	GCA_009745215.1
AIA65026.1	006367	Cluster6155_1clades	181	S13_229	Cronobacter phage S13	GCA_001503575.1
QHJ78908.1	006367	Cluster6155_1clades	312	-	Myoviridae sp.	GCA_012593985.1
BAW19240.1	006368	Cluster6156_1clades	311	FDH28_gp155	Ralstonia phage RP12	GCA_002617345.1
BAW19526.1	006368	Cluster6156_1clades	311	-	Ralstonia phage RP31	GCA_002617365.1
AWY08373.1	006369	Cluster6159_1clades	310	Alexandra_98	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58736.1	006369	Cluster6159_1clades	309	Y3_096	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AFU88113.1	006370	Cluster6160_1clades	309	CcrColossus_gp243	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68791.1	006370	Cluster6160_1clades	309	CcrPW_gp252	Caulobacter phage CcrPW	GCA_003443275.1
AMM44965.1	006371	MYND	309	SP15_167	Bacillus phage SP-15	GCA_001754685.1
AEO93551.1	006371	MYND	281	G_292	Bacillus virus G	GCA_000917535.1
BAW19080.1	006372	Mrr-N	308	FDH28_gp106	Ralstonia phage RP12	GCA_002617345.1
BAW19365.1	006372	Mrr-N	308	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000317	006373	Cluster6163_1clades	205	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000246	006373	Cluster6163_1clades	309	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000382	006374	TM+TM	309	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000308	006374	TM+TM	309	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03737.1	006375	Cluster6165_1clades	307	JOAD_178	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03493.1	006375	Cluster6165_1clades	307	RISINGSUN_177	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
BBI90660.1	006376	Cluster6166_1clades	306	HYO65_gp268	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90965.1	006376	Cluster6166_1clades	306	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAS04990.2	006377	Cluster6167_1clades	305	AVU11_gp198	Ralstonia phage RSF1	GCA_001500875.1
BAQ02719.2	006377	Cluster6167_1clades	305	-	Ralstonia phage RSL2	GCA_001503055.1
ASU03770.1	006378	Cluster6168_1clades	304	JOAD_145	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03526.1	006378	Cluster6168_1clades	304	RISINGSUN_144	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QDJ97406.1	006379	Cluster6170_1clades	304	D6_0247	Aeromonas phage D6	GCA_007051205.2
QDH47090.1	006379	Cluster6170_1clades	304	LAh10_159	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000351	006380	Cluster6171_1clades	172	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000277	006380	Cluster6171_1clades	305	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000512	006381	ZNR	271	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000387	006381	ZNR	305	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAG41683.1	006382	GT	255	RSL1_ORF234	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41682.1	006382	GT	302	RSL1_ORF233	Ralstonia phage phiRSL1	GCA_000879455.1
BBA65514.1	006383	SIG+ZNR	272	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96514.1	006383	SIG+ZNR	302	Xoosp13_328	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96749.1	006384	Cluster6176_1clades	301	PS1_0238	Aeromonas phage PS1	GCA_007051165.2
QFR59382.1	006384	Cluster6176_1clades	301	PS2_0240	Aeromonas phage PS2	GCA_009388305.2
QIG57739.1	006385	Cluster6177_1clades	301	SEA_PAULODIABOLI_1	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58040.1	006385	Cluster6177_1clades	301	SEA_PAULODIABOLI_356	Microbacterium phage PauloDiaboli	GCA_011067425.1
prev15ph1000000115	006386	DUF1566	302	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000501	006386	DUF1566	301	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44638.1	006387	Glycos_transf_2	300	PSSM2_261	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12333.1	006387	Glycos_transf_2	300	PRTG_00180	Prochlorococcus phage P-SSM5	GCA_002991095.1
AMM44955.1	006388	Uri-nuclease	236	SP15_157	Bacillus phage SP-15	GCA_001754685.1
AMM45016.1	006388	Uri-nuclease	299	SP15_216	Bacillus phage SP-15	GCA_001754685.1
BBI90649.1	006389	sf-sug	204	HYO65_gp257	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90955.1	006389	sf-sug	299	-	Tenacibaculum phage PTm5	GCA_009730715.1
ATA65683.1	006390	Cluster6182_1clades	298	2050HW_00348	Serratia phage 2050HW	GCA_002628125.1
QDB71104.1	006390	Cluster6182_1clades	298	CPT_Moabite_072	Serratia phage Moabite	GCA_006384735.1
prevph1000000217	006391	URI	156	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000170	006391	URI	299	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19155.1	006392	Cluster6184_1clades	288	FDH28_gp240	Ralstonia phage RP12	GCA_002617345.1
BAW19441.1	006392	Cluster6184_1clades	297	-	Ralstonia phage RP31	GCA_002617365.1
AMS01301.1	006393	Cluster6185_1clades	296	AR9_g217	Bacillus phage AR9	GCA_001743835.1
AST99930.1	006393	Cluster6185_1clades	296	PBI_PBS1_108	Bacillus virus PBS1	GCA_002601325.1
QDJ97265.1	006394	Cluster6186_1clades	283	D6_0105	Aeromonas phage D6	GCA_007051205.2
QDH47094.1	006394	Cluster6186_1clades	296	LAh10_37	Aeromonas phage LAh10	GCA_006863975.1
AFC21508.1	006395	HEPN	295	GAP32_060	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43629.1	006395	HEPN	295	CBB_64	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
BAW19049.1	006396	Cluster6189_1clades	295	FDH28_gp075	Ralstonia phage RP12	GCA_002617345.1
BAW19334.1	006396	Cluster6189_1clades	295	-	Ralstonia phage RP31	GCA_002617365.1
BAW19032.1	006397	Cluster6190_1clades	283	FDH28_gp058	Ralstonia phage RP12	GCA_002617345.1
BAW19317.1	006397	Cluster6190_1clades	295	-	Ralstonia phage RP31	GCA_002617365.1
AUZ95241.1	006398	DCM	278	FDI40_gp482	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95242.1	006398	DCM	294	FDI40_gp483	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXG67238.1	006399	Cluster6192_1clades	281	AD1_194	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08468.1	006399	Cluster6192_1clades	294	Alexandra_204	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBX32527.1	006400	Cluster6193_1clades	294	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42100.1	006400	Cluster6193_1clades	294	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22974.1	006401	Glyco_transf_17	294	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50556.1	006401	Glyco_transf_17	294	-	Synechococcus phage S-B43	GCA_006869725.1
prevph1000000335	006402	RADICAL-SAM	295	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000264	006402	RADICAL-SAM	295	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44445.1	006403	Cluster6196_1clades	293	PSSM2_067	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12207.1	006403	Cluster6196_1clades	293	PRTG_00049	Prochlorococcus phage P-SSM5	GCA_002991095.1
ABY63065.1	006404	Cluster6197_1clades	293	201phi2-1p236	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76855.1	006404	Cluster6197_1clades	292	PHABIO_224	Pseudomonas phage Phabio	GCA_002624965.1
BAW19157.1	006405	Cluster6198_1clades	293	FDH28_gp238	Ralstonia phage RP12	GCA_002617345.1
BAW19443.1	006405	Cluster6198_1clades	293	-	Ralstonia phage RP31	GCA_002617365.1
BAW19116.1	006406	Cluster6199_1clades	292	FDH28_gp279	Ralstonia phage RP12	GCA_002617345.1
BAW19402.1	006406	Cluster6199_1clades	292	-	Ralstonia phage RP31	GCA_002617365.1
BAW19231.1	006407	Cluster6200_1clades	292	FDH28_gp164	Ralstonia phage RP12	GCA_002617345.1
BAW19517.1	006407	Cluster6200_1clades	292	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000007	006408	THF_DHG_CYH+THF_DHG_CYH_C	293	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000008	006408	THF_DHG_CYH+THF_DHG_CYH_C	293	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000252	006409	Cluster6202_1clades	293	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000200	006409	Cluster6202_1clades	293	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88139.1	006410	SIG+PRTase	291	CcrColossus_gp269	Caulobacter phage CcrColossus	GCA_000899635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ68815.1	006410	SIG+PRTase	291	CcrPW_gp276	Caulobacter phage CcrPW	GCA_003443275.1
BAW19106.1	006411	Cluster6204_1clades	291	FDH28_gp289	Ralstonia phage RP12	GCA_002617345.1
BAW19392.1	006411	Cluster6204_1clades	291	-	Ralstonia phage RP31	GCA_002617365.1
ATA65570.1	006412	Cluster6205_1clades	288	2050HW_00235	Serratia phage 2050HW	GCA_002628125.1
QDB71333.1	006412	Cluster6205_1clades	290	CPT_Moabite_303	Serratia phage Moabite	GCA_006384735.1
prevph1000000013	006413	RADICAL-SAM	291	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000012	006413	RADICAL-SAM	291	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFO71447.1	006414	Cluster6207_1clades	197	CR5_227	Cronobacter phage CR5	GCA_000910235.1
ANZ50431.1	006414	Cluster6207_1clades	289	PHOBOS_241	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ATA65696.1	006415	Cluster6208_1clades	289	2050HW_00361	Serratia phage 2050HW	GCA_002628125.1
QDB71123.1	006415	Cluster6208_1clades	289	CPT_Moabite_093	Serratia phage Moabite	GCA_006384735.1
prevph1000000185	006416	SAICAR_synt	290	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000148	006416	SAICAR_synt	290	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65499.1	006417	Cluster6210_1clades	286	2050HW_00164	Serratia phage 2050HW	GCA_002628125.1
QDB71269.1	006417	Cluster6210_1clades	288	CPT_Moabite_239	Serratia phage Moabite	GCA_006384735.1
AAX44643.1	006418	Glyco_transf_4	287	PSSM2_266	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12328.1	006418	Glyco_transf_4	287	PRTG_00175	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ69358.1	006419	Cluster6212_1clades	287	CcrBL9_gp334	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69917.1	006419	Cluster6212_1clades	285	CcrSC_gp335	Caulobacter phage CcrSC	GCA_003443315.1
AFH14783.1	006420	Cluster6213_1clades	267	Lu11_0247	Pseudomonas phage Lu11	GCA_000897175.1
AGS82128.1	006420	Cluster6213_1clades	286	PaBG_00253	Pseudomonas phage PaBG	GCA_000912555.1
BBA65480.1	006421	Cluster6214_1clades	286	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96488.1	006421	Cluster6214_1clades	286	Xoosp13_302	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AFU87922.1	006422	Cluster6215_1clades	285	CcrColossus_gp052	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68595.1	006422	Cluster6215_1clades	271	CcrPW_gp056	Caulobacter phage CcrPW	GCA_003443275.1
BBA65379.1	006423	Cluster6216_1clades	285	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96407.1	006423	Cluster6216_1clades	158	Xoosp13_221	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000619	006424	Cluster6217_1clades	285	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000438	006424	Cluster6217_1clades	285	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000745	006425	Cluster6218_1clades	285	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000497	006425	Cluster6218_1clades	285	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14830.1	006426	Cluster6219_1clades	283	Lu11_0292	Pseudomonas phage Lu11	GCA_000897175.1
AGS81944.1	006426	Cluster6219_1clades	275	PaBG_00060	Pseudomonas phage PaBG	GCA_000912555.1
BAW19034.1	006427	Cluster6220_1clades	282	FDH28_gp060	Ralstonia phage RP12	GCA_002617345.1
BAW19319.1	006427	Cluster6220_1clades	271	-	Ralstonia phage RP31	GCA_002617365.1
AFU88112.1	006428	SIG+CsgG	281	CcrColossus_gp242	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68790.1	006428	SIG+CsgG	281	CcrPW_gp251	Caulobacter phage CcrPW	GCA_003443275.1
ABY63166.1	006429	Cluster6222_1clades	271	201phi2-1p341	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76969.1	006429	Cluster6222_1clades	281	PHABIO_338	Pseudomonas phage Phabio	GCA_002624965.1
ABY62972.1	006430	Cluster6223_1clades	135	201phi2-1p141	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77251.1	006430	Cluster6223_1clades	281	NOXIFER_80	Pseudomonas phage Noxifer	GCA_002625005.1
BAW19022.1	006431	Cluster6224_1clades	281	FDH28_gp048	Ralstonia phage RP12	GCA_002617345.1
BAW19308.1	006431	Cluster6224_1clades	281	-	Ralstonia phage RP31	GCA_002617365.1
BBI90545.1	006432	Cluster6225_1clades	281	HYO65_gp153	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90853.1	006432	Cluster6225_1clades	281	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000608	006433	Cluster6226_1clades	282	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000427	006433	Cluster6226_1clades	282	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000833	006434	Cluster6227_1clades	282	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000576	006434	Cluster6227_1clades	214	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAS04993.1	006435	Cluster6228_1clades	280	AVU11_gp201	Ralstonia phage RSF1	GCA_001500875.1
BAQ02722.2	006435	Cluster6228_1clades	271	-	Ralstonia phage RSL2	GCA_001503055.1
ATA65368.1	006436	Cluster6229_1clades	279	2050HW_00033	Serratia phage 2050HW	GCA_002628125.1
QDB71153.1	006436	Cluster6229_1clades	279	CPT_Moabite_123	Serratia phage Moabite	GCA_006384735.1
BBA65470.1	006437	PTSEIIA1	279	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96479.1	006437	PTSEIIA1	270	Xoosp13_293	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90629.1	006438	Cluster6231_1clades	279	HYO65_gp237	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90935.1	006438	Cluster6231_1clades	279	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAW19054.1	006439	DUF3050	278	FDH28_gp080	Ralstonia phage RP12	GCA_002617345.1
BAW19339.1	006439	DUF3050	278	-	Ralstonia phage RP31	GCA_002617365.1
AFH14614.1	006440	Cluster6233_1clades	252	Lu11_0082	Pseudomonas phage Lu11	GCA_000897175.1
AGS82087.1	006440	Cluster6233_1clades	277	PaBG_00212	Pseudomonas phage PaBG	GCA_000912555.1
ASV44127.1	006441	Cluster6234_1clades	273	PBI_SCTP2_112	Salicola phage SCTP-2	GCA_002625545.1
ASV44129.1	006441	Cluster6234_1clades	277	PBI_SCTP2_114	Salicola phage SCTP-2	GCA_002625545.1
QDJ97234.1	006442	Cluster6235_1clades	277	D6_0074	Aeromonas phage D6	GCA_007051205.2
QDH47101.1	006442	Cluster6235_1clades	277	LAh10_7	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000518	006443	Cluster6236_1clades	278	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000393	006443	Cluster6236_1clades	278	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBX06832.1	006444	Cluster6237_1clades	276	BcepSaruman_419	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74801.1	006444	Cluster6237_1clades	276	BcepSauron_421	Burkholderia phage BcepSauron	GCA_005394215.1
BAS04825.2	006445	Cluster6238_1clades	275	AVU11_gp033	Ralstonia phage RSF1	GCA_001500875.1
BAQ02558.2	006445	Cluster6238_1clades	270	-	Ralstonia phage RSL2	GCA_001503055.1
QBX32517.1	006446	Cluster6239_1clades	275	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42090.1	006446	Cluster6239_1clades	275	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22968.1	006447	Glyco_tranf_2_4	275	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50562.1	006447	Glyco_tranf_2_4	275	-	Synechococcus phage S-B43	GCA_006869725.1
prevph1000000219	006448	Cluster6241_1clades	276	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000171	006448	Cluster6241_1clades	276	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AYD81426.1	006449	Toast-rack	274	SEA_JUSTBECAUSE_271	Streptomyces phage JustBecause	GCA_003613775.1
QJD53831.1	006449	Toast-rack	274	SEA_KELA_271	Streptomyces phage Kela	GCA_012934305.1
QBZ71929.1	006450	Cluster6243_1clades	273	SEA_KRADAL_30	Streptomyces phage Kradal	GCA_004799925.1
AXH66191.1	006450	Cluster6243_1clades	273	SEA_SATIS_30	Streptomyces phage Satis	GCA_003366315.1
QBX06760.1	006451	Cluster6244_1clades	177	BcepSaruman_347	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74730.1	006451	Cluster6244_1clades	273	BcepSauron_350	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06817.1	006452	Cluster6245_1clades	273	BcepSaruman_404	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74786.1	006452	Cluster6245_1clades	272	BcepSauron_406	Burkholderia phage BcepSauron	GCA_005394215.1
QNI21170.1	006453	Cluster6246_1clades	273	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26101.1	006453	Cluster6246_1clades	131	g077	Yersinia phage phiR1-37	GCA_000895615.1
ASR76254.1	006454	RmlD_sub_bind	272	PBI_BELLAMY_218	Synechococcus phage Bellamy	GCA_002627525.1
QJT70205.1	006454	RmlD_sub_bind	272	SynMITS9220M01_199	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BAW18986.1	006455	Cluster6248_1clades	272	FDH28_gp012	Ralstonia phage RP12	GCA_002617345.1
BAW19274.1	006455	Cluster6248_1clades	272	-	Ralstonia phage RP31	GCA_002617365.1
QGT54672.1	006456	SIG+Band_7	272	b23_0044	Synechococcus phage B23	GCA_009745195.1
QGT54302.1	006456	SIG+Band_7	272	b3_0044	Synechococcus phage B3	GCA_009745215.1
QBZ70838.1	006457	Cluster6250_1clades	149	pETSU_257	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89468.1	006457	Cluster6250_1clades	271	OBP_031	Pseudomonas phage OBP	GCA_000896635.1
BAW19243.1	006458	ABhydrolase	271	FDH28_gp152	Ralstonia phage RP12	GCA_002617345.1
BAW19529.1	006458	ABhydrolase	271	-	Ralstonia phage RP31	GCA_002617365.1
BAS05005.1	006459	Cluster6252_1clades	267	AVU11_gp213	Ralstonia phage RSF1	GCA_001500875.1
BAQ02735.1	006459	Cluster6252_1clades	270	AVU38_gp207	Ralstonia phage RSL2	GCA_001503055.1
AEO93672.1	006460	Cluster6253_1clades	221	G_414	Bacillus virus G	GCA_000917535.1
AEO93674.1	006460	Cluster6253_1clades	269	G_416	Bacillus virus G	GCA_000917535.1
AFC21868.1	006461	Cluster6254_1clades	269	GAP32_415	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43994.1	006461	Cluster6254_1clades	266	CBB_431	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01250.1	006462	Cluster6255_1clades	269	AR9_g166	Bacillus phage AR9	GCA_001743835.1
AST99876.1	006462	Cluster6255_1clades	269	PBI_PBS1_54	Bacillus virus PBS1	GCA_002601325.1
AXC36995.1	006463	Cluster6256_1clades	269	-	Escherichia phage UB	GCA_003341455.1
AFA44653.1	006463	Cluster6256_1clades	200	RaK2_00380	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
CAG27183.1	006464	Cluster6257_1clades	261	PPEV_gp089	Pseudomonas phage EL	GCA_000866825.1
CAG27186.1	006464	Cluster6257_1clades	268	PPEV_gp092	Pseudomonas phage EL	GCA_000866825.1
ATA65628.1	006465	Cluster6258_1clades	228	2050HW_00293	Serratia phage 2050HW	GCA_002628125.1
QDB71055.1	006465	Cluster6258_1clades	268	CPT_Moabite_023	Serratia phage Moabite	GCA_006384735.1
QGT54821.1	006466	TM	268	b23_0206	Synechococcus phage B23	GCA_009745195.1
QGT54451.1	006466	TM	268	b3_0208	Synechococcus phage B3	GCA_009745215.1
AAX44576.2	006467	tRNA-synt_2	267	PSSM2_198	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12397.1	006467	tRNA-synt_2	246	PRTG_00244	Prochlorococcus phage P-SSM5	GCA_002991095.1
AMS01154.1	006468	Cluster6261_1clades	267	AR9_g070	Bacillus phage AR9	GCA_001743835.1
ASU00083.1	006468	Cluster6261_1clades	263	PBI_PBS1_261	Bacillus virus PBS1	GCA_002601325.1
AMS01184.1	006469	Cluster6262_1clades	267	AR9_g100	Bacillus phage AR9	GCA_001743835.1
ASU00118.1	006469	Cluster6262_1clades	267	PBI_PBS1_296	Bacillus virus PBS1	GCA_002601325.1
BAW19090.1	006470	Cluster6263_1clades	267	FDH28_gp116	Ralstonia phage RP12	GCA_002617345.1
BAW19376.1	006470	Cluster6263_1clades	267	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000227	006471	TM	268	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000177	006471	TM	268	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14718.1	006472	BAM	266	Lu11_0181	Pseudomonas phage Lu11	GCA_000897175.1
AGS81994.2	006472	BAM	260	PaBG_00109	Pseudomonas phage PaBG	GCA_000912555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69077.1	006473	Cluster6266_1clades	260	CcrBL9_gp053c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69637.1	006473	Cluster6266_1clades	266	CcrSC_gp055c	Caulobacter phage CcrSC	GCA_003443315.1
prevph1000000050	006474	Cluster6267_1clades	267	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000039	006474	Cluster6267_1clades	267	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000646	006475	Cluster6268_1clades	267	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000461	006475	Cluster6268_1clades	267	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000757	006476	Cluster6269_1clades	267	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000509	006476	Cluster6269_1clades	267	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAW19078.1	006477	TM	265	FDH28_gp104	Ralstonia phage RP12	GCA_002617345.1
BAW19363.1	006477	TM	265	-	Ralstonia phage RP31	GCA_002617365.1
QBX32512.1	006478	Cluster6272_1clades	265	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42085.1	006478	Cluster6272_1clades	265	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ALN97862.1	006479	Cluster6273_1clades	256	Bp8pS_183	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97863.1	006479	Cluster6273_1clades	264	Bp8pS_184	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
QBX06515.1	006480	Cluster6274_1clades	264	BcepSaruman_102	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74481.1	006480	Cluster6274_1clades	242	BcepSauron_101	Burkholderia phage BcepSauron	GCA_005394215.1
BAW19230.1	006481	Cluster6275_1clades	263	FDH28_gp165	Ralstonia phage RP12	GCA_002617345.1
BAW19516.1	006481	Cluster6275_1clades	263	-	Ralstonia phage RP31	GCA_002617365.1
BBI90541.1	006482	Cluster6276_1clades	254	HYO65_gp149	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90849.1	006482	Cluster6276_1clades	263	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000629	006483	Glyco_transf_25	264	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000447	006483	Glyco_transf_25	254	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03901.1	006484	Cluster6278_1clades	257	JOAD_14	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03656.1	006484	Cluster6278_1clades	262	RISINGSUN_14	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AUZ94876.1	006485	Cluster6279_1clades	262	FDI40_gp064	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44030.1	006485	Cluster6279_1clades	252	PBI_SCTP2_15	Salicola phage SCTP-2	GCA_002625545.1
AXQ69319.1	006486	Cluster6280_1clades	262	CcrBL9_gp295	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69879.1	006486	Cluster6280_1clades	262	CcrSC_gp297	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69518.1	006487	Cluster6281_1clades	262	CcrBL9_gp494	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70063.1	006487	Cluster6281_1clades	249	CcrSC_gp481	Caulobacter phage CcrSC	GCA_003443315.1
BAE47710.1	006488	Phage_pRha+ANT	262	CST012	Clostridium phage c-st	GCA_000865225.1
BAE47868.1	006488	Phage_pRha+ANT	240	CST170	Clostridium phage c-st	GCA_000865225.1
BAW19166.1	006489	SIG+SBP_bac_11	262	FDH28_gp229	Ralstonia phage RP12	GCA_002617345.1
BAW19452.1	006489	SIG+SBP_bac_11	262	-	Ralstonia phage RP31	GCA_002617365.1
CCH63498.1	006490	Cluster6284_1clades	262	CP21_036	Campylobacter virus CP21	GCA_000902535.1
CCH63703.1	006490	Cluster6284_1clades	230	CP21_243	Campylobacter virus CP21	GCA_000902535.1
QHJ86079.1	006491	SIG+RnaseH	160	KKIINIFJ_00167	Pseudomonas phage PN05	GCA_009931935.1
QHJ86189.1	006491	SIG+RnaseH	262	KKIINIFJ_00279	Pseudomonas phage PN05	GCA_009931935.1
AIX30708.1	006492	Cluster6286_1clades	261	Syn7803US37_231	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30505.1	006492	Cluster6286_1clades	253	Syn7803US37_28	Synechococcus phage ACG-2014f	GCA_002594065.1
ARV77184.1	006493	Cluster6287_1clades	261	NOXIFER_13	Pseudomonas phage Noxifer	GCA_002625005.1
BAG41739.1	006493	Cluster6287_1clades	164	RSL1_ORF293	Ralstonia phage phiRSL1	GCA_000879455.1
ATA65445.1	006494	MACRODOMAIN	261	2050HW_00110	Serratia phage 2050HW	GCA_002628125.1
QDB71215.1	006494	MACRODOMAIN	261	CPT_Moabite_185	Serratia phage Moabite	GCA_006384735.1
QBX32173.1	006495	Cluster6289_1clades	261	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41753.1	006495	Cluster6289_1clades	261	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97334.1	006496	Cluster6290_1clades	261	D6_0175	Aeromonas phage D6	GCA_007051205.2
QDH47104.1	006496	Cluster6290_1clades	261	LAh10_94	Aeromonas phage LAh10	GCA_006863975.1
QDJ97171.1	006497	Cluster6291_1clades	261	D6_0012	Aeromonas phage D6	GCA_007051205.2
QDH47105.1	006497	Cluster6291_1clades	261	LAh10_180.1	Aeromonas phage LAh10	GCA_006863975.1
AMS01318.1	006498	Cluster6292_1clades	260	AR9_g234	Bacillus phage AR9	GCA_001743835.1
AST99947.1	006498	Cluster6292_1clades	260	PBI_PBS1_125	Bacillus virus PBS1	GCA_002601325.1
AAX44637.1	006499	BACTERIALFRINGE	243	PSSM2_260	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12334.1	006499	BACTERIALFRINGE	259	PRTG_00181	Prochlorococcus phage P-SSM5	GCA_002991095.1
QCW22966.1	006500	NodZ	259	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50564.1	006500	NodZ	259	-	Synechococcus phage S-B43	GCA_006869725.1
AND75340.1	006501	LysM	258	ME3_179	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AFH14645.1	006501	LysM	208	Lu11_0113	Pseudomonas phage Lu11	GCA_000897175.1
QGT54742.1	006502	TRPR-HTH+TM	258	b23_0127	Synechococcus phage B23	GCA_009745195.1
QGT54372.1	006502	TRPR-HTH+TM	258	b3_0128	Synechococcus phage B3	GCA_009745215.1
BAW19010.1	006503	Cluster6299_1clades	257	FDH28_gp036	Ralstonia phage RP12	GCA_002617345.1
BAW19296.1	006503	Cluster6299_1clades	257	-	Ralstonia phage RP31	GCA_002617365.1
BBI90683.1	006504	Cluster6300_1clades	257	HYO65_gp291	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90990.1	006504	Cluster6300_1clades	257	-	Tenacibaculum phage PTm5	GCA_009730715.1
ABS83622.1	006505	SIG+GrpE	235	0305phi8-36p062	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44872.1	006505	SIG+GrpE	256	SP15_073	Bacillus phage SP-15	GCA_001754685.1
AMS01330.1	006506	Cluster6304_1clades	256	AR9_g246	Bacillus phage AR9	GCA_001743835.1
AST99959.1	006506	Cluster6304_1clades	254	PBI_PBS1_138	Bacillus virus PBS1	GCA_002601325.1
BAW19179.1	006507	Cluster6305_1clades	256	FDH28_gp216	Ralstonia phage RP12	GCA_002617345.1
BAW19465.1	006507	Cluster6305_1clades	256	-	Ralstonia phage RP31	GCA_002617365.1
QBX06740.1	006508	Cluster6306_1clades	256	BcepSaruman_327	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74709.1	006508	Cluster6306_1clades	252	BcepSauron_329	Burkholderia phage BcepSauron	GCA_005394215.1
AXG67079.1	006509	Phage-tail-tape	255	AD1_035	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08312.1	006509	Phage-tail-tape	224	Alexandra_32	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXQ69296.1	006510	Myosin_tail_1	251	CcrBL9_gp272c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69855.1	006510	Myosin_tail_1	255	CcrSC_gp273c	Caulobacter phage CcrSC	GCA_003443315.1
BAS04985.1	006511	Cluster6309_1clades	254	AVU11_gp193	Ralstonia phage RSF1	GCA_001500875.1
BAQ02714.1	006511	Cluster6309_1clades	255	AVU38_gp186	Ralstonia phage RSL2	GCA_001503055.1
prevph1000000195	006512	Cluster6310_1clades	199	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000158	006512	Cluster6310_1clades	256	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44948.1	006513	SIG+GGDEF	183	SP15_150	Bacillus phage SP-15	GCA_001754685.1
AEO93609.1	006513	SIG+GGDEF	254	G_350	Bacillus virus G	GCA_000917535.1
AFU88121.1	006514	Casc1_N	254	CcrColossus_gp251	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68799.1	006514	Casc1_N	176	CcrPW_gp260	Caulobacter phage CcrPW	GCA_003443275.1
QBX32177.1	006515	Cluster6313_1clades	254	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41756.1	006515	Cluster6313_1clades	254	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000019	006516	Cluster6314_1clades	255	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000017	006516	Cluster6314_1clades	255	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03905.1	006517	Cluster6315_1clades	253	JOAD_10	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03660.1	006517	Cluster6315_1clades	253	RISINGSUN_10	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXF51260.1	006518	Cluster6316_1clades	253	WELLINGTON_130	Erwinia phage Wellington	GCA_003344985.1
ANZ49480.1	006518	Cluster6316_1clades	252	KWAN_128	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXQ70515.1	006519	Cluster6317_1clades	240	HOU04_gp116	Synechococcus phage S-T4	GCA_003443335.1
AXQ70514.1	006519	Cluster6317_1clades	253	HOU04_gp115	Synechococcus phage S-T4	GCA_003443335.1
BAS04989.1	006520	Cluster6318_1clades	231	AVU11_gp197	Ralstonia phage RSF1	GCA_001500875.1
BAQ02718.1	006520	Cluster6318_1clades	253	AVU38_gp190	Ralstonia phage RSL2	GCA_001503055.1
AXH71030.1	006521	Cluster6319_1clades	246	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21124.1	006521	Cluster6319_1clades	253	-	Vibrio phage vB_pir03	GCA_014319855.1
prevph1000000046	006522	Cluster6320_1clades	254	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000037	006522	Cluster6320_1clades	254	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000852	006523	Cluster6321_1clades	254	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000590	006523	Cluster6321_1clades	254	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXG67324.1	006524	Cluster6322_1clades	252	AD1_280	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08551.1	006524	Cluster6322_1clades	169	Alexandra_295	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BBI90518.1	006525	Cluster6323_1clades	211	HYO65_gp126	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90826.1	006525	Cluster6323_1clades	252	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ96781.1	006526	Cluster6324_1clades	252	PS1_0022	Aeromonas phage PS1	GCA_007051165.2
QFR59413.1	006526	Cluster6324_1clades	252	PS2_0022	Aeromonas phage PS2	GCA_009388305.2
AFA44563.1	006527	SIG+Tox-NucA	226	RaK2_00290	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72873.1	006527	SIG+Tox-NucA	251	-	Myoviridae sp.	GCA_003657725.1
BAS04954.2	006528	Cluster6326_1clades	251	AVU11_agp33	Ralstonia phage RSF1	GCA_001500875.1
BAQ02679.2	006528	Cluster6326_1clades	251	-	Ralstonia phage RSL2	GCA_001503055.1
QGT54850.1	006529	C3RHD	251	b23_0236	Synechococcus phage B23	GCA_009745195.1
QGT54484.1	006529	C3RHD	251	b3_0242	Synechococcus phage B3	GCA_009745215.1
AAX44590.1	006530	Cluster6328_1clades	250	PSSM2_213	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12381.1	006530	Cluster6328_1clades	250	PRTG_00228	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXH70881.1	006531	Cluster6329_1clades	250	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21132.1	006531	Cluster6329_1clades	240	-	Vibrio phage vB_pir03	GCA_014319855.1
BAS04901.2	006532	Cluster6332_1clades	250	AVU11_gp109	Ralstonia phage RSF1	GCA_001500875.1
BAQ02627.1	006532	Cluster6332_1clades	242	AVU38_gp099	Ralstonia phage RSL2	GCA_001503055.1
QBZ70700.1	006533	Cluster6335_1clades	241	pETSU_119	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89589.1	006533	Cluster6335_1clades	249	OBP_152	Pseudomonas phage OBP	GCA_000896635.1
AMS01153.1	006534	Cluster6336_1clades	249	AR9_g069	Bacillus phage AR9	GCA_001743835.1
ASU00082.1	006534	Cluster6336_1clades	249	PBI_PBS1_260	Bacillus virus PBS1	GCA_002601325.1
BBI90404.1	006535	Cluster6337_1clades	249	HYO65_gp012	Tenacibaculum phage PTm1	GCA_009730695.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBI90713.1	006535	Cluster6337_1clades	249	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90646.1	006536	Cluster6338_1clades	249	HYO65_gp254	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90952.1	006536	Cluster6338_1clades	249	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ97285.1	006537	Cluster6339_1clades	249	D6_0125	Aeromonas phage D6	GCA_007051205.2
QDH47110.1	006537	Cluster6339_1clades	249	LAh10_55	Aeromonas phage LAh10	GCA_006863975.1
QGT54926.1	006538	TM	249	b23_0313	Synechococcus phage B23	GCA_009745195.1
QGT54561.1	006538	TM	249	b3_0320	Synechococcus phage B3	GCA_009745215.1
ABS83621.1	006539	ICAD	248	0305phi8-36p061	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44974.1	006539	ICAD	232	SP15_176	Bacillus phage SP-15	GCA_001754685.1
ABS83801.1	006540	Cluster6342_1clades	248	0305phi8-36p101	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83798.1	006540	Cluster6342_1clades	248	0305phi8-36p101R	Bacillus phage 0305phi8-36	GCA_000871045.1
AGH07549.1	006541	PMM	230	CYVG_00105	Cyanophage S-SSM6a	GCA_002710385.1
AIR93462.1	006541	PMM	248	AVU42_gp126	Prochlorococcus phage P-TIM68	GCA_001503075.1
AXQ69375.1	006542	Cluster6344_1clades	248	CcrBL9_gp351	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69935.1	006542	Cluster6344_1clades	246	CcrSC_gp353	Caulobacter phage CcrSC	GCA_003443315.1
AMM44891.1	006543	NUDIX	219	SP15_092	Bacillus phage SP-15	GCA_001754685.1
ARV77410.1	006543	NUDIX	247	NOXIFER_245	Pseudomonas phage Noxifer	GCA_002625005.1
AXQ69439.1	006544	Cluster6346_1clades	247	CcrBL9_gp415	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69990.1	006544	Cluster6346_1clades	247	CcrSC_gp408	Caulobacter phage CcrSC	GCA_003443315.1
BBA65463.1	006545	Cluster6347_1clades	244	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96472.1	006545	Cluster6347_1clades	247	Xoosp13_286	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65479.1	006546	Cluster6348_1clades	246	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96487.1	006546	Cluster6348_1clades	247	Xoosp13_301	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96790.1	006547	Cluster6349_1clades	247	PS1_0031	Aeromonas phage PS1	GCA_007051165.2
QFR59421.1	006547	Cluster6349_1clades	247	PS2_0030	Aeromonas phage PS2	GCA_009388305.2
QGT54735.1	006548	Cluster6350_1clades	246	b23_0120	Synechococcus phage B23	GCA_009745195.1
QGT54365.1	006548	Cluster6350_1clades	246	b3_0121	Synechococcus phage B3	GCA_009745215.1
prevph1000000321	006549	Cluster6351_1clades	247	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000250	006549	Cluster6351_1clades	247	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXF51265.1	006550	Cluster6352_1clades	245	WELLINGTON_135	Erwinia phage Wellington	GCA_003344985.1
ANZ49486.1	006550	Cluster6352_1clades	245	KWAN_134	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
BAS04946.1	006551	DnaB	186	AVU11_gp154	Ralstonia phage RSF1	GCA_001500875.1
BAQ02670.1	006551	DnaB	245	AVU38_gp142	Ralstonia phage RSL2	GCA_001503055.1
BAW19006.1	006552	DUF1281_C	245	FDH28_gp032	Ralstonia phage RP12	GCA_002617345.1
BAW19292.1	006552	DUF1281_C	245	-	Ralstonia phage RP31	GCA_002617365.1
BAW19165.1	006553	SIG+TM+TM+TM+TM+TM	245	FDH28_gp230	Ralstonia phage RP12	GCA_002617345.1
BAW19451.1	006553	SIG+TM+TM+TM+TM+TM	245	-	Ralstonia phage RP31	GCA_002617365.1
QBX06830.1	006554	Cluster6356_1clades	245	BcepSaruman_417	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74799.1	006554	Cluster6356_1clades	245	BcepSauron_419	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06525.1	006555	TM	245	BcepSaruman_112	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74491.1	006555	TM	197	BcepSauron_111	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97180.1	006556	Cluster6358_1clades	245	D6_0020	Aeromonas phage D6	GCA_007051205.2
QDH47115.1	006556	Cluster6358_1clades	244	LAh10_188	Aeromonas phage LAh10	GCA_006863975.1
AIA64855.1	006557	TM	244	S13_056	Cronobacter phage S13	GCA_001503575.1
QHJ78810.1	006557	TM	245	-	Myoviridae sp.	GCA_012593985.1
prevph1000000387	006558	Cluster6360_1clades	107	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000313	006558	Cluster6360_1clades	246	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000827	006559	SIG+Intein_splicing	147	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000571	006559	SIG+Intein_splicing	246	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83574.1	006560	Mobilization_B	182	0305phi8-36p009	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83575.1	006560	Mobilization_B	244	0305phi8-36p010	Bacillus phage 0305phi8-36	GCA_000871045.1
APU01760.1	006561	Cluster6363_1clades	240	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53403.1	006561	Cluster6363_1clades	244	65p396	Aeromonas virus 65	GCA_000893255.1
BBA65500.1	006562	Cluster6364_1clades	244	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96508.1	006562	Cluster6364_1clades	244	Xoosp13_322	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90567.1	006563	Cluster6365_1clades	244	HYO65_gp175	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90875.1	006563	Cluster6365_1clades	244	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ97310.1	006564	Cluster6366_1clades	244	D6_0150	Aeromonas phage D6	GCA_007051205.2
QDH47114.1	006564	Cluster6366_1clades	244	LAh10_75	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000066	006565	Cluster6367_1clades	245	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000052	006565	Cluster6367_1clades	245	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65498.1	006566	Cluster6368_1clades	243	2050HW_00163	Serratia phage 2050HW	GCA_002628125.1
QDB71266.1	006566	Cluster6368_1clades	243	CPT_Moabite_236	Serratia phage Moabite	GCA_006384735.1
AEO93439.1	006567	Cluster6370_1clades	242	G_179	Bacillus virus G	GCA_000917535.1
AEO93440.1	006567	Cluster6370_1clades	188	G_180	Bacillus virus G	GCA_000917535.1
ASV44411.1	006568	Cluster6371_1clades	236	PBI_SCTP2_396	Salicola phage SCTP-2	GCA_002625545.1
ASV44412.1	006568	Cluster6371_1clades	242	PBI_SCTP2_397	Salicola phage SCTP-2	GCA_002625545.1
BAS04986.1	006569	Cluster6372_1clades	242	AVU11_gp194	Ralstonia phage RSF1	GCA_001500875.1
BAQ02715.2	006569	Cluster6372_1clades	194	-	Ralstonia phage RSL2	GCA_001503055.1
ASV44722.1	006570	Cluster6374_1clades	232	FDI40_gp148	Agrobacterium phage Atu_ph07	GCA_002628245.1
AKF13644.1	006570	Cluster6374_1clades	241	PHIN3_381	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01319.1	006571	Cluster6375_1clades	241	AR9_g235	Bacillus phage AR9	GCA_001743835.1
AST99948.1	006571	Cluster6375_1clades	241	PBI_PBS1_126	Bacillus virus PBS1	GCA_002601325.1
AOO14242.1	006572	Cluster6376_1clades	241	Sn110110_048	Cyanophage S-RIM14	GCA_002599065.1
AOO14894.1	006572	Cluster6376_1clades	241	W1230910_048	Cyanophage S-RIM14	GCA_002599125.1
AXQ69254.1	006573	tRNA-synt_His	241	CcrBL9_gp230c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69811.1	006573	tRNA-synt_His	241	CcrSC_gp229c	Caulobacter phage CcrSC	GCA_003443315.1
AYD81268.1	006574	Cluster6378_1clades	241	SEA_JUSTBECAUSE_99	Streptomyces phage JustBecause	GCA_003613775.1
QJD53671.1	006574	Cluster6378_1clades	241	SEA_KELA_100	Streptomyces phage Kela	GCA_012934305.1
prevph1000000256	006575	Cluster6379_1clades	242	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000203	006575	Cluster6379_1clades	242	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BBI90712.1	006576	Cluster6380_2clades	135	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000462	006576	Cluster6380_2clades	242	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AFU88076.1	006577	Cluster6381_1clades	240	CcrColossus_gp206	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68753.1	006577	Cluster6381_1clades	222	CcrPW_gp214c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01320.1	006578	Cluster6382_1clades	240	AR9_g236	Bacillus phage AR9	GCA_001743835.1
AST99949.1	006578	Cluster6382_1clades	240	PBI_PBS1_127	Bacillus virus PBS1	GCA_002601325.1
QCW22971.1	006579	Cluster6383_1clades	240	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50559.1	006579	Cluster6383_1clades	240	-	Synechococcus phage S-B43	GCA_006869725.1
prevph1000000353	006580	Cluster6384_1clades	241	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000279	006580	Cluster6384_1clades	241	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000378	006581	Cluster6385_1clades	241	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000304	006581	Cluster6385_1clades	241	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000770	006582	Cluster6386_1clades	241	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000523	006582	Cluster6386_1clades	241	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44434.1	006583	Cluster6387_1clades	239	PSSM2_056	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12218.1	006583	Cluster6387_1clades	239	PRTG_00060	Prochlorococcus phage P-SSM5	GCA_002991095.1
ARM70870.1	006584	SIS	211	phiC120_c165	Escherichia phage phiC120	GCA_002621185.1
AFF28210.1	006584	SIS	239	PAU_212	Sphingomonas phage PAU	GCA_000902455.1
ALN97681.1	006585	Cluster6389_1clades	239	Bp8pS_002	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97719.1	006585	Cluster6389_1clades	234	Bp8pS_040	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AXQ69085.1	006586	Cluster6390_1clades	239	CcrBL9_gp061c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69640.1	006586	Cluster6390_1clades	153	CcrSC_gp058c	Caulobacter phage CcrSC	GCA_003443315.1
BBI90421.1	006587	Cluster6391_1clades	239	HYO65_gp029	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90728.1	006587	Cluster6391_1clades	239	-	Tenacibaculum phage PTm5	GCA_009730715.1
AFU88178.1	006588	Cluster6392_1clades	238	CcrColossus_gp308	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68855.1	006588	Cluster6392_1clades	238	CcrPW_gp316	Caulobacter phage CcrPW	GCA_003443275.1
AOO14232.1	006589	Cluster6393_1clades	238	Sn110110_038	Cyanophage S-RIM14	GCA_002599065.1
AOO14884.1	006589	Cluster6393_1clades	238	W1230910_038	Cyanophage S-RIM14	GCA_002599125.1
AXH72846.1	006590	ATP_bind_3	238	-	Myoviridae sp.	GCA_003657725.1
QCG76301.1	006590	ATP_bind_3	203	EST35_0433	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QDJ97179.1	006591	Cluster6395_1clades	221	D6_0019	Aeromonas phage D6	GCA_007051205.2
QDH47120.1	006591	Cluster6395_1clades	238	LAh10_187	Aeromonas phage LAh10	GCA_006863975.1
QDJ96750.1	006592	Cluster6396_1clades	238	PS1_0239	Aeromonas phage PS1	GCA_007051165.2
QFR59383.1	006592	Cluster6396_1clades	238	PS2_0241	Aeromonas phage PS2	GCA_009388305.2
AMS01204.1	006593	Cluster6397_1clades	237	AR9_g120	Bacillus phage AR9	GCA_001743835.1
AST99828.1	006593	Cluster6397_1clades	237	PBI_PBS1_6	Bacillus virus PBS1	GCA_002601325.1
BAG41752.1	006594	Cluster6398_1clades	237	RSL1_ORF306	Ralstonia phage phiRSL1	GCA_000879455.1
AQW88969.1	006594	Cluster6398_1clades	227	BF_0444	Serratia phage BF	GCA_002619745.1
BBA65427.1	006595	Tox-ABHYDROLASE3	237	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96446.1	006595	Tox-ABHYDROLASE3	236	Xoosp13_260	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QCW22969.1	006596	BACTERIALFRINGE	237	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50561.1	006596	BACTERIALFRINGE	237	-	Synechococcus phage S-B43	GCA_006869725.1
QDJ97186.1	006597	Cluster6401_1clades	237	D6_0026	Aeromonas phage D6	GCA_007051205.2
QDH47121.1	006597	Cluster6401_1clades	237	LAh10_194	Aeromonas phage LAh10	GCA_006863975.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000099	006598	Cluster6402_1clades	162	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000069	006598	Cluster6402_1clades	238	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEH03703.1	006599	Cluster6403_1clades	102	280	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03704.1	006599	Cluster6403_1clades	236	281	Pseudomonas phage PhiPA3	GCA_001502095.1
AMS01194.1	006600	Cluster6404_1clades	236	AR9_g110	Bacillus phage AR9	GCA_001743835.1
ASU00128.1	006600	Cluster6404_1clades	236	PBI_PBS1_306	Bacillus virus PBS1	GCA_002601325.1
AXG67289.1	006601	Cluster6405_1clades	234	AD1_245	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08512.1	006601	Cluster6405_1clades	236	Alexandra_255	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QDJ97170.1	006602	Cluster6406_1clades	236	D6_0011	Aeromonas phage D6	GCA_007051205.2
QDH47123.1	006602	Cluster6406_1clades	236	LAh10_180	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000139	006603	Cluster6407_1clades	237	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000107	006603	Cluster6407_1clades	237	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ALN97683.1	006604	Novel-BECR	235	Bp8pS_004	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97684.1	006604	Novel-BECR	219	Bp8pS_005	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AMS01376.1	006605	SIG+TM	235	AR9_g292	Bacillus phage AR9	GCA_001743835.1
ASU00007.1	006605	SIG+TM	235	PBI_PBS1_185	Bacillus virus PBS1	GCA_002601325.1
BAW19136.1	006606	Cluster6410_1clades	235	FDH28_gp259	Ralstonia phage RP12	GCA_002617345.1
BAW19422.1	006606	Cluster6410_1clades	235	-	Ralstonia phage RP31	GCA_002617365.1
BAW19161.1	006607	Cluster6411_1clades	235	FDH28_gp234	Ralstonia phage RP12	GCA_002617345.1
BAW19447.1	006607	Cluster6411_1clades	235	-	Ralstonia phage RP31	GCA_002617365.1
AJK27618.1	006608	Cluster6412_1clades	210	PTIM40_204	Cyanophage P-TIM40	GCA_001470935.1
AGG54377.1	006608	Cluster6412_1clades	234	CYWG_00093	Cyanophage S-SSM6b	GCA_002710425.1
AFU88046.1	006609	Cluster6413_1clades	232	CcrColossus_gp176	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68723.1	006609	Cluster6413_1clades	234	CcrPW_gp184c	Caulobacter phage CcrPW	GCA_003443275.1
BBI90558.1	006610	TM	234	HYO65_gp166	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90866.1	006610	TM	234	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBZ70832.1	006611	Cluster6416_1clades	233	pETSU_251	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89462.1	006611	Cluster6416_1clades	233	OBP_025	Pseudomonas phage OBP	GCA_000896635.1
QBX06439.1	006612	Cluster6417_1clades	233	BcepSaruman_026	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74407.1	006612	Cluster6417_1clades	233	BcepSauron_027	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97290.1	006613	Cluster6418_1clades	233	D6_0130	Aeromonas phage D6	GCA_007051205.2
QDH47124.1	006613	Cluster6418_1clades	233	LAh10_57	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000210	006614	Cluster6419_1clades	234	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000166	006614	Cluster6419_1clades	234	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44877.1	006615	Cluster6421_1clades	232	SP15_078	Bacillus phage SP-15	GCA_001754685.1
AMM45017.1	006615	Cluster6421_1clades	202	SP15_217	Bacillus phage SP-15	GCA_001754685.1
AXQ69124.1	006616	Cluster6423_1clades	232	CcrBL9_gp100	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69678.1	006616	Cluster6423_1clades	232	CcrSC_gp096	Caulobacter phage CcrSC	GCA_003443315.1
BBI90430.1	006617	Cluster6424_1clades	232	HYO65_gp038	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90737.1	006617	Cluster6424_1clades	232	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90661.1	006618	Amidase_2	232	HYO65_gp269	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90966.1	006618	Amidase_2	232	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ97416.1	006619	Cluster6426_1clades	232	D6_0257	Aeromonas phage D6	GCA_007051205.2
QDH47125.1	006619	Cluster6426_1clades	232	LAh10_168	Aeromonas phage LAh10	GCA_006863975.1
AFU88163.1	006620	Cluster6428_1clades	231	CcrColossus_gp293	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68839.1	006620	Cluster6428_1clades	221	CcrPW_gp300	Caulobacter phage CcrPW	GCA_003443275.1
AFU88168.1	006621	Imm34	231	CcrColossus_gp298	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68845.1	006621	Imm34	231	CcrPW_gp306	Caulobacter phage CcrPW	GCA_003443275.1
ATA65403.1	006622	Cluster6430_1clades	231	2050HW_00068	Serratia phage 2050HW	GCA_002628125.1
QDB71182.1	006622	Cluster6430_1clades	231	CPT_Moabite_152	Serratia phage Moabite	GCA_006384735.1
QBX32352.1	006623	Cluster6431_1clades	231	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41926.1	006623	Cluster6431_1clades	231	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54956.1	006624	TylF	231	b23_0350	Synechococcus phage B23	GCA_009745195.1
QGT54591.1	006624	TylF	231	b3_0356	Synechococcus phage B3	GCA_009745215.1
ALN97690.1	006625	tRNA-synt_2b	217	Bp8pS_011	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93546.1	006625	tRNA-synt_2b	230	G_287	Bacillus virus G	GCA_000917535.1
QBZ70712.1	006626	Cluster6434_1clades	223	pETSU_131	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89641.1	006626	Cluster6434_1clades	230	OBP_204	Pseudomonas phage OBP	GCA_000896635.1
AMS01090.1	006627	DUF2786	230	AR9_g005	Bacillus phage AR9	GCA_001743835.1
ASU00012.1	006627	DUF2786	230	PBI_PBS1_190	Bacillus virus PBS1	GCA_002601325.1
AMS01149.1	006628	Cluster6436_1clades	230	AR9_g065	Bacillus phage AR9	GCA_001743835.1
ASU00078.1	006628	Cluster6436_1clades	230	PBI_PBS1_256	Bacillus virus PBS1	GCA_002601325.1
AXF51215.1	006629	Cluster6437_1clades	230	WELLINGTON_85	Erwinia phage Wellington	GCA_003344985.1
ANZ49437.1	006629	Cluster6437_1clades	230	KWAN_85	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51220.1	006630	Cluster6438_1clades	230	WELLINGTON_90	Erwinia phage Wellington	GCA_003344985.1
ANZ49441.1	006630	Cluster6438_1clades	230	KWAN_89	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
BBA65373.1	006631	SGT1	230	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96401.1	006631	SGT1	218	Xoosp13_215	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06469.1	006632	Cluster6441_1clades	166	BcepSaruman_056	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74436.1	006632	Cluster6441_1clades	230	BcepSauron_056	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54858.1	006633	Cluster6442_1clades	230	b23_0244	Synechococcus phage B23	GCA_009745195.1
QGT54492.1	006633	Cluster6442_1clades	230	b3_0250	Synechococcus phage B3	GCA_009745215.1
AMM44995.1	006634	NMDAR2_C	226	SP15_195	Bacillus phage SP-15	GCA_001754685.1
SBV38524.1	006634	NMDAR2_C	230	BN7874_289	Phage NCTB	GCA_900092385.1
AFU87920.1	006635	Cluster6444_1clades	227	CcrColossus_gp050	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68592.1	006635	Cluster6444_1clades	229	CcrPW_gp053	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69366.1	006636	SIG+Gcw_chp	229	CcrBL9_gp342	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69926.1	006636	SIG+Gcw_chp	229	CcrSC_gp344	Caulobacter phage CcrSC	GCA_003443315.1
BAS04880.1	006637	ILEI	219	AVU11_gp088	Ralstonia phage RSF1	GCA_001500875.1
BAQ02610.1	006637	ILEI	229	AVU38_gp082	Ralstonia phage RSL2	GCA_001503055.1
BAS05001.2	006638	Cluster6447_1clades	228	AVU11_gp209	Ralstonia phage RSF1	GCA_001500875.1
BAQ02730.1	006638	Cluster6447_1clades	229	AVU38_gp202	Ralstonia phage RSL2	GCA_001503055.1
BAW19178.1	006639	Cluster6448_1clades	229	FDH28_gp217	Ralstonia phage RP12	GCA_002617345.1
BAW19464.1	006639	Cluster6448_1clades	229	-	Ralstonia phage RP31	GCA_002617365.1
BBI90685.1	006640	Cluster6450_1clades	229	HYO65_gp293	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90992.1	006640	Cluster6450_1clades	229	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ97369.1	006641	SIG+TM+TM+TM	229	D6_0210	Aeromonas phage D6	GCA_007051205.2
QDH47127.1	006641	SIG+TM+TM+TM	229	LAh10_124	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000753	006642	Cluster6453_1clades	230	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000505	006642	Cluster6453_1clades	230	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000760	006643	Cluster6454_1clades	210	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000512	006643	Cluster6454_1clades	230	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000774	006644	Cluster6455_1clades	230	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000527	006644	Cluster6455_1clades	230	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14633.1	006645	Cluster6456_1clades	228	Lu11_0101	Pseudomonas phage Lu11	GCA_000897175.1
AGS82075.1	006645	Cluster6456_1clades	227	PaBG_00200	Pseudomonas phage PaBG	GCA_000912555.1
AIA65015.1	006646	Cluster6457_1clades	228	S13_218	Cronobacter phage S13	GCA_001503575.1
QHJ78917.1	006646	Cluster6457_1clades	216	-	Myoviridae sp.	GCA_012593985.1
prevph1000000137	006647	Cluster6458_1clades	142	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000105	006647	Cluster6458_1clades	229	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QCW22970.1	006648	Cluster6459_1clades	227	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50560.1	006648	Cluster6459_1clades	227	-	Synechococcus phage S-B43	GCA_006869725.1
QDJ96779.1	006649	Cluster6460_1clades	227	PS1_0020	Aeromonas phage PS1	GCA_007051165.2
QFR59411.1	006649	Cluster6460_1clades	227	PS2_0020	Aeromonas phage PS2	GCA_009388305.2
prevph1000000418	006650	Cluster6461_1clades	228	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000329	006650	Cluster6461_1clades	228	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65509.1	006651	Cluster6462_1clades	226	2050HW_00174	Serratia phage 2050HW	GCA_002628125.1
QDB71277.1	006651	Cluster6462_1clades	226	CPT_Moabite_247	Serratia phage Moabite	GCA_006384735.1
BBA65377.1	006652	SIG+Phage_tail_APC	226	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96405.1	006652	SIG+Phage_tail_APC	226	Xoosp13_219	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65586.1	006653	Cluster6465_1clades	172	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65583.1	006653	Cluster6465_1clades	226	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ97309.1	006654	Cluster6466_1clades	226	D6_0149	Aeromonas phage D6	GCA_007051205.2
QDH47129.1	006654	Cluster6466_1clades	226	LAh10_74	Aeromonas phage LAh10	GCA_006863975.1
BBA65417.1	006655	Cluster6467_1clades	216	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96440.1	006655	Cluster6467_1clades	226	Xoosp13_254	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AAX44682.1	006656	Cluster6469_1clades	225	PSSM2_305	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12294.1	006656	Cluster6469_1clades	225	PRTG_00141	Prochlorococcus phage P-SSM5	GCA_002991095.1
CCH63604.1	006657	Cluster6470_1clades	225	CP21_142	Campylobacter virus CP21	GCA_000902535.1
QAU04559.1	006657	Cluster6470_1clades	216	ValB1MD_276	Vibrio phage ValB1MD	GCA_004138815.1
QBX06478.1	006658	Cluster6471_1clades	225	BcepSaruman_065	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74445.1	006658	Cluster6471_1clades	225	BcepSauron_065	Burkholderia phage BcepSauron	GCA_005394215.1
ABS83803.1	006659	Cluster6472_1clades	224	0305phi8-36p103	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83800.1	006659	Cluster6472_1clades	224	0305phi8-36p103R	Bacillus phage 0305phi8-36	GCA_000871045.1
AFU88138.1	006660	HAD	224	CcrColossus_gp268	Caulobacter phage CcrColossus	GCA_000899635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ68814.1	006660	HAD	224	CcrPW_gp275	Caulobacter phage CcrPW	GCA_003443275.1
AXF51261.1	006661	Cluster6474_1clades	224	WELLINGTON_131	Erwinia phage Wellington	GCA_003344985.1
ANZ49481.1	006661	Cluster6474_1clades	224	KWAN_129	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
BAS04810.2	006662	Cluster6475_1clades	156	AVU11_agp07	Ralstonia phage RSF1	GCA_001500875.1
BAQ02546.2	006662	Cluster6475_1clades	224	-	Ralstonia phage RSL2	GCA_001503055.1
QDJ97339.1	006663	Cluster6476_1clades	224	D6_0180	Aeromonas phage D6	GCA_007051205.2
QDH47131.1	006663	Cluster6476_1clades	224	LAh10_99	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000004	006664	Cluster6477_1clades	225	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000004	006664	Cluster6477_1clades	225	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASR76241.1	006665	PfkB	223	PBI_BELLAMY_205	Synechococcus phage Bellamy	GCA_002627525.1
QJT70197.1	006665	PfkB	223	SynMITS9220M01_191	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASU03855.1	006666	Cluster6479_1clades	223	JOAD_60	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03610.1	006666	Cluster6479_1clades	223	RISINGSUN_60	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
CCH63478.1	006667	Cluster6480_1clades	223	CP21_016	Campylobacter virus CP21	GCA_000902535.1
QAU04515.1	006667	Cluster6480_1clades	218	ValB1MD_182	Vibrio phage ValB1MD	GCA_004138815.1
CCH63642.1	006668	Cluster6481_1clades	223	CP21_180	Campylobacter virus CP21	GCA_000902535.1
CCH63644.1	006668	Cluster6481_1clades	172	CP21_182	Campylobacter virus CP21	GCA_000902535.1
AXH71031.1	006669	Cluster6483_1clades	222	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21125.1	006669	Cluster6483_1clades	223	-	Vibrio phage vB_pir03	GCA_014319855.1
AFH14663.1	006670	Cluster6484_1clades	222	Lu11_0129	Pseudomonas phage Lu11	GCA_000897175.1
AGS82041.1	006670	Cluster6484_1clades	147	PaBG_00159	Pseudomonas phage PaBG	GCA_000912555.1
AIA65066.1	006671	Cluster6485_1clades	222	S13_269	Cronobacter phage S13	GCA_001503575.1
QHJ78865.1	006671	Cluster6485_1clades	217	-	Myoviridae sp.	GCA_012593985.1
ASU03904.1	006672	Cluster6486_1clades	222	JOAD_11	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03659.1	006672	Cluster6486_1clades	222	RISINGSUN_11	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65690.1	006673	Cluster6487_1clades	222	2050HW_00355	Serratia phage 2050HW	GCA_002628125.1
QDB71117.1	006673	Cluster6487_1clades	222	CPT_Moabite_087	Serratia phage Moabite	GCA_006384735.1
AXG67322.1	006674	Cluster6488_1clades	209	AD1_278	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08548.1	006674	Cluster6488_1clades	222	Alexandra_292	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AYD81359.1	006675	Cluster6489_1clades	222	SEA_JUSTBECAUSE_194	Streptomyces phage JustBecause	GCA_003613775.1
QJD53762.1	006675	Cluster6489_1clades	222	SEA_KELA_192	Streptomyces phage Kela	GCA_012934305.1
BAW19194.1	006676	Cluster6490_1clades	222	FDH28_gp201	Ralstonia phage RP12	GCA_002617345.1
BAW19480.1	006676	Cluster6490_1clades	222	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000748	006677	Cluster6491_1clades	109	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000500	006677	Cluster6491_1clades	223	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44676.1	006678	Cluster6492_1clades	221	PSSM2_299	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12300.1	006678	Cluster6492_1clades	221	PRTG_00147	Prochlorococcus phage P-SSM5	GCA_002991095.1
AOO14400.1	006679	2OG-FeII_Oxy_5	221	Sn110110_207	Cyanophage S-RIM14	GCA_002599065.1
AOO15049.1	006679	2OG-FeII_Oxy_5	221	W1230910_204	Cyanophage S-RIM14	GCA_002599125.1
QGT54846.1	006680	SIG+GDSL	221	b23_0232	Synechococcus phage B23	GCA_009745195.1
QGT54480.1	006680	SIG+GDSL	221	b3_0238	Synechococcus phage B3	GCA_009745215.1
prevph1000000134	006681	Cluster6495_1clades	222	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000102	006681	Cluster6495_1clades	222	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000333	006682	Cluster6496_1clades	222	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000262	006682	Cluster6496_1clades	222	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000857	006683	Cluster6497_1clades	222	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000595	006683	Cluster6497_1clades	222	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXF51221.1	006684	Cluster6498_1clades	220	WELLINGTON_91	Erwinia phage Wellington	GCA_003344985.1
ANZ49442.1	006684	Cluster6498_1clades	219	KWAN_90	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
BAW19094.1	006685	Cluster6499_1clades	220	FDH28_gp120	Ralstonia phage RP12	GCA_002617345.1
BAW19380.1	006685	Cluster6499_1clades	220	-	Ralstonia phage RP31	GCA_002617365.1
QDJ96780.1	006686	Cluster6500_1clades	220	PS1_0021	Aeromonas phage PS1	GCA_007051165.2
QFR59412.1	006686	Cluster6500_1clades	220	PS2_0021	Aeromonas phage PS2	GCA_009388305.2
QGT54938.1	006687	Cluster6501_1clades	220	b23_0327	Synechococcus phage B23	GCA_009745195.1
QGT54573.1	006687	Cluster6501_1clades	220	b3_0333	Synechococcus phage B3	GCA_009745215.1
prevph1000000381	006688	Cluster6502_1clades	221	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000307	006688	Cluster6502_1clades	221	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000552	006689	Cluster6503_1clades	109	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000408	006689	Cluster6503_1clades	221	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ95025.1	006690	Cluster6504_1clades	219	FDI40_gp243	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65841.1	006690	Cluster6504_1clades	116	phiOC_p176	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BAW19242.1	006691	Cluster6506_1clades	219	FDH28_gp153	Ralstonia phage RP12	GCA_002617345.1
BAW19528.1	006691	Cluster6506_1clades	219	-	Ralstonia phage RP31	GCA_002617365.1
BBI90624.1	006692	SIG+Tox-ABHYDROLASE	219	HYO65_gp232	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90930.1	006692	SIG+Tox-ABHYDROLASE	219	-	Tenacibaculum phage PTm5	GCA_009730715.1
AXF51322.1	006693	Cluster6508_1clades	218	WELLINGTON_194	Erwinia phage Wellington	GCA_003344985.1
ANZ49547.1	006693	Cluster6508_1clades	218	KWAN_195	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03743.1	006694	Cluster6509_1clades	218	JOAD_172	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03499.1	006694	Cluster6509_1clades	218	RISINGSUN_171	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
SOK58843.1	006695	Cluster6510_1clades	212	g035	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58304.1	006695	Cluster6510_1clades	218	g027	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000119	006696	Cluster6511_1clades	219	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000088	006696	Cluster6511_1clades	219	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65405.1	006697	Cluster6512_1clades	217	2050HW_00070	Serratia phage 2050HW	GCA_002628125.1
QDB71184.1	006697	Cluster6512_1clades	217	CPT_Moabite_154	Serratia phage Moabite	GCA_006384735.1
BAS04907.1	006698	Cluster6513_1clades	217	AVU11_gp115	Ralstonia phage RSF1	GCA_001500875.1
BAQ02634.2	006698	Cluster6513_1clades	214	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65685.1	006699	Cluster6514_1clades	217	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65226.1	006699	Cluster6514_1clades	217	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65580.1	006700	Cluster6515_1clades	214	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96563.1	006700	Cluster6515_1clades	217	Xoosp13_377	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ASR76253.1	006701	NTP_transferase	216	PBI_BELLAMY_217	Synechococcus phage Bellamy	GCA_002627525.1
QJT70204.1	006701	NTP_transferase	216	SynMITS9220M01_198	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASU03751.1	006702	Cluster6517_1clades	216	JOAD_164	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03507.1	006702	Cluster6517_1clades	216	RISINGSUN_163	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
BAW19027.1	006703	TM	216	FDH28_gp053	Ralstonia phage RP12	GCA_002617345.1
BAW19313.1	006703	TM	216	-	Ralstonia phage RP31	GCA_002617365.1
BAW19133.1	006704	Cluster6519_1clades	216	FDH28_gp262	Ralstonia phage RP12	GCA_002617345.1
BAW19419.1	006704	Cluster6519_1clades	216	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000183	006705	HAM	217	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000146	006705	HAM	217	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000772	006706	Cluster6521_1clades	217	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000525	006706	Cluster6521_1clades	217	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000813	006707	HDRnase	217	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000558	006707	HDRnase	217	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANZ48409.1	006708	SIG+PVC-AAA	215	CAITLIN_114	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48681.1	006708	SIG+PVC-AAA	215	CHRISDB_119	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51259.1	006709	Cluster6524_1clades	215	WELLINGTON_129	Erwinia phage Wellington	GCA_003344985.1
ANZ49479.1	006709	Cluster6524_1clades	215	KWAN_127	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03781.1	006710	Cluster6525_1clades	215	JOAD_134	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03537.1	006710	Cluster6525_1clades	215	RISINGSUN_133	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65619.1	006711	Cluster6526_1clades	215	2050HW_00284	Serratia phage 2050HW	GCA_002628125.1
QDB71047.1	006711	Cluster6526_1clades	215	CPT_Moabite_015	Serratia phage Moabite	GCA_006384735.1
AUZ95133.1	006712	SIG+TM+TM+TM	176	FDI40_gp374	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95130.1	006712	SIG+TM+TM+TM	215	FDI40_gp371	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAS04812.1	006713	Cluster6528_1clades	215	AVU11_gp020	Ralstonia phage RSF1	GCA_001500875.1
BAQ02547.2	006713	Cluster6528_1clades	209	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19055.1	006714	Cluster6529_1clades	215	FDH28_gp081	Ralstonia phage RP12	GCA_002617345.1
BAW19340.1	006714	Cluster6529_1clades	215	-	Ralstonia phage RP31	GCA_002617365.1
BAW19233.1	006715	DUF5565	215	FDH28_gp162	Ralstonia phage RP12	GCA_002617345.1
BAW19519.1	006715	DUF5565	215	-	Ralstonia phage RP31	GCA_002617365.1
BBA65318.1	006716	Cluster6531_1clades	215	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96353.1	006716	Cluster6531_1clades	206	Xoosp13_166	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000181	006717	HisG	216	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000144	006717	HisG	216	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
BAV39312.1	006718	Amidase_3	203	BPT24_187	Tenacibaculum phage pT24	GCA_002611925.1
prev15ph1000000321	006718	Amidase_3	216	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44421.1	006719	PRTase	214	PSSM2_043	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12230.1	006719	PRTase	214	PRTG_00072	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88141.1	006720	Cluster6535_1clades	214	CcrColossus_gp271	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68817.1	006720	Cluster6535_1clades	214	CcrPW_gp278	Caulobacter phage CcrPW	GCA_003443275.1
AXF51222.1	006721	Cluster6536_1clades	214	WELLINGTON_92	Erwinia phage Wellington	GCA_003344985.1
ANZ49443.1	006721	Cluster6536_1clades	214	KWAN_91	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
BBI90573.1	006722	Cluster6537_1clades	214	HYO65_gp181	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90881.1	006722	Cluster6537_1clades	214	-	Tenacibaculum phage PTm5	GCA_009730715.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06678.1	006723	Cluster6538_1clades	214	BcepSaruman_265	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74648.1	006723	Cluster6538_1clades	214	BcepSauron_268	Burkholderia phage BcepSauron	GCA_005394215.1
ABY62905.1	006724	Cluster6539_1clades	213	201phi2-1p072	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76687.1	006724	Cluster6539_1clades	210	PHABIO_56	Pseudomonas phage Phabio	GCA_002624965.1
AXQ69360.1	006725	Cluster6540_1clades	213	CcrBL9_gp336	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69920.1	006725	Cluster6540_1clades	213	CcrSC_gp338	Caulobacter phage CcrSC	GCA_003443315.1
BAS04899.1	006726	Cluster6541_1clades	194	AVU11_gp107	Ralstonia phage RSF1	GCA_001500875.1
BAQ02625.1	006726	Cluster6541_1clades	213	AVU38_gp097	Ralstonia phage RSL2	GCA_001503055.1
BAS04917.1	006727	Cluster6542_1clades	213	AVU11_gp125	Ralstonia phage RSF1	GCA_001500875.1
BAQ02646.2	006727	Cluster6542_1clades	211	-	Ralstonia phage RSL2	GCA_001503055.1
QGH72103.1	006728	Cluster6543_1clades	213	N1M2_240	Klebsiella phage N1M2	GCA_010092605.1
AEV89740.1	006728	Cluster6543_1clades	212	OBP_303	Pseudomonas phage OBP	GCA_000896635.1
AAX44646.1	006729	Cluster6545_1clades	212	PSSM2_269	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12325.1	006729	Cluster6545_1clades	212	PRTG_00172	Prochlorococcus phage P-SSM5	GCA_002991095.1
BBI90600.1	006730	Cluster6546_1clades	212	HYO65_gp208	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90907.1	006730	Cluster6546_1clades	212	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000752	006731	Cluster6547_1clades	213	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000504	006731	Cluster6547_1clades	213	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44614.1	006732	Cluster6548_1clades	211	PSSM2_237	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12357.1	006732	Cluster6548_1clades	211	PRTG_00204	Prochlorococcus phage P-SSM5	GCA_002991095.1
ASU03790.1	006733	35exo	211	JOAD_125	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03546.1	006733	35exo	211	RISINGSUN_124	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXF51258.1	006734	Cluster6553_1clades	210	WELLINGTON_128	Erwinia phage Wellington	GCA_003344985.1
ANZ49478.1	006734	Cluster6553_1clades	210	KWAN_126	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AMS01151.1	006735	Gamma_PGA_hydro	208	AR9_g067	Bacillus phage AR9	GCA_001743835.1
ASU00080.1	006735	Gamma_PGA_hydro	210	PBI_PBS1_258	Bacillus virus PBS1	GCA_002601325.1
ASU03745.1	006736	Cluster6555_1clades	210	JOAD_170	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03501.1	006736	Cluster6555_1clades	210	RISINGSUN_169	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AUZ95389.1	006737	Cluster6556_1clades	110	FDI40_gp630	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95388.1	006737	Cluster6556_1clades	210	FDI40_gp629	Agrobacterium phage Atu_ph07	GCA_002628245.1
BBI90516.1	006738	Cluster6557_1clades	210	HYO65_gp124	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90824.1	006738	Cluster6557_1clades	210	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32284.1	006739	Cluster6558_1clades	210	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41857.1	006739	Cluster6558_1clades	210	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22924.1	006740	Cluster6559_1clades	210	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50639.1	006740	Cluster6559_1clades	210	-	Synechococcus phage S-B43	GCA_006869725.1
QBZ70846.1	006741	Cluster6560_1clades	205	pETSU_265	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71878.1	006741	Cluster6560_1clades	210	N1M2_15	Klebsiella phage N1M2	GCA_010092605.1
AMM43702.1	006742	DEOR-HTH	208	CBB_137	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK58404.1	006742	DEOR-HTH	210	g127	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QBP07446.1	006743	Cluster6562_1clades	209	DERBICUS_20	Erwinia phage Derbicus	GCA_004521655.1
ANZ48870.1	006743	Cluster6562_1clades	209	EARLPHILLIPIV_20	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ATA65402.1	006744	Cluster6563_1clades	209	2050HW_00067	Serratia phage 2050HW	GCA_002628125.1
QDB71181.1	006744	Cluster6563_1clades	209	CPT_Moabite_151	Serratia phage Moabite	GCA_006384735.1
AFU88202.1	006745	Cluster6564_1clades	198	CcrColossus_gp332	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68879.1	006745	Cluster6564_1clades	209	CcrPW_gp340	Caulobacter phage CcrPW	GCA_003443275.1
BBI90651.1	006746	Thymidylate_kin	209	HYO65_gp259	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90956.1	006746	Thymidylate_kin	209	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90688.1	006747	Cluster6566_1clades	209	HYO65_gp296	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90995.1	006747	Cluster6566_1clades	209	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ96782.1	006748	Cluster6567_1clades	194	PS1_0023	Aeromonas phage PS1	GCA_007051165.2
QFR59414.1	006748	Cluster6567_1clades	209	PS2_0023	Aeromonas phage PS2	GCA_009388305.2
prevph1000000652	006749	SERAprotease	115	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000464	006749	SERAprotease	210	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000808	006750	SIG+TM	210	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000554	006750	SIG+TM	210	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000741	006751	Cluster6571_1clades	210	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000493	006751	Cluster6571_1clades	209	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88164.1	006752	Cluster6572_1clades	208	CcrColossus_gp294	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68840.1	006752	Cluster6572_1clades	208	CcrPW_gp301	Caulobacter phage CcrPW	GCA_003443275.1
QBX32167.1	006753	Cluster6573_1clades	208	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41748.1	006753	Cluster6573_1clades	208	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
SOK59158.1	006754	Cluster6575_1clades	208	g350	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58626.1	006754	Cluster6575_1clades	208	g349	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFU88204.1	006755	Cluster6576_1clades	207	CcrColossus_gp334	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68881.1	006755	Cluster6576_1clades	205	CcrPW_gp342	Caulobacter phage CcrPW	GCA_003443275.1
AXF51203.1	006756	Cluster6577_1clades	207	WELLINGTON_73	Erwinia phage Wellington	GCA_003344985.1
ANZ49425.1	006756	Cluster6577_1clades	207	KWAN_73	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65584.1	006757	Cluster6578_1clades	207	2050HW_00249	Serratia phage 2050HW	GCA_002628125.1
QDB71349.1	006757	Cluster6578_1clades	207	CPT_Moabite_319	Serratia phage Moabite	GCA_006384735.1
BBI90401.1	006758	Cluster6579_1clades	207	HYO65_gp009	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90709.1	006758	Cluster6579_1clades	207	-	Tenacibaculum phage PTm5	GCA_009730715.1
CCH63615.1	006759	Cluster6580_1clades	201	CP21_153	Campylobacter virus CP21	GCA_000902535.1
QAU04567.1	006759	Cluster6580_1clades	207	ValB1MD_287	Vibrio phage ValB1MD	GCA_004138815.1
QBX06606.1	006760	Cluster6581_1clades	206	BcepSaruman_193	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74572.1	006760	Cluster6581_1clades	207	BcepSauron_192	Burkholderia phage BcepSauron	GCA_005394215.1
QCW18980.1	006761	Cluster6582_1clades	207	7t3_0459	Salmonella phage 7t3	GCA_006083215.1
QIG62756.1	006761	Cluster6582_1clades	207	SEPL_143	Salmonella phage SE_PL	GCA_011067555.1
prevph1000000106	006762	Cluster6583_1clades	208	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000076	006762	Cluster6583_1clades	208	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000176	006763	Cluster6584_1clades	208	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000139	006763	Cluster6584_1clades	208	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83807.1	006764	Cluster6585_1clades	206	0305phi8-36p107	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83665.1	006764	Cluster6585_1clades	206	0305phi8-36p107R	Bacillus phage 0305phi8-36	GCA_000871045.1
BBA65598.1	006765	Cluster6586_1clades	206	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96578.1	006765	Cluster6586_1clades	194	Xoosp13_392	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ97414.1	006766	Cluster6587_1clades	206	D6_0255	Aeromonas phage D6	GCA_007051205.2
QDH47138.1	006766	Cluster6587_1clades	206	LAh10_167	Aeromonas phage LAh10	GCA_006863975.1
QGT54920.1	006767	Cluster6588_1clades	206	b23_0307	Synechococcus phage B23	GCA_009745195.1
QGT54555.1	006767	Cluster6588_1clades	206	b3_0314	Synechococcus phage B3	GCA_009745215.1
AXH70745.1	006768	Cluster6589_1clades	194	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI20954.1	006768	Cluster6589_1clades	206	-	Vibrio phage vB_pir03	GCA_014319855.1
prevph1000000376	006769	Cluster6590_1clades	207	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000302	006769	Cluster6590_1clades	207	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88188.1	006770	Cluster6591_1clades	205	CcrColossus_gp318	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68865.1	006770	Cluster6591_1clades	205	CcrPW_gp326	Caulobacter phage CcrPW	GCA_003443275.1
AFU88222.1	006771	Cluster6592_1clades	205	CcrColossus_gp352	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68899.1	006771	Cluster6592_1clades	205	CcrPW_gp360	Caulobacter phage CcrPW	GCA_003443275.1
AXG67312.1	006772	Cluster6593_1clades	205	AD1_268	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08537.1	006772	Cluster6593_1clades	77	Alexandra_280	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BAW18995.1	006773	Cluster6594_1clades	205	FDH28_gp021	Ralstonia phage RP12	GCA_002617345.1
BAW19283.1	006773	Cluster6594_1clades	205	-	Ralstonia phage RP31	GCA_002617365.1
BBA65549.1	006774	Cluster6595_1clades	205	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96544.1	006774	Cluster6595_1clades	127	Xoosp13_358	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90418.1	006775	Cluster6596_1clades	195	HYO65_gp026	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90726.1	006775	Cluster6596_1clades	205	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06459.1	006776	Cluster6597_1clades	205	BcepSaruman_046	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74427.1	006776	Cluster6597_1clades	205	BcepSauron_047	Burkholderia phage BcepSauron	GCA_005394215.1
QBZ70845.1	006777	Cluster6598_1clades	205	pETSU_264	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH71877.1	006777	Cluster6598_1clades	203	N1M2_14	Klebsiella phage N1M2	GCA_010092605.1
QCW22852.1	006778	TM+TM	205	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50711.1	006778	TM+TM	85	-	Synechococcus phage S-B43	GCA_006869725.1
BBA65493.1	006779	Cluster6600_1clades	202	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96501.1	006779	Cluster6600_1clades	205	Xoosp13_315	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QIG57755.1	006780	Cluster6601_1clades	205	SEA_PAULODIABOLI_18	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58056.1	006780	Cluster6601_1clades	205	SEA_PAULODIABOLI_373	Microbacterium phage PauloDiaboli	GCA_011067425.1
AAX44577.1	006781	Tox-ABHYDROLASE3	204	PSSM2_200	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12396.1	006781	Tox-ABHYDROLASE3	204	PRTG_00243	Prochlorococcus phage P-SSM5	GCA_002991095.1
QBZ71932.1	006782	Cluster6603_1clades	204	SEA_KRADAL_33	Streptomyces phage Kradal	GCA_004799925.1
AXH66194.1	006782	Cluster6603_1clades	204	SEA_SATIS_33	Streptomyces phage Satis	GCA_003366315.1
AXQ69365.1	006783	Cluster6604_1clades	204	CcrBL9_gp341	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69925.1	006783	Cluster6604_1clades	199	CcrSC_gp343	Caulobacter phage CcrSC	GCA_003443315.1
BBA65258.1	006784	Cluster6605_1clades	204	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65717.1	006784	Cluster6605_1clades	204	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65261.1	006785	TM+TM	204	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65720.1	006785	TM+TM	204	-	Xanthomonas phage XacN1	GCA_003173815.1
ATA65573.1	006786	TM	199	2050HW_00238	Serratia phage 2050HW	GCA_002628125.1
QDB71338.1	006786	TM	204	CPT_Moabite_308	Serratia phage Moabite	GCA_006384735.1
QDJ97291.1	006787	Cluster6608_1clades	204	D6_0131	Aeromonas phage D6	GCA_007051205.2
QDH47140.1	006787	Cluster6608_1clades	204	LAh10_58	Aeromonas phage LAh10	GCA_006863975.1
QDH83531.1	006788	Cluster6609_1clades	204	H1O15_gp257	Achromobacter phage Motura	GCA_006964305.1
BAG41505.1	006788	Cluster6609_1clades	137	RSL1_ORF059	Ralstonia phage phiRSL1	GCA_000879455.1
BBA65533.1	006789	Cluster6610_1clades	200	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96530.1	006789	Cluster6610_1clades	204	Xoosp13_344	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000613	006790	Cluster6611_1clades	205	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000432	006790	Cluster6611_1clades	205	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AJT61020.1	006791	Cluster6612_1clades	203	AVU32_gp179	Vibrio phage ValKK3	GCA_001501635.1
ALP47066.1	006791	Cluster6612_1clades	203	phiGrn1_0196	Vibrio phage phi-Grn1	GCA_002757115.1
ABY62879.1	006792	Cluster6613_1clades	125	201phi2-1p046	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76663.1	006792	Cluster6613_1clades	203	PHABIO_32	Pseudomonas phage Phabio	GCA_002624965.1
QBZ72061.1	006793	Cluster6614_1clades	203	SEA_KRADAL_165	Streptomyces phage Kradal	GCA_004799925.1
AXH66324.1	006793	Cluster6614_1clades	203	SEA_SATIS_165	Streptomyces phage Satis	GCA_003366315.1
BBA65489.1	006794	Cluster6615_1clades	203	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96496.1	006794	Cluster6615_1clades	193	Xoosp13_310	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90640.1	006795	Cluster6616_1clades	203	HYO65_gp248	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90947.1	006795	Cluster6616_1clades	203	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIX30591.1	006796	Cluster6617_1clades	202	Syn7803US37_114	Synechococcus phage ACG-2014f	GCA_002594065.1
AXQ70599.1	006796	Cluster6617_1clades	200	HOU04_gp200	Synechococcus phage S-T4	GCA_003443335.1
ASU03704.1	006797	Cluster6618_1clades	202	JOAD_211	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03461.1	006797	Cluster6618_1clades	202	RISINGSUN_209	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65623.1	006798	Cluster6619_1clades	202	2050HW_00288	Serratia phage 2050HW	GCA_002628125.1
QDB71050.1	006798	Cluster6619_1clades	202	CPT_Moabite_018	Serratia phage Moabite	GCA_006384735.1
AXQ69438.1	006799	Cluster6620_1clades	202	CcrBL9_gp414	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69989.1	006799	Cluster6620_1clades	202	CcrSC_gp407	Caulobacter phage CcrSC	GCA_003443315.1
BAW19098.1	006800	Cluster6621_1clades	202	FDH28_gp124	Ralstonia phage RP12	GCA_002617345.1
BAW19384.1	006800	Cluster6621_1clades	202	-	Ralstonia phage RP31	GCA_002617365.1
BAW19118.1	006801	Cluster6622_1clades	202	FDH28_gp277	Ralstonia phage RP12	GCA_002617345.1
BAW19404.1	006801	Cluster6622_1clades	202	-	Ralstonia phage RP31	GCA_002617365.1
BBA65181.1	006802	PRTase	202	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65640.1	006802	PRTase	202	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90449.1	006803	SIG+TM	202	HYO65_gp057	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90757.1	006803	SIG+TM	202	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32433.1	006804	Cluster6625_1clades	202	-	Pseudomonas phage PA1C	GCA_004785505.1
ARV76961.1	006804	Cluster6625_1clades	199	PHABIO_330	Pseudomonas phage Phabio	GCA_002624965.1
QDJ97370.1	006805	Cluster6627_1clades	202	D6_0211	Aeromonas phage D6	GCA_007051205.2
QDH47144.1	006805	Cluster6627_1clades	202	LAh10_125	Aeromonas phage LAh10	GCA_006863975.1
AXF51280.1	006806	Cluster6629_1clades	198	WELLINGTON_151	Erwinia phage Wellington	GCA_003344985.1
ANZ49503.1	006806	Cluster6629_1clades	201	KWAN_151	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXQ68555.1	006807	Cluster6630_1clades	201	CcrPW_gp016	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69004.1	006807	Cluster6630_1clades	201	CcrPW_gp465	Caulobacter phage CcrPW	GCA_003443275.1
AFU88142.1	006808	Cluster6631_1clades	197	CcrColossus_gp272	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68818.1	006808	Cluster6631_1clades	201	CcrPW_gp279	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69491.1	006809	Cluster6632_1clades	201	CcrBL9_gp467	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70039.1	006809	Cluster6632_1clades	195	CcrSC_gp457	Caulobacter phage CcrSC	GCA_003443315.1
BAW18996.1	006810	Cluster6633_1clades	201	FDH28_gp022	Ralstonia phage RP12	GCA_002617345.1
BAW19284.1	006810	Cluster6633_1clades	201	-	Ralstonia phage RP31	GCA_002617365.1
BBA65442.1	006811	Cluster6634_1clades	201	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96458.1	006811	Cluster6634_1clades	198	Xoosp13_272	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65448.1	006812	Cluster6635_1clades	201	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96463.1	006812	Cluster6635_1clades	116	Xoosp13_277	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX32478.1	006813	Cluster6636_1clades	201	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42050.1	006813	Cluster6636_1clades	201	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97337.1	006814	Cluster6637_1clades	201	D6_0178	Aeromonas phage D6	GCA_007051205.2
QDH47145.1	006814	Cluster6637_1clades	201	LAh10_97	Aeromonas phage LAh10	GCA_006863975.1
QDJ97413.1	006815	Cluster6638_1clades	201	D6_0254	Aeromonas phage D6	GCA_007051205.2
QDH47147.1	006815	Cluster6638_1clades	201	LAh10_166	Aeromonas phage LAh10	GCA_006863975.1
QGT54668.1	006816	35exo	201	b23_0040	Synechococcus phage B23	GCA_009745195.1
QGT54298.1	006816	35exo	201	b3_0040	Synechococcus phage B3	GCA_009745215.1
AIX30529.1	006817	EAD11	200	Syn7803US37_52	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76132.1	006817	EAD11	187	PBI_BELLAMY_87	Synechococcus phage Bellamy	GCA_002627525.1
BBI90539.1	006818	Cluster6642_1clades	200	HYO65_gp147	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90847.1	006818	Cluster6642_1clades	200	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54973.1	006819	Cluster6643_1clades	200	b23_0367	Synechococcus phage B23	GCA_009745195.1
QGT54608.1	006819	Cluster6643_1clades	200	b3_0373	Synechococcus phage B3	GCA_009745215.1
prevph1000000655	006820	GrpE	201	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000467	006820	GrpE	201	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000663	006821	SIG+Glucosaminidase	201	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000475	006821	SIG+Glucosaminidase	201	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXQ69238.1	006822	Cluster6646_1clades	199	CcrBL9_gp214c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69792.1	006822	Cluster6646_1clades	199	CcrSC_gp210c	Caulobacter phage CcrSC	GCA_003443315.1
QBX06452.1	006823	Cluster6647_1clades	199	BcepSaruman_039	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74419.1	006823	Cluster6647_1clades	198	BcepSauron_039	Burkholderia phage BcepSauron	GCA_005394215.1
AAX44592.1	006824	Cluster6648_1clades	198	PSSM2_215	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12379.1	006824	Cluster6648_1clades	198	PRTG_00226	Prochlorococcus phage P-SSM5	GCA_002991095.1
AQW88990.1	006825	Tox-HNH	198	BF_0465	Serratia phage BF	GCA_002619745.1
AGN30363.1	006825	Tox-HNH	147	VPFG_00366	Vibrio phage nt-1	GCA_000910195.2
ASU03776.1	006826	SIG+DUF4671	198	JOAD_139	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03532.1	006826	SIG+DUF4671	198	RISINGSUN_138	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
BAW18992.1	006827	Cluster6651_1clades	198	FDH28_gp018	Ralstonia phage RP12	GCA_002617345.1
BAW19280.1	006827	Cluster6651_1clades	185	-	Ralstonia phage RP31	GCA_002617365.1
BBA65398.1	006828	Cluster6652_1clades	197	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96423.1	006828	Cluster6652_1clades	198	Xoosp13_237	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ATA65679.1	006829	Cluster6653_1clades	197	2050HW_00344	Serratia phage 2050HW	GCA_002628125.1
QDB71100.1	006829	Cluster6653_1clades	197	CPT_Moabite_068	Serratia phage Moabite	GCA_006384735.1
AXQ69125.1	006830	Cluster6654_1clades	188	CcrBL9_gp101	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69679.1	006830	Cluster6654_1clades	197	CcrSC_gp097	Caulobacter phage CcrSC	GCA_003443315.1
BBA65371.1	006831	35exo	197	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96399.1	006831	35exo	195	Xoosp13_213	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000192	006832	Cluster6656_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000155	006832	Cluster6656_1clades	198	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000416	006833	Cluster6657_1clades	198	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000327	006833	Cluster6657_1clades	198	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44569.1	006834	MGS+AICARFT_IMPCHas	196	PSSM2_191	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12404.1	006834	MGS+AICARFT_IMPCHas	196	PRTG_00251	Prochlorococcus phage P-SSM5	GCA_002991095.1
AMS01239.1	006835	Cluster6659_1clades	196	AR9_g155	Bacillus phage AR9	GCA_001743835.1
AST99865.1	006835	Cluster6659_1clades	196	PBI_PBS1_43	Bacillus virus PBS1	GCA_002601325.1
QBX32436.1	006836	SIG+TM+TM	193	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42006.1	006836	SIG+TM+TM	196	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AEH03675.1	006837	Cluster6661_1clades	195	252	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03677.1	006837	Cluster6661_1clades	135	254	Pseudomonas phage PhiPA3	GCA_001502095.1
AXQ69301.1	006838	Cluster6662_1clades	195	CcrBL9_gp277c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69860.1	006838	Cluster6662_1clades	195	CcrSC_gp278c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69309.1	006839	Cluster6663_1clades	195	CcrBL9_gp285	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69868.1	006839	Cluster6663_1clades	195	CcrSC_gp286	Caulobacter phage CcrSC	GCA_003443315.1
BAS04912.1	006840	Cluster6664_1clades	195	AVU11_gp120	Ralstonia phage RSF1	GCA_001500875.1
BAQ02641.2	006840	Cluster6664_1clades	132	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65438.1	006841	XIS-HTH	195	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96455.1	006841	XIS-HTH	192	Xoosp13_269	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AAX44629.1	006842	SIG+TM+TM	194	PSSM2_252	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12341.1	006842	SIG+TM+TM	194	PRTG_00188	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88107.1	006843	SIG+TM+TM	194	CcrColossus_gp237	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68784.1	006843	SIG+TM+TM	177	CcrPW_gp245	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68544.1	006844	Cluster6668_1clades	194	CcrPW_gp005	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68994.1	006844	Cluster6668_1clades	194	CcrPW_gp455	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69371.1	006845	Cluster6670_1clades	194	CcrBL9_gp347	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69931.1	006845	Cluster6670_1clades	194	CcrSC_gp349	Caulobacter phage CcrSC	GCA_003443315.1
BBA65474.1	006846	BACTERIALFRINGE	173	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96484.1	006846	BACTERIALFRINGE	194	Xoosp13_298	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65545.1	006847	ASCH	176	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96540.1	006847	ASCH	194	Xoosp13_354	Xanthomonas phage Xoo-sp13	GCA_013364725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIA64875.1	006848	Cluster6673_1clades	193	S13_076	Cronobacter phage S13	GCA_001503575.1
QHJ79064.1	006848	Cluster6673_1clades	194	-	Myoviridae sp.	GCA_012593985.1
AFU88189.1	006849	Cluster6674_1clades	193	CcrColossus_gp319	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68866.1	006849	Cluster6674_1clades	188	CcrPW_gp327	Caulobacter phage CcrPW	GCA_003443275.1
AFU88200.1	006850	Spermine_synth	193	CcrColossus_gp330	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68877.1	006850	Spermine_synth	193	CcrPW_gp338	Caulobacter phage CcrPW	GCA_003443275.1
AGG54466.1	006851	HNH	193	CYWG_00182	Cyanophage S-SSM6b	GCA_002710425.1
QJT70160.1	006851	HNH	176	SynMITS9220M01_147	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ARV77372.1	006852	SIG+TM+TM	193	NOXIFER_203	Pseudomonas phage Noxifer	GCA_002625005.1
QAU04577.1	006852	SIG+TM+TM	193	ValB1MD_323	Vibrio phage ValB1MD	GCA_004138815.1
ASU03703.1	006853	Cluster6678_1clades	193	JOAD_212	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03460.1	006853	Cluster6678_1clades	193	RISINGSUN_210	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65465.1	006854	SIG+TM+TM	193	2050HW_00130	Serratia phage 2050HW	GCA_002628125.1
QDB71234.1	006854	SIG+TM+TM	193	CPT_Moabite_204	Serratia phage Moabite	GCA_006384735.1
AXQ69612.1	006855	Cluster6680_1clades	193	CcrSC_gp030	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70112.1	006855	Cluster6680_1clades	193	CcrSC_gp530	Caulobacter phage CcrSC	GCA_003443315.1
BAS04938.1	006856	Cluster6681_1clades	165	AVU11_gp146	Ralstonia phage RSF1	GCA_001500875.1
BAQ02662.1	006856	Cluster6681_1clades	193	AVU38_gp134	Ralstonia phage RSL2	GCA_001503055.1
BAW19132.1	006857	Cluster6682_1clades	193	FDH28_gp263	Ralstonia phage RP12	GCA_002617345.1
BAW19418.1	006857	Cluster6682_1clades	193	-	Ralstonia phage RP31	GCA_002617365.1
QDJ97174.1	006858	Cluster6683_1clades	164	D6_0014	Aeromonas phage D6	GCA_007051205.2
QDH47150.1	006858	Cluster6683_1clades	193	LAh10_182	Aeromonas phage LAh10	GCA_006863975.1
ATA65492.1	006859	Cluster6684_1clades	192	2050HW_00157	Serratia phage 2050HW	GCA_002628125.1
QDB71260.1	006859	Cluster6684_1clades	192	CPT_Moabite_230	Serratia phage Moabite	GCA_006384735.1
ATA65624.1	006860	Cluster6685_1clades	192	2050HW_00289	Serratia phage 2050HW	GCA_002628125.1
QDB71051.1	006860	Cluster6685_1clades	192	CPT_Moabite_019	Serratia phage Moabite	GCA_006384735.1
QBZ72201.1	006861	Cluster6686_1clades	192	SEA_KRADAL_315	Streptomyces phage Kradal	GCA_004799925.1
AXH66464.1	006861	Cluster6686_1clades	192	SEA_SATIS_315	Streptomyces phage Satis	GCA_003366315.1
AFU88119.1	006862	Cluster6687_1clades	190	CcrColossus_gp249	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68797.1	006862	Cluster6687_1clades	192	CcrPW_gp258	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69434.1	006863	Cluster6688_1clades	192	CcrBL9_gp410	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69986.1	006863	Cluster6688_1clades	191	CcrSC_gp404	Caulobacter phage CcrSC	GCA_003443315.1
AYD81455.1	006864	Cluster6689_1clades	192	SEA_JUSTBECAUSE_300	Streptomyces phage JustBecause	GCA_003613775.1
QJD53860.1	006864	Cluster6689_1clades	192	SEA_KELA_300	Streptomyces phage Kela	GCA_012934305.1
BAW19258.1	006865	Cluster6690_1clades	192	FDH28_gp137	Ralstonia phage RP12	GCA_002617345.1
BAW19544.1	006865	Cluster6690_1clades	192	-	Ralstonia phage RP31	GCA_002617365.1
QDJ97294.1	006866	Cluster6692_1clades	192	D6_0134	Aeromonas phage D6	GCA_007051205.2
QDH47154.1	006866	Cluster6692_1clades	182	LAh10_60	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000318	006867	Cluster6693_1clades	193	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000247	006867	Cluster6693_1clades	193	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01759.1	006868	Cluster6694_1clades	191	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53402.1	006868	Cluster6694_1clades	191	65p395	Aeromonas virus 65	GCA_000893255.1
AFC21624.1	006869	Cluster6695_1clades	191	GAP32_174	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43745.1	006869	Cluster6695_1clades	182	CBB_180	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AJK27455.1	006870	Ferredoxin-RRM	191	PTIM40_28	Cyanophage P-TIM40	GCA_001470935.1
AIR93567.1	006870	Ferredoxin-RRM	191	ndhI	Prochlorococcus phage P-TIM68	GCA_001503075.1
AYD81377.1	006871	Cluster6697_1clades	191	SEA_JUSTBECAUSE_222	Streptomyces phage JustBecause	GCA_003613775.1
QJD53780.1	006871	Cluster6697_1clades	191	SEA_KELA_220	Streptomyces phage Kela	GCA_012934305.1
BAS04802.2	006872	Cluster6698_1clades	191	AVU11_agp05	Ralstonia phage RSF1	GCA_001500875.1
BAQ02538.2	006872	Cluster6698_1clades	191	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19072.1	006873	Cluster6699_1clades	191	FDH28_gp098	Ralstonia phage RP12	GCA_002617345.1
BAW19357.1	006873	Cluster6699_1clades	191	-	Ralstonia phage RP31	GCA_002617365.1
BBI90508.1	006874	Cluster6700_1clades	191	HYO65_gp116	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90816.1	006874	Cluster6700_1clades	188	-	Tenacibaculum phage PTm5	GCA_009730715.1
QIG57766.1	006875	Cluster6701_1clades	191	SEA_PAULODIABOLI_31	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58067.1	006875	Cluster6701_1clades	191	SEA_PAULODIABOLI_386	Microbacterium phage PauloDiaboli	GCA_011067425.1
QKN85837.1	006876	Cluster6702_1clades	191	ACEC001_0010	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QNI20720.1	006876	Cluster6702_1clades	191	-	Salmonella phage JN03	GCA_014319805.1
prevph1000000177	006877	Cluster6703_1clades	192	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000140	006877	Cluster6703_1clades	192	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AIA65064.1	006878	Cluster6704_1clades	190	S13_267	Cronobacter phage S13	GCA_001503575.1
QHJ78867.1	006878	Cluster6704_1clades	190	-	Myoviridae sp.	GCA_012593985.1
ALN97731.1	006879	Cluster6705_1clades	189	Bp8pS_052	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97738.1	006879	Cluster6705_1clades	190	Bp8pS_059	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ATA65676.1	006880	Cluster6706_1clades	190	2050HW_00341	Serratia phage 2050HW	GCA_002628125.1
QDB71098.1	006880	Cluster6706_1clades	190	CPT_Moabite_066	Serratia phage Moabite	GCA_006384735.1
AXQ69087.1	006881	Cluster6707_1clades	190	CcrBL9_gp063c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69643.1	006881	Cluster6707_1clades	190	CcrSC_gp061c	Caulobacter phage CcrSC	GCA_003443315.1
BBI90436.1	006882	Cluster6708_1clades	190	HYO65_gp044	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90743.1	006882	Cluster6708_1clades	190	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000330	006883	Cluster6709_1clades	191	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000259	006883	Cluster6709_1clades	191	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGH07523.1	006884	Cluster6710_1clades	187	CYVG_00079	Cyanophage S-SSM6a	GCA_002710385.1
AGG54428.1	006884	Cluster6710_1clades	189	CYWG_00144	Cyanophage S-SSM6b	GCA_002710425.1
AGH56971.1	006885	TET-JBP	189	CPXG_00168	Cyanophage P-RSM6	GCA_000906155.1
AJK27490.1	006885	TET-JBP	180	PTIM40_63	Cyanophage P-TIM40	GCA_001470935.1
ASU03794.1	006886	Cluster6712_1clades	189	JOAD_121	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03549.1	006886	Cluster6712_1clades	189	RISINGSUN_121	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65370.1	006887	Cluster6713_1clades	189	2050HW_00035	Serratia phage 2050HW	GCA_002628125.1
QDB71155.1	006887	Cluster6713_1clades	189	CPT_Moabite_125	Serratia phage Moabite	GCA_006384735.1
BBI90525.1	006888	Cluster6714_1clades	189	HYO65_gp133	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90833.1	006888	Cluster6714_1clades	189	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32447.1	006889	Cluster6715_1clades	189	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42018.1	006889	Cluster6715_1clades	189	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000793	006890	Cluster6716_1clades	190	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000541	006890	Cluster6716_1clades	190	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGS82179.1	006891	Cluster6717_1clades	188	PaBG_00308	Pseudomonas phage PaBG	GCA_000912555.1
AGS82180.1	006891	Cluster6717_1clades	168	PaBG_00309	Pseudomonas phage PaBG	GCA_000912555.1
ATA65448.1	006892	HAMP	188	2050HW_00113	Serratia phage 2050HW	GCA_002628125.1
QDB71219.1	006892	HAMP	188	CPT_Moabite_189	Serratia phage Moabite	GCA_006384735.1
ATA65449.1	006893	Cluster6719_1clades	188	2050HW_00114	Serratia phage 2050HW	GCA_002628125.1
QDB71220.1	006893	Cluster6719_1clades	188	CPT_Moabite_190	Serratia phage Moabite	GCA_006384735.1
QBZ72209.1	006894	Cluster6720_1clades	188	SEA_KRADAL_323	Streptomyces phage Kradal	GCA_004799925.1
AXH66472.1	006894	Cluster6720_1clades	188	SEA_SATIS_323	Streptomyces phage Satis	GCA_003366315.1
BAS04923.1	006895	Cluster6721_1clades	182	AVU11_gp131	Ralstonia phage RSF1	GCA_001500875.1
BAQ02651.1	006895	Cluster6721_1clades	188	AVU38_gp123	Ralstonia phage RSL2	GCA_001503055.1
BBI90512.1	006896	Cluster6722_1clades	188	HYO65_gp120	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90820.1	006896	Cluster6722_1clades	188	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32183.1	006897	Cluster6723_1clades	188	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41761.1	006897	Cluster6723_1clades	188	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AUE22569.1	006898	VirB11	187	Ah1_00028	Aeromonas phage Ah1	GCA_002957415.1
AAQ17681.1	006898	VirB11	183	Aeh1ORF024c	Aeromonas virus Aeh1	GCA_000843245.1
AXQ69267.1	006899	Cluster6725_1clades	187	CcrBL9_gp243c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69823.1	006899	Cluster6725_1clades	187	CcrSC_gp241c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69363.1	006900	Cluster6726_1clades	177	CcrBL9_gp339	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69923.1	006900	Cluster6726_1clades	187	CcrSC_gp341	Caulobacter phage CcrSC	GCA_003443315.1
BAW18991.1	006901	Cluster6727_1clades	187	FDH28_gp017	Ralstonia phage RP12	GCA_002617345.1
BAW19279.1	006901	Cluster6727_1clades	187	-	Ralstonia phage RP31	GCA_002617365.1
BAW19069.1	006902	Cluster6728_1clades	187	FDH28_gp095	Ralstonia phage RP12	GCA_002617345.1
BAW19354.1	006902	Cluster6728_1clades	187	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000236	006903	Cluster6729_1clades	188	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000186	006903	Cluster6729_1clades	188	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000332	006904	Cluster6730_1clades	188	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000261	006904	Cluster6730_1clades	188	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88109.1	006905	Cluster6731_1clades	186	CcrColossus_gp239	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68786.1	006905	Cluster6731_1clades	186	CcrPW_gp247	Caulobacter phage CcrPW	GCA_003443275.1
AFU88218.1	006906	Cluster6732_1clades	186	CcrColossus_gp348	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68895.1	006906	Cluster6732_1clades	186	CcrPW_gp356	Caulobacter phage CcrPW	GCA_003443275.1
AMS01374.1	006907	Cluster6733_1clades	186	AR9_g290	Bacillus phage AR9	GCA_001743835.1
ASU00005.1	006907	Cluster6733_1clades	186	PBI_PBS1_183	Bacillus virus PBS1	GCA_002601325.1
AXF51317.1	006908	Cluster6734_1clades	186	WELLINGTON_189	Erwinia phage Wellington	GCA_003344985.1
ANZ49542.1	006908	Cluster6734_1clades	186	KWAN_190	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXQ69076.1	006909	Cluster6735_1clades	176	CcrBL9_gp052c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69636.1	006909	Cluster6735_1clades	186	CcrSC_gp054c	Caulobacter phage CcrSC	GCA_003443315.1
BAS04863.1	006910	Cluster6736_1clades	186	AVU11_gp071	Ralstonia phage RSF1	GCA_001500875.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAQ02596.1	006910	Cluster6736_1clades	186	AVU38_gp068	Ralstonia phage RSL2	GCA_001503055.1
AFF28096.1	006911	Cluster6737_1clades	183	PAU_98	Sphingomonas phage PAU	GCA_000902455.1
BAV39250.1	006911	Cluster6737_1clades	186	BPT24_125	Tenacibaculum phage pT24	GCA_002611925.1
BAW18993.1	006912	Cluster6738_1clades	186	FDH28_gp019	Ralstonia phage RP12	GCA_002617345.1
BAW19281.1	006912	Cluster6738_1clades	186	-	Ralstonia phage RP31	GCA_002617365.1
QBX32450.1	006913	Cluster6739_1clades	186	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42022.1	006913	Cluster6739_1clades	186	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32515.1	006914	Cluster6740_1clades	186	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42088.1	006914	Cluster6740_1clades	186	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000437	006915	Cluster6741_1clades	180	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000349	006915	Cluster6741_1clades	187	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM43617.1	006916	Cluster6742_1clades	185	CBB_52	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44168.1	006916	Cluster6742_1clades	185	CBB_605	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01242.1	006917	Cluster6743_1clades	185	AR9_g158	Bacillus phage AR9	GCA_001743835.1
AST99868.1	006917	Cluster6743_1clades	185	PBI_PBS1_46	Bacillus virus PBS1	GCA_002601325.1
ATA65673.1	006918	Cluster6744_1clades	185	2050HW_00338	Serratia phage 2050HW	GCA_002628125.1
QDB71094.1	006918	Cluster6744_1clades	185	CPT_Moabite_062	Serratia phage Moabite	GCA_006384735.1
BBI90528.1	006919	Cluster6745_1clades	185	HYO65_gp136	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90836.1	006919	Cluster6745_1clades	185	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90555.1	006920	ParB	185	HYO65_gp163	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90863.1	006920	ParB	151	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIA65006.1	006921	Cluster6747_1clades	184	S13_209	Cronobacter phage S13	GCA_001503575.1
QHJ78925.1	006921	Cluster6747_1clades	185	-	Myoviridae sp.	GCA_012593985.1
prevph1000000157	006922	Cluster6748_1clades	186	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000118	006922	Cluster6748_1clades	186	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000508	006923	Cluster6749_1clades	82	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000384	006923	Cluster6749_1clades	186	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000773	006924	Cluster6750_1clades	186	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000526	006924	Cluster6750_1clades	186	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93822.1	006925	UPF0302+IDEAL	184	G_577	Bacillus virus G	GCA_000917535.1
AEO93843.1	006925	UPF0302+IDEAL	183	G_598	Bacillus virus G	GCA_000917535.1
AFU87919.1	006926	ParA-Soj-PloopNTPase	183	CcrColossus_gp049	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68591.1	006926	ParA-Soj-PloopNTPase	184	CcrPW_gp052	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69305.1	006927	SIG+tRNA-Endonuclease	184	CcrBL9_gp281	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69864.1	006927	SIG+tRNA-Endonuclease	184	CcrSC_gp282	Caulobacter phage CcrSC	GCA_003443315.1
BAS04949.1	006928	Cluster6754_1clades	182	AVU11_gp157	Ralstonia phage RSF1	GCA_001500875.1
BAQ02674.2	006928	Cluster6754_1clades	184	-	Ralstonia phage RSL2	GCA_001503055.1
QBX06831.1	006929	Cluster6755_1clades	184	BcepSaruman_418	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74800.1	006929	Cluster6755_1clades	184	BcepSauron_420	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32410.1	006930	Cluster6756_1clades	184	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41981.1	006930	Cluster6756_1clades	184	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65680.1	006931	Cluster6757_1clades	171	2050HW_00345	Serratia phage 2050HW	GCA_002628125.1
QDB71101.1	006931	Cluster6757_1clades	184	CPT_Moabite_069	Serratia phage Moabite	GCA_006384735.1
SBV38357.1	006932	Cluster6759_1clades	184	BN7874_188	Phage NCTB	GCA_900092385.1
SBV38363.1	006932	Cluster6759_1clades	179	BN7874_194	Phage NCTB	GCA_900092385.1
SOK59159.1	006933	Cluster6760_1clades	184	g351	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58627.1	006933	Cluster6760_1clades	184	g350	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000008	006934	Cluster6761_1clades	185	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000009	006934	Cluster6761_1clades	185	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000322	006935	SIG+TM	185	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000251	006935	SIG+TM	185	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88173.1	006936	TGS	183	CcrColossus_gp303	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68850.1	006936	TGS	183	CcrPW_gp311	Caulobacter phage CcrPW	GCA_003443275.1
AFH14784.1	006937	Cluster6764_1clades	168	Lu11_0248	Pseudomonas phage Lu11	GCA_000897175.1
AGS82130.1	006937	Cluster6764_1clades	183	PaBG_00255	Pseudomonas phage PaBG	GCA_000912555.1
AND75262.1	006938	DUF4376	183	ME3_101	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75263.1	006938	DUF4376	181	ME3_102	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ANZ48369.1	006939	SIG+MED12	183	CAITLIN_74	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48643.1	006939	SIG+MED12	183	CHRISDB_81	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51323.1	006940	Cluster6767_1clades	183	WELLINGTON_195	Erwinia phage Wellington	GCA_003344985.1
ANZ49548.1	006940	Cluster6767_1clades	183	KWAN_196	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AQW88746.1	006941	TM	167	BF_0221	Serratia phage BF	GCA_002619745.1
AQW88747.1	006941	TM	183	BF_0222	Serratia phage BF	GCA_002619745.1
ASU03760.1	006942	Cluster6769_1clades	183	JOAD_155	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03516.1	006942	Cluster6769_1clades	183	RISINGSUN_154	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QGT54704.1	006943	Cluster6771_1clades	183	b23_0089	Synechococcus phage B23	GCA_009745195.1
QGT54334.1	006943	Cluster6771_1clades	183	b3_0090	Synechococcus phage B3	GCA_009745215.1
prevph1000000189	006944	Cluster6772_1clades	184	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000152	006944	Cluster6772_1clades	184	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AIA64992.1	006945	Cluster6773_1clades	182	S13_195	Cronobacter phage S13	GCA_001503575.1
QHJ78940.1	006945	Cluster6773_1clades	169	-	Myoviridae sp.	GCA_012593985.1
AXQ69139.1	006946	Cluster6774_1clades	182	CcrBL9_gp115	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69693.1	006946	Cluster6774_1clades	182	CcrSC_gp111	Caulobacter phage CcrSC	GCA_003443315.1
BBI90610.1	006947	Cluster6775_1clades	182	HYO65_gp218	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90916.1	006947	Cluster6775_1clades	182	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBO63936.1	006948	Cluster6776_1clades	182	Goslar_00143	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63937.1	006948	Cluster6776_1clades	177	Goslar_00144	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBX06593.1	006949	Cluster6777_1clades	182	BcepSaruman_180	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74558.1	006949	Cluster6777_1clades	182	BcepSauron_178	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06595.1	006950	ZetaToxin	182	BcepSaruman_182	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74560.1	006950	ZetaToxin	182	BcepSauron_180	Burkholderia phage BcepSauron	GCA_005394215.1
prevph1000000617	006951	Cluster6779_1clades	183	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000436	006951	Cluster6779_1clades	183	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ALP47089.1	006952	Cluster6781_1clades	181	phiGrn1_0284	Vibrio phage phi-Grn1	GCA_002757115.1
AFN37401.1	006952	Cluster6781_1clades	179	pp2_168	Vibriophage phi-pp2	GCA_002630725.1
AOO14342.1	006953	Cluster6782_1clades	181	Sn110110_148	Cyanophage S-RIM14	GCA_002599065.1
AOO14991.1	006953	Cluster6782_1clades	181	W1230910_145	Cyanophage S-RIM14	GCA_002599125.1
QBZ72216.1	006954	Cluster6784_1clades	181	SEA_KRADAL_330	Streptomyces phage Kradal	GCA_004799925.1
AXH66479.1	006954	Cluster6784_1clades	181	SEA_SATIS_330	Streptomyces phage Satis	GCA_003366315.1
AXH72406.1	006955	Cluster6785_1clades	168	-	Myoviridae sp.	GCA_003657725.1
AXH72405.1	006955	Cluster6785_1clades	181	-	Myoviridae sp.	GCA_003657725.1
AFU88193.1	006956	Cluster6786_1clades	172	CcrColossus_gp323	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68870.1	006956	Cluster6786_1clades	181	CcrPW_gp331	Caulobacter phage CcrPW	GCA_003443275.1
BBA65402.1	006957	Cluster6787_1clades	181	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96426.1	006957	Cluster6787_1clades	166	Xoosp13_240	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QHJ86163.1	006958	Cluster6788_1clades	181	KKIINIFJ_00253	Pseudomonas phage PN05	GCA_009931935.1
BBA65401.1	006958	Cluster6788_1clades	178	-	Xanthomonas phage XacN1	GCA_003173815.1
prevph1000000003	006959	Cluster6789_1clades	182	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000003	006959	Cluster6789_1clades	182	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000078	006960	Cluster6790_1clades	182	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000063	006960	Cluster6790_1clades	182	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000265	006961	Cluster6791_1clades	182	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000212	006961	Cluster6791_1clades	182	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000298	006962	Cluster6792_1clades	182	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000230	006962	Cluster6792_1clades	182	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASR76208.1	006963	DSBH	180	PBI_BELLAMY_164	Synechococcus phage Bellamy	GCA_002627525.1
QJT70161.1	006963	DSBH	180	SynMITS9220M01_148	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ATA65674.1	006964	Cluster6794_1clades	180	2050HW_00339	Serratia phage 2050HW	GCA_002628125.1
QDB71096.1	006964	Cluster6794_1clades	180	CPT_Moabite_064	Serratia phage Moabite	GCA_006384735.1
BAW18982.1	006965	Cluster6795_1clades	180	FDH28_gp008	Ralstonia phage RP12	GCA_002617345.1
BAW19270.1	006965	Cluster6795_1clades	180	-	Ralstonia phage RP31	GCA_002617365.1
BBA65484.1	006966	Cluster6796_1clades	180	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96491.1	006966	Cluster6796_1clades	178	Xoosp13_305	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06519.1	006967	Cluster6797_1clades	180	BcepSaruman_106	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74485.1	006967	Cluster6797_1clades	180	BcepSauron_105	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06550.1	006968	Cluster6798_1clades	180	BcepSaruman_137	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74516.1	006968	Cluster6798_1clades	174	BcepSauron_136	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65511.1	006969	Cluster6799_1clades	174	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96511.1	006969	Cluster6799_1clades	180	Xoosp13_325	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QIW90472.1	006970	Cluster6800_1clades	115	GCAPEGMB_00125	Vibrio phage V07	GCA_012361095.1
QIW90957.1	006970	Cluster6800_1clades	180	COHAPHLL_00094	Vibrio phage V09	GCA_012361135.1
prevph1000000135	006971	Cluster6801_1clades	181	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000103	006971	Cluster6801_1clades	181	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000490	006972	Cluster6802_1clades	181	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000371	006972	Cluster6802_1clades	181	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48570.1	006973	Cluster6803_1clades	179	CAITLIN_275	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48848.1	006973	Cluster6803_1clades	175	CHRISDB_286	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
QDH83455.1	006974	Cluster6804_1clades	142	H1O15_gp047	Achromobacter phage Motura	GCA_006964305.1
BAG41493.2	006974	Cluster6804_1clades	179	RSL1_ORF048	Ralstonia phage phiRSL1	GCA_000879455.1
BBA65694.1	006975	SIG+TM+TM	179	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65235.1	006975	SIG+TM+TM	179	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90575.1	006976	Cluster6806_1clades	179	HYO65_gp183	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90883.1	006976	Cluster6806_1clades	179	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06828.1	006977	Cluster6807_1clades	179	BcepSaruman_415	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74797.1	006977	Cluster6807_1clades	179	BcepSauron_417	Burkholderia phage BcepSauron	GCA_005394215.1
QNH80851.1	006978	Cluster6808_1clades	134	D6_0190	Aeromonas phage D6	GCA_007051205.2
QDH47160.1	006978	Cluster6808_1clades	179	LAh10_108	Aeromonas phage LAh10	GCA_006863975.1
QDJ97176.1	006979	Cluster6809_1clades	179	D6_0016	Aeromonas phage D6	GCA_007051205.2
QDH47161.1	006979	Cluster6809_1clades	179	LAh10_184	Aeromonas phage LAh10	GCA_006863975.1
ALN97725.1	006980	Cluster6810_1clades	175	Bp8pS_046	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97726.1	006980	Cluster6810_1clades	178	Bp8pS_047	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AXF51324.1	006981	Cluster6811_1clades	178	WELLINGTON_196	Erwinia phage Wellington	GCA_003344985.1
ANZ49549.1	006981	Cluster6811_1clades	178	KWAN_197	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASR76240.1	006982	HAD	178	PBI_BELLAMY_204	Synechococcus phage Bellamy	GCA_002627525.1
QJT70196.1	006982	HAD	178	SynMITS9220M01_190	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ASV44087.1	006983	Cluster6813_1clades	178	PBI_SCTP2_72	Salicola phage SCTP-2	GCA_002625545.1
QAU04465.1	006983	Cluster6813_1clades	152	ValB1MD_062	Vibrio phage ValB1MD	GCA_004138815.1
BAW19153.1	006984	Cluster6814_1clades	178	FDH28_gp242	Ralstonia phage RP12	GCA_002617345.1
BAW19439.1	006984	Cluster6814_1clades	178	-	Ralstonia phage RP31	GCA_002617365.1
BBA65275.1	006985	Cluster6815_1clades	178	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65734.1	006985	Cluster6815_1clades	178	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90562.1	006986	Cluster6816_1clades	178	HYO65_gp170	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90870.1	006986	Cluster6816_1clades	178	-	Tenacibaculum phage PTm5	GCA_009730715.1
AFF28114.1	006987	Cluster6817_1clades	172	PAU_116	Sphingomonas phage PAU	GCA_000902455.1
AFF28037.1	006987	Cluster6817_1clades	177	PAU_39	Sphingomonas phage PAU	GCA_000902455.1
ABY63012.1	006988	Cluster6818_1clades	175	201phi2-1p182	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76641.1	006988	Cluster6818_1clades	177	PHABIO_10	Pseudomonas phage Phabio	GCA_002624965.1
ASU03895.1	006989	Cluster6819_1clades	177	JOAD_20	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03650.1	006989	Cluster6819_1clades	177	RISINGSUN_20	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65384.1	006990	Cluster6820_1clades	177	2050HW_00049	Serratia phage 2050HW	GCA_002628125.1
QDB71166.1	006990	Cluster6820_1clades	177	CPT_Moabite_136	Serratia phage Moabite	GCA_006384735.1
AXQ69136.1	006991	Cluster6821_1clades	177	CcrBL9_gp112	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69690.1	006991	Cluster6821_1clades	149	CcrSC_gp108	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69338.1	006992	TM	177	CcrBL9_gp314	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69898.1	006992	TM	175	CcrSC_gp316	Caulobacter phage CcrSC	GCA_003443315.1
BAS04955.2	006993	Cluster6823_1clades	112	AVU11_agp34	Ralstonia phage RSF1	GCA_001500875.1
BAQ02680.1	006993	Cluster6823_1clades	177	AVU38_gp152	Ralstonia phage RSL2	GCA_001503055.1
BAW19164.1	006994	Cluster6824_1clades	177	FDH28_gp231	Ralstonia phage RP12	GCA_002617345.1
BAW19450.1	006994	Cluster6824_1clades	177	-	Ralstonia phage RP31	GCA_002617365.1
BBI90652.1	006995	Cluster6825_1clades	140	HYO65_gp260	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90957.1	006995	Cluster6825_1clades	177	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ96846.1	006996	Fib_alpha	177	PS1_0087	Aeromonas phage PS1	GCA_007051165.2
QFR59476.1	006996	Fib_alpha	177	PS2_0085	Aeromonas phage PS2	GCA_009388305.2
QDJ96688.1	006997	Cluster6827_1clades	176	PS1_0177	Aeromonas phage PS1	GCA_007051165.2
QFR59321.1	006997	Cluster6827_1clades	177	PS2_0179	Aeromonas phage PS2	GCA_009388305.2
prevph1000000259	006998	DUF3310	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000206	006998	DUF3310	178	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000628	006999	Cluster6829_1clades	116	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000446	006999	Cluster6829_1clades	178	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000777	007000	Cluster6830_1clades	178	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000530	007000	Cluster6830_1clades	178	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS06030.1	007001	Cluster6831_1clades	176	ABCD_0253	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78793.1	007001	Cluster6831_1clades	176	RB43ORF271w	Escherichia virus RB43	GCA_000863505.1
APU01592.1	007002	Cluster6832_1clades	176	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53216.1	007002	Cluster6832_1clades	176	65p208	Aeromonas virus 65	GCA_000893255.1
AFC21616.1	007003	Cluster6833_1clades	176	GAP32_166	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW88691.1	007003	Cluster6833_1clades	124	BF_0166	Serratia phage BF	GCA_002619745.1
AFU88108.1	007004	Cluster6834_1clades	170	CcrColossus_gp238	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68785.1	007004	Cluster6834_1clades	176	CcrPW_gp246	Caulobacter phage CcrPW	GCA_003443275.1
BAS04903.1	007005	Cluster6835_1clades	176	AVU11_gp111	Ralstonia phage RSF1	GCA_001500875.1
BAQ02630.1	007005	Cluster6835_1clades	176	AVU38_gp102	Ralstonia phage RSL2	GCA_001503055.1
QBX06453.1	007006	SWC5	176	BcepSaruman_040	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74420.1	007006	SWC5	176	BcepSauron_040	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32523.1	007007	Cluster6837_1clades	176	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42096.1	007007	Cluster6837_1clades	176	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ96685.1	007008	WYL	175	PS1_0174	Aeromonas phage PS1	GCA_007051165.2
QFR59318.1	007008	WYL	176	PS2_0176	Aeromonas phage PS2	GCA_009388305.2
prevph1000000117	007009	Cluster6840_1clades	177	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000086	007009	Cluster6840_1clades	177	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000131	007010	Cluster6841_1clades	177	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000099	007010	Cluster6841_1clades	177	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000354	007011	Cluster6842_1clades	177	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000280	007011	Cluster6842_1clades	177	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000657	007012	Cluster6843_1clades	177	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000469	007012	Cluster6843_1clades	177	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88215.1	007013	Cluster6845_1clades	175	CcrColossus_gp345	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68891.1	007013	Cluster6845_1clades	172	CcrPW_gp352	Caulobacter phage CcrPW	GCA_003443275.1
ALN97851.1	007014	Cluster6846_1clades	175	Bp8pS_172	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97852.1	007014	Cluster6846_1clades	137	Bp8pS_173	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ARM70831.1	007015	motB	139	phiC120_c125	Escherichia phage phiC120	GCA_002621185.1
ARM70832.1	007015	motB	175	phiC120_c126	Escherichia phage phiC120	GCA_002621185.1
AYD81371.1	007016	Cluster6848_1clades	175	SEA_JUSTBECAUSE_216	Streptomyces phage JustBecause	GCA_003613775.1
QJD53774.1	007016	Cluster6848_1clades	175	SEA_KELA_214	Streptomyces phage Kela	GCA_012934305.1
prevph1000000435	007017	Cluster6849_1clades	176	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000347	007017	Cluster6849_1clades	176	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44398.1	007018	DUF2345	174	PSSM2_020	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12252.1	007018	DUF2345	174	PRTG_00095	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44429.1	007019	FormylT	174	PSSM2_051	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12222.1	007019	FormylT	174	PRTG_00064	Prochlorococcus phage P-SSM5	GCA_002991095.1
AMM43967.1	007020	Cluster6852_1clades	174	CBB_404	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88924.1	007020	Cluster6852_1clades	174	BF_0399	Serratia phage BF	GCA_002619745.1
AXG67257.1	007021	Cluster6853_1clades	174	AD1_213	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
ARW58858.1	007021	Cluster6853_1clades	174	Y3_218	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ATA65622.1	007022	Cluster6854_1clades	174	2050HW_00287	Serratia phage 2050HW	GCA_002628125.1
QDB71049.1	007022	Cluster6854_1clades	174	CPT_Moabite_017	Serratia phage Moabite	GCA_006384735.1
AXG67098.1	007023	Cluster6855_1clades	174	AD1_054	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08333.1	007023	Cluster6855_1clades	125	Alexandra_53	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXH70953.1	007024	PADR-HTH	174	-	Vibrio phage BONAISHI	GCA_003441475.1
AQT28039.1	007024	PADR-HTH	141	pVa21_098	Vibrio phage pVa-21	GCA_002619305.1
AXQ69121.1	007025	Cluster6857_1clades	174	CcrBL9_gp097	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69675.1	007025	Cluster6857_1clades	174	CcrSC_gp093	Caulobacter phage CcrSC	GCA_003443315.1
BBI90619.1	007026	Cluster6858_1clades	174	HYO65_gp227	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90925.1	007026	Cluster6858_1clades	174	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06838.1	007027	SIG+Osmo_CC	174	BcepSaruman_425	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74807.1	007027	SIG+Osmo_CC	174	BcepSauron_427	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32492.1	007028	Cluster6860_1clades	174	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42065.1	007028	Cluster6860_1clades	174	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000053	007029	Cluster6861_1clades	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000041	007029	Cluster6861_1clades	175	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000076	007030	TM	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000061	007030	TM	175	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000307	007031	NUDIX	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000239	007031	NUDIX	175	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000357	007032	Cluster6864_1clades	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000283	007032	Cluster6864_1clades	175	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000634	007033	Cluster6865_1clades	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000451	007033	Cluster6865_1clades	175	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000163	007034	Ruc-ZnR+Tox-HNH	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000125	007034	Ruc-ZnR+Tox-HNH	139	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44408.1	007035	Phage_tail_APC	173	PSSM2_030	Prochlorococcus phage P-SSM2	GCA_000859585.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGN12243.1	007035	Phage_tail_APC	173	PRTG_00085	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88063.1	007036	TM	173	CcrColossus_gp193	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68741.1	007036	TM	172	CcrPW_gp202c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88094.1	007037	Cluster6869_1clades	173	CcrColossus_gp224	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68770.1	007037	Cluster6869_1clades	145	CcrPW_gp231c	Caulobacter phage CcrPW	GCA_003443275.1
AGR48126.1	007038	TM+TM	173	SmphiM12_494	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13663.1	007038	TM+TM	173	PHIN3_400	Sinorhizobium phage phiN3	GCA_001501175.1
QCW18732.1	007039	Cluster6871_1clades	173	7t3_0211	Salmonella phage 7t3	GCA_006083215.1
AZU98002.1	007039	Cluster6871_1clades	173	CPT_Munch_058	Salmonella phage Munch	GCA_004015485.1
BAW18994.1	007040	Cluster6872_1clades	172	FDH28_gp020	Ralstonia phage RP12	GCA_002617345.1
BAW19282.1	007040	Cluster6872_1clades	173	-	Ralstonia phage RP31	GCA_002617365.1
BBA65524.1	007041	Cluster6873_1clades	173	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96522.1	007041	Cluster6873_1clades	153	Xoosp13_336	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06609.1	007042	Cluster6874_1clades	147	BcepSaruman_196	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74575.1	007042	Cluster6874_1clades	173	BcepSauron_195	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ96848.1	007043	Cluster6875_1clades	173	PS1_0089	Aeromonas phage PS1	GCA_007051165.2
QFR59479.1	007043	Cluster6875_1clades	173	PS2_0088	Aeromonas phage PS2	GCA_009388305.2
AUZ95410.1	007044	OmpA-beta-barrel	159	FDI40_gp651	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65986.1	007044	OmpA-beta-barrel	173	phiOC_p344	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ASU03774.1	007045	Cluster6877_1clades	172	JOAD_141	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03530.1	007045	Cluster6877_1clades	172	RISINGSUN_140	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65533.1	007046	SIG+TM+TM	172	2050HW_00198	Serratia phage 2050HW	GCA_002628125.1
QDB71297.1	007046	SIG+TM+TM	172	CPT_Moabite_267	Serratia phage Moabite	GCA_006384735.1
QBZ72205.1	007047	Cluster6879_1clades	172	SEA_KRADAL_319	Streptomyces phage Kradal	GCA_004799925.1
AXH66468.1	007047	Cluster6879_1clades	172	SEA_SATIS_319	Streptomyces phage Satis	GCA_003366315.1
AXQ69069.1	007048	Cluster6880_1clades	172	CcrBL9_gp045c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69629.1	007048	Cluster6880_1clades	172	CcrSC_gp047c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69505.1	007049	Cluster6881_1clades	172	CcrBL9_gp481	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70054.1	007049	Cluster6881_1clades	172	CcrSC_gp472	Caulobacter phage CcrSC	GCA_003443315.1
AYD81472.1	007050	Cluster6882_1clades	172	SEA_JUSTBECAUSE_317	Streptomyces phage JustBecause	GCA_003613775.1
QJD53875.1	007050	Cluster6882_1clades	172	SEA_KELA_315	Streptomyces phage Kela	GCA_012934305.1
BAW19138.1	007051	Cluster6883_1clades	172	FDH28_gp257	Ralstonia phage RP12	GCA_002617345.1
BAW19424.1	007051	Cluster6883_1clades	172	-	Ralstonia phage RP31	GCA_002617365.1
QBX06600.1	007052	DUF3310	172	BcepSaruman_187	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74565.1	007052	DUF3310	172	BcepSauron_185	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97315.1	007053	Cluster6885_1clades	172	D6_0155	Aeromonas phage D6	GCA_007051205.2
QDH47164.1	007053	Cluster6885_1clades	172	LAh10_78	Aeromonas phage LAh10	GCA_006863975.1
QBX32501.1	007054	Cluster6886_1clades	107	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42074.1	007054	Cluster6886_1clades	172	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000372	007055	Cluster6887_1clades	173	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000298	007055	Cluster6887_1clades	173	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14680.1	007056	SFI-Repeat	171	Lu11_0147	Pseudomonas phage Lu11	GCA_000897175.1
AGS82027.1	007056	SFI-Repeat	171	PaBG_00144	Pseudomonas phage PaBG	GCA_000912555.1
AMS01124.1	007057	Cluster6889_1clades	171	AR9_g039	Bacillus phage AR9	GCA_001743835.1
ASU00048.1	007057	Cluster6889_1clades	171	PBI_PBS1_226	Bacillus virus PBS1	GCA_002601325.1
AMS01270.1	007058	ZetaToxin	171	AR9_g186	Bacillus phage AR9	GCA_001743835.1
AST99897.1	007058	ZetaToxin	171	PBI_PBS1_75	Bacillus virus PBS1	GCA_002601325.1
AUZ94829.1	007059	Cluster6892_1clades	168	FDI40_gp017	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72570.1	007059	Cluster6892_1clades	171	-	Myoviridae sp.	GCA_003657725.1
AXQ69420.1	007060	Cluster6893_1clades	171	CcrBL9_gp396	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69975.1	007060	Cluster6893_1clades	171	CcrSC_gp393	Caulobacter phage CcrSC	GCA_003443315.1
BAS05000.1	007061	Cluster6894_1clades	169	AVU11_gp208	Ralstonia phage RSF1	GCA_001500875.1
BAQ02729.2	007061	Cluster6894_1clades	171	-	Ralstonia phage RSL2	GCA_001503055.1
BAW18985.1	007062	Cluster6895_1clades	171	FDH28_gp011	Ralstonia phage RP12	GCA_002617345.1
BAW19273.1	007062	Cluster6895_1clades	171	-	Ralstonia phage RP31	GCA_002617365.1
BAW18989.1	007063	Cluster6896_1clades	171	FDH28_gp015	Ralstonia phage RP12	GCA_002617345.1
BAW19277.1	007063	Cluster6896_1clades	159	-	Ralstonia phage RP31	GCA_002617365.1
BAW19154.1	007064	Cluster6897_1clades	171	FDH28_gp241	Ralstonia phage RP12	GCA_002617345.1
BAW19440.1	007064	Cluster6897_1clades	171	-	Ralstonia phage RP31	GCA_002617365.1
BBI90674.1	007065	Cluster6898_1clades	144	HYO65_gp282	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90981.1	007065	Cluster6898_1clades	171	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06767.1	007066	Cluster6899_1clades	171	BcepSaruman_354	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74737.1	007066	Cluster6899_1clades	171	BcepSauron_357	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32423.1	007067	Cluster6900_1clades	171	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41994.1	007067	Cluster6900_1clades	171	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32499.1	007068	Cluster6901_1clades	171	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42072.1	007068	Cluster6901_1clades	171	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54845.1	007069	HNH	171	b23_0230	Synechococcus phage B23	GCA_009745195.1
QGT54479.1	007069	HNH	171	b3_0236	Synechococcus phage B3	GCA_009745215.1
prevph1000000360	007070	Cluster6903_1clades	172	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000286	007070	Cluster6903_1clades	172	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANM45044.1	007071	Cluster6904_1clades	170	KTN4_286	Pseudomonas phage KTN4	GCA_002607225.1
QJB22920.1	007071	Cluster6904_1clades	170	fnug_277	Pseudomonas phage fnug	GCA_012837215.1
ANZ48308.1	007072	Cluster6905_1clades	170	CAITLIN_13	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48581.1	007072	Cluster6905_1clades	169	CHRISDB_19	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ATA65597.1	007073	DEAM	170	2050HW_00262	Serratia phage 2050HW	GCA_002628125.1
QDB71361.1	007073	DEAM	170	CPT_Moabite_331	Serratia phage Moabite	GCA_006384735.1
ATA65692.1	007074	Cluster6907_1clades	170	2050HW_00357	Serratia phage 2050HW	GCA_002628125.1
QDB71119.1	007074	Cluster6907_1clades	170	CPT_Moabite_089	Serratia phage Moabite	GCA_006384735.1
AXQ69378.1	007075	Cluster6908_1clades	170	CcrBL9_gp354	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69938.1	007075	Cluster6908_1clades	170	CcrSC_gp356	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69252.1	007076	Cluster6909_1clades	169	CcrBL9_gp228c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69809.1	007076	Cluster6909_1clades	170	CcrSC_gp227c	Caulobacter phage CcrSC	GCA_003443315.1
BAS04936.2	007077	Cluster6910_1clades	169	AVU11_gp144	Ralstonia phage RSF1	GCA_001500875.1
BAU71407.1	007077	Cluster6910_1clades	170	-	Ralstonia phage RSL2	GCA_001503055.1
QBX06857.1	007078	Cluster6911_1clades	170	BcepSaruman_444	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74826.1	007078	Cluster6911_1clades	170	BcepSauron_446	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97327.1	007079	Cluster6912_1clades	156	D6_0169	Aeromonas phage D6	GCA_007051205.2
QDH47165.1	007079	Cluster6912_1clades	170	LAh10_89	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000038	007080	Cluster6913_1clades	171	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000030	007080	Cluster6913_1clades	171	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS06035.1	007081	Cluster6914_1clades	169	ABCD_0248	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78787.1	007081	Cluster6914_1clades	169	RB43ORF265w	Escherichia virus RB43	GCA_000863505.1
AFH14656.1	007082	Cluster6915_1clades	85	Lu11_0124	Pseudomonas phage Lu11	GCA_000897175.1
AFH14657.1	007082	Cluster6915_1clades	169	Lu11_0125	Pseudomonas phage Lu11	GCA_000897175.1
BAS04942.1	007083	Cluster6916_1clades	169	AVU11_gp150	Ralstonia phage RSF1	GCA_001500875.1
BAQ02666.1	007083	Cluster6916_1clades	163	AVU38_gp138	Ralstonia phage RSL2	GCA_001503055.1
QBX06450.1	007084	Cluster6917_1clades	167	BcepSaruman_037	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74417.1	007084	Cluster6917_1clades	169	BcepSauron_037	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32506.1	007085	Cluster6918_1clades	169	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42078.1	007085	Cluster6918_1clades	169	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000740	007086	Cluster6919_1clades	170	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000492	007086	Cluster6919_1clades	170	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU87954.1	007087	Cluster6920_1clades	168	CcrColossus_gp084	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68629.1	007087	Cluster6920_1clades	165	CcrPW_gp090	Caulobacter phage CcrPW	GCA_003443275.1
AFU88199.1	007088	Cluster6921_1clades	168	CcrColossus_gp329	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68876.1	007088	Cluster6921_1clades	168	CcrPW_gp337	Caulobacter phage CcrPW	GCA_003443275.1
ASU03867.1	007089	Cluster6922_1clades	168	JOAD_48	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03622.1	007089	Cluster6922_1clades	168	RISINGSUN_48	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXH72474.1	007090	Cluster6923_1clades	165	-	Myoviridae sp.	GCA_003657725.1
AXH72436.1	007090	Cluster6923_1clades	168	-	Myoviridae sp.	GCA_003657725.1
BAS04826.1	007091	Cluster6924_1clades	168	AVU11_gp034	Ralstonia phage RSF1	GCA_001500875.1
BAQ02559.1	007091	Cluster6924_1clades	168	AVU38_gp031	Ralstonia phage RSL2	GCA_001503055.1
ATA65501.1	007092	Cluster6925_1clades	97	2050HW_00166	Serratia phage 2050HW	GCA_002628125.1
QDB71273.1	007092	Cluster6925_1clades	168	CPT_Moabite_243	Serratia phage Moabite	GCA_006384735.1
QNH80850.1	007093	Cluster6926_1clades	140	D6_0173	Aeromonas phage D6	GCA_007051205.2
QDH47166.1	007093	Cluster6926_1clades	168	LAh10_92	Aeromonas phage LAh10	GCA_006863975.1
QDJ96786.1	007094	Cluster6927_1clades	168	PS1_0027	Aeromonas phage PS1	GCA_007051165.2
QFR59417.1	007094	Cluster6927_1clades	168	PS2_0026	Aeromonas phage PS2	GCA_009388305.2
prevph1000000637	007095	Cluster6928_1clades	169	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000453	007095	Cluster6928_1clades	169	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65636.1	007096	Cluster6929_1clades	167	2050HW_00301	Serratia phage 2050HW	GCA_002628125.1
QDB71064.1	007096	Cluster6929_1clades	167	CPT_Moabite_032	Serratia phage Moabite	GCA_006384735.1
BAS04839.2	007097	Cluster6930_1clades	167	AVU11_gp047	Ralstonia phage RSF1	GCA_001500875.1
BAQ02572.2	007097	Cluster6930_1clades	77	-	Ralstonia phage RSL2	GCA_001503055.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAW19008.1	007098	Cluster6931_1clades	166	FDH28_gp034	Ralstonia phage RP12	GCA_002617345.1
BAW19294.1	007098	Cluster6931_1clades	167	-	Ralstonia phage RP31	GCA_002617365.1
BBA65187.1	007099	Cluster6932_1clades	167	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65646.1	007099	Cluster6932_1clades	167	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06477.1	007100	Cluster6934_1clades	167	BcepSaruman_064	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74444.1	007100	Cluster6934_1clades	167	BcepSauron_064	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97385.1	007101	Cluster6935_1clades	167	D6_0226	Aeromonas phage D6	GCA_007051205.2
QDH47167.1	007101	Cluster6935_1clades	167	LAh10_140	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000194	007102	Cluster6936_1clades	83	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000157	007102	Cluster6936_1clades	168	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000517	007103	TM	168	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000391	007103	TM	168	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000802	007104	Cluster6938_1clades	168	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000549	007104	Cluster6938_1clades	168	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88206.1	007105	Cluster6939_1clades	166	CcrColossus_gp336	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68883.1	007105	Cluster6939_1clades	166	CcrPW_gp344	Caulobacter phage CcrPW	GCA_003443275.1
AIA65021.1	007106	Tox-HNH	166	S13_224	Cronobacter phage S13	GCA_001503575.1
QHJ78910.1	007106	Tox-HNH	166	-	Myoviridae sp.	GCA_012593985.1
AGH07554.1	007107	HD	152	CYVG_00110	Cyanophage S-SSM6a	GCA_002710385.1
AIR93512.1	007107	HD	166	AVU42_gp175	Prochlorococcus phage P-TIM68	GCA_001503075.1
AMS01222.1	007108	TM	166	AR9_g138	Bacillus phage AR9	GCA_001743835.1
AST99847.1	007108	TM	166	PBI_PBS1_25	Bacillus virus PBS1	GCA_002601325.1
AXQ69307.1	007109	Myosin_N	166	CcrBL9_gp283	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69866.1	007109	Myosin_N	166	CcrSC_gp284	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69310.1	007110	Cluster6944_1clades	166	CcrBL9_gp286	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69869.1	007110	Cluster6944_1clades	165	CcrSC_gp287	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69311.1	007111	Cluster6945_1clades	166	CcrBL9_gp287	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69870.1	007111	Cluster6945_1clades	166	CcrSC_gp288	Caulobacter phage CcrSC	GCA_003443315.1
QBX06720.1	007112	Cluster6946_1clades	159	BcepSaruman_307	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74688.1	007112	Cluster6946_1clades	166	BcepSauron_308	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ96730.1	007113	Cluster6947_1clades	166	PS1_0219	Aeromonas phage PS1	GCA_007051165.2
QFR59363.1	007113	Cluster6947_1clades	166	PS2_0221	Aeromonas phage PS2	GCA_009388305.2
QDJ97341.1	007114	Cluster6948_1clades	166	D6_0182	Aeromonas phage D6	GCA_007051205.2
QDH47169.1	007114	Cluster6948_1clades	165	LAh10_101	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000014	007115	V-SNARE	167	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000013	007115	V-SNARE	167	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000334	007116	Cluster6950_1clades	167	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000263	007116	Cluster6950_1clades	167	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000751	007117	DSPc	167	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000503	007117	DSPc	167	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000766	007118	Cluster6952_1clades	167	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000519	007118	Cluster6952_1clades	167	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMS01285.1	007119	Cluster6954_1clades	165	AR9_g201	Bacillus phage AR9	GCA_001743835.1
AST99913.1	007119	Cluster6954_1clades	165	PBI_PBS1_91	Bacillus virus PBS1	GCA_002601325.1
AXQ69345.1	007120	Cluster6955_1clades	165	CcrBL9_gp321	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69904.1	007120	Cluster6955_1clades	165	CcrSC_gp322	Caulobacter phage CcrSC	GCA_003443315.1
BAS04889.1	007121	TM	165	AVU11_gp097	Ralstonia phage RSF1	GCA_001500875.1
BAQ02616.1	007121	TM	165	AVU38_gp088	Ralstonia phage RSL2	GCA_001503055.1
BAW19226.1	007122	Cluster6957_1clades	165	FDH28_gp169	Ralstonia phage RP12	GCA_002617345.1
BAW19512.1	007122	Cluster6957_1clades	165	-	Ralstonia phage RP31	GCA_002617365.1
prevph1000000336	007123	Cluster6958_1clades	166	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000265	007123	Cluster6958_1clades	166	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AYD81298.1	007124	Cluster6959_1clades	164	SEA_JUSTBECAUSE_129	Streptomyces phage JustBecause	GCA_003613775.1
QJD53701.1	007124	Cluster6959_1clades	164	SEA_KELA_130	Streptomyces phage Kela	GCA_012934305.1
BAS04850.1	007125	Cluster6960_1clades	164	AVU11_gp058	Ralstonia phage RSF1	GCA_001500875.1
BAQ02584.2	007125	Cluster6960_1clades	130	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65412.1	007126	Cluster6961_1clades	164	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96435.1	007126	Cluster6961_1clades	164	Xoosp13_249	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06467.1	007127	Cluster6962_1clades	164	BcepSaruman_054	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74435.1	007127	Cluster6962_1clades	164	BcepSauron_055	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32374.1	007128	Cluster6963_1clades	164	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41947.1	007128	Cluster6963_1clades	164	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCG76309.1	007129	PTSEIIA1	164	EST35_0441	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BBA65571.1	007129	PTSEIIA1	159	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ97412.1	007130	Cluster6965_1clades	164	D6_0253	Aeromonas phage D6	GCA_007051205.2
QDH47170.1	007130	Cluster6965_1clades	164	LAh10_165	Aeromonas phage LAh10	GCA_006863975.1
SOK59273.1	007131	Cluster6966_1clades	164	g465	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58737.1	007131	Cluster6966_1clades	126	g460	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000640	007132	Cluster6967_1clades	165	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000456	007132	Cluster6967_1clades	165	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABY63249.1	007133	Cluster6968_1clades	163	201phi2-1p426	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77065.1	007133	Cluster6968_1clades	148	PHABIO_434	Pseudomonas phage Phabio	GCA_002624965.1
AFU88079.1	007134	Cluster6969_1clades	163	CcrColossus_gp209	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68756.1	007134	Cluster6969_1clades	163	CcrPW_gp217c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88111.1	007135	SIG+TM	163	CcrColossus_gp241	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68789.1	007135	SIG+TM	163	CcrPW_gp250	Caulobacter phage CcrPW	GCA_003443275.1
AIA65057.1	007136	Cluster6971_1clades	163	S13_260	Cronobacter phage S13	GCA_001503575.1
QHJ78875.1	007136	Cluster6971_1clades	161	-	Myoviridae sp.	GCA_012593985.1
AMS01094.1	007137	Cluster6972_1clades	163	AR9_g009	Bacillus phage AR9	GCA_001743835.1
ASU00016.1	007137	Cluster6972_1clades	163	PBI_PBS1_194	Bacillus virus PBS1	GCA_002601325.1
ANS06038.1	007138	Cluster6973_1clades	163	ABCD_0246	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78785.1	007138	Cluster6973_1clades	108	RB43ORF263w	Escherichia virus RB43	GCA_000863505.1
AOV59655.1	007139	C1q	163	S330809_194	Synechococcus phage S-CAM4	GCA_002366065.1
AOV59417.1	007139	C1q	163	C440309_194	Synechococcus phage S-CAM4	GCA_002922145.1
ASU03779.1	007140	Cluster6975_1clades	163	JOAD_136	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03535.1	007140	Cluster6975_1clades	163	RISINGSUN_135	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03809.1	007141	Cluster6976_1clades	163	JOAD_106	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03564.1	007141	Cluster6976_1clades	163	RISINGSUN_106	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QBX06842.1	007142	Cluster6979_1clades	163	BcepSaruman_429	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74811.1	007142	Cluster6979_1clades	163	BcepSauron_431	Burkholderia phage BcepSauron	GCA_005394215.1
SOK59312.1	007143	Cluster6981_1clades	163	g504	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58776.1	007143	Cluster6981_1clades	163	g499	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000191	007144	Cluster6982_1clades	164	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000154	007144	Cluster6982_1clades	164	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000244	007145	Cluster6983_1clades	121	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000194	007145	Cluster6983_1clades	164	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000661	007146	Cluster6984_1clades	164	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000473	007146	Cluster6984_1clades	164	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44440.2	007147	Cluster6985_1clades	162	PSSM2_062	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12212.1	007147	Cluster6985_1clades	151	PRTG_00054	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88229.1	007148	Cupin	162	CcrColossus_gp359	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68906.1	007148	Cupin	162	CcrPW_gp367	Caulobacter phage CcrPW	GCA_003443275.1
AMS01334.1	007149	Cluster6987_1clades	162	AR9_g250	Bacillus phage AR9	GCA_001743835.1
AST99964.1	007149	Cluster6987_1clades	162	PBI_PBS1_143	Bacillus virus PBS1	GCA_002601325.1
AFO71276.1	007150	Cluster6988_1clades	157	CR5_056	Cronobacter phage CR5	GCA_000910235.1
ANZ50248.1	007150	Cluster6988_1clades	162	PHOBOS_58	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ASU03903.1	007151	Cluster6990_1clades	162	JOAD_12	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03658.1	007151	Cluster6990_1clades	162	RISINGSUN_12	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QBZ72035.1	007152	Cluster6991_1clades	162	SEA_KRADAL_137	Streptomyces phage Kradal	GCA_004799925.1
AXH66298.1	007152	Cluster6991_1clades	162	SEA_SATIS_137	Streptomyces phage Satis	GCA_003366315.1
AXQ69478.1	007153	Cluster6992_1clades	162	CcrBL9_gp454	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70027.1	007153	Cluster6992_1clades	162	CcrSC_gp445	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69514.1	007154	Cluster6993_1clades	162	CcrBL9_gp490	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70061.1	007154	Cluster6993_1clades	157	CcrSC_gp479	Caulobacter phage CcrSC	GCA_003443315.1
BAS04842.1	007155	Cluster6994_1clades	162	AVU11_gp050	Ralstonia phage RSF1	GCA_001500875.1
BAQ02575.1	007155	Cluster6994_1clades	158	AVU38_gp047	Ralstonia phage RSL2	GCA_001503055.1
QBP07622.1	007156	Cluster6995_1clades	162	DERBICUS_196	Erwinia phage Derbicus	GCA_004521655.1
ANZ49046.1	007156	Cluster6995_1clades	151	EARLPHILLIPIV_197	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
QBX32414.1	007157	Cluster6996_1clades	162	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41985.1	007157	Cluster6996_1clades	162	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000379	007158	Cluster6997_1clades	163	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000305	007158	Cluster6997_1clades	163	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABY63261.1	007159	Cluster6998_1clades	161	201phi2-1p438	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76884.1	007159	Cluster6998_1clades	157	PHABIO_253	Pseudomonas phage Phabio	GCA_002624965.1
ARV77465.1	007160	Cluster6999_1clades	161	NOXIFER_300	Pseudomonas phage Noxifer	GCA_002625005.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEH03590.1	007160	Cluster6999_1clades	134	167	Pseudomonas phage PhiPA3	GCA_001502095.1
ASU03674.1	007161	Cluster7000_1clades	161	JOAD_241	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03431.1	007161	Cluster7000_1clades	161	RISINGSUN_239	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65476.1	007162	SspB	161	2050HW_00141	Serratia phage 2050HW	GCA_002628125.1
QDB71246.1	007162	SspB	161	CPT_Moabite_216	Serratia phage Moabite	GCA_006384735.1
AXG67210.1	007163	Cluster7002_1clades	160	AD1_166	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08441.1	007163	Cluster7002_1clades	161	Alexandra_171	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXH72383.1	007164	Cluster7003_1clades	159	-	Myoviridae sp.	GCA_003657725.1
AXH72382.1	007164	Cluster7003_1clades	161	-	Myoviridae sp.	GCA_003657725.1
AXQ69486.1	007165	Cluster7004_1clades	161	CcrBL9_gp462	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70034.1	007165	Cluster7004_1clades	161	CcrSC_gp452	Caulobacter phage CcrSC	GCA_003443315.1
BAS04805.2	007166	SIG+TM+TM	130	AVU11_gp013	Ralstonia phage RSF1	GCA_001500875.1
BAQ02541.1	007166	SIG+TM+TM	161	AVU38_gp013	Ralstonia phage RSL2	GCA_001503055.1
QBO63924.1	007167	DUF4262	161	Goslar_00131	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
BAG41475.1	007167	DUF4262	159	RSL1_ORF030	Ralstonia phage phiRSL1	GCA_000879455.1
QBX06479.1	007168	Cluster7007_1clades	150	BcepSaruman_066	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74446.1	007168	Cluster7007_1clades	161	BcepSauron_066	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65444.1	007169	Cluster7008_1clades	150	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96460.1	007169	Cluster7008_1clades	161	Xoosp13_274	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54747.1	007170	Cluster7010_1clades	161	b23_0132	Synechococcus phage B23	GCA_009745195.1
QGT54377.1	007170	Cluster7010_1clades	161	b3_0133	Synechococcus phage B3	GCA_009745215.1
prevph1000000618	007171	Cluster7011_1clades	162	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000437	007171	Cluster7011_1clades	162	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000746	007172	Cluster7012_1clades	162	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000498	007172	Cluster7012_1clades	162	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88165.1	007173	Cluster7013_1clades	160	CcrColossus_gp295	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68841.1	007173	Cluster7013_1clades	160	CcrPW_gp302	Caulobacter phage CcrPW	GCA_003443275.1
AJT60917.1	007174	Cluster7015_1clades	157	AVU32_gp076	Vibrio phage ValKK3	GCA_001501635.1
ALP47112.1	007174	Cluster7015_1clades	160	phiGrn1_0297	Vibrio phage phi-Grn1	GCA_002757115.1
AFC21962.1	007175	Cluster7016_1clades	153	GAP32_503	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW89043.1	007175	Cluster7016_1clades	160	BF_0518	Serratia phage BF	GCA_002619745.1
ATA65487.1	007176	Cluster7017_1clades	160	2050HW_00152	Serratia phage 2050HW	GCA_002628125.1
QDB71257.1	007176	Cluster7017_1clades	160	CPT_Moabite_227	Serratia phage Moabite	GCA_006384735.1
AUZ95055.1	007177	Cluster7018_1clades	135	FDI40_gp283	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72729.1	007177	Cluster7018_1clades	160	-	Myoviridae sp.	GCA_003657725.1
AFU88102.1	007178	Cluster7019_1clades	159	CcrColossus_gp232	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68779.1	007178	Cluster7019_1clades	160	CcrPW_gp240	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69152.1	007179	Cluster7020_1clades	160	CcrBL9_gp128	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69706.1	007179	Cluster7020_1clades	160	CcrSC_gp124	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69283.1	007180	Cluster7021_1clades	160	CcrBL9_gp259c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69840.1	007180	Cluster7021_1clades	160	CcrSC_gp258c	Caulobacter phage CcrSC	GCA_003443315.1
AFF28250.1	007181	Cluster7022_1clades	77	PAU_252	Sphingomonas phage PAU	GCA_000902455.1
BAV39236.1	007181	Cluster7022_1clades	160	BPT24_111	Tenacibaculum phage pT24	GCA_002611925.1
BAW19170.1	007182	Cluster7023_1clades	160	FDH28_gp225	Ralstonia phage RP12	GCA_002617345.1
BAW19456.1	007182	Cluster7023_1clades	160	-	Ralstonia phage RP31	GCA_002617365.1
BBI90423.1	007183	Cluster7024_1clades	160	HYO65_gp031	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90730.1	007183	Cluster7024_1clades	160	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90458.1	007184	Cluster7025_1clades	160	HYO65_gp066	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90766.1	007184	Cluster7025_1clades	160	-	Tenacibaculum phage PTm5	GCA_009730715.1
prevph1000000132	007185	Cluster7026_1clades	161	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000100	007185	Cluster7026_1clades	161	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000492	007186	Cluster7027_1clades	161	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000373	007186	Cluster7027_1clades	161	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AOO14243.1	007187	Cluster7028_1clades	159	Sn110110_049	Cyanophage S-RIM14	GCA_002599065.1
AOO14895.1	007187	Cluster7028_1clades	159	W1230910_049	Cyanophage S-RIM14	GCA_002599125.1
ATA65416.1	007188	Cluster7029_1clades	159	2050HW_00081	Serratia phage 2050HW	GCA_002628125.1
QDB71195.1	007188	Cluster7029_1clades	159	CPT_Moabite_165	Serratia phage Moabite	GCA_006384735.1
ATA65486.1	007189	Cluster7030_1clades	159	2050HW_00151	Serratia phage 2050HW	GCA_002628125.1
QDB71256.1	007189	Cluster7030_1clades	159	CPT_Moabite_226	Serratia phage Moabite	GCA_006384735.1
ATA65510.1	007190	SIG+TM	159	2050HW_00175	Serratia phage 2050HW	GCA_002628125.1
QDB71278.1	007190	SIG+TM	159	CPT_Moabite_248	Serratia phage Moabite	GCA_006384735.1
ATA65634.1	007191	Cluster7032_1clades	159	2050HW_00299	Serratia phage 2050HW	GCA_002628125.1
QDB71062.1	007191	Cluster7032_1clades	159	CPT_Moabite_030	Serratia phage Moabite	GCA_006384735.1
QAY01472.1	007192	Cluster7033_1clades	159	ASwh1_413	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01473.1	007192	Cluster7033_1clades	156	ASwh1_414	Aeromonas phage Aswh_1	GCA_004146945.1
QBX32454.1	007193	Cluster7034_1clades	159	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42026.1	007193	Cluster7034_1clades	159	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AFU88125.1	007194	Cluster7035_1clades	158	CcrColossus_gp255	Caulobacter phage CcrColossus	GCA_000899635.1
AGX01834.1	007194	Cluster7035_1clades	145	CF95_gp112	Erwinia phage PhiEaH1	GCA_000914555.1
AMS01131.1	007195	Cluster7036_1clades	158	AR9_g046	Bacillus phage AR9	GCA_001743835.1
ASU00058.1	007195	Cluster7036_1clades	153	PBI_PBS1_236	Bacillus virus PBS1	GCA_002601325.1
ARV77272.1	007196	TM	75	NOXIFER_103	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77352.1	007196	TM	158	NOXIFER_183	Pseudomonas phage Noxifer	GCA_002625005.1
ASU03759.1	007197	Cluster7038_1clades	158	JOAD_156	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03515.1	007197	Cluster7038_1clades	158	RISINGSUN_155	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASV44365.1	007198	Cluster7039_1clades	91	PBI_SCTP2_350	Salicola phage SCTP-2	GCA_002625545.1
ASV44436.1	007198	Cluster7039_1clades	158	PBI_SCTP2_421	Salicola phage SCTP-2	GCA_002625545.1
ATA65694.1	007199	Cluster7040_1clades	158	2050HW_00359	Serratia phage 2050HW	GCA_002628125.1
QDB71121.1	007199	Cluster7040_1clades	158	CPT_Moabite_091	Serratia phage Moabite	GCA_006384735.1
AFU87934.1	007200	Cluster7041_1clades	157	CcrColossus_gp064	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68606.1	007200	Cluster7041_1clades	158	CcrPW_gp067	Caulobacter phage CcrPW	GCA_003443275.1
BAS04965.1	007201	Cluster7042_1clades	156	AVU11_gp173	Ralstonia phage RSF1	GCA_001500875.1
BAQ02690.1	007201	Cluster7042_1clades	158	AVU38_gp162	Ralstonia phage RSL2	GCA_001503055.1
BAS04979.1	007202	Cluster7043_1clades	158	AVU11_gp187	Ralstonia phage RSF1	GCA_001500875.1
BAQ02705.1	007202	Cluster7043_1clades	158	AVU38_gp177	Ralstonia phage RSL2	GCA_001503055.1
BAW19023.1	007203	Cluster7044_1clades	158	FDH28_gp049	Ralstonia phage RP12	GCA_002617345.1
BAW19309.1	007203	Cluster7044_1clades	158	-	Ralstonia phage RP31	GCA_002617365.1
BAW19115.1	007204	Cluster7045_1clades	158	FDH28_gp280	Ralstonia phage RP12	GCA_002617345.1
BAW19401.1	007204	Cluster7045_1clades	158	-	Ralstonia phage RP31	GCA_002617365.1
BAW19152.1	007205	Cluster7046_1clades	158	FDH28_gp243	Ralstonia phage RP12	GCA_002617345.1
BAW19438.1	007205	Cluster7046_1clades	158	-	Ralstonia phage RP31	GCA_002617365.1
BBI90470.1	007206	Cluster7047_1clades	158	HYO65_gp078	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90777.1	007206	Cluster7047_1clades	158	-	Tenacibaculum phage PTm5	GCA_009730715.1
QDJ97304.1	007207	Cluster7048_1clades	158	D6_0144	Aeromonas phage D6	GCA_007051205.2
QDH47174.1	007207	Cluster7048_1clades	158	LAh10_68	Aeromonas phage LAh10	GCA_006863975.1
QBX32404.1	007208	Cluster7049_1clades	137	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41974.1	007208	Cluster7049_1clades	158	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63283.1	007209	Cluster7050_1clades	158	DAC16_50	Bacteroides phage DAC16	GCA_013387695.1
QIG64328.1	007209	Cluster7050_1clades	158	DAC23_50	Bacteroides phage DAC23	GCA_013387745.1
prevph1000000471	007210	Cluster7051_1clades	121	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000357	007210	Cluster7051_1clades	159	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AXF51366.1	007211	Cluster7052_1clades	157	WELLINGTON_240	Erwinia phage Wellington	GCA_003344985.1
ANZ49593.1	007211	Cluster7052_1clades	157	KWAN_241	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03746.1	007212	Cluster7053_1clades	157	JOAD_169	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03502.1	007212	Cluster7053_1clades	157	RISINGSUN_168	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QBZ72088.1	007213	Cluster7054_1clades	157	SEA_KRADAL_192	Streptomyces phage Kradal	GCA_004799925.1
AXH66350.1	007213	Cluster7054_1clades	157	SEA_SATIS_191	Streptomyces phage Satis	GCA_003366315.1
QBZ72141.1	007214	Cluster7055_1clades	157	SEA_KRADAL_255	Streptomyces phage Kradal	GCA_004799925.1
AXH66403.1	007214	Cluster7055_1clades	157	SEA_SATIS_254	Streptomyces phage Satis	GCA_003366315.1
AXH72563.1	007215	Cluster7056_1clades	107	-	Myoviridae sp.	GCA_003657725.1
AXH72633.1	007215	Cluster7056_1clades	157	-	Myoviridae sp.	GCA_003657725.1
QBX06855.1	007216	Cluster7057_1clades	157	BcepSaruman_442	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74824.1	007216	Cluster7057_1clades	157	BcepSauron_444	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06816.1	007217	Cluster7058_1clades	157	BcepSaruman_403	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74785.1	007217	Cluster7058_1clades	153	BcepSauron_405	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ96701.1	007218	Cluster7059_1clades	157	PS1_0190	Aeromonas phage PS1	GCA_007051165.2
QFR59334.1	007218	Cluster7059_1clades	157	PS2_0192	Aeromonas phage PS2	GCA_009388305.2
QGT54758.1	007219	Cluster7060_1clades	157	b23_0143	Synechococcus phage B23	GCA_009745195.1
QGT54388.1	007219	Cluster7060_1clades	157	b3_0144	Synechococcus phage B3	GCA_009745215.1
SOK59216.1	007220	Cluster7061_1clades	157	g408	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58682.1	007220	Cluster7061_1clades	157	g405	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AMS01221.1	007221	Cluster7062_1clades	156	AR9_g137	Bacillus phage AR9	GCA_001743835.1
AST99846.1	007221	Cluster7062_1clades	156	PBI_PBS1_24	Bacillus virus PBS1	GCA_002601325.1
AXF51271.1	007222	Cluster7063_1clades	156	WELLINGTON_141	Erwinia phage Wellington	GCA_003344985.1
ANZ49492.1	007222	Cluster7063_1clades	156	KWAN_140	Erwinia phage vB_EamM_Kwan	GCA_001744315.1

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ASU03902.1	007223	Cluster7064_1clades	156	JOAD_13	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03657.1	007223	Cluster7064_1clades	156	RISINGSUN_13	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
BAS04953.1	007224	Cluster7065_1clades	156	AVU11_gp161	Ralstonia phage RSF1	GCA_001500875.1
BAQ02678.1	007224	Cluster7065_1clades	156	AVU38_gp150	Ralstonia phage RSL2	GCA_001503055.1
BAW19237.1	007225	Cluster7066_1clades	156	FDH28_gp158	Ralstonia phage RP12	GCA_002617345.1
BAW19523.1	007225	Cluster7066_1clades	156	-	Ralstonia phage RP31	GCA_002617365.1
QBX06564.1	007226	Cluster7067_1clades	156	BcepSaruman_151	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74532.1	007226	Cluster7067_1clades	156	BcepSauron_152	Burkholderia phage BcepSauron	GCA_005394215.1
QIG57751.1	007227	Cluster7068_1clades	156	SEA_PAULODIABOLI_13	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58052.1	007227	Cluster7068_1clades	156	SEA_PAULODIABOLI_368	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000260	007228	Cluster7069_1clades	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000207	007228	Cluster7069_1clades	157	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000329	007229	Cluster7070_1clades	157	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000258	007229	Cluster7070_1clades	157	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000610	007230	Cluster7071_1clades	157	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000429	007230	Cluster7071_1clades	157	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14791.1	007231	Peptidase_M15_3	148	Lu11_0255	Pseudomonas phage Lu11	GCA_000897175.1
AGS82149.1	007231	Peptidase_M15_3	155	PaBG_00276	Pseudomonas phage PaBG	GCA_000912555.1
ATA65478.1	007232	Cluster7073_1clades	155	2050HW_00143	Serratia phage 2050HW	GCA_002628125.1
QDB71248.1	007232	Cluster7073_1clades	155	CPT_Moabite_218	Serratia phage Moabite	GCA_006384735.1
BAS04800.2	007233	Cluster7074_1clades	150	AVU11_gp008	Ralstonia phage RSF1	GCA_001500875.1
BAQ02536.2	007233	Cluster7074_1clades	155	-	Ralstonia phage RSL2	GCA_001503055.1
BAS05014.1	007234	Cluster7075_1clades	155	AVU11_gp222	Ralstonia phage RSF1	GCA_001500875.1
BAQ02744.1	007234	Cluster7075_1clades	149	AVU38_gp216	Ralstonia phage RSL2	GCA_001503055.1
BBA65494.1	007235	Cluster7076_1clades	155	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96502.1	007235	Cluster7076_1clades	155	Xoosp13_316	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90570.1	007236	Cluster7077_1clades	155	HYO65_gp178	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90878.1	007236	Cluster7077_1clades	155	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32449.1	007237	Cluster7079_1clades	155	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42021.1	007237	Cluster7079_1clades	155	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32522.1	007238	Cluster7080_1clades	155	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42095.1	007238	Cluster7080_1clades	155	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000068	007239	Cluster7081_1clades	156	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000054	007239	Cluster7081_1clades	156	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000151	007240	SMPB	156	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000114	007240	SMPB	156	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ATA65575.1	007241	SIG+TM+TM	154	2050HW_00240	Serratia phage 2050HW	GCA_002628125.1
QDB71340.1	007241	SIG+TM+TM	149	CPT_Moabite_310	Serratia phage Moabite	GCA_006384735.1
AUZ95394.1	007242	Cluster7085_1clades	154	FDI40_gp635	Agrobacterium phage Atu_ph07	GCA_002628245.1
AKF13279.1	007242	Cluster7085_1clades	136	PHIN3_12	Sinorhizobium phage phiN3	GCA_001501175.1
BAW19059.1	007243	SIG+TCAD1	154	FDH28_gp085	Ralstonia phage RP12	GCA_002617345.1
BAW19344.1	007243	SIG+TCAD1	154	-	Ralstonia phage RP31	GCA_002617365.1
QBX06622.1	007244	Cluster7087_1clades	154	BcepSaruman_209	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74590.1	007244	Cluster7087_1clades	154	BcepSauron_210	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06810.1	007245	Cluster7088_1clades	154	BcepSaruman_397	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74779.1	007245	Cluster7088_1clades	154	BcepSauron_399	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97354.1	007246	TM	139	D6_0195	Aeromonas phage D6	GCA_007051205.2
QDH47177.1	007246	TM	154	LAh10_113	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000370	007247	Cluster7090_1clades	155	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000296	007247	Cluster7090_1clades	155	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000436	007248	Cluster7091_1clades	155	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000348	007248	Cluster7091_1clades	155	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000809	007249	Cluster7092_1clades	155	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000555	007249	Cluster7092_1clades	155	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU87945.1	007250	DnaJ_CXXCXGXG	153	CcrColossus_gp075	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68618.1	007250	DnaJ_CXXCXGXG	150	CcrPW_gp079	Caulobacter phage CcrPW	GCA_003443275.1
AFU88059.1	007251	YqeY	153	CcrColossus_gp189	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68737.1	007251	YqeY	153	CcrPW_gp198c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88116.1	007252	Cluster7095_1clades	153	CcrColossus_gp246	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68794.1	007252	Cluster7095_1clades	153	CcrPW_gp255	Caulobacter phage CcrPW	GCA_003443275.1
AGX01764.1	007253	Cluster7096_1clades	130	CF95_gp042	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01765.1	007253	Cluster7096_1clades	153	CF95_gp043	Erwinia phage PhiEaH1	GCA_000914555.1
QAY01445.1	007254	Cluster7097_1clades	152	ASwh1_386	Aeromonas phage Aswh_1	GCA_004146945.1
ALY07141.1	007254	Cluster7097_1clades	153	VmeM32_00155	Vibrio phage vB_VmeM-32	GCA_002608825.1
AMS01233.1	007255	fvmYukDl-Nterm	153	AR9_g149	Bacillus phage AR9	GCA_001743835.1
AST99859.1	007255	fvmYukDl-Nterm	153	PBI_PBS1_37	Bacillus virus PBS1	GCA_002601325.1
ANZ48484.1	007256	Cluster7099_1clades	148	CAITLIN_189	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48763.1	007256	Cluster7099_1clades	153	CHRISDB_201	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
QBP07483.1	007257	Cluster7100_1clades	153	DERBICUS_57	Erwinia phage Derbicus	GCA_004521655.1
ANZ48907.1	007257	Cluster7100_1clades	153	EARLPHILLIPIV_57	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ABY63095.1	007258	Cluster7101_1clades	143	201phi2-1p267	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76887.1	007258	Cluster7101_1clades	153	PHABIO_256	Pseudomonas phage Phabio	GCA_002624965.1
ASR76094.1	007259	Cluster7102_1clades	138	PBI_BELLAMY_49	Synechococcus phage Bellamy	GCA_002627525.1
ASR76097.1	007259	Cluster7102_1clades	153	PBI_BELLAMY_52	Synechococcus phage Bellamy	GCA_002627525.1
ASU03798.1	007260	Cluster7103_1clades	153	JOAD_117	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03553.1	007260	Cluster7103_1clades	153	RISINGSUN_117	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03866.1	007261	Cluster7104_1clades	153	JOAD_49	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03621.1	007261	Cluster7104_1clades	153	RISINGSUN_49	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65550.1	007262	Cluster7105_1clades	153	2050HW_00215	Serratia phage 2050HW	GCA_002628125.1
QDB71315.1	007262	Cluster7105_1clades	153	CPT_Moabite_285	Serratia phage Moabite	GCA_006384735.1
AXQ69407.1	007263	ZNR+FXSXX	153	CcrBL9_gp383	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69963.1	007263	ZNR+FXSXX	153	CcrSC_gp381	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69282.1	007264	Cluster7107_1clades	95	CcrBL9_gp258c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69839.1	007264	Cluster7107_1clades	153	CcrSC_gp257c	Caulobacter phage CcrSC	GCA_003443315.1
BAS04807.1	007265	Cluster7108_1clades	153	AVU11_gp015	Ralstonia phage RSF1	GCA_001500875.1
BAQ02543.1	007265	Cluster7108_1clades	153	AVU38_gp015	Ralstonia phage RSL2	GCA_001503055.1
BAS04940.1	007266	Cluster7109_1clades	153	AVU11_gp148	Ralstonia phage RSF1	GCA_001500875.1
BAQ02664.1	007266	Cluster7109_1clades	151	AVU38_gp136	Ralstonia phage RSL2	GCA_001503055.1
BBI90433.1	007267	Cluster7110_1clades	153	HYO65_gp041	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90740.1	007267	Cluster7110_1clades	153	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90435.1	007268	SIG+TM	153	HYO65_gp043	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90742.1	007268	SIG+TM	153	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06553.1	007269	Cluster7113_1clades	153	BcepSaruman_140	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74520.1	007269	Cluster7113_1clades	153	BcepSauron_140	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06647.1	007270	Cluster7114_1clades	153	BcepSaruman_234	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74616.1	007270	Cluster7114_1clades	153	BcepSauron_236	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97364.1	007271	SIG+TM+TM	78	D6_0205	Aeromonas phage D6	GCA_007051205.2
QDH47179.1	007271	SIG+TM+TM	153	LAh10_120	Aeromonas phage LAh10	GCA_006863975.1
QGT54898.1	007272	Cluster7116_1clades	153	b23_0285	Synechococcus phage B23	GCA_009745195.1
QGT54533.1	007272	Cluster7116_1clades	153	b3_0292	Synechococcus phage B3	GCA_009745215.1
AIA65018.1	007273	Cluster7117_1clades	125	S13_221	Cronobacter phage S13	GCA_001503575.1
QHJ78914.1	007273	Cluster7117_1clades	153	-	Myoviridae sp.	GCA_012593985.1
prevph1000000182	007274	Cluster7118_1clades	154	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000145	007274	Cluster7118_1clades	154	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88180.1	007275	Cluster7120_1clades	152	CcrColossus_gp310	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68857.1	007275	Cluster7120_1clades	152	CcrPW_gp318	Caulobacter phage CcrPW	GCA_003443275.1
AFU88184.1	007276	Cluster7121_1clades	152	CcrColossus_gp314	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68860.1	007276	Cluster7121_1clades	152	CcrPW_gp321	Caulobacter phage CcrPW	GCA_003443275.1
AFU88227.1	007277	Cluster7122_1clades	152	CcrColossus_gp357	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68904.1	007277	Cluster7122_1clades	152	CcrPW_gp365	Caulobacter phage CcrPW	GCA_003443275.1
ATA65515.1	007278	Cluster7123_1clades	152	2050HW_00180	Serratia phage 2050HW	GCA_002628125.1
QDB71282.1	007278	Cluster7123_1clades	152	CPT_Moabite_252	Serratia phage Moabite	GCA_006384735.1
ATA65558.1	007279	Cluster7124_1clades	152	2050HW_00223	Serratia phage 2050HW	GCA_002628125.1
QDB71323.1	007279	Cluster7124_1clades	152	CPT_Moabite_293	Serratia phage Moabite	GCA_006384735.1
AXH72487.1	007280	Cluster7125_1clades	117	-	Myoviridae sp.	GCA_003657725.1
AXH72564.1	007280	Cluster7125_1clades	152	-	Myoviridae sp.	GCA_003657725.1
AXQ69237.1	007281	S2P	101	CcrBL9_gp213	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69791.1	007281	S2P	152	CcrSC_gp209	Caulobacter phage CcrSC	GCA_003443315.1
AYD81479.1	007282	Cluster7127_1clades	152	SEA_JUSTBECAUSE_324	Streptomyces phage JustBecause	GCA_003613775.1
QJD53882.1	007282	Cluster7127_1clades	152	SEA_KELA_322	Streptomyces phage Kela	GCA_012934305.1
QBX06457.1	007283	Cluster7128_1clades	152	BcepSaruman_044	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74425.1	007283	Cluster7128_1clades	152	BcepSauron_045	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97432.1	007284	SIG+TM+TM+TM	152	D6_0005	Aeromonas phage D6	GCA_007051205.2
QDH47181.1	007284	SIG+TM+TM+TM	152	LAh10_179	Aeromonas phage LAh10	GCA_006863975.1
QGT54843.1	007285	Cluster7130_1clades	152	b23_0228	Synechococcus phage B23	GCA_009745195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54477.1	007285	Cluster7130_1clades	152	b3_0234	Synechococcus phage B3	GCA_009745215.1
QIG57752.1	007286	Cluster7131_1clades	152	SEA_PAULODIABOLI_15	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58053.1	007286	Cluster7131_1clades	152	SEA_PAULODIABOLI_370	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH70858.1	007287	TM	103	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21108.1	007287	TM	152	-	Vibrio phage vB_pir03	GCA_014319855.1
AMS01338.1	007288	Cluster7133_1clades	151	AR9_g254	Bacillus phage AR9	GCA_001743835.1
AST99968.1	007288	Cluster7133_1clades	151	PBI_PBS1_147	Bacillus virus PBS1	GCA_002601325.1
ATA65521.1	007289	Cluster7134_1clades	151	2050HW_00186	Serratia phage 2050HW	GCA_002628125.1
QDB71288.1	007289	Cluster7134_1clades	151	CPT_Moabite_258	Serratia phage Moabite	GCA_006384735.1
ATA65639.1	007290	Cluster7135_1clades	151	2050HW_00304	Serratia phage 2050HW	GCA_002628125.1
QDB71067.1	007290	Cluster7135_1clades	151	CPT_Moabite_035	Serratia phage Moabite	GCA_006384735.1
AXQ69325.1	007291	Cluster7137_1clades	151	CcrBL9_gp301	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69885.1	007291	Cluster7137_1clades	151	CcrSC_gp303	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69457.1	007292	Cluster7138_1clades	151	CcrBL9_gp433	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70006.1	007292	Cluster7138_1clades	151	CcrSC_gp424	Caulobacter phage CcrSC	GCA_003443315.1
BAW19131.1	007293	Cluster7139_1clades	151	FDH28_gp264	Ralstonia phage RP12	GCA_002617345.1
BAW19417.1	007293	Cluster7139_1clades	151	-	Ralstonia phage RP31	GCA_002617365.1
BAW19175.1	007294	Cluster7140_1clades	151	FDH28_gp220	Ralstonia phage RP12	GCA_002617345.1
BAW19461.1	007294	Cluster7140_1clades	113	-	Ralstonia phage RP31	GCA_002617365.1
QBX06766.1	007295	Cluster7141_1clades	151	BcepSaruman_353	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74736.1	007295	Cluster7141_1clades	151	BcepSauron_356	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32342.1	007296	Cluster7142_1clades	151	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41916.1	007296	Cluster7142_1clades	151	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBZ71907.1	007297	Cluster7143_1clades	151	SEA_KRADAL_8	Streptomyces phage Kradal	GCA_004799925.1
AXH66169.1	007297	Cluster7143_1clades	130	SEA_SATIS_8	Streptomyces phage Satis	GCA_003366315.1
QGH71924.1	007298	Cluster7144_1clades	151	N1M2_61	Klebsiella phage N1M2	GCA_010092605.1
QGH71925.1	007298	Cluster7144_1clades	149	N1M2_62	Klebsiella phage N1M2	GCA_010092605.1
QGH72043.1	007299	Cluster7145_1clades	151	N1M2_180	Klebsiella phage N1M2	GCA_010092605.1
AEV89664.1	007299	Cluster7145_1clades	145	OBP_227	Pseudomonas phage OBP	GCA_000896635.1
QGH72040.1	007300	Cluster7146_1clades	139	N1M2_177	Klebsiella phage N1M2	GCA_010092605.1
AEV89661.1	007300	Cluster7146_1clades	150	OBP_224	Pseudomonas phage OBP	GCA_000896635.1
AMS01172.1	007301	Cluster7147_1clades	150	AR9_g088	Bacillus phage AR9	GCA_001743835.1
ASU00105.1	007301	Cluster7147_1clades	150	PBI_PBS1_283	Bacillus virus PBS1	GCA_002601325.1
ATA65535.1	007302	Cluster7148_1clades	150	2050HW_00200	Serratia phage 2050HW	GCA_002628125.1
QDB71299.1	007302	Cluster7148_1clades	150	CPT_Moabite_269	Serratia phage Moabite	GCA_006384735.1
AXQ69503.1	007303	Cluster7150_1clades	146	CcrBL9_gp479	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70053.1	007303	Cluster7150_1clades	150	CcrSC_gp471	Caulobacter phage CcrSC	GCA_003443315.1
BAS04798.1	007304	Cluster7151_1clades	150	AVU11_gp006	Ralstonia phage RSF1	GCA_001500875.1
BAQ02534.1	007304	Cluster7151_1clades	150	AVU38_gp006	Ralstonia phage RSL2	GCA_001503055.1
BAS04947.2	007305	Cluster7152_1clades	142	AVU11_gp155	Ralstonia phage RSF1	GCA_001500875.1
BAQ02671.2	007305	Cluster7152_1clades	150	-	Ralstonia phage RSL2	GCA_001503055.1
BAS04827.1	007306	Cluster7153_1clades	150	AVU11_gp035	Ralstonia phage RSF1	GCA_001500875.1
BAQ02560.1	007306	Cluster7153_1clades	147	AVU38_gp032	Ralstonia phage RSL2	GCA_001503055.1
BAW19105.1	007307	Cluster7154_1clades	150	FDH28_gp131	Ralstonia phage RP12	GCA_002617345.1
BAW19391.1	007307	Cluster7154_1clades	150	-	Ralstonia phage RP31	GCA_002617365.1
BAW19191.1	007308	Cluster7155_1clades	150	FDH28_gp204	Ralstonia phage RP12	GCA_002617345.1
BAW19477.1	007308	Cluster7155_1clades	150	-	Ralstonia phage RP31	GCA_002617365.1
BAW19223.1	007309	Cluster7156_1clades	150	FDH28_gp172	Ralstonia phage RP12	GCA_002617345.1
BAW19509.1	007309	Cluster7156_1clades	150	-	Ralstonia phage RP31	GCA_002617365.1
QBX06533.1	007310	Cluster7158_1clades	150	BcepSaruman_120	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74499.1	007310	Cluster7158_1clades	150	BcepSauron_119	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97192.1	007311	Cluster7159_1clades	150	D6_0032	Aeromonas phage D6	GCA_007051205.2
QDH47184.1	007311	Cluster7159_1clades	150	LAh10_199	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000044	007312	Cluster7160_1clades	151	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000035	007312	Cluster7160_1clades	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000180	007313	Cluster7161_1clades	151	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000143	007313	Cluster7161_1clades	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000228	007314	ATHOOK	151	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000178	007314	ATHOOK	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000472	007315	Cluster7163_1clades	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000358	007315	Cluster7163_1clades	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFA44469.1	007316	Cluster7164_1clades	145	RaK2_00196	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44491.1	007316	Cluster7164_1clades	149	RaK2_00218	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFU88250.1	007317	Cluster7165_1clades	149	CcrColossus_gp380	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68925.1	007317	Cluster7165_1clades	149	CcrPW_gp386	Caulobacter phage CcrPW	GCA_003443275.1
AMS01122.1	007318	Cluster7166_1clades	149	AR9_g037	Bacillus phage AR9	GCA_001743835.1
ASU00046.1	007318	Cluster7166_1clades	149	PBI_PBS1_224	Bacillus virus PBS1	GCA_002601325.1
AMM44020.1	007319	Cluster7167_1clades	144	CBB_457	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88979.1	007319	Cluster7167_1clades	149	BF_0454	Serratia phage BF	GCA_002619745.1
AWY08524.1	007320	Cluster7168_1clades	149	Alexandra_267	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58903.1	007320	Cluster7168_1clades	147	Y3_263	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXG67354.1	007321	Cluster7169_1clades	149	AD1_310	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AQT28781.1	007321	Cluster7169_1clades	109	YOLOSWAG_312	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
BBA65394.1	007322	Cluster7171_1clades	149	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96421.1	007322	Cluster7171_1clades	125	Xoosp13_235	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90654.1	007323	TM	149	HYO65_gp262	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90959.1	007323	TM	149	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06741.1	007324	Cluster7173_1clades	149	BcepSaruman_328	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74710.1	007324	Cluster7173_1clades	149	BcepSauron_330	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32458.1	007325	Cluster7174_1clades	149	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42030.1	007325	Cluster7174_1clades	149	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AMS01117.1	007326	Cluster7175_1clades	148	AR9_g032	Bacillus phage AR9	GCA_001743835.1
ASU00041.1	007326	Cluster7175_1clades	148	PBI_PBS1_219	Bacillus virus PBS1	GCA_002601325.1
AOO14209.1	007327	Cluster7176_1clades	148	Sn110110_015	Cyanophage S-RIM14	GCA_002599065.1
AOO14861.1	007327	Cluster7176_1clades	148	W1230910_015	Cyanophage S-RIM14	GCA_002599125.1
ATA65553.1	007328	Cluster7177_1clades	148	2050HW_00218	Serratia phage 2050HW	GCA_002628125.1
QDB71318.1	007328	Cluster7177_1clades	148	CPT_Moabite_288	Serratia phage Moabite	GCA_006384735.1
AXG67305.1	007329	Cluster7178_1clades	147	AD1_261	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08531.1	007329	Cluster7178_1clades	148	Alexandra_274	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72184.1	007330	Cluster7179_1clades	148	SEA_KRADAL_298	Streptomyces phage Kradal	GCA_004799925.1
AXH66447.1	007330	Cluster7179_1clades	148	SEA_SATIS_298	Streptomyces phage Satis	GCA_003366315.1
AXQ69349.1	007331	DUF1416	148	CcrBL9_gp325	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69908.1	007331	DUF1416	144	CcrSC_gp326	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69470.1	007332	Cluster7181_1clades	148	CcrBL9_gp446	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70019.1	007332	Cluster7181_1clades	148	CcrSC_gp437	Caulobacter phage CcrSC	GCA_003443315.1
AYD81370.1	007333	Cluster7182_1clades	148	SEA_JUSTBECAUSE_215	Streptomyces phage JustBecause	GCA_003613775.1
QJD53773.1	007333	Cluster7182_1clades	148	SEA_KELA_213	Streptomyces phage Kela	GCA_012934305.1
BAW18978.1	007334	Cluster7183_1clades	148	FDH28_gp004	Ralstonia phage RP12	GCA_002617345.1
BAW19266.1	007334	Cluster7183_1clades	148	-	Ralstonia phage RP31	GCA_002617365.1
BAW19134.1	007335	Cluster7184_1clades	148	FDH28_gp261	Ralstonia phage RP12	GCA_002617345.1
BAW19420.1	007335	Cluster7184_1clades	148	-	Ralstonia phage RP31	GCA_002617365.1
QGT54941.1	007336	Cluster7185_1clades	148	b23_0330	Synechococcus phage B23	GCA_009745195.1
QGT54576.1	007336	Cluster7185_1clades	148	b3_0336	Synechococcus phage B3	GCA_009745215.1
QAX98621.1	007337	GxC-R	146	ASfcp2_288	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52761.1	007337	GxC-R	147	PX29p042	Aeromonas phage PX29	GCA_000920195.1
AFH14625.1	007338	Cluster7187_1clades	147	Lu11_0093	Pseudomonas phage Lu11	GCA_000897175.1
AGS82083.2	007338	Cluster7187_1clades	145	PaBG_00208	Pseudomonas phage PaBG	GCA_000912555.1
AFU88234.1	007339	ZDNA-HTH	147	CcrColossus_gp364	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68910.1	007339	ZDNA-HTH	140	CcrPW_gp371c	Caulobacter phage CcrPW	GCA_003443275.1
ASU03736.1	007340	Cluster7189_1clades	147	JOAD_179	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03492.1	007340	Cluster7189_1clades	147	RISINGSUN_178	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65580.1	007341	Cluster7190_1clades	147	2050HW_00245	Serratia phage 2050HW	GCA_002628125.1
QDB71345.1	007341	Cluster7190_1clades	147	CPT_Moabite_315	Serratia phage Moabite	GCA_006384735.1
QBZ72187.1	007342	Cluster7191_1clades	147	SEA_KRADAL_301	Streptomyces phage Kradal	GCA_004799925.1
AXH66450.1	007342	Cluster7191_1clades	147	SEA_SATIS_301	Streptomyces phage Satis	GCA_003366315.1
QBZ72190.1	007343	Cluster7192_1clades	147	SEA_KRADAL_304	Streptomyces phage Kradal	GCA_004799925.1
AXH66453.1	007343	Cluster7192_1clades	147	SEA_SATIS_304	Streptomyces phage Satis	GCA_003366315.1
AXQ69262.1	007344	Cluster7193_1clades	147	CcrBL9_gp238c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69819.1	007344	Cluster7193_1clades	147	CcrSC_gp237c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69465.1	007345	Cluster7194_1clades	147	CcrBL9_gp441	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70014.1	007345	Cluster7194_1clades	147	CcrSC_gp432	Caulobacter phage CcrSC	GCA_003443315.1
BAG41524.1	007346	Cluster7195_1clades	143	RSL1_ORF078	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41523.1	007346	Cluster7195_1clades	147	RSL1_ORF077	Ralstonia phage phiRSL1	GCA_000879455.1
BAS04838.2	007347	Cluster7196_1clades	137	AVU11_agp12	Ralstonia phage RSF1	GCA_001500875.1
BAQ02571.2	007347	Cluster7196_1clades	147	-	Ralstonia phage RSL2	GCA_001503055.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBI90444.1	007348	Cluster7198_1clades	147	HYO65_gp052	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90752.1	007348	Cluster7198_1clades	147	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06463.1	007349	Cluster7199_1clades	147	BcepSaruman_050	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74431.1	007349	Cluster7199_1clades	147	BcepSauron_051	Burkholderia phage BcepSauron	GCA_005394215.1
ATA65428.1	007350	Cluster7201_1clades	138	2050HW_00093	Serratia phage 2050HW	GCA_002628125.1
QDB71204.1	007350	Cluster7201_1clades	147	CPT_Moabite_174	Serratia phage Moabite	GCA_006384735.1
QDJ97292.1	007351	Cluster7202_1clades	131	D6_0132	Aeromonas phage D6	GCA_007051205.2
QDH47187.1	007351	Cluster7202_1clades	147	LAh10_59	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000188	007352	Cluster7203_1clades	148	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000151	007352	Cluster7203_1clades	148	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFC21908.1	007353	Cluster7204_1clades	146	GAP32_452	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
SOK58738.1	007353	Cluster7204_1clades	132	g461	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFU88072.1	007354	Cluster7205_1clades	146	CcrColossus_gp202	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68749.1	007354	Cluster7205_1clades	145	CcrPW_gp210c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01368.1	007355	Cluster7206_1clades	146	AR9_g284	Bacillus phage AR9	GCA_001743835.1
AST99998.1	007355	Cluster7206_1clades	146	PBI_PBS1_177	Bacillus virus PBS1	GCA_002601325.1
AXF51226.1	007356	CDC73	146	WELLINGTON_96	Erwinia phage Wellington	GCA_003344985.1
ANZ49447.1	007356	CDC73	146	KWAN_95	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51362.1	007357	Cluster7208_1clades	146	WELLINGTON_236	Erwinia phage Wellington	GCA_003344985.1
ANZ49588.1	007357	Cluster7208_1clades	146	KWAN_236	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ARV77275.1	007358	Arc	146	NOXIFER_106	Pseudomonas phage Noxifer	GCA_002625005.1
AGS82173.2	007358	Arc	138	PaBG_00302	Pseudomonas phage PaBG	GCA_000912555.1
ASU03747.1	007359	Imm12	146	JOAD_168	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03503.1	007359	Imm12	146	RISINGSUN_167	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65505.1	007360	Cluster7211_1clades	146	2050HW_00170	Serratia phage 2050HW	GCA_002628125.1
QDB71274.1	007360	Cluster7211_1clades	146	CPT_Moabite_244	Serratia phage Moabite	GCA_006384735.1
ATA65520.1	007361	Cluster7212_1clades	146	2050HW_00185	Serratia phage 2050HW	GCA_002628125.1
QDB71287.1	007361	Cluster7212_1clades	146	CPT_Moabite_257	Serratia phage Moabite	GCA_006384735.1
ATA65546.1	007362	Cluster7213_1clades	146	2050HW_00211	Serratia phage 2050HW	GCA_002628125.1
QDB71311.1	007362	Cluster7213_1clades	146	CPT_Moabite_281	Serratia phage Moabite	GCA_006384735.1
ATA65638.1	007363	Cluster7214_1clades	146	2050HW_00303	Serratia phage 2050HW	GCA_002628125.1
QDB71066.1	007363	Cluster7214_1clades	146	CPT_Moabite_034	Serratia phage Moabite	GCA_006384735.1
AXQ69318.1	007364	MarR-HTH	146	CcrBL9_gp294	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69878.1	007364	MarR-HTH	144	CcrSC_gp296	Caulobacter phage CcrSC	GCA_003443315.1
BAW19151.1	007365	Cluster7216_1clades	146	FDH28_gp244	Ralstonia phage RP12	GCA_002617345.1
BAW19437.1	007365	Cluster7216_1clades	146	-	Ralstonia phage RP31	GCA_002617365.1
BAW19228.1	007366	Cluster7217_1clades	146	FDH28_gp167	Ralstonia phage RP12	GCA_002617345.1
BAW19514.1	007366	Cluster7217_1clades	146	-	Ralstonia phage RP31	GCA_002617365.1
QDJ97373.1	007367	Cluster7218_1clades	146	D6_0214	Aeromonas phage D6	GCA_007051205.2
QDH47188.1	007367	Cluster7218_1clades	146	LAh10_128	Aeromonas phage LAh10	GCA_006863975.1
ABS83585.1	007368	Cluster7219_1clades	145	0305phi8-36p020	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93468.1	007368	Cluster7219_1clades	140	G_209	Bacillus virus G	GCA_000917535.1
QBZ70701.1	007369	Cluster7220_1clades	125	pETSU_120	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89625.1	007369	Cluster7220_1clades	145	OBP_188	Pseudomonas phage OBP	GCA_000896635.1
AXF51202.1	007370	Cluster7221_1clades	145	WELLINGTON_72	Erwinia phage Wellington	GCA_003344985.1
ANZ49424.1	007370	Cluster7221_1clades	145	KWAN_72	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ARV77495.1	007371	Cluster7222_1clades	145	NOXIFER_330	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77496.1	007371	Cluster7222_1clades	139	NOXIFER_331	Pseudomonas phage Noxifer	GCA_002625005.1
AXH72420.1	007372	Cluster7223_1clades	139	-	Myoviridae sp.	GCA_003657725.1
AXH72409.1	007372	Cluster7223_1clades	145	-	Myoviridae sp.	GCA_003657725.1
AXQ69441.1	007373	Cluster7224_1clades	145	CcrBL9_gp417	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69992.1	007373	Cluster7224_1clades	110	CcrSC_gp410	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69481.1	007374	Cluster7225_1clades	145	CcrBL9_gp457	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70030.1	007374	Cluster7225_1clades	145	CcrSC_gp448	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69452.1	007375	Cluster7226_1clades	144	CcrBL9_gp428	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70002.1	007375	Cluster7226_1clades	145	CcrSC_gp420	Caulobacter phage CcrSC	GCA_003443315.1
BAS04840.2	007376	Cluster7227_1clades	142	AVU11_agp13	Ralstonia phage RSF1	GCA_001500875.1
BAQ02573.2	007376	Cluster7227_1clades	145	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65374.1	007377	Cluster7228_1clades	145	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96402.1	007377	Cluster7228_1clades	145	Xoosp13_216	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90653.1	007378	TM+TM+TM	145	HYO65_gp261	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90958.1	007378	TM+TM+TM	145	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06441.1	007379	Cluster7230_1clades	145	BcepSaruman_028	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74409.1	007379	Cluster7230_1clades	145	BcepSauron_029	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06616.1	007380	Cluster7231_1clades	145	BcepSaruman_203	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74582.1	007380	Cluster7231_1clades	145	BcepSauron_202	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06796.1	007381	Cluster7232_1clades	145	BcepSaruman_383	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74766.1	007381	Cluster7232_1clades	145	BcepSauron_386	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54650.1	007382	Cluster7233_1clades	145	b23_0022	Synechococcus phage B23	GCA_009745195.1
QGT54280.1	007382	Cluster7233_1clades	145	b3_0022	Synechococcus phage B3	GCA_009745215.1
prevph1000000662	007383	WYL	146	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000474	007383	WYL	146	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000747	007384	Cluster7235_1clades	146	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000499	007384	Cluster7235_1clades	131	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AMM44818.1	007385	SIG+TrkAC	144	SP15_019	Bacillus phage SP-15	GCA_001754685.1
AEO93897.1	007385	SIG+TrkAC	93	G_654	Bacillus virus G	GCA_000917535.1
ASU03869.1	007386	Cluster7237_1clades	144	JOAD_46	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03624.1	007386	Cluster7237_1clades	144	RISINGSUN_46	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65562.1	007387	Cluster7238_1clades	144	2050HW_00227	Serratia phage 2050HW	GCA_002628125.1
QDB71327.1	007387	Cluster7238_1clades	144	CPT_Moabite_297	Serratia phage Moabite	GCA_006384735.1
AXH72481.1	007388	Cluster7239_1clades	141	-	Myoviridae sp.	GCA_003657725.1
AXH72478.1	007388	Cluster7239_1clades	144	-	Myoviridae sp.	GCA_003657725.1
BAS04987.2	007389	RnasePH	144	AVU11_agp40	Ralstonia phage RSF1	GCA_001500875.1
BAQ02716.2	007389	RnasePH	130	-	Ralstonia phage RSL2	GCA_001503055.1
BAW18984.1	007390	Cluster7241_1clades	144	FDH28_gp010	Ralstonia phage RP12	GCA_002617345.1
BAW19272.1	007390	Cluster7241_1clades	144	-	Ralstonia phage RP31	GCA_002617365.1
BAW19244.1	007391	Cluster7242_1clades	144	FDH28_gp151	Ralstonia phage RP12	GCA_002617345.1
BAW19530.1	007391	Cluster7242_1clades	144	-	Ralstonia phage RP31	GCA_002617365.1
QBX06567.1	007392	Cluster7243_1clades	144	BcepSaruman_154	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74534.1	007392	Cluster7243_1clades	144	BcepSauron_154	Burkholderia phage BcepSauron	GCA_005394215.1
ATA65528.1	007393	Cluster7244_1clades	140	2050HW_00193	Serratia phage 2050HW	GCA_002628125.1
QDB71292.1	007393	Cluster7244_1clades	144	CPT_Moabite_262	Serratia phage Moabite	GCA_006384735.1
BBA65534.1	007394	Cluster7245_1clades	140	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96531.1	007394	Cluster7245_1clades	144	Xoosp13_345	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54817.1	007395	SIG+TM	144	b23_0202	Synechococcus phage B23	GCA_009745195.1
QGT54447.1	007395	SIG+TM	144	b3_0204	Synechococcus phage B3	GCA_009745215.1
AFU88027.1	007396	TM+TM	143	CcrColossus_gp157	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68704.1	007396	TM+TM	143	CcrPW_gp165c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88247.1	007397	Cluster7248_1clades	143	CcrColossus_gp377	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68922.1	007397	Cluster7248_1clades	143	CcrPW_gp383c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88305.1	007398	Cluster7249_1clades	143	CcrColossus_gp435	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68979.1	007398	Cluster7249_1clades	143	CcrPW_gp440c	Caulobacter phage CcrPW	GCA_003443275.1
ASU03883.1	007399	Cluster7250_1clades	143	JOAD_32	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03638.1	007399	Cluster7250_1clades	143	RISINGSUN_32	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65667.1	007400	sGTP	143	2050HW_00332	Serratia phage 2050HW	GCA_002628125.1
QDB71089.1	007400	sGTP	143	CPT_Moabite_057	Serratia phage Moabite	GCA_006384735.1
AXG67275.1	007401	Cluster7252_1clades	143	AD1_231	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08500.1	007401	Cluster7252_1clades	142	Alexandra_240	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72161.1	007402	Cluster7253_1clades	143	SEA_KRADAL_275	Streptomyces phage Kradal	GCA_004799925.1
AXH66424.1	007402	Cluster7253_1clades	143	SEA_SATIS_275	Streptomyces phage Satis	GCA_003366315.1
AXQ69396.1	007403	COQ7	143	CcrBL9_gp372	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69954.1	007403	COQ7	143	CcrSC_gp372	Caulobacter phage CcrSC	GCA_003443315.1
BAW19089.1	007404	Cluster7256_1clades	143	FDH28_gp115	Ralstonia phage RP12	GCA_002617345.1
BAW19375.1	007404	Cluster7256_1clades	143	-	Ralstonia phage RP31	GCA_002617365.1
BBI90537.1	007405	Cluster7257_1clades	143	HYO65_gp145	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90845.1	007405	Cluster7257_1clades	143	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06623.1	007406	Cluster7258_1clades	140	BcepSaruman_210	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74591.1	007406	Cluster7258_1clades	143	BcepSauron_211	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32424.1	007407	Cluster7259_1clades	143	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41995.1	007407	Cluster7259_1clades	143	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97182.1	007408	Cluster7260_1clades	128	D6_0022	Aeromonas phage D6	GCA_007051205.2
QDH47190.1	007408	Cluster7260_1clades	143	LAh10_190	Aeromonas phage LAh10	GCA_006863975.1
QGT54855.1	007409	Cluster7261_1clades	143	b23_0241	Synechococcus phage B23	GCA_009745195.1
QGT54489.1	007409	Cluster7261_1clades	143	b3_0247	Synechococcus phage B3	GCA_009745215.1
ASU03749.1	007410	Cluster7262_1clades	142	JOAD_166	Erwinia phage vB_EamM_Joad	GCA_002629065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU03505.1	007410	Cluster7262_1clades	142	RISINGSUN_165	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXG67284.1	007411	Cluster7263_1clades	139	AD1_240	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08508.1	007411	Cluster7263_1clades	142	Alexandra_249	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
BAS04939.1	007412	Cluster7264_1clades	141	AVU11_gp147	Ralstonia phage RSF1	GCA_001500875.1
BAQ02663.1	007412	Cluster7264_1clades	142	AVU38_gp135	Ralstonia phage RSL2	GCA_001503055.1
BAW19081.1	007413	Cluster7265_1clades	142	FDH28_gp107	Ralstonia phage RP12	GCA_002617345.1
BAW19367.1	007413	Cluster7265_1clades	142	-	Ralstonia phage RP31	GCA_002617365.1
BBI90538.1	007414	Cluster7266_1clades	142	HYO65_gp146	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90846.1	007414	Cluster7266_1clades	142	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06737.1	007415	TIM-Barrel	137	BcepSaruman_324	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74706.1	007415	TIM-Barrel	142	BcepSauron_326	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06798.1	007416	Cluster7268_1clades	142	BcepSaruman_385	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74768.1	007416	Cluster7268_1clades	142	BcepSauron_388	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32185.1	007417	Cluster7269_1clades	142	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41763.1	007417	Cluster7269_1clades	142	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32268.1	007418	Cluster7270_1clades	142	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41842.1	007418	Cluster7270_1clades	142	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDH83652.1	007419	Cluster7271_1clades	110	H1O15_gp098	Achromobacter phage Motura	GCA_006964305.1
QDH83653.1	007419	Cluster7271_1clades	142	H1O15_gp097	Achromobacter phage Motura	GCA_006964305.1
QDJ96686.1	007420	Cluster7272_1clades	142	PS1_0175	Aeromonas phage PS1	GCA_007051165.2
QFR59319.1	007420	Cluster7272_1clades	133	PS2_0177	Aeromonas phage PS2	GCA_009388305.2
QGT54860.1	007421	Cluster7273_1clades	142	b23_0246	Synechococcus phage B23	GCA_009745195.1
QGT54495.1	007421	Cluster7273_1clades	142	b3_0253	Synechococcus phage B3	GCA_009745215.1
prevph1000000820	007422	Cluster7274_1clades	143	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000563	007422	Cluster7274_1clades	143	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU87977.1	007423	TM	141	CcrColossus_gp107	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68654.1	007423	TM	141	CcrPW_gp115	Caulobacter phage CcrPW	GCA_003443275.1
AFC21548.1	007424	Cluster7276_1clades	140	GAP32_100	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43666.1	007424	Cluster7276_1clades	141	CBB_101	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AXQ69393.1	007425	Cluster7277_1clades	141	CcrBL9_gp369	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69952.1	007425	Cluster7277_1clades	141	CcrSC_gp370	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69455.1	007426	Cluster7278_1clades	141	CcrBL9_gp431	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70004.1	007426	Cluster7278_1clades	141	CcrSC_gp422	Caulobacter phage CcrSC	GCA_003443315.1
BAW19038.1	007427	SIG+TM	141	FDH28_gp064	Ralstonia phage RP12	GCA_002617345.1
BAW19323.1	007427	SIG+TM	141	-	Ralstonia phage RP31	GCA_002617365.1
BAW19181.1	007428	Cluster7280_1clades	140	FDH28_gp214	Ralstonia phage RP12	GCA_002617345.1
BAW19467.1	007428	Cluster7280_1clades	141	-	Ralstonia phage RP31	GCA_002617365.1
BBI90620.1	007429	Cluster7281_1clades	110	HYO65_gp228	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90926.1	007429	Cluster7281_1clades	141	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAX98428.1	007430	Cluster7282_1clades	141	ASfcp2_84	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52883.1	007430	Cluster7282_1clades	102	PX29p164	Aeromonas phage PX29	GCA_000920195.1
BBA65578.1	007431	APP_N	131	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96561.1	007431	APP_N	141	Xoosp13_375	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000233	007432	Cluster7284_1clades	142	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000183	007432	Cluster7284_1clades	142	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44403.1	007433	Cluster7285_1clades	140	PSSM2_025	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12248.1	007433	Cluster7285_1clades	140	PRTG_00090	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88016.1	007434	Cluster7286_1clades	140	CcrColossus_gp146	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68693.1	007434	Cluster7286_1clades	140	CcrPW_gp154c	Caulobacter phage CcrPW	GCA_003443275.1
AGH26241.1	007435	SIG+TM+TM+TM	140	CPMG_00140	Prochlorococcus phage MED4-213	GCA_000904535.1
AIR93566.1	007435	SIG+TM+TM+TM	134	AVU42_gp229	Prochlorococcus phage P-TIM68	GCA_001503075.1
ANZ48436.1	007436	Cluster7288_1clades	140	CAITLIN_141	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48711.1	007436	Cluster7288_1clades	140	CHRISDB_149	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49872.1	007437	TM	127	MACHINA_234	Erwinia phage Machina	GCA_002758035.1
ANZ48529.1	007437	TM	140	CAITLIN_234	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
AXH72689.1	007438	Cluster7290_1clades	130	-	Myoviridae sp.	GCA_003657725.1
AXH72697.1	007438	Cluster7290_1clades	140	-	Myoviridae sp.	GCA_003657725.1
AXQ68514.1	007439	Cluster7291_1clades	140	CcrBL10_gp310	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86803.1	007439	Cluster7291_1clades	137	CcrRogue_gp321	Caulobacter virus Rogue	GCA_000900555.1
BAS05017.2	007440	Cluster7292_1clades	124	AVU11_agp44	Ralstonia phage RSF1	GCA_001500875.1
BAQ02747.2	007440	Cluster7292_1clades	140	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65369.1	007441	Cluster7294_1clades	140	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96397.1	007441	Cluster7294_1clades	123	Xoosp13_211	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90554.1	007442	Cluster7295_1clades	140	HYO65_gp162	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90862.1	007442	Cluster7295_1clades	140	-	Tenacibaculum phage PTm5	GCA_009730715.1
CCH63667.1	007443	SIG+OrfB_Zn_ribbon	140	CP21_205	Campylobacter virus CP21	GCA_000902535.1
prevph1000000496	007443	SIG+OrfB_Zn_ribbon	94	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QBX32181.1	007444	Cluster7297_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41759.1	007444	Cluster7297_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32203.1	007445	Cluster7298_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41780.1	007445	Cluster7298_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32209.1	007446	Cluster7299_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41787.1	007446	Cluster7299_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32401.1	007447	Cluster7300_1clades	140	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41971.1	007447	Cluster7300_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BBA65559.1	007448	Cluster7301_1clades	128	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96552.1	007448	Cluster7301_1clades	140	Xoosp13_366	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX32484.1	007449	Cluster7302_1clades	138	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42056.1	007449	Cluster7302_1clades	140	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG63285.1	007450	Cluster7303_1clades	140	DAC16_52	Bacteroides phage DAC16	GCA_013387695.1
QIG64330.1	007450	Cluster7303_1clades	140	DAC23_52	Bacteroides phage DAC23	GCA_013387745.1
AIA65065.1	007451	Cluster7304_1clades	139	S13_268	Cronobacter phage S13	GCA_001503575.1
QHJ78866.1	007451	Cluster7304_1clades	133	-	Myoviridae sp.	GCA_012593985.1
ALN97972.1	007452	Cluster7305_1clades	139	Bp8pS_293	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97973.1	007452	Cluster7305_1clades	136	Bp8pS_294	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AMS01294.1	007453	SIG+RFC-AAA	139	AR9_g210	Bacillus phage AR9	GCA_001743835.1
AST99923.1	007453	SIG+RFC-AAA	139	PBI_PBS1_101	Bacillus virus PBS1	GCA_002601325.1
AND75414.1	007454	Cluster7307_1clades	139	ME3_253	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AQT28516.1	007454	Cluster7307_1clades	123	YOLOSWAG_31	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ASU03692.1	007455	Cluster7308_1clades	139	JOAD_223	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03449.1	007455	Cluster7308_1clades	139	RISINGSUN_221	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03825.1	007456	Cluster7309_1clades	139	JOAD_90	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03580.1	007456	Cluster7309_1clades	139	RISINGSUN_90	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65589.1	007457	Cluster7310_1clades	139	2050HW_00254	Serratia phage 2050HW	GCA_002628125.1
QDB71354.1	007457	Cluster7310_1clades	139	CPT_Moabite_324	Serratia phage Moabite	GCA_006384735.1
AXQ69123.1	007458	Cluster7311_1clades	139	CcrBL9_gp099	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69677.1	007458	Cluster7311_1clades	139	CcrSC_gp095	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69144.1	007459	Cluster7312_1clades	139	CcrBL9_gp120	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69698.1	007459	Cluster7312_1clades	137	CcrSC_gp116	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69336.1	007460	Cluster7313_1clades	139	CcrBL9_gp312	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69896.1	007460	Cluster7313_1clades	139	CcrSC_gp314	Caulobacter phage CcrSC	GCA_003443315.1
BBA65229.1	007461	Cluster7314_1clades	139	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65688.1	007461	Cluster7314_1clades	139	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90460.1	007462	Cluster7315_1clades	139	HYO65_gp068	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90768.1	007462	Cluster7315_1clades	139	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90585.1	007463	Cluster7316_1clades	139	HYO65_gp193	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90893.1	007463	Cluster7316_1clades	139	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06517.1	007464	Cluster7317_1clades	138	BcepSaruman_104	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74483.1	007464	Cluster7317_1clades	139	BcepSauron_103	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32341.1	007465	Cluster7318_1clades	139	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41915.1	007465	Cluster7318_1clades	139	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBZ70725.1	007466	Cluster7319_1clades	139	pETSU_144	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89657.1	007466	Cluster7319_1clades	136	OBP_220	Pseudomonas phage OBP	GCA_000896635.1
prevph1000000616	007467	Cluster7320_1clades	140	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000435	007467	Cluster7320_1clades	140	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFA44652.1	007468	Cluster7321_1clades	138	RaK2_00379	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44654.1	007468	Cluster7321_1clades	131	RaK2_00381	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXF51321.1	007469	Cluster7322_1clades	138	WELLINGTON_193	Erwinia phage Wellington	GCA_003344985.1
ANZ49546.1	007469	Cluster7322_1clades	138	KWAN_194	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ABY62840.1	007470	Cluster7323_1clades	135	201phi2-1p006	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76638.1	007470	Cluster7323_1clades	138	PHABIO_7	Pseudomonas phage Phabio	GCA_002624965.1
QBZ72083.1	007471	Cluster7324_1clades	138	SEA_KRADAL_187	Streptomyces phage Kradal	GCA_004799925.1
AXH66345.1	007471	Cluster7324_1clades	138	SEA_SATIS_186	Streptomyces phage Satis	GCA_003366315.1
AXH70877.1	007472	SIG+TM+TM+TM	136	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70876.1	007472	SIG+TM+TM+TM	138	-	Vibrio phage BONAISHI	GCA_003441475.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH72613.1	007473	Cluster7326_1clades	128	-	Myoviridae sp.	GCA_003657725.1
AXH72679.1	007473	Cluster7326_1clades	138	-	Myoviridae sp.	GCA_003657725.1
AXQ69032.1	007474	Cluster7327_1clades	138	CcrBL9_gp008	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69548.1	007474	Cluster7327_1clades	138	CcrBL9_gp524	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69351.1	007475	Cluster7328_1clades	138	CcrBL9_gp327	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69910.1	007475	Cluster7328_1clades	138	CcrSC_gp328	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69385.1	007476	Cluster7329_1clades	138	CcrBL9_gp361	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69945.1	007476	Cluster7329_1clades	134	CcrSC_gp363	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69476.1	007477	Cluster7330_1clades	138	CcrBL9_gp452	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70025.1	007477	Cluster7330_1clades	138	CcrSC_gp443	Caulobacter phage CcrSC	GCA_003443315.1
BAW19037.1	007478	Cluster7331_1clades	138	FDH28_gp063	Ralstonia phage RP12	GCA_002617345.1
BAW19322.1	007478	Cluster7331_1clades	138	-	Ralstonia phage RP31	GCA_002617365.1
BAW19124.1	007479	Cluster7332_1clades	138	FDH28_gp271	Ralstonia phage RP12	GCA_002617345.1
BAW19410.1	007479	Cluster7332_1clades	138	-	Ralstonia phage RP31	GCA_002617365.1
QBX06436.1	007480	Cluster7333_1clades	138	BcepSaruman_023	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74404.1	007480	Cluster7333_1clades	138	BcepSauron_024	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06636.1	007481	Pkinase	138	BcepSaruman_223	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74606.1	007481	Pkinase	138	BcepSauron_226	Burkholderia phage BcepSauron	GCA_005394215.1
ATA65633.1	007482	Cluster7335_1clades	128	2050HW_00298	Serratia phage 2050HW	GCA_002628125.1
QDB71061.1	007482	Cluster7335_1clades	138	CPT_Moabite_029	Serratia phage Moabite	GCA_006384735.1
QDJ97331.1	007483	Cluster7336_1clades	138	D6_0172	Aeromonas phage D6	GCA_007051205.2
QDH47193.1	007483	Cluster7336_1clades	138	LAh10_91	Aeromonas phage LAh10	GCA_006863975.1
AIA64970.1	007484	Cluster7337_1clades	137	S13_171	Cronobacter phage S13	GCA_001503575.1
QHJ78963.1	007484	Cluster7337_1clades	138	-	Myoviridae sp.	GCA_012593985.1
prevph1000000059	007485	Cluster7338_1clades	139	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000045	007485	Cluster7338_1clades	139	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000300	007486	Cluster7339_1clades	139	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000232	007486	Cluster7339_1clades	139	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000371	007487	Cluster7340_1clades	139	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000297	007487	Cluster7340_1clades	139	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABY63255.1	007488	Cluster7341_1clades	137	201phi2-1p432	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77074.1	007488	Cluster7341_1clades	118	PHABIO_443	Pseudomonas phage Phabio	GCA_002624965.1
AIA65020.1	007489	Cluster7342_1clades	137	S13_223	Cronobacter phage S13	GCA_001503575.1
QHJ78912.1	007489	Cluster7342_1clades	134	-	Myoviridae sp.	GCA_012593985.1
AMO43072.1	007490	Cluster7343_1clades	137	R1080702_063	Cyanophage S-RIM32	GCA_001754165.1
QDH50611.1	007490	Cluster7343_1clades	122	-	Synechococcus phage S-B43	GCA_006869725.1
AMS01259.1	007491	Cluster7344_1clades	137	AR9_g175	Bacillus phage AR9	GCA_001743835.1
AST99885.1	007491	Cluster7344_1clades	137	PBI_PBS1_63	Bacillus virus PBS1	GCA_002601325.1
ASU03752.1	007492	Cluster7345_1clades	137	JOAD_163	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03508.1	007492	Cluster7345_1clades	137	RISINGSUN_162	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65339.1	007493	SIG+CCDC158	137	2050HW_00004	Serratia phage 2050HW	GCA_002628125.1
QDB71127.1	007493	SIG+CCDC158	137	CPT_Moabite_097	Serratia phage Moabite	GCA_006384735.1
QBZ71934.1	007494	Cluster7347_1clades	137	SEA_KRADAL_35	Streptomyces phage Kradal	GCA_004799925.1
AXH66196.1	007494	Cluster7347_1clades	137	SEA_SATIS_35	Streptomyces phage Satis	GCA_003366315.1
AXQ69279.1	007495	Cluster7348_1clades	137	CcrBL9_gp255c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69836.1	007495	Cluster7348_1clades	137	CcrSC_gp254c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69466.1	007496	Cluster7349_1clades	137	CcrBL9_gp442	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70015.1	007496	Cluster7349_1clades	137	CcrSC_gp433	Caulobacter phage CcrSC	GCA_003443315.1
QBX06559.1	007497	Cluster7351_1clades	137	BcepSaruman_146	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74526.1	007497	Cluster7351_1clades	137	BcepSauron_146	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65446.1	007498	Cluster7352_1clades	131	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96462.1	007498	Cluster7352_1clades	137	Xoosp13_276	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QIG65834.1	007499	Cluster7353_1clades	137	phiOC_p169	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65837.1	007499	Cluster7353_1clades	132	phiOC_p172	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AYD81212.1	007500	ANAPC2	120	SEA_JUSTBECAUSE_43	Streptomyces phage JustBecause	GCA_003613775.1
QJD53615.1	007500	ANAPC2	137	SEA_KELA_44	Streptomyces phage Kela	GCA_012934305.1
prevph1000000040	007501	POLYSACPOLYMERASE	138	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000031	007501	POLYSACPOLYMERASE	138	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000398	007502	Cluster7356_1clades	114	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000317	007502	Cluster7356_1clades	138	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44609.1	007503	Cluster7357_1clades	136	PSSM2_232	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12361.1	007503	Cluster7357_1clades	136	PRTG_00208	Prochlorococcus phage P-SSM5	GCA_002991095.1
AMM45112.1	007504	Cluster7358_1clades	136	SP15_304	Bacillus phage SP-15	GCA_001754685.1
AEO93871.1	007504	Cluster7358_1clades	135	G_626	Bacillus virus G	GCA_000917535.1
AMS01123.1	007505	Cluster7359_1clades	136	AR9_g038	Bacillus phage AR9	GCA_001743835.1
ASU00047.1	007505	Cluster7359_1clades	136	PBI_PBS1_225	Bacillus virus PBS1	GCA_002601325.1
AXF51252.1	007506	Cluster7360_1clades	136	WELLINGTON_122	Erwinia phage Wellington	GCA_003344985.1
ANZ49473.1	007506	Cluster7360_1clades	136	KWAN_121	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51380.1	007507	Cluster7361_1clades	101	WELLINGTON_254	Erwinia phage Wellington	GCA_003344985.1
ANZ49607.1	007507	Cluster7361_1clades	136	KWAN_255	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03769.1	007508	TM	136	JOAD_146	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03525.1	007508	TM	136	RISINGSUN_145	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65617.1	007509	Cluster7363_1clades	136	2050HW_00282	Serratia phage 2050HW	GCA_002628125.1
QDB71045.1	007509	Cluster7363_1clades	136	CPT_Moabite_013	Serratia phage Moabite	GCA_006384735.1
AXQ69442.1	007510	Cluster7364_1clades	136	CcrBL9_gp418	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69993.1	007510	Cluster7364_1clades	135	CcrSC_gp411	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69469.1	007511	Cluster7365_1clades	136	CcrBL9_gp445	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70018.1	007511	Cluster7365_1clades	118	CcrSC_gp436	Caulobacter phage CcrSC	GCA_003443315.1
BAW19246.1	007512	Cluster7366_1clades	136	FDH28_gp149	Ralstonia phage RP12	GCA_002617345.1
BAW19532.1	007512	Cluster7366_1clades	136	-	Ralstonia phage RP31	GCA_002617365.1
BBA65710.1	007513	Cluster7367_1clades	136	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65251.1	007513	Cluster7367_1clades	136	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06476.1	007514	Cluster7368_1clades	136	BcepSaruman_063	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74443.1	007514	Cluster7368_1clades	136	BcepSauron_063	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06617.1	007515	Cluster7369_1clades	136	BcepSaruman_204	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74583.1	007515	Cluster7369_1clades	136	BcepSauron_203	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97340.1	007516	Cluster7370_1clades	136	D6_0181	Aeromonas phage D6	GCA_007051205.2
QDH47194.1	007516	Cluster7370_1clades	136	LAh10_100	Aeromonas phage LAh10	GCA_006863975.1
QGT54803.1	007517	Cluster7371_1clades	136	b23_0188	Synechococcus phage B23	GCA_009745195.1
QGT54433.1	007517	Cluster7371_1clades	136	b3_0189	Synechococcus phage B3	GCA_009745215.1
QIG57771.1	007518	Cluster7372_1clades	136	SEA_PAULODIABOLI_36	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58072.1	007518	Cluster7372_1clades	136	SEA_PAULODIABOLI_391	Microbacterium phage PauloDiaboli	GCA_011067425.1
SOK58916.1	007519	Cluster7373_1clades	136	g108	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58381.1	007519	Cluster7373_1clades	136	g104	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000037	007520	SIG+TM+TM	137	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000029	007520	SIG+TM+TM	137	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000641	007521	Cluster7375_1clades	137	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000457	007521	Cluster7375_1clades	137	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000270	007522	Cluster7376_1clades	137	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000215	007522	Cluster7376_1clades	130	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83734.1	007523	SIG+TM+TM+TM	135	0305phi8-36p176	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44865.1	007523	SIG+TM+TM+TM	129	SP15_066	Bacillus phage SP-15	GCA_001754685.1
QAX98539.1	007524	Cluster7378_1clades	135	ASfcp2_203	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53002.1	007524	Cluster7378_1clades	135	PX29p283	Aeromonas phage PX29	GCA_000920195.1
APU01602.1	007525	Cluster7379_1clades	135	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53226.1	007525	Cluster7379_1clades	135	65p218	Aeromonas virus 65	GCA_000893255.1
QBZ70807.1	007526	Cluster7380_1clades	133	pETSU_226	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89746.1	007526	Cluster7380_1clades	135	OBP_309	Pseudomonas phage OBP	GCA_000896635.1
AFU87937.1	007527	Cluster7381_1clades	135	CcrColossus_gp067	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68609.1	007527	Cluster7381_1clades	135	CcrPW_gp070	Caulobacter phage CcrPW	GCA_003443275.1
AFU88106.1	007528	Cluster7382_1clades	135	CcrColossus_gp236	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68783.1	007528	Cluster7382_1clades	135	CcrPW_gp244	Caulobacter phage CcrPW	GCA_003443275.1
AGH56949.1	007529	Cluster7383_1clades	127	CPXG_00146	Cyanophage P-RSM6	GCA_000906155.1
AJK27503.1	007529	Cluster7383_1clades	135	PTIM40_76	Cyanophage P-TIM40	GCA_001470935.1
AXF51330.1	007530	Cluster7384_1clades	135	WELLINGTON_202	Erwinia phage Wellington	GCA_003344985.1
ANZ49555.1	007530	Cluster7384_1clades	135	KWAN_203	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65691.1	007531	Cluster7385_1clades	135	2050HW_00356	Serratia phage 2050HW	GCA_002628125.1
QDB71118.1	007531	Cluster7385_1clades	135	CPT_Moabite_088	Serratia phage Moabite	GCA_006384735.1
AUZ95418.1	007532	SIG+Lysozyme	135	FDI40_gp661	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65810.1	007532	SIG+Lysozyme	129	phiOC_p145	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AXQ69297.1	007533	SIG+TM+TM	135	CcrBL9_gp273c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69856.1	007533	SIG+TM+TM	135	CcrSC_gp274c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69392.1	007534	Cluster7388_1clades	135	CcrBL9_gp368	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69951.1	007534	Cluster7388_1clades	135	CcrSC_gp369	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69449.1	007535	CR-REase1	135	CcrBL9_gp425	Caulobacter phage CcrBL9	GCA_003443295.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69999.1	007535	CR-REase1	135	CcrSC_gp417	Caulobacter phage CcrSC	GCA_003443315.1
AXQ68627.1	007536	Cluster7390_1clades	132	CcrPW_gp088c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69728.1	007536	Cluster7390_1clades	135	CcrSC_gp146c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69291.1	007537	Cluster7391_1clades	115	CcrBL9_gp267c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69848.1	007537	Cluster7391_1clades	135	CcrSC_gp266c	Caulobacter phage CcrSC	GCA_003443315.1
BAW19093.1	007538	Cluster7392_1clades	135	FDH28_gp119	Ralstonia phage RP12	GCA_002617345.1
BAW19379.1	007538	Cluster7392_1clades	118	-	Ralstonia phage RP31	GCA_002617365.1
BAW19199.1	007539	Cluster7393_1clades	135	FDH28_gp196	Ralstonia phage RP12	GCA_002617345.1
BAW19485.1	007539	Cluster7393_1clades	135	-	Ralstonia phage RP31	GCA_002617365.1
BAW19024.1	007540	Cluster7394_1clades	102	FDH28_gp050	Ralstonia phage RP12	GCA_002617345.1
BAW19310.1	007540	Cluster7394_1clades	135	-	Ralstonia phage RP31	GCA_002617365.1
BBA65657.1	007541	Cluster7395_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65198.1	007541	Cluster7395_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65362.1	007542	Cluster7396_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96389.1	007542	Cluster7396_1clades	88	Xoosp13_203	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65553.1	007543	Cluster7397_1clades	135	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96548.1	007543	Cluster7397_1clades	121	Xoosp13_362	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AEH03618.1	007544	Cluster7398_1clades	131	195	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02692.1	007544	Cluster7398_1clades	135	PSA21_165	Pseudomonas phage Psa21	GCA_004340405.1
QBX06839.1	007545	Cluster7399_1clades	135	BcepSaruman_426	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74808.1	007545	Cluster7399_1clades	135	BcepSauron_428	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06713.1	007546	Cluster7400_1clades	135	BcepSaruman_300	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74681.1	007546	Cluster7400_1clades	133	BcepSauron_301	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32186.1	007547	SIG+TM+TM+TM	135	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41764.1	007547	SIG+TM+TM+TM	135	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65637.1	007548	Cluster7402_1clades	92	2050HW_00302	Serratia phage 2050HW	GCA_002628125.1
QDB71065.1	007548	Cluster7402_1clades	135	CPT_Moabite_033	Serratia phage Moabite	GCA_006384735.1
QGT54752.1	007549	Cluster7403_1clades	135	b23_0137	Synechococcus phage B23	GCA_009745195.1
QGT54382.1	007549	Cluster7403_1clades	135	b3_0138	Synechococcus phage B3	GCA_009745215.1
QGH71869.1	007550	Cluster7404_1clades	130	N1M2_6	Klebsiella phage N1M2	GCA_010092605.1
AEV89461.1	007550	Cluster7404_1clades	134	OBP_024	Pseudomonas phage OBP	GCA_000896635.1
AGR48122.2	007551	Cluster7405_1clades	134	SmphiM12_490	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13660.1	007551	Cluster7405_1clades	134	PHIN3_397	Sinorhizobium phage phiN3	GCA_001501175.1
ATA65475.1	007552	Cluster7406_1clades	134	2050HW_00140	Serratia phage 2050HW	GCA_002628125.1
QDB71245.1	007552	Cluster7406_1clades	134	CPT_Moabite_215	Serratia phage Moabite	GCA_006384735.1
ATA65654.1	007553	SIG+TM+TM+TM	134	2050HW_00319	Serratia phage 2050HW	GCA_002628125.1
QDB71078.1	007553	SIG+TM+TM+TM	134	CPT_Moabite_046	Serratia phage Moabite	GCA_006384735.1
AXQ69496.1	007554	Cluster7408_1clades	134	CcrBL9_gp472	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70044.1	007554	Cluster7408_1clades	128	CcrSC_gp462	Caulobacter phage CcrSC	GCA_003443315.1
QDH83687.1	007555	SIG+DUF1190	127	H1O15_gp274	Achromobacter phage Motura	GCA_006964305.1
BAG41497.2	007555	SIG+DUF1190	134	RSL1_ORF051	Ralstonia phage phiRSL1	GCA_000879455.1
BBA65319.1	007556	Cluster7410_1clades	134	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96354.1	007556	Cluster7410_1clades	118	Xoosp13_167	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65375.1	007557	Cluster7411_1clades	134	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96403.1	007557	Cluster7411_1clades	69	Xoosp13_217	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBP07634.1	007558	Cluster7412_1clades	134	DERBICUS_208	Erwinia phage Derbicus	GCA_004521655.1
ANZ49058.1	007558	Cluster7412_1clades	123	EARLPHILLIPIV_209	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
QBX06534.1	007559	Cluster7413_1clades	134	BcepSaruman_121	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74500.1	007559	Cluster7413_1clades	134	BcepSauron_120	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06771.1	007560	Cluster7414_1clades	134	BcepSaruman_358	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74741.1	007560	Cluster7414_1clades	134	BcepSauron_361	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06776.1	007561	Cluster7415_1clades	134	BcepSaruman_363	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74746.1	007561	Cluster7415_1clades	134	BcepSauron_366	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06756.1	007562	Cluster7416_1clades	134	BcepSaruman_343	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74726.1	007562	Cluster7416_1clades	113	BcepSauron_346	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32430.1	007563	Cluster7417_1clades	134	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42001.1	007563	Cluster7417_1clades	134	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32451.1	007564	Cluster7418_1clades	134	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42023.1	007564	Cluster7418_1clades	134	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QNH80845.1	007565	Cluster7419_1clades	129	D6_0148	Aeromonas phage D6	GCA_007051205.2
QDH47196.1	007565	Cluster7419_1clades	134	LAh10_73	Aeromonas phage LAh10	GCA_006863975.1
SOK59008.1	007566	Cluster7420_1clades	134	g200	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58473.1	007566	Cluster7420_1clades	134	g196	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000234	007567	Cluster7421_1clades	135	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000184	007567	Cluster7421_1clades	135	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000275	007568	Cluster7422_1clades	135	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000220	007568	Cluster7422_1clades	135	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000485	007569	Cluster7423_1clades	135	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000366	007569	Cluster7423_1clades	135	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000506	007570	Cluster7424_1clades	126	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000817	007570	Cluster7424_1clades	135	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AGR48105.1	007571	YodL	133	SmphiM12_473	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13638.1	007571	YodL	133	PHIN3_375	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21634.1	007572	Cluster7426_1clades	131	GAP32_184	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43754.1	007572	Cluster7426_1clades	133	CBB_189	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01369.1	007573	Cluster7427_1clades	133	AR9_g285	Bacillus phage AR9	GCA_001743835.1
AST99999.1	007573	Cluster7427_1clades	133	PBI_PBS1_178	Bacillus virus PBS1	GCA_002601325.1
AND75278.1	007574	Cluster7428_1clades	129	ME3_117	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75279.1	007574	Cluster7428_1clades	133	ME3_118	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AFQ96731.1	007575	Cluster7429_1clades	85	G173_gp186	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50439.1	007575	Cluster7429_1clades	133	STRATTON_2	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ASU03791.1	007576	Cluster7430_1clades	133	JOAD_124	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03547.1	007576	Cluster7430_1clades	133	RISINGSUN_123	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AUZ94815.1	007577	Cluster7431_1clades	115	FDI40_gp003	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44311.1	007577	Cluster7431_1clades	133	PBI_SCTP2_296	Salicola phage SCTP-2	GCA_002625545.1
AXH70815.1	007578	Cluster7433_1clades	133	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21060.1	007578	Cluster7433_1clades	133	-	Vibrio phage vB_pir03	GCA_014319855.1
AXH72665.1	007579	WCAK	129	-	Myoviridae sp.	GCA_003657725.1
AXH72675.1	007579	WCAK	133	-	Myoviridae sp.	GCA_003657725.1
AFU88278.1	007580	Cluster7435_1clades	130	CcrColossus_gp408	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68955.1	007580	Cluster7435_1clades	133	CcrPW_gp416c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69328.1	007581	GDC-P	133	CcrBL9_gp304	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69888.1	007581	GDC-P	133	CcrSC_gp306	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69415.1	007582	Cluster7437_1clades	133	CcrBL9_gp391	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69972.1	007582	Cluster7437_1clades	133	CcrSC_gp390	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69459.1	007583	Cluster7438_1clades	131	CcrBL9_gp435	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70008.1	007583	Cluster7438_1clades	133	CcrSC_gp426	Caulobacter phage CcrSC	GCA_003443315.1
BAS04920.1	007584	Cluster7439_1clades	126	AVU11_gp128	Ralstonia phage RSF1	GCA_001500875.1
BAQ02649.1	007584	Cluster7439_1clades	133	AVU38_gp121	Ralstonia phage RSL2	GCA_001503055.1
BBA65161.1	007585	Cluster7440_1clades	133	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65620.1	007585	Cluster7440_1clades	133	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90426.1	007586	TM	133	HYO65_gp034	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90733.1	007586	TM	74	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90477.1	007587	Cluster7442_1clades	133	HYO65_gp085	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90785.1	007587	Cluster7442_1clades	133	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90500.1	007588	Cluster7443_1clades	133	HYO65_gp108	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90808.1	007588	Cluster7443_1clades	99	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06536.1	007589	Cluster7444_1clades	133	BcepSaruman_123	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74502.1	007589	Cluster7444_1clades	133	BcepSauron_122	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97311.1	007590	SIG+TCAD13+TM	133	D6_0151	Aeromonas phage D6	GCA_007051205.2
QDH47197.1	007590	SIG+TCAD13+TM	133	LAh10_76	Aeromonas phage LAh10	GCA_006863975.1
QDJ97335.1	007591	Cluster7446_1clades	133	D6_0176	Aeromonas phage D6	GCA_007051205.2
QDH47198.1	007591	Cluster7446_1clades	133	LAh10_95	Aeromonas phage LAh10	GCA_006863975.1
ABY63134.1	007592	Cluster7447_1clades	132	201phi2-1p308	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76948.1	007592	Cluster7447_1clades	128	PHABIO_317	Pseudomonas phage Phabio	GCA_002624965.1
AIA65005.1	007593	Cluster7448_1clades	132	S13_208	Cronobacter phage S13	GCA_001503575.1
QHJ78926.1	007593	Cluster7448_1clades	131	-	Myoviridae sp.	GCA_012593985.1
AFC21889.1	007594	Cluster7449_1clades	131	GAP32_435	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44017.1	007594	Cluster7449_1clades	132	CBB_454	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AXQ69468.1	007595	Cluster7450_1clades	132	CcrBL9_gp444	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70017.1	007595	Cluster7450_1clades	131	CcrSC_gp435	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69483.1	007596	Cluster7451_1clades	120	CcrBL9_gp459	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70032.1	007596	Cluster7451_1clades	132	CcrSC_gp450	Caulobacter phage CcrSC	GCA_003443315.1
AYD81486.1	007597	Cluster7452_1clades	132	SEA_JUSTBECAUSE_331	Streptomyces phage JustBecause	GCA_003613775.1
QJD53889.1	007597	Cluster7452_1clades	132	SEA_KELA_329	Streptomyces phage Kela	GCA_012934305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65621.1	007598	Cluster7453_1clades	132	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65162.1	007598	Cluster7453_1clades	132	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90429.1	007599	Cluster7454_1clades	132	HYO65_gp037	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90736.1	007599	Cluster7454_1clades	132	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06719.1	007600	Cluster7455_1clades	132	BcepSaruman_306	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74687.1	007600	Cluster7455_1clades	80	BcepSauron_307	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97359.1	007601	Cluster7456_1clades	132	D6_0200	Aeromonas phage D6	GCA_007051205.2
QDH47199.1	007601	Cluster7456_1clades	132	LAh10_117	Aeromonas phage LAh10	GCA_006863975.1
QGT54798.1	007602	Cluster7457_1clades	132	b23_0183	Synechococcus phage B23	GCA_009745195.1
QGT54428.1	007602	Cluster7457_1clades	132	b3_0184	Synechococcus phage B3	GCA_009745215.1
prevph1000000341	007603	Cluster7458_1clades	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000270	007603	Cluster7458_1clades	133	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000358	007604	Cluster7459_1clades	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000284	007604	Cluster7459_1clades	133	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000612	007605	Cluster7460_1clades	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000431	007605	Cluster7460_1clades	133	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000762	007606	DUF488	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000514	007606	DUF488	133	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000837	007607	SIG+DUF3048_C	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000579	007607	SIG+DUF3048_C	124	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFC21903.1	007608	Cluster7463_1clades	131	GAP32_448	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44032.1	007608	Cluster7463_1clades	131	CBB_469	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFQ96714.1	007609	Cluster7464_1clades	131	G173_gp169	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50696.1	007609	Cluster7464_1clades	131	STRATTON_271	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AXQ68495.1	007610	Cluster7465_1clades	131	CcrBL10_gp291	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86784.1	007610	Cluster7465_1clades	131	CcrRogue_gp302	Caulobacter virus Rogue	GCA_000900555.1
AIA64853.1	007611	GNTR-HTH	131	S13_054	Cronobacter phage S13	GCA_001503575.1
QHJ78812.1	007611	GNTR-HTH	130	-	Myoviridae sp.	GCA_012593985.1
AMS01191.1	007612	Cluster7467_1clades	131	AR9_g107	Bacillus phage AR9	GCA_001743835.1
ASU00125.1	007612	Cluster7467_1clades	131	PBI_PBS1_303	Bacillus virus PBS1	GCA_002601325.1
AMS01370.1	007613	Cluster7468_1clades	131	AR9_g286	Bacillus phage AR9	GCA_001743835.1
ASU00001.1	007613	Cluster7468_1clades	131	PBI_PBS1_179	Bacillus virus PBS1	GCA_002601325.1
AXF51328.1	007614	Cluster7469_1clades	131	WELLINGTON_200	Erwinia phage Wellington	GCA_003344985.1
ANZ49553.1	007614	Cluster7469_1clades	131	KWAN_201	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65427.1	007615	Cluster7470_1clades	131	2050HW_00092	Serratia phage 2050HW	GCA_002628125.1
QDB71203.1	007615	Cluster7470_1clades	131	CPT_Moabite_173	Serratia phage Moabite	GCA_006384735.1
ATA65506.1	007616	Cluster7471_1clades	131	2050HW_00171	Serratia phage 2050HW	GCA_002628125.1
QDB71275.1	007616	Cluster7471_1clades	131	CPT_Moabite_245	Serratia phage Moabite	GCA_006384735.1
AXH72461.1	007617	Cluster7472_1clades	124	-	Myoviridae sp.	GCA_003657725.1
AXH72462.1	007617	Cluster7472_1clades	131	-	Myoviridae sp.	GCA_003657725.1
AFU88260.1	007618	Cluster7473_1clades	127	CcrColossus_gp390	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68934.1	007618	Cluster7473_1clades	131	CcrPW_gp395	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69321.1	007619	Cluster7474_1clades	131	CcrBL9_gp297	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69881.1	007619	Cluster7474_1clades	131	CcrSC_gp299	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69482.1	007620	Cluster7475_1clades	129	CcrBL9_gp458	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70031.1	007620	Cluster7475_1clades	131	CcrSC_gp449	Caulobacter phage CcrSC	GCA_003443315.1
BAW18983.1	007621	Cluster7476_1clades	131	FDH28_gp009	Ralstonia phage RP12	GCA_002617345.1
BAW19271.1	007621	Cluster7476_1clades	131	-	Ralstonia phage RP31	GCA_002617365.1
BBA65546.1	007622	Cluster7477_1clades	131	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96541.1	007622	Cluster7477_1clades	128	Xoosp13_355	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90446.1	007623	Cluster7478_1clades	131	HYO65_gp054	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90754.1	007623	Cluster7478_1clades	131	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06648.1	007624	Cluster7479_1clades	131	BcepSaruman_235	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74617.1	007624	Cluster7479_1clades	129	BcepSauron_237	Burkholderia phage BcepSauron	GCA_005394215.1
QBZ72089.1	007625	Cluster7480_1clades	131	SEA_KRADAL_193	Streptomyces phage Kradal	GCA_004799925.1
AXH66351.1	007625	Cluster7480_1clades	125	SEA_SATIS_192	Streptomyces phage Satis	GCA_003366315.1
QDJ96669.1	007626	Cluster7481_1clades	131	PS1_0158	Aeromonas phage PS1	GCA_007051165.2
QFR59303.1	007626	Cluster7481_1clades	131	PS2_0162	Aeromonas phage PS2	GCA_009388305.2
QDJ96677.1	007627	Tail_spike_N	131	PS1_0166	Aeromonas phage PS1	GCA_007051165.2
QFR59311.1	007627	Tail_spike_N	130	PS2_0170	Aeromonas phage PS2	GCA_009388305.2
QMP24096.1	007628	Peptidase_M15_4	131	-	Proteus phage 10	GCA_014071245.1
QHJ86188.1	007628	Peptidase_M15_4	115	KKIINIFJ_00278	Pseudomonas phage PN05	GCA_009931935.1
prevph1000000102	007629	TM+TM	105	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000073	007629	TM+TM	132	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000356	007630	Cluster7485_1clades	132	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000282	007630	Cluster7485_1clades	132	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000488	007631	Cluster7486_1clades	132	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000369	007631	Cluster7486_1clades	132	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01398.1	007632	Cluster7487_1clades	130	-	Aeromonas phage 65.2	GCA_002618145.1
AAR90932.1	007632	Cluster7487_1clades	130	65p007	Aeromonas virus 65	GCA_000893255.1
AFU88171.1	007633	Cluster7488_1clades	130	CcrColossus_gp301	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68848.1	007633	Cluster7488_1clades	85	CcrPW_gp309	Caulobacter phage CcrPW	GCA_003443275.1
AFU88214.1	007634	Cluster7489_1clades	130	CcrColossus_gp344	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68890.1	007634	Cluster7489_1clades	125	CcrPW_gp351	Caulobacter phage CcrPW	GCA_003443275.1
AMS01171.1	007635	Cluster7490_1clades	130	AR9_g087	Bacillus phage AR9	GCA_001743835.1
ASU00103.1	007635	Cluster7490_1clades	130	PBI_PBS1_281	Bacillus virus PBS1	GCA_002601325.1
AOO14264.1	007636	Cluster7491_1clades	130	Sn110110_070	Cyanophage S-RIM14	GCA_002599065.1
AOO14913.1	007636	Cluster7491_1clades	130	W1230910_067	Cyanophage S-RIM14	GCA_002599125.1
AOO14330.1	007637	HNH	130	Sn110110_136	Cyanophage S-RIM14	GCA_002599065.1
AOO14979.1	007637	HNH	128	W1230910_133	Cyanophage S-RIM14	GCA_002599125.1
APU01646.1	007638	Cluster7493_1clades	130	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53273.1	007638	Cluster7493_1clades	86	65p265	Aeromonas virus 65	GCA_000893255.1
ATA65529.1	007639	Cluster7494_1clades	130	2050HW_00194	Serratia phage 2050HW	GCA_002628125.1
QDB71293.1	007639	Cluster7494_1clades	130	CPT_Moabite_263	Serratia phage Moabite	GCA_006384735.1
ATA65631.1	007640	Cluster7495_1clades	130	2050HW_00296	Serratia phage 2050HW	GCA_002628125.1
QDB71059.1	007640	Cluster7495_1clades	130	CPT_Moabite_027	Serratia phage Moabite	GCA_006384735.1
AXQ69458.1	007641	Cluster7496_1clades	124	CcrBL9_gp434	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70007.1	007641	Cluster7496_1clades	130	CcrSC_gp425	Caulobacter phage CcrSC	GCA_003443315.1
AYD81241.1	007642	Cluster7497_1clades	130	SEA_JUSTBECAUSE_72	Streptomyces phage JustBecause	GCA_003613775.1
QJD53644.1	007642	Cluster7497_1clades	130	SEA_KELA_73	Streptomyces phage Kela	GCA_012934305.1
BAS04908.2	007643	Cluster7498_1clades	130	AVU11_gp116	Ralstonia phage RSF1	GCA_001500875.1
BAQ02635.2	007643	Cluster7498_1clades	116	-	Ralstonia phage RSL2	GCA_001503055.1
BBI90556.1	007644	Cluster7499_1clades	130	HYO65_gp164	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90864.1	007644	Cluster7499_1clades	130	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06604.1	007645	Cluster7500_1clades	130	BcepSaruman_191	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74570.1	007645	Cluster7500_1clades	130	BcepSauron_190	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32194.1	007646	Cluster7501_1clades	130	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41771.1	007646	Cluster7501_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32453.1	007647	Cluster7502_1clades	130	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42025.1	007647	Cluster7502_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32480.1	007648	Cluster7503_1clades	130	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42052.1	007648	Cluster7503_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65483.1	007649	Cluster7504_1clades	129	2050HW_00148	Serratia phage 2050HW	GCA_002628125.1
QDB71253.1	007649	Cluster7504_1clades	130	CPT_Moabite_223	Serratia phage Moabite	GCA_006384735.1
ATA65494.1	007650	Cluster7505_1clades	75	2050HW_00159	Serratia phage 2050HW	GCA_002628125.1
QDB71262.1	007650	Cluster7505_1clades	130	CPT_Moabite_232	Serratia phage Moabite	GCA_006384735.1
QDJ96668.1	007651	Cluster7506_1clades	130	PS1_0157	Aeromonas phage PS1	GCA_007051165.2
QFR59302.1	007651	Cluster7506_1clades	130	PS2_0161	Aeromonas phage PS2	GCA_009388305.2
QBX32486.1	007652	Cluster7507_1clades	85	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42058.1	007652	Cluster7507_1clades	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54665.1	007653	Cluster7508_1clades	130	b23_0037	Synechococcus phage B23	GCA_009745195.1
QGT54295.1	007653	Cluster7508_1clades	130	b3_0037	Synechococcus phage B3	GCA_009745215.1
QGT54866.1	007654	ACET	130	b23_0252	Synechococcus phage B23	GCA_009745195.1
QGT54501.1	007654	ACET	130	b3_0259	Synechococcus phage B3	GCA_009745215.1
prevph1000000305	007655	Cluster7510_1clades	131	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000237	007655	Cluster7510_1clades	131	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000844	007656	Cluster7511_1clades	131	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000586	007656	Cluster7511_1clades	131	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFH14815.1	007657	Cluster7512_1clades	129	Lu11_0278	Pseudomonas phage Lu11	GCA_000897175.1
QKE11211.1	007657	Cluster7512_1clades	123	PaBG_00133	Pseudomonas phage PaBG	GCA_000912555.1
AFU88186.1	007658	Cluster7513_1clades	129	CcrColossus_gp316	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68863.1	007658	Cluster7513_1clades	129	CcrPW_gp324	Caulobacter phage CcrPW	GCA_003443275.1
AFU88301.1	007659	Cluster7514_1clades	129	CcrColossus_gp431	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68976.1	007659	Cluster7514_1clades	129	CcrPW_gp437c	Caulobacter phage CcrPW	GCA_003443275.1
AND75420.1	007660	Cluster7515_1clades	122	ME3_259	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AND75430.1	007660	Cluster7515_1clades	129	ME3_269	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AWY08297.1	007661	Cluster7516_1clades	127	Alexandra_16	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58656.1	007661	Cluster7516_1clades	129	Y3_016	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ASU03755.1	007662	Cluster7517_1clades	129	JOAD_160	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03511.1	007662	Cluster7517_1clades	129	RISINGSUN_159	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03766.1	007663	Cluster7518_1clades	129	JOAD_149	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03522.1	007663	Cluster7518_1clades	129	RISINGSUN_148	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QKE11213.1	007664	Cluster7519_1clades	110	PaBG_00148	Pseudomonas phage PaBG	GCA_000912555.1
ASV44474.1	007664	Cluster7519_1clades	129	PBI_SCTP2_459	Salicola phage SCTP-2	GCA_002625545.1
ATA65519.1	007665	Cluster7520_1clades	129	2050HW_00184	Serratia phage 2050HW	GCA_002628125.1
QDB71286.1	007665	Cluster7520_1clades	129	CPT_Moabite_256	Serratia phage Moabite	GCA_006384735.1
ATA65530.1	007666	Cluster7521_1clades	129	2050HW_00195	Serratia phage 2050HW	GCA_002628125.1
QDB71294.1	007666	Cluster7521_1clades	129	CPT_Moabite_264	Serratia phage Moabite	GCA_006384735.1
AXQ69435.1	007667	Cluster7522_1clades	129	CcrBL9_gp411	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69987.1	007667	Cluster7522_1clades	118	CcrSC_gp405	Caulobacter phage CcrSC	GCA_003443315.1
AYD81417.1	007668	Cluster7523_1clades	129	SEA_JUSTBECAUSE_262	Streptomyces phage JustBecause	GCA_003613775.1
QJD53822.1	007668	Cluster7523_1clades	129	SEA_KELA_262	Streptomyces phage Kela	GCA_012934305.1
BAW19096.1	007669	Cluster7524_1clades	129	FDH28_gp122	Ralstonia phage RP12	GCA_002617345.1
BAW19382.1	007669	Cluster7524_1clades	129	-	Ralstonia phage RP31	GCA_002617365.1
BBA65151.1	007670	Cluster7525_1clades	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65610.1	007670	Cluster7525_1clades	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65616.1	007671	Cluster7526_1clades	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65157.1	007671	Cluster7526_1clades	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65247.1	007672	Cluster7527_1clades	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65706.1	007672	Cluster7527_1clades	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90454.1	007673	Cluster7528_1clades	129	HYO65_gp062	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90762.1	007673	Cluster7528_1clades	129	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90526.1	007674	Cluster7529_1clades	129	HYO65_gp134	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90834.1	007674	Cluster7529_1clades	129	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06472.1	007675	Cluster7530_1clades	129	BcepSaruman_059	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74439.1	007675	Cluster7530_1clades	129	BcepSauron_059	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06732.1	007676	aGPT-PPlase	123	BcepSaruman_319	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74701.1	007676	aGPT-PPlase	129	BcepSauron_321	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32333.1	007677	Cluster7532_1clades	129	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41906.1	007677	Cluster7532_1clades	108	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW18680.1	007678	Cluster7533_1clades	129	7t3_0159	Salmonella phage 7t3	GCA_006083215.1
QIG63022.1	007678	Cluster7533_1clades	129	SEPL_409	Salmonella phage SE_PL	GCA_011067555.1
QDJ97343.1	007679	Cluster7534_1clades	129	D6_0184	Aeromonas phage D6	GCA_007051205.2
QDH47203.1	007679	Cluster7534_1clades	129	LAh10_103	Aeromonas phage LAh10	GCA_006863975.1
BBA65368.1	007680	Cluster7535_1clades	126	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96396.1	007680	Cluster7535_1clades	129	Xoosp13_210	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AUZ95220.1	007681	Cluster7536_1clades	120	FDI40_gp461	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65894.1	007681	Cluster7536_1clades	129	phiOC_p233	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
prevph1000000369	007682	Cluster7537_1clades	130	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000295	007682	Cluster7537_1clades	130	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000375	007683	Cluster7538_1clades	130	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000301	007683	Cluster7538_1clades	130	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000795	007684	Cluster7539_1clades	130	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000543	007684	Cluster7539_1clades	130	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88242.1	007685	Cluster7540_1clades	128	CcrColossus_gp372	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68917.1	007685	Cluster7540_1clades	127	CcrPW_gp378c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88286.1	007686	Cluster7541_1clades	128	CcrColossus_gp416	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68960.1	007686	Cluster7541_1clades	128	CcrPW_gp421c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88287.1	007687	Phage_BR0599	128	CcrColossus_gp417	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68962.1	007687	Phage_BR0599	60	CcrPW_gp423c	Caulobacter phage CcrPW	GCA_003443275.1
AXF51251.1	007688	Cluster7543_1clades	128	WELLINGTON_121	Erwinia phage Wellington	GCA_003344985.1
ANZ49472.1	007688	Cluster7543_1clades	128	KWAN_120	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51336.1	007689	Cluster7544_1clades	128	WELLINGTON_208	Erwinia phage Wellington	GCA_003344985.1
ANZ49561.1	007689	Cluster7544_1clades	128	KWAN_209	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
SOK58739.1	007690	Cluster7545_2clades	128	g462	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AQW88993.1	007690	Cluster7545_2clades	128	BF_0468	Serratia phage BF	GCA_002619745.1
ASU03768.1	007691	TM	128	JOAD_147	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03524.1	007691	TM	128	RISINGSUN_146	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65516.1	007692	Cluster7547_1clades	128	2050HW_00181	Serratia phage 2050HW	GCA_002628125.1
QDB71283.1	007692	Cluster7547_1clades	128	CPT_Moabite_253	Serratia phage Moabite	GCA_006384735.1
ATA65531.1	007693	Cluster7548_1clades	128	2050HW_00196	Serratia phage 2050HW	GCA_002628125.1
QDB71295.1	007693	Cluster7548_1clades	128	CPT_Moabite_265	Serratia phage Moabite	GCA_006384735.1
AUZ94855.1	007694	Cluster7549_1clades	128	FDI40_gp043	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72777.1	007694	Cluster7549_1clades	122	-	Myoviridae sp.	GCA_003657725.1
QBZ71923.1	007695	Cluster7550_1clades	128	SEA_KRADAL_24	Streptomyces phage Kradal	GCA_004799925.1
AXH66185.1	007695	Cluster7550_1clades	128	SEA_SATIS_24	Streptomyces phage Satis	GCA_003366315.1
AXH72484.1	007696	Cluster7551_1clades	126	-	Myoviridae sp.	GCA_003657725.1
AXH72560.1	007696	Cluster7551_1clades	128	-	Myoviridae sp.	GCA_003657725.1
AXQ69348.1	007697	Cluster7552_1clades	128	CcrBL9_gp324	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69907.1	007697	Cluster7552_1clades	128	CcrSC_gp325	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69410.1	007698	Cluster7553_1clades	128	CcrBL9_gp386	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69966.1	007698	Cluster7553_1clades	128	CcrSC_gp384	Caulobacter phage CcrSC	GCA_003443315.1
QBX32443.1	007699	Cluster7555_1clades	128	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42014.1	007699	Cluster7555_1clades	128	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97307.1	007700	Cluster7556_1clades	128	D6_0147	Aeromonas phage D6	GCA_007051205.2
QDH47206.1	007700	Cluster7556_1clades	128	LAh10_72	Aeromonas phage LAh10	GCA_006863975.1
BBA65529.1	007701	Cluster7557_1clades	120	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96527.1	007701	Cluster7557_1clades	128	Xoosp13_341	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96674.1	007702	SIG+TM	128	PS1_0163	Aeromonas phage PS1	GCA_007051165.2
QFR59308.1	007702	SIG+TM	128	PS2_0167	Aeromonas phage PS2	GCA_009388305.2
QDB70310.1	007703	Cluster7559_1clades	124	CF8_0142	Aeromonas phage CF8	GCA_006384595.2
QFR59287.1	007703	Cluster7559_1clades	128	PS2_0146	Aeromonas phage PS2	GCA_009388305.2
QGT54799.1	007704	Cluster7560_1clades	128	b23_0184	Synechococcus phage B23	GCA_009745195.1
QGT54429.1	007704	Cluster7560_1clades	128	b3_0185	Synechococcus phage B3	GCA_009745215.1
QGT54836.1	007705	Cluster7561_1clades	128	b23_0221	Synechococcus phage B23	GCA_009745195.1
QGT54466.1	007705	Cluster7561_1clades	128	b3_0223	Synechococcus phage B3	GCA_009745215.1
prevph1000000169	007706	TM+TM	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000131	007706	TM+TM	129	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFO71421.1	007707	Cluster7563_1clades	127	CR5_201	Cronobacter phage CR5	GCA_000910235.1
ANZ50405.1	007707	Cluster7563_1clades	122	PHOBOS_215	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AFU88156.1	007708	Cluster7564_1clades	127	CcrColossus_gp286	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68831.1	007708	Cluster7564_1clades	127	CcrPW_gp292	Caulobacter phage CcrPW	GCA_003443275.1
AFU88223.1	007709	Cluster7565_1clades	127	CcrColossus_gp353	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68900.1	007709	Cluster7565_1clades	127	CcrPW_gp361	Caulobacter phage CcrPW	GCA_003443275.1
ANZ48434.1	007710	Cluster7566_1clades	127	CAITLIN_139	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48709.1	007710	Cluster7566_1clades	125	CHRISDB_147	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AMS01321.1	007711	Cluster7567_1clades	126	AR9_g237	Bacillus phage AR9	GCA_001743835.1
AST99950.1	007711	Cluster7567_1clades	127	PBI_PBS1_128	Bacillus virus PBS1	GCA_002601325.1
AXQ69447.1	007712	Cluster7568_1clades	127	CcrBL9_gp423	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69997.1	007712	Cluster7568_1clades	127	CcrSC_gp415	Caulobacter phage CcrSC	GCA_003443315.1
BAW19203.1	007713	TM+TM	127	FDH28_gp192	Ralstonia phage RP12	GCA_002617345.1
BAW19489.1	007713	TM+TM	127	-	Ralstonia phage RP31	GCA_002617365.1
BBI90596.1	007714	TM+TM	127	HYO65_gp204	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90903.1	007714	TM+TM	127	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90498.1	007715	Cluster7571_1clades	109	HYO65_gp106	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90806.1	007715	Cluster7571_1clades	127	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06759.1	007716	Cluster7572_1clades	127	BcepSaruman_346	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74729.1	007716	Cluster7572_1clades	127	BcepSauron_349	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97189.1	007717	Cluster7573_1clades	127	D6_0029	Aeromonas phage D6	GCA_007051205.2
QDH47208.1	007717	Cluster7573_1clades	127	LAh10_197	Aeromonas phage LAh10	GCA_006863975.1
QGT54805.1	007718	Cluster7574_1clades	127	b23_0190	Synechococcus phage B23	GCA_009745195.1
QGT54435.1	007718	Cluster7574_1clades	127	b3_0191	Synechococcus phage B3	GCA_009745215.1
QIG57767.1	007719	PG-binding	127	SEA_PAULODIABOLI_32	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58068.1	007719	PG-binding	127	SEA_PAULODIABOLI_387	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000306	007720	Cluster7576_1clades	128	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000238	007720	Cluster7576_1clades	128	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000524	007721	Cluster7577_1clades	128	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000398	007721	Cluster7577_1clades	128	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000763	007722	Cluster7578_1clades	128	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000515	007722	Cluster7578_1clades	71	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAX44557.2	007723	DUF1257	126	PSSM2_179	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12415.1	007723	DUF1257	126	PRTG_00263	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01596.1	007724	Cluster7580_1clades	126	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53220.1	007724	Cluster7580_1clades	126	65p212	Aeromonas virus 65	GCA_000893255.1
AFH14604.1	007725	Cluster7581_1clades	126	Lu11_0072	Pseudomonas phage Lu11	GCA_000897175.1
AGS82100.1	007725	Cluster7581_1clades	113	PaBG_00225	Pseudomonas phage PaBG	GCA_000912555.1
AFU88190.1	007726	Cluster7582_1clades	126	CcrColossus_gp320	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68868.1	007726	Cluster7582_1clades	126	CcrPW_gp329	Caulobacter phage CcrPW	GCA_003443275.1
AMS01218.1	007727	Cluster7583_1clades	126	AR9_g134	Bacillus phage AR9	GCA_001743835.1
AST99843.1	007727	Cluster7583_1clades	126	PBI_PBS1_21	Bacillus virus PBS1	GCA_002601325.1
AXF51209.1	007728	Cluster7584_1clades	126	WELLINGTON_79	Erwinia phage Wellington	GCA_003344985.1
ANZ49431.1	007728	Cluster7584_1clades	126	KWAN_79	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51331.1	007729	Cluster7585_1clades	126	WELLINGTON_203	Erwinia phage Wellington	GCA_003344985.1
ANZ49556.1	007729	Cluster7585_1clades	126	KWAN_204	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51361.1	007730	Cluster7586_1clades	126	WELLINGTON_235	Erwinia phage Wellington	GCA_003344985.1
ANZ49587.1	007730	Cluster7586_1clades	126	KWAN_235	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ABY63247.1	007731	Cluster7587_1clades	125	201phi2-1p424	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77055.1	007731	Cluster7587_1clades	126	PHABIO_424	Pseudomonas phage Phabio	GCA_002624965.1
ASU03729.1	007732	Cluster7588_1clades	126	JOAD_186	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03486.1	007732	Cluster7588_1clades	126	RISINGSUN_184	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AFU88217.1	007733	Cluster7589_1clades	125	CcrColossus_gp347	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68894.1	007733	Cluster7589_1clades	126	CcrPW_gp355	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69511.1	007734	Cluster7590_1clades	126	CcrBL9_gp487	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70058.1	007734	Cluster7590_1clades	123	CcrSC_gp476	Caulobacter phage CcrSC	GCA_003443315.1
BAS04957.1	007735	Cluster7591_1clades	126	AVU11_gp165	Ralstonia phage RSF1	GCA_001500875.1
BAQ02682.1	007735	Cluster7591_1clades	79	AVU38_gp154	Ralstonia phage RSL2	GCA_001503055.1
BAW19146.1	007736	Cluster7592_1clades	126	FDH28_gp249	Ralstonia phage RP12	GCA_002617345.1
BAW19432.1	007736	Cluster7592_1clades	126	-	Ralstonia phage RP31	GCA_002617365.1
BAW19192.1	007737	Cluster7593_1clades	126	FDH28_gp203	Ralstonia phage RP12	GCA_002617345.1
BAW19478.1	007737	Cluster7593_1clades	126	-	Ralstonia phage RP31	GCA_002617365.1
BBA65210.1	007738	HNH	126	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65669.1	007738	HNH	126	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06571.1	007739	Cluster7595_1clades	126	BcepSaruman_158	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74538.1	007739	Cluster7595_1clades	126	BcepSauron_158	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06755.1	007740	Cluster7596_1clades	122	BcepSaruman_342	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74725.1	007740	Cluster7596_1clades	126	BcepSauron_345	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32498.1	007741	Cluster7597_1clades	126	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42071.1	007741	Cluster7597_1clades	126	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65640.1	007742	Cluster7598_1clades	81	2050HW_00305	Serratia phage 2050HW	GCA_002628125.1
QDB71068.1	007742	Cluster7598_1clades	126	CPT_Moabite_036	Serratia phage Moabite	GCA_006384735.1
QDJ97352.1	007743	Cluster7599_1clades	126	D6_0193	Aeromonas phage D6	GCA_007051205.2
QDH47209.1	007743	Cluster7599_1clades	126	LAh10_111	Aeromonas phage LAh10	GCA_006863975.1
QNH80835.1	007744	Cluster7600_1clades	108	D6_0024	Aeromonas phage D6	GCA_007051205.2
QDH47210.1	007744	Cluster7600_1clades	126	LAh10_192	Aeromonas phage LAh10	GCA_006863975.1
QGT54746.1	007745	SIG+ENDO3	126	b23_0131	Synechococcus phage B23	GCA_009745195.1
QGT54376.1	007745	SIG+ENDO3	126	b3_0132	Synechococcus phage B3	GCA_009745215.1
QGT54828.1	007746	Cluster7602_1clades	126	b23_0213	Synechococcus phage B23	GCA_009745195.1
QGT54458.1	007746	Cluster7602_1clades	126	b3_0215	Synechococcus phage B3	GCA_009745215.1
SOK59309.1	007747	Cluster7603_1clades	126	g501	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58774.1	007747	Cluster7603_1clades	126	g497	Yersinia phage fHe-Yen9-04	GCA_002990485.1
APU01516.1	007748	Cluster7604_1clades	125	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53139.1	007748	Cluster7604_1clades	125	65p131	Aeromonas virus 65	GCA_000893255.1
AFU88044.1	007749	Cluster7605_1clades	125	CcrColossus_gp174	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68721.1	007749	Cluster7605_1clades	125	CcrPW_gp182c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88151.1	007750	Cluster7606_1clades	125	CcrColossus_gp281	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68827.1	007750	Cluster7606_1clades	125	CcrPW_gp288	Caulobacter phage CcrPW	GCA_003443275.1
AIA64997.1	007751	Cluster7607_1clades	125	S13_200	Cronobacter phage S13	GCA_001503575.1
QHJ78934.1	007751	Cluster7607_1clades	123	-	Myoviridae sp.	GCA_012593985.1
AMS01366.1	007752	Cluster7608_1clades	125	AR9_g282	Bacillus phage AR9	GCA_001743835.1
AST99996.1	007752	Cluster7608_1clades	125	PBI_PBS1_175	Bacillus virus PBS1	GCA_002601325.1
AXF51163.1	007753	Cluster7609_1clades	125	WELLINGTON_32	Erwinia phage Wellington	GCA_003344985.1
ANZ49384.1	007753	Cluster7609_1clades	125	KWAN_32	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03772.1	007754	TM	125	JOAD_143	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03528.1	007754	TM	125	RISINGSUN_142	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65614.1	007755	Cluster7611_1clades	125	2050HW_00279	Serratia phage 2050HW	GCA_002628125.1
QDB71043.1	007755	Cluster7611_1clades	125	CPT_Moabite_011	Serratia phage Moabite	GCA_006384735.1
BAW19048.1	007756	Cluster7612_1clades	125	FDH28_gp074	Ralstonia phage RP12	GCA_002617345.1
BAW19333.1	007756	Cluster7612_1clades	125	-	Ralstonia phage RP31	GCA_002617365.1
BAW19088.1	007757	Cluster7613_1clades	125	FDH28_gp114	Ralstonia phage RP12	GCA_002617345.1
BAW19374.1	007757	Cluster7613_1clades	125	-	Ralstonia phage RP31	GCA_002617365.1
BAW19077.1	007758	Cluster7614_1clades	122	FDH28_gp103	Ralstonia phage RP12	GCA_002617345.1
BAW19362.1	007758	Cluster7614_1clades	125	-	Ralstonia phage RP31	GCA_002617365.1
QBX06738.1	007759	Cluster7615_1clades	124	BcepSaruman_325	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74707.1	007759	Cluster7615_1clades	125	BcepSauron_327	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06813.1	007760	Cluster7616_1clades	125	BcepSaruman_400	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74782.1	007760	Cluster7616_1clades	125	BcepSauron_402	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32487.1	007761	Cluster7617_1clades	125	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42059.1	007761	Cluster7617_1clades	125	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54654.1	007762	Cluster7618_1clades	115	b23_0026	Synechococcus phage B23	GCA_009745195.1
QGT54284.1	007762	Cluster7618_1clades	125	b3_0026	Synechococcus phage B3	GCA_009745215.1
prevph1000000031	007763	Cluster7619_1clades	126	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000023	007763	Cluster7619_1clades	126	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000525	007764	Cluster7620_1clades	126	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000399	007764	Cluster7620_1clades	126	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000565	007765	Cluster7621_1clades	126	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000412	007765	Cluster7621_1clades	126	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88018.1	007766	DAGKIN	124	CcrColossus_gp148	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68695.1	007766	DAGKIN	124	CcrPW_gp156c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88148.1	007767	Cluster7623_1clades	124	CcrColossus_gp278	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68824.1	007767	Cluster7623_1clades	124	CcrPW_gp285	Caulobacter phage CcrPW	GCA_003443275.1
AFU88216.1	007768	Cluster7624_1clades	124	CcrColossus_gp346	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68893.1	007768	Cluster7624_1clades	121	CcrPW_gp354	Caulobacter phage CcrPW	GCA_003443275.1
AIA64982.1	007769	Cluster7625_1clades	124	S13_185	Cronobacter phage S13	GCA_001503575.1
QHJ78953.1	007769	Cluster7625_1clades	122	-	Myoviridae sp.	GCA_012593985.1
AMS01135.1	007770	Cluster7626_1clades	124	AR9_g050	Bacillus phage AR9	GCA_001743835.1
ASU00062.1	007770	Cluster7626_1clades	124	PBI_PBS1_240	Bacillus virus PBS1	GCA_002601325.1
ANZ48516.1	007771	Cluster7627_1clades	124	CAITLIN_221	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48793.1	007771	Cluster7627_1clades	121	CHRISDB_231	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ASU03800.1	007772	Cluster7628_1clades	124	JOAD_115	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03555.1	007772	Cluster7628_1clades	124	RISINGSUN_115	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03892.1	007773	Cluster7629_1clades	124	JOAD_23	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03647.1	007773	Cluster7629_1clades	124	RISINGSUN_23	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65587.1	007774	Cluster7630_1clades	124	2050HW_00252	Serratia phage 2050HW	GCA_002628125.1
QDB71352.1	007774	Cluster7630_1clades	124	CPT_Moabite_322	Serratia phage Moabite	GCA_006384735.1
AXQ69249.1	007775	Cluster7631_1clades	124	CcrBL9_gp225	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69804.1	007775	Cluster7631_1clades	124	CcrSC_gp222	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69285.1	007776	Cluster7632_1clades	124	CcrBL9_gp261c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69842.1	007776	Cluster7632_1clades	124	CcrSC_gp260c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69330.1	007777	Cluster7633_1clades	124	CcrBL9_gp306	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69890.1	007777	Cluster7633_1clades	124	CcrSC_gp308	Caulobacter phage CcrSC	GCA_003443315.1
BBI90486.1	007778	Cluster7634_1clades	124	HYO65_gp094	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90794.1	007778	Cluster7634_1clades	124	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90665.1	007779	Cluster7635_1clades	124	HYO65_gp273	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90970.1	007779	Cluster7635_1clades	124	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06473.1	007780	Cluster7636_1clades	124	BcepSaruman_060	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74440.1	007780	Cluster7636_1clades	124	BcepSauron_060	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06507.1	007781	Cluster7637_1clades	124	BcepSaruman_094	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74473.1	007781	Cluster7637_1clades	124	BcepSauron_093	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06727.1	007782	Cluster7638_1clades	124	BcepSaruman_314	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74696.1	007782	Cluster7638_1clades	124	BcepSauron_316	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54760.1	007783	Cluster7639_1clades	124	b23_0145	Synechococcus phage B23	GCA_009745195.1
QGT54390.1	007783	Cluster7639_1clades	124	b3_0146	Synechococcus phage B3	GCA_009745215.1
SOK59243.1	007784	Cluster7641_1clades	124	g435	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58709.1	007784	Cluster7641_1clades	124	g432	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000323	007785	SIG+TM+TM	125	-	Prevotella_phage_Lak-B8	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prev15ph1000000252	007785	SIG+TM+TM	124	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01678.1	007786	Cluster7643_1clades	123	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53312.1	007786	Cluster7643_1clades	123	65p304	Aeromonas virus 65	GCA_000893255.1
APU01772.1	007787	Cluster7644_1clades	123	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53415.1	007787	Cluster7644_1clades	123	65p408	Aeromonas virus 65	GCA_000893255.1
AEO93526.1	007788	SIG+SASP	123	G_267	Bacillus virus G	GCA_000917535.1
AEO93675.1	007788	SIG+SASP	81	G_417	Bacillus virus G	GCA_000917535.1
AMS01134.1	007789	TM+LysM	123	AR9_g049	Bacillus phage AR9	GCA_001743835.1
ASU00061.1	007789	TM+LysM	123	PBI_PBS1_239	Bacillus virus PBS1	GCA_002601325.1
ARV76721.1	007790	Cluster7647_1clades	123	PHABIO_90	Pseudomonas phage Phabio	GCA_002624965.1
ARV76722.1	007790	Cluster7647_1clades	122	PHABIO_91	Pseudomonas phage Phabio	GCA_002624965.1
ARW58671.1	007791	AntA	123	Y3_031	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28512.1	007791	AntA	122	YOLOSWAG_26	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ASU03731.1	007792	Cluster7649_1clades	107	JOAD_184	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03487.1	007792	Cluster7649_1clades	123	RISINGSUN_183	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03758.1	007793	Cluster7650_1clades	123	JOAD_157	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03514.1	007793	Cluster7650_1clades	123	RISINGSUN_156	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03787.1	007794	Cluster7651_1clades	123	JOAD_128	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03543.1	007794	Cluster7651_1clades	123	RISINGSUN_127	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03828.1	007795	TM+TM+TM	123	JOAD_87	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03583.1	007795	TM+TM+TM	123	RISINGSUN_87	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03908.1	007796	DUF2829	123	JOAD_7	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03663.1	007796	DUF2829	123	RISINGSUN_7	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QBZ72134.1	007797	Cluster7654_1clades	123	SEA_KRADAL_248	Streptomyces phage Kradal	GCA_004799925.1
AXH66396.1	007797	Cluster7654_1clades	123	SEA_SATIS_247	Streptomyces phage Satis	GCA_003366315.1
QBZ72198.1	007798	Cluster7655_1clades	123	SEA_KRADAL_312	Streptomyces phage Kradal	GCA_004799925.1
AXH66461.1	007798	Cluster7655_1clades	123	SEA_SATIS_312	Streptomyces phage Satis	GCA_003366315.1
AXQ69327.1	007799	Cluster7656_1clades	123	CcrBL9_gp303	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69887.1	007799	Cluster7656_1clades	123	CcrSC_gp305	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69347.1	007800	Cluster7657_1clades	123	CcrBL9_gp323	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69906.1	007800	Cluster7657_1clades	123	CcrSC_gp324	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69355.1	007801	Cluster7658_1clades	123	CcrBL9_gp331	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69914.1	007801	Cluster7658_1clades	123	CcrSC_gp332	Caulobacter phage CcrSC	GCA_003443315.1
BAW18987.1	007802	Cluster7659_1clades	123	FDH28_gp013	Ralstonia phage RP12	GCA_002617345.1
BAW19275.1	007802	Cluster7659_1clades	123	-	Ralstonia phage RP31	GCA_002617365.1
BBA65248.1	007803	Cluster7660_1clades	123	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65707.1	007803	Cluster7660_1clades	123	-	Xanthomonas phage XacN1	GCA_003173815.1
QGT54861.1	007804	tRNA_lig_CPD	123	b23_0247	Synechococcus phage B23	GCA_009745195.1
QGT54496.1	007804	tRNA_lig_CPD	123	b3_0254	Synechococcus phage B3	GCA_009745215.1
QGT54900.1	007805	Cluster7662_1clades	123	b23_0287	Synechococcus phage B23	GCA_009745195.1
QGT54535.1	007805	Cluster7662_1clades	123	b3_0294	Synechococcus phage B3	GCA_009745215.1
ABY63112.1	007806	AFG1-AAA	122	201phi2-1p285	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76907.1	007806	AFG1-AAA	120	PHABIO_276	Pseudomonas phage Phabio	GCA_002624965.1
ABY63125.1	007807	Cluster7664_1clades	122	201phi2-1p299	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76926.1	007807	Cluster7664_1clades	120	PHABIO_295	Pseudomonas phage Phabio	GCA_002624965.1
APU01713.1	007808	Cluster7665_1clades	122	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53353.1	007808	Cluster7665_1clades	122	65p345	Aeromonas virus 65	GCA_000893255.1
APU01789.1	007809	Cluster7666_1clades	122	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53432.1	007809	Cluster7666_1clades	122	65p426	Aeromonas virus 65	GCA_000893255.1
QBZ70827.1	007810	Cluster7667_1clades	117	pETSU_246	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89458.1	007810	Cluster7667_1clades	122	OBP_021	Pseudomonas phage OBP	GCA_000896635.1
AFU88297.1	007811	Cluster7668_1clades	122	CcrColossus_gp427	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68972.1	007811	Cluster7668_1clades	122	CcrPW_gp433c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01268.1	007812	Cluster7669_1clades	122	AR9_g184	Bacillus phage AR9	GCA_001743835.1
AST99895.1	007812	Cluster7669_1clades	122	PBI_PBS1_73	Bacillus virus PBS1	GCA_002601325.1
AMS01333.1	007813	RnaseHII+CHTH	122	AR9_g249	Bacillus phage AR9	GCA_001743835.1
AST99963.1	007813	RnaseHII+CHTH	122	PBI_PBS1_142	Bacillus virus PBS1	GCA_002601325.1
ASU03868.1	007814	Cluster7671_1clades	122	JOAD_47	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03623.1	007814	Cluster7671_1clades	122	RISINGSUN_47	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65563.1	007815	Cluster7672_1clades	122	2050HW_00228	Serratia phage 2050HW	GCA_002628125.1
QDB71328.1	007815	Cluster7672_1clades	122	CPT_Moabite_298	Serratia phage Moabite	GCA_006384735.1
QBZ72147.1	007816	Cluster7673_1clades	122	SEA_KRADAL_261	Streptomyces phage Kradal	GCA_004799925.1
AXH66410.1	007816	Cluster7673_1clades	122	SEA_SATIS_261	Streptomyces phage Satis	GCA_003366315.1
AXQ69513.1	007817	Cluster7674_1clades	122	CcrBL9_gp489	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70059.1	007817	Cluster7674_1clades	122	CcrSC_gp477	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69346.1	007818	Cluster7675_1clades	121	CcrBL9_gp322	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69905.1	007818	Cluster7675_1clades	122	CcrSC_gp323	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70608.1	007819	Cluster7676_1clades	122	HOU04_gp007	Synechococcus phage S-T4	GCA_003443335.1
AXQ70406.1	007819	Cluster7676_1clades	122	HOU04_gp007	Synechococcus phage S-T4	GCA_003443335.1
AYD81485.1	007820	Cluster7677_1clades	122	SEA_JUSTBECAUSE_330	Streptomyces phage JustBecause	GCA_003613775.1
QJD53888.1	007820	Cluster7677_1clades	122	SEA_KELA_328	Streptomyces phage Kela	GCA_012934305.1
BBA65487.1	007821	TM	122	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96494.1	007821	TM	92	Xoosp13_308	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65557.1	007822	4HBT	122	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96551.1	007822	4HBT	122	Xoosp13_365	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90499.1	007823	Cluster7680_1clades	122	HYO65_gp107	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90807.1	007823	Cluster7680_1clades	122	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06773.1	007824	Cluster7681_1clades	122	BcepSaruman_360	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74743.1	007824	Cluster7681_1clades	122	BcepSauron_363	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06603.1	007825	Cluster7682_1clades	122	BcepSaruman_190	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74568.1	007825	Cluster7682_1clades	119	BcepSauron_188	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97322.1	007826	Cluster7683_1clades	122	D6_0162	Aeromonas phage D6	GCA_007051205.2
QDH47211.1	007826	Cluster7683_1clades	122	LAh10_83	Aeromonas phage LAh10	GCA_006863975.1
QDJ97181.1	007827	SIG+TM	122	D6_0021	Aeromonas phage D6	GCA_007051205.2
QDH47213.1	007827	SIG+TM	122	LAh10_189	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000000	007828	Cluster7685_1clades	123	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000000	007828	Cluster7685_1clades	123	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000115	007829	Cluster7686_1clades	123	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000082	007829	Cluster7686_1clades	123	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000363	007830	CXC3	123	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000289	007830	CXC3	123	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44475.1	007831	Cluster7688_1clades	121	PSSM2_097	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12177.1	007831	Cluster7688_1clades	121	PRTG_00019	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFF28051.1	007832	Cluster7689_1clades	121	PAU_53	Sphingomonas phage PAU	GCA_000902455.1
BAV39375.1	007832	Cluster7689_1clades	110	BPT24_256	Tenacibaculum phage pT24	GCA_002611925.1
AFU87932.1	007833	Cluster7690_1clades	121	CcrColossus_gp062	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68604.1	007833	Cluster7690_1clades	118	CcrPW_gp065	Caulobacter phage CcrPW	GCA_003443275.1
AFU88224.1	007834	SIG+TM+TM	121	CcrColossus_gp354	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68901.1	007834	SIG+TM+TM	99	CcrPW_gp362	Caulobacter phage CcrPW	GCA_003443275.1
AGH56813.1	007835	Cluster7692_1clades	102	CPXG_00010	Cyanophage P-RSM6	GCA_000906155.1
AJK27633.1	007835	Cluster7692_1clades	121	PTIM40_227	Cyanophage P-TIM40	GCA_001470935.1
AND75427.1	007836	Cluster7693_1clades	113	ME3_266	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75428.1	007836	Cluster7693_1clades	121	ME3_267	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXF51160.1	007837	Cluster7694_1clades	121	WELLINGTON_29	Erwinia phage Wellington	GCA_003344985.1
ANZ49381.1	007837	Cluster7694_1clades	121	KWAN_29	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXG67320.1	007838	Cluster7695_1clades	117	AD1_276	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
ARW58920.1	007838	Cluster7695_1clades	121	Y3_280	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ASU03738.1	007839	Cluster7696_1clades	121	JOAD_177	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03494.1	007839	Cluster7696_1clades	97	RISINGSUN_176	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65378.1	007840	Cluster7697_1clades	121	2050HW_00043	Serratia phage 2050HW	GCA_002628125.1
QDB71162.1	007840	Cluster7697_1clades	121	CPT_Moabite_132	Serratia phage Moabite	GCA_006384735.1
ATA65538.1	007841	Cluster7698_1clades	121	2050HW_00203	Serratia phage 2050HW	GCA_002628125.1
QDB71303.1	007841	Cluster7698_1clades	121	CPT_Moabite_273	Serratia phage Moabite	GCA_006384735.1
ATA65632.1	007842	Cluster7699_1clades	121	2050HW_00297	Serratia phage 2050HW	GCA_002628125.1
QDB71060.1	007842	Cluster7699_1clades	121	CPT_Moabite_028	Serratia phage Moabite	GCA_006384735.1
AXQ69350.1	007843	Cluster7700_1clades	121	CcrBL9_gp326	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69909.1	007843	Cluster7700_1clades	121	CcrSC_gp327	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69445.1	007844	TM	57	CcrBL9_gp421	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69995.1	007844	TM	121	CcrSC_gp413	Caulobacter phage CcrSC	GCA_003443315.1
AYD81488.1	007845	Cluster7702_1clades	121	SEA_JUSTBECAUSE_333	Streptomyces phage JustBecause	GCA_003613775.1
QJD53891.1	007845	Cluster7702_1clades	119	SEA_KELA_331	Streptomyces phage Kela	GCA_012934305.1
BBA65651.1	007846	Cluster7703_1clades	121	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65192.1	007846	Cluster7703_1clades	121	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65237.1	007847	Cluster7704_1clades	121	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65696.1	007847	Cluster7704_1clades	121	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBI90427.1	007848	Cluster7705_1clades	121	HYO65_gp035	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90734.1	007848	Cluster7705_1clades	121	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06542.1	007849	SIG+TM	121	BcepSaruman_129	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74508.1	007849	SIG+TM	121	BcepSauron_128	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06690.1	007850	Cluster7707_1clades	121	BcepSaruman_277	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74658.1	007850	Cluster7707_1clades	121	BcepSauron_278	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97407.1	007851	Cluster7708_1clades	121	D6_0248	Aeromonas phage D6	GCA_007051205.2
QDH47215.1	007851	Cluster7708_1clades	121	LAh10_160	Aeromonas phage LAh10	GCA_006863975.1
QDJ97185.1	007852	Cluster7709_1clades	121	D6_0025	Aeromonas phage D6	GCA_007051205.2
QDH47216.1	007852	Cluster7709_1clades	121	LAh10_193	Aeromonas phage LAh10	GCA_006863975.1
QDJ96681.1	007853	DUF483	121	PS1_0170	Aeromonas phage PS1	GCA_007051165.2
QHJ86070.1	007853	DUF483	99	KKIINIFJ_00158	Pseudomonas phage PN05	GCA_009931935.1
QGH71996.1	007854	HTH	121	N1M2_133	Klebsiella phage N1M2	GCA_010092605.1
AEV89603.1	007854	HTH	118	OBP_166	Pseudomonas phage OBP	GCA_000896635.1
QGT54790.1	007855	AbiJ-NTD3	121	b23_0175	Synechococcus phage B23	GCA_009745195.1
QGT54420.1	007855	AbiJ-NTD3	121	b3_0176	Synechococcus phage B3	GCA_009745215.1
QNH80834.1	007856	SIG+TM	121	D6_0017	Aeromonas phage D6	GCA_007051205.2
QDH47219.1	007856	SIG+TM	120	LAh10_185	Aeromonas phage LAh10	GCA_006863975.1
prevph1000000034	007857	Cluster7714_1clades	122	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000026	007857	Cluster7714_1clades	122	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000061	007858	Cluster7715_1clades	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000047	007858	Cluster7715_1clades	122	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000175	007859	Cluster7716_1clades	122	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000138	007859	Cluster7716_1clades	122	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000716	007860	Cluster7717_1clades	88	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000485	007860	Cluster7717_1clades	122	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01568.1	007861	Cluster7718_1clades	120	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53191.1	007861	Cluster7718_1clades	120	65p183	Aeromonas virus 65	GCA_000893255.1
AGR48109.1	007862	Cluster7719_1clades	120	SmphiM12_477	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13655.1	007862	Cluster7719_1clades	120	PHIN3_392	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01111.1	007863	Cluster7720_1clades	116	AR9_g026	Bacillus phage AR9	GCA_001743835.1
ASU00033.1	007863	Cluster7720_1clades	120	PBI_PBS1_211	Bacillus virus PBS1	GCA_002601325.1
AFQ96596.1	007864	Cluster7721_1clades	82	G173_gp051	Erwinia phage phiEaH2	GCA_000902915.1
AXF51057.1	007864	Cluster7721_1clades	120	MLDJOKPK_00019	Salmonella phage SPAsTU	GCA_003183805.1
AXF51339.1	007865	Cluster7722_1clades	120	WELLINGTON_213	Erwinia phage Wellington	GCA_003344985.1
ANZ49566.1	007865	Cluster7722_1clades	107	KWAN_214	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXQ69284.1	007866	Cluster7723_1clades	120	CcrBL9_gp260c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69841.1	007866	Cluster7723_1clades	120	CcrSC_gp259c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69440.1	007867	Cluster7724_1clades	120	CcrBL9_gp416	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69991.1	007867	Cluster7724_1clades	67	CcrSC_gp409	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70422.1	007868	Cluster7725_1clades	120	HOU04_gp023	Synechococcus phage S-T4	GCA_003443335.1
AXQ70624.1	007868	Cluster7725_1clades	120	HOU04_gp023	Synechococcus phage S-T4	GCA_003443335.1
BBA65609.1	007869	NarQ	120	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65150.1	007869	NarQ	120	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90608.1	007870	Cluster7727_1clades	120	HYO65_gp216	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90914.1	007870	Cluster7727_1clades	120	-	Tenacibaculum phage PTm5	GCA_009730715.1
AEH03760.1	007871	Cluster7729_1clades	115	337	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02903.1	007871	Cluster7729_1clades	120	PSA21_377	Pseudomonas phage Psa21	GCA_004340405.1
QBX06510.1	007872	Cluster7730_1clades	120	BcepSaruman_097	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74476.1	007872	Cluster7730_1clades	120	BcepSauron_096	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06538.1	007873	SIG+TM+TM	120	BcepSaruman_125	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74504.1	007873	SIG+TM+TM	120	BcepSauron_124	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06722.1	007874	Cluster7732_1clades	120	BcepSaruman_309	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74690.1	007874	Cluster7732_1clades	120	BcepSauron_310	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06784.1	007875	Cluster7733_1clades	120	BcepSaruman_371	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74754.1	007875	Cluster7733_1clades	120	BcepSauron_374	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06847.1	007876	Cluster7734_1clades	96	BcepSaruman_434	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74816.1	007876	Cluster7734_1clades	120	BcepSauron_436	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06739.1	007877	Cluster7735_1clades	120	BcepSaruman_326	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74708.1	007877	Cluster7735_1clades	119	BcepSauron_328	Burkholderia phage BcepSauron	GCA_005394215.1
QBZ70723.1	007878	Cluster7736_1clades	120	pETSU_142	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89656.1	007878	Cluster7736_1clades	110	OBP_219	Pseudomonas phage OBP	GCA_000896635.1
QDJ97313.1	007879	Cluster7737_1clades	120	D6_0153	Aeromonas phage D6	GCA_007051205.2
QDH47217.1	007879	Cluster7737_1clades	120	LAh10_77	Aeromonas phage LAh10	GCA_006863975.1
QDJ97353.1	007880	Cluster7738_1clades	120	D6_0194	Aeromonas phage D6	GCA_007051205.2
QDH47218.1	007880	Cluster7738_1clades	120	LAh10_112	Aeromonas phage LAh10	GCA_006863975.1
QDJ96752.1	007881	Cluster7739_1clades	120	PS1_0241	Aeromonas phage PS1	GCA_007051165.2
QFR59385.1	007881	Cluster7739_1clades	120	PS2_0243	Aeromonas phage PS2	GCA_009388305.2
QGT54702.1	007882	Cluster7740_1clades	120	b23_0087	Synechococcus phage B23	GCA_009745195.1
QGT54332.1	007882	Cluster7740_1clades	120	b3_0088	Synechococcus phage B3	GCA_009745215.1
QGT54802.1	007883	Cluster7741_1clades	120	b23_0187	Synechococcus phage B23	GCA_009745195.1
QGT54432.1	007883	Cluster7741_1clades	120	b3_0188	Synechococcus phage B3	GCA_009745215.1
AYD81433.1	007884	Cluster7742_1clades	119	SEA_JUSTBECAUSE_278	Streptomyces phage JustBecause	GCA_003613775.1
QJD53839.1	007884	Cluster7742_1clades	120	SEA_KELA_279	Streptomyces phage Kela	GCA_012934305.1
SOK59197.1	007885	Cluster7743_1clades	120	g389	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58661.1	007885	Cluster7743_1clades	120	g384	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000174	007886	Cluster7744_1clades	121	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000136	007886	Cluster7744_1clades	114	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44531.1	007887	Cluster7745_1clades	119	PSSM2_153	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12439.1	007887	Cluster7745_1clades	119	PRTG_00290	Prochlorococcus phage P-SSM5	GCA_002991095.1
ABY63129.1	007888	Cluster7746_1clades	119	201phi2-1p303	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76928.1	007888	Cluster7746_1clades	119	PHABIO_297	Pseudomonas phage Phabio	GCA_002624965.1
AUE22826.1	007889	Cluster7747_1clades	119	Ah1_00308	Aeromonas phage Ah1	GCA_002957415.1
ADM79927.1	007889	Cluster7747_1clades	119	phiAS5_ORF0084	Aeromonas phage phiAS5	GCA_000887715.1
AFA44765.1	007890	Cluster7748_1clades	119	RaK2_00492	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXH72439.1	007890	Cluster7748_1clades	118	-	Myoviridae sp.	GCA_003657725.1
AFU88221.1	007891	Cluster7749_1clades	119	CcrColossus_gp351	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68898.1	007891	Cluster7749_1clades	119	CcrPW_gp359	Caulobacter phage CcrPW	GCA_003443275.1
AFU88246.1	007892	Cluster7750_1clades	119	CcrColossus_gp376	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68921.1	007892	Cluster7750_1clades	119	CcrPW_gp382c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01327.1	007893	Cluster7751_1clades	119	AR9_g243	Bacillus phage AR9	GCA_001743835.1
AST99956.1	007893	Cluster7751_1clades	119	PBI_PBS1_134	Bacillus virus PBS1	GCA_002601325.1
ABY63013.1	007894	Cluster7752_1clades	118	201phi2-1p183	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76796.1	007894	Cluster7752_1clades	119	PHABIO_165	Pseudomonas phage Phabio	GCA_002624965.1
ATA65536.1	007895	Cluster7753_1clades	119	2050HW_00201	Serratia phage 2050HW	GCA_002628125.1
QDB71300.1	007895	Cluster7753_1clades	119	CPT_Moabite_270	Serratia phage Moabite	GCA_006384735.1
AXQ69213.1	007896	SIG+TM	119	CcrBL9_gp189	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69767.1	007896	SIG+TM	119	CcrSC_gp185	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69164.1	007897	Cluster7755_1clades	118	CcrBL9_gp140c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69719.1	007897	Cluster7755_1clades	119	CcrSC_gp137c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69474.1	007898	Cluster7756_1clades	64	CcrBL9_gp450	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70023.1	007898	Cluster7756_1clades	119	CcrSC_gp441	Caulobacter phage CcrSC	GCA_003443315.1
BAS04799.2	007899	Cluster7757_1clades	119	AVU11_gp007	Ralstonia phage RSF1	GCA_001500875.1
BAQ02535.2	007899	Cluster7757_1clades	114	-	Ralstonia phage RSL2	GCA_001503055.1
BBI90412.1	007900	Cluster7759_1clades	119	HYO65_gp020	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90720.1	007900	Cluster7759_1clades	119	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90445.1	007901	Cluster7760_1clades	119	HYO65_gp053	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90753.1	007901	Cluster7760_1clades	119	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90478.1	007902	Cluster7761_1clades	119	HYO65_gp086	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90786.1	007902	Cluster7761_1clades	119	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06599.1	007903	Cluster7762_1clades	118	BcepSaruman_186	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74564.1	007903	Cluster7762_1clades	119	BcepSauron_184	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06646.1	007904	Cluster7763_1clades	119	BcepSaruman_233	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74615.1	007904	Cluster7763_1clades	119	BcepSauron_235	Burkholderia phage BcepSauron	GCA_005394215.1
QGH71998.1	007905	SIG+HNH	119	N1M2_135	Klebsiella phage N1M2	GCA_010092605.1
AEV89607.1	007905	SIG+HNH	117	OBP_170	Pseudomonas phage OBP	GCA_000896635.1
QGT54825.1	007906	Cluster7765_1clades	119	b23_0210	Synechococcus phage B23	GCA_009745195.1
QGT54455.1	007906	Cluster7765_1clades	119	b3_0212	Synechococcus phage B3	GCA_009745215.1
prevph1000000630	007907	Cluster7766_1clades	120	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000448	007907	Cluster7766_1clades	120	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000739	007908	Cluster7767_1clades	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000491	007908	Cluster7767_1clades	120	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000764	007909	Cluster7768_1clades	120	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000517	007909	Cluster7768_1clades	92	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01409.1	007910	Cluster7769_1clades	118	-	Aeromonas phage 65.2	GCA_002618145.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AAR90920.1	007910	Cluster7769_1clades	118	65p018	Aeromonas virus 65	GCA_000893255.1
ABY63204.1	007911	Cluster7770_1clades	118	201phi2-1p379	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77030.1	007911	Cluster7770_1clades	117	PHABIO_399	Pseudomonas phage Phabio	GCA_002624965.1
QAY01119.1	007912	Cluster7771_1clades	114	ASwh1_52	Aeromonas phage Aswh_1	GCA_004146945.1
ADQ53352.1	007912	Cluster7771_1clades	118	65p344	Aeromonas virus 65	GCA_000893255.1
AFQ96600.1	007913	Cluster7772_1clades	118	G173_gp055	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50577.1	007913	Cluster7772_1clades	118	STRATTON_152	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AMS01287.1	007914	Cluster7773_1clades	118	AR9_g203	Bacillus phage AR9	GCA_001743835.1
AST99915.1	007914	Cluster7773_1clades	118	PBI_PBS1_93	Bacillus virus PBS1	GCA_002601325.1
AXG67300.1	007915	Cluster7774_1clades	117	AD1_256	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
ARW58905.1	007915	Cluster7774_1clades	118	Y3_265	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AMS01091.1	007916	Cluster7775_1clades	89	AR9_g006	Bacillus phage AR9	GCA_001743835.1
ASU00013.1	007916	Cluster7775_1clades	118	PBI_PBS1_191	Bacillus virus PBS1	GCA_002601325.1
ATA65464.1	007917	Cluster7776_1clades	118	2050HW_00129	Serratia phage 2050HW	GCA_002628125.1
QDB71233.1	007917	Cluster7776_1clades	118	CPT_Moabite_203	Serratia phage Moabite	GCA_006384735.1
AXH72600.1	007918	Cluster7777_1clades	116	-	Myoviridae sp.	GCA_003657725.1
AXH72602.1	007918	Cluster7777_1clades	118	-	Myoviridae sp.	GCA_003657725.1
AXQ69373.1	007919	DUF4170	118	CcrBL9_gp349	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69933.1	007919	DUF4170	83	CcrSC_gp351	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69433.1	007920	Cluster7779_1clades	118	CcrBL9_gp409	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69985.1	007920	Cluster7779_1clades	118	CcrSC_gp403	Caulobacter phage CcrSC	GCA_003443315.1
AYD81337.1	007921	Cluster7780_1clades	118	SEA_JUSTBECAUSE_172	Streptomyces phage JustBecause	GCA_003613775.1
QJD53740.1	007921	Cluster7780_1clades	118	SEA_KELA_170	Streptomyces phage Kela	GCA_012934305.1
AYD81487.1	007922	Cluster7781_1clades	118	SEA_JUSTBECAUSE_332	Streptomyces phage JustBecause	GCA_003613775.1
QJD53890.1	007922	Cluster7781_1clades	118	SEA_KELA_330	Streptomyces phage Kela	GCA_012934305.1
BAS04801.2	007923	Cluster7782_1clades	70	AVU11_agp04	Ralstonia phage RSF1	GCA_001500875.1
BAQ02537.2	007923	Cluster7782_1clades	118	-	Ralstonia phage RSL2	GCA_001503055.1
BAS04941.1	007924	DUF1202	118	AVU11_gp149	Ralstonia phage RSF1	GCA_001500875.1
BAQ02665.2	007924	DUF1202	81	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19095.1	007925	Cluster7784_1clades	118	FDH28_gp121	Ralstonia phage RP12	GCA_002617345.1
BAW19381.1	007925	Cluster7784_1clades	118	-	Ralstonia phage RP31	GCA_002617365.1
BAW19111.1	007926	Cluster7785_1clades	118	FDH28_gp284	Ralstonia phage RP12	GCA_002617345.1
BAW19397.1	007926	Cluster7785_1clades	118	-	Ralstonia phage RP31	GCA_002617365.1
BAW19171.1	007927	Cluster7786_1clades	118	FDH28_gp224	Ralstonia phage RP12	GCA_002617345.1
BAW19457.1	007927	Cluster7786_1clades	118	-	Ralstonia phage RP31	GCA_002617365.1
BBA65231.1	007928	Cluster7787_1clades	118	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65690.1	007928	Cluster7787_1clades	118	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90611.1	007929	Cluster7788_1clades	67	HYO65_gp219	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90917.1	007929	Cluster7788_1clades	118	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06470.1	007930	Cluster7789_1clades	118	BcepSaruman_057	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74437.1	007930	Cluster7789_1clades	118	BcepSauron_057	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06474.1	007931	Cluster7790_1clades	118	BcepSaruman_061	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74441.1	007931	Cluster7790_1clades	118	BcepSauron_061	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06563.1	007932	Cluster7791_1clades	118	BcepSaruman_150	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74531.1	007932	Cluster7791_1clades	118	BcepSauron_151	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06811.1	007933	Cluster7792_1clades	117	BcepSaruman_398	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74780.1	007933	Cluster7792_1clades	118	BcepSauron_400	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06845.1	007934	Cluster7793_1clades	118	BcepSaruman_432	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74814.1	007934	Cluster7793_1clades	118	BcepSauron_434	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32489.1	007935	Cluster7794_1clades	118	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42061.1	007935	Cluster7794_1clades	118	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BBA65353.1	007936	Cluster7795_1clades	115	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96385.1	007936	Cluster7795_1clades	118	Xoosp13_199	Xanthomonas phage Xoo-sp13	GCA_013364725.1
prevph1000000170	007937	Cluster7796_1clades	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000132	007937	Cluster7796_1clades	119	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000504	007938	Cluster7797_1clades	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000381	007938	Cluster7797_1clades	119	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000858	007939	Cluster7798_1clades	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000596	007939	Cluster7798_1clades	119	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88172.1	007940	Cluster7799_1clades	117	CcrColossus_gp302	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68849.1	007940	Cluster7799_1clades	116	CcrPW_gp310	Caulobacter phage CcrPW	GCA_003443275.1
AMM43598.1	007941	TM	117	CBB_33	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44149.1	007941	TM	117	CBB_586	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ARW58922.1	007942	Cluster7801_1clades	111	Y3_282	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28746.1	007942	Cluster7801_1clades	117	YOLOSWAG_274	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
SBV38282.1	007943	DUF1890	109	BN7874_113	Phage NCTB	GCA_900092385.1
ARV77433.1	007943	DUF1890	117	NOXIFER_268	Pseudomonas phage Noxifer	GCA_002625005.1
ASU03773.1	007944	Cluster7803_1clades	117	JOAD_142	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03529.1	007944	Cluster7803_1clades	117	RISINGSUN_141	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXQ69070.1	007945	Cluster7804_1clades	117	CcrBL9_gp046c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69630.1	007945	Cluster7804_1clades	116	CcrSC_gp048c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69102.1	007946	Cluster7805_1clades	117	CcrBL9_gp078c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69657.1	007946	Cluster7805_1clades	112	CcrSC_gp075c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69417.1	007947	Cluster7806_1clades	117	CcrBL9_gp393	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69973.1	007947	Cluster7806_1clades	117	CcrSC_gp391	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69426.1	007948	Cluster7807_1clades	111	CcrBL9_gp402	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69980.1	007948	Cluster7807_1clades	117	CcrSC_gp398	Caulobacter phage CcrSC	GCA_003443315.1
AYD81206.1	007949	Cluster7808_1clades	117	SEA_JUSTBECAUSE_37	Streptomyces phage JustBecause	GCA_003613775.1
QJD53609.1	007949	Cluster7808_1clades	117	SEA_KELA_38	Streptomyces phage Kela	GCA_012934305.1
BBA65675.1	007950	Cluster7809_1clades	117	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65216.1	007950	Cluster7809_1clades	117	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06490.1	007951	Cluster7810_1clades	117	BcepSaruman_077	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74457.1	007951	Cluster7810_1clades	117	BcepSauron_077	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06494.1	007952	Cluster7811_1clades	117	BcepSaruman_081	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74461.1	007952	Cluster7811_1clades	117	BcepSauron_081	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06566.1	007953	Cluster7812_1clades	117	BcepSaruman_153	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74533.1	007953	Cluster7812_1clades	117	BcepSauron_153	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06812.1	007954	Cluster7813_1clades	117	BcepSaruman_399	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74781.1	007954	Cluster7813_1clades	117	BcepSauron_401	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06846.1	007955	Cluster7814_1clades	117	BcepSaruman_433	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74815.1	007955	Cluster7814_1clades	117	BcepSauron_435	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97183.1	007956	Cluster7815_1clades	117	D6_0023	Aeromonas phage D6	GCA_007051205.2
QDH47221.1	007956	Cluster7815_1clades	117	LAh10_191	Aeromonas phage LAh10	GCA_006863975.1
QDH83486.1	007957	Cluster7816_1clades	107	H1O15_gp320	Achromobacter phage Motura	GCA_006964305.1
QDH83487.1	007957	Cluster7816_1clades	117	H1O15_gp319	Achromobacter phage Motura	GCA_006964305.1
QGT54757.1	007958	Cluster7817_1clades	117	b23_0142	Synechococcus phage B23	GCA_009745195.1
QGT54387.1	007958	Cluster7817_1clades	117	b3_0143	Synechococcus phage B3	GCA_009745215.1
prevph1000000060	007959	Cluster7818_1clades	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000046	007959	Cluster7818_1clades	118	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000421	007960	Cluster7819_1clades	114	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000332	007960	Cluster7819_1clades	118	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000843	007961	Cluster7820_1clades	118	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000585	007961	Cluster7820_1clades	118	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03784.1	007962	SIG+TM	116	JOAD_131	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03540.1	007962	SIG+TM	116	RISINGSUN_130	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65481.1	007963	SIG+TM+TM	116	2050HW_00146	Serratia phage 2050HW	GCA_002628125.1
QDB71251.1	007963	SIG+TM+TM	95	CPT_Moabite_221	Serratia phage Moabite	GCA_006384735.1
ATA65485.1	007964	Cluster7823_1clades	116	2050HW_00150	Serratia phage 2050HW	GCA_002628125.1
QDB71255.1	007964	Cluster7823_1clades	116	CPT_Moabite_225	Serratia phage Moabite	GCA_006384735.1
ATA65554.1	007965	Cluster7824_1clades	116	2050HW_00219	Serratia phage 2050HW	GCA_002628125.1
QDB71319.1	007965	Cluster7824_1clades	116	CPT_Moabite_289	Serratia phage Moabite	GCA_006384735.1
ATA65613.1	007966	Cluster7825_1clades	116	2050HW_00278	Serratia phage 2050HW	GCA_002628125.1
QDB71042.1	007966	Cluster7825_1clades	116	CPT_Moabite_010	Serratia phage Moabite	GCA_006384735.1
BAW19083.1	007967	Cluster7826_1clades	116	FDH28_gp109	Ralstonia phage RP12	GCA_002617345.1
BAW19369.1	007967	Cluster7826_1clades	116	-	Ralstonia phage RP31	GCA_002617365.1
BAW19107.1	007968	Cluster7827_1clades	116	FDH28_gp288	Ralstonia phage RP12	GCA_002617345.1
BAW19393.1	007968	Cluster7827_1clades	116	-	Ralstonia phage RP31	GCA_002617365.1
BAW19147.1	007969	Cluster7828_1clades	116	FDH28_gp248	Ralstonia phage RP12	GCA_002617345.1
BAW19433.1	007969	Cluster7828_1clades	116	-	Ralstonia phage RP31	GCA_002617365.1
BAW19172.1	007970	Cluster7829_1clades	116	FDH28_gp223	Ralstonia phage RP12	GCA_002617345.1
BAW19458.1	007970	Cluster7829_1clades	116	-	Ralstonia phage RP31	GCA_002617365.1
BAW19190.1	007971	TM	116	FDH28_gp205	Ralstonia phage RP12	GCA_002617345.1
BAW19476.1	007971	TM	116	-	Ralstonia phage RP31	GCA_002617365.1
BBA65732.1	007972	Cluster7831_1clades	116	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65273.1	007972	Cluster7831_1clades	116	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65392.1	007973	Cluster7832_1clades	116	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96420.1	007973	Cluster7832_1clades	113	Xoosp13_234	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06610.1	007974	Cluster7834_1clades	116	BcepSaruman_197	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74576.1	007974	Cluster7834_1clades	116	BcepSauron_196	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06621.1	007975	TM	116	BcepSaruman_208	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74589.1	007975	TM	116	BcepSauron_209	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32473.1	007976	SIG+TM	116	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42045.1	007976	SIG+TM	116	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32483.1	007977	Cluster7837_1clades	116	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42055.1	007977	Cluster7837_1clades	116	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97172.1	007978	TM	116	D6_0013	Aeromonas phage D6	GCA_007051205.2
QDH47222.1	007978	TM	116	LAh10_181	Aeromonas phage LAh10	GCA_006863975.1
QDJ97178.1	007979	Cluster7839_1clades	116	D6_0018	Aeromonas phage D6	GCA_007051205.2
QDH47223.1	007979	Cluster7839_1clades	116	LAh10_186	Aeromonas phage LAh10	GCA_006863975.1
QDJ97201.1	007980	Cluster7840_1clades	116	D6_0041	Aeromonas phage D6	GCA_007051205.2
QDH47224.1	007980	Cluster7840_1clades	116	LAh10_207	Aeromonas phage LAh10	GCA_006863975.1
AIA64980.1	007981	Cluster7841_1clades	115	S13_183	Cronobacter phage S13	GCA_001503575.1
QHJ78955.1	007981	Cluster7841_1clades	116	-	Myoviridae sp.	GCA_012593985.1
prevph1000000342	007982	Cluster7842_1clades	117	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000271	007982	Cluster7842_1clades	117	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000367	007983	Cluster7843_1clades	117	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000293	007983	Cluster7843_1clades	117	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000493	007984	Cluster7844_1clades	117	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000374	007984	Cluster7844_1clades	117	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABY63133.1	007985	Cluster7845_1clades	115	201phi2-1p307	Pseudomonas phage 201phi2-1	GCA_000875305.1
QKE54550.1	007985	Cluster7845_1clades	106	ACSA002_2340	Salmonella phage vB_SalM_SA002	GCA_014131285.1
APU01774.1	007986	Cluster7846_1clades	115	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53417.1	007986	Cluster7846_1clades	115	65p410	Aeromonas virus 65	GCA_000893255.1
AFA44582.1	007987	TM+TM+TM	115	RaK2_00309	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44583.1	007987	TM+TM+TM	115	RaK2_00310	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFU88104.1	007988	FIS-HTH	115	CcrColossus_gp234	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68781.1	007988	FIS-HTH	100	CcrPW_gp242	Caulobacter phage CcrPW	GCA_003443275.1
AFU88212.1	007989	Cluster7849_1clades	115	CcrColossus_gp342	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68889.1	007989	Cluster7849_1clades	91	CcrPW_gp350	Caulobacter phage CcrPW	GCA_003443275.1
AQW88559.1	007990	Cluster7851_1clades	115	BF_0034	Serratia phage BF	GCA_002619745.1
SOK58834.1	007990	Cluster7851_1clades	115	g026	Yersinia phage fHe-Yen9-03	GCA_002990515.1
ASU03836.1	007991	SIG+PyocinS	115	JOAD_79	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03591.1	007991	SIG+PyocinS	115	RISINGSUN_79	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65618.1	007992	Cluster7853_1clades	115	2050HW_00283	Serratia phage 2050HW	GCA_002628125.1
QDB71046.1	007992	Cluster7853_1clades	115	CPT_Moabite_014	Serratia phage Moabite	GCA_006384735.1
QBZ71937.1	007993	Cluster7854_1clades	115	SEA_KRADAL_38	Streptomyces phage Kradal	GCA_004799925.1
AXH66199.1	007993	Cluster7854_1clades	115	SEA_SATIS_38	Streptomyces phage Satis	GCA_003366315.1
QBZ72215.1	007994	Cluster7855_1clades	115	SEA_KRADAL_329	Streptomyces phage Kradal	GCA_004799925.1
AXH66478.1	007994	Cluster7855_1clades	115	SEA_SATIS_329	Streptomyces phage Satis	GCA_003366315.1
AUZ94827.1	007995	SIG+Smr	109	FDI40_gp015	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72911.1	007995	SIG+Smr	115	-	Myoviridae sp.	GCA_003657725.1
AXQ68212.1	007996	Cluster7857_1clades	115	CcrBL10_gp008	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68530.1	007996	Cluster7857_1clades	115	CcrBL10_gp326	Caulobacter phage CcrBL10	GCA_003443255.1
BAS04933.1	007997	Cluster7858_1clades	115	AVU11_gp141	Ralstonia phage RSF1	GCA_001500875.1
BAQ02658.2	007997	Cluster7858_1clades	108	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19073.1	007998	Cluster7859_1clades	115	FDH28_gp099	Ralstonia phage RP12	GCA_002617345.1
BAW19358.1	007998	Cluster7859_1clades	115	-	Ralstonia phage RP31	GCA_002617365.1
BAW19198.1	007999	Cluster7860_1clades	115	FDH28_gp197	Ralstonia phage RP12	GCA_002617345.1
BAW19484.1	007999	Cluster7860_1clades	115	-	Ralstonia phage RP31	GCA_002617365.1
BBA65737.1	008000	Cluster7861_1clades	115	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65278.1	008000	Cluster7861_1clades	115	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90578.1	008001	Cluster7862_1clades	79	HYO65_gp186	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90886.1	008001	Cluster7862_1clades	115	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06598.1	008002	Cluster7863_1clades	115	BcepSaruman_185	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74563.1	008002	Cluster7863_1clades	115	BcepSauron_183	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32463.1	008003	Cluster7864_1clades	115	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42035.1	008003	Cluster7864_1clades	115	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97175.1	008004	Cluster7865_1clades	89	D6_0015	Aeromonas phage D6	GCA_007051205.2
QDH47225.1	008004	Cluster7865_1clades	115	LAh10_183	Aeromonas phage LAh10	GCA_006863975.1
BBA65418.1	008005	Cluster7866_1clades	109	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96441.1	008005	Cluster7866_1clades	115	Xoosp13_255	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54826.1	008006	Cluster7867_1clades	115	b23_0211	Synechococcus phage B23	GCA_009745195.1
QGT54456.1	008006	Cluster7867_1clades	115	b3_0213	Synechococcus phage B3	GCA_009745215.1
prevph1000000054	008007	Cluster7868_1clades	116	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000042	008007	Cluster7868_1clades	116	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000511	008008	SIG+TM	116	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000386	008008	SIG+TM	116	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83804.1	008009	Cluster7870_1clades	114	0305phi8-36p104	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83662.1	008009	Cluster7870_1clades	114	0305phi8-36p104R	Bacillus phage 0305phi8-36	GCA_000871045.1
AFU88078.1	008010	Cluster7871_1clades	114	CcrColossus_gp208	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68755.1	008010	Cluster7871_1clades	114	CcrPW_gp216c	Caulobacter phage CcrPW	GCA_003443275.1
AIA64915.1	008011	Cluster7872_1clades	114	S13_116	Cronobacter phage S13	GCA_001503575.1
QHJ79012.1	008011	Cluster7872_1clades	104	-	Myoviridae sp.	GCA_012593985.1
AIA64952.1	008012	Cluster7873_1clades	114	S13_153	Cronobacter phage S13	GCA_001503575.1
QHJ78994.1	008012	Cluster7873_1clades	113	-	Myoviridae sp.	GCA_012593985.1
AIA65000.1	008013	Cluster7874_1clades	114	S13_203	Cronobacter phage S13	GCA_001503575.1
QHJ78931.1	008013	Cluster7874_1clades	113	-	Myoviridae sp.	GCA_012593985.1
AFC21809.1	008014	Cluster7875_1clades	111	GAP32_359	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43932.1	008014	Cluster7875_1clades	114	CBB_369	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01192.1	008015	Cluster7876_1clades	114	AR9_g108	Bacillus phage AR9	GCA_001743835.1
ASU00126.1	008015	Cluster7876_1clades	114	PBI_PBS1_304	Bacillus virus PBS1	GCA_002601325.1
AXF51200.1	008016	Cluster7877_1clades	114	WELLINGTON_70	Erwinia phage Wellington	GCA_003344985.1
ANZ49422.1	008016	Cluster7877_1clades	114	KWAN_70	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03797.1	008017	Cluster7878_1clades	114	JOAD_118	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03552.1	008017	Cluster7878_1clades	114	RISINGSUN_118	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03893.1	008018	Cluster7879_1clades	114	JOAD_22	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03648.1	008018	Cluster7879_1clades	114	RISINGSUN_22	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03894.1	008019	Cluster7880_1clades	114	JOAD_21	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03649.1	008019	Cluster7880_1clades	114	RISINGSUN_21	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXQ69374.1	008020	Cluster7881_1clades	114	CcrBL9_gp350	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69934.1	008020	Cluster7881_1clades	114	CcrSC_gp352	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69451.1	008021	Cluster7882_1clades	114	CcrBL9_gp427	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70001.1	008021	Cluster7882_1clades	114	CcrSC_gp419	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69316.1	008022	Cluster7883_1clades	68	CcrBL9_gp292	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69876.1	008022	Cluster7883_1clades	114	CcrSC_gp294	Caulobacter phage CcrSC	GCA_003443315.1
BAW19156.1	008023	Cluster7884_1clades	114	FDH28_gp239	Ralstonia phage RP12	GCA_002617345.1
BAW19442.1	008023	Cluster7884_1clades	114	-	Ralstonia phage RP31	GCA_002617365.1
BAW19250.1	008024	Cluster7885_1clades	114	FDH28_gp145	Ralstonia phage RP12	GCA_002617345.1
BAW19536.1	008024	Cluster7885_1clades	114	-	Ralstonia phage RP31	GCA_002617365.1
BBA65164.1	008025	pEK499_p136	114	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65623.1	008025	pEK499_p136	114	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65281.1	008026	SIG+TM+TM	114	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65740.1	008026	SIG+TM+TM	114	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06481.1	008027	Cluster7888_1clades	114	BcepSaruman_068	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74448.1	008027	Cluster7888_1clades	114	BcepSauron_068	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06800.1	008028	Cluster7889_1clades	114	BcepSaruman_387	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74769.1	008028	Cluster7889_1clades	114	BcepSauron_389	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06801.1	008029	Cluster7890_1clades	114	BcepSaruman_388	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74770.1	008029	Cluster7890_1clades	114	BcepSauron_390	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32349.1	008030	Cluster7891_1clades	114	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41923.1	008030	Cluster7891_1clades	114	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32472.1	008031	Cluster7892_1clades	114	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42044.1	008031	Cluster7892_1clades	114	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97205.1	008032	Cluster7893_1clades	87	D6_0045	Aeromonas phage D6	GCA_007051205.2
QDH47226.1	008032	Cluster7893_1clades	114	LAh10_212	Aeromonas phage LAh10	GCA_006863975.1
QDH83430.1	008033	Cluster7894_1clades	114	H1O15_gp022	Achromobacter phage Motura	GCA_006964305.1
QCG76040.1	008033	Cluster7894_1clades	101	EST35_0158	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QDJ96690.1	008034	Cluster7895_1clades	114	PS1_0179	Aeromonas phage PS1	GCA_007051165.2
QFR59323.1	008034	Cluster7895_1clades	114	PS2_0181	Aeromonas phage PS2	GCA_009388305.2
QGT54740.1	008035	Cluster7896_1clades	114	b23_0125	Synechococcus phage B23	GCA_009745195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54370.1	008035	Cluster7896_1clades	114	b3_0126	Synechococcus phage B3	GCA_009745215.1
QIG58048.1	008036	Cluster7897_1clades	114	SEA_PAULODIABOLI_364	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57747.1	008036	Cluster7897_1clades	114	SEA_PAULODIABOLI_9	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000732	008037	Cluster7898_1clades	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000733	008037	Cluster7898_1clades	115	-	Prevotella_phage_Lak-B8	GCA_004379655.1
APU01644.1	008038	Cluster7899_1clades	113	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53271.1	008038	Cluster7899_1clades	113	65p263	Aeromonas virus 65	GCA_000893255.1
AFC21844.1	008039	Cluster7900_1clades	113	GAP32_392	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43964.1	008039	Cluster7900_1clades	113	CBB_401	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU88041.1	008040	Cluster7901_1clades	113	CcrColossus_gp171	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68718.1	008040	Cluster7901_1clades	113	CcrPW_gp179c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01353.1	008041	Cluster7902_1clades	113	AR9_g269	Bacillus phage AR9	GCA_001743835.1
AST99982.1	008041	Cluster7902_1clades	113	PBI_PBS1_161	Bacillus virus PBS1	GCA_002601325.1
AXF51213.1	008042	Cluster7903_1clades	113	WELLINGTON_83	Erwinia phage Wellington	GCA_003344985.1
ANZ49435.1	008042	Cluster7903_1clades	113	KWAN_83	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65537.1	008043	Cluster7904_1clades	113	2050HW_00202	Serratia phage 2050HW	GCA_002628125.1
QDB71302.1	008043	Cluster7904_1clades	113	CPT_Moabite_272	Serratia phage Moabite	GCA_006384735.1
ATA65557.1	008044	Cluster7905_1clades	113	2050HW_00222	Serratia phage 2050HW	GCA_002628125.1
QDB71322.1	008044	Cluster7905_1clades	113	CPT_Moabite_292	Serratia phage Moabite	GCA_006384735.1
AXG67338.1	008045	SIG+TM	71	AD1_294	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08620.1	008045	SIG+TM	113	Alexandra_311	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXH72678.1	008046	Cluster7907_1clades	113	-	Myoviridae sp.	GCA_003657725.1
QDJ96223.1	008046	Cluster7907_1clades	101	Xoosp13_36	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AXQ69180.1	008047	SIG+TM	113	CcrBL9_gp156	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69733.1	008047	SIG+TM	113	CcrSC_gp151	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69270.1	008048	Cluster7909_1clades	113	CcrBL9_gp246c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69826.1	008048	Cluster7909_1clades	113	CcrSC_gp244c	Caulobacter phage CcrSC	GCA_003443315.1
AYD81242.1	008049	Cluster7910_1clades	113	SEA_JUSTBECAUSE_73	Streptomyces phage JustBecause	GCA_003613775.1
QJD53645.1	008049	Cluster7910_1clades	113	SEA_KELA_74	Streptomyces phage Kela	GCA_012934305.1
BBI90553.1	008050	Cluster7911_1clades	113	HYO65_gp161	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90861.1	008050	Cluster7911_1clades	113	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90639.1	008051	Cluster7912_1clades	113	HYO65_gp247	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90946.1	008051	Cluster7912_1clades	113	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06644.1	008052	Cluster7913_1clades	113	BcepSaruman_231	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74613.1	008052	Cluster7913_1clades	113	BcepSauron_233	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06724.1	008053	Cluster7914_1clades	113	BcepSaruman_311	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74692.1	008053	Cluster7914_1clades	113	BcepSauron_312	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06570.1	008054	Cluster7915_1clades	113	BcepSaruman_157	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74537.1	008054	Cluster7915_1clades	89	BcepSauron_157	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32469.1	008055	Cluster7916_1clades	113	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42041.1	008055	Cluster7916_1clades	113	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QIG57758.1	008056	Cluster7917_1clades	113	SEA_PAULODIABOLI_21	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58059.1	008056	Cluster7917_1clades	113	SEA_PAULODIABOLI_376	Microbacterium phage PauloDiaboli	GCA_011067425.1
QNH80852.1	008057	SIG+TM+TM	113	D6_0198	Aeromonas phage D6	GCA_007051205.2
QDH47233.1	008057	SIG+TM+TM	102	LAh10_116	Aeromonas phage LAh10	GCA_006863975.1
SOK58818.1	008058	Cluster7919_1clades	113	g010	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58286.1	008058	Cluster7919_1clades	113	g009	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000350	008059	Cluster7920_1clades	101	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000276	008059	Cluster7920_1clades	114	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000407	008060	Cluster7921_1clades	114	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000323	008060	Cluster7921_1clades	114	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01693.1	008061	Cluster7922_1clades	112	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53331.1	008061	Cluster7922_1clades	112	65p323	Aeromonas virus 65	GCA_000893255.1
QGH72017.1	008062	Cluster7923_1clades	111	N1M2_154	Klebsiella phage N1M2	GCA_010092605.1
AEV89631.1	008062	Cluster7923_1clades	112	OBP_194	Pseudomonas phage OBP	GCA_000896635.1
AFU87913.1	008063	Cluster7924_1clades	112	CcrColossus_gp043	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68585.1	008063	Cluster7924_1clades	106	CcrPW_gp046	Caulobacter phage CcrPW	GCA_003443275.1
AFU88157.1	008064	Cluster7925_1clades	112	CcrColossus_gp287	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68832.1	008064	Cluster7925_1clades	112	CcrPW_gp293	Caulobacter phage CcrPW	GCA_003443275.1
AFU88266.1	008065	Cluster7926_1clades	112	CcrColossus_gp396	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68940.1	008065	Cluster7926_1clades	112	CcrPW_gp401	Caulobacter phage CcrPW	GCA_003443275.1
AXF51284.1	008066	Cluster7927_1clades	112	WELLINGTON_155	Erwinia phage Wellington	GCA_003344985.1
ANZ49508.1	008066	Cluster7927_1clades	112	KWAN_156	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03756.1	008067	TM	112	JOAD_159	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03512.1	008067	TM	112	RISINGSUN_158	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AFU87941.1	008068	Cluster7929_1clades	109	CcrColossus_gp071	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68613.1	008068	Cluster7929_1clades	112	CcrPW_gp074	Caulobacter phage CcrPW	GCA_003443275.1
AFU88295.1	008069	Cluster7930_1clades	111	CcrColossus_gp425	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68971.1	008069	Cluster7930_1clades	112	CcrPW_gp432c	Caulobacter phage CcrPW	GCA_003443275.1
BAS04888.1	008070	Cluster7931_1clades	112	AVU11_gp096	Ralstonia phage RSF1	GCA_001500875.1
BAQ02615.1	008070	Cluster7931_1clades	112	AVU38_gp087	Ralstonia phage RSL2	GCA_001503055.1
BAW19058.1	008071	Cluster7932_1clades	112	FDH28_gp084	Ralstonia phage RP12	GCA_002617345.1
BAW19343.1	008071	Cluster7932_1clades	112	-	Ralstonia phage RP31	GCA_002617365.1
QBX06619.1	008072	Cluster7933_1clades	112	BcepSaruman_206	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74587.1	008072	Cluster7933_1clades	112	BcepSauron_207	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32431.1	008073	Cluster7934_1clades	112	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42002.1	008073	Cluster7934_1clades	112	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32452.1	008074	Cluster7935_1clades	112	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42024.1	008074	Cluster7935_1clades	112	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ97404.1	008075	Cluster7936_1clades	112	D6_0245	Aeromonas phage D6	GCA_007051205.2
QDH47227.1	008075	Cluster7936_1clades	112	LAh10_158	Aeromonas phage LAh10	GCA_006863975.1
QDJ96784.1	008076	Cluster7937_1clades	112	PS1_0025	Aeromonas phage PS1	GCA_007051165.2
QFR59415.1	008076	Cluster7937_1clades	112	PS2_0024	Aeromonas phage PS2	GCA_009388305.2
QGT54832.1	008077	Cluster7938_1clades	112	b23_0217	Synechococcus phage B23	GCA_009745195.1
QGT54462.1	008077	Cluster7938_1clades	112	b3_0219	Synechococcus phage B3	GCA_009745215.1
QIG65999.1	008078	Cluster7939_1clades	112	phiOC_p357	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QHJ86105.1	008078	Cluster7939_1clades	108	KKIINIFJ_00194	Pseudomonas phage PN05	GCA_009931935.1
SOK59205.1	008079	Cluster7940_1clades	112	g397	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58670.1	008079	Cluster7940_1clades	112	g393	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AFU88066.1	008080	Cluster7942_1clades	111	CcrColossus_gp196	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68743.1	008080	Cluster7942_1clades	71	CcrPW_gp204c	Caulobacter phage CcrPW	GCA_003443275.1
AIA64868.1	008081	HIN-HTH	111	S13_069	Cronobacter phage S13	GCA_001503575.1
QHJ79071.1	008081	HIN-HTH	104	-	Myoviridae sp.	GCA_012593985.1
AMM43580.1	008082	Cluster7944_1clades	111	CBB_15	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44131.1	008082	Cluster7944_1clades	111	CBB_568	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01329.1	008083	Cluster7945_1clades	111	AR9_g245	Bacillus phage AR9	GCA_001743835.1
AST99958.1	008083	Cluster7945_1clades	111	PBI_PBS1_137	Bacillus virus PBS1	GCA_002601325.1
AMS01350.1	008084	Cluster7946_1clades	111	AR9_g266	Bacillus phage AR9	GCA_001743835.1
AST99979.1	008084	Cluster7946_1clades	111	PBI_PBS1_158	Bacillus virus PBS1	GCA_002601325.1
ATA65574.1	008085	SIG+TM	111	2050HW_00239	Serratia phage 2050HW	GCA_002628125.1
QDB71339.1	008085	SIG+TM	111	CPT_Moabite_309	Serratia phage Moabite	GCA_006384735.1
ATI17248.1	008086	Cluster7948_1clades	111	-	Aeromonas phage AS-szw	GCA_002743635.1
QAX97691.1	008086	Cluster7948_1clades	111	ASswx1_45	Aeromonas phage Asswx_1	GCA_004146865.1
AXG67106.1	008087	Cluster7949_1clades	108	AD1_062	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08342.1	008087	Cluster7949_1clades	111	Alexandra_62	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72153.1	008088	Cluster7950_1clades	111	SEA_KRADAL_267	Streptomyces phage Kradal	GCA_004799925.1
AXH66416.1	008088	Cluster7950_1clades	111	SEA_SATIS_267	Streptomyces phage Satis	GCA_003366315.1
BAW19082.1	008089	Cluster7951_1clades	109	FDH28_gp108	Ralstonia phage RP12	GCA_002617345.1
BAW19368.1	008089	Cluster7951_1clades	111	-	Ralstonia phage RP31	GCA_002617365.1
BBI90425.1	008090	Cluster7952_1clades	110	HYO65_gp033	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90732.1	008090	Cluster7952_1clades	111	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06627.1	008091	Cluster7953_1clades	111	BcepSaruman_214	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74595.1	008091	Cluster7953_1clades	111	BcepSauron_215	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06806.1	008092	Cluster7954_1clades	111	BcepSaruman_393	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74775.1	008092	Cluster7954_1clades	111	BcepSauron_395	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32471.1	008093	Cluster7955_1clades	111	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42043.1	008093	Cluster7955_1clades	111	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BBA65365.1	008094	Cluster7956_1clades	105	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96393.1	008094	Cluster7956_1clades	111	Xoosp13_207	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65367.1	008095	Cluster7957_1clades	109	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96395.1	008095	Cluster7957_1clades	111	Xoosp13_209	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54859.1	008096	Cluster7958_1clades	111	b23_0245	Synechococcus phage B23	GCA_009745195.1
QGT54493.1	008096	Cluster7958_1clades	111	b3_0251	Synechococcus phage B3	GCA_009745215.1
AIA64846.1	008097	Cluster7960_1clades	108	S13_047	Cronobacter phage S13	GCA_001503575.1
QHJ78817.1	008097	Cluster7960_1clades	111	-	Myoviridae sp.	GCA_012593985.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000430	008098	Cluster7961_1clades	112	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000342	008098	Cluster7961_1clades	112	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000011	008099	Cluster7962_1clades	112	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000283	008099	Cluster7962_1clades	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AXQ68513.1	008100	Cluster7963_1clades	110	CcrBL10_gp309	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86802.1	008100	Cluster7963_1clades	110	CcrRogue_gp320	Caulobacter virus Rogue	GCA_000900555.1
AKF12679.1	008101	Cluster7964_1clades	110	PHIM7_133	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13411.1	008101	Cluster7964_1clades	110	PHIN3_148	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01168.1	008102	Cluster7965_1clades	110	AR9_g084	Bacillus phage AR9	GCA_001743835.1
ASU00099.1	008102	Cluster7965_1clades	110	PBI_PBS1_277	Bacillus virus PBS1	GCA_002601325.1
AMS01373.1	008103	Cluster7966_1clades	110	AR9_g289	Bacillus phage AR9	GCA_001743835.1
ASU00004.1	008103	Cluster7966_1clades	110	PBI_PBS1_182	Bacillus virus PBS1	GCA_002601325.1
AND75261.1	008104	MNS	110	ME3_100	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75259.1	008104	MNS	97	ME3_98	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
ATA65512.1	008105	Cluster7968_1clades	110	2050HW_00177	Serratia phage 2050HW	GCA_002628125.1
QDB71280.1	008105	Cluster7968_1clades	110	CPT_Moabite_250	Serratia phage Moabite	GCA_006384735.1
ATA65610.1	008106	Cluster7969_1clades	110	2050HW_00275	Serratia phage 2050HW	GCA_002628125.1
QDB71039.1	008106	Cluster7969_1clades	110	CPT_Moabite_007	Serratia phage Moabite	GCA_006384735.1
AXG67240.1	008107	Cluster7970_1clades	105	AD1_196	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08470.1	008107	Cluster7970_1clades	110	Alexandra_206	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72217.1	008108	Cluster7971_1clades	110	SEA_KRADAL_331	Streptomyces phage Kradal	GCA_004799925.1
AXH66480.1	008108	Cluster7971_1clades	110	SEA_SATIS_331	Streptomyces phage Satis	GCA_003366315.1
AXQ69489.1	008109	Cluster7972_1clades	110	CcrBL9_gp465	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70037.1	008109	Cluster7972_1clades	75	CcrSC_gp455	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69097.1	008110	Cluster7973_1clades	107	CcrBL9_gp073c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69653.1	008110	Cluster7973_1clades	110	CcrSC_gp071c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69383.1	008111	D6	91	CcrBL9_gp359	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69943.1	008111	D6	110	CcrSC_gp361	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69462.1	008112	Cluster7975_1clades	108	CcrBL9_gp438	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70011.1	008112	Cluster7975_1clades	110	CcrSC_gp429	Caulobacter phage CcrSC	GCA_003443315.1
BAS04922.1	008113	Cluster7976_1clades	110	AVU11_gp130	Ralstonia phage RSF1	GCA_001500875.1
BAQ02650.1	008113	Cluster7976_1clades	104	AVU38_gp122	Ralstonia phage RSL2	GCA_001503055.1
BAW19087.1	008114	Cluster7977_1clades	110	FDH28_gp113	Ralstonia phage RP12	GCA_002617345.1
BAW19373.1	008114	Cluster7977_1clades	110	-	Ralstonia phage RP31	GCA_002617365.1
QBX06822.1	008115	Cluster7978_1clades	110	BcepSaruman_409	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74791.1	008115	Cluster7978_1clades	110	BcepSauron_411	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06728.1	008116	Cluster7979_1clades	110	BcepSaruman_315	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74697.1	008116	Cluster7979_1clades	75	BcepSauron_317	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54683.1	008117	Cluster7980_1clades	110	b23_0065	Synechococcus phage B23	GCA_009745195.1
QGT54313.1	008117	Cluster7980_1clades	110	b3_0065	Synechococcus phage B3	GCA_009745215.1
QIG57760.1	008118	Cluster7981_1clades	110	SEA_PAULODIABOLI_24	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58061.1	008118	Cluster7981_1clades	110	SEA_PAULODIABOLI_379	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58076.1	008119	Cluster7982_1clades	110	SEA_PAULODIABOLI_395	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57775.1	008119	Cluster7982_1clades	110	SEA_PAULODIABOLI_40	Microbacterium phage PauloDiaboli	GCA_011067425.1
SBV38232.1	008120	Cluster7983_1clades	110	BN7874_063	Phage NCTB	GCA_900092385.1
AFH14564.1	008120	Cluster7983_1clades	86	Lu11_0033	Pseudomonas phage Lu11	GCA_000897175.1
AFU88225.1	008121	Cluster7984_1clades	109	CcrColossus_gp355	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68902.1	008121	Cluster7984_1clades	109	CcrPW_gp363	Caulobacter phage CcrPW	GCA_003443275.1
AIA64918.1	008122	Cluster7985_1clades	109	S13_119	Cronobacter phage S13	GCA_001503575.1
QHJ79025.1	008122	Cluster7985_1clades	94	-	Myoviridae sp.	GCA_012593985.1
AMS01252.1	008123	Cluster7986_1clades	109	AR9_g168	Bacillus phage AR9	GCA_001743835.1
AST99878.1	008123	Cluster7986_1clades	109	PBI_PBS1_56	Bacillus virus PBS1	GCA_002601325.1
AXF51311.1	008124	TM	109	WELLINGTON_183	Erwinia phage Wellington	GCA_003344985.1
ANZ49536.1	008124	TM	109	KWAN_184	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03782.1	008125	Cluster7988_1clades	109	JOAD_133	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03538.1	008125	Cluster7988_1clades	109	RISINGSUN_132	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65542.1	008126	SIG+TM+TM	109	2050HW_00207	Serratia phage 2050HW	GCA_002628125.1
QDB71307.1	008126	SIG+TM+TM	109	CPT_Moabite_277	Serratia phage Moabite	GCA_006384735.1
AUZ95204.1	008127	Cluster7990_1clades	107	FDI40_gp445	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95207.1	008127	Cluster7990_1clades	109	FDI40_gp448	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69137.1	008128	Cluster7991_1clades	109	CcrBL9_gp113	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69691.1	008128	Cluster7991_1clades	109	CcrSC_gp109	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69304.1	008129	Cluster7992_1clades	109	CcrBL9_gp280	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69863.1	008129	Cluster7992_1clades	90	CcrSC_gp281	Caulobacter phage CcrSC	GCA_003443315.1
AYD81468.1	008130	Cluster7993_1clades	109	SEA_JUSTBECAUSE_313	Streptomyces phage JustBecause	GCA_003613775.1
QJD53871.1	008130	Cluster7993_1clades	109	SEA_KELA_311	Streptomyces phage Kela	GCA_012934305.1
BBA65388.1	008131	Cluster7994_1clades	109	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96416.1	008131	Cluster7994_1clades	104	Xoosp13_230	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90443.1	008132	Cluster7995_1clades	109	HYO65_gp051	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90751.1	008132	Cluster7995_1clades	109	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90519.1	008133	Cluster7996_1clades	109	HYO65_gp127	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90827.1	008133	Cluster7996_1clades	109	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06485.1	008134	Cluster7997_1clades	109	BcepSaruman_072	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74452.1	008134	Cluster7997_1clades	109	BcepSauron_072	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06765.1	008135	Cluster7998_1clades	103	BcepSaruman_352	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74735.1	008135	Cluster7998_1clades	109	BcepSauron_355	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06789.1	008136	Cluster7999_1clades	93	BcepSaruman_376	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74759.1	008136	Cluster7999_1clades	109	BcepSauron_379	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06834.1	008137	Cluster8000_1clades	109	BcepSaruman_421	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74803.1	008137	Cluster8000_1clades	109	BcepSauron_423	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32271.1	008138	Cluster8001_1clades	109	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41845.1	008138	Cluster8001_1clades	109	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54800.1	008139	Cluster8002_1clades	109	b23_0185	Synechococcus phage B23	GCA_009745195.1
QGT54430.1	008139	Cluster8002_1clades	109	b3_0186	Synechococcus phage B3	GCA_009745215.1
prevph1000000838	008140	Mononeg_RNA_pol	110	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000580	008140	Mononeg_RNA_pol	110	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS06085.1	008141	Cluster8004_1clades	108	ABCD_0058	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78581.1	008141	Cluster8004_1clades	108	RB43ORF059w	Escherichia virus RB43	GCA_000863505.1
QGH71882.1	008142	Cluster8005_1clades	108	N1M2_19	Klebsiella phage N1M2	GCA_010092605.1
AEV89475.1	008142	Cluster8005_1clades	108	OBP_038	Pseudomonas phage OBP	GCA_000896635.1
AIA64833.1	008143	Cluster8006_1clades	108	S13_034	Cronobacter phage S13	GCA_001503575.1
QHJ78829.1	008143	Cluster8006_1clades	89	-	Myoviridae sp.	GCA_012593985.1
AMS01193.1	008144	SIG+NUDE_C	108	AR9_g109	Bacillus phage AR9	GCA_001743835.1
ASU00127.1	008144	SIG+NUDE_C	108	PBI_PBS1_305	Bacillus virus PBS1	GCA_002601325.1
AMS01339.1	008145	Cluster8008_1clades	108	AR9_g255	Bacillus phage AR9	GCA_001743835.1
AST99969.1	008145	Cluster8008_1clades	108	PBI_PBS1_148	Bacillus virus PBS1	GCA_002601325.1
ABY62935.1	008146	Cluster8009_1clades	101	201phi2-1p102	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76711.1	008146	Cluster8009_1clades	108	PHABIO_80	Pseudomonas phage Phabio	GCA_002624965.1
AXF51278.1	008147	Cluster8010_1clades	108	WELLINGTON_149	Erwinia phage Wellington	GCA_003344985.1
ANZ49501.1	008147	Cluster8010_1clades	107	KWAN_149	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QBZ72093.1	008148	Cluster8011_1clades	108	SEA_KRADAL_207	Streptomyces phage Kradal	GCA_004799925.1
AXH66354.1	008148	Cluster8011_1clades	108	SEA_SATIS_205	Streptomyces phage Satis	GCA_003366315.1
AXQ69268.1	008149	Cluster8012_1clades	108	CcrBL9_gp244c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69824.1	008149	Cluster8012_1clades	100	CcrSC_gp242c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69332.1	008150	Cluster8013_1clades	108	CcrBL9_gp308	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69892.1	008150	Cluster8013_1clades	108	CcrSC_gp310	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69506.1	008151	SIG+TM	108	CcrBL9_gp482	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70055.1	008151	SIG+TM	105	CcrSC_gp473	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69495.1	008152	SIG+UvrD_C_2	107	CcrBL9_gp471	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70043.1	008152	SIG+UvrD_C_2	108	CcrSC_gp461	Caulobacter phage CcrSC	GCA_003443315.1
BAS04963.1	008153	Cluster8016_1clades	98	AVU11_gp171	Ralstonia phage RSF1	GCA_001500875.1
BAQ02688.1	008153	Cluster8016_1clades	108	AVU38_gp160	Ralstonia phage RSL2	GCA_001503055.1
BAW19085.1	008154	Cluster8017_1clades	108	FDH28_gp111	Ralstonia phage RP12	GCA_002617345.1
BAW19371.1	008154	Cluster8017_1clades	108	-	Ralstonia phage RP31	GCA_002617365.1
BAW19182.1	008155	Cluster8018_1clades	108	FDH28_gp213	Ralstonia phage RP12	GCA_002617345.1
BAW19468.1	008155	Cluster8018_1clades	108	-	Ralstonia phage RP31	GCA_002617365.1
BBA65492.1	008156	Cluster8019_1clades	108	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96500.1	008156	Cluster8019_1clades	106	Xoosp13_314	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90536.1	008157	Cluster8020_1clades	88	HYO65_gp144	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90844.1	008157	Cluster8020_1clades	108	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06814.1	008158	Cluster8021_1clades	108	BcepSaruman_401	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74783.1	008158	Cluster8021_1clades	108	BcepSauron_403	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06818.1	008159	Cluster8022_1clades	108	BcepSaruman_405	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74787.1	008159	Cluster8022_1clades	108	BcepSauron_407	Burkholderia phage BcepSauron	GCA_005394215.1
QCW22872.1	008160	Cluster8023_1clades	108	-	Synechococcus phage S-B05	GCA_006083695.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDH50486.1	008160	Cluster8023_1clades	107	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54857.1	008161	Cluster8024_1clades	108	b23_0243	Synechococcus phage B23	GCA_009745195.1
QGT54491.1	008161	Cluster8024_1clades	108	b3_0249	Synechococcus phage B3	GCA_009745215.1
AMM43701.1	008162	Cluster8025_1clades	106	CBB_136	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK58403.1	008162	Cluster8025_1clades	108	g126	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000432	008163	Cluster8026_1clades	109	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000344	008163	Cluster8026_1clades	109	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000788	008164	Cluster8027_1clades	87	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000536	008164	Cluster8027_1clades	109	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88137.1	008165	Cluster8028_1clades	107	CcrColossus_gp267	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68813.1	008165	Cluster8028_1clades	107	CcrPW_gp274	Caulobacter phage CcrPW	GCA_003443275.1
AFC21944.1	008166	Cluster8029_1clades	101	GAP32_486	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44071.1	008166	Cluster8029_1clades	107	CBB_508	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01103.1	008167	Cluster8030_1clades	107	AR9_g018	Bacillus phage AR9	GCA_001743835.1
ASU00025.1	008167	Cluster8030_1clades	107	PBL_PBS1_203	Bacillus virus PBS1	GCA_002601325.1
AXF51404.1	008168	Cluster8031_1clades	107	WELLINGTON_278	Erwinia phage Wellington	GCA_003344985.1
ANZ49629.1	008168	Cluster8031_1clades	107	KWAN_277	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03806.1	008169	Cluster8032_1clades	107	JOAD_109	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03561.1	008169	Cluster8032_1clades	107	RISINGSUN_109	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXG67208.1	008170	Cluster8033_1clades	107	AD1_164	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08439.1	008170	Cluster8033_1clades	105	Alexandra_169	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXQ69091.1	008171	Cluster8034_1clades	107	CcrBL9_gp067c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69647.1	008171	Cluster8034_1clades	100	CcrSC_gp065c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69176.1	008172	DUF1653	107	CcrBL9_gp152	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69729.1	008172	DUF1653	107	CcrSC_gp147	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69444.1	008173	Cluster8036_1clades	107	CcrBL9_gp420	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69994.1	008173	Cluster8036_1clades	107	CcrSC_gp412	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69536.1	008174	Cluster8037_1clades	107	CcrBL9_gp512	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70079.1	008174	Cluster8037_1clades	107	CcrSC_gp497	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69112.1	008175	Cluster8038_1clades	106	CcrBL9_gp088	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69666.1	008175	Cluster8038_1clades	107	CcrSC_gp084	Caulobacter phage CcrSC	GCA_003443315.1
AYD81423.1	008176	Cluster8039_1clades	107	SEA_JUSTBECAUSE_268	Streptomyces phage JustBecause	GCA_003613775.1
QJD53828.1	008176	Cluster8039_1clades	107	SEA_KELA_268	Streptomyces phage Kela	GCA_012934305.1
BAW19121.1	008177	Cluster8040_1clades	107	FDH28_gp274	Ralstonia phage RP12	GCA_002617345.1
BAW19407.1	008177	Cluster8040_1clades	107	-	Ralstonia phage RP31	GCA_002617365.1
BAW19158.1	008178	Cluster8041_1clades	107	FDH28_gp237	Ralstonia phage RP12	GCA_002617345.1
BAW19444.1	008178	Cluster8041_1clades	107	-	Ralstonia phage RP31	GCA_002617365.1
BBA65535.1	008179	Cluster8042_1clades	107	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96532.1	008179	Cluster8042_1clades	107	Xoosp13_346	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90613.1	008180	Cluster8043_1clades	107	HYO65_gp221	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90919.1	008180	Cluster8043_1clades	107	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAY00700.1	008181	Cluster8044_1clades	107	Ecwhy1_425	Escherichia phage Ecwhy_1	GCA_004146585.1
AXC36996.1	008181	Cluster8044_1clades	41	-	Escherichia phage UB	GCA_003341455.1
QBX06592.1	008182	Cluster8045_1clades	107	BcepSaruman_179	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74557.1	008182	Cluster8045_1clades	107	BcepSauron_177	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06611.1	008183	Cluster8046_1clades	107	BcepSaruman_198	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74577.1	008183	Cluster8046_1clades	107	BcepSauron_197	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06819.1	008184	Cluster8047_1clades	107	BcepSaruman_406	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74788.1	008184	Cluster8047_1clades	107	BcepSauron_408	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32277.1	008185	Cluster8048_1clades	107	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41851.1	008185	Cluster8048_1clades	107	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
ATA65482.1	008186	Cluster8049_1clades	59	2050HW_00147	Serratia phage 2050HW	GCA_002628125.1
QDB71252.1	008186	Cluster8049_1clades	107	CPT_Moabite_222	Serratia phage Moabite	GCA_006384735.1
QDJ97306.1	008187	Cluster8050_1clades	106	D6_0146	Aeromonas phage D6	GCA_007051205.2
QDH47230.1	008187	Cluster8050_1clades	107	LAh10_71	Aeromonas phage LAh10	GCA_006863975.1
QGT54769.1	008188	ParB	107	b23_0154	Synechococcus phage B23	GCA_009745195.1
QGT54399.1	008188	ParB	107	b3_0155	Synechococcus phage B3	GCA_009745215.1
prevph1000000273	008189	Cluster8052_1clades	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000218	008189	Cluster8052_1clades	108	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000327	008190	Cluster8053_1clades	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000256	008190	Cluster8053_1clades	108	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000498	008191	Cluster8054_1clades	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000378	008191	Cluster8054_1clades	108	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44679.1	008192	Cluster8055_1clades	106	PSSM2_302	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12297.1	008192	Cluster8055_1clades	106	PRTG_00144	Prochlorococcus phage P-SSM5	GCA_002991095.1
AEO93872.1	008193	Cluster8056_1clades	96	G_627	Bacillus virus G	GCA_000917535.1
AEO93874.1	008193	Cluster8056_1clades	106	G_629	Bacillus virus G	GCA_000917535.1
AXQ68347.1	008194	Cluster8057_1clades	102	CcrBL10_gp143c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86631.1	008194	Cluster8057_1clades	106	CcrRogue_gp149	Caulobacter virus Rogue	GCA_000900555.1
QBP07503.1	008195	Cluster8058_1clades	106	DERBICUS_77	Erwinia phage Derbicus	GCA_004521655.1
ANZ48927.1	008195	Cluster8058_1clades	106	EARLPHILLIPIV_77	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ASR76243.1	008196	DSBH	106	PBL_BELLAMY_207	Synechococcus phage Bellamy	GCA_002627525.1
QJT70199.1	008196	DSBH	46	SynMITS9220M01_193	Synechococcus phage SynMITS9220M01	GCA_013187275.1
ATA65470.1	008197	Cluster8060_1clades	106	2050HW_00135	Serratia phage 2050HW	GCA_002628125.1
QDB71239.1	008197	Cluster8060_1clades	106	CPT_Moabite_209	Serratia phage Moabite	GCA_006384735.1
ATA65534.1	008198	Cluster8061_1clades	106	2050HW_00199	Serratia phage 2050HW	GCA_002628125.1
QDB71298.1	008198	Cluster8061_1clades	106	CPT_Moabite_268	Serratia phage Moabite	GCA_006384735.1
AXQ69281.1	008199	Cluster8062_1clades	106	CcrBL9_gp257c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69838.1	008199	Cluster8062_1clades	106	CcrSC_gp256c	Caulobacter phage CcrSC	GCA_003443315.1
QDH83642.1	008200	Cluster8063_1clades	95	H1O15_gp146	Achromobacter phage Motura	GCA_006964305.1
BAG41659.1	008200	Cluster8063_1clades	106	RSL1_ORF210	Ralstonia phage phiRSL1	GCA_000879455.1
BAS04887.1	008201	TM	106	AVU11_gp095	Ralstonia phage RSF1	GCA_001500875.1
BAQ02614.1	008201	TM	96	AVU38_gp086	Ralstonia phage RSL2	GCA_001503055.1
BBA65312.1	008202	XIS-HTH	106	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96347.1	008202	XIS-HTH	104	Xoosp13_160	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90574.1	008203	Cluster8066_1clades	106	HYO65_gp182	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90882.1	008203	Cluster8066_1clades	106	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06791.1	008204	Cluster8067_1clades	106	BcepSaruman_378	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74761.1	008204	Cluster8067_1clades	106	BcepSauron_381	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54775.1	008205	Cluster8068_1clades	106	b23_0160	Synechococcus phage B23	GCA_009745195.1
QGT54405.1	008205	Cluster8068_1clades	106	b3_0161	Synechococcus phage B3	GCA_009745215.1
QIG57773.1	008206	Cluster8069_1clades	106	SEA_PAULODIABOLI_38	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58074.1	008206	Cluster8069_1clades	106	SEA_PAULODIABOLI_393	Microbacterium phage PauloDiaboli	GCA_011067425.1
SOK59229.1	008207	Cluster8070_1clades	106	g421	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58695.1	008207	Cluster8070_1clades	106	g418	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AAX44438.1	008208	Cluster8071_1clades	105	PSSM2_060	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12214.1	008208	Cluster8071_1clades	105	PRTG_00056	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGH07646.1	008209	Cluster8072_1clades	105	CYVG_00203	Cyanophage S-SSM6a	GCA_002710385.1
AGN12229.1	008209	Cluster8072_1clades	98	PRTG_00071	Prochlorococcus phage P-SSM5	GCA_002991095.1
ATA65556.1	008210	Cluster8073_1clades	105	2050HW_00221	Serratia phage 2050HW	GCA_002628125.1
QDB71321.1	008210	Cluster8073_1clades	105	CPT_Moabite_291	Serratia phage Moabite	GCA_006384735.1
AFU88275.1	008211	Cluster8074_1clades	104	CcrColossus_gp405	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68951.1	008211	Cluster8074_1clades	105	CcrPW_gp412c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88282.1	008212	Cluster8075_1clades	89	CcrColossus_gp412	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68958.1	008212	Cluster8075_1clades	105	CcrPW_gp419c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69492.1	008213	Cluster8076_1clades	103	CcrBL9_gp468	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70040.1	008213	Cluster8076_1clades	105	CcrSC_gp458	Caulobacter phage CcrSC	GCA_003443315.1
QBX06417.1	008214	Cluster8077_1clades	105	BcepSaruman_004	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74385.1	008214	Cluster8077_1clades	105	BcepSauron_005	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06826.1	008215	Cluster8078_1clades	105	BcepSaruman_413	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74795.1	008215	Cluster8078_1clades	105	BcepSauron_415	Burkholderia phage BcepSauron	GCA_005394215.1
QCW22843.1	008216	Cluster8079_1clades	105	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50510.1	008216	Cluster8079_1clades	104	-	Synechococcus phage S-B43	GCA_006869725.1
BBA65331.1	008217	Cluster8080_1clades	50	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96370.1	008217	Cluster8080_1clades	105	Xoosp13_183	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96671.1	008218	Cluster8081_1clades	105	PS1_0160	Aeromonas phage PS1	GCA_007051165.2
QFR59305.1	008218	Cluster8081_1clades	105	PS2_0164	Aeromonas phage PS2	GCA_009388305.2
QGT54762.1	008219	Cluster8082_1clades	105	b23_0147	Synechococcus phage B23	GCA_009745195.1
QGT54392.1	008219	Cluster8082_1clades	105	b3_0148	Synechococcus phage B3	GCA_009745215.1
QGT54804.1	008220	TM	105	b23_0189	Synechococcus phage B23	GCA_009745195.1
QGT54434.1	008220	TM	105	b3_0190	Synechococcus phage B3	GCA_009745215.1
QGT54848.1	008221	Cluster8084_1clades	105	b23_0234	Synechococcus phage B23	GCA_009745195.1
QGT54482.1	008221	Cluster8084_1clades	105	b3_0240	Synechococcus phage B3	GCA_009745215.1
AIA64832.1	008222	Cluster8085_1clades	96	S13_033	Cronobacter phage S13	GCA_001503575.1
QHJ78830.1	008222	Cluster8085_1clades	105	-	Myoviridae sp.	GCA_012593985.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000032	008223	TM	106	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000024	008223	TM	106	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000016	008224	YacG	106	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000408	008224	YacG	97	-	Prevotella_phage_Lak-B8	GCA_004379655.1
APU01696.1	008225	Cluster8088_1clades	104	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53335.1	008225	Cluster8088_1clades	104	65p327	Aeromonas virus 65	GCA_000893255.1
AXQ68511.1	008226	Cluster8089_1clades	90	CcrBL10_gp307	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86800.1	008226	Cluster8089_1clades	104	CcrRogue_gp318	Caulobacter virus Rogue	GCA_000900555.1
AGR48102.2	008227	Cluster8090_1clades	103	SmphiM12_470	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13634.1	008227	Cluster8090_1clades	104	PHIN3_371	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01352.1	008228	Cluster8091_1clades	104	AR9_g268	Bacillus phage AR9	GCA_001743835.1
AST99981.1	008228	Cluster8091_1clades	104	PBI_PBS1_160	Bacillus virus PBS1	GCA_002601325.1
AXF51281.1	008229	Cluster8092_1clades	104	WELLINGTON_152	Erwinia phage Wellington	GCA_003344985.1
ANZ49504.1	008229	Cluster8092_1clades	104	KWAN_152	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASR76210.1	008230	Cluster8093_1clades	104	PBI_BELLAMY_166	Synechococcus phage Bellamy	GCA_002627525.1
QJT70163.1	008230	Cluster8093_1clades	68	SynMITS9220M01_150	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AWY08625.1	008231	Cluster8094_1clades	104	Alexandra_312	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28765.1	008231	Cluster8094_1clades	103	YOLOSWAG_295	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXH72589.1	008232	Cluster8095_1clades	103	-	Myoviridae sp.	GCA_003657725.1
AXH72587.1	008232	Cluster8095_1clades	104	-	Myoviridae sp.	GCA_003657725.1
AXQ69079.1	008233	Cluster8096_1clades	104	CcrBL9_gp055c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69638.1	008233	Cluster8096_1clades	104	CcrSC_gp056c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69094.1	008234	Cluster8097_1clades	104	CcrBL9_gp070c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69650.1	008234	Cluster8097_1clades	101	CcrSC_gp068c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69436.1	008235	Cluster8098_1clades	104	CcrBL9_gp412	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69988.1	008235	Cluster8098_1clades	104	CcrSC_gp406	Caulobacter phage CcrSC	GCA_003443315.1
BBA65236.1	008236	Cluster8099_1clades	104	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65695.1	008236	Cluster8099_1clades	104	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90461.1	008237	Cluster8100_1clades	104	HYO65_gp069	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90769.1	008237	Cluster8100_1clades	104	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90598.1	008238	Cluster8101_1clades	104	HYO65_gp206	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90905.1	008238	Cluster8101_1clades	104	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06792.1	008239	Cluster8102_1clades	104	BcepSaruman_379	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74762.1	008239	Cluster8102_1clades	104	BcepSauron_382	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06802.1	008240	Cluster8103_1clades	104	BcepSaruman_389	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74771.1	008240	Cluster8103_1clades	104	BcepSauron_391	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06807.1	008241	Cluster8104_1clades	104	BcepSaruman_394	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74776.1	008241	Cluster8104_1clades	104	BcepSauron_396	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32400.1	008242	APATPase	104	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41970.1	008242	APATPase	104	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000130	008243	Cluster8106_1clades	105	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000098	008243	Cluster8106_1clades	105	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000250	008244	Cluster8107_1clades	105	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000198	008244	Cluster8107_1clades	105	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABY63209.1	008245	Cluster8108_1clades	103	201phi2-1p384	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76882.1	008245	Cluster8108_1clades	103	PHABIO_251	Pseudomonas phage Phabio	GCA_002624965.1
AFC21808.1	008246	Cluster8109_1clades	103	GAP32_358	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43931.1	008246	Cluster8109_1clades	103	CBB_368	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU88115.1	008247	Cluster8110_1clades	103	CcrColossus_gp245	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68793.1	008247	Cluster8110_1clades	103	CcrPW_gp254	Caulobacter phage CcrPW	GCA_003443275.1
ATI17295.1	008248	Cluster8111_1clades	102	-	Aeromonas phage AS-szw	GCA_002743635.1
ASU00301.1	008248	Cluster8111_1clades	103	HWB28_gp251	Aeromonas phage AS-zj	GCA_002627665.1
AXF51416.1	008249	Cluster8112_1clades	103	WELLINGTON_292	Erwinia phage Wellington	GCA_003344985.1
ANZ49641.1	008249	Cluster8112_1clades	63	KWAN_290	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXQ69129.1	008250	Cluster8114_1clades	103	CcrBL9_gp105	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69683.1	008250	Cluster8114_1clades	103	CcrSC_gp101	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69205.1	008251	SIG+TM	103	CcrBL9_gp181	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69758.1	008251	SIG+TM	103	CcrSC_gp176	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69484.1	008252	Cluster8116_1clades	103	CcrBL9_gp460	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70033.1	008252	Cluster8116_1clades	103	CcrSC_gp451	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69467.1	008253	Cluster8117_1clades	101	CcrBL9_gp443	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70016.1	008253	Cluster8117_1clades	103	CcrSC_gp434	Caulobacter phage CcrSC	GCA_003443315.1
BBA65693.1	008254	Cluster8118_1clades	103	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65234.1	008254	Cluster8118_1clades	103	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65337.1	008255	Cluster8119_1clades	103	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96374.1	008255	Cluster8119_1clades	103	Xoosp13_188	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90622.1	008256	Cluster8121_1clades	103	HYO65_gp230	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90928.1	008256	Cluster8121_1clades	49	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06527.1	008257	Cluster8122_1clades	103	BcepSaruman_114	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74493.1	008257	Cluster8122_1clades	103	BcepSauron_113	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06827.1	008258	Cluster8123_1clades	103	BcepSaruman_414	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74796.1	008258	Cluster8123_1clades	103	BcepSauron_416	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32350.1	008259	Cluster8124_1clades	103	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41924.1	008259	Cluster8124_1clades	103	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32448.1	008260	Cluster8125_1clades	103	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42020.1	008260	Cluster8125_1clades	103	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32475.1	008261	Cluster8126_1clades	103	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42047.1	008261	Cluster8126_1clades	103	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54851.1	008262	Cluster8128_1clades	103	b23_0237	Synechococcus phage B23	GCA_009745195.1
QGT54485.1	008262	Cluster8128_1clades	103	b3_0243	Synechococcus phage B3	GCA_009745215.1
QGT54899.1	008263	Cluster8129_1clades	103	b23_0286	Synechococcus phage B23	GCA_009745195.1
QGT54534.1	008263	Cluster8129_1clades	103	b3_0293	Synechococcus phage B3	GCA_009745215.1
AYD81204.1	008264	Cluster8130_1clades	99	SEA_JUSTBECAUSE_35	Streptomyces phage JustBecause	GCA_003613775.1
QJD53607.1	008264	Cluster8130_1clades	103	SEA_KELA_36	Streptomyces phage Kela	GCA_012934305.1
SOK59327.1	008265	SIG+TM+TM	103	g519	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58789.1	008265	SIG+TM+TM	103	g512	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000274	008266	Cluster8132_1clades	104	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000219	008266	Cluster8132_1clades	104	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000366	008267	Cluster8133_1clades	104	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000292	008267	Cluster8133_1clades	104	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01591.1	008268	Cluster8134_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53215.1	008268	Cluster8134_1clades	102	65p207	Aeromonas virus 65	GCA_000893255.1
APU01748.1	008269	Cluster8135_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53389.1	008269	Cluster8135_1clades	102	65p382	Aeromonas virus 65	GCA_000893255.1
APU01749.1	008270	Cluster8136_1clades	102	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53390.1	008270	Cluster8136_1clades	102	65p383	Aeromonas virus 65	GCA_000893255.1
AXQ68393.1	008271	Cluster8137_1clades	102	CcrBL10_gp189c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86679.1	008271	Cluster8137_1clades	102	CcrRogue_gp197	Caulobacter virus Rogue	GCA_000900555.1
AFU87935.1	008272	Cluster8138_1clades	102	CcrColossus_gp065	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68607.1	008272	Cluster8138_1clades	102	CcrPW_gp068	Caulobacter phage CcrPW	GCA_003443275.1
AMS01262.1	008273	Cluster8139_1clades	102	AR9_g178	Bacillus phage AR9	GCA_001743835.1
AST99889.1	008273	Cluster8139_1clades	95	PBI_PBS1_67	Bacillus virus PBS1	GCA_002601325.1
AMS01267.1	008274	Cluster8140_1clades	102	AR9_g183	Bacillus phage AR9	GCA_001743835.1
AST99894.1	008274	Cluster8140_1clades	102	PBI_PBS1_72	Bacillus virus PBS1	GCA_002601325.1
ANZ48432.1	008275	Cluster8141_1clades	94	CAITLIN_137	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48707.1	008275	Cluster8141_1clades	102	CHRISDB_145	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AOO14278.1	008276	Cluster8142_1clades	102	Sn110110_084	Cyanophage S-RIM14	GCA_002599065.1
AOO14927.1	008276	Cluster8142_1clades	102	W1230910_081	Cyanophage S-RIM14	GCA_002599125.1
ASU03739.1	008277	Cluster8143_1clades	102	JOAD_176	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03495.1	008277	Cluster8143_1clades	102	RISINGSUN_175	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXG67343.1	008278	Cluster8144_1clades	102	AD1_299	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08570.1	008278	Cluster8144_1clades	102	Alexandra_318	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72178.1	008279	Cluster8145_1clades	102	SEA_KRADAL_292	Streptomyces phage Kradal	GCA_004799925.1
AXH66441.1	008279	Cluster8145_1clades	102	SEA_SATIS_292	Streptomyces phage Satis	GCA_003366315.1
QBZ72182.1	008280	Cluster8146_1clades	102	SEA_KRADAL_296	Streptomyces phage Kradal	GCA_004799925.1
AXH66445.1	008280	Cluster8146_1clades	102	SEA_SATIS_296	Streptomyces phage Satis	GCA_003366315.1
AFU87943.1	008281	Cluster8147_1clades	84	CcrColossus_gp073	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68615.1	008281	Cluster8147_1clades	102	CcrPW_gp076	Caulobacter phage CcrPW	GCA_003443275.1
AFU88249.1	008282	Cluster8148_1clades	101	CcrColossus_gp379	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68924.1	008282	Cluster8148_1clades	102	CcrPW_gp385c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69090.1	008283	Cluster8149_1clades	102	CcrBL9_gp066c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69646.1	008283	Cluster8149_1clades	102	CcrSC_gp064c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69165.1	008284	Cluster8150_1clades	102	CcrBL9_gp141	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69720.1	008284	Cluster8150_1clades	102	CcrSC_gp138	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69089.1	008285	Cluster8151_1clades	98	CcrBL9_gp065c	Caulobacter phage CcrBL9	GCA_003443295.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69645.1	008285	Cluster8151_1clades	102	CcrSC_gp063c	Caulobacter phage CcrSC	GCA_003443315.1
AYD81450.1	008286	Cluster8152_1clades	102	SEA_JUSTBECAUSE_295	Streptomyces phage JustBecause	GCA_003613775.1
QJD53855.1	008286	Cluster8152_1clades	102	SEA_KELA_295	Streptomyces phage Kela	GCA_012934305.1
AYD81462.1	008287	Cluster8153_1clades	102	SEA_JUSTBECAUSE_307	Streptomyces phage JustBecause	GCA_003613775.1
QJD53865.1	008287	Cluster8153_1clades	102	SEA_KELA_305	Streptomyces phage Kela	GCA_012934305.1
BAS04879.1	008288	Cluster8154_1clades	102	AVU11_gp087	Ralstonia phage RSF1	GCA_001500875.1
BAU71406.1	008288	Cluster8154_1clades	102	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19204.1	008289	SIG+TM+TM	102	FDH28_gp191	Ralstonia phage RP12	GCA_002617345.1
BAW19490.1	008289	SIG+TM+TM	102	-	Ralstonia phage RP31	GCA_002617365.1
BBA65663.1	008290	TM+TM	102	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65204.1	008290	TM+TM	102	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65280.1	008291	Cluster8157_1clades	102	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65739.1	008291	Cluster8157_1clades	102	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90455.1	008292	Cluster8158_1clades	102	HYO65_gp063	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90763.1	008292	Cluster8158_1clades	102	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90527.1	008293	Cluster8159_1clades	102	HYO65_gp135	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90835.1	008293	Cluster8159_1clades	93	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06551.1	008294	Cluster8160_1clades	102	BcepSaruman_138	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74517.1	008294	Cluster8160_1clades	102	BcepSauron_137	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06640.1	008295	Cluster8161_1clades	102	BcepSaruman_227	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74610.1	008295	Cluster8161_1clades	102	BcepSauron_230	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06704.1	008296	Cluster8162_1clades	70	BcepSaruman_291	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74672.1	008296	Cluster8162_1clades	102	BcepSauron_292	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06809.1	008297	Cluster8163_1clades	100	BcepSaruman_396	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74778.1	008297	Cluster8163_1clades	102	BcepSauron_398	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06837.1	008298	Cluster8164_1clades	102	BcepSaruman_424	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74806.1	008298	Cluster8164_1clades	102	BcepSauron_426	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06844.1	008299	Cluster8165_1clades	82	BcepSaruman_431	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74813.1	008299	Cluster8165_1clades	102	BcepSauron_433	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06851.1	008300	Cluster8166_1clades	102	BcepSaruman_438	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74820.1	008300	Cluster8166_1clades	102	BcepSauron_440	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32406.1	008301	Cluster8167_1clades	102	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41977.1	008301	Cluster8167_1clades	59	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32429.1	008302	Cluster8168_1clades	102	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42000.1	008302	Cluster8168_1clades	102	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54710.1	008303	Cluster8169_1clades	102	b23_0095	Synechococcus phage B23	GCA_009745195.1
QGT54340.1	008303	Cluster8169_1clades	102	b3_0096	Synechococcus phage B3	GCA_009745215.1
QGT54791.1	008304	Cluster8170_1clades	102	b23_0176	Synechococcus phage B23	GCA_009745195.1
QGT54421.1	008304	Cluster8170_1clades	102	b3_0177	Synechococcus phage B3	GCA_009745215.1
AIA65035.1	008305	Cluster8171_1clades	101	S13_238	Cronobacter phage S13	GCA_001503575.1
QHJ78897.1	008305	Cluster8171_1clades	102	-	Myoviridae sp.	GCA_012593985.1
QIG57748.1	008306	Cluster8172_1clades	102	SEA_PAULODIABOLI_10	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58049.1	008306	Cluster8172_1clades	102	SEA_PAULODIABOLI_365	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000021	008307	Cluster8173_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000019	008307	Cluster8173_1clades	103	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000172	008308	Cluster8174_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000134	008308	Cluster8174_1clades	103	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000239	008309	Cluster8175_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000189	008309	Cluster8175_1clades	103	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000255	008310	Cluster8176_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000202	008310	Cluster8176_1clades	103	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000365	008311	Cluster8177_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000291	008311	Cluster8177_1clades	103	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000771	008312	Cluster8178_1clades	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000524	008312	Cluster8178_1clades	103	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88248.1	008313	Cluster8179_1clades	101	CcrColossus_gp378	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68923.1	008313	Cluster8179_1clades	100	CcrPW_gp384c	Caulobacter phage CcrPW	GCA_003443275.1
AIA65019.1	008314	Cluster8180_1clades	101	S13_222	Cronobacter phage S13	GCA_001503575.1
QHJ78913.1	008314	Cluster8180_1clades	100	-	Myoviridae sp.	GCA_012593985.1
AXF51256.1	008315	Cluster8181_1clades	101	WELLINGTON_126	Erwinia phage Wellington	GCA_003344985.1
ANZ49476.1	008315	Cluster8181_1clades	101	KWAN_124	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51337.1	008316	SIG+TM	101	WELLINGTON_211	Erwinia phage Wellington	GCA_003344985.1
ANZ49564.1	008316	SIG+TM	101	KWAN_212	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AWY08327.1	008317	Cluster8183_1clades	49	Alexandra_47	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AQT28529.1	008317	Cluster8183_1clades	101	YOLOSWAG_44	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ATA65560.1	008318	Cluster8184_1clades	101	2050HW_00225	Serratia phage 2050HW	GCA_002628125.1
QDB71325.1	008318	Cluster8184_1clades	101	CPT_Moabite_295	Serratia phage Moabite	GCA_006384735.1
AXQ69292.1	008319	Cluster8185_1clades	101	CcrBL9_gp268c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69849.1	008319	Cluster8185_1clades	101	CcrSC_gp267c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69323.1	008320	Cluster8186_1clades	101	CcrBL9_gp299	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69883.1	008320	Cluster8186_1clades	101	CcrSC_gp301	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69255.1	008321	Cluster8187_1clades	69	CcrBL9_gp231c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69812.1	008321	Cluster8187_1clades	101	CcrSC_gp230c	Caulobacter phage CcrSC	GCA_003443315.1
AYD81413.1	008322	Cluster8188_1clades	101	SEA_JUSTBECAUSE_258	Streptomyces phage JustBecause	GCA_003613775.1
QJD53820.1	008322	Cluster8188_1clades	101	SEA_KELA_260	Streptomyces phage Kela	GCA_012934305.1
AYD81418.1	008323	Cluster8189_1clades	101	SEA_JUSTBECAUSE_263	Streptomyces phage JustBecause	GCA_003613775.1
QJD53823.1	008323	Cluster8189_1clades	101	SEA_KELA_263	Streptomyces phage Kela	GCA_012934305.1
BAW19247.1	008324	SIG+TM	101	FDH28_gp148	Ralstonia phage RP12	GCA_002617345.1
BAW19533.1	008324	SIG+TM	101	-	Ralstonia phage RP31	GCA_002617365.1
QGZ14440.1	008325	Cluster8192_1clades	101	HWC77_gp077	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04294.1	008325	Cluster8192_1clades	101	HWC03_gp139	Vibrio phage 2 TSL-2019	GCA_006964105.1
QBX06546.1	008326	Cluster8193_1clades	101	BcepSaruman_133	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74512.1	008326	Cluster8193_1clades	101	BcepSauron_132	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ97199.1	008327	Cluster8194_1clades	50	D6_0039	Aeromonas phage D6	GCA_007051205.2
QDH47234.1	008327	Cluster8194_1clades	101	LAh10_205	Aeromonas phage LAh10	GCA_006863975.1
QDJ96662.1	008328	Cluster8195_1clades	101	PS1_0151	Aeromonas phage PS1	GCA_007051165.2
QFR59296.1	008328	Cluster8195_1clades	101	PS2_0155	Aeromonas phage PS2	GCA_009388305.2
QGT54766.1	008329	Cluster8196_1clades	101	b23_0151	Synechococcus phage B23	GCA_009745195.1
QGT54396.1	008329	Cluster8196_1clades	101	b3_0152	Synechococcus phage B3	GCA_009745215.1
prevph1000000020	008330	Cluster8197_1clades	102	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000018	008330	Cluster8197_1clades	102	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000361	008331	Cluster8198_1clades	102	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000287	008331	Cluster8198_1clades	102	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000822	008332	Cluster8199_1clades	102	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000566	008332	Cluster8199_1clades	102	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44581.1	008333	Cluster8200_1clades	100	PSSM2_204	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12392.1	008333	Cluster8200_1clades	100	PRTG_00239	Prochlorococcus phage P-SSM5	GCA_002991095.1
ADQ52756.1	008334	Cluster8201_1clades	100	PX29p037	Aeromonas phage PX29	GCA_000920195.1
ADM80012.1	008334	Cluster8201_1clades	90	phiAS5_ORF0169	Aeromonas phage phiAS5	GCA_000887715.1
AFO71393.1	008335	Cluster8202_1clades	100	CR5_173	Cronobacter phage CR5	GCA_000910235.1
ANZ50376.1	008335	Cluster8202_1clades	100	PHOBOS_186	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
AFU87965.1	008336	Cluster8203_1clades	100	CcrColossus_gp095	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68641.1	008336	Cluster8203_1clades	64	CcrPW_gp102	Caulobacter phage CcrPW	GCA_003443275.1
AFU88160.1	008337	Cluster8204_1clades	100	CcrColossus_gp290	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68836.1	008337	Cluster8204_1clades	100	CcrPW_gp297	Caulobacter phage CcrPW	GCA_003443275.1
AGH56937.1	008338	Cluster8205_1clades	79	CPXG_00134	Cyanophage P-RSM6	GCA_000906155.1
AJK27519.1	008338	Cluster8205_1clades	100	PTIM40_92	Cyanophage P-TIM40	GCA_001470935.1
ANZ49495.1	008339	Cluster8206_1clades	100	KWAN_143	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QFP93251.1	008339	Cluster8206_1clades	92	-	Serratia phage PCH45	GCA_009187865.1
ATA65693.1	008340	Cluster8207_1clades	100	2050HW_00358	Serratia phage 2050HW	GCA_002628125.1
QDB71120.1	008340	Cluster8207_1clades	100	CPT_Moabite_090	Serratia phage Moabite	GCA_006384735.1
AXQ69225.1	008341	Cluster8208_1clades	100	CcrBL9_gp201	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69779.1	008341	Cluster8208_1clades	100	CcrSC_gp197	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69287.1	008342	Cluster8209_1clades	100	CcrBL9_gp263c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69844.1	008342	Cluster8209_1clades	100	CcrSC_gp262c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69471.1	008343	Cluster8210_1clades	100	CcrBL9_gp447	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70020.1	008343	Cluster8210_1clades	100	CcrSC_gp438	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69490.1	008344	Cluster8211_1clades	100	CcrBL9_gp466	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70038.1	008344	Cluster8211_1clades	100	CcrSC_gp456	Caulobacter phage CcrSC	GCA_003443315.1
BBI90424.1	008345	Cluster8212_1clades	100	HYO65_gp032	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90731.1	008345	Cluster8212_1clades	100	-	Tenacibaculum phage PTm5	GCA_009730715.1
ARV77037.1	008346	Cluster8213_1clades	96	PHABIO_406	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02884.1	008346	Cluster8213_1clades	100	PSA21_358	Pseudomonas phage Psa21	GCA_004340405.1
QBX06698.1	008347	Cluster8214_1clades	100	BcepSaruman_285	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74666.1	008347	Cluster8214_1clades	100	BcepSauron_286	Burkholderia phage BcepSauron	GCA_005394215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06521.1	008348	Cluster8215_1clades	100	BcepSaruman_108	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74487.1	008348	Cluster8215_1clades	99	BcepSauron_107	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32225.1	008349	SIG+TM	100	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41803.1	008349	SIG+TM	100	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCG76226.1	008350	Cluster8217_1clades	100	EST35_0345	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44145.1	008350	Cluster8217_1clades	89	PBI_SCTP2_130	Salicola phage SCTP-2	GCA_002625545.1
QCW22930.1	008351	Cluster8218_1clades	100	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50615.1	008351	Cluster8218_1clades	100	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54797.1	008352	Cluster8219_1clades	100	b23_0182	Synechococcus phage B23	GCA_009745195.1
QGT54427.1	008352	Cluster8219_1clades	100	b3_0183	Synechococcus phage B3	GCA_009745215.1
QGT54849.1	008353	Cluster8220_1clades	100	b23_0235	Synechococcus phage B23	GCA_009745195.1
QGT54483.1	008353	Cluster8220_1clades	100	b3_0241	Synechococcus phage B3	GCA_009745215.1
QIG58046.1	008354	Cluster8221_1clades	100	SEA_PAULODIABOLI_362	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57745.1	008354	Cluster8221_1clades	100	SEA_PAULODIABOLI_7	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57763.1	008355	LPD40	100	SEA_PAULODIABOLI_28	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58064.1	008355	LPD40	100	SEA_PAULODIABOLI_383	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000319	008356	Cluster8223_1clades	101	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000248	008356	Cluster8223_1clades	101	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000331	008357	Cluster8224_1clades	101	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000260	008357	Cluster8224_1clades	101	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000647	008358	Cluster8225_1clades	101	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000462	008358	Cluster8225_1clades	101	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01604.1	008359	Cluster8226_1clades	99	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53228.1	008359	Cluster8226_1clades	99	65p220	Aeromonas virus 65	GCA_000893255.1
QAX97696.1	008360	Cluster8227_1clades	99	ASswx1_50	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39200.1	008360	Cluster8227_1clades	99	CC2_062	Aeromonas phage CC2	GCA_000903495.1
AFU88175.1	008361	Cluster8228_1clades	99	CcrColossus_gp305	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68852.1	008361	Cluster8228_1clades	99	CcrPW_gp313	Caulobacter phage CcrPW	GCA_003443275.1
AFU88268.1	008362	Cluster8229_1clades	99	CcrColossus_gp398	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68943.1	008362	Cluster8229_1clades	99	CcrPW_gp404	Caulobacter phage CcrPW	GCA_003443275.1
AXF51162.1	008363	Cluster8230_1clades	99	WELLINGTON_31	Erwinia phage Wellington	GCA_003344985.1
ANZ49383.1	008363	Cluster8230_1clades	99	KWAN_31	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51342.1	008364	GTP_EFTU	99	WELLINGTON_216	Erwinia phage Wellington	GCA_003344985.1
ANZ49569.1	008364	GTP_EFTU	99	KWAN_217	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65543.1	008365	TM+TM+TM	99	2050HW_00208	Serratia phage 2050HW	GCA_002628125.1
QDB71308.1	008365	TM+TM+TM	99	CPT_Moabite_278	Serratia phage Moabite	GCA_006384735.1
ATA65581.1	008366	Cluster8233_1clades	99	2050HW_00246	Serratia phage 2050HW	GCA_002628125.1
QDB71346.1	008366	Cluster8233_1clades	99	CPT_Moabite_316	Serratia phage Moabite	GCA_006384735.1
AUZ95301.1	008367	Cluster8234_1clades	99	FDI40_gp542	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44410.1	008367	Cluster8234_1clades	93	PBI_SCTP2_395	Salicola phage SCTP-2	GCA_002625545.1
AXG67306.1	008368	Cluster8235_1clades	75	AD1_262	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08532.1	008368	Cluster8235_1clades	99	Alexandra_275	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXQ69227.1	008369	SIG+TM	97	CcrBL9_gp203	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69781.1	008369	SIG+TM	99	CcrSC_gp199	Caulobacter phage CcrSC	GCA_003443315.1
AYD81465.1	008370	Cluster8237_1clades	99	SEA_JUSTBECAUSE_310	Streptomyces phage JustBecause	GCA_003613775.1
QJD53868.1	008370	Cluster8237_1clades	99	SEA_KELA_308	Streptomyces phage Kela	GCA_012934305.1
BAS04848.2	008371	Cluster8238_1clades	94	AVU11_agp15	Ralstonia phage RSF1	GCA_001500875.1
BAU71404.1	008371	Cluster8238_1clades	99	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19234.1	008372	SIG+KAP-NTPase	99	FDH28_gp161	Ralstonia phage RP12	GCA_002617345.1
BAW19520.1	008372	SIG+KAP-NTPase	99	-	Ralstonia phage RP31	GCA_002617365.1
BBI90413.1	008373	Cluster8240_1clades	99	HYO65_gp021	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90721.1	008373	Cluster8240_1clades	83	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06484.1	008374	Cluster8241_1clades	99	BcepSaruman_071	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74451.1	008374	Cluster8241_1clades	99	BcepSauron_071	Burkholderia phage BcepSauron	GCA_005394215.1
BBA65335.1	008375	Cluster8242_1clades	93	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96588.1	008375	Cluster8242_1clades	99	Xoosp13_186	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54737.1	008376	Cluster8243_1clades	99	b23_0122	Synechococcus phage B23	GCA_009745195.1
QGT54367.1	008376	Cluster8243_1clades	99	b3_0123	Synechococcus phage B3	GCA_009745215.1
QGT54787.1	008377	Cluster8244_1clades	99	b23_0172	Synechococcus phage B23	GCA_009745195.1
QGT54417.1	008377	Cluster8244_1clades	99	b3_0173	Synechococcus phage B3	GCA_009745215.1
QGT54827.1	008378	Cluster8245_1clades	99	b23_0212	Synechococcus phage B23	GCA_009745195.1
QGT54457.1	008378	Cluster8245_1clades	99	b3_0214	Synechococcus phage B3	GCA_009745215.1
QIG57754.1	008379	Cluster8246_1clades	99	SEA_PAULODIABOLI_17	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58055.1	008379	Cluster8246_1clades	99	SEA_PAULODIABOLI_372	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000268	008380	Cluster8247_1clades	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000214	008380	Cluster8247_1clades	100	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000338	008381	Cluster8248_1clades	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000267	008381	Cluster8248_1clades	100	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000611	008382	Cluster8249_1clades	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000430	008382	Cluster8249_1clades	100	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000856	008383	Cluster8250_1clades	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000594	008383	Cluster8250_1clades	100	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU87911.1	008384	Cluster8251_1clades	98	CcrColossus_gp041	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68583.1	008384	Cluster8251_1clades	98	CcrPW_gp044	Caulobacter phage CcrPW	GCA_003443275.1
AFU87924.1	008385	Cluster8252_1clades	98	CcrColossus_gp054	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68596.1	008385	Cluster8252_1clades	98	CcrPW_gp057	Caulobacter phage CcrPW	GCA_003443275.1
AFU87933.1	008386	Cluster8253_1clades	98	CcrColossus_gp063	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68605.1	008386	Cluster8253_1clades	98	CcrPW_gp066	Caulobacter phage CcrPW	GCA_003443275.1
AFU87947.1	008387	Cluster8254_1clades	98	CcrColossus_gp077	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68620.1	008387	Cluster8254_1clades	98	CcrPW_gp081	Caulobacter phage CcrPW	GCA_003443275.1
AFU88117.1	008388	EFTS	98	CcrColossus_gp247	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68795.1	008388	EFTS	98	CcrPW_gp256	Caulobacter phage CcrPW	GCA_003443275.1
AFU88312.1	008389	Cluster8256_1clades	98	CcrColossus_gp442	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68983.1	008389	Cluster8256_1clades	98	CcrPW_gp444	Caulobacter phage CcrPW	GCA_003443275.1
AGH56902.1	008390	Cluster8257_1clades	98	CPXG_00099	Cyanophage P-RSM6	GCA_000906155.1
AJK27560.1	008390	Cluster8257_1clades	84	PTIM40_133	Cyanophage P-TIM40	GCA_001470935.1
AHI60383.1	008391	Cluster8258_1clades	98	Ea357_230	Erwinia phage Ea35-70	GCA_000914635.1
AUG86986.1	008391	Cluster8258_1clades	98	MORTIMER_238	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AJT61168.1	008392	Cluster8259_1clades	98	AVU32_gp327	Vibrio phage ValKK3	GCA_001501635.1
ALP47209.1	008392	Cluster8259_1clades	98	phiGrn1_0052	Vibrio phage phi-Grn1	GCA_002757115.1
AMS01195.1	008393	Cluster8260_1clades	98	AR9_g111	Bacillus phage AR9	GCA_001743835.1
ASU00129.1	008393	Cluster8260_1clades	98	PBI_PBS1_307	Bacillus virus PBS1	GCA_002601325.1
ANZ48324.1	008394	Cluster8261_1clades	96	CAITLIN_29	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48596.1	008394	Cluster8261_1clades	98	CHRISDB_34	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ATA65571.1	008395	Cluster8262_1clades	98	2050HW_00236	Serratia phage 2050HW	GCA_002628125.1
QDB71335.1	008395	Cluster8262_1clades	91	CPT_Moabite_305	Serratia phage Moabite	GCA_006384735.1
QBZ72204.1	008396	Cluster8263_1clades	98	SEA_KRADAL_318	Streptomyces phage Kradal	GCA_004799925.1
AXH66467.1	008396	Cluster8263_1clades	98	SEA_SATIS_318	Streptomyces phage Satis	GCA_003366315.1
AFU88252.1	008397	Cluster8264_1clades	96	CcrColossus_gp382	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68928.1	008397	Cluster8264_1clades	98	CcrPW_gp389c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69088.1	008398	Cluster8265_1clades	98	CcrBL9_gp064c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69644.1	008398	Cluster8265_1clades	95	CcrSC_gp062c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69101.1	008399	Cluster8266_1clades	98	CcrBL9_gp077c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69656.1	008399	Cluster8266_1clades	98	CcrSC_gp074c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69463.1	008400	ATR13	98	CcrBL9_gp439	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70012.1	008400	ATR13	91	CcrSC_gp430	Caulobacter phage CcrSC	GCA_003443315.1
BAW19007.1	008401	Cluster8268_1clades	98	FDH28_gp033	Ralstonia phage RP12	GCA_002617345.1
BAW19293.1	008401	Cluster8268_1clades	98	-	Ralstonia phage RP31	GCA_002617365.1
BBA65310.1	008402	Cluster8269_1clades	98	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96345.1	008402	Cluster8269_1clades	95	Xoosp13_158	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QBX06446.1	008403	Cluster8271_1clades	98	BcepSaruman_033	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74413.1	008403	Cluster8271_1clades	98	BcepSauron_033	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06475.1	008404	Cluster8272_1clades	98	BcepSaruman_062	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74442.1	008404	Cluster8272_1clades	98	BcepSauron_062	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54768.1	008405	Cluster8273_1clades	98	b23_0153	Synechococcus phage B23	GCA_009745195.1
QGT54398.1	008405	Cluster8273_1clades	98	b3_0154	Synechococcus phage B3	GCA_009745215.1
QGT54887.1	008406	Cluster8274_1clades	98	b23_0274	Synechococcus phage B23	GCA_009745195.1
QGT54522.1	008406	Cluster8274_1clades	98	b3_0281	Synechococcus phage B3	GCA_009745215.1
AIA65049.1	008407	Phage_head_chap	97	S13_252	Cronobacter phage S13	GCA_001503575.1
QHJ78883.1	008407	Phage_head_chap	98	-	Myoviridae sp.	GCA_012593985.1
QIG63322.1	008408	Cluster8276_1clades	98	DAC16_89	Bacteroides phage DAC16	GCA_013387695.1
QIG64366.1	008408	Cluster8276_1clades	98	DAC23_88	Bacteroides phage DAC23	GCA_013387745.1
prevph1000000165	008409	Cluster8277_1clades	45	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000126	008409	Cluster8277_1clades	99	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000491	008410	Cluster8278_1clades	99	-	Prevotella_phage_Lak-B8	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prev15ph1000000372	008410	Cluster8278_1clades	99	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000303	008411	Cluster8279_1clades	55	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000495	008411	Cluster8279_1clades	99	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AEO93617.1	008412	Cluster8280_1clades	97	G_358	Bacillus virus G	GCA_000917535.1
AEO93627.1	008412	Cluster8280_1clades	97	G_368	Bacillus virus G	GCA_000917535.1
AFC21856.1	008413	SIG+TM	96	GAP32_403	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43978.1	008413	SIG+TM	97	CBB_415	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ANZ48485.1	008414	Cluster8282_1clades	97	CAITLIN_190	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48764.1	008414	Cluster8282_1clades	83	CHRISDB_202	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ASU03765.1	008415	Cluster8283_1clades	97	JOAD_150	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03521.1	008415	Cluster8283_1clades	97	RISINGSUN_149	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65588.1	008416	Cluster8284_1clades	97	2050HW_00253	Serratia phage 2050HW	GCA_002628125.1
QDB71353.1	008416	Cluster8284_1clades	97	CPT_Moabite_323	Serratia phage Moabite	GCA_006384735.1
AUZ95189.1	008417	Cluster8285_1clades	95	FDI40_gp430	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95185.1	008417	Cluster8285_1clades	97	FDI40_gp426	Agrobacterium phage Atu_ph07	GCA_002628245.1
QBZ72160.1	008418	Cluster8286_1clades	97	SEA_KRADAL_274	Streptomyces phage Kradal	GCA_004799925.1
AXH66423.1	008418	Cluster8286_1clades	97	SEA_SATIS_274	Streptomyces phage Satis	GCA_003366315.1
QBZ72175.1	008419	Cluster8287_1clades	97	SEA_KRADAL_289	Streptomyces phage Kradal	GCA_004799925.1
AXH66438.1	008419	Cluster8287_1clades	97	SEA_SATIS_289	Streptomyces phage Satis	GCA_003366315.1
AFU87973.1	008420	DUF4170	90	CcrColossus_gp103	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68650.1	008420	DUF4170	97	CcrPW_gp111	Caulobacter phage CcrPW	GCA_003443275.1
AFU88273.1	008421	Cluster8289_1clades	93	CcrColossus_gp403	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68949.1	008421	Cluster8289_1clades	97	CcrPW_gp410c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69312.1	008422	Cluster8290_1clades	97	CcrBL9_gp288	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69872.1	008422	Cluster8290_1clades	85	CcrSC_gp290	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69354.1	008423	Cluster8291_1clades	97	CcrBL9_gp330	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69913.1	008423	Cluster8291_1clades	97	CcrSC_gp331	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69428.1	008424	Cluster8292_1clades	95	CcrBL9_gp404	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69982.1	008424	Cluster8292_1clades	97	CcrSC_gp400	Caulobacter phage CcrSC	GCA_003443315.1
BAS04925.2	008425	Cluster8293_1clades	87	AVU11_gp133	Ralstonia phage RSF1	GCA_001500875.1
BAQ02652.2	008425	Cluster8293_1clades	97	-	Ralstonia phage RSL2	GCA_001503055.1
BBI90462.1	008426	Cluster8295_1clades	97	HYO65_gp070	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90770.1	008426	Cluster8295_1clades	97	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54711.1	008427	Cluster8296_1clades	97	b23_0096	Synechococcus phage B23	GCA_009745195.1
QGT54341.1	008427	Cluster8296_1clades	97	b3_0097	Synechococcus phage B3	GCA_009745215.1
QGT54820.1	008428	Cluster8297_1clades	97	b23_0205	Synechococcus phage B23	GCA_009745195.1
QGT54450.1	008428	Cluster8297_1clades	97	b3_0207	Synechococcus phage B3	GCA_009745215.1
SOK59164.1	008429	Cluster8298_1clades	97	g356	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58632.1	008429	Cluster8298_1clades	97	g355	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000159	008430	Cluster8299_1clades	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000120	008430	Cluster8299_1clades	98	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000791	008431	Cluster8300_1clades	98	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000539	008431	Cluster8300_1clades	98	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGN30248.1	008432	Cluster8301_1clades	96	VPFG_00249	Vibrio phage nt-1	GCA_000910195.2
ALP47305.1	008432	Cluster8301_1clades	64	phiGrn1_0307	Vibrio phage phi-Grn1	GCA_002757115.1
AIA64830.1	008433	Cluster8302_1clades	96	S13_031	Cronobacter phage S13	GCA_001503575.1
QHJ78832.1	008433	Cluster8302_1clades	96	-	Myoviridae sp.	GCA_012593985.1
AFC21857.1	008434	Cluster8303_1clades	83	GAP32_404	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43980.1	008434	Cluster8303_1clades	96	CBB_417	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMO43225.1	008435	Thioredoxin	96	R1080702_220	Cyanophage S-RIM32	GCA_001754165.1
QDH50668.1	008435	Thioredoxin	75	-	Synechococcus phage S-B43	GCA_006869725.1
ANS06102.1	008436	Cluster8305_1clades	96	ABCD_0083	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97096.1	008436	Cluster8305_1clades	96	E_088	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ASU03897.1	008437	Cluster8306_1clades	96	JOAD_18	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03652.1	008437	Cluster8306_1clades	96	RISINGSUN_18	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65681.1	008438	Cluster8307_1clades	96	2050HW_00346	Serratia phage 2050HW	GCA_002628125.1
QDB71102.1	008438	Cluster8307_1clades	96	CPT_Moabite_070	Serratia phage Moabite	GCA_006384735.1
QBZ72168.1	008439	Cluster8308_1clades	96	SEA_KRADAL_282	Streptomyces phage Kradal	GCA_004799925.1
AXH66431.1	008439	Cluster8308_1clades	96	SEA_SATIS_282	Streptomyces phage Satis	GCA_003366315.1
AXQ69400.1	008440	PWI	96	CcrBL9_gp376	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69957.1	008440	PWI	96	CcrSC_gp375	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69454.1	008441	Cluster8310_1clades	96	CcrBL9_gp430	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70003.1	008441	Cluster8310_1clades	96	CcrSC_gp421	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69408.1	008442	Cluster8311_1clades	93	CcrBL9_gp384	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69964.1	008442	Cluster8311_1clades	96	CcrSC_gp382	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70619.1	008443	Cluster8312_1clades	96	HOU04_gp018	Synechococcus phage S-T4	GCA_003443335.1
AXQ70417.1	008443	Cluster8312_1clades	96	HOU04_gp018	Synechococcus phage S-T4	GCA_003443335.1
BBI90417.1	008444	Cluster8313_1clades	96	HYO65_gp025	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90725.1	008444	Cluster8313_1clades	96	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90515.1	008445	Cluster8314_1clades	96	HYO65_gp123	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90823.1	008445	Cluster8314_1clades	96	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06775.1	008446	Cluster8315_1clades	96	BcepSaruman_362	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74745.1	008446	Cluster8315_1clades	96	BcepSauron_365	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54682.1	008447	Cluster8316_1clades	96	b23_0064	Synechococcus phage B23	GCA_009745195.1
QGT54312.1	008447	Cluster8316_1clades	96	b3_0064	Synechococcus phage B3	GCA_009745215.1
prevph1000000133	008448	DUF2812	97	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000101	008448	DUF2812	97	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUE22543.1	008449	Cluster8318_1clades	95	Ah1_00002	Aeromonas phage Ah1	GCA_002957415.1
AAQ17657.1	008449	Cluster8318_1clades	95	Aeh1ORF002c	Aeromonas virus Aeh1	GCA_000843245.1
AAX44604.1	008450	Cluster8319_1clades	95	PSSM2_227	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12366.1	008450	Cluster8319_1clades	95	PRTG_00213	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFC21618.1	008451	Cluster8320_1clades	95	GAP32_168	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43737.1	008451	Cluster8320_1clades	95	CBB_172	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU88133.1	008452	Cluster8321_1clades	95	CcrColossus_gp263	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68810.1	008452	Cluster8321_1clades	89	CcrPW_gp271	Caulobacter phage CcrPW	GCA_003443275.1
AFU88219.1	008453	Cluster8322_1clades	95	CcrColossus_gp349	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68896.1	008453	Cluster8322_1clades	95	CcrPW_gp357	Caulobacter phage CcrPW	GCA_003443275.1
AFU88284.1	008454	Cluster8323_1clades	95	CcrColossus_gp414	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68959.1	008454	Cluster8323_1clades	61	CcrPW_gp420c	Caulobacter phage CcrPW	GCA_003443275.1
AGR47640.1	008455	Cluster8324_1clades	95	SmphiM12_008	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13275.1	008455	Cluster8324_1clades	95	PHIN3_8	Sinorhizobium phage phiN3	GCA_001501175.1
AIA65013.1	008456	Cluster8325_1clades	95	S13_216	Cronobacter phage S13	GCA_001503575.1
QHJ78919.1	008456	Cluster8325_1clades	95	-	Myoviridae sp.	GCA_012593985.1
AMS01244.1	008457	Cluster8326_1clades	95	AR9_g160	Bacillus phage AR9	GCA_001743835.1
AST99870.1	008457	Cluster8326_1clades	95	PBI_PBS1_48	Bacillus virus PBS1	GCA_002601325.1
ANZ48300.1	008458	Cluster8327_1clades	69	ASESINO_287	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50711.1	008458	Cluster8327_1clades	95	STRATTON_286	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARV77049.1	008459	Cluster8328_1clades	95	PHABIO_418	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02914.1	008459	Cluster8328_1clades	93	PSA21_388	Pseudomonas phage Psa21	GCA_004340405.1
ASU03810.1	008460	Cluster8329_1clades	95	JOAD_105	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03565.1	008460	Cluster8329_1clades	95	RISINGSUN_105	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65591.1	008461	Cluster8330_1clades	95	2050HW_00256	Serratia phage 2050HW	GCA_002628125.1
QDB71356.1	008461	Cluster8330_1clades	95	CPT_Moabite_326	Serratia phage Moabite	GCA_006384735.1
QBZ71909.1	008462	Cluster8331_1clades	95	SEA_KRADAL_10	Streptomyces phage Kradal	GCA_004799925.1
AXH66171.1	008462	Cluster8331_1clades	95	SEA_SATIS_10	Streptomyces phage Satis	GCA_003366315.1
AXQ69288.1	008463	Cluster8332_1clades	95	CcrBL9_gp264c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69845.1	008463	Cluster8332_1clades	95	CcrSC_gp263c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69092.1	008464	Cluster8333_1clades	88	CcrBL9_gp068c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69648.1	008464	Cluster8333_1clades	95	CcrSC_gp066c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69329.1	008465	Cluster8334_1clades	90	CcrBL9_gp305	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69889.1	008465	Cluster8334_1clades	95	CcrSC_gp307	Caulobacter phage CcrSC	GCA_003443315.1
AYD81324.1	008466	Cluster8335_1clades	95	SEA_JUSTBECAUSE_159	Streptomyces phage JustBecause	GCA_003613775.1
QJD53727.1	008466	Cluster8335_1clades	95	SEA_KELA_157	Streptomyces phage Kela	GCA_012934305.1
BBA65158.1	008467	Cluster8336_1clades	95	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65617.1	008467	Cluster8336_1clades	95	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90533.1	008468	Cluster8337_1clades	95	HYO65_gp141	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90841.1	008468	Cluster8337_1clades	95	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06423.1	008469	Cluster8338_1clades	95	BcepSaruman_010	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74391.1	008469	Cluster8338_1clades	95	BcepSauron_011	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06460.1	008470	Cluster8339_1clades	95	BcepSaruman_047	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74428.1	008470	Cluster8339_1clades	95	BcepSauron_048	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06618.1	008471	Cluster8340_1clades	95	BcepSaruman_205	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74584.1	008471	Cluster8340_1clades	95	BcepSauron_204	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06689.1	008472	Cluster8341_1clades	95	BcepSaruman_276	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74657.1	008472	Cluster8341_1clades	95	BcepSauron_277	Burkholderia phage BcepSauron	GCA_005394215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX06762.1	008473	Cluster8342_1clades	95	BcepSaruman_349	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74732.1	008473	Cluster8342_1clades	95	BcepSauron_352	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06780.1	008474	Cluster8343_1clades	95	BcepSaruman_367	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74750.1	008474	Cluster8343_1clades	95	BcepSauron_370	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54724.1	008475	Cluster8344_1clades	95	b23_0109	Synechococcus phage B23	GCA_009745195.1
QGT54354.1	008475	Cluster8344_1clades	95	b3_0110	Synechococcus phage B3	GCA_009745215.1
QGT54830.1	008476	Cluster8345_1clades	95	b23_0215	Synechococcus phage B23	GCA_009745195.1
QGT54460.1	008476	Cluster8345_1clades	95	b3_0217	Synechococcus phage B3	GCA_009745215.1
QHJ78946.1	008477	Cluster8346_1clades	77	-	Myoviridae sp.	GCA_012593985.1
QIW90762.1	008477	Cluster8346_1clades	95	GCAPEGMB_00443	Vibrio phage V07	GCA_012361095.1
SOK59191.1	008478	Cluster8347_1clades	95	g383	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58655.1	008478	Cluster8347_1clades	95	g378	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000337	008479	SIG+TM	86	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000266	008479	SIG+TM	96	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AGH56805.1	008480	TM	94	CPXG_00002	Cyanophage P-RSM6	GCA_000906155.1
AGH57024.1	008480	TM	61	CPXG_00221	Cyanophage P-RSM6	GCA_000906155.1
AXF51254.1	008481	Cluster8351_1clades	94	WELLINGTON_124	Erwinia phage Wellington	GCA_003344985.1
ANZ49475.1	008481	Cluster8351_1clades	94	KWAN_123	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65488.1	008482	Cluster8352_1clades	94	2050HW_00153	Serratia phage 2050HW	GCA_002628125.1
QDB71258.1	008482	Cluster8352_1clades	94	CPT_Moabite_228	Serratia phage Moabite	GCA_006384735.1
ATA65507.1	008483	Cluster8353_1clades	94	2050HW_00172	Serratia phage 2050HW	GCA_002628125.1
QDB71276.1	008483	Cluster8353_1clades	94	CPT_Moabite_246	Serratia phage Moabite	GCA_006384735.1
ATA65541.1	008484	SIG+TM+TM	94	2050HW_00206	Serratia phage 2050HW	GCA_002628125.1
QDB71306.1	008484	SIG+TM+TM	94	CPT_Moabite_276	Serratia phage Moabite	GCA_006384735.1
QBP07427.1	008485	SIG+TM	81	REBECCA_85	Erwinia phage Rebecca	GCA_004521635.1
AUG86834.1	008485	SIG+TM	94	MORTIMER_85	Erwinia phage vB_EamM_Mortimer	GCA_002957765.1
AWY08619.1	008486	Cluster8356_1clades	94	Alexandra_309	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58939.1	008486	Cluster8356_1clades	87	Y3_299	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXQ69103.1	008487	Cluster8357_1clades	94	CcrBL9_gp079c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69658.1	008487	Cluster8357_1clades	94	CcrSC_gp076c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69150.1	008488	Cluster8358_1clades	94	CcrBL9_gp126	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69704.1	008488	Cluster8358_1clades	94	CcrSC_gp122	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69224.1	008489	Cluster8359_1clades	94	CcrBL9_gp200	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69778.1	008489	Cluster8359_1clades	94	CcrSC_gp196	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69314.1	008490	SIG+PC-Esterase+TM	94	CcrBL9_gp290	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69874.1	008490	SIG+PC-Esterase+TM	94	CcrSC_gp292	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69498.1	008491	Cluster8361_1clades	68	CcrBL9_gp474	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70047.1	008491	Cluster8361_1clades	94	CcrSC_gp465	Caulobacter phage CcrSC	GCA_003443315.1
AYD81411.1	008492	Cluster8362_1clades	94	SEA_JUSTBECAUSE_256	Streptomyces phage JustBecause	GCA_003613775.1
QJD53818.1	008492	Cluster8362_1clades	94	SEA_KELA_258	Streptomyces phage Kela	GCA_012934305.1
AYD81440.1	008493	Cluster8363_1clades	94	SEA_JUSTBECAUSE_285	Streptomyces phage JustBecause	GCA_003613775.1
QJD53845.1	008493	Cluster8363_1clades	94	SEA_KELA_285	Streptomyces phage Kela	GCA_012934305.1
BAS04806.1	008494	Cluster8364_1clades	94	AVU11_gp014	Ralstonia phage RSF1	GCA_001500875.1
BAQ02542.1	008494	Cluster8364_1clades	94	AVU38_gp014	Ralstonia phage RSL2	GCA_001503055.1
BAS04970.2	008495	Cluster8365_1clades	81	AVU11_gp178	Ralstonia phage RSF1	GCA_001500875.1
BAQ02696.2	008495	Cluster8365_1clades	94	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19176.1	008496	Cluster8366_1clades	94	FDH28_gp219	Ralstonia phage RP12	GCA_002617345.1
BAW19462.1	008496	Cluster8366_1clades	94	-	Ralstonia phage RP31	GCA_002617365.1
BBA65645.1	008497	Cluster8367_1clades	94	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65186.1	008497	Cluster8367_1clades	94	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90603.1	008498	Cluster8368_1clades	94	HYO65_gp211	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90910.1	008498	Cluster8368_1clades	94	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90625.1	008499	Cluster8369_1clades	94	HYO65_gp233	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90931.1	008499	Cluster8369_1clades	94	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54693.1	008500	Cluster8370_1clades	94	b23_0078	Synechococcus phage B23	GCA_009745195.1
QGT54323.1	008500	Cluster8370_1clades	94	b3_0079	Synechococcus phage B3	GCA_009745215.1
prevph1000000644	008501	Cluster8371_1clades	95	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000459	008501	Cluster8371_1clades	95	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000845	008502	Cluster8372_1clades	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000587	008502	Cluster8372_1clades	95	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000855	008503	Cluster8373_1clades	95	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000593	008503	Cluster8373_1clades	95	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QGH71919.1	008504	Cluster8374_1clades	89	N1M2_56	Klebsiella phage N1M2	GCA_010092605.1
AEV89519.1	008504	Cluster8374_1clades	93	OBP_082	Pseudomonas phage OBP	GCA_000896635.1
AFC21536.1	008505	Cluster8375_1clades	93	GAP32_088	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43655.1	008505	Cluster8375_1clades	90	CBB_90	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QMV28864.1	008506	Cluster8376_1clades	93	AP1_0157	Aeromonas phage AP1	GCA_014183365.1
AFN39146.1	008506	Cluster8376_1clades	93	CC2_012	Aeromonas phage CC2	GCA_000903495.1
AXQ68518.1	008507	Cluster8377_1clades	91	CcrBL10_gp314	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86808.1	008507	Cluster8377_1clades	93	CcrRogue_gp326	Caulobacter virus Rogue	GCA_000900555.1
AFU87917.1	008508	Cluster8378_1clades	93	CcrColossus_gp047	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68589.1	008508	Cluster8378_1clades	77	CcrPW_gp050	Caulobacter phage CcrPW	GCA_003443275.1
AMS01178.1	008509	Cluster8379_1clades	93	AR9_g094	Bacillus phage AR9	GCA_001743835.1
ASU00112.1	008509	Cluster8379_1clades	93	PBI_PBS1_290	Bacillus virus PBS1	GCA_002601325.1
ATA65578.1	008510	SIG+TM	93	2050HW_00243	Serratia phage 2050HW	GCA_002628125.1
QDB71343.1	008510	SIG+TM	93	CPT_Moabite_313	Serratia phage Moabite	GCA_006384735.1
AXQ68447.1	008511	Cluster8381_1clades	93	CcrBL10_gp243	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86733.1	008511	Cluster8381_1clades	92	CcrRogue_gp251	Caulobacter virus Rogue	GCA_000900555.1
AXQ69113.1	008512	Cluster8382_1clades	93	CcrBL9_gp089	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69667.1	008512	Cluster8382_1clades	93	CcrSC_gp085	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69126.1	008513	Cluster8383_1clades	93	CcrBL9_gp102	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69680.1	008513	Cluster8383_1clades	92	CcrSC_gp098	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69293.1	008514	Cluster8384_1clades	93	CcrBL9_gp269c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69850.1	008514	Cluster8384_1clades	93	CcrSC_gp268c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69446.1	008515	Cluster8385_1clades	93	CcrBL9_gp422	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69996.1	008515	Cluster8385_1clades	93	CcrSC_gp414	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69479.1	008516	Cluster8386_1clades	93	CcrBL9_gp455	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70028.1	008516	Cluster8386_1clades	93	CcrSC_gp446	Caulobacter phage CcrSC	GCA_003443315.1
AYD81289.1	008517	Cluster8387_1clades	93	SEA_JUSTBECAUSE_120	Streptomyces phage JustBecause	GCA_003613775.1
QJD53692.1	008517	Cluster8387_1clades	93	SEA_KELA_121	Streptomyces phage Kela	GCA_012934305.1
AYD81483.1	008518	Cluster8388_1clades	93	SEA_JUSTBECAUSE_328	Streptomyces phage JustBecause	GCA_003613775.1
QJD53886.1	008518	Cluster8388_1clades	93	SEA_KELA_326	Streptomyces phage Kela	GCA_012934305.1
BAW19057.1	008519	TM	93	FDH28_gp083	Ralstonia phage RP12	GCA_002617345.1
BAW19342.1	008519	TM	93	-	Ralstonia phage RP31	GCA_002617365.1
BAW19125.1	008520	Cluster8390_1clades	93	FDH28_gp270	Ralstonia phage RP12	GCA_002617345.1
BAW19411.1	008520	Cluster8390_1clades	73	-	Ralstonia phage RP31	GCA_002617365.1
BBA65252.1	008521	Cluster8391_1clades	93	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65711.1	008521	Cluster8391_1clades	93	-	Xanthomonas phage XacN1	GCA_003173815.1
QAX97706.1	008522	Cluster8392_1clades	92	ASswx1_60	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01438.1	008522	Cluster8392_1clades	93	ASwh1_379	Aeromonas phage Aswh_1	GCA_004146945.1
QBX06464.1	008523	Cluster8393_1clades	93	BcepSaruman_051	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74432.1	008523	Cluster8393_1clades	93	BcepSauron_052	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06725.1	008524	Cluster8394_1clades	93	BcepSaruman_312	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74693.1	008524	Cluster8394_1clades	93	BcepSauron_313	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32273.1	008525	Cluster8395_1clades	93	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41847.1	008525	Cluster8395_1clades	93	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32444.1	008526	Cluster8396_1clades	93	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42015.1	008526	Cluster8396_1clades	93	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54669.1	008527	Cluster8397_1clades	93	b23_0041	Synechococcus phage B23	GCA_009745195.1
QGT54299.1	008527	Cluster8397_1clades	93	b3_0041	Synechococcus phage B3	GCA_009745215.1
QGT54720.1	008528	Cluster8398_1clades	93	b23_0105	Synechococcus phage B23	GCA_009745195.1
QGT54350.1	008528	Cluster8398_1clades	93	b3_0106	Synechococcus phage B3	GCA_009745215.1
QGT54809.1	008529	Cluster8399_1clades	93	b23_0194	Synechococcus phage B23	GCA_009745195.1
QGT54439.1	008529	Cluster8399_1clades	93	b3_0196	Synechococcus phage B3	GCA_009745215.1
AIA65014.1	008530	SIG+TM	88	S13_217	Cronobacter phage S13	GCA_001503575.1
QHJ78918.1	008530	SIG+TM	93	-	Myoviridae sp.	GCA_012593985.1
prevph1000000744	008531	Cluster8401_1clades	94	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000496	008531	Cluster8401_1clades	94	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS06119.1	008532	Cluster8402_1clades	90	ABCD_0129	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78652.1	008532	Cluster8402_1clades	92	RB43ORF130c	Escherichia virus RB43	GCA_000863505.1
QBZ70680.1	008533	HTH	91	pETSU_099	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89604.1	008533	HTH	92	OBP_167	Pseudomonas phage OBP	GCA_000896635.1
AGH07517.1	008534	Cluster8404_1clades	92	CYVG_00073	Cyanophage S-SSM6a	GCA_002710385.1
AGH26228.1	008534	Cluster8404_1clades	91	CPMG_00127	Prochlorococcus phage MED4-213	GCA_000904535.1
AGR48127.1	008535	Cluster8405_1clades	91	SmphiM12_495	Sinorhizobium phage phiM12	GCA_001023565.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF13664.1	008535	Cluster8405_1clades	92	PHIN3_401	Sinorhizobium phage phiN3	GCA_001501175.1
AND75426.1	008536	Cluster8406_1clades	92	ME3_265	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QIG65781.1	008536	Cluster8406_1clades	88	phiOC_p116	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AFQ96632.1	008537	SIG+TM+TM	81	G173_gp087	Erwinia phage phiEaH2	GCA_000902915.1
ANZ48197.1	008537	SIG+TM+TM	92	ASESINO_184	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ATA65595.1	008538	APATPase	92	2050HW_00260	Serratia phage 2050HW	GCA_002628125.1
QDB71359.1	008538	APATPase	92	CPT_Moabite_329	Serratia phage Moabite	GCA_006384735.1
AFU88205.1	008539	Cluster8409_1clades	91	CcrColossus_gp335	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68882.1	008539	Cluster8409_1clades	92	CcrPW_gp343	Caulobacter phage CcrPW	GCA_003443275.1
AFU88230.1	008540	Cluster8410_1clades	82	CcrColossus_gp360	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68907.1	008540	Cluster8410_1clades	92	CcrPW_gp368	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69377.1	008541	Cluster8411_1clades	92	CcrBL9_gp353	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69937.1	008541	Cluster8411_1clades	92	CcrSC_gp355	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69487.1	008542	Cluster8412_1clades	92	CcrBL9_gp463	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70035.1	008542	Cluster8412_1clades	92	CcrSC_gp453	Caulobacter phage CcrSC	GCA_003443315.1
BAS04797.2	008543	Cluster8413_1clades	92	AVU11_agp03	Ralstonia phage RSF1	GCA_001500875.1
BAQ02533.2	008543	Cluster8413_1clades	31	-	Ralstonia phage RSL2	GCA_001503055.1
BAS04900.2	008544	Cluster8414_1clades	92	AVU11_gp108	Ralstonia phage RSF1	GCA_001500875.1
BAQ02626.1	008544	Cluster8414_1clades	90	AVU38_gp098	Ralstonia phage RSL2	GCA_001503055.1
BBA65238.1	008545	Cluster8415_1clades	92	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65697.1	008545	Cluster8415_1clades	92	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06434.1	008546	Cluster8416_1clades	92	BcepSaruman_021	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74401.1	008546	Cluster8416_1clades	92	BcepSauron_021	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06590.1	008547	Cluster8417_1clades	92	BcepSaruman_177	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74555.1	008547	Cluster8417_1clades	92	BcepSauron_175	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06779.1	008548	Cluster8418_1clades	92	BcepSaruman_366	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74749.1	008548	Cluster8418_1clades	92	BcepSauron_369	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32184.1	008549	Cluster8419_1clades	92	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41762.1	008549	Cluster8419_1clades	92	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ96711.1	008550	TM+TM	92	PS1_0200	Aeromonas phage PS1	GCA_007051165.2
QFR59344.1	008550	TM+TM	92	PS2_0202	Aeromonas phage PS2	GCA_009388305.2
QGT54666.1	008551	Cluster8421_1clades	92	b23_0038	Synechococcus phage B23	GCA_009745195.1
QGT54296.1	008551	Cluster8421_1clades	92	b3_0038	Synechococcus phage B3	GCA_009745215.1
QIG57764.1	008552	TM	92	SEA_PAULODIABOLI_29	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58065.1	008552	TM	92	SEA_PAULODIABOLI_384	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57774.1	008553	Cluster8423_1clades	92	SEA_PAULODIABOLI_39	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58075.1	008553	Cluster8423_1clades	92	SEA_PAULODIABOLI_394	Microbacterium phage PauloDiaboli	GCA_011067425.1
QCW23031.1	008554	Cluster8424_1clades	69	-	Synechococcus phage S-B05	GCA_006083695.1
QJT70243.1	008554	Cluster8424_1clades	92	SynMITS9220M01_237	Synechococcus phage SynMITS9220M01	GCA_013187275.1
prevph1000000768	008555	Cluster8425_1clades	93	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000521	008555	Cluster8425_1clades	93	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44423.1	008556	Cluster8426_1clades	91	PSSM2_045	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12227.1	008556	Cluster8426_1clades	91	PRTG_00069	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44426.1	008557	Cluster8427_1clades	91	PSSM2_048	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12225.1	008557	Cluster8427_1clades	91	PRTG_00067	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44680.1	008558	Cluster8428_1clades	91	PSSM2_303	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12296.1	008558	Cluster8428_1clades	91	PRTG_00143	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFC21465.1	008559	Cluster8429_1clades	77	GAP32_018	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFA44617.1	008559	Cluster8429_1clades	91	RaK2_00344	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44649.1	008560	Cluster8430_1clades	91	RaK2_00376	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44665.1	008560	Cluster8430_1clades	90	RaK2_00392	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AXQ68489.1	008561	SIG+TM	91	CcrBL10_gp285	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86777.1	008561	SIG+TM	91	CcrRogue_gp295	Caulobacter virus Rogue	GCA_000900555.1
AUZ95310.1	008562	Cluster8432_1clades	72	FDI40_gp551	Agrobacterium phage Atu_ph07	GCA_002628245.1
AKF13642.1	008562	Cluster8432_1clades	91	PHIN3_379	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01275.1	008563	Cluster8433_1clades	91	AR9_g191	Bacillus phage AR9	GCA_001743835.1
AST99903.1	008563	Cluster8433_1clades	86	PBI_PBS1_81	Bacillus virus PBS1	GCA_002601325.1
APU01519.1	008564	Cluster8434_1clades	91	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53142.1	008564	Cluster8434_1clades	45	65p134	Aeromonas virus 65	GCA_000893255.1
QBZ72075.1	008565	Cluster8435_1clades	91	SEA_KRADAL_179	Streptomyces phage Kradal	GCA_004799925.1
AXH66338.1	008565	Cluster8435_1clades	91	SEA_SATIS_179	Streptomyces phage Satis	GCA_003366315.1
AXQ69480.1	008566	SIG+35exo	91	CcrBL9_gp456	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70029.1	008566	SIG+35exo	91	CcrSC_gp447	Caulobacter phage CcrSC	GCA_003443315.1
AYD81277.1	008567	Cluster8437_1clades	91	SEA_JUSTBECAUSE_108	Streptomyces phage JustBecause	GCA_003613775.1
QJD53680.1	008567	Cluster8437_1clades	91	SEA_KELA_109	Streptomyces phage Kela	GCA_012934305.1
AYD81448.1	008568	Cluster8438_1clades	91	SEA_JUSTBECAUSE_293	Streptomyces phage JustBecause	GCA_003613775.1
QJD53853.1	008568	Cluster8438_1clades	91	SEA_KELA_293	Streptomyces phage Kela	GCA_012934305.1
BAS04831.1	008569	Cluster8439_1clades	91	AVU11_gp039	Ralstonia phage RSF1	GCA_001500875.1
BAQ02564.1	008569	Cluster8439_1clades	90	AVU38_gp036	Ralstonia phage RSL2	GCA_001503055.1
BBA65703.1	008570	Cluster8440_1clades	91	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65244.1	008570	Cluster8440_1clades	91	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90416.1	008571	Cluster8441_1clades	91	HYO65_gp024	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90724.1	008571	Cluster8441_1clades	91	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90535.1	008572	Cluster8442_1clades	91	HYO65_gp143	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90843.1	008572	Cluster8442_1clades	91	-	Tenacibaculum phage PTm5	GCA_009730715.1
ATA65598.1	008573	Cluster8443_1clades	65	2050HW_00263	Serratia phage 2050HW	GCA_002628125.1
QDB71362.1	008573	Cluster8443_1clades	91	CPT_Moabite_332	Serratia phage Moabite	GCA_006384735.1
QBZ70718.1	008574	Cluster8444_1clades	83	pETSU_137	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72033.1	008574	Cluster8444_1clades	91	N1M2_170	Klebsiella phage N1M2	GCA_010092605.1
QGT54667.1	008575	Cluster8445_1clades	91	b23_0039	Synechococcus phage B23	GCA_009745195.1
QGT54297.1	008575	Cluster8445_1clades	91	b3_0039	Synechococcus phage B3	GCA_009745215.1
QGT54718.1	008576	Cluster8446_1clades	91	b23_0103	Synechococcus phage B23	GCA_009745195.1
QGT54348.1	008576	Cluster8446_1clades	91	b3_0104	Synechococcus phage B3	GCA_009745215.1
prevph1000000355	008577	Cluster8447_1clades	92	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000281	008577	Cluster8447_1clades	92	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000841	008578	Cluster8448_1clades	92	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000583	008578	Cluster8448_1clades	92	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABY62848.1	008579	Cluster8449_1clades	90	201phi2-1p014	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76640.1	008579	Cluster8449_1clades	82	PHABIO_9	Pseudomonas phage Phabio	GCA_002624965.1
ADM80085.1	008580	Cluster8450_1clades	90	phiAS5_ORF0242	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17772.1	008580	Cluster8450_1clades	89	Aeh1gORF131c	Aeromonas virus Aeh1	GCA_000843245.1
APU01688.1	008581	Cluster8451_1clades	90	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53324.1	008581	Cluster8451_1clades	90	65p316	Aeromonas virus 65	GCA_000893255.1
AGH07694.1	008582	Cluster8452_1clades	80	CYVG_00251	Cyanophage S-SSM6a	GCA_002710385.1
AGH26163.1	008582	Cluster8452_1clades	90	CPMG_00062	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH57000.1	008583	Cluster8453_1clades	90	CPXG_00197	Cyanophage P-RSM6	GCA_000906155.1
AJK27461.1	008583	Cluster8453_1clades	84	PTIM40_34	Cyanophage P-TIM40	GCA_001470935.1
ALY07158.1	008584	Cluster8454_1clades	78	VmeM32_00172	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07162.1	008584	Cluster8454_1clades	90	VmeM32_00176	Vibrio phage vB_VmeM-32	GCA_002608825.1
QBP07587.1	008585	Cluster8455_1clades	90	DERBICUS_161	Erwinia phage Derbicus	GCA_004521655.1
ANZ49010.1	008585	Cluster8455_1clades	90	EARLPHILLIPIV_161	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
AOO14265.1	008586	Cluster8456_1clades	90	Sn110110_071	Cyanophage S-RIM14	GCA_002599065.1
AOO14914.1	008586	Cluster8456_1clades	90	W1230910_068	Cyanophage S-RIM14	GCA_002599125.1
ASU03753.1	008587	Cluster8458_1clades	90	JOAD_162	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03509.1	008587	Cluster8458_1clades	90	RISINGSUN_161	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QBZ72145.1	008588	Cluster8459_1clades	90	SEA_KRADAL_259	Streptomyces phage Kradal	GCA_004799925.1
AXH66407.1	008588	Cluster8459_1clades	90	SEA_SATIS_258	Streptomyces phage Satis	GCA_003366315.1
AFU88191.1	008589	IMM	86	CcrColossus_gp321	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68869.1	008589	IMM	90	CcrPW_gp330	Caulobacter phage CcrPW	GCA_003443275.1
AFU88263.1	008590	Cluster8461_1clades	88	CcrColossus_gp393	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68938.1	008590	Cluster8461_1clades	90	CcrPW_gp399	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69169.1	008591	Cluster8462_1clades	90	CcrBL9_gp145	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69723.1	008591	Cluster8462_1clades	90	CcrSC_gp141	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69265.1	008592	Cluster8463_1clades	90	CcrBL9_gp241c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69821.1	008592	Cluster8463_1clades	90	CcrSC_gp239c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69397.1	008593	Cluster8464_1clades	90	CcrBL9_gp373	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69955.1	008593	Cluster8464_1clades	90	CcrSC_gp373	Caulobacter phage CcrSC	GCA_003443315.1
AYD81199.1	008594	Cluster8465_1clades	90	SEA_JUSTBECAUSE_30	Streptomyces phage JustBecause	GCA_003613775.1
QJD53601.1	008594	Cluster8465_1clades	78	SEA_KELA_30	Streptomyces phage Kela	GCA_012934305.1
BAS05020.2	008595	Cluster8466_1clades	84	AVU11_agp45	Ralstonia phage RSF1	GCA_001500875.1
BAQ02750.1	008595	Cluster8466_1clades	90	AVU38_gp222	Ralstonia phage RSL2	GCA_001503055.1
BBI90529.1	008596	Cluster8467_1clades	90	HYO65_gp137	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90837.1	008596	Cluster8467_1clades	90	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32224.1	008597	SIG+TM	90	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41802.1	008597	SIG+TM	90	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBX32456.1	008598	SIG+TM+TM	90	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42028.1	008598	SIG+TM+TM	90	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22845.1	008599	Cluster8470_1clades	90	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50702.1	008599	Cluster8470_1clades	87	-	Synechococcus phage S-B43	GCA_006869725.1
QDJ96705.1	008600	SIG+TM	90	PS1_0194	Aeromonas phage PS1	GCA_007051165.2
QFR59338.1	008600	SIG+TM	90	PS2_0196	Aeromonas phage PS2	GCA_009388305.2
QGT54731.1	008601	Cluster8472_1clades	90	b23_0116	Synechococcus phage B23	GCA_009745195.1
QGT54361.1	008601	Cluster8472_1clades	90	b3_0117	Synechococcus phage B3	GCA_009745215.1
prevph1000000075	008602	Cluster8473_1clades	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000060	008602	Cluster8473_1clades	91	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000243	008603	Cluster8474_1clades	91	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000193	008603	Cluster8474_1clades	91	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000324	008604	Cluster8475_1clades	91	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000253	008604	Cluster8475_1clades	91	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44428.1	008605	Cluster8476_1clades	89	PSSM2_050	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12223.1	008605	Cluster8476_1clades	89	PRTG_00065	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01464.1	008606	Cluster8477_1clades	66	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53086.1	008606	Cluster8477_1clades	89	65p076	Aeromonas virus 65	GCA_000893255.1
APU01661.1	008607	Cluster8478_1clades	89	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53292.1	008607	Cluster8478_1clades	89	65p284	Aeromonas virus 65	GCA_000893255.1
AFU88040.1	008608	SIG+TM	89	CcrColossus_gp170	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68717.1	008608	SIG+TM	89	CcrPW_gp178c	Caulobacter phage CcrPW	GCA_003443275.1
AIA65028.1	008609	Cluster8480_1clades	89	S13_231	Cronobacter phage S13	GCA_001503575.1
QHJ78907.1	008609	Cluster8480_1clades	83	-	Myoviridae sp.	GCA_012593985.1
AMM43979.1	008610	Cluster8481_1clades	88	CBB_416	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88939.1	008610	Cluster8481_1clades	89	BF_0414	Serratia phage BF	GCA_002619745.1
AMS01093.1	008611	SIG+TM	80	AR9_g008	Bacillus phage AR9	GCA_001743835.1
ASU00015.1	008611	SIG+TM	89	PBI_PBS1_193	Bacillus virus PBS1	GCA_002601325.1
ATA65532.1	008612	SIG+TM+TM	89	2050HW_00197	Serratia phage 2050HW	GCA_002628125.1
QDB71296.1	008612	SIG+TM+TM	89	CPT_Moabite_266	Serratia phage Moabite	GCA_006384735.1
ATA65586.1	008613	Cluster8484_1clades	89	2050HW_00251	Serratia phage 2050HW	GCA_002628125.1
QDB71351.1	008613	Cluster8484_1clades	89	CPT_Moabite_321	Serratia phage Moabite	GCA_006384735.1
QBZ72210.1	008614	Cluster8485_1clades	89	SEA_KRADAL_324	Streptomyces phage Kradal	GCA_004799925.1
AXH66473.1	008614	Cluster8485_1clades	89	SEA_SATIS_324	Streptomyces phage Satis	GCA_003366315.1
AUZ95452.1	008615	SIG+Ribosomal_S21	83	FDI40_gp713	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72842.1	008615	SIG+Ribosomal_S21	89	-	Myoviridae sp.	GCA_003657725.1
AFU88084.1	008616	Cluster8487_1clades	87	CcrColossus_gp214	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68760.1	008616	Cluster8487_1clades	89	CcrPW_gp221c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69320.1	008617	Cluster8488_1clades	89	CcrBL9_gp296	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69880.1	008617	Cluster8488_1clades	77	CcrSC_gp298	Caulobacter phage CcrSC	GCA_003443315.1
BBA65708.1	008618	Cluster8489_1clades	89	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65249.1	008618	Cluster8489_1clades	89	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90612.1	008619	Cluster8490_1clades	89	HYO65_gp220	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90918.1	008619	Cluster8490_1clades	89	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06664.1	008620	DUF3175	89	BcepSaruman_251	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74633.1	008620	DUF3175	89	BcepSauron_253	Burkholderia phage BcepSauron	GCA_005394215.1
ATA65682.1	008621	Cluster8492_1clades	84	2050HW_00347	Serratia phage 2050HW	GCA_002628125.1
QDB71103.1	008621	Cluster8492_1clades	89	CPT_Moabite_071	Serratia phage Moabite	GCA_006384735.1
SOK59285.1	008622	Cluster8493_1clades	89	g477	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58750.1	008622	Cluster8493_1clades	89	g473	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000801	008623	Cluster8494_1clades	90	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000548	008623	Cluster8494_1clades	90	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44615.1	008624	Cluster8495_1clades	88	PSSM2_238	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12356.1	008624	Cluster8495_1clades	88	PRTG_00203	Prochlorococcus phage P-SSM5	GCA_002991095.1
AON97195.1	008625	Cluster8496_1clades	88	E_187	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78712.1	008625	Cluster8496_1clades	88	RB43ORF190c	Escherichia virus RB43	GCA_000863505.1
AFU88196.1	008626	Cluster8497_1clades	88	CcrColossus_gp326	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68873.1	008626	Cluster8497_1clades	88	CcrPW_gp334	Caulobacter phage CcrPW	GCA_003443275.1
AXF51351.1	008627	SIG+TM	88	WELLINGTON_225	Erwinia phage Wellington	GCA_003344985.1
ANZ49577.1	008627	SIG+TM	88	KWAN_225	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03799.1	008628	Cluster8500_1clades	88	JOAD_116	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03554.1	008628	Cluster8500_1clades	88	RISINGSUN_116	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXF51119.1	008629	SIG+TM	88	MLDJOKPK_00240	Salmonella phage SPAsTU	GCA_003183805.1
AEP84033.1	008629	SIG+TM	86	SPN3US_0200	Salmonella phage SPN3US	GCA_001042275.1
AXQ69271.1	008630	Cluster8502_1clades	88	CcrBL9_gp247c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69827.1	008630	Cluster8502_1clades	85	CcrSC_gp245c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69519.1	008631	ZDNA-HTH	86	CcrBL9_gp495	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70064.1	008631	ZDNA-HTH	88	CcrSC_gp482	Caulobacter phage CcrSC	GCA_003443315.1
BAW19193.1	008632	TM	88	FDH28_gp202	Ralstonia phage RP12	GCA_002617345.1
BAW19479.1	008632	TM	88	-	Ralstonia phage RP31	GCA_002617365.1
BAW19196.1	008633	Cluster8505_1clades	88	FDH28_gp199	Ralstonia phage RP12	GCA_002617345.1
BAW19482.1	008633	Cluster8505_1clades	88	-	Ralstonia phage RP31	GCA_002617365.1
BBA65195.1	008634	Cluster8506_1clades	88	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65654.1	008634	Cluster8506_1clades	88	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90438.1	008635	Cluster8507_1clades	88	HYO65_gp046	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90745.1	008635	Cluster8507_1clades	88	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90447.1	008636	Cluster8508_1clades	88	HYO65_gp055	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90755.1	008636	Cluster8508_1clades	88	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBO61544.1	008637	Cluster8509_1clades	88	G17_00048	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62150.1	008637	Cluster8509_1clades	88	G17_00661	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBX06558.1	008638	Cluster8510_1clades	88	BcepSaruman_145	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74525.1	008638	Cluster8510_1clades	88	BcepSauron_145	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06747.1	008639	Cluster8511_1clades	88	BcepSaruman_334	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74716.1	008639	Cluster8511_1clades	88	BcepSauron_336	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06421.1	008640	Cluster8512_1clades	88	BcepSaruman_008	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74389.1	008640	Cluster8512_1clades	66	BcepSauron_009	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06524.1	008641	Cluster8513_1clades	88	BcepSaruman_111	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74490.1	008641	Cluster8513_1clades	84	BcepSauron_110	Burkholderia phage BcepSauron	GCA_005394215.1
SOK58873.1	008642	Cluster8514_1clades	88	g065	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58336.1	008642	Cluster8514_1clades	88	g059	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58880.1	008643	Cluster8515_1clades	88	g072	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58343.1	008643	Cluster8515_1clades	88	g066	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000743	008644	Cluster8516_1clades	47	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000495	008644	Cluster8516_1clades	89	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ADM79938.1	008645	Cluster8517_1clades	85	phiAS5_ORF0095	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17966.1	008645	Cluster8517_1clades	87	Aeh1ORF297c	Aeromonas virus Aeh1	GCA_000843245.1
AAX44459.1	008646	Cluster8518_1clades	87	PSSM2_081	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12194.1	008646	Cluster8518_1clades	87	PRTG_00036	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01697.1	008647	Cluster8519_1clades	87	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53336.1	008647	Cluster8519_1clades	87	65p328	Aeromonas virus 65	GCA_000893255.1
AFU88093.1	008648	Cluster8520_1clades	87	CcrColossus_gp223	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68769.1	008648	Cluster8520_1clades	87	CcrPW_gp230c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88132.1	008649	Cluster8521_1clades	87	CcrColossus_gp262	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68809.1	008649	Cluster8521_1clades	87	CcrPW_gp270	Caulobacter phage CcrPW	GCA_003443275.1
AGR47639.1	008650	Cluster8522_1clades	87	SmphiM12_007	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13274.1	008650	Cluster8522_1clades	87	PHIN3_7	Sinorhizobium phage phiN3	GCA_001501175.1
AGR48100.1	008651	Cluster8523_1clades	87	SmphiM12_468	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13632.1	008651	Cluster8523_1clades	87	PHIN3_369	Sinorhizobium phage phiN3	GCA_001501175.1
AFC21900.1	008652	Cluster8524_1clades	86	GAP32_445	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44029.1	008652	Cluster8524_1clades	87	CBB_466	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01232.1	008653	Herpes_UL6	87	AR9_g148	Bacillus phage AR9	GCA_001743835.1
AST99858.1	008653	Herpes_UL6	87	PBI_PBS1_36	Bacillus virus PBS1	GCA_002601325.1
AXF51270.1	008654	Cluster8526_1clades	87	WELLINGTON_140	Erwinia phage Wellington	GCA_003344985.1
ANZ49491.1	008654	Cluster8526_1clades	87	KWAN_139	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03780.1	008655	SIG+TM	87	JOAD_135	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03536.1	008655	SIG+TM	87	RISINGSUN_134	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASV44235.1	008656	Cluster8528_1clades	82	PBI_SCTP2_220	Salicola phage SCTP-2	GCA_002625545.1
ASV44236.1	008656	Cluster8528_1clades	87	PBI_SCTP2_221	Salicola phage SCTP-2	GCA_002625545.1
QBZ72057.1	008657	Cluster8529_1clades	87	SEA_KRADAL_161	Streptomyces phage Kradal	GCA_004799925.1
AXH66320.1	008657	Cluster8529_1clades	87	SEA_SATIS_161	Streptomyces phage Satis	GCA_003366315.1
AFU88162.1	008658	Cluster8530_1clades	85	CcrColossus_gp292	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68838.1	008658	Cluster8530_1clades	87	CcrPW_gp299	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69073.1	008659	Cluster8531_1clades	87	CcrBL9_gp049c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69633.1	008659	Cluster8531_1clades	87	CcrSC_gp051c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69131.1	008660	Cluster8532_1clades	87	CcrBL9_gp107	Caulobacter phage CcrBL9	GCA_003443295.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69685.1	008660	Cluster8532_1clades	87	CcrSC_gp103	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69356.1	008661	Cluster8533_1clades	87	CcrBL9_gp332	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69915.1	008661	Cluster8533_1clades	87	CcrSC_gp333	Caulobacter phage CcrSC	GCA_003443315.1
BAW19137.1	008662	Cluster8534_1clades	87	FDH28_gp258	Ralstonia phage RP12	GCA_002617345.1
BAW19423.1	008662	Cluster8534_1clades	87	-	Ralstonia phage RP31	GCA_002617365.1
BBI90581.1	008663	Cluster8535_1clades	87	HYO65_gp189	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90889.1	008663	Cluster8535_1clades	87	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90459.1	008664	Cluster8536_1clades	39	HYO65_gp067	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90767.1	008664	Cluster8536_1clades	87	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06853.1	008665	Cluster8537_1clades	87	BcepSaruman_440	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74822.1	008665	Cluster8537_1clades	87	BcepSauron_442	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ96691.1	008666	SIG+TM	87	PS1_0180	Aeromonas phage PS1	GCA_007051165.2
QFR59324.1	008666	SIG+TM	87	PS2_0182	Aeromonas phage PS2	GCA_009388305.2
QDJ96767.1	008667	Cluster8539_1clades	87	PS1_0009	Aeromonas phage PS1	GCA_007051165.2
QFR59400.1	008667	Cluster8539_1clades	87	PS2_0009	Aeromonas phage PS2	GCA_009388305.2
QGT54723.1	008668	Cluster8540_1clades	87	b23_0108	Synechococcus phage B23	GCA_009745195.1
QGT54353.1	008668	Cluster8540_1clades	87	b3_0109	Synechococcus phage B3	GCA_009745215.1
QGT54755.1	008669	Cluster8541_1clades	87	b23_0140	Synechococcus phage B23	GCA_009745195.1
QGT54385.1	008669	Cluster8541_1clades	87	b3_0141	Synechococcus phage B3	GCA_009745215.1
QGT54765.1	008670	Cluster8542_1clades	87	b23_0150	Synechococcus phage B23	GCA_009745195.1
QGT54395.1	008670	Cluster8542_1clades	87	b3_0151	Synechococcus phage B3	GCA_009745215.1
QGT54770.1	008671	NAD_synthase	87	b23_0155	Synechococcus phage B23	GCA_009745195.1
QGT54400.1	008671	NAD_synthase	87	b3_0156	Synechococcus phage B3	GCA_009745215.1
QIG57749.1	008672	Cluster8544_1clades	87	SEA_PAULODIABOLI_11	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58050.1	008672	Cluster8544_1clades	87	SEA_PAULODIABOLI_366	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000114	008673	Cluster8545_1clades	88	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000081	008673	Cluster8545_1clades	88	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000240	008674	Cluster8546_1clades	88	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000190	008674	Cluster8546_1clades	88	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000301	008675	Cluster8547_1clades	88	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000233	008675	Cluster8547_1clades	88	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000339	008676	Cluster8548_1clades	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000268	008676	Cluster8548_1clades	88	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44493.1	008677	Cluster8549_1clades	86	PSSM2_115	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12473.1	008677	Cluster8549_1clades	86	PRTG_00326	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88077.1	008678	Cluster8550_1clades	86	CcrColossus_gp207	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68754.1	008678	Cluster8550_1clades	86	CcrPW_gp215c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88300.1	008679	Cluster8551_1clades	86	CcrColossus_gp430	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68975.1	008679	Cluster8551_1clades	86	CcrPW_gp436c	Caulobacter phage CcrPW	GCA_003443275.1
AGH56945.1	008680	Cluster8552_1clades	64	CPXG_00142	Cyanophage P-RSM6	GCA_000906155.1
AIR93599.1	008680	Cluster8552_1clades	86	AVU42_gp054	Prochlorococcus phage P-TIM68	GCA_001503075.1
AMM43992.1	008681	Cluster8553_1clades	86	CBB_429	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88949.1	008681	Cluster8553_1clades	85	BF_0424	Serratia phage BF	GCA_002619745.1
AOO14402.1	008682	Cluster8554_1clades	86	Sn110110_209	Cyanophage S-RIM14	GCA_002599065.1
AOO15051.1	008682	Cluster8554_1clades	86	W1230910_206	Cyanophage S-RIM14	GCA_002599125.1
ASU03722.1	008683	SIG+TM+TM	86	JOAD_193	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03479.1	008683	SIG+TM+TM	86	RISINGSUN_191	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03762.1	008684	Cluster8556_1clades	86	JOAD_153	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03518.1	008684	Cluster8556_1clades	86	RISINGSUN_152	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
QCG76137.1	008685	SIG+Ribosomal_S21	68	EST35_0256	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44208.1	008685	SIG+Ribosomal_S21	86	PBI_SCTP2_193	Salicola phage SCTP-2	GCA_002625545.1
ATA65675.1	008686	Cluster8558_1clades	86	2050HW_00340	Serratia phage 2050HW	GCA_002628125.1
QDB71097.1	008686	Cluster8558_1clades	86	CPT_Moabite_065	Serratia phage Moabite	GCA_006384735.1
AXQ68541.1	008687	Cluster8559_1clades	86	CcrPW_gp002c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68991.1	008687	Cluster8559_1clades	86	CcrPW_gp452c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69362.1	008688	Cluster8560_1clades	85	CcrBL9_gp338	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69922.1	008688	Cluster8560_1clades	86	CcrSC_gp340	Caulobacter phage CcrSC	GCA_003443315.1
BAW19084.1	008689	LRRNT	86	FDH28_gp110	Ralstonia phage RP12	GCA_002617345.1
BAW19370.1	008689	LRRNT	86	-	Ralstonia phage RP31	GCA_002617365.1
BBI90657.1	008690	Cluster8562_1clades	86	HYO65_gp265	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90962.1	008690	Cluster8562_1clades	86	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90658.1	008691	Cluster8563_1clades	86	HYO65_gp266	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90963.1	008691	Cluster8563_1clades	86	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90679.1	008692	Cluster8564_1clades	86	HYO65_gp287	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90986.1	008692	Cluster8564_1clades	86	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06547.1	008693	Cluster8565_1clades	86	BcepSaruman_134	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74513.1	008693	Cluster8565_1clades	86	BcepSauron_133	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06548.1	008694	Cluster8566_1clades	86	BcepSaruman_135	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74514.1	008694	Cluster8566_1clades	86	BcepSauron_134	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06782.1	008695	Cluster8567_1clades	86	BcepSaruman_369	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74752.1	008695	Cluster8567_1clades	86	BcepSauron_372	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32228.1	008696	Cluster8568_1clades	86	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41806.1	008696	Cluster8568_1clades	86	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32529.1	008697	Cluster8569_1clades	86	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42102.1	008697	Cluster8569_1clades	86	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54686.1	008698	Cluster8570_1clades	86	b23_0069	Synechococcus phage B23	GCA_009745195.1
QGT54316.1	008698	Cluster8570_1clades	86	b3_0070	Synechococcus phage B3	GCA_009745215.1
QGT54786.1	008699	Cluster8571_1clades	86	b23_0171	Synechococcus phage B23	GCA_009745195.1
QGT54416.1	008699	Cluster8571_1clades	86	b3_0172	Synechococcus phage B3	GCA_009745215.1
prevph1000000660	008700	Cluster8572_1clades	87	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000472	008700	Cluster8572_1clades	87	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000819	008701	Thioredoxin	87	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000562	008701	Thioredoxin	87	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88270.1	008702	Cluster8574_1clades	85	CcrColossus_gp400	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68946.1	008702	Cluster8574_1clades	85	CcrPW_gp407	Caulobacter phage CcrPW	GCA_003443275.1
AMO43128.1	008703	Cluster8575_1clades	85	R1080702_119	Cyanophage S-RIM32	GCA_001754165.1
AGH26114.1	008703	Cluster8575_1clades	85	CPMG_00013	Prochlorococcus phage MED4-213	GCA_000904535.1
AXF51229.1	008704	Cluster8576_1clades	85	WELLINGTON_99	Erwinia phage Wellington	GCA_003344985.1
ANZ49450.1	008704	Cluster8576_1clades	85	KWAN_98	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51344.1	008705	Cluster8577_1clades	85	WELLINGTON_218	Erwinia phage Wellington	GCA_003344985.1
ANZ49571.1	008705	Cluster8577_1clades	85	KWAN_219	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ARV76788.1	008706	Cluster8578_1clades	85	PHABIO_157	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02678.1	008706	Cluster8578_1clades	83	PSA21_151	Pseudomonas phage Psa21	GCA_004340405.1
ASU03733.1	008707	Cluster8579_1clades	84	JOAD_182	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03489.1	008707	Cluster8579_1clades	85	RISINGSUN_181	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03899.1	008708	Cluster8580_1clades	85	JOAD_16	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03654.1	008708	Cluster8580_1clades	85	RISINGSUN_16	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXQ69333.1	008709	Cluster8581_1clades	85	CcrBL9_gp309	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69894.1	008709	Cluster8581_1clades	85	CcrSC_gp312	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69618.1	008710	Cluster8582_1clades	85	CcrSC_gp036	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70118.1	008710	Cluster8582_1clades	85	CcrSC_gp536	Caulobacter phage CcrSC	GCA_003443315.1
AZU97960.1	008711	Cluster8583_1clades	85	CPT_Munch_016	Salmonella phage Munch	GCA_004015485.1
QIG63018.1	008711	Cluster8583_1clades	85	SEPL_405	Salmonella phage SE_PL	GCA_011067555.1
BAS04994.2	008712	Cluster8584_1clades	85	AVU11_agp41	Ralstonia phage RSF1	GCA_001500875.1
BAQ02723.2	008712	Cluster8584_1clades	85	-	Ralstonia phage RSL2	GCA_001503055.1
BAS04902.2	008713	TM	85	AVU11_gp110	Ralstonia phage RSF1	GCA_001500875.1
BAQ02629.2	008713	TM	84	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65243.1	008714	Cluster8586_1clades	85	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65702.1	008714	Cluster8586_1clades	85	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65413.1	008715	Cluster8587_1clades	85	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96436.1	008715	Cluster8587_1clades	84	Xoosp13_250	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90406.1	008716	Cluster8588_1clades	85	HYO65_gp014	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90715.1	008716	Cluster8588_1clades	85	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90469.1	008717	Cluster8589_1clades	85	HYO65_gp077	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90776.1	008717	Cluster8589_1clades	85	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90481.1	008718	Cluster8590_1clades	85	HYO65_gp089	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90789.1	008718	Cluster8590_1clades	85	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90511.1	008719	Cluster8591_1clades	85	HYO65_gp119	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90819.1	008719	Cluster8591_1clades	66	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06442.1	008720	Cluster8592_1clades	85	BcepSaruman_029	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74410.1	008720	Cluster8592_1clades	85	BcepSauron_030	Burkholderia phage BcepSauron	GCA_005394215.1
QBZ70789.1	008721	Cluster8593_1clades	85	pETSU_208	Edwardsiella virus pEt-SU	GCA_004800915.1
AEV89727.1	008721	Cluster8593_1clades	81	OBP_290	Pseudomonas phage OBP	GCA_000896635.1
QGT54784.1	008722	Cluster8594_1clades	85	b23_0169	Synechococcus phage B23	GCA_009745195.1
QGT54414.1	008722	Cluster8594_1clades	85	b3_0170	Synechococcus phage B3	GCA_009745215.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU88043.1	008723	Cluster8595_1clades	84	CcrColossus_gp173	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68720.1	008723	Cluster8595_1clades	81	CcrPW_gp181c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01188.1	008724	Cluster8596_1clades	84	AR9_g104	Bacillus phage AR9	GCA_001743835.1
ASU00122.1	008724	Cluster8596_1clades	84	PBI_PBS1_300	Bacillus virus PBS1	GCA_002601325.1
AMS01217.1	008725	Cluster8597_1clades	84	AR9_g133	Bacillus phage AR9	GCA_001743835.1
AST99842.1	008725	Cluster8597_1clades	84	PBI_PBS1_20	Bacillus virus PBS1	GCA_002601325.1
AMS01219.1	008726	Cluster8598_1clades	84	AR9_g135	Bacillus phage AR9	GCA_001743835.1
AST99844.1	008726	Cluster8598_1clades	84	PBI_PBS1_22	Bacillus virus PBS1	GCA_002601325.1
ATA65424.1	008727	Cluster8599_1clades	84	2050HW_00089	Serratia phage 2050HW	GCA_002628125.1
QDB71200.1	008727	Cluster8599_1clades	84	CPT_Moabite_170	Serratia phage Moabite	GCA_006384735.1
ATA65463.1	008728	Cluster8600_1clades	84	2050HW_00128	Serratia phage 2050HW	GCA_002628125.1
QDB71232.1	008728	Cluster8600_1clades	84	CPT_Moabite_202	Serratia phage Moabite	GCA_006384735.1
ATA65684.1	008729	Cluster8601_1clades	84	2050HW_00349	Serratia phage 2050HW	GCA_002628125.1
QDB71105.1	008729	Cluster8601_1clades	84	CPT_Moabite_073	Serratia phage Moabite	GCA_006384735.1
QBZ71940.1	008730	Cluster8602_1clades	84	SEA_KRADAL_41	Streptomyces phage Kradal	GCA_004799925.1
AXH66202.1	008730	Cluster8602_1clades	84	SEA_SATIS_41	Streptomyces phage Satis	GCA_003366315.1
AXQ69099.1	008731	Cluster8603_1clades	84	CcrBL9_gp075c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69654.1	008731	Cluster8603_1clades	84	CcrSC_gp072c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69391.1	008732	Cluster8604_1clades	83	CcrBL9_gp367	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69950.1	008732	Cluster8604_1clades	84	CcrSC_gp368	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69493.1	008733	Cluster8605_1clades	73	CcrBL9_gp469	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70041.1	008733	Cluster8605_1clades	84	CcrSC_gp459	Caulobacter phage CcrSC	GCA_003443315.1
AYD81328.1	008734	Cluster8606_1clades	84	SEA_JUSTBECAUSE_163	Streptomyces phage JustBecause	GCA_003613775.1
QJD53731.1	008734	Cluster8606_1clades	84	SEA_KELA_161	Streptomyces phage Kela	GCA_012934305.1
BAS04943.1	008735	Cluster8607_1clades	82	AVU11_gp151	Ralstonia phage RSF1	GCA_001500875.1
BAQ02667.1	008735	Cluster8607_1clades	84	AVU38_gp139	Ralstonia phage RSL2	GCA_001503055.1
BBI90496.1	008736	Cluster8608_1clades	84	HYO65_gp104	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90804.1	008736	Cluster8608_1clades	84	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90572.1	008737	Cluster8609_1clades	84	HYO65_gp180	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90880.1	008737	Cluster8609_1clades	84	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06591.1	008738	Cluster8610_1clades	84	BcepSaruman_178	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74556.1	008738	Cluster8610_1clades	84	BcepSauron_176	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54844.1	008739	Cluster8611_1clades	84	b23_0229	Synechococcus phage B23	GCA_009745195.1
QGT54478.1	008739	Cluster8611_1clades	84	b3_0235	Synechococcus phage B3	GCA_009745215.1
prevph1000000226	008740	Cluster8612_1clades	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000176	008740	Cluster8612_1clades	85	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000257	008741	Cluster8613_1clades	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000204	008741	Cluster8613_1clades	85	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000364	008742	Cluster8614_1clades	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000290	008742	Cluster8614_1clades	85	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000861	008743	Cluster8615_1clades	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000599	008743	Cluster8615_1clades	85	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ANS06142.1	008744	Cluster8616_1clades	83	ABCD_0133	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78655.1	008744	Cluster8616_1clades	83	RB43ORF133c	Escherichia virus RB43	GCA_000863505.1
AFU88067.1	008745	Cluster8617_1clades	83	CcrColossus_gp197	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68744.1	008745	Cluster8617_1clades	83	CcrPW_gp205c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88290.1	008746	Cluster8618_1clades	83	CcrColossus_gp420	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68963.1	008746	Cluster8618_1clades	83	CcrPW_gp424c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88316.1	008747	Cluster8619_1clades	83	CcrColossus_gp446	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68987.1	008747	Cluster8619_1clades	83	CcrPW_gp448	Caulobacter phage CcrPW	GCA_003443275.1
AIA64903.1	008748	Cluster8620_1clades	83	S13_104	Cronobacter phage S13	GCA_001503575.1
QHJ79036.1	008748	Cluster8620_1clades	82	-	Myoviridae sp.	GCA_012593985.1
ANS06143.1	008749	Cluster8621_1clades	83	ABCD_0167	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97179.1	008749	Cluster8621_1clades	83	E_171	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AOO14335.1	008750	Cluster8622_1clades	83	Sn110110_141	Cyanophage S-RIM14	GCA_002599065.1
AOO14984.1	008750	Cluster8622_1clades	83	W1230910_138	Cyanophage S-RIM14	GCA_002599125.1
QBZ72206.1	008751	Cluster8623_1clades	83	SEA_KRADAL_320	Streptomyces phage Kradal	GCA_004799925.1
AXH66469.1	008751	Cluster8623_1clades	83	SEA_SATIS_320	Streptomyces phage Satis	GCA_003366315.1
AFU87942.1	008752	SIG+TM	72	CcrColossus_gp072	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68614.1	008752	SIG+TM	83	CcrPW_gp075	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69114.1	008753	Cluster8625_1clades	83	CcrBL9_gp090	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69668.1	008753	Cluster8625_1clades	83	CcrSC_gp086	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69315.1	008754	SIG+TM+TM	83	CcrBL9_gp291	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69875.1	008754	SIG+TM+TM	83	CcrSC_gp293	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69370.1	008755	Cluster8627_1clades	83	CcrBL9_gp346	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69930.1	008755	Cluster8627_1clades	82	CcrSC_gp348	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69472.1	008756	Cluster8628_1clades	83	CcrBL9_gp448	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70021.1	008756	Cluster8628_1clades	83	CcrSC_gp439	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69116.1	008757	Cluster8629_1clades	82	CcrBL9_gp092	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69670.1	008757	Cluster8629_1clades	83	CcrSC_gp088	Caulobacter phage CcrSC	GCA_003443315.1
BBA65194.1	008758	Cluster8630_1clades	83	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65653.1	008758	Cluster8630_1clades	83	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90488.1	008759	Cluster8631_1clades	83	HYO65_gp096	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90796.1	008759	Cluster8631_1clades	83	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06437.1	008760	Cluster8632_1clades	83	BcepSaruman_024	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74405.1	008760	Cluster8632_1clades	83	BcepSauron_025	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06451.1	008761	Cluster8633_1clades	83	BcepSaruman_038	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74418.1	008761	Cluster8633_1clades	83	BcepSauron_038	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06532.1	008762	Cluster8634_1clades	83	BcepSaruman_119	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74498.1	008762	Cluster8634_1clades	83	BcepSauron_118	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32412.1	008763	Cluster8635_1clades	83	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41983.1	008763	Cluster8635_1clades	83	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22866.1	008764	Cluster8636_1clades	83	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50717.1	008764	Cluster8636_1clades	81	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54653.1	008765	XIS-HTH	83	b23_0025	Synechococcus phage B23	GCA_009745195.1
QGT54283.1	008765	XIS-HTH	83	b3_0025	Synechococcus phage B3	GCA_009745215.1
QGT54709.1	008766	Cluster8638_1clades	83	b23_0094	Synechococcus phage B23	GCA_009745195.1
QGT54339.1	008766	Cluster8638_1clades	83	b3_0095	Synechococcus phage B3	GCA_009745215.1
QGT54806.1	008767	APG5	83	b23_0191	Synechococcus phage B23	GCA_009745195.1
QGT54436.1	008767	APG5	83	b3_0192	Synechococcus phage B3	GCA_009745215.1
QGT54818.1	008768	Cluster8640_1clades	83	b23_0203	Synechococcus phage B23	GCA_009745195.1
QGT54448.1	008768	Cluster8640_1clades	83	b3_0205	Synechococcus phage B3	GCA_009745215.1
QIG58045.1	008769	Cluster8641_1clades	83	SEA_PAULODIABOLI_361	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57744.1	008769	Cluster8641_1clades	83	SEA_PAULODIABOLI_6	Microbacterium phage PauloDiaboli	GCA_011067425.1
AYD81480.1	008770	Cluster8642_1clades	81	SEA_JUSTBECAUSE_325	Streptomyces phage JustBecause	GCA_003613775.1
QJD53883.1	008770	Cluster8642_1clades	83	SEA_KELA_323	Streptomyces phage Kela	GCA_012934305.1
prevph1000000171	008771	Cluster8643_1clades	82	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000133	008771	Cluster8643_1clades	84	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000231	008772	Cluster8644_1clades	84	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000181	008772	Cluster8644_1clades	84	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000478	008773	Cluster8645_1clades	54	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000361	008773	Cluster8645_1clades	84	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000656	008774	Cluster8646_1clades	57	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000468	008774	Cluster8646_1clades	84	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAQ64277.1	008775	Cluster8647_1clades	82	KVP40.0208	Vibrio phage KVP40	GCA_000843785.1
QIW91205.1	008775	Cluster8647_1clades	62	COHAPHLL_00369	Vibrio phage V09	GCA_012361135.1
APU01537.1	008776	Cluster8648_1clades	82	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53159.1	008776	Cluster8648_1clades	82	65p151	Aeromonas virus 65	GCA_000893255.1
APU01548.1	008777	Cluster8649_1clades	82	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53170.1	008777	Cluster8649_1clades	82	65p162	Aeromonas virus 65	GCA_000893255.1
APU01614.1	008778	Cluster8650_1clades	82	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53239.1	008778	Cluster8650_1clades	82	65p231	Aeromonas virus 65	GCA_000893255.1
QKN86037.1	008779	Cluster8651_1clades	82	ACEC001_1940	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AEP84028.1	008779	Cluster8651_1clades	82	SPN3US_0195	Salmonella phage SPN3US	GCA_001042275.1
AGC34940.1	008780	Cluster8652_1clades	80	ACQ29_gp260	Escherichia phage PBECO4	GCA_001041035.1
AFA44613.1	008780	Cluster8652_1clades	82	RaK2_00340	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFC21913.1	008781	Cluster8653_1clades	82	GAP32_456	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44038.1	008781	Cluster8653_1clades	82	CBB_475	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU87928.1	008782	Cluster8654_1clades	82	CcrColossus_gp058	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68600.1	008782	Cluster8654_1clades	81	CcrPW_gp061	Caulobacter phage CcrPW	GCA_003443275.1
AFU88277.1	008783	PADR-HTH	82	CcrColossus_gp407	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68953.1	008783	PADR-HTH	42	CcrPW_gp414c	Caulobacter phage CcrPW	GCA_003443275.1
AGH56952.1	008784	Cluster8656_1clades	82	CPXG_00149	Cyanophage P-RSM6	GCA_000906155.1
AGH07685.1	008784	Cluster8656_1clades	79	CYVG_00242	Cyanophage S-SSM6a	GCA_002710385.1
AMM44023.1	008785	Cluster8657_1clades	82	CBB_460	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SOK58728.1	008785	Cluster8657_1clades	76	g451	Yersinia phage fHe-Yen9-04	GCA_002990485.1
ANS06145.1	008786	Cluster8658_1clades	82	ABCD_0121	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78644.1	008786	Cluster8658_1clades	81	RB43ORF122c	Escherichia virus RB43	GCA_000863505.1
AFO71344.1	008787	Cluster8659_1clades	77	CR5_124	Cronobacter phage CR5	GCA_000910235.1
ANZ50316.1	008787	Cluster8659_1clades	82	PHOBOS_126	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ATA65545.1	008788	SIG+TM+TM	82	2050HW_00210	Serratia phage 2050HW	GCA_002628125.1
QDB71310.1	008788	SIG+TM+TM	82	CPT_Moabite_280	Serratia phage Moabite	GCA_006384735.1
QBZ71975.1	008789	SIG+TM	82	SEA_KRADAL_77	Streptomyces phage Kradal	GCA_004799925.1
AXH66238.1	008789	SIG+TM	82	SEA_SATIS_77	Streptomyces phage Satis	GCA_003366315.1
AFU88034.1	008790	Cluster8662_1clades	74	CcrColossus_gp164	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68711.1	008790	Cluster8662_1clades	82	CcrPW_gp172c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88054.1	008791	Cluster8663_1clades	77	CcrColossus_gp184	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68733.1	008791	Cluster8663_1clades	82	CcrPW_gp194c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69128.1	008792	DUF2992	82	CcrBL9_gp104	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69682.1	008792	DUF2992	82	CcrSC_gp100	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69109.1	008793	Cluster8665_1clades	81	CcrBL9_gp085	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69663.1	008793	Cluster8665_1clades	82	CcrSC_gp081	Caulobacter phage CcrSC	GCA_003443315.1
BBA65211.1	008794	Cluster8666_1clades	82	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65670.1	008794	Cluster8666_1clades	82	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65246.1	008795	Cluster8667_1clades	82	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65705.1	008795	Cluster8667_1clades	82	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90437.1	008796	Cluster8668_1clades	82	HYO65_gp045	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90744.1	008796	Cluster8668_1clades	68	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90551.1	008797	Cluster8669_1clades	82	HYO65_gp159	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90859.1	008797	Cluster8669_1clades	82	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90656.1	008798	Cullin	82	HYO65_gp264	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90961.1	008798	Cullin	82	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06466.1	008799	Cluster8672_1clades	82	BcepSaruman_053	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74434.1	008799	Cluster8672_1clades	82	BcepSauron_054	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32426.1	008800	Cluster8673_1clades	82	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41997.1	008800	Cluster8673_1clades	82	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ96704.1	008801	SIG+TM	82	PS1_0193	Aeromonas phage PS1	GCA_007051165.2
QFR59337.1	008801	SIG+TM	82	PS2_0195	Aeromonas phage PS2	GCA_009388305.2
QGT54688.1	008802	Cluster8675_1clades	82	b23_0073	Synechococcus phage B23	GCA_009745195.1
QGT54318.1	008802	Cluster8675_1clades	82	b3_0074	Synechococcus phage B3	GCA_009745215.1
QGT54708.1	008803	Cluster8676_1clades	82	b23_0093	Synechococcus phage B23	GCA_009745195.1
QGT54338.1	008803	Cluster8676_1clades	82	b3_0094	Synechococcus phage B3	GCA_009745215.1
QGT54972.1	008804	Cluster8677_1clades	82	b23_0366	Synechococcus phage B23	GCA_009745195.1
QGT54607.1	008804	Cluster8677_1clades	82	b3_0372	Synechococcus phage B3	GCA_009745215.1
AAX44460.1	008805	Cluster8678_1clades	81	PSSM2_082	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12193.1	008805	Cluster8678_1clades	81	PRTG_00035	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01785.1	008806	Cluster8679_1clades	81	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53428.1	008806	Cluster8679_1clades	81	65p422	Aeromonas virus 65	GCA_000893255.1
AFU88140.1	008807	Cluster8680_1clades	81	CcrColossus_gp270	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68816.1	008807	Cluster8680_1clades	81	CcrPW_gp277	Caulobacter phage CcrPW	GCA_003443275.1
AMM43990.1	008808	Cluster8681_1clades	81	CBB_427	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88947.1	008808	Cluster8681_1clades	77	BF_0422	Serratia phage BF	GCA_002619745.1
AMS01186.1	008809	Cluster8682_1clades	81	AR9_g102	Bacillus phage AR9	GCA_001743835.1
ASU00120.1	008809	Cluster8682_1clades	81	PBI_PBS1_298	Bacillus virus PBS1	GCA_002601325.1
ANS06146.1	008810	Cluster8683_1clades	81	ABCD_0130	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97139.1	008810	Cluster8683_1clades	80	E_131	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AXF51326.1	008811	Cluster8684_1clades	81	WELLINGTON_198	Erwinia phage Wellington	GCA_003344985.1
ANZ49551.1	008811	Cluster8684_1clades	81	KWAN_199	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51345.1	008812	Cluster8685_1clades	81	WELLINGTON_219	Erwinia phage Wellington	GCA_003344985.1
ANZ49572.1	008812	Cluster8685_1clades	81	KWAN_220	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ48713.1	008813	Cluster8686_1clades	75	CHRISDB_151	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51055.1	008813	Cluster8686_1clades	81	MLDJOKPK_00016	Salmonella phage SPAsTU	GCA_003183805.1
AFU88237.1	008814	Cluster8687_1clades	80	CcrColossus_gp367	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68913.1	008814	Cluster8687_1clades	81	CcrPW_gp374c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69236.1	008815	Cluster8688_1clades	81	CcrBL9_gp212c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69790.1	008815	Cluster8688_1clades	81	CcrSC_gp208c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69300.1	008816	Cluster8689_1clades	81	CcrBL9_gp276c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69859.1	008816	Cluster8689_1clades	81	CcrSC_gp277c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69353.1	008817	Cluster8690_1clades	81	CcrBL9_gp329	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69912.1	008817	Cluster8690_1clades	81	CcrSC_gp330	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69386.1	008818	Cluster8691_1clades	81	CcrBL9_gp362	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69946.1	008818	Cluster8691_1clades	81	CcrSC_gp364	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69477.1	008819	Cluster8692_1clades	81	CcrBL9_gp453	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70026.1	008819	Cluster8692_1clades	81	CcrSC_gp444	Caulobacter phage CcrSC	GCA_003443315.1
AYD81325.1	008820	Cluster8693_1clades	81	SEA_JUSTBECAUSE_160	Streptomyces phage JustBecause	GCA_003613775.1
QJD53728.1	008820	Cluster8693_1clades	81	SEA_KELA_158	Streptomyces phage Kela	GCA_012934305.1
AYD81470.1	008821	Cluster8694_1clades	81	SEA_JUSTBECAUSE_315	Streptomyces phage JustBecause	GCA_003613775.1
QJD53873.1	008821	Cluster8694_1clades	81	SEA_KELA_313	Streptomyces phage Kela	GCA_012934305.1
AYD81478.1	008822	VIT1	81	SEA_JUSTBECAUSE_323	Streptomyces phage JustBecause	GCA_003613775.1
QJD53881.1	008822	VIT1	79	SEA_KELA_321	Streptomyces phage Kela	GCA_012934305.1
BAW19173.1	008823	Cluster8696_1clades	81	FDH28_gp222	Ralstonia phage RP12	GCA_002617345.1
BAW19459.1	008823	Cluster8696_1clades	81	-	Ralstonia phage RP31	GCA_002617365.1
BBA65655.1	008824	Cluster8697_1clades	81	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65196.1	008824	Cluster8697_1clades	81	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65424.1	008825	Cluster8698_1clades	81	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96445.1	008825	Cluster8698_1clades	77	Xoosp13_259	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90463.1	008826	Cluster8699_1clades	81	HYO65_gp071	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90771.1	008826	Cluster8699_1clades	81	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06492.1	008827	Cluster8700_1clades	81	BcepSaruman_079	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74459.1	008827	Cluster8700_1clades	81	BcepSauron_079	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06613.1	008828	Cluster8701_1clades	81	BcepSaruman_200	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74579.1	008828	Cluster8701_1clades	81	BcepSauron_199	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06633.1	008829	Cluster8702_1clades	81	BcepSaruman_220	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74602.1	008829	Cluster8702_1clades	81	BcepSauron_222	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06823.1	008830	Cluster8703_1clades	81	BcepSaruman_410	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74792.1	008830	Cluster8703_1clades	81	BcepSauron_412	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06824.1	008831	Imm_superinfect	75	BcepSaruman_411	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74793.1	008831	Imm_superinfect	81	BcepSauron_413	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54698.1	008832	Cluster8705_1clades	81	b23_0083	Synechococcus phage B23	GCA_009745195.1
QGT54328.1	008832	Cluster8705_1clades	81	b3_0084	Synechococcus phage B3	GCA_009745215.1
QGT54794.1	008833	Cluster8706_1clades	81	b23_0179	Synechococcus phage B23	GCA_009745195.1
QGT54424.1	008833	Cluster8706_1clades	81	b3_0180	Synechococcus phage B3	GCA_009745215.1
QGT54947.1	008834	Cluster8707_1clades	81	b23_0337	Synechococcus phage B23	GCA_009745195.1
QGT54582.1	008834	Cluster8707_1clades	81	b3_0343	Synechococcus phage B3	GCA_009745215.1
QIG63284.1	008835	Cluster8708_1clades	81	DAC16_51	Bacteroides phage DAC16	GCA_013387695.1
QIG64329.1	008835	Cluster8708_1clades	81	DAC23_51	Bacteroides phage DAC23	GCA_013387745.1
AYD81308.1	008836	Cluster8709_1clades	46	SEA_JUSTBECAUSE_140	Streptomyces phage JustBecause	GCA_003613775.1
QJD53711.1	008836	Cluster8709_1clades	81	SEA_KELA_140	Streptomyces phage Kela	GCA_012934305.1
AAX44567.1	008837	Cluster8710_1clades	80	PSSM2_189	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12406.1	008837	Cluster8710_1clades	80	PRTG_00253	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44574.1	008838	Cluster8711_1clades	80	PSSM2_196	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12399.1	008838	Cluster8711_1clades	80	PRTG_00246	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01708.1	008839	Cluster8712_1clades	80	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53347.1	008839	Cluster8712_1clades	80	65p339	Aeromonas virus 65	GCA_000893255.1
QGH71904.1	008840	TM	55	N1M2_41	Klebsiella phage N1M2	GCA_010092605.1
AEV89499.1	008840	TM	80	OBP_062	Pseudomonas phage OBP	GCA_000896635.1
AFH14852.1	008841	Cluster8714_1clades	80	Lu11_0314	Pseudomonas phage Lu11	GCA_000897175.1
ASV44530.1	008841	Cluster8714_1clades	79	PBI_SCTP2_515	Salicola phage SCTP-2	GCA_002625545.1
AXQ68384.1	008842	Cluster8715_1clades	80	CcrBL10_gp180c	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86669.1	008842	Cluster8715_1clades	80	CcrRogue_gp187	Caulobacter virus Rogue	GCA_000900555.1
AXQ68478.1	008843	Cluster8716_1clades	80	CcrBL10_gp274	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86763.1	008843	Cluster8716_1clades	80	CcrRogue_gp281	Caulobacter virus Rogue	GCA_000900555.1
AFU88240.1	008844	Cluster8717_1clades	80	CcrColossus_gp370	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68915.1	008844	Cluster8717_1clades	80	CcrPW_gp376c	Caulobacter phage CcrPW	GCA_003443275.1
AMS01341.1	008845	HTH	80	AR9_g257	Bacillus phage AR9	GCA_001743835.1
AST99971.1	008845	HTH	80	PBI_PBS1_150	Bacillus virus PBS1	GCA_002601325.1
ANS06147.1	008846	Cluster8719_1clades	80	ABCD_0122	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97133.1	008846	Cluster8719_1clades	80	E_125	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ASU03884.1	008847	Cluster8720_1clades	80	JOAD_31	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03639.1	008847	Cluster8720_1clades	80	RISINGSUN_31	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ATA65404.1	008848	Cluster8721_1clades	80	2050HW_00069	Serratia phage 2050HW	GCA_002628125.1
QDB71183.1	008848	Cluster8721_1clades	80	CPT_Moabite_153	Serratia phage Moabite	GCA_006384735.1
QBZ71938.1	008849	Cluster8722_1clades	80	SEA_KRADAL_39	Streptomyces phage Kradal	GCA_004799925.1
AXH66200.1	008849	Cluster8722_1clades	80	SEA_SATIS_39	Streptomyces phage Satis	GCA_003366315.1
AXQ68228.1	008850	Cluster8723_1clades	80	CcrBL10_gp024	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86509.1	008850	Cluster8723_1clades	79	CcrRogue_gp027	Caulobacter virus Rogue	GCA_000900555.1
AXQ69110.1	008851	Cluster8724_1clades	80	CcrBL9_gp086	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69664.1	008851	Cluster8724_1clades	80	CcrSC_gp082	Caulobacter phage CcrSC	GCA_003443315.1
BAS04995.2	008852	Cluster8725_1clades	80	AVU11_agp42	Ralstonia phage RSF1	GCA_001500875.1
BAQ02724.2	008852	Cluster8725_1clades	80	-	Ralstonia phage RSL2	GCA_001503055.1
BAW18981.1	008853	Cluster8726_1clades	80	FDH28_gp007	Ralstonia phage RP12	GCA_002617345.1
BAW19269.1	008853	Cluster8726_1clades	80	-	Ralstonia phage RP31	GCA_002617365.1
BAW19119.1	008854	Cluster8727_1clades	80	FDH28_gp276	Ralstonia phage RP12	GCA_002617345.1
BAW19405.1	008854	Cluster8727_1clades	80	-	Ralstonia phage RP31	GCA_002617365.1
BBA65232.1	008855	Cluster8728_1clades	80	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65691.1	008855	Cluster8728_1clades	80	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65256.1	008856	Cluster8729_1clades	80	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65715.1	008856	Cluster8729_1clades	80	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06735.1	008857	Cluster8730_1clades	76	BcepSaruman_322	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74704.1	008857	Cluster8730_1clades	80	BcepSauron_324	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32180.1	008858	Cluster8731_1clades	80	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41758.1	008858	Cluster8731_1clades	80	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54719.1	008859	Cluster8732_1clades	80	b23_0104	Synechococcus phage B23	GCA_009745195.1
QGT54349.1	008859	Cluster8732_1clades	80	b3_0105	Synechococcus phage B3	GCA_009745215.1
QGT54974.1	008860	Cluster8733_1clades	80	b23_0368	Synechococcus phage B23	GCA_009745195.1
QGT54609.1	008860	Cluster8733_1clades	80	b3_0374	Synechococcus phage B3	GCA_009745215.1
QKE54379.1	008861	TM	72	ACSA002_0650	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54561.1	008861	TM	80	ACSA002_2450	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ANS06160.1	008862	Cluster8735_1clades	72	ABCD_0247	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78786.1	008862	Cluster8735_1clades	79	RB43ORF264w	Escherichia virus RB43	GCA_000863505.1
ABY63241.1	008863	Cluster8736_1clades	79	201phi2-1p417	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77047.1	008863	Cluster8736_1clades	75	PHABIO_416	Pseudomonas phage Phabio	GCA_002624965.1
APU01765.1	008864	Cluster8737_1clades	79	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53408.1	008864	Cluster8737_1clades	79	65p401	Aeromonas virus 65	GCA_000893255.1
QAX97821.1	008865	Cluster8738_1clades	79	ASswx1_177	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39159.1	008865	Cluster8738_1clades	79	CC2_359	Aeromonas phage CC2	GCA_000903495.1
AFU87925.1	008866	Cluster8739_1clades	79	CcrColossus_gp055	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68597.1	008866	Cluster8739_1clades	65	CcrPW_gp058	Caulobacter phage CcrPW	GCA_003443275.1
AOO14247.1	008867	Cluster8740_1clades	79	Sn110110_053	Cyanophage S-RIM14	GCA_002599065.1
AOO14899.1	008867	Cluster8740_1clades	79	W1230910_053	Cyanophage S-RIM14	GCA_002599125.1
ARV76914.1	008868	Cluster8741_1clades	79	PHABIO_283	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02785.1	008868	Cluster8741_1clades	79	PSA21_259	Pseudomonas phage Psa21	GCA_004340405.1
ATA65484.1	008869	Cluster8742_1clades	79	2050HW_00149	Serratia phage 2050HW	GCA_002628125.1
QDB71254.1	008869	Cluster8742_1clades	79	CPT_Moabite_224	Serratia phage Moabite	GCA_006384735.1
QBZ72033.1	008870	Cluster8743_1clades	79	SEA_KRADAL_135	Streptomyces phage Kradal	GCA_004799925.1
AXH66296.1	008870	Cluster8743_1clades	79	SEA_SATIS_135	Streptomyces phage Satis	GCA_003366315.1
AXQ68551.1	008871	Cluster8744_1clades	79	CcrPW_gp012	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69001.1	008871	Cluster8744_1clades	79	CcrPW_gp462	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69086.1	008872	Cluster8745_1clades	79	CcrBL9_gp062c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69642.1	008872	Cluster8745_1clades	77	CcrSC_gp060c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69111.1	008873	Cluster8746_1clades	79	CcrBL9_gp087	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69665.1	008873	Cluster8746_1clades	79	CcrSC_gp083	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69286.1	008874	Cluster8747_1clades	79	CcrBL9_gp262c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69843.1	008874	Cluster8747_1clades	79	CcrSC_gp261c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69298.1	008875	DUF1487	79	CcrBL9_gp274c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69857.1	008875	DUF1487	79	CcrSC_gp275c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69515.1	008876	Cluster8749_1clades	79	CcrBL9_gp491	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70062.1	008876	Cluster8749_1clades	77	CcrSC_gp480	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69357.1	008877	Cluster8750_1clades	71	CcrBL9_gp333	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69916.1	008877	Cluster8750_1clades	79	CcrSC_gp334	Caulobacter phage CcrSC	GCA_003443315.1
AYD81401.1	008878	Cluster8751_1clades	79	SEA_JUSTBECAUSE_246	Streptomyces phage JustBecause	GCA_003613775.1
QJD53805.1	008878	Cluster8751_1clades	79	SEA_KELA_245	Streptomyces phage Kela	GCA_012934305.1
AYD81431.1	008879	Cluster8752_1clades	79	SEA_JUSTBECAUSE_276	Streptomyces phage JustBecause	GCA_003613775.1
QJD53837.1	008879	Cluster8752_1clades	79	SEA_KELA_277	Streptomyces phage Kela	GCA_012934305.1
CCH63495.1	008880	Cluster8753_1clades	65	CP21_033	Campylobacter virus CP21	GCA_000902535.1
CCH63496.1	008880	Cluster8753_1clades	79	CP21_034	Campylobacter virus CP21	GCA_000902535.1
QBX06549.1	008881	Cluster8754_1clades	79	BcepSaruman_136	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74515.1	008881	Cluster8754_1clades	79	BcepSauron_135	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06706.1	008882	Cluster8755_1clades	79	BcepSaruman_293	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74674.1	008882	Cluster8755_1clades	79	BcepSauron_294	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06786.1	008883	Cluster8756_1clades	79	BcepSaruman_373	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74756.1	008883	Cluster8756_1clades	79	BcepSauron_376	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06615.1	008884	Cluster8757_1clades	79	BcepSaruman_202	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74581.1	008884	Cluster8757_1clades	74	BcepSauron_201	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32229.1	008885	SIG+TM	79	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41807.1	008885	SIG+TM	79	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22867.1	008886	Cluster8759_1clades	79	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50718.1	008886	Cluster8759_1clades	66	-	Synechococcus phage S-B43	GCA_006869725.1
QCW23026.1	008887	Cluster8760_1clades	79	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50519.1	008887	Cluster8760_1clades	79	-	Synechococcus phage S-B43	GCA_006869725.1
QCW23093.1	008888	Cluster8761_1clades	79	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50485.1	008888	Cluster8761_1clades	79	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54713.1	008889	Cluster8762_1clades	79	b23_0098	Synechococcus phage B23	GCA_009745195.1
QGT54343.1	008889	Cluster8762_1clades	79	b3_0099	Synechococcus phage B3	GCA_009745215.1
QGT54773.1	008890	Cluster8763_1clades	79	b23_0158	Synechococcus phage B23	GCA_009745195.1
QGT54403.1	008890	Cluster8763_1clades	79	b3_0159	Synechococcus phage B3	GCA_009745215.1
QGT54984.1	008891	Cluster8764_1clades	79	b23_0378	Synechococcus phage B23	GCA_009745195.1
QGT54619.1	008891	Cluster8764_1clades	79	b3_0384	Synechococcus phage B3	GCA_009745215.1
QIG57770.1	008892	Cluster8765_1clades	79	SEA_PAULODIABOLI_35	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58071.1	008892	Cluster8765_1clades	79	SEA_PAULODIABOLI_390	Microbacterium phage PauloDiaboli	GCA_011067425.1
APU01421.1	008893	Cluster8766_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
AAR90908.1	008893	Cluster8766_1clades	78	65p030	Aeromonas virus 65	GCA_000893255.1
APU01722.1	008894	Cluster8767_1clades	78	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53362.1	008894	Cluster8767_1clades	78	65p354	Aeromonas virus 65	GCA_000893255.1
AXQ68235.1	008895	Cluster8768_1clades	78	CcrBL10_gp031	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86517.1	008895	Cluster8768_1clades	78	CcrRogue_gp035	Caulobacter virus Rogue	GCA_000900555.1
AFU87978.1	008896	Cluster8769_1clades	78	CcrColossus_gp108	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68655.1	008896	Cluster8769_1clades	78	CcrPW_gp116	Caulobacter phage CcrPW	GCA_003443275.1
AMS01177.1	008897	PC4	78	AR9_g093	Bacillus phage AR9	GCA_001743835.1
ASU00111.1	008897	PC4	78	PBI_PBS1_289	Bacillus virus PBS1	GCA_002601325.1
AMS01214.1	008898	Cluster8771_1clades	78	AR9_g130	Bacillus phage AR9	GCA_001743835.1
AST99839.1	008898	Cluster8771_1clades	78	PBI_PBS1_17	Bacillus virus PBS1	GCA_002601325.1
AMS01337.1	008899	Cluster8772_1clades	78	AR9_g253	Bacillus phage AR9	GCA_001743835.1
AST99967.1	008899	Cluster8772_1clades	78	PBI_PBS1_146	Bacillus virus PBS1	GCA_002601325.1
ANZ48425.1	008900	SIG+TM	77	CAITLIN_130	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48698.1	008900	SIG+TM	78	CHRISDB_136	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AOO14291.1	008901	Cluster8774_1clades	78	Sn110110_097	Cyanophage S-RIM14	GCA_002599065.1
AOO14940.1	008901	Cluster8774_1clades	78	W1230910_094	Cyanophage S-RIM14	GCA_002599125.1
AMM43997.1	008902	Cluster8775_1clades	75	CBB_434	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AQW88957.1	008902	Cluster8775_1clades	78	BF_0432	Serratia phage BF	GCA_002619745.1
AXG67319.1	008903	PLUS3	65	AD1_275	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08545.1	008903	PLUS3	78	Alexandra_289	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AXQ69263.1	008904	Cluster8777_1clades	78	CcrBL9_gp239c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69820.1	008904	Cluster8777_1clades	78	CcrSC_gp238c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69322.1	008905	Cluster8778_1clades	78	CcrBL9_gp298	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69882.1	008905	Cluster8778_1clades	78	CcrSC_gp300	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69352.1	008906	Cluster8779_1clades	78	CcrBL9_gp328	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69911.1	008906	Cluster8779_1clades	78	CcrSC_gp329	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69359.1	008907	Cluster8780_1clades	78	CcrBL9_gp335	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69919.1	008907	Cluster8780_1clades	68	CcrSC_gp337	Caulobacter phage CcrSC	GCA_003443315.1
BAW19148.1	008908	SIG+TM	78	FDH28_gp247	Ralstonia phage RP12	GCA_002617345.1
BAW19434.1	008908	SIG+TM	78	-	Ralstonia phage RP31	GCA_002617365.1
BBA65618.1	008909	Cluster8782_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65159.1	008909	Cluster8782_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65179.1	008910	Cluster8783_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65638.1	008910	Cluster8783_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65215.1	008911	Cluster8784_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65674.1	008911	Cluster8784_1clades	78	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90451.1	008912	Cluster8785_1clades	78	HYO65_gp059	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90759.1	008912	Cluster8785_1clades	78	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06569.1	008913	Cluster8786_1clades	78	BcepSaruman_156	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74536.1	008913	Cluster8786_1clades	78	BcepSauron_156	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06808.1	008914	Cluster8787_1clades	78	BcepSaruman_395	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74777.1	008914	Cluster8787_1clades	78	BcepSauron_397	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32479.1	008915	Cluster8788_1clades	78	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42051.1	008915	Cluster8788_1clades	78	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22874.1	008916	Cluster8789_1clades	78	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50483.1	008916	Cluster8789_1clades	78	-	Synechococcus phage S-B43	GCA_006869725.1
QIG57750.1	008917	Cluster8790_1clades	78	SEA_PAULODIABOLI_12	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58051.1	008917	Cluster8790_1clades	78	SEA_PAULODIABOLI_367	Microbacterium phage PauloDiaboli	GCA_011067425.1
QMV29075.1	008918	Cluster8791_1clades	78	AP1_0368	Aeromonas phage AP1	GCA_014183365.1
ATI17354.1	008918	Cluster8791_1clades	46	-	Aeromonas phage AS-szw	GCA_002743635.1
prevph1000000186	008919	Cluster8792_1clades	79	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000149	008919	Cluster8792_1clades	79	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000249	008920	DUF4494	79	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000197	008920	DUF4494	79	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44556.1	008921	DUF2997	77	PSSM2_178	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12416.1	008921	DUF2997	77	PRTG_00264	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFC21893.1	008922	Cluster8795_1clades	77	GAP32_439	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44022.1	008922	Cluster8795_1clades	76	CBB_459	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU88055.1	008923	SIG+TM	77	CcrColossus_gp185	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68734.1	008923	SIG+TM	75	CcrPW_gp195c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88101.1	008924	Cluster8797_1clades	77	CcrColossus_gp231	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68778.1	008924	Cluster8797_1clades	77	CcrPW_gp239	Caulobacter phage CcrPW	GCA_003443275.1
AJK27550.1	008925	Cluster8798_1clades	55	PTIM40_123	Cyanophage P-TIM40	GCA_001470935.1
AGG54499.1	008925	Cluster8798_1clades	77	CYWG_00215	Cyanophage S-SSM6b	GCA_002710425.1
AGH56944.1	008926	Cluster8799_1clades	77	CPXG_00141	Cyanophage P-RSM6	GCA_000906155.1
AJK27515.1	008926	Cluster8799_1clades	56	PTIM40_88	Cyanophage P-TIM40	GCA_001470935.1
AGR47637.2	008927	Cluster8800_1clades	74	SmphiM12_005	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13273.1	008927	Cluster8800_1clades	77	PHIN3_6	Sinorhizobium phage phiN3	GCA_001501175.1
ARV77076.1	008928	Cluster8801_1clades	77	PHABIO_445	Pseudomonas phage Phabio	GCA_002624965.1
QBJ02925.1	008928	Cluster8801_1clades	76	PSA21_399	Pseudomonas phage Psa21	GCA_004340405.1
ASU03785.1	008929	Cluster8802_1clades	77	JOAD_130	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03541.1	008929	Cluster8802_1clades	77	RISINGSUN_129	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65469.1	008930	SIG+TM	77	2050HW_00134	Serratia phage 2050HW	GCA_002628125.1
QDB71238.1	008930	SIG+TM	77	CPT_Moabite_208	Serratia phage Moabite	GCA_006384735.1
AXQ69100.1	008931	Cluster8804_1clades	77	CcrBL9_gp076c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69655.1	008931	Cluster8804_1clades	77	CcrSC_gp073c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69456.1	008932	Cluster8805_1clades	76	CcrBL9_gp432	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70005.1	008932	Cluster8805_1clades	77	CcrSC_gp423	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70605.1	008933	Cluster8806_1clades	77	HOU04_gp004	Synechococcus phage S-T4	GCA_003443335.1
AXQ70403.1	008933	Cluster8806_1clades	77	HOU04_gp004	Synechococcus phage S-T4	GCA_003443335.1
BBA65608.1	008934	Cluster8807_1clades	77	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65149.1	008934	Cluster8807_1clades	77	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65635.1	008935	Cluster8808_1clades	77	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65176.1	008935	Cluster8808_1clades	77	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90464.1	008936	Cluster8809_1clades	77	HYO65_gp072	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90772.1	008936	Cluster8809_1clades	77	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90568.1	008937	Cluster8810_1clades	77	HYO65_gp176	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90876.1	008937	Cluster8810_1clades	77	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06529.1	008938	Cluster8811_1clades	77	BcepSaruman_116	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74495.1	008938	Cluster8811_1clades	77	BcepSauron_115	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06778.1	008939	Cluster8812_1clades	77	BcepSaruman_365	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74748.1	008939	Cluster8812_1clades	77	BcepSauron_368	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54813.1	008940	Cluster8813_1clades	77	b23_0198	Synechococcus phage B23	GCA_009745195.1
QGT54443.1	008940	Cluster8813_1clades	77	b3_0200	Synechococcus phage B3	GCA_009745215.1
QGT54840.1	008941	Cluster8814_1clades	77	b23_0225	Synechococcus phage B23	GCA_009745195.1
QGT54474.1	008941	Cluster8814_1clades	77	b3_0231	Synechococcus phage B3	GCA_009745215.1
QGT54952.1	008942	SIG+TM	77	b23_0346	Synechococcus phage B23	GCA_009745195.1
QGT54587.1	008942	SIG+TM	77	b3_0352	Synechococcus phage B3	GCA_009745215.1
QGT54970.1	008943	Cluster8816_1clades	77	b23_0364	Synechococcus phage B23	GCA_009745195.1
QGT54605.1	008943	Cluster8816_1clades	77	b3_0370	Synechococcus phage B3	GCA_009745215.1
QIG57756.1	008944	Cluster8817_1clades	77	SEA_PAULODIABOLI_19	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58057.1	008944	Cluster8817_1clades	77	SEA_PAULODIABOLI_374	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57982.1	008945	SIG+TM	77	SEA_PAULODIABOLI_298	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57983.1	008945	SIG+TM	70	SEA_PAULODIABOLI_299	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000261	008946	SIG+DOC	78	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000208	008946	SIG+DOC	78	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AON97100.1	008947	Cluster8820_1clades	76	E_092	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78609.1	008947	Cluster8820_1clades	76	RB43ORF087w	Escherichia virus RB43	GCA_000863505.1
QAX98648.1	008948	Cluster8821_1clades	76	ASfcp2_315	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ52789.1	008948	Cluster8821_1clades	76	PX29p070	Aeromonas phage PX29	GCA_000920195.1
AFC21947.1	008949	HTH	76	GAP32_488	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44074.1	008949	HTH	76	CBB_511	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFC21954.1	008950	Cluster8823_1clades	76	GAP32_495	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AQW89036.1	008950	Cluster8823_1clades	72	BF_0511	Serratia phage BF	GCA_002619745.1
AFU87971.1	008951	Cluster8824_1clades	76	CcrColossus_gp101	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68648.1	008951	Cluster8824_1clades	76	CcrPW_gp109	Caulobacter phage CcrPW	GCA_003443275.1
AFU88207.1	008952	Cluster8825_1clades	76	CcrColossus_gp337	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68884.1	008952	Cluster8825_1clades	76	CcrPW_gp345	Caulobacter phage CcrPW	GCA_003443275.1
AIA64975.1	008953	Cluster8826_1clades	76	S13_177	Cronobacter phage S13	GCA_001503575.1
QHJ78956.1	008953	Cluster8826_1clades	76	-	Myoviridae sp.	GCA_012593985.1
AOO14355.1	008954	Cluster8827_1clades	76	Sn110110_161	Cyanophage S-RIM14	GCA_002599065.1
AOO15004.1	008954	Cluster8827_1clades	76	W1230910_158	Cyanophage S-RIM14	GCA_002599125.1
ASU03889.1	008955	Cluster8828_1clades	76	JOAD_26	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03644.1	008955	Cluster8828_1clades	76	RISINGSUN_26	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXQ69033.1	008956	Cluster8829_1clades	76	CcrBL9_gp009	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69549.1	008956	Cluster8829_1clades	76	CcrBL9_gp525	Caulobacter phage CcrBL9	GCA_003443295.1
AYD81200.1	008957	Cluster8830_1clades	76	SEA_JUSTBECAUSE_31	Streptomyces phage JustBecause	GCA_003613775.1
QJD53602.1	008957	Cluster8830_1clades	76	SEA_KELA_31	Streptomyces phage Kela	GCA_012934305.1
BBA65172.1	008958	Cluster8831_1clades	76	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65631.1	008958	Cluster8831_1clades	76	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65632.1	008959	LPD1	76	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65173.1	008959	LPD1	76	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65644.1	008960	Cluster8833_1clades	76	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65185.1	008960	Cluster8833_1clades	76	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06705.1	008961	Cluster8834_1clades	76	BcepSaruman_292	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74673.1	008961	Cluster8834_1clades	76	BcepSauron_293	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06718.1	008962	SIG+TM	76	BcepSaruman_305	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74686.1	008962	SIG+TM	76	BcepSauron_306	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32188.1	008963	Cluster8836_1clades	76	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41766.1	008963	Cluster8836_1clades	76	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32495.1	008964	Cluster8837_1clades	76	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42068.1	008964	Cluster8837_1clades	76	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54736.1	008965	Cluster8838_1clades	76	b23_0121	Synechococcus phage B23	GCA_009745195.1
QGT54366.1	008965	Cluster8838_1clades	76	b3_0122	Synechococcus phage B3	GCA_009745215.1
QGT54823.1	008966	CAGE1	76	b23_0208	Synechococcus phage B23	GCA_009745195.1
QGT54453.1	008966	CAGE1	76	b3_0210	Synechococcus phage B3	GCA_009745215.1
QGT54948.1	008967	Cluster8840_1clades	76	b23_0338	Synechococcus phage B23	GCA_009745195.1
QGT54583.1	008967	Cluster8840_1clades	76	b3_0344	Synechococcus phage B3	GCA_009745215.1
QIG57757.1	008968	Glutaredoxin	76	SEA_PAULODIABOLI_20	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58058.1	008968	Glutaredoxin	76	SEA_PAULODIABOLI_375	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58079.1	008969	Cluster8842_1clades	76	SEA_PAULODIABOLI_14	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58088.1	008969	Cluster8842_1clades	76	SEA_PAULODIABOLI_369	Microbacterium phage PauloDiaboli	GCA_011067425.1
SOK59190.1	008970	Cluster8843_1clades	76	g382	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58654.1	008970	Cluster8843_1clades	76	g377	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000368	008971	Cluster8844_1clades	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000294	008971	Cluster8844_1clades	77	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000380	008972	Cluster8845_1clades	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000306	008972	Cluster8845_1clades	77	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000860	008973	TM	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000598	008973	TM	77	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01608.1	008974	Cluster8847_1clades	75	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53232.1	008974	Cluster8847_1clades	75	65p224	Aeromonas virus 65	GCA_000893255.1
AXQ68484.1	008975	Cluster8848_1clades	72	CcrBL10_gp280	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86772.1	008975	Cluster8848_1clades	75	CcrRogue_gp290	Caulobacter virus Rogue	GCA_000900555.1
AFU88261.1	008976	SIG+TM	75	CcrColossus_gp391	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68935.1	008976	SIG+TM	75	CcrPW_gp396	Caulobacter phage CcrPW	GCA_003443275.1
AFU88262.1	008977	Cluster8850_1clades	75	CcrColossus_gp392	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68936.1	008977	Cluster8850_1clades	70	CcrPW_gp397	Caulobacter phage CcrPW	GCA_003443275.1
AIA64826.1	008978	Cluster8851_1clades	75	S13_027	Cronobacter phage S13	GCA_001503575.1
QHJ78836.1	008978	Cluster8851_1clades	75	-	Myoviridae sp.	GCA_012593985.1
AMM43578.1	008979	Cluster8852_1clades	75	CBB_13	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44129.1	008979	Cluster8852_1clades	75	CBB_566	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
ANZ48494.1	008980	SIG+TM	75	CAITLIN_199	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48773.1	008980	SIG+TM	71	CHRISDB_211	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51385.1	008981	Cluster8854_1clades	75	WELLINGTON_259	Erwinia phage Wellington	GCA_003344985.1
ANZ49611.1	008981	Cluster8854_1clades	75	KWAN_259	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASR76226.1	008982	Cluster8855_1clades	75	PBI_BELLAMY_183	Synechococcus phage Bellamy	GCA_002627525.1
QJT70180.1	008982	Cluster8855_1clades	74	SynMITS9220M01_168	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AUG86019.1	008983	Cluster8856_1clades	75	BOSOLAPHORUS_233	Erwinia phage vB_EamM_Bosolaphorus	GCA_002957735.1
AUG86338.1	008983	Cluster8856_1clades	75	DESERTFOX_231	Erwinia phage vB_EamM_Desertfox	GCA_002957745.1
AXQ69072.1	008984	Cluster8857_1clades	75	CcrBL9_gp048c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69632.1	008984	Cluster8857_1clades	74	CcrSC_gp050c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69093.1	008985	Cluster8858_1clades	75	CcrBL9_gp069c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69649.1	008985	Cluster8858_1clades	75	CcrSC_gp067c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69399.1	008986	Cluster8859_1clades	75	CcrBL9_gp375	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69956.1	008986	Cluster8859_1clades	75	CcrSC_gp374	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69535.1	008987	SIG+TM	75	CcrBL9_gp511	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70078.1	008987	SIG+TM	75	CcrSC_gp496	Caulobacter phage CcrSC	GCA_003443315.1
BAS05003.1	008988	Cluster8861_1clades	75	AVU11_gp211	Ralstonia phage RSF1	GCA_001500875.1
BAQ02733.1	008988	Cluster8861_1clades	74	AVU38_gp205	Ralstonia phage RSL2	GCA_001503055.1
BBA65700.1	008989	DEAM	75	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65241.1	008989	DEAM	75	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65555.1	008990	Cluster8863_1clades	75	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96550.1	008990	Cluster8863_1clades	74	Xoosp13_364	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90482.1	008991	Cluster8864_1clades	75	HYO65_gp090	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90790.1	008991	Cluster8864_1clades	75	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06443.1	008992	Cluster8865_1clades	75	BcepSaruman_030	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74411.1	008992	Cluster8865_1clades	75	BcepSauron_031	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06557.1	008993	Cluster8866_1clades	75	BcepSaruman_144	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74524.1	008993	Cluster8866_1clades	75	BcepSauron_144	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06594.1	008994	Cluster8867_1clades	75	BcepSaruman_181	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74559.1	008994	Cluster8867_1clades	75	BcepSauron_179	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06631.1	008995	Cluster8868_1clades	75	BcepSaruman_218	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74600.1	008995	Cluster8868_1clades	75	BcepSauron_220	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06769.1	008996	Cluster8869_1clades	75	BcepSaruman_356	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74739.1	008996	Cluster8869_1clades	75	BcepSauron_359	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06772.1	008997	Cluster8870_1clades	75	BcepSaruman_359	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74742.1	008997	Cluster8870_1clades	75	BcepSauron_362	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32305.1	008998	Cluster8871_1clades	75	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41878.1	008998	Cluster8871_1clades	75	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBZ70703.1	008999	Cluster8872_1clades	75	pETSU_122	Edwardsiella virus pEt-SU	GCA_004800915.1
QGH72014.1	008999	Cluster8872_1clades	70	N1M2_151	Klebsiella phage N1M2	GCA_010092605.1
QGT54691.1	009000	Cluster8873_1clades	75	b23_0076	Synechococcus phage B23	GCA_009745195.1
QGT54321.1	009000	Cluster8873_1clades	75	b3_0077	Synechococcus phage B3	GCA_009745215.1
QGT54779.1	009001	Cluster8874_1clades	75	b23_0164	Synechococcus phage B23	GCA_009745195.1
QGT54409.1	009001	Cluster8874_1clades	75	b3_0165	Synechococcus phage B3	GCA_009745215.1
prevph1000000320	009002	Cluster8875_1clades	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000249	009002	Cluster8875_1clades	76	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000790	009003	Cluster8876_1clades	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000538	009003	Cluster8876_1clades	76	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ADM80064.1	009004	Cluster8877_1clades	73	phiAS5_ORF0221	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17751.1	009004	Cluster8877_1clades	74	Aeh1ORF090c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ64390.1	009005	Cluster8878_1clades	74	KVP40.0320	Vibrio phage KVP40	GCA_000843785.1
QHJ74502.1	009005	Cluster8878_1clades	74	VH12019_00202	Vibrio phage VH1_2019	GCA_009931825.1
AAX44465.1	009006	Cluster8879_1clades	74	PSSM2_087	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12188.1	009006	Cluster8879_1clades	74	PRTG_00030	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44468.1	009007	Cluster8880_1clades	74	PSSM2_090	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12184.1	009007	Cluster8880_1clades	74	PRTG_00026	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44517.1	009008	Cluster8881_1clades	74	PSSM2_139	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12450.1	009008	Cluster8881_1clades	74	PRTG_00302	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44620.1	009009	Cluster8882_1clades	74	PSSM2_243	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12351.1	009009	Cluster8882_1clades	74	PRTG_00198	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01633.1	009010	Cluster8883_1clades	74	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53259.1	009010	Cluster8883_1clades	74	65p251	Aeromonas virus 65	GCA_000893255.1
AFU88069.1	009011	Cluster8884_1clades	74	CcrColossus_gp199	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68746.1	009011	Cluster8884_1clades	45	CcrPW_gp207c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88087.1	009012	Cluster8885_1clades	74	CcrColossus_gp217	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68763.1	009012	Cluster8885_1clades	64	CcrPW_gp224c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88195.1	009013	Cluster8886_1clades	74	CcrColossus_gp325	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68872.1	009013	Cluster8886_1clades	74	CcrPW_gp333	Caulobacter phage CcrPW	GCA_003443275.1
AJK27460.1	009014	Cluster8887_1clades	62	PTIM40_33	Cyanophage P-TIM40	GCA_001470935.1
AGG54354.1	009014	Cluster8887_1clades	74	CYWG_00070	Cyanophage S-SSM6b	GCA_002710425.1
AIA65022.1	009015	Cluster8888_1clades	74	S13_225	Cronobacter phage S13	GCA_001503575.1
QHJ78911.1	009015	Cluster8888_1clades	65	-	Myoviridae sp.	GCA_012593985.1
AMO43077.1	009016	Cluster8889_1clades	74	R1080702_068	Cyanophage S-RIM32	GCA_001754165.1
QCW23004.1	009016	Cluster8889_1clades	66	-	Synechococcus phage S-B05	GCA_006083695.1
AMS01266.1	009017	Cluster8890_1clades	74	AR9_g182	Bacillus phage AR9	GCA_001743835.1
AST99893.1	009017	Cluster8890_1clades	74	PBI_PBS1_71	Bacillus virus PBS1	GCA_002601325.1
AOO14212.1	009018	Cluster8891_1clades	74	Sn110110_018	Cyanophage S-RIM14	GCA_002599065.1
AOO14864.1	009018	Cluster8891_1clades	74	W1230910_018	Cyanophage S-RIM14	GCA_002599125.1
AOO14245.1	009019	Cluster8892_1clades	74	Sn110110_051	Cyanophage S-RIM14	GCA_002599065.1
AOO14897.1	009019	Cluster8892_1clades	74	W1230910_051	Cyanophage S-RIM14	GCA_002599125.1
AQW88529.1	009020	Cluster8893_1clades	74	BF_0004	Serratia phage BF	GCA_002619745.1
SOK58811.1	009020	Cluster8893_1clades	74	g003	Yersinia phage fHe-Yen9-03	GCA_002990515.1
ASU03742.1	009021	Cluster8894_1clades	74	JOAD_173	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03498.1	009021	Cluster8894_1clades	74	RISINGSUN_172	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AXG67053.1	009022	Cluster8895_1clades	44	AD1_009	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08291.1	009022	Cluster8895_1clades	74	Alexandra_9	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AFU88244.1	009023	Cluster8896_1clades	69	CcrColossus_gp374	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68919.1	009023	Cluster8896_1clades	74	CcrPW_gp380c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69074.1	009024	TM	74	CcrBL9_gp050c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69634.1	009024	TM	74	CcrSC_gp052c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69266.1	009025	Cluster8898_1clades	74	CcrBL9_gp242c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69822.1	009025	Cluster8898_1clades	74	CcrSC_gp240c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69422.1	009026	Cluster8899_1clades	74	CcrBL9_gp398	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69977.1	009026	Cluster8899_1clades	74	CcrSC_gp395	Caulobacter phage CcrSC	GCA_003443315.1
BAW19064.1	009027	SIG+TM	74	FDH28_gp090	Ralstonia phage RP12	GCA_002617345.1
BAW19349.1	009027	SIG+TM	74	-	Ralstonia phage RP31	GCA_002617365.1
BAW19235.1	009028	Cluster8901_1clades	74	FDH28_gp160	Ralstonia phage RP12	GCA_002617345.1
BAW19521.1	009028	Cluster8901_1clades	74	-	Ralstonia phage RP31	GCA_002617365.1
BBA65208.1	009029	Cluster8902_1clades	74	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65667.1	009029	Cluster8902_1clades	74	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65686.1	009030	Cluster8903_1clades	74	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65227.1	009030	Cluster8903_1clades	74	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90583.1	009031	Cluster8904_1clades	74	HYO65_gp191	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90891.1	009031	Cluster8904_1clades	74	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06774.1	009032	Cluster8905_1clades	74	BcepSaruman_361	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74744.1	009032	Cluster8905_1clades	74	BcepSauron_364	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54685.1	009033	Cluster8906_1clades	74	b23_0067	Synechococcus phage B23	GCA_009745195.1
QGT54315.1	009033	Cluster8906_1clades	74	b3_0067	Synechococcus phage B3	GCA_009745215.1
QGT54730.1	009034	TAP42	74	b23_0115	Synechococcus phage B23	GCA_009745195.1
QGT54360.1	009034	TAP42	74	b3_0116	Synechococcus phage B3	GCA_009745215.1
QGT54763.1	009035	TUDOR	74	b23_0148	Synechococcus phage B23	GCA_009745195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54393.1	009035	TUDOR	74	b3_0149	Synechococcus phage B3	GCA_009745215.1
QGT54780.1	009036	Cluster8909_1clades	74	b23_0165	Synechococcus phage B23	GCA_009745195.1
QGT54410.1	009036	Cluster8909_1clades	74	b3_0166	Synechococcus phage B3	GCA_009745215.1
AIA65034.1	009037	Cluster8910_1clades	70	S13_237	Cronobacter phage S13	GCA_001503575.1
QHJ78898.1	009037	Cluster8910_1clades	74	-	Myoviridae sp.	GCA_012593985.1
prevph1000000756	009038	Cluster8911_1clades	75	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000508	009038	Cluster8911_1clades	75	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000800	009039	Cluster8912_1clades	75	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000547	009039	Cluster8912_1clades	75	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88154.1	009040	Cluster8913_1clades	73	CcrColossus_gp284	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68829.1	009040	Cluster8913_1clades	73	CcrPW_gp290	Caulobacter phage CcrPW	GCA_003443275.1
AIA64801.1	009041	Cluster8914_1clades	73	S13_002	Cronobacter phage S13	GCA_001503575.1
QHJ78861.1	009041	Cluster8914_1clades	73	-	Myoviridae sp.	GCA_012593985.1
AKF13261.1	009042	Cluster8915_1clades	73	PHIM19_356	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12901.1	009042	Cluster8915_1clades	73	PHIM7_356	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01234.1	009043	TM	73	AR9_g150	Bacillus phage AR9	GCA_001743835.1
AST99860.1	009043	TM	73	PBI_PBS1_38	Bacillus virus PBS1	GCA_002601325.1
AOO14354.1	009044	TM	68	Sn110110_160	Cyanophage S-RIM14	GCA_002599065.1
AOO15003.1	009044	TM	73	W1230910_157	Cyanophage S-RIM14	GCA_002599125.1
AXQ69181.1	009045	Cluster8918_1clades	73	CcrBL9_gp157	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69734.1	009045	Cluster8918_1clades	73	CcrSC_gp152	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69207.1	009046	Cluster8919_1clades	44	CcrBL9_gp183	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69760.1	009046	Cluster8919_1clades	73	CcrSC_gp178	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69404.1	009047	Cluster8920_1clades	71	CcrBL9_gp380	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69961.1	009047	Cluster8920_1clades	73	CcrSC_gp379	Caulobacter phage CcrSC	GCA_003443315.1
AYD81364.1	009048	Cluster8921_1clades	73	SEA_JUSTBECAUSE_209	Streptomyces phage JustBecause	GCA_003613775.1
QJD53767.1	009048	Cluster8921_1clades	73	SEA_KELA_207	Streptomyces phage Kela	GCA_012934305.1
BAW19197.1	009049	Cluster8922_1clades	73	FDH28_gp198	Ralstonia phage RP12	GCA_002617345.1
BAW19483.1	009049	Cluster8922_1clades	73	-	Ralstonia phage RP31	GCA_002617365.1
BAW19202.1	009050	Cluster8923_1clades	73	FDH28_gp193	Ralstonia phage RP12	GCA_002617345.1
BAW19488.1	009050	Cluster8923_1clades	73	-	Ralstonia phage RP31	GCA_002617365.1
BBA65156.1	009051	Cluster8924_1clades	73	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65615.1	009051	Cluster8924_1clades	73	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65736.1	009052	SIG+TM	73	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65277.1	009052	SIG+TM	73	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90699.1	009053	Cluster8926_1clades	73	HYO65_gp307	Tenacibaculum phage PTm1	GCA_009730695.1
BBI91005.1	009053	Cluster8926_1clades	73	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06552.1	009054	Cluster8927_1clades	72	BcepSaruman_139	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74519.1	009054	Cluster8927_1clades	73	BcepSauron_139	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06716.1	009055	SIG+TM	73	BcepSaruman_303	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74684.1	009055	SIG+TM	73	BcepSauron_304	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32175.1	009056	Cluster8929_1clades	73	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41754.1	009056	Cluster8929_1clades	73	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54712.1	009057	Cluster8930_1clades	73	b23_0097	Synechococcus phage B23	GCA_009745195.1
QGT54342.1	009057	Cluster8930_1clades	73	b3_0098	Synechococcus phage B3	GCA_009745215.1
QGT54728.1	009058	Cluster8931_1clades	73	b23_0113	Synechococcus phage B23	GCA_009745195.1
QGT54358.1	009058	Cluster8931_1clades	73	b3_0114	Synechococcus phage B3	GCA_009745215.1
QGT54793.1	009059	Cluster8932_1clades	73	b23_0178	Synechococcus phage B23	GCA_009745195.1
QGT54423.1	009059	Cluster8932_1clades	73	b3_0179	Synechococcus phage B3	GCA_009745215.1
QGT54816.1	009060	Cluster8933_1clades	73	b23_0201	Synechococcus phage B23	GCA_009745195.1
QGT54446.1	009060	Cluster8933_1clades	73	b3_0203	Synechococcus phage B3	GCA_009745215.1
SOK59278.1	009061	Cluster8934_1clades	73	g470	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58743.1	009061	Cluster8934_1clades	73	g466	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000043	009062	Cluster8935_1clades	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000034	009062	Cluster8935_1clades	74	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000326	009063	SIG+Lar_restr_allev	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000255	009063	SIG+Lar_restr_allev	74	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000434	009064	Cluster8937_1clades	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000346	009064	Cluster8937_1clades	74	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44497.1	009065	Cluster8938_1clades	72	PSSM2_119	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12469.1	009065	Cluster8938_1clades	72	PRTG_00322	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44575.1	009066	Cluster8939_1clades	72	PSSM2_197	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12398.1	009066	Cluster8939_1clades	72	PRTG_00245	Prochlorococcus phage P-SSM5	GCA_002991095.1
QAX98583.1	009067	Cluster8940_1clades	72	ASfcp2_249	Aeromonas phage AsFcp_2	GCA_004146885.1
ADQ53048.1	009067	Cluster8940_1clades	72	PX29p331	Aeromonas phage PX29	GCA_000920195.1
AFC21523.1	009068	SIG+TM	72	GAP32_075	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43643.1	009068	SIG+TM	67	CBB_78	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU88124.1	009069	Cluster8942_1clades	72	CcrColossus_gp254	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68802.1	009069	Cluster8942_1clades	56	CcrPW_gp263	Caulobacter phage CcrPW	GCA_003443275.1
AFU88257.1	009070	Cluster8943_1clades	72	CcrColossus_gp387	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68931.1	009070	Cluster8943_1clades	72	CcrPW_gp392	Caulobacter phage CcrPW	GCA_003443275.1
AHI60353.1	009071	Cluster8944_1clades	72	Ea357_200A	Erwinia phage Ea35-70	GCA_000914635.1
ASB43076.1	009071	Cluster8944_1clades	72	SIMMY50_208	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
AIA64910.1	009072	Cluster8945_1clades	72	S13_111	Cronobacter phage S13	GCA_001503575.1
QHJ79033.1	009072	Cluster8945_1clades	69	-	Myoviridae sp.	GCA_012593985.1
AMS01104.1	009073	Cluster8947_1clades	72	AR9_g019	Bacillus phage AR9	GCA_001743835.1
ASU00026.1	009073	Cluster8947_1clades	72	PBI_PBS1_204	Bacillus virus PBS1	GCA_002601325.1
AMS01190.1	009074	Cluster8948_1clades	72	AR9_g106	Bacillus phage AR9	GCA_001743835.1
ASU00124.1	009074	Cluster8948_1clades	72	PBI_PBS1_302	Bacillus virus PBS1	GCA_002601325.1
AND75338.1	009075	Cluster8949_1clades	71	ME3_177	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75357.1	009075	Cluster8949_1clades	72	ME3_196	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AOO14271.1	009076	Cluster8950_1clades	72	Sn110110_077	Cyanophage S-RIM14	GCA_002599065.1
AOO14920.1	009076	Cluster8950_1clades	72	W1230910_074	Cyanophage S-RIM14	GCA_002599125.1
QBZ72135.1	009077	Cluster8952_1clades	72	SEA_KRADAL_249	Streptomyces phage Kradal	GCA_004799925.1
AXH66397.1	009077	Cluster8952_1clades	72	SEA_SATIS_248	Streptomyces phage Satis	GCA_003366315.1
AXQ69497.1	009078	Cluster8953_1clades	72	CcrBL9_gp473	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70045.1	009078	Cluster8953_1clades	72	CcrSC_gp463	Caulobacter phage CcrSC	GCA_003443315.1
AYD81346.1	009079	Cluster8954_1clades	72	SEA_JUSTBECAUSE_181	Streptomyces phage JustBecause	GCA_003613775.1
QJD53749.1	009079	Cluster8954_1clades	72	SEA_KELA_179	Streptomyces phage Kela	GCA_012934305.1
AYD81476.1	009080	Cluster8955_1clades	72	SEA_JUSTBECAUSE_321	Streptomyces phage JustBecause	GCA_003613775.1
QJD53879.1	009080	Cluster8955_1clades	72	SEA_KELA_319	Streptomyces phage Kela	GCA_012934305.1
BBA65625.1	009081	Cluster8956_1clades	72	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65166.1	009081	Cluster8956_1clades	72	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65175.1	009082	Cluster8957_1clades	72	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65634.1	009082	Cluster8957_1clades	72	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90456.1	009083	Cluster8958_1clades	72	HYO65_gp064	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90764.1	009083	Cluster8958_1clades	72	-	Tenacibaculum phage PTm5	GCA_009730715.1
AIT14235.1	009084	Cluster8959_1clades	69	PBI_121Q_345	Escherichia phage 121Q	GCA_000926855.1
BBM61912.1	009084	Cluster8959_1clades	72	EO157G_3230	Escherichia phage SP27	GCA_008033345.1
QAY01363.1	009085	Cluster8960_1clades	72	ASwh1_303	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39287.1	009085	Cluster8960_1clades	70	CC2_391	Aeromonas phage CC2	GCA_000903495.1
QBX06432.1	009086	Cluster8961_1clades	72	BcepSaruman_019	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74399.1	009086	Cluster8961_1clades	72	BcepSauron_019	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06518.1	009087	Cluster8962_1clades	72	BcepSaruman_105	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74484.1	009087	Cluster8962_1clades	72	BcepSauron_104	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06680.1	009088	Cluster8963_1clades	72	BcepSaruman_267	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74650.1	009088	Cluster8963_1clades	72	BcepSauron_270	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54741.1	009089	Cluster8964_1clades	72	b23_0126	Synechococcus phage B23	GCA_009745195.1
QGT54371.1	009089	Cluster8964_1clades	72	b3_0127	Synechococcus phage B3	GCA_009745215.1
QGT54721.1	009090	Cluster8965_1clades	72	b23_0106	Synechococcus phage B23	GCA_009745195.1
QGT54351.1	009090	Cluster8965_1clades	58	b3_0107	Synechococcus phage B3	GCA_009745215.1
QIG58047.1	009091	Cluster8966_1clades	72	SEA_PAULODIABOLI_363	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57746.1	009091	Cluster8966_1clades	72	SEA_PAULODIABOLI_8	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000645	009092	Cluster8967_1clades	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000460	009092	Cluster8967_1clades	73	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000759	009093	Cluster8968_1clades	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000511	009093	Cluster8968_1clades	73	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01555.1	009094	TM	71	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53178.1	009094	TM	71	65p170	Aeromonas virus 65	GCA_000893255.1
AXQ68455.1	009095	Cluster8970_1clades	70	CcrBL10_gp251	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86742.1	009095	Cluster8970_1clades	71	CcrRogue_gp260	Caulobacter virus Rogue	GCA_000900555.1
AFU87938.1	009096	Cluster8971_1clades	71	CcrColossus_gp068	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68610.1	009096	Cluster8971_1clades	71	CcrPW_gp071	Caulobacter phage CcrPW	GCA_003443275.1
AFU88236.1	009097	Cluster8972_1clades	71	CcrColossus_gp366	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68912.1	009097	Cluster8972_1clades	71	CcrPW_gp373c	Caulobacter phage CcrPW	GCA_003443275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFU88239.1	009098	Cluster8973_1clades	71	CcrColossus_gp369	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68914.1	009098	Cluster8973_1clades	71	CcrPW_gp375c	Caulobacter phage CcrPW	GCA_003443275.1
AFC21635.1	009099	Cluster8974_1clades	69	GAP32_185	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43756.1	009099	Cluster8974_1clades	71	CBB_191	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01156.1	009100	Cluster8975_1clades	71	AR9_g072	Bacillus phage AR9	GCA_001743835.1
ASU00085.1	009100	Cluster8975_1clades	71	PBI_PBS1_263	Bacillus virus PBS1	GCA_002601325.1
AMS01220.1	009101	Cluster8976_1clades	71	AR9_g136	Bacillus phage AR9	GCA_001743835.1
AST99845.1	009101	Cluster8976_1clades	71	PBI_PBS1_23	Bacillus virus PBS1	GCA_002601325.1
AXQ69130.1	009102	Cluster8977_1clades	71	CcrBL9_gp106	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69684.1	009102	Cluster8977_1clades	71	CcrSC_gp102	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69427.1	009103	Cluster8978_1clades	71	CcrBL9_gp403	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69981.1	009103	Cluster8978_1clades	71	CcrSC_gp399	Caulobacter phage CcrSC	GCA_003443315.1
BBA65268.1	009104	Cluster8979_1clades	71	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65727.1	009104	Cluster8979_1clades	71	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65537.1	009105	DUF4381	71	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96534.1	009105	DUF4381	64	Xoosp13_348	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90476.1	009106	Cluster8981_1clades	71	HYO65_gp084	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90783.1	009106	Cluster8981_1clades	71	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAY00312.1	009107	SIG+TM	71	Ecwhy1_30	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61714.1	009107	SIG+TM	56	EO157G_1250	Escherichia phage SP27	GCA_008033345.1
QBX06440.1	009108	Cluster8983_1clades	71	BcepSaruman_027	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74408.1	009108	Cluster8983_1clades	71	BcepSauron_028	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06556.1	009109	Cluster8984_1clades	71	BcepSaruman_143	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74523.1	009109	Cluster8984_1clades	71	BcepSauron_143	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06702.1	009110	Cluster8985_1clades	71	BcepSaruman_289	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74670.1	009110	Cluster8985_1clades	71	BcepSauron_290	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06757.1	009111	Cluster8986_1clades	71	BcepSaruman_344	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74727.1	009111	Cluster8986_1clades	71	BcepSauron_347	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06820.1	009112	Cluster8987_1clades	71	BcepSaruman_407	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74789.1	009112	Cluster8987_1clades	71	BcepSauron_409	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32164.1	009113	Cluster8988_1clades	71	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41745.1	009113	Cluster8988_1clades	41	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32534.1	009114	Cluster8989_1clades	71	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42107.1	009114	Cluster8989_1clades	71	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ96835.1	009115	Cluster8990_1clades	71	PS1_0076	Aeromonas phage PS1	GCA_007051165.2
QFR59465.1	009115	Cluster8990_1clades	71	PS2_0074	Aeromonas phage PS2	GCA_009388305.2
QBX32470.1	009116	Cluster8991_1clades	51	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42042.1	009116	Cluster8991_1clades	71	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54687.1	009117	Cluster8992_1clades	71	b23_0070	Synechococcus phage B23	GCA_009745195.1
QGT54317.1	009117	Cluster8992_1clades	71	b3_0071	Synechococcus phage B3	GCA_009745215.1
QGT54789.1	009118	Cluster8993_1clades	71	b23_0174	Synechococcus phage B23	GCA_009745195.1
QGT54419.1	009118	Cluster8993_1clades	71	b3_0175	Synechococcus phage B3	GCA_009745215.1
QIG57759.1	009119	Cluster8994_1clades	71	SEA_PAULODIABOLI_22	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58060.1	009119	Cluster8994_1clades	71	SEA_PAULODIABOLI_377	Microbacterium phage PauloDiaboli	GCA_011067425.1
SOK58986.1	009120	Cluster8995_1clades	71	g178	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58452.1	009120	Cluster8995_1clades	71	g175	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000603	009121	Cluster8996_1clades	72	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000423	009121	Cluster8996_1clades	72	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000859	009122	Cluster8997_1clades	72	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000597	009122	Cluster8997_1clades	72	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44578.1	009123	Cluster8998_1clades	70	PSSM2_201	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12395.1	009123	Cluster8998_1clades	70	PRTG_00242	Prochlorococcus phage P-SSM5	GCA_002991095.1
ANS06161.1	009124	Cluster8999_1clades	70	ABCD_0014	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78535.1	009124	Cluster8999_1clades	70	RB43ORF013c	Escherichia virus RB43	GCA_000863505.1
ABY62918.1	009125	Cluster9000_1clades	70	201phi2-1p085	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV76699.1	009125	Cluster9000_1clades	66	PHABIO_68	Pseudomonas phage Phabio	GCA_002624965.1
AXQ68241.1	009126	SelB-HTH	68	CcrBL10_gp037	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86523.1	009126	SelB-HTH	70	CcrRogue_gp041	Caulobacter virus Rogue	GCA_000900555.1
AFU88038.1	009127	TM+TM	70	CcrColossus_gp168	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68715.1	009127	TM+TM	70	CcrPW_gp176c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88169.1	009128	Cluster9003_1clades	70	CcrColossus_gp299	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68846.1	009128	Cluster9003_1clades	70	CcrPW_gp307	Caulobacter phage CcrPW	GCA_003443275.1
AAX44466.1	009129	Cluster9004_1clades	69	PSSM2_088	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12187.1	009129	Cluster9004_1clades	70	PRTG_00029	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGH56956.1	009130	Cluster9005_1clades	68	CPXG_00153	Cyanophage P-RSM6	GCA_000906155.1
AJK27499.1	009130	Cluster9005_1clades	70	PTIM40_72	Cyanophage P-TIM40	GCA_001470935.1
AXF51148.1	009131	SIG+TM	70	WELLINGTON_17	Erwinia phage Wellington	GCA_003344985.1
ANZ49370.1	009131	SIG+TM	70	KWAN_17	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AGN12389.1	009132	Cluster9007_1clades	53	PRTG_00236	Prochlorococcus phage P-SSM5	GCA_002991095.1
ASR76219.1	009132	Cluster9007_1clades	70	PBI_BELLAMY_176	Synechococcus phage Bellamy	GCA_002627525.1
QBZ72139.1	009133	Cluster9008_1clades	70	SEA_KRADAL_253	Streptomyces phage Kradal	GCA_004799925.1
AXH66401.1	009133	Cluster9008_1clades	70	SEA_SATIS_252	Streptomyces phage Satis	GCA_003366315.1
AXQ69412.1	009134	Cluster9009_1clades	65	CcrBL9_gp388	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69969.1	009134	Cluster9009_1clades	70	CcrSC_gp387	Caulobacter phage CcrSC	GCA_003443315.1
BBA65664.1	009135	Cluster9010_1clades	70	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65205.1	009135	Cluster9010_1clades	70	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65714.1	009136	Cluster9011_1clades	70	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65255.1	009136	Cluster9011_1clades	70	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90561.1	009137	Cluster9012_1clades	70	HYO65_gp169	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90869.1	009137	Cluster9012_1clades	70	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06620.1	009138	Cluster9013_1clades	70	BcepSaruman_207	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74588.1	009138	Cluster9013_1clades	70	BcepSauron_208	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06749.1	009139	Cluster9014_1clades	70	BcepSaruman_336	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74718.1	009139	Cluster9014_1clades	70	BcepSauron_338	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32160.1	009140	Cluster9015_1clades	70	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41741.1	009140	Cluster9015_1clades	70	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54689.1	009141	Cluster9016_1clades	70	b23_0074	Synechococcus phage B23	GCA_009745195.1
QGT54319.1	009141	Cluster9016_1clades	70	b3_0075	Synechococcus phage B3	GCA_009745215.1
QGT54842.1	009142	Cluster9017_1clades	70	b23_0227	Synechococcus phage B23	GCA_009745195.1
QGT54476.1	009142	Cluster9017_1clades	70	b3_0233	Synechococcus phage B3	GCA_009745215.1
QGT54867.1	009143	Cluster9018_1clades	70	b23_0253	Synechococcus phage B23	GCA_009745195.1
QGT54502.1	009143	Cluster9018_1clades	70	b3_0260	Synechococcus phage B3	GCA_009745215.1
SOK58862.1	009144	Cluster9019_1clades	70	g054	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58325.1	009144	Cluster9019_1clades	70	g048	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000792	009145	Cluster9020_1clades	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000540	009145	Cluster9020_1clades	71	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44467.1	009146	Cluster9021_1clades	69	PSSM2_089	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12186.1	009146	Cluster9021_1clades	69	PRTG_00028	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01553.1	009147	TM+TM	69	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53176.1	009147	TM+TM	69	65p168	Aeromonas virus 65	GCA_000893255.1
APU01706.1	009148	Cluster9023_1clades	65	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53345.1	009148	Cluster9023_1clades	69	65p337	Aeromonas virus 65	GCA_000893255.1
AXQ68471.1	009149	Cluster9024_1clades	69	CcrBL10_gp267	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86756.1	009149	Cluster9024_1clades	69	CcrRogue_gp274	Caulobacter virus Rogue	GCA_000900555.1
QHJ74292.1	009150	Cluster9025_1clades	67	VH12019_00373	Vibrio phage VH1_2019	GCA_009931825.1
AGN30160.1	009150	Cluster9025_1clades	69	VPFG_00158	Vibrio phage nt-1	GCA_000910195.2
AGR48104.1	009151	Cluster9026_1clades	69	SmphiM12_472	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13637.1	009151	Cluster9026_1clades	69	PHIN3_374	Sinorhizobium phage phiN3	GCA_001501175.1
AIA64989.1	009152	Cluster9027_1clades	69	S13_192	Cronobacter phage S13	GCA_001503575.1
QHJ78943.1	009152	Cluster9027_1clades	64	-	Myoviridae sp.	GCA_012593985.1
AMS01150.1	009153	SIG+TM	69	AR9_g066	Bacillus phage AR9	GCA_001743835.1
ASU00079.1	009153	SIG+TM	69	PBI_PBS1_257	Bacillus virus PBS1	GCA_002601325.1
AXF51421.1	009154	Cluster9029_1clades	69	WELLINGTON_5	Erwinia phage Wellington	GCA_003344985.1
ANZ49645.1	009154	Cluster9029_1clades	69	KWAN_5	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
APU01570.1	009155	Cluster9030_1clades	69	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53193.1	009155	Cluster9030_1clades	57	65p185	Aeromonas virus 65	GCA_000893255.1
ASU03900.1	009156	Cluster9031_1clades	55	JOAD_15	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03655.1	009156	Cluster9031_1clades	69	RISINGSUN_15	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65660.1	009157	Cluster9032_1clades	69	2050HW_00325	Serratia phage 2050HW	GCA_002628125.1
QDB71084.1	009157	Cluster9032_1clades	69	CPT_Moabite_052	Serratia phage Moabite	GCA_006384735.1
AXG67066.1	009158	Cluster9033_1clades	69	AD1_022	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08303.1	009158	Cluster9033_1clades	69	Alexandra_23	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72096.1	009159	Cluster9034_1clades	69	SEA_KRADAL_210	Streptomyces phage Kradal	GCA_004799925.1
AXH66357.1	009159	Cluster9034_1clades	69	SEA_SATIS_208	Streptomyces phage Satis	GCA_003366315.1
AXQ69095.1	009160	PMR5N	69	CcrBL9_gp071c	Caulobacter phage CcrBL9	GCA_003443295.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69652.1	009160	PMR5N	68	CcrSC_gp070c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69388.1	009161	Cluster9036_1clades	69	CcrBL9_gp364	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69948.1	009161	Cluster9036_1clades	69	CcrSC_gp366	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69119.1	009162	SIG+MNS	66	CcrBL9_gp095	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69673.1	009162	SIG+MNS	69	CcrSC_gp091	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69278.1	009163	Cluster9038_1clades	66	CcrBL9_gp254c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69835.1	009163	Cluster9038_1clades	69	CcrSC_gp253c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69532.1	009164	SIG+TM	68	CcrBL9_gp508	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70074.1	009164	SIG+TM	69	CcrSC_gp492	Caulobacter phage CcrSC	GCA_003443315.1
AYD81338.1	009165	Cluster9040_1clades	69	SEA_JUSTBECAUSE_173	Streptomyces phage JustBecause	GCA_003613775.1
QJD53741.1	009165	Cluster9040_1clades	69	SEA_KELA_171	Streptomyces phage Kela	GCA_012934305.1
QCW19101.1	009166	Cluster9041_1clades	69	7t3_0583	Salmonella phage 7t3	GCA_006083215.1
AZU98340.1	009166	Cluster9041_1clades	69	CPT_Munch_398	Salmonella phage Munch	GCA_004015485.1
BBA65250.1	009167	TM+TM	69	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65709.1	009167	TM+TM	69	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06427.1	009168	Cluster9043_1clades	69	BcepSaruman_014	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74394.1	009168	Cluster9043_1clades	69	BcepSauron_014	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06597.1	009169	SIG+TM	65	BcepSaruman_184	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74562.1	009169	SIG+TM	69	BcepSauron_182	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06742.1	009170	Cluster9045_1clades	69	BcepSaruman_329	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74711.1	009170	Cluster9045_1clades	69	BcepSauron_331	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06744.1	009171	Cluster9046_1clades	69	BcepSaruman_331	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74713.1	009171	Cluster9046_1clades	69	BcepSauron_333	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06748.1	009172	Cluster9047_1clades	69	BcepSaruman_335	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74717.1	009172	Cluster9047_1clades	69	BcepSauron_337	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32226.1	009173	SIG+TM	69	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41804.1	009173	SIG+TM	64	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32413.1	009174	Cluster9049_1clades	69	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41984.1	009174	Cluster9049_1clades	69	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22868.1	009175	Cluster9050_1clades	69	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50719.1	009175	Cluster9050_1clades	69	-	Synechococcus phage S-B43	GCA_006869725.1
QBX32513.1	009176	Cluster9051_1clades	36	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42086.1	009176	Cluster9051_1clades	69	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
prevph1000000352	009177	Cluster9052_1clades	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000278	009177	Cluster9052_1clades	70	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44597.1	009178	Cluster9053_1clades	68	PSSM2_220	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12373.1	009178	Cluster9053_1clades	68	PRTG_00220	Prochlorococcus phage P-SSM5	GCA_002991095.1
ANS06167.1	009179	Cluster9054_1clades	68	ABCD_0084	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78606.1	009179	Cluster9054_1clades	68	RB43ORF084w	Escherichia virus RB43	GCA_000863505.1
AGR48125.1	009180	Cluster9055_1clades	68	SmphiM12_493	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13662.1	009180	Cluster9055_1clades	68	PHIN3_399	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13145.1	009181	Cluster9056_1clades	68	PHIM19_240	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12784.1	009181	Cluster9056_1clades	68	PHIM7_239	Sinorhizobium phage phiM7	GCA_002622405.1
AXF51257.1	009182	Cluster9057_1clades	68	WELLINGTON_127	Erwinia phage Wellington	GCA_003344985.1
ANZ49477.1	009182	Cluster9057_1clades	68	KWAN_125	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AOO14254.1	009183	Cluster9058_1clades	68	Sn110110_060	Cyanophage S-RIM14	GCA_002599065.1
AOO14906.1	009183	Cluster9058_1clades	68	W1230910_060	Cyanophage S-RIM14	GCA_002599125.1
ASU03735.1	009184	Cluster9059_1clades	68	JOAD_180	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03491.1	009184	Cluster9059_1clades	68	RISINGSUN_179	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ASU03805.1	009185	Cluster9060_1clades	68	JOAD_110	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03560.1	009185	Cluster9060_1clades	68	RISINGSUN_110	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65466.1	009186	Cluster9061_1clades	68	2050HW_00131	Serratia phage 2050HW	GCA_002628125.1
QDB71235.1	009186	Cluster9061_1clades	68	CPT_Moabite_205	Serratia phage Moabite	GCA_006384735.1
AXQ69450.1	009187	Cluster9062_1clades	68	CcrBL9_gp426	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70000.1	009187	Cluster9062_1clades	68	CcrSC_gp418	Caulobacter phage CcrSC	GCA_003443315.1
BAS04904.2	009188	Cluster9063_1clades	57	AVU11_agp25	Ralstonia phage RSF1	GCA_001500875.1
BAQ02631.1	009188	Cluster9063_1clades	68	AVU38_gp103	Ralstonia phage RSL2	GCA_001503055.1
BBA65704.1	009189	Cluster9064_1clades	68	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65245.1	009189	Cluster9064_1clades	68	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90599.1	009190	Cluster9065_1clades	68	HYO65_gp207	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90906.1	009190	Cluster9065_1clades	68	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06754.1	009191	Cluster9066_1clades	68	BcepSaruman_341	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74723.1	009191	Cluster9066_1clades	68	BcepSauron_343	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32441.1	009192	Cluster9067_1clades	68	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42012.1	009192	Cluster9067_1clades	68	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54706.1	009193	Cluster9068_1clades	68	b23_0091	Synechococcus phage B23	GCA_009745195.1
QGT54336.1	009193	Cluster9068_1clades	68	b3_0092	Synechococcus phage B3	GCA_009745215.1
QGT54774.1	009194	Cluster9069_1clades	68	b23_0159	Synechococcus phage B23	GCA_009745195.1
QGT54404.1	009194	Cluster9069_1clades	68	b3_0160	Synechococcus phage B3	GCA_009745215.1
QGT54783.1	009195	Cluster9070_1clades	68	b23_0168	Synechococcus phage B23	GCA_009745195.1
QGT54413.1	009195	Cluster9070_1clades	68	b3_0169	Synechococcus phage B3	GCA_009745215.1
QDJ96809.1	009196	Cluster9071_1clades	52	PS1_0050	Aeromonas phage PS1	GCA_007051165.2
QHE95176.1	009196	Cluster9071_1clades	68	PS2_0049	Aeromonas phage PS2	GCA_009388305.2
SOK58984.1	009197	Cluster9072_1clades	68	g176	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58450.1	009197	Cluster9072_1clades	67	g173	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000328	009198	Cluster9073_1clades	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000257	009198	Cluster9073_1clades	69	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000615	009199	Cluster9074_1clades	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000434	009199	Cluster9074_1clades	69	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000754	009200	Cluster9075_1clades	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000506	009200	Cluster9075_1clades	69	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000769	009201	Cluster9076_1clades	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000522	009201	Cluster9076_1clades	69	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44470.1	009202	Cluster9077_1clades	67	PSSM2_092	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12182.1	009202	Cluster9077_1clades	67	PRTG_00024	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44571.1	009203	Cluster9078_1clades	67	PSSM2_193	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12402.1	009203	Cluster9078_1clades	67	PRTG_00249	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44602.1	009204	Cluster9079_1clades	67	PSSM2_225	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12368.1	009204	Cluster9079_1clades	67	PRTG_00215	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ68238.1	009205	Cluster9080_1clades	67	CcrBL10_gp034	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86520.1	009205	Cluster9080_1clades	67	CcrRogue_gp038	Caulobacter virus Rogue	GCA_000900555.1
AXQ68486.1	009206	Cluster9081_1clades	67	CcrBL10_gp282	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86774.1	009206	Cluster9081_1clades	67	CcrRogue_gp292	Caulobacter virus Rogue	GCA_000900555.1
AFU88253.1	009207	Cluster9082_1clades	67	CcrColossus_gp383	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68929.1	009207	Cluster9082_1clades	67	CcrPW_gp390c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88274.1	009208	Cluster9083_1clades	67	CcrColossus_gp404	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68950.1	009208	Cluster9083_1clades	67	CcrPW_gp411c	Caulobacter phage CcrPW	GCA_003443275.1
AIA64983.1	009209	Cluster9084_1clades	67	S13_186	Cronobacter phage S13	GCA_001503575.1
QHJ78952.1	009209	Cluster9084_1clades	66	-	Myoviridae sp.	GCA_012593985.1
AIA65009.1	009210	Cluster9085_1clades	67	S13_212	Cronobacter phage S13	GCA_001503575.1
QHJ78923.1	009210	Cluster9085_1clades	63	-	Myoviridae sp.	GCA_012593985.1
AGH07683.1	009211	Cluster9086_1clades	63	CYVG_00240	Cyanophage S-SSM6a	GCA_002710385.1
AIR93623.1	009211	Cluster9086_1clades	67	AVU42_gp078	Prochlorococcus phage P-TIM68	GCA_001503075.1
AMS01086.1	009212	Cluster9087_1clades	67	AR9_g001	Bacillus phage AR9	GCA_001743835.1
ASU00008.1	009212	Cluster9087_1clades	67	PBI_PBS1_186	Bacillus virus PBS1	GCA_002601325.1
AMS01181.1	009213	Cluster9088_1clades	67	AR9_g097	Bacillus phage AR9	GCA_001743835.1
ASU00115.1	009213	Cluster9088_1clades	67	PBI_PBS1_293	Bacillus virus PBS1	GCA_002601325.1
AMS01303.1	009214	Cluster9089_1clades	67	AR9_g219	Bacillus phage AR9	GCA_001743835.1
AST99932.1	009214	Cluster9089_1clades	60	PBI_PBS1_110	Bacillus virus PBS1	GCA_002601325.1
AXF51230.1	009215	Cluster9090_1clades	67	WELLINGTON_100	Erwinia phage Wellington	GCA_003344985.1
ANZ49451.1	009215	Cluster9090_1clades	67	KWAN_99	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51423.1	009216	Cluster9091_1clades	67	WELLINGTON_145	Erwinia phage Wellington	GCA_003344985.1
ANZ49497.1	009216	Cluster9091_1clades	67	KWAN_145	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65462.1	009217	Cluster9092_1clades	67	2050HW_00127	Serratia phage 2050HW	GCA_002628125.1
QDB71231.1	009217	Cluster9092_1clades	67	CPT_Moabite_201	Serratia phage Moabite	GCA_006384735.1
ATA65467.1	009218	Cluster9093_1clades	67	2050HW_00132	Serratia phage 2050HW	GCA_002628125.1
QDB71236.1	009218	Cluster9093_1clades	67	CPT_Moabite_206	Serratia phage Moabite	GCA_006384735.1
AXQ69253.1	009219	Cluster9094_1clades	67	CcrBL9_gp229c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69810.1	009219	Cluster9094_1clades	67	CcrSC_gp228c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69387.1	009220	Cluster9095_1clades	55	CcrBL9_gp363	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69947.1	009220	Cluster9095_1clades	67	CcrSC_gp365	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70618.1	009221	Cluster9096_1clades	67	HOU04_gp017	Synechococcus phage S-T4	GCA_003443335.1
AXQ70416.1	009221	Cluster9096_1clades	67	HOU04_gp017	Synechococcus phage S-T4	GCA_003443335.1
QCW18790.1	009222	Cluster9097_1clades	67	7t3_0269	Salmonella phage 7t3	GCA_006083215.1
AZU98055.1	009222	Cluster9097_1clades	67	CPT_Munch_111	Salmonella phage Munch	GCA_004015485.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65165.1	009223	SCP2	67	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65624.1	009223	SCP2	67	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65699.1	009224	Cluster9099_1clades	67	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65240.1	009224	Cluster9099_1clades	67	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65600.1	009225	Cluster9100_1clades	67	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96579.1	009225	Cluster9100_1clades	66	Xoosp13_393	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90615.1	009226	RE_ApaLI	67	HYO65_gp223	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90921.1	009226	RE_ApaLI	67	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06430.1	009227	Cluster9102_1clades	67	BcepSaruman_017	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74397.1	009227	Cluster9102_1clades	67	BcepSauron_017	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06777.1	009228	Cluster9103_1clades	67	BcepSaruman_364	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74747.1	009228	Cluster9103_1clades	67	BcepSauron_367	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32516.1	009229	Cluster9104_1clades	67	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42089.1	009229	Cluster9104_1clades	67	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW18883.1	009230	Cluster9105_1clades	67	7t3_0362	Salmonella phage 7t3	GCA_006083215.1
AZU98141.1	009230	Cluster9105_1clades	66	CPT_Munch_197	Salmonella phage Munch	GCA_004015485.1
QGT54680.1	009231	Cluster9106_1clades	67	b23_0055	Synechococcus phage B23	GCA_009745195.1
QGT54310.1	009231	Cluster9106_1clades	67	b3_0055	Synechococcus phage B3	GCA_009745215.1
QGT54715.1	009232	Cluster9107_1clades	67	b23_0100	Synechococcus phage B23	GCA_009745195.1
QGT54345.1	009232	Cluster9107_1clades	67	b3_0101	Synechococcus phage B3	GCA_009745215.1
QGT54810.1	009233	Cluster9108_1clades	67	b23_0195	Synechococcus phage B23	GCA_009745195.1
QGT54440.1	009233	Cluster9108_1clades	67	b3_0197	Synechococcus phage B3	GCA_009745215.1
prevph1000000297	009234	Cluster9109_1clades	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000229	009234	Cluster9109_1clades	68	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000373	009235	Cluster9110_1clades	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000299	009235	Cluster9110_1clades	68	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44462.1	009236	Cluster9111_1clades	66	PSSM2_084	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12191.1	009236	Cluster9111_1clades	66	PRTG_00033	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFU88070.1	009237	Cluster9112_1clades	66	CcrColossus_gp200	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68747.1	009237	Cluster9112_1clades	66	CcrPW_gp208c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88127.1	009238	Cluster9113_1clades	66	CcrColossus_gp257	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68804.1	009238	Cluster9113_1clades	66	CcrPW_gp265	Caulobacter phage CcrPW	GCA_003443275.1
AFU88303.1	009239	Cluster9114_1clades	66	CcrColossus_gp433	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68978.1	009239	Cluster9114_1clades	66	CcrPW_gp439c	Caulobacter phage CcrPW	GCA_003443275.1
AGH07519.1	009240	SIG+TM	66	CYVG_00075	Cyanophage S-SSM6a	GCA_002710385.1
ASR76289.1	009240	SIG+TM	65	PBI_BELLAMY_253	Synechococcus phage Bellamy	GCA_002627525.1
AGR48124.1	009241	Cluster9116_1clades	66	SmphiM12_492	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13661.1	009241	Cluster9116_1clades	66	PHIN3_398	Sinorhizobium phage phiN3	GCA_001501175.1
AIT14191.1	009242	Cluster9117_1clades	66	PBI_121Q_301	Escherichia phage 121Q	GCA_000926855.1
QDF14130.1	009242	Cluster9117_1clades	66	vBEcoMphAPEC6_gp507c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AMS01147.1	009243	Cluster9118_1clades	66	AR9_g063	Bacillus phage AR9	GCA_001743835.1
ASU00075.1	009243	Cluster9118_1clades	57	PBI_PBS1_253	Bacillus virus PBS1	GCA_002601325.1
AMS01157.1	009244	Cluster9119_1clades	66	AR9_g073	Bacillus phage AR9	GCA_001743835.1
ASU00086.1	009244	Cluster9119_1clades	66	PBI_PBS1_264	Bacillus virus PBS1	GCA_002601325.1
AMS01314.1	009245	Cluster9120_1clades	66	AR9_g230	Bacillus phage AR9	GCA_001743835.1
AST99943.1	009245	Cluster9120_1clades	42	PBI_PBS1_121	Bacillus virus PBS1	GCA_002601325.1
ANZ49770.1	009246	SIG+TM	66	MACHINA_132	Erwinia phage Machina	GCA_002758035.1
ANZ48697.1	009246	SIG+TM	66	CHRISDB_135	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51422.1	009247	Cluster9122_1clades	66	WELLINGTON_56	Erwinia phage Wellington	GCA_003344985.1
ANZ49408.1	009247	Cluster9122_1clades	66	KWAN_56	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51419.1	009248	Cluster9123_1clades	66	WELLINGTON_295	Erwinia phage Wellington	GCA_003344985.1
ANZ49644.1	009248	Cluster9123_1clades	66	KWAN_293	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AOO14270.1	009249	Cluster9124_1clades	65	Sn110110_076	Cyanophage S-RIM14	GCA_002599065.1
AOO14919.1	009249	Cluster9124_1clades	66	W1230910_073	Cyanophage S-RIM14	GCA_002599125.1
ATA65688.1	009250	Cluster9125_1clades	66	2050HW_00353	Serratia phage 2050HW	GCA_002628125.1
QDB71115.1	009250	Cluster9125_1clades	66	CPT_Moabite_085	Serratia phage Moabite	GCA_006384735.1
AXG67101.1	009251	Cluster9126_1clades	66	AD1_057	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AWY08337.1	009251	Cluster9126_1clades	66	Alexandra_57	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
QBZ72105.1	009252	Cluster9127_1clades	66	SEA_KRADAL_219	Streptomyces phage Kradal	GCA_004799925.1
AXH66366.1	009252	Cluster9127_1clades	66	SEA_SATIS_217	Streptomyces phage Satis	GCA_003366315.1
QBZ72166.1	009253	Cluster9128_1clades	66	SEA_KRADAL_280	Streptomyces phage Kradal	GCA_004799925.1
AXH66429.1	009253	Cluster9128_1clades	66	SEA_SATIS_280	Streptomyces phage Satis	GCA_003366315.1
AFU88232.1	009254	Cluster9129_1clades	34	CcrColossus_gp362	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68909.1	009254	Cluster9129_1clades	66	CcrPW_gp370	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69138.1	009255	Cluster9130_1clades	66	CcrBL9_gp114	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69692.1	009255	Cluster9130_1clades	66	CcrSC_gp110	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69372.1	009256	Cluster9131_1clades	66	CcrBL9_gp348	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69932.1	009256	Cluster9131_1clades	66	CcrSC_gp350	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69421.1	009257	Cluster9132_1clades	65	CcrBL9_gp397	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69976.1	009257	Cluster9132_1clades	66	CcrSC_gp394	Caulobacter phage CcrSC	GCA_003443315.1
AYD81246.1	009258	Cluster9133_1clades	66	SEA_JUSTBECAUSE_77	Streptomyces phage JustBecause	GCA_003613775.1
QJD53649.1	009258	Cluster9133_1clades	66	SEA_KELA_78	Streptomyces phage Kela	GCA_012934305.1
BAS04808.1	009259	Cluster9134_1clades	66	AVU11_gp016	Ralstonia phage RSF1	GCA_001500875.1
BAQ02544.2	009259	Cluster9134_1clades	50	-	Ralstonia phage RSL2	GCA_001503055.1
BAW19075.1	009260	Cluster9135_1clades	66	FDH28_gp101	Ralstonia phage RP12	GCA_002617345.1
BAW19360.1	009260	Cluster9135_1clades	66	-	Ralstonia phage RP31	GCA_002617365.1
BBA65190.1	009261	Cluster9136_1clades	66	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65649.1	009261	Cluster9136_1clades	66	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90609.1	009262	Cluster9137_1clades	66	HYO65_gp217	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90915.1	009262	Cluster9137_1clades	66	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90670.1	009263	HTH	66	HYO65_gp278	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90975.1	009263	HTH	66	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90415.1	009264	Cluster9139_1clades	40	HYO65_gp023	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90723.1	009264	Cluster9139_1clades	66	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06568.1	009265	Cluster9140_1clades	66	BcepSaruman_155	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74535.1	009265	Cluster9140_1clades	66	BcepSauron_155	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06761.1	009266	Cluster9141_1clades	66	BcepSaruman_348	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74731.1	009266	Cluster9141_1clades	66	BcepSauron_351	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06788.1	009267	Cluster9142_1clades	66	BcepSaruman_375	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74758.1	009267	Cluster9142_1clades	65	BcepSauron_378	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32375.1	009268	Cluster9143_1clades	66	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41948.1	009268	Cluster9143_1clades	66	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW19078.1	009269	Cluster9144_1clades	66	7t3_0558	Salmonella phage 7t3	GCA_006083215.1
QIG62663.1	009269	Cluster9144_1clades	66	SEPL_050	Salmonella phage SE_PL	GCA_011067555.1
QCW23014.1	009270	TM	58	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50720.1	009270	TM	66	-	Synechococcus phage S-B43	GCA_006869725.1
QDJ96884.1	009271	Cluster9146_1clades	66	PS1_0125	Aeromonas phage PS1	GCA_007051165.2
QFR59516.1	009271	Cluster9146_1clades	66	PS2_0125	Aeromonas phage PS2	GCA_009388305.2
QGT54684.1	009272	Cluster9147_1clades	66	b23_0066	Synechococcus phage B23	GCA_009745195.1
QGT54314.1	009272	Cluster9147_1clades	66	b3_0066	Synechococcus phage B3	GCA_009745215.1
QGT54695.1	009273	Cluster9148_1clades	66	b23_0080	Synechococcus phage B23	GCA_009745195.1
QGT54325.1	009273	Cluster9148_1clades	66	b3_0081	Synechococcus phage B3	GCA_009745215.1
QGT54976.1	009274	Cluster9149_1clades	66	b23_0370	Synechococcus phage B23	GCA_009745195.1
QGT54611.1	009274	Cluster9149_1clades	66	b3_0376	Synechococcus phage B3	GCA_009745215.1
AIA65055.1	009275	Cluster9150_1clades	61	S13_258	Cronobacter phage S13	GCA_001503575.1
QHJ78876.1	009275	Cluster9150_1clades	66	-	Myoviridae sp.	GCA_012593985.1
SOK58885.1	009276	SIG+TM	66	g077	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58348.1	009276	SIG+TM	66	g071	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000362	009277	Cluster9152_1clades	67	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000288	009277	Cluster9152_1clades	67	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000383	009278	Cluster9153_1clades	67	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000309	009278	Cluster9153_1clades	67	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000384	009279	Cluster9154_1clades	67	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000310	009279	Cluster9154_1clades	67	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000522	009280	Cluster9155_1clades	67	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000396	009280	Cluster9155_1clades	67	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44454.1	009281	Cluster9156_1clades	65	PSSM2_076	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12200.1	009281	Cluster9156_1clades	65	PRTG_00042	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFC21872.1	009282	Cluster9157_1clades	65	GAP32_419	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44000.1	009282	Cluster9157_1clades	65	CBB_437	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU87967.1	009283	Cluster9158_1clades	65	CcrColossus_gp097	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68642.1	009283	Cluster9158_1clades	65	CcrPW_gp103	Caulobacter phage CcrPW	GCA_003443275.1
AGG54319.1	009284	Cluster9159_1clades	65	CYWG_00035	Cyanophage S-SSM6b	GCA_002710425.1
AGH26150.1	009284	Cluster9159_1clades	65	CPMG_00049	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH56891.1	009285	Cluster9160_1clades	65	CPXG_00088	Cyanophage P-RSM6	GCA_000906155.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGG54441.1	009285	Cluster9160_1clades	62	CYWG_00157	Cyanophage S-SSM6b	GCA_002710425.1
AJK27508.1	009286	Cluster9161_1clades	65	PTIM40_81	Cyanophage P-TIM40	GCA_001470935.1
AGG54320.1	009286	Cluster9161_1clades	62	CYWG_00036	Cyanophage S-SSM6b	GCA_002710425.1
AGH56943.1	009287	Cluster9162_1clades	64	CPXG_00140	Cyanophage P-RSM6	GCA_000906155.1
AJK27516.1	009287	Cluster9162_1clades	65	PTIM40_89	Cyanophage P-TIM40	GCA_001470935.1
AMS01197.1	009288	Cluster9163_1clades	65	AR9_g113	Bacillus phage AR9	GCA_001743835.1
ASU00131.1	009288	Cluster9163_1clades	65	PBI_PBS1_309	Bacillus virus PBS1	GCA_002601325.1
AXF51161.1	009289	Cluster9164_1clades	65	WELLINGTON_30	Erwinia phage Wellington	GCA_003344985.1
ANZ49382.1	009289	Cluster9164_1clades	65	KWAN_30	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51427.1	009290	Cluster9165_1clades	65	WELLINGTON_291	Erwinia phage Wellington	GCA_003344985.1
ANZ49647.1	009290	Cluster9165_1clades	65	KWAN_289	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ATA65577.1	009291	Cluster9166_1clades	65	2050HW_00242	Serratia phage 2050HW	GCA_002628125.1
QDB71342.1	009291	Cluster9166_1clades	65	CPT_Moabite_312	Serratia phage Moabite	GCA_006384735.1
QBZ72119.1	009292	SAM	65	SEA_KRADAL_233	Streptomyces phage Kradal	GCA_004799925.1
AXH66381.1	009292	SAM	65	SEA_SATIS_232	Streptomyces phage Satis	GCA_003366315.1
AYD81306.1	009293	Cluster9168_1clades	65	SEA_JUSTBECAUSE_138	Streptomyces phage JustBecause	GCA_003613775.1
QJD53709.1	009293	Cluster9168_1clades	65	SEA_KELA_138	Streptomyces phage Kela	GCA_012934305.1
BBA65628.1	009294	Cluster9169_1clades	65	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65169.1	009294	Cluster9169_1clades	65	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65662.1	009295	Cluster9170_1clades	65	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65203.1	009295	Cluster9170_1clades	65	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06438.1	009296	Cluster9171_1clades	65	BcepSaruman_025	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74406.1	009296	Cluster9171_1clades	65	BcepSauron_026	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06456.1	009297	SIG+TM	65	BcepSaruman_043	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74424.1	009297	SIG+TM	65	BcepSauron_044	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06628.1	009298	Cluster9173_1clades	64	BcepSaruman_215	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74597.1	009298	Cluster9173_1clades	65	BcepSauron_217	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06795.1	009299	Cluster9174_1clades	65	BcepSaruman_382	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74765.1	009299	Cluster9174_1clades	65	BcepSauron_385	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32272.1	009300	Cluster9175_1clades	65	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41846.1	009300	Cluster9175_1clades	65	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32491.1	009301	Cluster9176_1clades	65	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42064.1	009301	Cluster9176_1clades	65	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54645.1	009302	Cluster9177_1clades	65	b23_0017	Synechococcus phage B23	GCA_009745195.1
QGT54275.1	009302	Cluster9177_1clades	65	b3_0017	Synechococcus phage B3	GCA_009745215.1
QGT54692.1	009303	Cluster9178_1clades	65	b23_0077	Synechococcus phage B23	GCA_009745195.1
QGT54322.1	009303	Cluster9178_1clades	65	b3_0078	Synechococcus phage B3	GCA_009745215.1
QGT54694.1	009304	Cluster9179_1clades	65	b23_0079	Synechococcus phage B23	GCA_009745195.1
QGT54324.1	009304	Cluster9179_1clades	65	b3_0080	Synechococcus phage B3	GCA_009745215.1
QGT54767.1	009305	Cluster9180_1clades	65	b23_0152	Synechococcus phage B23	GCA_009745195.1
QGT54397.1	009305	Cluster9180_1clades	65	b3_0153	Synechococcus phage B3	GCA_009745215.1
QGT54788.1	009306	Cluster9181_1clades	65	b23_0173	Synechococcus phage B23	GCA_009745195.1
QGT54418.1	009306	Cluster9181_1clades	65	b3_0174	Synechococcus phage B3	GCA_009745215.1
QIG63269.1	009307	Cluster9182_1clades	65	DAC16_36	Bacteroides phage DAC16	GCA_013387695.1
QIG64314.1	009307	Cluster9182_1clades	65	DAC23_36	Bacteroides phage DAC23	GCA_013387745.1
prevph1000000124	009308	SIG+TM	66	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000094	009308	SIG+TM	66	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000761	009309	Cluster9184_1clades	66	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000513	009309	Cluster9184_1clades	66	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000507	009310	HEPN	66	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000816	009310	HEPN	66	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AAQ64383.1	009311	Cluster9186_1clades	64	KVP40.0313	Vibrio phage KVP40	GCA_000843785.1
AFN37544.1	009311	Cluster9186_1clades	64	pp2_311	Vibriophage phi-pp2	GCA_002630725.1
AAX44608.1	009312	Cluster9187_1clades	64	PSSM2_231	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12362.1	009312	Cluster9187_1clades	64	PRTG_00209	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ68227.1	009313	Cluster9188_1clades	64	CcrBL10_gp023	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86508.1	009313	Cluster9188_1clades	64	CcrRogue_gp026	Caulobacter virus Rogue	GCA_000900555.1
AFU88071.1	009314	SIG+TM	64	CcrColossus_gp201	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68748.1	009314	SIG+TM	64	CcrPW_gp209c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88276.1	009315	Cluster9190_1clades	64	CcrColossus_gp406	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68952.1	009315	Cluster9190_1clades	64	CcrPW_gp413c	Caulobacter phage CcrPW	GCA_003443275.1
QJB22736.1	009316	SIG+TM	64	fnug_93	Pseudomonas phage fnug	GCA_012837215.1
AGC26320.1	009316	SIG+TM	64	PHIKZ076.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGR47991.2	009317	Cluster9192_1clades	64	SmphiM12_359	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13178.1	009317	Cluster9192_1clades	64	PHIM19_273	Sinorhizobium phage phiM19	GCA_002605865.1
AMM44148.1	009318	Cluster9193_1clades	64	CBB_32	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43597.1	009318	Cluster9193_1clades	64	CBB_585	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44085.1	009319	SIG+TM	64	CBB_522	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SOK59314.1	009319	SIG+TM	61	g506	Yersinia phage fHe-Yen9-03	GCA_002990515.1
AMS01269.1	009320	Cluster9195_1clades	64	AR9_g185	Bacillus phage AR9	GCA_001743835.1
AST99896.1	009320	Cluster9195_1clades	64	PBI_PBS1_74	Bacillus virus PBS1	GCA_002601325.1
AMS01375.1	009321	Cluster9196_1clades	64	AR9_g291	Bacillus phage AR9	GCA_001743835.1
ASU00006.1	009321	Cluster9196_1clades	64	PBI_PBS1_184	Bacillus virus PBS1	GCA_002601325.1
QBZ72030.1	009322	Cluster9197_1clades	64	SEA_KRADAL_132	Streptomyces phage Kradal	GCA_004799925.1
AXH66293.1	009322	Cluster9197_1clades	64	SEA_SATIS_132	Streptomyces phage Satis	GCA_003366315.1
AXQ69143.1	009323	Cluster9198_1clades	64	CcrBL9_gp119	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69697.1	009323	Cluster9198_1clades	64	CcrSC_gp115	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69218.1	009324	TM	64	CcrBL9_gp194	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69772.1	009324	TM	64	CcrSC_gp190	Caulobacter phage CcrSC	GCA_003443315.1
AYD81405.1	009325	Cluster9200_1clades	64	SEA_JUSTBECAUSE_250	Streptomyces phage JustBecause	GCA_003613775.1
QJD53809.1	009325	Cluster9200_1clades	64	SEA_KELA_249	Streptomyces phage Kela	GCA_012934305.1
QCW18627.1	009326	Cluster9201_1clades	64	7t3_0106	Salmonella phage 7t3	GCA_006083215.1
AZU98452.1	009326	Cluster9201_1clades	64	CPT_Munch_520	Salmonella phage Munch	GCA_004015485.1
BAS04911.2	009327	Glutaredoxin	64	AVU11_agp26	Ralstonia phage RSF1	GCA_001500875.1
BAQ02640.2	009327	Glutaredoxin	64	-	Ralstonia phage RSL2	GCA_001503055.1
BAS04948.1	009328	Cluster9203_1clades	62	AVU11_gp156	Ralstonia phage RSF1	GCA_001500875.1
BAQ02672.1	009328	Cluster9203_1clades	64	AVU38_gp144	Ralstonia phage RSL2	GCA_001503055.1
BAS04996.1	009329	Cluster9204_1clades	64	AVU11_gp204	Ralstonia phage RSF1	GCA_001500875.1
BAQ02725.1	009329	Cluster9204_1clades	56	AVU38_gp197	Ralstonia phage RSL2	GCA_001503055.1
BAW19009.1	009330	Cluster9205_1clades	64	FDH28_gp035	Ralstonia phage RP12	GCA_002617345.1
BAW19295.1	009330	Cluster9205_1clades	64	-	Ralstonia phage RP31	GCA_002617365.1
BAW19014.1	009331	Cluster9206_1clades	64	FDH28_gp040	Ralstonia phage RP12	GCA_002617345.1
BAW19300.1	009331	Cluster9206_1clades	57	-	Ralstonia phage RP31	GCA_002617365.1
BBA65692.1	009332	Cluster9207_1clades	64	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65233.1	009332	Cluster9207_1clades	64	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90566.1	009333	Cluster9208_1clades	64	HYO65_gp174	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90874.1	009333	Cluster9208_1clades	64	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90592.1	009334	TM+TM	64	HYO65_gp200	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90900.1	009334	TM+TM	64	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90617.1	009335	Cluster9210_1clades	64	HYO65_gp225	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90923.1	009335	Cluster9210_1clades	64	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90700.1	009336	Cluster9211_1clades	64	HYO65_gp308	Tenacibaculum phage PTm1	GCA_009730695.1
BBI91006.1	009336	Cluster9211_1clades	64	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06426.1	009337	Cluster9212_1clades	64	BcepSaruman_013	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74393.1	009337	Cluster9212_1clades	64	BcepSauron_013	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06841.1	009338	Cluster9213_1clades	64	BcepSaruman_428	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74810.1	009338	Cluster9213_1clades	64	BcepSauron_430	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32461.1	009339	Cluster9214_1clades	64	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42033.1	009339	Cluster9214_1clades	64	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BBA65323.1	009340	Cluster9215_1clades	63	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96362.1	009340	Cluster9215_1clades	64	Xoosp13_175	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QGT54722.1	009341	Cluster9216_1clades	64	b23_0107	Synechococcus phage B23	GCA_009745195.1
QGT54352.1	009341	Cluster9216_1clades	64	b3_0108	Synechococcus phage B3	GCA_009745215.1
QGT54733.1	009342	Cluster9217_1clades	64	b23_0118	Synechococcus phage B23	GCA_009745195.1
QGT54363.1	009342	Cluster9217_1clades	64	b3_0119	Synechococcus phage B3	GCA_009745215.1
QGT54778.1	009343	Cluster9218_1clades	64	b23_0163	Synechococcus phage B23	GCA_009745195.1
QGT54408.1	009343	Cluster9218_1clades	64	b3_0164	Synechococcus phage B3	GCA_009745215.1
QGT54815.1	009344	Cluster9219_1clades	64	b23_0200	Synechococcus phage B23	GCA_009745195.1
QGT54445.1	009344	Cluster9219_1clades	64	b3_0202	Synechococcus phage B3	GCA_009745215.1
QIG57741.1	009345	Cluster9220_1clades	64	SEA_PAULODIABOLI_3	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58042.1	009345	Cluster9220_1clades	64	SEA_PAULODIABOLI_358	Microbacterium phage PauloDiaboli	GCA_011067425.1
SOK59226.1	009346	Cluster9221_1clades	64	g418	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58692.1	009346	Cluster9221_1clades	64	g415	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000229	009347	Cluster9222_1clades	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000179	009347	Cluster9222_1clades	65	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000798	009348	Cluster9223_1clades	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000546	009348	Cluster9223_1clades	65	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44480.1	009349	Cluster9224_1clades	63	PSSM2_102	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12168.1	009349	Cluster9224_1clades	63	PRTG_00010	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44657.1	009350	Cluster9225_1clades	63	PSSM2_280	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12318.1	009350	Cluster9225_1clades	63	PRTG_00165	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01732.1	009351	Cluster9226_1clades	53	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53374.1	009351	Cluster9226_1clades	63	65p366	Aeromonas virus 65	GCA_000893255.1
QAX97958.1	009352	Cluster9227_1clades	63	ASswx1_316	Aeromonas phage Asswx_1	GCA_004146865.1
AFN39262.1	009352	Cluster9227_1clades	63	CC2_216	Aeromonas phage CC2	GCA_000903495.1
ASU00279.1	009353	Cluster9228_1clades	63	HWB28_gp273	Aeromonas phage AS-zj	GCA_002627665.1
AFN39296.1	009353	Cluster9228_1clades	63	CC2_424	Aeromonas phage CC2	GCA_000903495.1
AFU88187.1	009354	Cluster9229_1clades	63	CcrColossus_gp317	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68864.1	009354	Cluster9229_1clades	63	CcrPW_gp325	Caulobacter phage CcrPW	GCA_003443275.1
AAX44479.1	009355	Cluster9230_1clades	45	PSSM2_101	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12171.1	009355	Cluster9230_1clades	63	PRTG_00013	Prochlorococcus phage P-SSM5	GCA_002991095.1
AMM43614.1	009356	Cluster9231_1clades	63	CBB_49	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44165.1	009356	Cluster9231_1clades	63	CBB_602	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01132.1	009357	SIG+TM	63	AR9_g047	Bacillus phage AR9	GCA_001743835.1
ASU00059.1	009357	SIG+TM	63	PBI_PBS1_237	Bacillus virus PBS1	GCA_002601325.1
AOO14211.1	009358	Cluster9233_1clades	63	Sn110110_017	Cyanophage S-RIM14	GCA_002599065.1
AOO14863.1	009358	Cluster9233_1clades	63	W1230910_017	Cyanophage S-RIM14	GCA_002599125.1
AOO14262.1	009359	Cluster9234_1clades	63	Sn110110_068	Cyanophage S-RIM14	GCA_002599065.1
AOO14911.1	009359	Cluster9234_1clades	63	W1230910_065	Cyanophage S-RIM14	GCA_002599125.1
ATA65590.1	009360	SUKH-SMI1	63	2050HW_00255	Serratia phage 2050HW	GCA_002628125.1
QDB71355.1	009360	SUKH-SMI1	63	CPT_Moabite_325	Serratia phage Moabite	GCA_006384735.1
AXQ69135.1	009361	BZIP	63	CcrBL9_gp111	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69689.1	009361	BZIP	63	CcrSC_gp107	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69229.1	009362	SIG+TM	63	CcrBL9_gp205	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69783.1	009362	SIG+TM	63	CcrSC_gp201	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69339.1	009363	SIG+TM	63	CcrBL9_gp315	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69899.1	009363	SIG+TM	63	CcrSC_gp317	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69423.1	009364	SIG+TM	63	CcrBL9_gp399	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69978.1	009364	SIG+TM	63	CcrSC_gp396	Caulobacter phage CcrSC	GCA_003443315.1
AYD81300.1	009365	Cluster9240_1clades	63	SEA_JUSTBECAUSE_131	Streptomyces phage JustBecause	GCA_003613775.1
QJD53703.1	009365	Cluster9240_1clades	63	SEA_KELA_132	Streptomyces phage Kela	GCA_012934305.1
AYD81307.1	009366	Cluster9241_1clades	63	SEA_JUSTBECAUSE_139	Streptomyces phage JustBecause	GCA_003613775.1
QJD53710.1	009366	Cluster9241_1clades	63	SEA_KELA_139	Streptomyces phage Kela	GCA_012934305.1
BAW19103.1	009367	Cluster9242_1clades	63	FDH28_gp129	Ralstonia phage RP12	GCA_002617345.1
BAW19389.1	009367	Cluster9242_1clades	63	-	Ralstonia phage RP31	GCA_002617365.1
BBA65613.1	009368	RecT-Redbeta	63	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65154.1	009368	RecT-Redbeta	63	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65184.1	009369	RNase_P_p30	63	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65643.1	009369	RNase_P_p30	63	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06447.1	009370	TM	63	BcepSaruman_034	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74415.1	009370	TM	61	BcepSauron_035	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06531.1	009371	Cluster9246_1clades	63	BcepSaruman_118	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74497.1	009371	Cluster9246_1clades	59	BcepSauron_117	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54717.1	009372	Cluster9247_1clades	63	b23_0102	Synechococcus phage B23	GCA_009745195.1
QGT54347.1	009372	Cluster9247_1clades	63	b3_0103	Synechococcus phage B3	GCA_009745215.1
QGT54862.1	009373	Cluster9248_1clades	63	b23_0248	Synechococcus phage B23	GCA_009745195.1
QGT54497.1	009373	Cluster9248_1clades	63	b3_0255	Synechococcus phage B3	GCA_009745215.1
QGT54868.1	009374	Cluster9249_1clades	63	b23_0254	Synechococcus phage B23	GCA_009745195.1
QGT54503.1	009374	Cluster9249_1clades	63	b3_0261	Synechococcus phage B3	GCA_009745215.1
ADQ52795.1	009375	Cluster9250_1clades	62	PX29p076	Aeromonas phage PX29	GCA_000920195.1
AAQ17738.1	009375	Cluster9250_1clades	62	Aeh1ORF078c	Aeromonas virus Aeh1	GCA_000843245.1
AAX44439.1	009376	Cluster9251_1clades	62	PSSM2_061	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12213.1	009376	Cluster9251_1clades	62	PRTG_00055	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44441.1	009377	Cluster9252_1clades	62	PSSM2_063	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12211.1	009377	Cluster9252_1clades	62	PRTG_00053	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01776.1	009378	SIG+IG	62	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53419.1	009378	SIG+IG	62	65p412	Aeromonas virus 65	GCA_000893255.1
QGH71965.1	009379	Cluster9254_1clades	60	N1M2_102	Klebsiella phage N1M2	GCA_010092605.1
AEV89566.1	009379	Cluster9254_1clades	62	OBP_129	Pseudomonas phage OBP	GCA_000896635.1
AFC21928.1	009380	Cluster9255_1clades	62	GAP32_470	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44054.1	009380	Cluster9255_1clades	62	CBB_491	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFU88176.1	009381	DUF1495	62	CcrColossus_gp306	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68853.1	009381	DUF1495	60	CcrPW_gp314	Caulobacter phage CcrPW	GCA_003443275.1
AGH56829.1	009382	Cluster9257_1clades	62	CPXG_00026	Cyanophage P-RSM6	GCA_000906155.1
AJK27612.1	009382	Cluster9257_1clades	60	PTIM40_197	Cyanophage P-TIM40	GCA_001470935.1
AIA64985.1	009383	Cluster9258_1clades	62	S13_188	Cronobacter phage S13	GCA_001503575.1
QHJ78950.1	009383	Cluster9258_1clades	61	-	Myoviridae sp.	GCA_012593985.1
AMM43567.1	009384	Cluster9259_1clades	62	CBB_2	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44118.1	009384	Cluster9259_1clades	62	CBB_555	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01133.1	009385	Cluster9260_1clades	62	AR9_g048	Bacillus phage AR9	GCA_001743835.1
ASU00060.1	009385	Cluster9260_1clades	62	PBI_PBS1_238	Bacillus virus PBS1	GCA_002601325.1
AMS01203.1	009386	Cluster9261_1clades	62	AR9_g119	Bacillus phage AR9	GCA_001743835.1
AST99827.1	009386	Cluster9261_1clades	62	PBI_PBS1_5	Bacillus virus PBS1	GCA_002601325.1
AOO14253.1	009387	Cluster9262_1clades	62	Sn110110_059	Cyanophage S-RIM14	GCA_002599065.1
AOO14905.1	009387	Cluster9262_1clades	62	W1230910_059	Cyanophage S-RIM14	GCA_002599125.1
AOO14385.1	009388	Cluster9263_1clades	62	Sn110110_191	Cyanophage S-RIM14	GCA_002599065.1
AOO15033.1	009388	Cluster9263_1clades	62	W1230910_187	Cyanophage S-RIM14	GCA_002599125.1
AXQ69379.1	009389	Cluster9264_1clades	62	CcrBL9_gp355	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69939.1	009389	Cluster9264_1clades	62	CcrSC_gp357	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69527.1	009390	Cluster9265_1clades	62	CcrBL9_gp503	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70070.1	009390	Cluster9265_1clades	62	CcrSC_gp488	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69528.1	009391	Cluster9266_1clades	62	CcrBL9_gp504	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70071.1	009391	Cluster9266_1clades	56	CcrSC_gp489	Caulobacter phage CcrSC	GCA_003443315.1
QCW18684.1	009392	Cluster9267_1clades	60	7t3_0163	Salmonella phage 7t3	GCA_006083215.1
AZU97959.1	009392	Cluster9267_1clades	62	CPT_Munch_015	Salmonella phage Munch	GCA_004015485.1
BBI90514.1	009393	Cluster9268_1clades	62	HYO65_gp122	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90822.1	009393	Cluster9268_1clades	62	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06626.1	009394	Cluster9269_1clades	62	BcepSaruman_213	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74594.1	009394	Cluster9269_1clades	62	BcepSauron_214	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06821.1	009395	SIG+TM	62	BcepSaruman_408	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74790.1	009395	SIG+TM	62	BcepSauron_410	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06414.1	009396	Cluster9271_1clades	62	BcepSaruman_001	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74381.1	009396	Cluster9271_1clades	61	BcepSauron_001	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32227.1	009397	Cluster9272_1clades	62	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41805.1	009397	Cluster9272_1clades	62	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54759.1	009398	Cluster9273_1clades	62	b23_0144	Synechococcus phage B23	GCA_009745195.1
QGT54389.1	009398	Cluster9273_1clades	62	b3_0145	Synechococcus phage B3	GCA_009745215.1
QGT54856.1	009399	Cluster9274_1clades	62	b23_0242	Synechococcus phage B23	GCA_009745195.1
QGT54490.1	009399	Cluster9274_1clades	62	b3_0248	Synechococcus phage B3	GCA_009745215.1
AIA64913.1	009400	Cluster9275_1clades	60	S13_114	Cronobacter phage S13	GCA_001503575.1
QHJ79027.1	009400	Cluster9275_1clades	62	-	Myoviridae sp.	GCA_012593985.1
QIG57765.1	009401	Cluster9276_1clades	62	SEA_PAULODIABOLI_30	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58066.1	009401	Cluster9276_1clades	62	SEA_PAULODIABOLI_385	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000489	009402	Cluster9277_1clades	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000370	009402	Cluster9277_1clades	63	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000606	009403	Cluster9278_1clades	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000425	009403	Cluster9278_1clades	63	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44469.1	009404	Cluster9279_1clades	61	PSSM2_091	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12183.1	009404	Cluster9279_1clades	61	PRTG_00025	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01689.1	009405	Cluster9280_1clades	61	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53325.1	009405	Cluster9280_1clades	61	65p317	Aeromonas virus 65	GCA_000893255.1
AFC21958.1	009406	Cluster9281_1clades	61	GAP32_499	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44083.1	009406	Cluster9281_1clades	61	CBB_520	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AIF27789.1	009407	Cluster9282_1clades	61	SmphiM12_471	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13635.1	009407	Cluster9282_1clades	61	PHIN3_372	Sinorhizobium phage phiN3	GCA_001501175.1
AGG54454.1	009408	TM	58	CYWG_00170	Cyanophage S-SSM6b	GCA_002710425.1
AIR93536.1	009408	TM	61	AVU42_gp199	Prochlorococcus phage P-TIM68	GCA_001503075.1
AGG54318.1	009409	Cluster9284_1clades	60	CYWG_00034	Cyanophage S-SSM6b	GCA_002710425.1
AIR93610.1	009409	Cluster9284_1clades	61	AVU42_gp065	Prochlorococcus phage P-TIM68	GCA_001503075.1
AMS01174.1	009410	Cluster9285_1clades	61	AR9_g090	Bacillus phage AR9	GCA_001743835.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASU00107.1	009410	Cluster9285_1clades	61	PBI_PBS1_285	Bacillus virus PBS1	GCA_002601325.1
AMS01367.1	009411	Cluster9286_1clades	61	AR9_g283	Bacillus phage AR9	GCA_001743835.1
AST99997.1	009411	Cluster9286_1clades	61	PBI_PBS1_176	Bacillus virus PBS1	GCA_002601325.1
ATA65438.1	009412	Cluster9287_1clades	61	2050HW_00103	Serratia phage 2050HW	GCA_002628125.1
QDB71209.1	009412	Cluster9287_1clades	61	CPT_Moabite_179	Serratia phage Moabite	GCA_006384735.1
QBZ72036.1	009413	Cluster9288_1clades	61	SEA_KRADAL_138	Streptomyces phage Kradal	GCA_004799925.1
AXH66299.1	009413	Cluster9288_1clades	61	SEA_SATIS_138	Streptomyces phage Satis	GCA_003366315.1
AXQ69431.1	009414	Cluster9289_1clades	61	CcrBL9_gp407	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69983.1	009414	Cluster9289_1clades	61	CcrSC_gp401	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70400.1	009415	Cluster9290_1clades	61	HOU04_gp001	Synechococcus phage S-T4	GCA_003443335.1
AXQ70602.1	009415	Cluster9290_1clades	61	HOU04_gp001	Synechococcus phage S-T4	GCA_003443335.1
QAY00786.1	009416	Cluster9291_1clades	61	Ecwhy1_513	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61820.1	009416	Cluster9291_1clades	61	EO157G_2310	Escherichia phage SP27	GCA_008033345.1
QAY00773.1	009417	Cluster9292_1clades	60	Ecwhy1_499	Escherichia phage Ecwhy_1	GCA_004146585.1
BBM61838.1	009417	Cluster9292_1clades	61	EO157G_2490	Escherichia phage SP27	GCA_008033345.1
QBX06707.1	009418	Cluster9293_1clades	61	BcepSaruman_294	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74675.1	009418	Cluster9293_1clades	61	BcepSauron_295	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06465.1	009419	Cluster9294_1clades	61	BcepSaruman_052	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74433.1	009419	Cluster9294_1clades	49	BcepSauron_053	Burkholderia phage BcepSauron	GCA_005394215.1
QCW22842.1	009420	Cluster9295_1clades	61	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50509.1	009420	Cluster9295_1clades	54	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54696.1	009421	Cluster9296_1clades	61	b23_0081	Synechococcus phage B23	GCA_009745195.1
QGT54326.1	009421	Cluster9296_1clades	61	b3_0082	Synechococcus phage B3	GCA_009745215.1
QGT54822.1	009422	Cluster9297_1clades	61	b23_0207	Synechococcus phage B23	GCA_009745195.1
QGT54452.1	009422	Cluster9297_1clades	61	b3_0209	Synechococcus phage B3	GCA_009745215.1
prevph1000000209	009423	Cluster9298_1clades	62	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000165	009423	Cluster9298_1clades	62	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAQ64115.1	009424	Cluster9299_1clades	60	KVP40.0044	Vibrio phage KVP40	GCA_000843785.1
QNJ54671.1	009424	Cluster9299_1clades	41	vBValMR10Z_130	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AAX44472.1	009425	Cluster9300_1clades	60	PSSM2_094	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12180.1	009425	Cluster9300_1clades	60	PRTG_00022	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44478.1	009426	Cluster9301_1clades	60	PSSM2_100	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12174.1	009426	Cluster9301_1clades	60	PRTG_00016	Prochlorococcus phage P-SSM5	GCA_002991095.1
ABY63272.1	009427	Cluster9302_1clades	60	201phi2-1p449	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBJ02932.1	009427	Cluster9302_1clades	60	PSA21_410	Pseudomonas phage Psa21	GCA_004340405.1
AFC21572.1	009428	Cluster9303_1clades	60	GAP32_123	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43689.1	009428	Cluster9303_1clades	60	CBB_124	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AFC21790.1	009429	Cluster9304_1clades	60	GAP32_340	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM43908.1	009429	Cluster9304_1clades	59	CBB_345	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
QMV28735.1	009430	Cluster9305_1clades	60	AP1_0017	Aeromonas phage AP1	GCA_014183365.1
AFN39243.1	009430	Cluster9305_1clades	60	CC2_169	Aeromonas phage CC2	GCA_000903495.1
AFU88201.1	009431	TM	60	CcrColossus_gp331	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68878.1	009431	TM	60	CcrPW_gp339	Caulobacter phage CcrPW	GCA_003443275.1
AIT14147.1	009432	Cluster9307_1clades	60	PBI_121Q_257	Escherichia phage 121Q	GCA_000926855.1
QBO61556.1	009432	Cluster9307_1clades	60	G17_00060	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AIT14150.1	009433	Cluster9308_1clades	60	PBI_121Q_260	Escherichia phage 121Q	GCA_000926855.1
QBO61553.1	009433	Cluster9308_1clades	60	G17_00057	Escherichia phage vB_EcoM_G17	GCA_004521135.1
AIT14154.1	009434	Cluster9309_1clades	60	PBI_121Q_264	Escherichia phage 121Q	GCA_000926855.1
SCA80143.1	009434	Cluster9309_1clades	60	PSLUR01_00166	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AMS01351.1	009435	Cluster9310_1clades	60	AR9_g267	Bacillus phage AR9	GCA_001743835.1
AST99980.1	009435	Cluster9310_1clades	60	PBI_PBS1_159	Bacillus virus PBS1	GCA_002601325.1
AXF51210.1	009436	Cluster9311_1clades	60	WELLINGTON_80	Erwinia phage Wellington	GCA_003344985.1
ANZ49432.1	009436	Cluster9311_1clades	60	KWAN_80	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ASU03801.1	009437	SIG+TM	60	JOAD_114	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03556.1	009437	SIG+TM	60	RISINGSUN_114	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65369.1	009438	Cluster9313_1clades	60	2050HW_00034	Serratia phage 2050HW	GCA_002628125.1
QDB71154.1	009438	Cluster9313_1clades	60	CPT_Moabite_124	Serratia phage Moabite	GCA_006384735.1
QBZ72046.1	009439	Cluster9314_1clades	60	SEA_KRADAL_150	Streptomyces phage Kradal	GCA_004799925.1
AXH66309.1	009439	Cluster9314_1clades	60	SEA_SATIS_150	Streptomyces phage Satis	GCA_003366315.1
AXQ69531.1	009440	SIG+TM	60	CcrBL9_gp507	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70073.1	009440	SIG+TM	59	CcrSC_gp491	Caulobacter phage CcrSC	GCA_003443315.1
BAW19120.1	009441	Cluster9316_1clades	60	FDH28_gp275	Ralstonia phage RP12	GCA_002617345.1
BAW19406.1	009441	Cluster9316_1clades	60	-	Ralstonia phage RP31	GCA_002617365.1
BAW19201.1	009442	SIG+TM	60	FDH28_gp194	Ralstonia phage RP12	GCA_002617345.1
BAW19487.1	009442	SIG+TM	60	-	Ralstonia phage RP31	GCA_002617365.1
BBA65152.1	009443	Cluster9318_1clades	60	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65611.1	009443	Cluster9318_1clades	60	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65316.1	009444	Cluster9319_1clades	60	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96351.1	009444	Cluster9319_1clades	60	Xoosp13_164	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBA65464.1	009445	Cluster9320_1clades	60	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96473.1	009445	Cluster9320_1clades	60	Xoosp13_287	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90468.1	009446	Cluster9321_1clades	60	HYO65_gp076	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90775.1	009446	Cluster9321_1clades	60	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90607.1	009447	Cluster9322_1clades	60	HYO65_gp215	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90913.1	009447	Cluster9322_1clades	52	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06743.1	009448	Cluster9323_1clades	59	BcepSaruman_330	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74712.1	009448	Cluster9323_1clades	60	BcepSauron_332	Burkholderia phage BcepSauron	GCA_005394215.1
QCW18649.1	009449	RCC1	60	7t3_0128	Salmonella phage 7t3	GCA_006083215.1
QIG63040.1	009449	RCC1	60	SEPL_427	Salmonella phage SE_PL	GCA_011067555.1
QGT54644.1	009450	Cluster9325_1clades	60	b23_0016	Synechococcus phage B23	GCA_009745195.1
QGT54274.1	009450	Cluster9325_1clades	60	b3_0016	Synechococcus phage B3	GCA_009745215.1
QGT54761.1	009451	Cluster9326_1clades	60	b23_0146	Synechococcus phage B23	GCA_009745195.1
QGT54391.1	009451	Cluster9326_1clades	60	b3_0147	Synechococcus phage B3	GCA_009745215.1
QGT54777.1	009452	Cluster9327_1clades	60	b23_0162	Synechococcus phage B23	GCA_009745195.1
QGT54407.1	009452	Cluster9327_1clades	60	b3_0163	Synechococcus phage B3	GCA_009745215.1
QGT54852.1	009453	Cluster9328_1clades	60	b23_0238	Synechococcus phage B23	GCA_009745195.1
QGT54486.1	009453	Cluster9328_1clades	60	b3_0244	Synechococcus phage B3	GCA_009745215.1
QIG57762.1	009454	Cluster9329_1clades	60	SEA_PAULODIABOLI_26	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58063.1	009454	Cluster9329_1clades	60	SEA_PAULODIABOLI_381	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58078.1	009455	Cluster9330_1clades	60	SEA_PAULODIABOLI_27	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58090.1	009455	Cluster9330_1clades	60	SEA_PAULODIABOLI_382	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG63282.1	009456	Cluster9331_1clades	60	DAC16_49	Bacteroides phage DAC16	GCA_013387695.1
QIG64327.1	009456	Cluster9331_1clades	60	DAC23_49	Bacteroides phage DAC23	GCA_013387745.1
SOK59241.1	009457	Cluster9332_1clades	60	g433	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58707.1	009457	Cluster9332_1clades	60	g430	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000001	009458	Cluster9333_1clades	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000001	009458	Cluster9333_1clades	61	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000419	009459	Cluster9334_1clades	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000330	009459	Cluster9334_1clades	61	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000631	009460	Cluster9335_1clades	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000449	009460	Cluster9335_1clades	61	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01597.1	009461	Cluster9336_1clades	59	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53221.1	009461	Cluster9336_1clades	59	65p213	Aeromonas virus 65	GCA_000893255.1
AXQ68440.1	009462	Cluster9337_1clades	59	CcrBL10_gp236	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86726.1	009462	Cluster9337_1clades	59	CcrRogue_gp244	Caulobacter virus Rogue	GCA_000900555.1
AMM43582.1	009463	Cluster9338_1clades	59	CBB_17	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44133.1	009463	Cluster9338_1clades	59	CBB_570	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01332.1	009464	Cluster9339_1clades	59	AR9_g248	Bacillus phage AR9	GCA_001743835.1
AST99962.1	009464	Cluster9339_1clades	59	PBI_PBS1_141	Bacillus virus PBS1	GCA_002601325.1
AXF51335.1	009465	Cluster9340_1clades	59	WELLINGTON_207	Erwinia phage Wellington	GCA_003344985.1
ANZ49560.1	009465	Cluster9340_1clades	59	KWAN_208	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
APU01656.1	009466	Cluster9341_1clades	59	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53286.1	009466	Cluster9341_1clades	30	65p278	Aeromonas virus 65	GCA_000893255.1
ARM70827.1	009467	Ruc-ZnR	59	phiC120_c121	Escherichia phage phiC120	GCA_002621185.1
QHJ79001.1	009467	Ruc-ZnR	57	-	Myoviridae sp.	GCA_012593985.1
ATA65635.1	009468	Cluster9343_1clades	59	2050HW_00300	Serratia phage 2050HW	GCA_002628125.1
QDB71063.1	009468	Cluster9343_1clades	59	CPT_Moabite_031	Serratia phage Moabite	GCA_006384735.1
QBZ72067.1	009469	Cluster9344_1clades	59	SEA_KRADAL_171	Streptomyces phage Kradal	GCA_004799925.1
AXH66330.1	009469	Cluster9344_1clades	59	SEA_SATIS_171	Streptomyces phage Satis	GCA_003366315.1
QBZ72111.1	009470	Cluster9345_1clades	59	SEA_KRADAL_225	Streptomyces phage Kradal	GCA_004799925.1
AXH66373.1	009470	Cluster9345_1clades	59	SEA_SATIS_224	Streptomyces phage Satis	GCA_003366315.1
AFU88299.1	009471	TM	58	CcrColossus_gp429	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68974.1	009471	TM	59	CcrPW_gp435c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69308.1	009472	Cluster9347_1clades	59	CcrBL9_gp284	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69867.1	009472	Cluster9347_1clades	59	CcrSC_gp285	Caulobacter phage CcrSC	GCA_003443315.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69507.1	009473	Cluster9348_1clades	59	CcrBL9_gp483	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70056.1	009473	Cluster9348_1clades	59	CcrSC_gp474	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69424.1	009474	Cluster9349_1clades	58	CcrBL9_gp400	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69979.1	009474	Cluster9349_1clades	59	CcrSC_gp397	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70402.1	009475	Cluster9350_1clades	59	HOU04_gp003	Synechococcus phage S-T4	GCA_003443335.1
AXQ70604.1	009475	Cluster9350_1clades	59	HOU04_gp003	Synechococcus phage S-T4	GCA_003443335.1
BAS04817.1	009476	Cluster9351_1clades	57	AVU11_gp025	Ralstonia phage RSF1	GCA_001500875.1
BAQ02550.2	009476	Cluster9351_1clades	59	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65178.1	009477	DUF2891	59	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65637.1	009477	DUF2891	59	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65201.1	009478	Cluster9353_1clades	59	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65660.1	009478	Cluster9353_1clades	59	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90544.1	009479	Cluster9354_1clades	59	HYO65_gp152	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90852.1	009479	Cluster9354_1clades	59	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90593.1	009480	Cluster9355_1clades	59	HYO65_gp201	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90901.1	009480	Cluster9355_1clades	59	-	Tenacibaculum phage PTm5	GCA_009730715.1
QAY00794.1	009481	Cluster9356_1clades	59	Ecwhy1_521	Escherichia phage Ecwhy_1	GCA_004146585.1
SCA80120.1	009481	Cluster9356_1clades	59	PSLUR01_00143	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QBX06420.1	009482	Cluster9357_1clades	59	BcepSaruman_007	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74388.1	009482	Cluster9357_1clades	59	BcepSauron_008	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06444.1	009483	Cluster9358_1clades	59	BcepSaruman_031	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74412.1	009483	Cluster9358_1clades	59	BcepSauron_032	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06833.1	009484	Cluster9359_1clades	58	BcepSaruman_420	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74802.1	009484	Cluster9359_1clades	59	BcepSauron_422	Burkholderia phage BcepSauron	GCA_005394215.1
QDJ96655.1	009485	Cluster9360_1clades	59	PS1_0144	Aeromonas phage PS1	GCA_007051165.2
QFR59532.1	009485	Cluster9360_1clades	59	PS2_0141	Aeromonas phage PS2	GCA_009388305.2
QGT54714.1	009486	Cluster9361_1clades	59	b23_0099	Synechococcus phage B23	GCA_009745195.1
QGT54344.1	009486	Cluster9361_1clades	59	b3_0100	Synechococcus phage B3	GCA_009745215.1
QGT54750.1	009487	Cluster9362_1clades	59	b23_0135	Synechococcus phage B23	GCA_009745195.1
QGT54380.1	009487	Cluster9362_1clades	59	b3_0136	Synechococcus phage B3	GCA_009745215.1
ASR76153.1	009488	Cluster9363_1clades	56	PBI_BELLAMY_108	Synechococcus phage Bellamy	GCA_002627525.1
QJT70093.1	009488	Cluster9363_1clades	59	SynMITS9220M01_080	Synechococcus phage SynMITS9220M01	GCA_013187275.1
SOK59154.1	009489	Cluster9364_1clades	59	g346	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58620.1	009489	Cluster9364_1clades	59	g343	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000178	009490	Cluster9365_1clades	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000141	009490	Cluster9365_1clades	60	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000523	009491	HC1-Chlam	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000397	009491	HC1-Chlam	60	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000607	009492	Cluster9367_1clades	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000426	009492	Cluster9367_1clades	60	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44418.1	009493	TM	58	PSSM2_040	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12233.1	009493	TM	58	PRTG_00075	Prochlorococcus phage P-SSM5	GCA_002991095.1
AON97161.1	009494	Mcm10	56	E_153	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AAX78677.1	009494	Mcm10	58	RB43ORF155c	Escherichia virus RB43	GCA_000863505.1
ABY62998.1	009495	Cluster9370_1clades	58	201phi2-1p168	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77021.1	009495	Cluster9370_1clades	58	PHABIO_390	Pseudomonas phage Phabio	GCA_002624965.1
AGH56951.1	009496	Cluster9371_1clades	50	CPXG_00148	Cyanophage P-RSM6	GCA_000906155.1
AGH07696.1	009496	Cluster9371_1clades	58	CYVG_00253	Cyanophage S-SSM6a	GCA_002710385.1
AGH56999.1	009497	Cluster9372_1clades	57	CPXG_00196	Cyanophage P-RSM6	GCA_000906155.1
AGH26144.1	009497	Cluster9372_1clades	58	CPMG_00043	Prochlorococcus phage MED4-213	GCA_000904535.1
AIA64883.1	009498	Cluster9373_1clades	58	S13_084	Cronobacter phage S13	GCA_001503575.1
QHJ79056.1	009498	Cluster9373_1clades	57	-	Myoviridae sp.	GCA_012593985.1
ANZ48146.1	009499	Cluster9374_1clades	58	ASESINO_133	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50562.1	009499	Cluster9374_1clades	58	STRATTON_137	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ATA65555.1	009500	Cluster9375_1clades	58	2050HW_00220	Serratia phage 2050HW	GCA_002628125.1
QDB71320.1	009500	Cluster9375_1clades	58	CPT_Moabite_290	Serratia phage Moabite	GCA_006384735.1
QBZ71913.1	009501	Cluster9376_1clades	58	SEA_KRADAL_14	Streptomyces phage Kradal	GCA_004799925.1
AXH66175.1	009501	Cluster9376_1clades	58	SEA_SATIS_14	Streptomyces phage Satis	GCA_003366315.1
AXQ69403.1	009502	Cluster9377_1clades	58	CcrBL9_gp379	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69960.1	009502	Cluster9377_1clades	58	CcrSC_gp378	Caulobacter phage CcrSC	GCA_003443315.1
BAS04926.2	009503	Cluster9378_1clades	33	AVU11_agp30	Ralstonia phage RSF1	GCA_001500875.1
BAQ02653.1	009503	Cluster9378_1clades	58	AVU38_gp125	Ralstonia phage RSL2	GCA_001503055.1
BBA65738.1	009504	Cluster9379_1clades	58	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65279.1	009504	Cluster9379_1clades	58	-	Xanthomonas phage XacN1	GCA_003173815.1
QBX06424.1	009505	Cluster9380_1clades	58	BcepSaruman_011	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74392.1	009505	Cluster9380_1clades	58	BcepSauron_012	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06428.1	009506	Cluster9381_1clades	58	BcepSaruman_015	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74395.1	009506	Cluster9381_1clades	58	BcepSauron_015	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06431.1	009507	Cluster9382_1clades	58	BcepSaruman_018	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74398.1	009507	Cluster9382_1clades	58	BcepSauron_018	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06537.1	009508	Cluster9383_1clades	58	BcepSaruman_124	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74503.1	009508	Cluster9383_1clades	58	BcepSauron_123	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06751.1	009509	Cluster9384_1clades	57	BcepSaruman_338	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74720.1	009509	Cluster9384_1clades	58	BcepSauron_340	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32528.1	009510	Cluster9385_1clades	58	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42101.1	009510	Cluster9385_1clades	58	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW23067.1	009511	Cluster9386_1clades	58	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50685.1	009511	Cluster9386_1clades	53	-	Synechococcus phage S-B43	GCA_006869725.1
QCW22990.1	009512	Cluster9387_1clades	54	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50714.1	009512	Cluster9387_1clades	58	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54764.1	009513	Cluster9388_1clades	58	b23_0149	Synechococcus phage B23	GCA_009745195.1
QGT54394.1	009513	Cluster9388_1clades	58	b3_0150	Synechococcus phage B3	GCA_009745215.1
QGT54945.1	009514	Cluster9389_1clades	58	b23_0335	Synechococcus phage B23	GCA_009745195.1
QGT54580.1	009514	Cluster9389_1clades	58	b3_0341	Synechococcus phage B3	GCA_009745215.1
AIA64852.1	009515	DUF2685	57	S13_053	Cronobacter phage S13	GCA_001503575.1
QHJ78813.1	009515	DUF2685	58	-	Myoviridae sp.	GCA_012593985.1
AIA64935.1	009516	Cluster9391_1clades	55	S13_136	Cronobacter phage S13	GCA_001503575.1
QHJ78992.1	009516	Cluster9391_1clades	58	-	Myoviridae sp.	GCA_012593985.1
QIG57772.1	009517	Cluster9392_1clades	58	SEA_PAULODIABOLI_37	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58073.1	009517	Cluster9392_1clades	58	SEA_PAULODIABOLI_392	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000299	009518	Cluster9393_1clades	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000231	009518	Cluster9393_1clades	59	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000385	009519	Cluster9394_1clades	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000311	009519	Cluster9394_1clades	59	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000765	009520	Cluster9395_1clades	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000518	009520	Cluster9395_1clades	59	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
APU01399.1	009521	Cluster9396_1clades	57	-	Aeromonas phage 65.2	GCA_002618145.1
AAR90931.1	009521	Cluster9396_1clades	57	65p007c	Aeromonas virus 65	GCA_000893255.1
AAX44437.1	009522	Cluster9397_1clades	57	PSSM2_059	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12215.1	009522	Cluster9397_1clades	57	PRTG_00057	Prochlorococcus phage P-SSM5	GCA_002991095.1
ABY63273.1	009523	TCAD11	57	201phi2-1p450	Pseudomonas phage 201phi2-1	GCA_000875305.1
QBJ02933.1	009523	TCAD11	56	PSA21_411	Pseudomonas phage Psa21	GCA_004340405.1
ADQ52901.1	009524	LAG1	57	PX29p182	Aeromonas phage PX29	GCA_000920195.1
ADM80168.1	009524	LAG1	40	phiAS5_ORF0325	Aeromonas phage phiAS5	GCA_000887715.1
AFC21955.1	009525	Cluster9400_1clades	57	GAP32_496	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44081.1	009525	Cluster9400_1clades	57	CBB_518	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AJK27505.1	009526	Cluster9401_1clades	57	PTIM40_78	Cyanophage P-TIM40	GCA_001470935.1
AGH26161.1	009526	Cluster9401_1clades	57	CPMG_00060	Prochlorococcus phage MED4-213	GCA_000904535.1
AGR47638.2	009527	Cluster9402_1clades	52	SmphiM12_006	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13271.1	009527	Cluster9402_1clades	57	PHIN3_4	Sinorhizobium phage phiN3	GCA_001501175.1
AMM43572.1	009528	Cluster9403_1clades	57	CBB_560	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44123.1	009528	Cluster9403_1clades	57	CBB_7	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01263.1	009529	SIG+TM	57	AR9_g179	Bacillus phage AR9	GCA_001743835.1
AST99890.1	009529	SIG+TM	57	PBI_PBS1_68	Bacillus virus PBS1	GCA_002601325.1
ASU03786.1	009530	TM	57	JOAD_129	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03542.1	009530	TM	56	RISINGSUN_128	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65576.1	009531	Cluster9406_1clades	57	2050HW_00241	Serratia phage 2050HW	GCA_002628125.1
QDB71341.1	009531	Cluster9406_1clades	57	CPT_Moabite_311	Serratia phage Moabite	GCA_006384735.1
QBZ72223.1	009532	Cluster9407_1clades	57	SEA_KRADAL_337	Streptomyces phage Kradal	GCA_004799925.1
AXH66486.1	009532	Cluster9407_1clades	57	SEA_SATIS_337	Streptomyces phage Satis	GCA_003366315.1
BBA65429.1	009533	Cluster9408_1clades	57	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96447.1	009533	Cluster9408_1clades	55	Xoosp13_261	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90520.1	009534	Cluster9409_1clades	44	HYO65_gp128	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90828.1	009534	Cluster9409_1clades	57	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06829.1	009535	Cluster9410_1clades	57	BcepSaruman_416	Burkholderia phage BcepSaruman	GCA_004771375.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBQ74798.1	009535	Cluster9410_1clades	57	BcepSauron_418	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06843.1	009536	SIG+TM	57	BcepSaruman_430	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74812.1	009536	SIG+TM	57	BcepSauron_432	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06458.1	009537	Cluster9412_1clades	57	BcepSaruman_045	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74426.1	009537	Cluster9412_1clades	55	BcepSauron_046	Burkholderia phage BcepSauron	GCA_005394215.1
prevph1000000197	009538	Cluster9413_1clades	58	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000160	009538	Cluster9413_1clades	58	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44427.1	009539	Cluster9415_1clades	56	PSSM2_049	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12224.1	009539	Cluster9415_1clades	56	PRTG_00066	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ68262.1	009540	Cluster9416_1clades	56	CcrBL10_gp058	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86545.1	009540	Cluster9416_1clades	56	CcrRogue_gp063	Caulobacter virus Rogue	GCA_000900555.1
AFU88313.1	009541	SIG+TM	56	CcrColossus_gp443	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68984.1	009541	SIG+TM	56	CcrPW_gp445	Caulobacter phage CcrPW	GCA_003443275.1
AIA65058.1	009542	Cluster9418_1clades	56	S13_261	Cronobacter phage S13	GCA_001503575.1
QHJ78874.1	009542	Cluster9418_1clades	56	-	Myoviridae sp.	GCA_012593985.1
AMS01106.1	009543	Cluster9419_1clades	56	AR9_g021	Bacillus phage AR9	GCA_001743835.1
ASU00028.1	009543	Cluster9419_1clades	56	PBI_PBS1_206	Bacillus virus PBS1	GCA_002601325.1
AMS01118.1	009544	Cluster9420_1clades	56	AR9_g033	Bacillus phage AR9	GCA_001743835.1
ASU00042.1	009544	Cluster9420_1clades	56	PBI_PBS1_220	Bacillus virus PBS1	GCA_002601325.1
AMS01243.1	009545	Cluster9421_1clades	56	AR9_g159	Bacillus phage AR9	GCA_001743835.1
AST99869.1	009545	Cluster9421_1clades	56	PBI_PBS1_47	Bacillus virus PBS1	GCA_002601325.1
ANM45046.1	009546	Nuc-transf	56	KTN4_288	Pseudomonas phage KTN4	GCA_002607225.1
QJB22921.1	009546	Nuc-transf	56	fnug_278	Pseudomonas phage fnug	GCA_012837215.1
ASR76206.1	009547	Cluster9423_1clades	56	PBI_BELLAMY_162	Synechococcus phage Bellamy	GCA_002627525.1
QJT70158.1	009547	Cluster9423_1clades	51	SynMITS9220M01_145	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXQ69179.1	009548	Cluster9424_1clades	56	CcrBL9_gp155	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69732.1	009548	Cluster9424_1clades	56	CcrSC_gp150	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69529.1	009549	Cluster9425_1clades	56	CcrBL9_gp505	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70072.1	009549	Cluster9425_1clades	52	CcrSC_gp490	Caulobacter phage CcrSC	GCA_003443315.1
QBX32460.1	009550	Cluster9426_1clades	56	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42032.1	009550	Cluster9426_1clades	56	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QGT54725.1	009551	Cluster9427_1clades	56	b23_0110	Synechococcus phage B23	GCA_009745195.1
QGT54355.1	009551	Cluster9427_1clades	56	b3_0111	Synechococcus phage B3	GCA_009745215.1
QGT54744.1	009552	Cluster9428_1clades	56	b23_0129	Synechococcus phage B23	GCA_009745195.1
QGT54374.1	009552	Cluster9428_1clades	56	b3_0130	Synechococcus phage B3	GCA_009745215.1
QGT54776.1	009553	Cluster9429_1clades	56	b23_0161	Synechococcus phage B23	GCA_009745195.1
QGT54406.1	009553	Cluster9429_1clades	56	b3_0162	Synechococcus phage B3	GCA_009745215.1
SOK59287.1	009554	Cluster9430_1clades	56	g479	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58752.1	009554	Cluster9430_1clades	54	g475	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000101	009555	Cluster9431_1clades	57	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000072	009555	Cluster9431_1clades	57	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFQ96732.1	009556	Cluster9432_1clades	55	G173_gp187	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50442.1	009556	Cluster9432_1clades	55	STRATTON_7	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AIR93585.1	009557	Cluster9433_1clades	53	AVU42_gp029	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93584.1	009557	Cluster9433_1clades	55	AVU42_gp025	Prochlorococcus phage P-TIM68	GCA_001503075.1
ANS06180.1	009558	Cluster9434_1clades	55	ABCD_0087	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97101.1	009558	Cluster9434_1clades	53	E_093	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AOO14282.1	009559	Cluster9435_1clades	55	Sn110110_088	Cyanophage S-RIM14	GCA_002599065.1
AOO14931.1	009559	Cluster9435_1clades	55	W1230910_085	Cyanophage S-RIM14	GCA_002599125.1
ARB14226.1	009560	Cluster9436_1clades	55	Ccr5_gp008	Caulobacter phage Ccr5	GCA_002619545.1
ARB14546.1	009560	Cluster9436_1clades	55	Ccr5_gp326	Caulobacter phage Ccr5	GCA_002619545.1
QBZ72020.1	009561	TM	55	SEA_KRADAL_122	Streptomyces phage Kradal	GCA_004799925.1
AXH66283.1	009561	TM	55	SEA_SATIS_122	Streptomyces phage Satis	GCA_003366315.1
AXQ69107.1	009562	Cluster9438_1clades	55	CcrBL9_gp083	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69661.1	009562	Cluster9438_1clades	55	CcrSC_gp079	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69302.1	009563	Cluster9439_1clades	55	CcrBL9_gp278c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69861.1	009563	Cluster9439_1clades	55	CcrSC_gp279c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69341.1	009564	Cluster9440_1clades	55	CcrBL9_gp317	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69901.1	009564	Cluster9440_1clades	55	CcrSC_gp319	Caulobacter phage CcrSC	GCA_003443315.1
BBA65626.1	009565	Cluster9441_1clades	55	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65167.1	009565	Cluster9441_1clades	55	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65378.1	009566	Cluster9442_1clades	55	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96406.1	009566	Cluster9442_1clades	55	Xoosp13_220	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BBI90466.1	009567	Cluster9443_1clades	55	HYO65_gp074	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90773.1	009567	Cluster9443_1clades	55	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90676.1	009568	TM	55	HYO65_gp284	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90983.1	009568	TM	55	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06486.1	009569	Cluster9445_1clades	55	BcepSaruman_073	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74453.1	009569	Cluster9445_1clades	55	BcepSauron_073	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06731.1	009570	Cluster9446_1clades	51	BcepSaruman_318	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74700.1	009570	Cluster9446_1clades	55	BcepSauron_320	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06753.1	009571	Cluster9447_1clades	55	BcepSaruman_340	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74722.1	009571	Cluster9447_1clades	55	BcepSauron_342	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54681.1	009572	Cluster9448_1clades	55	b23_0061	Synechococcus phage B23	GCA_009745195.1
QGT54311.1	009572	Cluster9448_1clades	55	b3_0061	Synechococcus phage B3	GCA_009745215.1
QGT54950.1	009573	Cluster9449_1clades	55	b23_0340	Synechococcus phage B23	GCA_009745195.1
QGT54585.1	009573	Cluster9449_1clades	55	b3_0346	Synechococcus phage B3	GCA_009745215.1
QIG57753.1	009574	Cluster9450_1clades	55	SEA_PAULODIABOLI_16	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58054.1	009574	Cluster9450_1clades	55	SEA_PAULODIABOLI_371	Microbacterium phage PauloDiaboli	GCA_011067425.1
ASR76229.1	009575	Cluster9451_1clades	51	PBI_BELLAMY_191	Synechococcus phage Bellamy	GCA_002627525.1
QJT70181.1	009575	Cluster9451_1clades	55	SynMITS9220M01_173	Synechococcus phage SynMITS9220M01	GCA_013187275.1
prevph1000000055	009576	Cluster9452_1clades	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000043	009576	Cluster9452_1clades	56	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000767	009577	Cluster9453_1clades	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000520	009577	Cluster9453_1clades	51	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44485.1	009578	Cluster9454_1clades	54	PSSM2_107	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12163.1	009578	Cluster9454_1clades	54	PRTG_00005	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01559.1	009579	Cluster9455_1clades	54	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53182.1	009579	Cluster9455_1clades	54	65p174	Aeromonas virus 65	GCA_000893255.1
AFU87976.1	009580	Cluster9456_1clades	54	CcrColossus_gp106	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68653.1	009580	Cluster9456_1clades	54	CcrPW_gp114	Caulobacter phage CcrPW	GCA_003443275.1
AMS01099.1	009581	DEOR-HTH	54	AR9_g014	Bacillus phage AR9	GCA_001743835.1
ASU00021.1	009581	DEOR-HTH	54	PBI_PBS1_199	Bacillus virus PBS1	GCA_002601325.1
AMS01176.1	009582	Cluster9458_1clades	54	AR9_g092	Bacillus phage AR9	GCA_001743835.1
ASU00110.1	009582	Cluster9458_1clades	54	PBI_PBS1_288	Bacillus virus PBS1	GCA_002601325.1
AXF51228.1	009583	Cluster9459_1clades	54	WELLINGTON_98	Erwinia phage Wellington	GCA_003344985.1
ANZ49449.1	009583	Cluster9459_1clades	54	KWAN_97	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AOO14272.1	009584	TM	54	Sn110110_078	Cyanophage S-RIM14	GCA_002599065.1
AOO14921.1	009584	TM	54	W1230910_075	Cyanophage S-RIM14	GCA_002599125.1
AXQ69289.1	009585	Cluster9461_1clades	54	CcrBL9_gp265c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69846.1	009585	Cluster9461_1clades	54	CcrSC_gp264c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70411.1	009586	Cluster9462_1clades	54	HOU04_gp012	Synechococcus phage S-T4	GCA_003443335.1
AXQ70613.1	009586	Cluster9462_1clades	54	HOU04_gp012	Synechococcus phage S-T4	GCA_003443335.1
BBA65209.1	009587	Cluster9463_1clades	54	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65668.1	009587	Cluster9463_1clades	54	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90489.1	009588	Cluster9464_1clades	54	HYO65_gp097	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90797.1	009588	Cluster9464_1clades	54	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90668.1	009589	Cluster9465_1clades	54	HYO65_gp276	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90973.1	009589	Cluster9465_1clades	54	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90696.1	009590	Cluster9466_1clades	54	HYO65_gp304	Tenacibaculum phage PTm1	GCA_009730695.1
BBI91002.1	009590	Cluster9466_1clades	54	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06433.1	009591	Cluster9467_1clades	54	BcepSaruman_020	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74400.1	009591	Cluster9467_1clades	54	BcepSauron_020	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06520.1	009592	SIG+TM	54	BcepSaruman_107	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74486.1	009592	SIG+TM	54	BcepSauron_106	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06555.1	009593	Cluster9469_1clades	54	BcepSaruman_142	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74522.1	009593	Cluster9469_1clades	54	BcepSauron_142	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06768.1	009594	Cluster9470_1clades	54	BcepSaruman_355	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74738.1	009594	Cluster9470_1clades	54	BcepSauron_358	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32201.1	009595	Cluster9471_1clades	54	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41778.1	009595	Cluster9471_1clades	54	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32266.1	009596	TM	54	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41840.1	009596	TM	54	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32420.1	009597	Cluster9473_1clades	54	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41991.1	009597	Cluster9473_1clades	54	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54671.1	009598	Cluster9474_1clades	54	b23_0043	Synechococcus phage B23	GCA_009745195.1
QGT54301.1	009598	Cluster9474_1clades	54	b3_0043	Synechococcus phage B3	GCA_009745215.1
QIG57768.1	009599	Cluster9475_1clades	54	SEA_PAULODIABOLI_33	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58069.1	009599	Cluster9475_1clades	54	SEA_PAULODIABOLI_388	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000045	009600	Cluster9476_1clades	55	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000036	009600	Cluster9476_1clades	55	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ADM80148.1	009601	Cluster9477_1clades	51	phiAS5_ORF0305	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17836.1	009601	Cluster9477_1clades	53	Aeh1ORF170c	Aeromonas virus Aeh1	GCA_000843245.1
AAX44473.1	009602	Cluster9478_1clades	53	PSSM2_095	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12179.1	009602	Cluster9478_1clades	53	PRTG_00021	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44627.1	009603	Cluster9479_1clades	53	PSSM2_250	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12343.1	009603	Cluster9479_1clades	53	PRTG_00190	Prochlorococcus phage P-SSM5	GCA_002991095.1
ABY63266.1	009604	Cluster9480_1clades	53	201phi2-1p443	Pseudomonas phage 201phi2-1	GCA_000875305.1
ATN94594.1	009604	Cluster9480_1clades	52	SL2_017	Pseudomonas phage SL2	GCA_002956015.1
AFU87939.1	009605	Cluster9481_1clades	53	CcrColossus_gp069	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68611.1	009605	Cluster9481_1clades	53	CcrPW_gp072	Caulobacter phage CcrPW	GCA_003443275.1
AFU88123.1	009606	Cluster9482_1clades	53	CcrColossus_gp253	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68801.1	009606	Cluster9482_1clades	53	CcrPW_gp262	Caulobacter phage CcrPW	GCA_003443275.1
AMS01342.1	009607	Cluster9483_1clades	53	AR9_g258	Bacillus phage AR9	GCA_001743835.1
AST99972.1	009607	Cluster9483_1clades	53	PBI_PBS1_151	Bacillus virus PBS1	GCA_002601325.1
AOO14398.1	009608	Cluster9484_1clades	53	Sn110110_205	Cyanophage S-RIM14	GCA_002599065.1
AOO15047.1	009608	Cluster9484_1clades	53	W1230910_202	Cyanophage S-RIM14	GCA_002599125.1
ATA65401.1	009609	SIG+TM	53	2050HW_00066	Serratia phage 2050HW	GCA_002628125.1
QDB71180.1	009609	SIG+TM	53	CPT_Moabite_150	Serratia phage Moabite	GCA_006384735.1
ATA65468.1	009610	Cluster9486_1clades	53	2050HW_00133	Serratia phage 2050HW	GCA_002628125.1
QDB71237.1	009610	Cluster9486_1clades	53	CPT_Moabite_207	Serratia phage Moabite	GCA_006384735.1
AXQ69303.1	009611	Cluster9487_1clades	53	CcrBL9_gp279c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69862.1	009611	Cluster9487_1clades	53	CcrSC_gp280c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69075.1	009612	Cluster9488_1clades	40	CcrBL9_gp051c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69635.1	009612	Cluster9488_1clades	53	CcrSC_gp053c	Caulobacter phage CcrSC	GCA_003443315.1
BAW19200.1	009613	Cluster9489_1clades	53	FDH28_gp195	Ralstonia phage RP12	GCA_002617345.1
BAW19486.1	009613	Cluster9489_1clades	53	-	Ralstonia phage RP31	GCA_002617365.1
BBI90450.1	009614	Cluster9490_1clades	53	HYO65_gp058	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90758.1	009614	Cluster9490_1clades	53	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90453.1	009615	Cluster9491_1clades	53	HYO65_gp061	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90761.1	009615	Cluster9491_1clades	53	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90473.1	009616	Cluster9492_1clades	53	HYO65_gp081	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90779.1	009616	Cluster9492_1clades	53	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90582.1	009617	Cluster9493_1clades	53	HYO65_gp190	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90890.1	009617	Cluster9493_1clades	53	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90666.1	009618	Cluster9494_1clades	53	HYO65_gp274	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90971.1	009618	Cluster9494_1clades	53	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06815.1	009619	Cluster9495_1clades	53	BcepSaruman_402	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74784.1	009619	Cluster9495_1clades	53	BcepSauron_404	Burkholderia phage BcepSauron	GCA_005394215.1
QCW23069.1	009620	Cluster9496_1clades	53	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50683.1	009620	Cluster9496_1clades	53	-	Synechococcus phage S-B43	GCA_006869725.1
ATA65572.1	009621	SIG+TM	30	2050HW_00237	Serratia phage 2050HW	GCA_002628125.1
QDB71336.1	009621	SIG+TM	53	CPT_Moabite_306	Serratia phage Moabite	GCA_006384735.1
QCW22890.1	009622	Cluster9498_1clades	52	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50656.1	009622	Cluster9498_1clades	53	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54814.1	009623	Cluster9499_1clades	53	b23_0199	Synechococcus phage B23	GCA_009745195.1
QGT54444.1	009623	Cluster9499_1clades	53	b3_0201	Synechococcus phage B3	GCA_009745215.1
AAX44451.1	009624	Cluster9500_1clades	52	PSSM2_073	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12203.1	009624	Cluster9500_1clades	52	PRTG_00045	Prochlorococcus phage P-SSM5	GCA_002991095.1
AXQ68237.1	009625	Cluster9501_1clades	52	CcrBL10_gp033	Caulobacter phage CcrBL10	GCA_003443255.1
AFU86519.1	009625	Cluster9501_1clades	52	CcrRogue_gp037	Caulobacter virus Rogue	GCA_000900555.1
AFU88008.1	009626	Cluster9502_1clades	52	CcrColossus_gp138	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68684.1	009626	Cluster9502_1clades	37	CcrPW_gp145	Caulobacter phage CcrPW	GCA_003443275.1
AMM43585.1	009627	Cluster9503_1clades	52	CBB_20	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44136.1	009627	Cluster9503_1clades	52	CBB_573	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AXF51319.1	009628	Cluster9504_1clades	52	WELLINGTON_191	Erwinia phage Wellington	GCA_003344985.1
ANZ49544.1	009628	Cluster9504_1clades	52	KWAN_192	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AOO14275.1	009629	Cluster9505_1clades	52	Sn110110_081	Cyanophage S-RIM14	GCA_002599065.1
AOO14924.1	009629	Cluster9505_1clades	52	W1230910_078	Cyanophage S-RIM14	GCA_002599125.1
AOO14359.1	009630	Cluster9506_1clades	52	Sn110110_165	Cyanophage S-RIM14	GCA_002599065.1
AOO15008.1	009630	Cluster9506_1clades	52	W1230910_162	Cyanophage S-RIM14	GCA_002599125.1
ATA65585.1	009631	Cluster9507_1clades	52	2050HW_00250	Serratia phage 2050HW	GCA_002628125.1
QDB71350.1	009631	Cluster9507_1clades	52	CPT_Moabite_320	Serratia phage Moabite	GCA_006384735.1
AXQ69525.1	009632	Cluster9508_1clades	52	CcrBL9_gp501	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70068.1	009632	Cluster9508_1clades	52	CcrSC_gp486	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70419.1	009633	Cluster9509_1clades	52	HOU04_gp020	Synechococcus phage S-T4	GCA_003443335.1
AXQ70621.1	009633	Cluster9509_1clades	52	HOU04_gp020	Synechococcus phage S-T4	GCA_003443335.1
BAS04927.1	009634	Cluster9510_1clades	52	AVU11_gp135	Ralstonia phage RSF1	GCA_001500875.1
BAQ02654.2	009634	Cluster9510_1clades	46	-	Ralstonia phage RSL2	GCA_001503055.1
BBA65633.1	009635	SIG+TM	52	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65174.1	009635	SIG+TM	52	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65253.1	009636	Cluster9512_1clades	52	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65712.1	009636	Cluster9512_1clades	52	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90614.1	009637	Cluster9513_1clades	52	HYO65_gp222	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90920.1	009637	Cluster9513_1clades	52	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90648.1	009638	Cluster9514_1clades	45	HYO65_gp256	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90954.1	009638	Cluster9514_1clades	52	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBO62095.1	009639	Cluster9515_1clades	52	G17_00606	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80199.1	009639	Cluster9515_1clades	52	PSLUR01_00222	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW22848.1	009640	Cluster9516_1clades	52	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50707.1	009640	Cluster9516_1clades	52	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54658.1	009641	Cluster9517_1clades	52	b23_0030	Synechococcus phage B23	GCA_009745195.1
QGT54288.1	009641	Cluster9517_1clades	52	b3_0030	Synechococcus phage B3	GCA_009745215.1
QGT54795.1	009642	Cluster9518_1clades	52	b23_0180	Synechococcus phage B23	GCA_009745195.1
QGT54425.1	009642	Cluster9518_1clades	52	b3_0181	Synechococcus phage B3	GCA_009745215.1
QGT54987.1	009643	Cluster9519_1clades	52	b23_0381	Synechococcus phage B23	GCA_009745195.1
QGT54622.1	009643	Cluster9519_1clades	52	b3_0387	Synechococcus phage B3	GCA_009745215.1
prevph1000000266	009644	Cluster9520_1clades	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000213	009644	Cluster9520_1clades	53	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000659	009645	Cluster9521_1clades	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000471	009645	Cluster9521_1clades	53	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44518.1	009646	Cluster9522_1clades	51	PSSM2_140	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12449.1	009646	Cluster9522_1clades	51	PRTG_00301	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44603.1	009647	Cluster9523_1clades	51	PSSM2_226	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12367.1	009647	Cluster9523_1clades	51	PRTG_00214	Prochlorococcus phage P-SSM5	GCA_002991095.1
QNJ54877.1	009648	Cluster9524_1clades	31	vBValMR10Z_337	Vibrio phage vB_ValM_R10Z	GCA_014337545.1
AFN37438.1	009648	Cluster9524_1clades	51	pp2_205	Vibriophage phi-pp2	GCA_002630725.1
AMS01291.1	009649	Cluster9525_1clades	51	AR9_g207	Bacillus phage AR9	GCA_001743835.1
AST99919.1	009649	Cluster9525_1clades	38	PBI_PBS1_97	Bacillus virus PBS1	GCA_002601325.1
ASR76167.1	009650	Cluster9526_1clades	51	PBI_BELLAMY_122	Synechococcus phage Bellamy	GCA_002627525.1
QJT70109.1	009650	Cluster9526_1clades	39	SynMITS9220M01_096	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AXQ69027.1	009651	Cluster9527_1clades	51	CcrBL9_gp003	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69543.1	009651	Cluster9527_1clades	51	CcrBL9_gp519	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69235.1	009652	Cluster9528_1clades	51	CcrBL9_gp211	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69789.1	009652	Cluster9528_1clades	51	CcrSC_gp207	Caulobacter phage CcrSC	GCA_003443315.1
BBI90493.1	009653	TM	51	HYO65_gp101	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90801.1	009653	TM	51	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06416.1	009654	Cluster9530_1clades	51	BcepSaruman_003	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74383.1	009654	Cluster9530_1clades	51	BcepSauron_003	Burkholderia phage BcepSauron	GCA_005394215.1
QCW22834.1	009655	Cluster9531_1clades	51	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50500.1	009655	Cluster9531_1clades	51	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54660.1	009656	Cluster9532_1clades	51	b23_0032	Synechococcus phage B23	GCA_009745195.1
QGT54290.1	009656	Cluster9532_1clades	51	b3_0032	Synechococcus phage B3	GCA_009745215.1
QGT54748.1	009657	Cluster9533_1clades	51	b23_0133	Synechococcus phage B23	GCA_009745195.1
QGT54378.1	009657	Cluster9533_1clades	51	b3_0134	Synechococcus phage B3	GCA_009745215.1
QGT54792.1	009658	Cluster9534_1clades	51	b23_0177	Synechococcus phage B23	GCA_009745195.1
QGT54422.1	009658	Cluster9534_1clades	51	b3_0178	Synechococcus phage B3	GCA_009745215.1
QGT54865.1	009659	Cluster9535_1clades	51	b23_0251	Synechococcus phage B23	GCA_009745195.1
QGT54500.1	009659	Cluster9535_1clades	51	b3_0258	Synechococcus phage B3	GCA_009745215.1
QGT54903.1	009660	Cluster9536_1clades	51	b23_0290	Synechococcus phage B23	GCA_009745195.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGT54538.1	009660	Cluster9536_1clades	51	b3_0297	Synechococcus phage B3	GCA_009745215.1
AYD81301.1	009661	Cluster9537_1clades	49	SEA_JUSTBECAUSE_132	Streptomyces phage JustBecause	GCA_003613775.1
QJD53704.1	009661	Cluster9537_1clades	51	SEA_KELA_133	Streptomyces phage Kela	GCA_012934305.1
AAX44536.1	009662	Cluster9538_1clades	50	PSSM2_158	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12435.1	009662	Cluster9538_1clades	50	PRTG_00285	Prochlorococcus phage P-SSM5	GCA_002991095.1
ANS06184.1	009663	TM	50	ABCD_0089	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AAX78611.1	009663	TM	50	RB43ORF089w	Escherichia virus RB43	GCA_000863505.1
AMM43573.1	009664	Cluster9540_1clades	50	CBB_561	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44124.1	009664	Cluster9540_1clades	50	CBB_8	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMS01257.1	009665	Cluster9541_1clades	50	AR9_g173	Bacillus phage AR9	GCA_001743835.1
AST99883.1	009665	Cluster9541_1clades	50	PBI_PBS1_61	Bacillus virus PBS1	GCA_002601325.1
AMS01264.1	009666	Cluster9542_1clades	50	AR9_g180	Bacillus phage AR9	GCA_001743835.1
AST99891.1	009666	Cluster9542_1clades	50	PBI_PBS1_69	Bacillus virus PBS1	GCA_002601325.1
ARB14633.1	009667	Cluster9543_1clades	50	Ccr29_gp076	Caulobacter phage Ccr29	GCA_002619485.1
ARB14989.1	009667	Cluster9543_1clades	50	Ccr32_gp070	Caulobacter phage Ccr32	GCA_002619505.1
AXQ68549.1	009668	Cluster9544_1clades	50	CcrPW_gp010	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68999.1	009668	Cluster9544_1clades	50	CcrPW_gp460	Caulobacter phage CcrPW	GCA_003443275.1
BBI90523.1	009669	Cluster9545_1clades	50	HYO65_gp131	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90831.1	009669	Cluster9545_1clades	50	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32276.1	009670	Cluster9546_1clades	50	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41850.1	009670	Cluster9546_1clades	50	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW22841.1	009671	Cluster9547_1clades	50	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50506.1	009671	Cluster9547_1clades	50	-	Synechococcus phage S-B43	GCA_006869725.1
QCW23184.1	009672	Cluster9548_1clades	50	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47545.1	009672	Cluster9548_1clades	50	HWC35_gp151	Vibrio phage USC-1	GCA_006864065.1
QDJ96800.1	009673	Cluster9549_1clades	50	PS1_0041	Aeromonas phage PS1	GCA_007051165.2
QFR59431.1	009673	Cluster9549_1clades	50	PS2_0040	Aeromonas phage PS2	GCA_009388305.2
QGT54657.1	009674	Cluster9550_1clades	50	b23_0029	Synechococcus phage B23	GCA_009745195.1
QGT54287.1	009674	Cluster9550_1clades	50	b3_0029	Synechococcus phage B3	GCA_009745215.1
QGT54690.1	009675	Cluster9551_1clades	50	b23_0075	Synechococcus phage B23	GCA_009745195.1
QGT54320.1	009675	Cluster9551_1clades	50	b3_0076	Synechococcus phage B3	GCA_009745215.1
QGT54771.1	009676	Cluster9552_1clades	50	b23_0156	Synechococcus phage B23	GCA_009745195.1
QGT54401.1	009676	Cluster9552_1clades	50	b3_0157	Synechococcus phage B3	GCA_009745215.1
QIG58080.1	009677	Cluster9553_1clades	50	SEA_PAULODIABOLI_23	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58089.1	009677	Cluster9553_1clades	50	SEA_PAULODIABOLI_378	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000129	009678	Cluster9554_1clades	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000097	009678	Cluster9554_1clades	51	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000794	009679	Cluster9555_1clades	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000542	009679	Cluster9555_1clades	51	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ADM79847.1	009680	Cluster9556_1clades	49	phiAS5_ORF0004	Aeromonas phage phiAS5	GCA_000887715.1
AAQ17872.1	009680	Cluster9556_1clades	49	Aeh1ORF209w	Aeromonas virus Aeh1	GCA_000843245.1
AAX44420.1	009681	Cluster9557_1clades	49	PSSM2_042	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12231.1	009681	Cluster9557_1clades	49	PRTG_00073	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44519.1	009682	Cluster9558_1clades	49	PSSM2_141	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12448.1	009682	Cluster9558_1clades	49	PRTG_00300	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44546.1	009683	Cluster9559_1clades	49	PSSM2_168	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12425.1	009683	Cluster9559_1clades	49	PRTG_00275	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44561.1	009684	Cluster9560_1clades	49	PSSM2_183	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12411.1	009684	Cluster9560_1clades	49	PRTG_00259	Prochlorococcus phage P-SSM5	GCA_002991095.1
AAX44633.1	009685	Cluster9561_1clades	49	PSSM2_256	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12338.1	009685	Cluster9561_1clades	49	PRTG_00185	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01634.1	009686	Cluster9562_1clades	49	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53260.1	009686	Cluster9562_1clades	49	65p252	Aeromonas virus 65	GCA_000893255.1
ANZ48492.1	009687	Cluster9563_1clades	49	CAITLIN_197	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48771.1	009687	Cluster9563_1clades	49	CHRISDB_209	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AUR81100.1	009688	Cluster9564_1clades	49	Aphrodite1_0032	Vibrio phage Aphrodite1	GCA_002958015.1
BAW98234.1	009688	Cluster9564_1clades	49	FDH33_gp025	Vibrio phage pTD1	GCA_002618825.1
QBZ72037.1	009689	Cluster9565_1clades	49	SEA_KRADAL_139	Streptomyces phage Kradal	GCA_004799925.1
AXH66300.1	009689	Cluster9565_1clades	49	SEA_SATIS_139	Streptomyces phage Satis	GCA_003366315.1
AFU87930.1	009690	TM	46	CcrColossus_gp060	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68602.1	009690	TM	49	CcrPW_gp063	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69526.1	009691	Cluster9567_1clades	49	CcrBL9_gp502	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70069.1	009691	Cluster9567_1clades	49	CcrSC_gp487	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69538.1	009692	Cluster9568_1clades	49	CcrBL9_gp514	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70081.1	009692	Cluster9568_1clades	49	CcrSC_gp499	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69539.1	009693	Cluster9569_1clades	48	CcrBL9_gp515	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70082.1	009693	Cluster9569_1clades	49	CcrSC_gp500	Caulobacter phage CcrSC	GCA_003443315.1
BAU71416.1	009694	TM	45	AVU11_agp06	Ralstonia phage RSF1	GCA_001500875.1
BAU71402.1	009694	TM	49	-	Ralstonia phage RSL2	GCA_001503055.1
QBX06418.1	009695	Cluster9571_1clades	49	BcepSaruman_005	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74386.1	009695	Cluster9571_1clades	49	BcepSauron_006	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06852.1	009696	Cluster9572_1clades	49	BcepSaruman_439	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74821.1	009696	Cluster9572_1clades	49	BcepSauron_441	Burkholderia phage BcepSauron	GCA_005394215.1
QCW22997.1	009697	Cluster9573_1clades	49	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50648.1	009697	Cluster9573_1clades	47	-	Synechococcus phage S-B43	GCA_006869725.1
ATA65480.1	009698	Cluster9574_1clades	42	2050HW_00145	Serratia phage 2050HW	GCA_002628125.1
QDB71250.1	009698	Cluster9574_1clades	49	CPT_Moabite_220	Serratia phage Moabite	GCA_006384735.1
QGT54663.1	009699	Cluster9575_1clades	49	b23_0035	Synechococcus phage B23	GCA_009745195.1
QGT54293.1	009699	Cluster9575_1clades	49	b3_0035	Synechococcus phage B3	GCA_009745215.1
QIG57740.1	009700	Cluster9576_1clades	49	SEA_PAULODIABOLI_2	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58041.1	009700	Cluster9576_1clades	49	SEA_PAULODIABOLI_357	Microbacterium phage PauloDiaboli	GCA_011067425.1
ASR76147.1	009701	Cluster9577_1clades	47	PBI_BELLAMY_102	Synechococcus phage Bellamy	GCA_002627525.1
QJT70087.1	009701	Cluster9577_1clades	49	SynMITS9220M01_074	Synechococcus phage SynMITS9220M01	GCA_013187275.1
prevph1000000487	009702	Cluster9578_1clades	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000368	009702	Cluster9578_1clades	50	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44698.1	009703	SIG+DUF4278	48	PSSM2_320	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12277.1	009703	SIG+DUF4278	48	PRTG_00124	Prochlorococcus phage P-SSM5	GCA_002991095.1
ABS83806.1	009704	Cluster9580_1clades	48	0305phi8-36p106	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83664.1	009704	Cluster9580_1clades	48	0305phi8-36p106R	Bacillus phage 0305phi8-36	GCA_000871045.1
AIT14183.1	009705	TM	48	PBI_121Q_293	Escherichia phage 121Q	GCA_000926855.1
AGC34933.1	009705	TM	48	ACQ29_gp253	Escherichia phage PBECO4	GCA_001041035.1
AKF12951.1	009706	Cluster9582_1clades	48	PHIM19_44	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12591.1	009706	Cluster9582_1clades	48	PHIM7_43	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13155.1	009707	Cluster9583_1clades	48	PHIM19_250	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12794.1	009707	Cluster9583_1clades	48	PHIM7_249	Sinorhizobium phage phiM7	GCA_002622405.1
AMS01182.1	009708	Cluster9584_1clades	48	AR9_g098	Bacillus phage AR9	GCA_001743835.1
ASU00116.1	009708	Cluster9584_1clades	48	PBI_PBS1_294	Bacillus virus PBS1	GCA_002601325.1
AOO14269.1	009709	Cluster9585_1clades	48	Sn110110_075	Cyanophage S-RIM14	GCA_002599065.1
AOO14918.1	009709	Cluster9585_1clades	48	W1230910_072	Cyanophage S-RIM14	GCA_002599125.1
AXQ69054.1	009710	Cluster9586_1clades	48	CcrBL9_gp030c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69570.1	009710	Cluster9586_1clades	48	CcrBL9_gp546c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69223.1	009711	Cluster9587_1clades	48	CcrBL9_gp199	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69777.1	009711	Cluster9587_1clades	48	CcrSC_gp195	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69586.1	009712	Cluster9588_1clades	48	CcrSC_gp004	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70086.1	009712	Cluster9588_1clades	48	CcrSC_gp504	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69589.1	009713	Cluster9589_1clades	48	CcrSC_gp007	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70089.1	009713	Cluster9589_1clades	48	CcrSC_gp507	Caulobacter phage CcrSC	GCA_003443315.1
QBX06612.1	009714	DUF1778	48	BcepSaruman_199	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74578.1	009714	DUF1778	48	BcepSauron_198	Burkholderia phage BcepSauron	GCA_005394215.1
QIG57761.1	009715	Cluster9591_1clades	48	SEA_PAULODIABOLI_25	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58062.1	009715	Cluster9591_1clades	48	SEA_PAULODIABOLI_380	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000173	009716	Cluster9592_1clades	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000135	009716	Cluster9592_1clades	49	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000214	009717	Cluster9593_1clades	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000168	009717	Cluster9593_1clades	49	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000497	009718	Cluster9594_1clades	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000377	009718	Cluster9594_1clades	49	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44653.1	009719	TM	47	PSSM2_276	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12320.1	009719	TM	47	PRTG_00167	Prochlorococcus phage P-SSM5	GCA_002991095.1
APU01512.1	009720	Cluster9596_1clades	47	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53135.1	009720	Cluster9596_1clades	47	65p127	Aeromonas virus 65	GCA_000893255.1
APU01703.1	009721	Cluster9597_1clades	47	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53342.1	009721	Cluster9597_1clades	47	65p334	Aeromonas virus 65	GCA_000893255.1
AMS01225.1	009722	Cluster9598_1clades	47	AR9_g141	Bacillus phage AR9	GCA_001743835.1
AST99850.1	009722	Cluster9598_1clades	47	PBI_PBS1_28	Bacillus virus PBS1	GCA_002601325.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMS01271.1	009723	Cluster9599_1clades	47	AR9_g187	Bacillus phage AR9	GCA_001743835.1
AST99898.1	009723	Cluster9599_1clades	47	PBI_PBS1_76	Bacillus virus PBS1	GCA_002601325.1
QBZ71998.1	009724	Cluster9600_1clades	47	SEA_KRADAL_100	Streptomyces phage Kradal	GCA_004799925.1
AXH66261.1	009724	Cluster9600_1clades	47	SEA_SATIS_100	Streptomyces phage Satis	GCA_003366315.1
AYD81266.1	009725	Cluster9601_1clades	47	SEA_JUSTBECAUSE_97	Streptomyces phage JustBecause	GCA_003613775.1
QJD53669.1	009725	Cluster9601_1clades	47	SEA_KELA_98	Streptomyces phage Kela	GCA_012934305.1
BAW19168.1	009726	Cluster9602_1clades	47	FDH28_gp227	Ralstonia phage RP12	GCA_002617345.1
BAW19454.1	009726	Cluster9602_1clades	47	-	Ralstonia phage RP31	GCA_002617365.1
BBI90672.1	009727	Cluster9603_1clades	47	HYO65_gp280	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90977.1	009727	Cluster9603_1clades	47	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90698.1	009728	Cluster9604_1clades	47	HYO65_gp306	Tenacibaculum phage PTm1	GCA_009730695.1
BBI91004.1	009728	Cluster9604_1clades	47	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06746.1	009729	Cluster9605_1clades	47	BcepSaruman_333	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74715.1	009729	Cluster9605_1clades	47	BcepSauron_335	Burkholderia phage BcepSauron	GCA_005394215.1
QBX32265.1	009730	TM	47	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41839.1	009730	TM	47	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QBX32354.1	009731	Cluster9607_1clades	47	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41928.1	009731	Cluster9607_1clades	47	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QDJ96785.1	009732	Cluster9608_1clades	47	PS1_0026	Aeromonas phage PS1	GCA_007051165.2
QFR59416.1	009732	Cluster9608_1clades	47	PS2_0025	Aeromonas phage PS2	GCA_009388305.2
QDJ96817.1	009733	Cluster9609_1clades	47	PS1_0058	Aeromonas phage PS1	GCA_007051165.2
QFR59446.1	009733	Cluster9609_1clades	47	PS2_0055	Aeromonas phage PS2	GCA_009388305.2
QGT54661.1	009734	Cluster9610_1clades	47	b23_0033	Synechococcus phage B23	GCA_009745195.1
QGT54291.1	009734	Cluster9610_1clades	47	b3_0033	Synechococcus phage B3	GCA_009745215.1
QGT54808.1	009735	Cluster9611_1clades	47	b23_0193	Synechococcus phage B23	GCA_009745195.1
QGT54438.1	009735	Cluster9611_1clades	47	b3_0195	Synechococcus phage B3	GCA_009745215.1
AUZ95216.1	009736	Cluster9612_1clades	42	FDI40_gp457	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIG65911.1	009736	Cluster9612_1clades	47	phiOC_p254	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
prevph1000000113	009737	Cluster9613_1clades	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000080	009737	Cluster9613_1clades	48	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000804	009738	Cluster9614_1clades	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000551	009738	Cluster9614_1clades	48	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFU88185.1	009739	TM	46	CcrColossus_gp315	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68862.1	009739	TM	46	CcrPW_gp323	Caulobacter phage CcrPW	GCA_003443275.1
ANZ48493.1	009740	Cluster9616_1clades	46	CAITLIN_198	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48772.1	009740	Cluster9616_1clades	46	CHRISDB_210	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AXF51426.1	009741	Cluster9617_1clades	46	WELLINGTON_210	Erwinia phage Wellington	GCA_003344985.1
ANZ49563.1	009741	Cluster9617_1clades	46	KWAN_211	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
APU01794.1	009742	DEAM	46	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53438.1	009742	DEAM	43	65p432	Aeromonas virus 65	GCA_000893255.1
AWY08462.1	009743	Cluster9619_1clades	45	Alexandra_197	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ARW58832.1	009743	Cluster9619_1clades	46	Y3_192	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AXQ69155.1	009744	Cluster9620_1clades	46	CcrBL9_gp131	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69710.1	009744	Cluster9620_1clades	46	CcrSC_gp128	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70420.1	009745	Cluster9621_1clades	46	HOU04_gp021	Synechococcus phage S-T4	GCA_003443335.1
AXQ70622.1	009745	Cluster9621_1clades	46	HOU04_gp021	Synechococcus phage S-T4	GCA_003443335.1
QCW18898.1	009746	Cluster9622_1clades	46	7t3_0377	Salmonella phage 7t3	GCA_006083215.1
AZU98155.1	009746	Cluster9622_1clades	46	CPT_Munch_211	Salmonella phage Munch	GCA_004015485.1
BAW19086.1	009747	Cluster9623_1clades	46	FDH28_gp112	Ralstonia phage RP12	GCA_002617345.1
BAW19372.1	009747	Cluster9623_1clades	46	-	Ralstonia phage RP31	GCA_002617365.1
BBA65639.1	009748	Cluster9624_1clades	46	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65180.1	009748	Cluster9624_1clades	46	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90602.1	009749	Cluster9625_1clades	46	HYO65_gp210	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90909.1	009749	Cluster9625_1clades	46	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06419.1	009750	Cluster9626_1clades	46	BcepSaruman_006	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74387.1	009750	Cluster9626_1clades	46	BcepSauron_007	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06461.1	009751	Cluster9627_1clades	46	BcepSaruman_048	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74429.1	009751	Cluster9627_1clades	46	BcepSauron_049	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06462.1	009752	Cluster9628_1clades	46	BcepSaruman_049	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74430.1	009752	Cluster9628_1clades	46	BcepSauron_050	Burkholderia phage BcepSauron	GCA_005394215.1
QBX06764.1	009753	Cluster9629_1clades	46	BcepSaruman_351	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74734.1	009753	Cluster9629_1clades	46	BcepSauron_354	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54847.1	009754	Cluster9630_1clades	46	b23_0233	Synechococcus phage B23	GCA_009745195.1
QGT54481.1	009754	Cluster9630_1clades	46	b3_0239	Synechococcus phage B3	GCA_009745215.1
AYD81459.1	009755	Cluster9631_1clades	33	SEA_JUSTBECAUSE_304	Streptomyces phage JustBecause	GCA_003613775.1
QJD53863.1	009755	Cluster9631_1clades	46	SEA_KELA_303	Streptomyces phage Kela	GCA_012934305.1
prevph1000000778	009756	TM	47	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000531	009756	TM	47	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44587.1	009757	Cluster9633_1clades	45	PSSM2_210	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12384.1	009757	Cluster9633_1clades	45	PRTG_00231	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGR48101.1	009758	Cluster9634_1clades	45	SmphiM12_469	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13633.1	009758	Cluster9634_1clades	45	PHIN3_370	Sinorhizobium phage phiN3	GCA_001501175.1
AMS01185.1	009759	Cluster9635_1clades	45	AR9_g101	Bacillus phage AR9	GCA_001743835.1
ASU00119.1	009759	Cluster9635_1clades	45	PBI_PBS1_297	Bacillus virus PBS1	GCA_002601325.1
AMS01328.1	009760	Cluster9636_1clades	45	AR9_g244	Bacillus phage AR9	GCA_001743835.1
AST99957.1	009760	Cluster9636_1clades	45	PBI_PBS1_136	Bacillus virus PBS1	GCA_002601325.1
AOO14366.1	009761	Cluster9637_1clades	45	Sn110110_172	Cyanophage S-RIM14	GCA_002599065.1
AOO15014.1	009761	Cluster9637_1clades	45	W1230910_168	Cyanophage S-RIM14	GCA_002599125.1
AXQ70405.1	009762	Cluster9638_1clades	45	HOU04_gp006	Synechococcus phage S-T4	GCA_003443335.1
AXQ70607.1	009762	Cluster9638_1clades	45	HOU04_gp006	Synechococcus phage S-T4	GCA_003443335.1
QGT54676.1	009763	Cluster9639_1clades	45	b23_0048	Synechococcus phage B23	GCA_009745195.1
QGT54306.1	009763	Cluster9639_1clades	45	b3_0048	Synechococcus phage B3	GCA_009745215.1
QIG58044.1	009764	Cluster9640_1clades	45	SEA_PAULODIABOLI_360	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57743.1	009764	Cluster9640_1clades	45	SEA_PAULODIABOLI_5	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000158	009765	Cluster9641_1clades	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000119	009765	Cluster9641_1clades	46	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000258	009766	Cluster9642_1clades	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000205	009766	Cluster9642_1clades	46	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000609	009767	Cluster9643_1clades	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000428	009767	Cluster9643_1clades	46	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AAX44699.1	009768	Cluster9644_1clades	44	PSSM2_321	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12276.1	009768	Cluster9644_1clades	44	PRTG_00123	Prochlorococcus phage P-SSM5	GCA_002991095.1
AFC21924.1	009769	Cluster9645_1clades	44	GAP32_466	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44051.1	009769	Cluster9645_1clades	43	CBB_488	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AXF51227.1	009770	Cluster9646_1clades	44	WELLINGTON_97	Erwinia phage Wellington	GCA_003344985.1
ANZ49448.1	009770	Cluster9646_1clades	44	KWAN_96	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QBZ72192.1	009771	Cluster9647_1clades	44	SEA_KRADAL_306	Streptomyces phage Kradal	GCA_004799925.1
AXH66455.1	009771	Cluster9647_1clades	44	SEA_SATIS_306	Streptomyces phage Satis	GCA_003366315.1
AXQ69108.1	009772	TM	44	CcrBL9_gp084	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69662.1	009772	TM	44	CcrSC_gp080	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69590.1	009773	Cluster9649_1clades	44	CcrSC_gp008	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70090.1	009773	Cluster9649_1clades	44	CcrSC_gp508	Caulobacter phage CcrSC	GCA_003443315.1
BAW19109.1	009774	Cluster9650_1clades	44	FDH28_gp286	Ralstonia phage RP12	GCA_002617345.1
BAW19395.1	009774	Cluster9650_1clades	44	-	Ralstonia phage RP31	GCA_002617365.1
BBA65701.1	009775	Cluster9651_1clades	44	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65242.1	009775	Cluster9651_1clades	44	-	Xanthomonas phage XacN1	GCA_003173815.1
BBI90543.1	009776	Cluster9652_1clades	44	HYO65_gp151	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90851.1	009776	Cluster9652_1clades	44	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90548.1	009777	Cluster9653_1clades	44	HYO65_gp156	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90856.1	009777	Cluster9653_1clades	44	-	Tenacibaculum phage PTm5	GCA_009730715.1
QGT54749.1	009778	Cluster9654_1clades	44	b23_0134	Synechococcus phage B23	GCA_009745195.1
QGT54379.1	009778	Cluster9654_1clades	44	b3_0135	Synechococcus phage B3	GCA_009745215.1
SOK58925.1	009779	Cluster9655_1clades	44	g117	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58390.1	009779	Cluster9655_1clades	44	g113	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000122	009780	Cluster9656_1clades	45	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000091	009780	Cluster9656_1clades	45	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ADQ52796.1	009781	Cluster9657_1clades	43	PX29p077	Aeromonas phage PX29	GCA_000920195.1
AAQ17739.1	009781	Cluster9657_1clades	43	Aeh1gORF094c	Aeromonas virus Aeh1	GCA_000843245.1
APU01701.1	009782	Cluster9658_1clades	43	-	Aeromonas phage 65.2	GCA_002618145.1
ADQ53340.1	009782	Cluster9658_1clades	43	65p332	Aeromonas virus 65	GCA_000893255.1
AMR59847.1	009783	Cluster9659_1clades	43	SEGD1_200	Enterobacteria phage SEGD1	GCA_002601865.1
AEP84030.1	009783	Cluster9659_1clades	43	SPN3US_0197	Salmonella phage SPN3US	GCA_001042275.1
ATA65479.1	009784	Cluster9660_1clades	43	2050HW_00144	Serratia phage 2050HW	GCA_002628125.1
QDB71249.1	009784	Cluster9660_1clades	43	CPT_Moabite_219	Serratia phage Moabite	GCA_006384735.1
QDJ96741.1	009785	Cluster9661_1clades	43	PS1_0230	Aeromonas phage PS1	GCA_007051165.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFR59374.1	009785	Cluster9661_1clades	43	PS2_0232	Aeromonas phage PS2	GCA_009388305.2
QBX32525.1	009786	TM	42	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM42098.1	009786	TM	43	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
SOK59215.1	009787	Cluster9663_1clades	43	g407	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58681.1	009787	Cluster9663_1clades	43	g404	Yersinia phage fHe-Yen9-04	GCA_002990485.1
AIT14127.1	009788	Cluster9664_1clades	42	PBI_121Q_237	Escherichia phage 121Q	GCA_000926855.1
AXC36552.1	009788	Cluster9664_1clades	42	-	Escherichia phage UB	GCA_003341455.1
AMR59839.1	009789	Cluster9665_1clades	42	SEGD1_192	Enterobacteria phage SEGD1	GCA_002601865.1
AWN09150.2	009789	Cluster9665_1clades	38	MLDJOKPK_00252	Salmonella phage SPAsTU	GCA_003183805.1
AYD81374.1	009790	Cluster9666_1clades	42	SEA_JUSTBECAUSE_219	Streptomyces phage JustBecause	GCA_003613775.1
QJD53777.1	009790	Cluster9666_1clades	41	SEA_KELA_217	Streptomyces phage Kela	GCA_012934305.1
AYD81474.1	009791	Cluster9667_1clades	42	SEA_JUSTBECAUSE_319	Streptomyces phage JustBecause	GCA_003613775.1
QJD53877.1	009791	Cluster9667_1clades	42	SEA_KELA_317	Streptomyces phage Kela	GCA_012934305.1
BBI90484.1	009792	Cluster9668_1clades	42	HYO65_gp092	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90792.1	009792	Cluster9668_1clades	42	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90491.1	009793	Cluster9669_1clades	42	HYO65_gp099	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90799.1	009793	Cluster9669_1clades	42	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90495.1	009794	Cluster9670_1clades	42	HYO65_gp103	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90803.1	009794	Cluster9670_1clades	42	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90506.1	009795	Cluster9671_1clades	42	HYO65_gp114	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90814.1	009795	Cluster9671_1clades	42	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX32176.1	009796	Cluster9672_1clades	42	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41755.1	009796	Cluster9672_1clades	42	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QCW23029.1	009797	Cluster9673_1clades	40	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50665.1	009797	Cluster9673_1clades	42	-	Synechococcus phage S-B43	GCA_006869725.1
QGT54662.1	009798	TM	42	b23_0034	Synechococcus phage B23	GCA_009745195.1
QGT54292.1	009798	TM	42	b3_0034	Synechococcus phage B3	GCA_009745215.1
prevph1000000658	009799	Cluster9675_1clades	43	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000470	009799	Cluster9675_1clades	43	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AFQ96657.1	009800	Cluster9676_1clades	41	G173_gp112	Erwinia phage phiEaH2	GCA_000902915.1
ANZ50634.1	009800	Cluster9676_1clades	41	STRATTON_209	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
AFU87910.1	009801	Cluster9677_1clades	41	CcrColossus_gp040	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68582.1	009801	Cluster9677_1clades	41	CcrPW_gp043	Caulobacter phage CcrPW	GCA_003443275.1
ALP47333.1	009802	Cluster9678_1clades	41	phiGrn1_0348	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47717.1	009802	Cluster9678_1clades	41	phiST2_0103	Vibrio phage phi-ST2	GCA_002757135.1
AMM44128.1	009803	Cluster9679_1clades	41	CBB_12	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43577.1	009803	Cluster9679_1clades	41	CBB_565	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43596.1	009804	Cluster9680_1clades	41	CBB_31	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44147.1	009804	Cluster9680_1clades	41	CBB_584	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AOO14315.1	009805	Cluster9681_1clades	41	Sn110110_121	Cyanophage S-RIM14	GCA_002599065.1
AOO14964.1	009805	Cluster9681_1clades	41	W1230910_118	Cyanophage S-RIM14	GCA_002599125.1
ATA65549.1	009806	Cluster9682_1clades	41	2050HW_00214	Serratia phage 2050HW	GCA_002628125.1
QDB71314.1	009806	Cluster9682_1clades	41	CPT_Moabite_284	Serratia phage Moabite	GCA_006384735.1
AYD81230.1	009807	Cluster9683_1clades	41	SEA_JUSTBECAUSE_61	Streptomyces phage JustBecause	GCA_003613775.1
QJD53633.1	009807	Cluster9683_1clades	41	SEA_KELA_62	Streptomyces phage Kela	GCA_012934305.1
AYD81458.1	009808	Cluster9684_1clades	41	SEA_JUSTBECAUSE_303	Streptomyces phage JustBecause	GCA_003613775.1
QJD53862.1	009808	Cluster9684_1clades	41	SEA_KELA_302	Streptomyces phage Kela	GCA_012934305.1
BAW19102.1	009809	Cluster9685_1clades	41	FDH28_gp128	Ralstonia phage RP12	GCA_002617345.1
BAW19388.1	009809	Cluster9685_1clades	41	-	Ralstonia phage RP31	GCA_002617365.1
BBA65614.1	009810	Cluster9686_1clades	41	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65155.1	009810	Cluster9686_1clades	41	-	Xanthomonas phage XacN1	GCA_003173815.1
ATA65548.1	009811	Cluster9687_1clades	40	2050HW_00213	Serratia phage 2050HW	GCA_002628125.1
QDB71313.1	009811	Cluster9687_1clades	41	CPT_Moabite_283	Serratia phage Moabite	GCA_006384735.1
QGT54659.1	009812	Cluster9688_1clades	41	b23_0031	Synechococcus phage B23	GCA_009745195.1
QGT54289.1	009812	Cluster9688_1clades	41	b3_0031	Synechococcus phage B3	GCA_009745215.1
QGT54729.1	009813	Cluster9689_1clades	41	b23_0114	Synechococcus phage B23	GCA_009745195.1
QGT54359.1	009813	Cluster9689_1clades	41	b3_0115	Synechococcus phage B3	GCA_009745215.1
ASR76285.1	009814	A18	39	PBI_BELLAMY_249	Synechococcus phage Bellamy	GCA_002627525.1
QJT70187.1	009814	A18	41	SynMITS9220M01_179	Synechococcus phage SynMITS9220M01	GCA_013187275.1
AMR59842.1	009815	Cluster9691_1clades	40	SEGD1_195	Enterobacteria phage SEGD1	GCA_002601865.1
AEP84023.1	009815	Cluster9691_1clades	40	SPN3US_0190	Salmonella phage SPN3US	GCA_001042275.1
AFU88100.1	009816	TM	40	CcrColossus_gp230	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68777.1	009816	TM	40	CcrPW_gp238	Caulobacter phage CcrPW	GCA_003443275.1
ASU03882.1	009817	Cluster9693_1clades	40	JOAD_33	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03637.1	009817	Cluster9693_1clades	40	RISINGSUN_33	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
ATA65601.1	009818	Cluster9694_1clades	40	2050HW_00266	Serratia phage 2050HW	GCA_002628125.1
QDB71365.1	009818	Cluster9694_1clades	40	CPT_Moabite_335	Serratia phage Moabite	GCA_006384735.1
AXQ70407.1	009819	Cluster9695_1clades	40	HOU04_gp008	Synechococcus phage S-T4	GCA_003443335.1
AXQ70609.1	009819	Cluster9695_1clades	40	HOU04_gp008	Synechococcus phage S-T4	GCA_003443335.1
AXQ70414.1	009820	Cluster9696_1clades	40	HOU04_gp015	Synechococcus phage S-T4	GCA_003443335.1
AXQ70616.1	009820	Cluster9696_1clades	40	HOU04_gp015	Synechococcus phage S-T4	GCA_003443335.1
AYD81360.1	009821	Cluster9697_1clades	40	SEA_JUSTBECAUSE_198	Streptomyces phage JustBecause	GCA_003613775.1
QJD53763.1	009821	Cluster9697_1clades	40	SEA_KELA_196	Streptomyces phage Kela	GCA_012934305.1
BBI90587.1	009822	Cluster9698_1clades	40	HYO65_gp195	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90894.1	009822	Cluster9698_1clades	40	-	Tenacibaculum phage PTm5	GCA_009730715.1
QCW22994.1	009823	Cluster9699_1clades	40	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50645.1	009823	Cluster9699_1clades	40	-	Synechococcus phage S-B43	GCA_006869725.1
QDJ96663.1	009824	Cluster9700_1clades	40	PS1_0152	Aeromonas phage PS1	GCA_007051165.2
QFR59297.1	009824	Cluster9700_1clades	40	PS2_0156	Aeromonas phage PS2	GCA_009388305.2
QDJ96834.1	009825	Cluster9701_1clades	40	PS1_0075	Aeromonas phage PS1	GCA_007051165.2
QFR59464.1	009825	Cluster9701_1clades	40	PS2_0073	Aeromonas phage PS2	GCA_009388305.2
AKF13071.1	009826	Cluster9702_1clades	39	PHIM19_166	Sinorhizobium phage phiM19	GCA_002605865.1
AKZ65589.1	009826	Cluster9702_1clades	39	PHIM7_166	Sinorhizobium phage phiM7	GCA_002622405.1
ANM44852.1	009827	Cluster9703_1clades	39	KTN4_094	Pseudomonas phage KTN4	GCA_002607225.1
ATN94861.1	009827	Cluster9703_1clades	36	SL2_284	Pseudomonas phage SL2	GCA_002956015.1
AXF51420.1	009828	Cluster9704_1clades	39	WELLINGTON_4	Erwinia phage Wellington	GCA_003344985.1
ANZ49366.1	009828	Cluster9704_1clades	39	KWAN_4	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXQ69173.1	009829	Cluster9705_1clades	39	CcrBL9_gp149	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69726.1	009829	Cluster9705_1clades	39	CcrSC_gp144	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69523.1	009830	Cluster9706_1clades	39	CcrBL9_gp499	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ70067.1	009830	Cluster9706_1clades	39	CcrSC_gp485	Caulobacter phage CcrSC	GCA_003443315.1
AYD81179.1	009831	Cluster9707_1clades	39	SEA_JUSTBECAUSE_10	Streptomyces phage JustBecause	GCA_003613775.1
QJD53581.1	009831	Cluster9707_1clades	38	SEA_KELA_10	Streptomyces phage Kela	GCA_012934305.1
BAW19042.1	009832	Cluster9708_1clades	39	FDH28_gp068	Ralstonia phage RP12	GCA_002617345.1
BAW19327.1	009832	Cluster9708_1clades	39	-	Ralstonia phage RP31	GCA_002617365.1
QGT54679.1	009833	Cluster9710_1clades	39	b23_0054	Synechococcus phage B23	GCA_009745195.1
QGT54309.1	009833	Cluster9710_1clades	39	b3_0054	Synechococcus phage B3	GCA_009745215.1
QGT54980.1	009834	Cluster9711_1clades	39	b23_0374	Synechococcus phage B23	GCA_009745195.1
QGT54615.1	009834	Cluster9711_1clades	39	b3_0380	Synechococcus phage B3	GCA_009745215.1
AFU87914.1	009835	Cluster9712_1clades	38	CcrColossus_gp044	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68586.1	009835	Cluster9712_1clades	38	CcrPW_gp047	Caulobacter phage CcrPW	GCA_003443275.1
AFU87915.1	009836	TM	38	CcrColossus_gp045	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68588.1	009836	TM	38	CcrPW_gp049	Caulobacter phage CcrPW	GCA_003443275.1
ANS06192.1	009837	Cluster9714_1clades	38	ABCD_0171	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
AON97184.1	009837	Cluster9714_1clades	38	E_176	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
ATA65540.1	009838	Cluster9715_1clades	38	2050HW_00205	Serratia phage 2050HW	GCA_002628125.1
QDB71305.1	009838	Cluster9715_1clades	38	CPT_Moabite_275	Serratia phage Moabite	GCA_006384735.1
QBZ72038.1	009839	Cluster9716_1clades	38	SEA_KRADAL_140	Streptomyces phage Kradal	GCA_004799925.1
AXH66301.1	009839	Cluster9716_1clades	38	SEA_SATIS_140	Streptomyces phage Satis	GCA_003366315.1
QBO61917.1	009840	Cluster9717_1clades	38	G17_00428	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80374.1	009840	Cluster9717_1clades	38	PSLUR01_00397	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QCW18940.1	009841	Cluster9718_1clades	38	7t3_0419	Salmonella phage 7t3	GCA_006083215.1
QIG62790.1	009841	Cluster9718_1clades	38	SEPL_177	Salmonella phage SE_PL	GCA_011067555.1
SOK58971.1	009842	Cluster9719_1clades	38	g163	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58437.1	009842	Cluster9719_1clades	38	g160	Yersinia phage fHe-Yen9-04	GCA_002990485.1
QHJ74498.1	009843	Cluster9720_1clades	37	VH12019_00197	Vibrio phage VH1_2019	GCA_009931825.1
AFN37548.1	009843	Cluster9720_1clades	37	pp2_316	Vibriophage phi-pp2	GCA_002630725.1
AFU88021.1	009844	Cluster9721_1clades	37	CcrColossus_gp151	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68698.1	009844	Cluster9721_1clades	37	CcrPW_gp159c	Caulobacter phage CcrPW	GCA_003443275.1
AFU88181.1	009845	Cluster9722_1clades	37	CcrColossus_gp311	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68858.1	009845	Cluster9722_1clades	37	CcrPW_gp319	Caulobacter phage CcrPW	GCA_003443275.1
QHJ74495.1	009846	Cluster9723_1clades	37	VH12019_00175	Vibrio phage VH1_2019	GCA_009931825.1
AIE13783.1	009846	Cluster9723_1clades	37	VPFG_p11	Vibrio phage nt-1	GCA_000910195.2
QBP07554.1	009847	Cluster9724_1clades	37	DERBICUS_128	Erwinia phage Derbicus	GCA_004521655.1
ANZ48977.1	009847	Cluster9724_1clades	37	EARLPHILLIPIV_128	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXF51303.1	009848	TM	37	WELLINGTON_174	Erwinia phage Wellington	GCA_003344985.1
ANZ49527.1	009848	TM	37	KWAN_175	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QCW23150.1	009849	Cluster9726_1clades	37	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
AUR81105.1	009849	Cluster9726_1clades	37	Aphrodite1_0190	Vibrio phage Aphrodite1	GCA_002958015.1
BBI90517.1	009850	Cluster9727_1clades	37	HYO65_gp125	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90825.1	009850	Cluster9727_1clades	37	-	Tenacibaculum phage PTm5	GCA_009730715.1
QBX06422.1	009851	Cluster9728_1clades	34	BcepSaruman_009	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74390.1	009851	Cluster9728_1clades	37	BcepSauron_010	Burkholderia phage BcepSauron	GCA_005394215.1
QCW19109.1	009852	Cluster9729_1clades	37	7t3_0592	Salmonella phage 7t3	GCA_006083215.1
QIG62636.1	009852	Cluster9729_1clades	37	SEPL_023	Salmonella phage SE_PL	GCA_011067555.1
QCW23195.1	009853	Cluster9730_1clades	37	-	Vibrio phage 5 TSL-2019	GCA_006964265.1
QDH47534.1	009853	Cluster9730_1clades	37	HWC35_gp140	Vibrio phage USC-1	GCA_006864065.1
QGT54751.1	009854	Cluster9731_1clades	37	b23_0136	Synechococcus phage B23	GCA_009745195.1
QGT54381.1	009854	Cluster9731_1clades	37	b3_0137	Synechococcus phage B3	GCA_009745215.1
QGT54811.1	009855	TM	37	b23_0196	Synechococcus phage B23	GCA_009745195.1
QGT54441.1	009855	TM	37	b3_0198	Synechococcus phage B3	GCA_009745215.1
prevph1000000162	009856	Cluster9733_1clades	38	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000123	009856	Cluster9733_1clades	38	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBZ71916.1	009857	Cluster9734_1clades	36	SEA_KRADAL_17	Streptomyces phage Kradal	GCA_004799925.1
AXH66178.1	009857	Cluster9734_1clades	36	SEA_SATIS_17	Streptomyces phage Satis	GCA_003366315.1
QDJ96703.1	009858	Cluster9735_1clades	36	PS1_0192	Aeromonas phage PS1	GCA_007051165.2
QFR59336.1	009858	Cluster9735_1clades	36	PS2_0194	Aeromonas phage PS2	GCA_009388305.2
QIG57769.1	009859	SIG+TM	36	SEA_PAULODIABOLI_34	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58070.1	009859	SIG+TM	36	SEA_PAULODIABOLI_389	Microbacterium phage PauloDiaboli	GCA_011067425.1
AKF13217.1	009860	Cluster9737_1clades	35	PHIM19_312	Sinorhizobium phage phiM19	GCA_002605865.1
AKF12858.1	009860	Cluster9737_1clades	35	PHIM7_312	Sinorhizobium phage phiM7	GCA_002622405.1
AXF51425.1	009861	Cluster9738_1clades	35	WELLINGTON_209	Erwinia phage Wellington	GCA_003344985.1
ANZ49562.1	009861	Cluster9738_1clades	35	KWAN_210	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
AXF51338.1	009862	Cluster9739_1clades	35	WELLINGTON_212	Erwinia phage Wellington	GCA_003344985.1
ANZ49565.1	009862	Cluster9739_1clades	35	KWAN_213	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
BBA65183.1	009863	Cluster9740_1clades	35	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65642.1	009863	Cluster9740_1clades	35	-	Xanthomonas phage XacN1	GCA_003173815.1
QGZ14524.1	009864	Cluster9741_1clades	35	HWC77_gp161	Photobacterium phage PDCC-1	GCA_009800445.1
QAU04210.1	009864	Cluster9741_1clades	35	HWC03_gp055	Vibrio phage 2 TSL-2019	GCA_006964105.1
QBO61929.1	009865	Cluster9742_1clades	34	G17_00440	Escherichia phage vB_EcoM_G17	GCA_004521135.1
SCA80362.1	009865	Cluster9742_1clades	34	PSLUR01_00385	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
QBX32269.1	009866	Cluster9743_1clades	34	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41843.1	009866	Cluster9743_1clades	34	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
SOK58970.1	009867	Cluster9744_1clades	34	g162	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58436.1	009867	Cluster9744_1clades	34	g159	Yersinia phage fHe-Yen9-04	GCA_002990485.1
prevph1000000062	009868	Cluster9745_1clades	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000048	009868	Cluster9745_1clades	35	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prevph1000000121	009869	Cluster9746_1clades	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000090	009869	Cluster9746_1clades	35	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ASU03906.1	009870	Cluster9747_1clades	33	JOAD_9	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03661.1	009870	Cluster9747_1clades	33	RISINGSUN_9	Erwinia phage vB_EamM_RisingSun	GCA_002629045.1
AYD81428.1	009871	Cluster9748_1clades	33	SEA_JUSTBECAUSE_273	Streptomyces phage JustBecause	GCA_003613775.1
QJD53833.1	009871	Cluster9748_1clades	33	SEA_KELA_273	Streptomyces phage Kela	GCA_012934305.1
prevph1000000755	009872	Cluster9749_1clades	34	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000507	009872	Cluster9749_1clades	34	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QBX32270.1	009873	Cluster9750_1clades	31	-	Pseudomonas phage PA1C	GCA_004785505.1
QEM41844.1	009873	Cluster9750_1clades	31	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AXF51346.1	009874	Cluster9751_1clades	30	WELLINGTON_220	Erwinia phage Wellington	GCA_003344985.1
ANZ49573.1	009874	Cluster9751_1clades	30	KWAN_221	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
QBX06785.1	009875	Cluster9752_1clades	30	BcepSaruman_372	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74755.1	009875	Cluster9752_1clades	30	BcepSauron_375	Burkholderia phage BcepSauron	GCA_005394215.1
QGT54678.1	009876	Cluster9753_1clades	30	b23_0050	Synechococcus phage B23	GCA_009745195.1
QGT54308.1	009876	Cluster9753_1clades	30	b3_0050	Synechococcus phage B3	GCA_009745215.1
QIG63270.1	009877	Cluster9754_1clades	29	DAC16_37	Bacteroides phage DAC16	GCA_013387695.1
QIG63531.1	009877	Cluster9754_1clades	30	DAC19_40	Bacteroides phage DAC19	GCA_013387715.1
ARB13617.1	009878	Cluster9755_1clades	24	Ccr10_gp088	Caulobacter phage Ccr10	GCA_002619445.1
ARB13962.1	009878	Cluster9755_1clades	24	Ccr2_gp087	Caulobacter phage Ccr2	GCA_002619465.1
QDH83508.1	000000	SIG+TM	57	H1O15_gp298	Achromobacter phage Motura	GCA_006964305.1
QDH83523.1	000000	SIG+TM	70	H1O15_gp283	Achromobacter phage Motura	GCA_006964305.1
AND75308.1	000000	SIG+TM	124	ME3_147	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75323.1	000000	SIG+TM	124	ME3_162	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75358.1	000000	SIG+TM	70	ME3_197	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75369.1	000000	SIG+TM	72	ME3_208	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75442.1	000000	SIG+TM	155	ME3_281	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75164.1	000000	SIG+TM	92	ME3_3	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75478.1	000000	SIG+TM	130	ME3_317	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75166.1	000000	SIG+TM	86	ME3_5	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01746.1	000000	SIG+TM	93	-	Aeromonas phage 65.2	GCA_002618145.1
APU01745.1	000000	SIG+TM	100	-	Aeromonas phage 65.2	GCA_002618145.1
QAY01269.1	000000	SIG+TM	73	ASwh1_206	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01073.1	000000	SIG+TM	166	ASwh1_5	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01131.1	000000	SIG+TM	79	ASwh1_64	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01137.1	000000	SIG+TM	81	ASwh1_71	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01147.1	000000	SIG+TM	95	ASwh1_81	Aeromonas phage Aswh_1	GCA_004146945.1
QGY75126.1	000000	SIG+TM	141	CF8_0156	Aeromonas phage CF8	GCA_006384595.2
QDB70358.1	000000	SIG+TM	95	CF8_0190	Aeromonas phage CF8	GCA_006384595.2
QDB70359.1	000000	SIG+TM	67	CF8_0191	Aeromonas phage CF8	GCA_006384595.2
QDB70365.1	000000	SIG+TM	88	CF8_0197	Aeromonas phage CF8	GCA_006384595.2
QDJ97312.1	000000	SIG+TM	53	D6_0152	Aeromonas phage D6	GCA_007051205.2
QDJ97320.1	000000	SIG+TM	76	D6_0160	Aeromonas phage D6	GCA_007051205.2
QDJ97345.1	000000	SIG+TM	73	D6_0186	Aeromonas phage D6	GCA_007051205.2
QDJ97358.1	000000	SIG+TM	93	D6_0199	Aeromonas phage D6	GCA_007051205.2
QDJ97360.1	000000	SIG+TM	71	D6_0201	Aeromonas phage D6	GCA_007051205.2
QDJ97361.1	000000	SIG+TM	73	D6_0202	Aeromonas phage D6	GCA_007051205.2
ADQ53006.1	000000	SIG+TM	66	PX29p287	Aeromonas phage PX29	GCA_000920195.1
ADM80030.1	000000	SIG+TM	46	phiAS5_ORF0187	Aeromonas phage phiAS5	GCA_000887715.1
ADM80041.1	000000	SIG+TM	51	phiAS5_ORF0198	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53196.1	000000	SIG+TM	55	65p188	Aeromonas virus 65	GCA_000893255.1
ADQ53236.1	000000	SIG+TM	36	65p228	Aeromonas virus 65	GCA_000893255.1
ADQ53304.1	000000	SIG+TM	45	65p296	Aeromonas virus 65	GCA_000893255.1
ADQ53315.1	000000	SIG+TM	78	65p307	Aeromonas virus 65	GCA_000893255.1
ADQ53366.1	000000	SIG+TM	76	65p358	Aeromonas virus 65	GCA_000893255.1
AAQ17735.1	000000	SIG+TM	62	Aeh1ORF075c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95208.1	000000	SIG+TM	60	FDI40_gp449	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95422.1	000000	SIG+TM	52	FDI40_gp665	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95199.1	000000	SIG+TM	39	FDI40_gp440	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95134.1	000000	SIG+TM	86	FDI40_gp375	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95330.1	000000	SIG+TM	68	FDI40_gp571	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95244.1	000000	SIG+TM	79	FDI40_gp485	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83769.1	000000	SIG+TM	122	0305phi8-36p211	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44984.1	000000	SIG+TM	72	SP15_184B	Bacillus phage SP-15	GCA_001754685.1
AMM44998.1	000000	SIG+TM	103	SP15_198	Bacillus phage SP-15	GCA_001754685.1
AMM45011.1	000000	SIG+TM	128	SP15_211	Bacillus phage SP-15	GCA_001754685.1
AMM45043.1	000000	SIG+TM	51	SP15_239A	Bacillus phage SP-15	GCA_001754685.1
ALN97692.1	000000	SIG+TM	126	Bp8pS_013	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97818.1	000000	SIG+TM	55	Bp8pS_139	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97819.1	000000	SIG+TM	63	Bp8pS_140	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93587.1	000000	SIG+TM	60	G_328	Bacillus virus G	GCA_000917535.1
AEO93304.1	000000	SIG+TM	50	G_33	Bacillus virus G	GCA_000917535.1
AEO93660.1	000000	SIG+TM	93	G_401	Bacillus virus G	GCA_000917535.1
AEO93941.1	000000	SIG+TM	90	G_402	Bacillus virus G	GCA_000917535.1
AEO93699.1	000000	SIG+TM	183	G_441	Bacillus virus G	GCA_000917535.1
AEO93762.1	000000	SIG+TM	97	G_504	Bacillus virus G	GCA_000917535.1
AEO93801.1	000000	SIG+TM	64	G_545	Bacillus virus G	GCA_000917535.1
AEO93816.1	000000	SIG+TM	118	G_570	Bacillus virus G	GCA_000917535.1
AEO93820.1	000000	SIG+TM	46	G_574	Bacillus virus G	GCA_000917535.1
AEO93831.1	000000	SIG+TM	81	G_586	Bacillus virus G	GCA_000917535.1
AEO93335.1	000000	SIG+TM	84	G_64	Bacillus virus G	GCA_000917535.1
AEO93945.1	000000	SIG+TM	27	G_640	Bacillus virus G	GCA_000917535.1
AEO93906.1	000000	SIG+TM	79	G_663	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEO93342.1	000000	SIG+TM	92	G_71	Bacillus virus G	GCA_000917535.1
CCH63481.1	000000	SIG+TM	130	CP21_019	Campylobacter virus CP21	GCA_000902535.1
CCH63494.1	000000	SIG+TM	77	CP21_032	Campylobacter virus CP21	GCA_000902535.1
CCH63575.1	000000	SIG+TM	365	CP21_113	Campylobacter virus CP21	GCA_000902535.1
AXQ68390.1	000000	SIG+TM	71	CcrBL10_gp186c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68396.1	000000	SIG+TM	65	CcrBL10_gp192c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69530.1	000000	SIG+TM	63	CcrBL9_gp506	Caulobacter phage CcrBL9	GCA_003443295.1
AFU88152.1	000000	SIG+TM	72	CcrColossus_gp282	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68587.1	000000	SIG+TM	56	CcrPW_gp048	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68964.1	000000	SIG+TM	53	CcrPW_gp425c	Caulobacter phage CcrPW	GCA_003443275.1
BAE47762.1	000000	SIG+TM	61	CST064	Clostridium phage c-st	GCA_000865225.1
AIA64921.1	000000	SIG+TM	59	S13_122	Cronobacter phage S13	GCA_001503575.1
AIA64926.1	000000	SIG+TM	73	S13_127	Cronobacter phage S13	GCA_001503575.1
AIA64927.1	000000	SIG+TM	76	S13_128	Cronobacter phage S13	GCA_001503575.1
AIA64938.1	000000	SIG+TM	77	S13_139	Cronobacter phage S13	GCA_001503575.1
AIA64943.1	000000	SIG+TM	70	S13_144	Cronobacter phage S13	GCA_001503575.1
AIA64947.1	000000	SIG+TM	71	S13_148	Cronobacter phage S13	GCA_001503575.1
AIA64948.1	000000	SIG+TM	62	S13_149	Cronobacter phage S13	GCA_001503575.1
AFC21851.1	000000	SIG+TM	64	GAP32_398A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21960.1	000000	SIG+TM	65	GAP32_501	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AJK27447.1	000000	SIG+TM	1289	PTIM40_20	Cyanophage P-TIM40	GCA_001470935.1
QBZ70688.1	000000	SIG+TM	81	pETSU_107	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70735.1	000000	SIG+TM	85	pETSU_154	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70736.1	000000	SIG+TM	114	pETSU_155	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70739.1	000000	SIG+TM	61	pETSU_158	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70749.1	000000	SIG+TM	182	pETSU_168	Edwardsiella virus pEt-SU	GCA_004800915.1
AGX01947.1	000000	SIG+TM	460	CF95_gp225	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ48151.1	000000	SIG+TM	72	ASESINO_138	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ50372.1	000000	SIG+TM	63	PHOBOS_182	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ARW58703.1	000000	SIG+TM	76	Y3_063	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28507.1	000000	SIG+TM	80	YOLOSWAG_20	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28738.1	000000	SIG+TM	89	YOLOSWAG_265	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28760.1	000000	SIG+TM	172	YOLOSWAG_290	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ARM70956.1	000000	SIG+TM	123	phiC120_c251	Escherichia phage phiC120	GCA_002621185.1
QBO63915.1	000000	SIG+TM	94	Goslar_00122	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13635.1	000000	SIG+TM	100	vBEcoMphAPEC6_gp004	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13881.1	000000	SIG+TM	57	vBEcoMphAPEC6_gp252c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QGH72003.1	000000	SIG+TM	75	N1M2_140	Klebsiella phage N1M2	GCA_010092605.1
QGH72032.1	000000	SIG+TM	131	N1M2_169	Klebsiella phage N1M2	GCA_010092605.1
QGH72048.1	000000	SIG+TM	74	N1M2_185	Klebsiella phage N1M2	GCA_010092605.1
QGH72056.1	000000	SIG+TM	130	N1M2_193	Klebsiella phage N1M2	GCA_010092605.1
AFA44420.1	000000	SIG+TM	118	RaK2_00147	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44479.1	000000	SIG+TM	79	RaK2_00206	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44510.1	000000	SIG+TM	148	RaK2_00237	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44571.1	000000	SIG+TM	81	RaK2_00298	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44586.1	000000	SIG+TM	101	RaK2_00313	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44789.1	000000	SIG+TM	77	RaK2_00516	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57873.1	000000	SIG+TM	102	SEA_PAULODIABOLI_181	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57889.1	000000	SIG+TM	103	SEA_PAULODIABOLI_202	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57895.1	000000	SIG+TM	54	SEA_PAULODIABOLI_209	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57948.1	000000	SIG+TM	93	SEA_PAULODIABOLI_264	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57949.1	000000	SIG+TM	112	SEA_PAULODIABOLI_265	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57952.1	000000	SIG+TM	88	SEA_PAULODIABOLI_268	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57954.1	000000	SIG+TM	142	SEA_PAULODIABOLI_270	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57957.1	000000	SIG+TM	142	SEA_PAULODIABOLI_273	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57959.1	000000	SIG+TM	139	SEA_PAULODIABOLI_275	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57962.1	000000	SIG+TM	734	SEA_PAULODIABOLI_278	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57966.1	000000	SIG+TM	91	SEA_PAULODIABOLI_282	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57967.1	000000	SIG+TM	69	SEA_PAULODIABOLI_283	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57986.1	000000	SIG+TM	99	SEA_PAULODIABOLI_302	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57988.1	000000	SIG+TM	91	SEA_PAULODIABOLI_304	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57989.1	000000	SIG+TM	71	SEA_PAULODIABOLI_305	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57990.1	000000	SIG+TM	69	SEA_PAULODIABOLI_306	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57992.1	000000	SIG+TM	49	SEA_PAULODIABOLI_308	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58034.1	000000	SIG+TM	72	SEA_PAULODIABOLI_350	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58036.1	000000	SIG+TM	84	SEA_PAULODIABOLI_352	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58038.1	000000	SIG+TM	75	SEA_PAULODIABOLI_354	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57815.1	000000	SIG+TM	94	SEA_PAULODIABOLI_81	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72572.1	000000	SIG+TM	83	-	Myoviridae sp.	GCA_003657725.1
AXH72533.1	000000	SIG+TM	83	-	Myoviridae sp.	GCA_003657725.1
AXH72707.1	000000	SIG+TM	129	-	Myoviridae sp.	GCA_003657725.1
AXH72468.1	000000	SIG+TM	113	-	Myoviridae sp.	GCA_003657725.1
AXH72619.1	000000	SIG+TM	82	-	Myoviridae sp.	GCA_003657725.1
AXH72712.1	000000	SIG+TM	89	-	Myoviridae sp.	GCA_003657725.1
AXH72705.1	000000	SIG+TM	119	-	Myoviridae sp.	GCA_003657725.1
AXH72446.1	000000	SIG+TM	236	-	Myoviridae sp.	GCA_003657725.1
QHJ78984.1	000000	SIG+TM	130	-	Myoviridae sp.	GCA_012593985.1
QHJ79008.1	000000	SIG+TM	55	-	Myoviridae sp.	GCA_012593985.1
QHJ79023.1	000000	SIG+TM	70	-	Myoviridae sp.	GCA_012593985.1
QIG65854.1	000000	SIG+TM	168	phiOC_p189	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65857.1	000000	SIG+TM	70	phiOC_p192	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65955.1	000000	SIG+TM	54	phiOC_p313	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66027.1	000000	SIG+TM	89	phiOC_p385	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
SBV38197.1	000000	SIG+TM	62	BN7874_028	Phage NCTB	GCA_900092385.1
SBV38212.1	000000	SIG+TM	82	BN7874_043	Phage NCTB	GCA_900092385.1
SBV38328.1	000000	SIG+TM	138	BN7874_159	Phage NCTB	GCA_900092385.1
SBV38465.1	000000	SIG+TM	110	BN7874_260	Phage NCTB	GCA_900092385.1
SBV38466.1	000000	SIG+TM	81	BN7874_261	Phage NCTB	GCA_900092385.1
AIR93625.1	000000	SIG+TM	89	AVU42_gp080	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93541.1	000000	SIG+TM	66	AVU42_gp204	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93559.1	000000	SIG+TM	123	psaJF	Prochlorococcus phage P-TIM68	GCA_001503075.1
QMP24036.1	000000	SIG+TM	250	-	Proteus phage 10	GCA_014071245.1
QMP24147.1	000000	SIG+TM	77	-	Proteus phage 10	GCA_014071245.1
ABY62844.1	000000	SIG+TM	85	201phi2-1p010	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62964.1	000000	SIG+TM	77	201phi2-1p132	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63093.1	000000	SIG+TM	79	201phi2-1p265	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63174.1	000000	SIG+TM	54	201phi2-1p348	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63200.1	000000	SIG+TM	76	201phi2-1p375	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63231.1	000000	SIG+TM	83	201phi2-1p407	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63169.1	000000	SIG+TM	70	201phi2-1p469	Pseudomonas phage 201phi2-1	GCA_000875305.1
AFH14575.1	000000	SIG+TM	90	Lu11_0044	Pseudomonas phage Lu11	GCA_000897175.1
AFH14576.1	000000	SIG+TM	86	Lu11_0045	Pseudomonas phage Lu11	GCA_000897175.1
AFH14807.1	000000	SIG+TM	70	Lu11_0270	Pseudomonas phage Lu11	GCA_000897175.1
AFH14820.1	000000	SIG+TM	64	Lu11_0282	Pseudomonas phage Lu11	GCA_000897175.1
AFH14863.1	000000	SIG+TM	74	Lu11_0325	Pseudomonas phage Lu11	GCA_000897175.1
AFH14872.1	000000	SIG+TM	72	Lu11_0334	Pseudomonas phage Lu11	GCA_000897175.1
AFH14905.1	000000	SIG+TM	88	Lu11_0367	Pseudomonas phage Lu11	GCA_000897175.1
AFH14917.1	000000	SIG+TM	119	Lu11_0379	Pseudomonas phage Lu11	GCA_000897175.1
ARV77285.1	000000	SIG+TM	104	NOXIFER_116	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77286.1	000000	SIG+TM	104	NOXIFER_117	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77350.1	000000	SIG+TM	48	NOXIFER_181	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77397.1	000000	SIG+TM	176	NOXIFER_232	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77450.1	000000	SIG+TM	97	NOXIFER_285	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89608.1	000000	SIG+TM	84	OBP_171	Pseudomonas phage OBP	GCA_000896635.1
AEV89609.1	000000	SIG+TM	81	OBP_172	Pseudomonas phage OBP	GCA_000896635.1
AEV89615.1	000000	SIG+TM	78	OBP_178	Pseudomonas phage OBP	GCA_000896635.1
AEV89637.1	000000	SIG+TM	76	OBP_200	Pseudomonas phage OBP	GCA_000896635.1
AEV89649.1	000000	SIG+TM	94	OBP_212	Pseudomonas phage OBP	GCA_000896635.1
AEV89650.1	000000	SIG+TM	85	OBP_213	Pseudomonas phage OBP	GCA_000896635.1
AEV89653.1	000000	SIG+TM	129	OBP_216	Pseudomonas phage OBP	GCA_000896635.1
AEV89654.1	000000	SIG+TM	110	OBP_217	Pseudomonas phage OBP	GCA_000896635.1
AEV89669.1	000000	SIG+TM	81	OBP_232	Pseudomonas phage OBP	GCA_000896635.1
AEV89670.1	000000	SIG+TM	80	OBP_233	Pseudomonas phage OBP	GCA_000896635.1
AEV89680.1	000000	SIG+TM	71	OBP_243	Pseudomonas phage OBP	GCA_000896635.1
AEV89682.1	000000	SIG+TM	189	OBP_245	Pseudomonas phage OBP	GCA_000896635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QHJ86074.1	000000	SIG+TM	49	KKIINIFJ_00162	Pseudomonas phage PN05	GCA_009931935.1
AGS81910.1	000000	SIG+TM	88	PaBG_00026	Pseudomonas phage PaBG	GCA_000912555.1
AGS82187.1	000000	SIG+TM	87	PaBG_00316	Pseudomonas phage PaBG	GCA_000912555.1
ARV76747.1	000000	SIG+TM	53	PHABIO_116	Pseudomonas phage Phabio	GCA_002624965.1
ARV76750.1	000000	SIG+TM	70	PHABIO_119	Pseudomonas phage Phabio	GCA_002624965.1
ARV76975.1	000000	SIG+TM	77	PHABIO_344	Pseudomonas phage Phabio	GCA_002624965.1
ARV76979.1	000000	SIG+TM	76	PHABIO_348	Pseudomonas phage Phabio	GCA_002624965.1
ARV77010.1	000000	SIG+TM	57	PHABIO_379	Pseudomonas phage Phabio	GCA_002624965.1
ARV77011.1	000000	SIG+TM	73	PHABIO_380	Pseudomonas phage Phabio	GCA_002624965.1
ARV77038.1	000000	SIG+TM	87	PHABIO_407	Pseudomonas phage Phabio	GCA_002624965.1
ARV77039.1	000000	SIG+TM	75	PHABIO_408	Pseudomonas phage Phabio	GCA_002624965.1
ARV77058.1	000000	SIG+TM	84	PHABIO_427	Pseudomonas phage Phabio	GCA_002624965.1
ARV77059.1	000000	SIG+TM	79	PHABIO_428	Pseudomonas phage Phabio	GCA_002624965.1
ARV77060.1	000000	SIG+TM	70	PHABIO_429	Pseudomonas phage Phabio	GCA_002624965.1
AEH03430.1	000000	SIG+TM	71	004	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03493.1	000000	SIG+TM	74	069	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03494.1	000000	SIG+TM	96	070	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03495.1	000000	SIG+TM	86	071	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03496.1	000000	SIG+TM	78	072	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03706.1	000000	SIG+TM	88	283	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03718.1	000000	SIG+TM	113	295	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02648.1	000000	SIG+TM	57	PSA21_120	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02657.1	000000	SIG+TM	67	PSA21_130	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02669.1	000000	SIG+TM	82	PSA21_142	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02901.1	000000	SIG+TM	179	PSA21_375	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02913.1	000000	SIG+TM	72	PSA21_387	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02915.1	000000	SIG+TM	56	PSA21_389	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02608.1	000000	SIG+TM	67	PSA21_79	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02609.1	000000	SIG+TM	58	PSA21_80	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02610.1	000000	SIG+TM	80	PSA21_81	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02949.1	000000	SIG+TM	73	PSA21_82	Pseudomonas phage Psa21	GCA_004340405.1
QCG75928.1	000000	SIG+TM	70	EST35_0045	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75950.1	000000	SIG+TM	62	EST35_0067	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75963.1	000000	SIG+TM	75	EST35_0081	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76131.1	000000	SIG+TM	106	EST35_0250	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76217.1	000000	SIG+TM	151	EST35_0336	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76222.1	000000	SIG+TM	80	EST35_0341	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76264.1	000000	SIG+TM	80	EST35_0384	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76300.1	000000	SIG+TM	93	EST35_0432	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76320.1	000000	SIG+TM	102	EST35_0452	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AGC26331.1	000000	SIG+TM	69	PHIKZ117.1	Pseudomonas virus phiKZ	GCA_000842965.1
BAS04934.2	000000	SIG+TM	78	AVU11_gp142	Ralstonia phage RSF1	GCA_001500875.1
BAG41451.1	000000	SIG+TM	45	RSL1_ORF006	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41751.1	000000	SIG+TM	102	RSL1_ORF305	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41758.1	000000	SIG+TM	124	RSL1_ORF311	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44042.1	000000	SIG+TM	83	PBI_SCTP2_27	Salicola phage SCTP-2	GCA_002625545.1
ASV44328.1	000000	SIG+TM	66	PBI_SCTP2_313	Salicola phage SCTP-2	GCA_002625545.1
ASV44335.1	000000	SIG+TM	97	PBI_SCTP2_320	Salicola phage SCTP-2	GCA_002625545.1
ASV44415.1	000000	SIG+TM	80	PBI_SCTP2_400	Salicola phage SCTP-2	GCA_002625545.1
ASV44441.1	000000	SIG+TM	161	PBI_SCTP2_426	Salicola phage SCTP-2	GCA_002625545.1
ASV44446.1	000000	SIG+TM	85	PBI_SCTP2_431	Salicola phage SCTP-2	GCA_002625545.1
ASV44454.1	000000	SIG+TM	87	PBI_SCTP2_439	Salicola phage SCTP-2	GCA_002625545.1
ASV44505.1	000000	SIG+TM	80	PBI_SCTP2_490	Salicola phage SCTP-2	GCA_002625545.1
QCW18719.1	000000	SIG+TM	51	7t3_0198	Salmonella phage 7t3	GCA_006083215.1
AXF51069.1	000000	SIG+TM	67	MLDJOKPK_00039	Salmonella phage SPAsTU	GCA_003183805.1
QKE54352.1	000000	SIG+TM	96	ACSA002_0380	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54354.1	000000	SIG+TM	74	ACSA002_0400	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54398.1	000000	SIG+TM	99	ACSA002_0840	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54438.1	000000	SIG+TM	125	ACSA002_1240	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54444.1	000000	SIG+TM	121	ACSA002_1300	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AQW88544.1	000000	SIG+TM	100	BF_0019	Serratia phage BF	GCA_002619745.1
AQW89002.1	000000	SIG+TM	84	BF_0477	Serratia phage BF	GCA_002619745.1
AGR47755.1	000000	SIG+TM	199	SmphiM12_123	Sinorhizobium phage phiM12	GCA_001023565.1
AFF28159.1	000000	SIG+TM	70	PAU_161	Sphingomonas phage PAU	GCA_000902455.1
AFF28285.1	000000	SIG+TM	66	PAU_287	Sphingomonas phage PAU	GCA_000902455.1
AFF28287.1	000000	SIG+TM	109	PAU_289	Sphingomonas phage PAU	GCA_000902455.1
AIX30569.1	000000	SIG+TM	103	Syn7803US37_92	Synechococcus phage ACG-2014f	GCA_002594065.1
BAX25546.1	000000	SIG+TM	207	BPT24_005	Tenacibaculum phage pT24	GCA_002611925.1
BAV39181.1	000000	SIG+TM	123	BPT24_058	Tenacibaculum phage pT24	GCA_002611925.1
BAV39244.1	000000	SIG+TM	120	BPT24_119	Tenacibaculum phage pT24	GCA_002611925.1
BAV39246.1	000000	SIG+TM	127	BPT24_121	Tenacibaculum phage pT24	GCA_002611925.1
BAV39383.1	000000	SIG+TM	48	BPT24_265	Tenacibaculum phage pT24	GCA_002611925.1
BAV39409.1	000000	SIG+TM	79	BPT24_291	Tenacibaculum phage pT24	GCA_002611925.1
AXH70956.1	000000	SIG+TM	77	-	Vibrio phage BONAISHI	GCA_003441475.1
QIW90722.1	000000	SIG+TM	107	GCAPEGMB_00403	Vibrio phage V07	GCA_012361095.1
QIW90764.1	000000	SIG+TM	99	GCAPEGMB_00445	Vibrio phage V07	GCA_012361095.1
QIW90815.1	000000	SIG+TM	95	GCAPEGMB_00497	Vibrio phage V07	GCA_012361095.1
AJT61028.1	000000	SIG+TM	98	AVU32_gp187	Vibrio phage ValKK3	GCA_001501635.1
AGN30101.1	000000	SIG+TM	71	VPFG_00099	Vibrio phage nt-1	GCA_000910195.2
AGN30221.1	000000	SIG+TM	58	VPFG_00221	Vibrio phage nt-1	GCA_000910195.2
BAW98232.1	000000	SIG+TM	57	FDH33_gp023	Vibrio phage pTD1	GCA_002618825.1
AQT28010.1	000000	SIG+TM	85	pVa21_069	Vibrio phage pVa-21	GCA_002619305.1
AQT28102.1	000000	SIG+TM	187	pVa21_161	Vibrio phage pVa-21	GCA_002619305.1
AQT28134.1	000000	SIG+TM	87	pVa21_193	Vibrio phage pVa-21	GCA_002619305.1
ALY07232.1	000000	SIG+TM	89	VmeM32_00246	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI20959.1	000000	SIG+TM	127	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65528.1	000000	SIG+TM	148	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65593.1	000000	SIG+TM	74	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96318.1	000000	SIG+TM	95	Xoosp13_131	Xanthomonas phage Xoo-sp13	GCA_013364725.1
CCE26119.1	000000	SIG+TM	169	g095	Yersinia phage phiR1-37	GCA_000895615.1
CCE26168.1	000000	SIG+TM	526	g144	Yersinia phage phiR1-37	GCA_000895615.1
CCE26179.1	000000	SIG+TM	85	g155	Yersinia phage phiR1-37	GCA_000895615.1
CCE26182.1	000000	SIG+TM	118	g158	Yersinia phage phiR1-37	GCA_000895615.1
CCE26238.1	000000	SIG+TM	123	g215	Yersinia phage phiR1-37	GCA_000895615.1
CCE26285.1	000000	SIG+TM	82	g262	Yersinia phage phiR1-37	GCA_000895615.1
CCE26325.1	000000	SIG+TM	109	g302	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000035	000000	SIG+TM	86	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000269	000000	SIG+TM	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
QDH83727.1	000000	TM	65	H1O15_gp126	Achromobacter phage Motura	GCA_006964305.1
QDH83457.1	000000	TM	83	H1O15_gp049	Achromobacter phage Motura	GCA_006964305.1
QDH83527.1	000000	TM	340	H1O15_gp279	Achromobacter phage Motura	GCA_006964305.1
AND75173.1	000000	TM	546	ME3_12	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75409.1	000000	TM	163	ME3_248	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75461.1	000000	TM	65	ME3_300	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUE22712.1	000000	TM	58	Ah1_00192	Aeromonas phage Ah1	GCA_002957415.1
ADM80052.1	000000	TM	48	phiAS5_ORF0209	Aeromonas phage phiAS5	GCA_000887715.1
ADM80100.1	000000	TM	115	phiAS5_ORF0257	Aeromonas phage phiAS5	GCA_000887715.1
AUZ94900.1	000000	TM	72	FDI40_gp098	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95400.1	000000	TM	44	FDI40_gp641	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95427.1	000000	TM	93	FDI40_gp674	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95132.1	000000	TM	39	FDI40_gp373	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95396.1	000000	TM	121	FDI40_gp637	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94860.1	000000	TM	81	FDI40_gp048	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95420.1	000000	TM	127	FDI40_gp663	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83763.1	000000	TM	171	0305phi8-36p205	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM45018.1	000000	TM	55	SP15_217A	Bacillus phage SP-15	GCA_001754685.1
AMM45053.1	000000	TM	47	SP15_248	Bacillus phage SP-15	GCA_001754685.1
AMM45088.1	000000	TM	94	SP15_280	Bacillus phage SP-15	GCA_001754685.1
AEO93407.1	000000	TM	107	G_145	Bacillus virus G	GCA_000917535.1
AEO93939.1	000000	TM	60	G_148	Bacillus virus G	GCA_000917535.1
AEO93411.1	000000	TM	45	G_151	Bacillus virus G	GCA_000917535.1
AEO93474.1	000000	TM	108	G_215	Bacillus virus G	GCA_000917535.1
AEO93785.1	000000	TM	37	G_527	Bacillus virus G	GCA_000917535.1
CCH63484.1	000000	TM	152	CP21_022	Campylobacter virus CP21	GCA_000902535.1
CCH63566.1	000000	TM	149	CP21_104	Campylobacter virus CP21	GCA_000902535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
CCH63639.1	000000	TM	70	CP21_177	Campylobacter virus CP21	GCA_000902535.1
AFU87892.1	000000	TM	24	CcrColossus_gp022	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68771.1	000000	TM	37	CcrPW_gp232	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68861.1	000000	TM	114	CcrPW_gp322	Caulobacter phage CcrPW	GCA_003443275.1
BAE47699.1	000000	TM	45	CST001	Clostridium phage c-st	GCA_000865225.1
BAE47707.1	000000	TM	69	CST009	Clostridium phage c-st	GCA_000865225.1
BAE47767.1	000000	TM	240	CST069	Clostridium phage c-st	GCA_000865225.1
BAE47786.1	000000	TM	84	CST088	Clostridium phage c-st	GCA_000865225.1
BAE47801.1	000000	TM	122	CST103	Clostridium phage c-st	GCA_000865225.1
BAE47885.1	000000	TM	59	CST187	Clostridium phage c-st	GCA_000865225.1
BAE47890.1	000000	TM	58	CST192	Clostridium phage c-st	GCA_000865225.1
AGH56819.1	000000	TM	66	CPXG_00016	Cyanophage P-RSM6	GCA_000906155.1
AJK27567.1	000000	TM	56	PTIM40_140	Cyanophage P-TIM40	GCA_001470935.1
AJK27625.1	000000	TM	45	PTIM40_216	Cyanophage P-TIM40	GCA_001470935.1
AJK27628.1	000000	TM	32	PTIM40_222	Cyanophage P-TIM40	GCA_001470935.1
AMO43102.1	000000	TM	38	R1080702_093	Cyanophage S-RIM32	GCA_001754165.1
AGH07481.1	000000	TM	55	CYVG_00037	Cyanophage S-SSM6a	GCA_002710385.1
AGG54445.1	000000	TM	63	CYWG_00161	Cyanophage S-SSM6b	GCA_002710425.1
AXG67103.1	000000	TM	71	AD1_059	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
QBZ70691.1	000000	TM	107	pETSU_110	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59672.1	000000	TM	349	SEGD1_021	Enterobacteria phage SEGD1	GCA_002601865.1
AGX01879.1	000000	TM	181	CF95_gp157	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01859.1	000000	TM	267	CF95_gp137	Erwinia phage PhiEaH1	GCA_000914555.1
ANZ48034.1	000000	TM	74	ASESINO_21	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48462.1	000000	TM	50	CAITLIN_167	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48741.1	000000	TM	44	CHRISDB_179	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
AQT28532.1	000000	TM	77	YOLOSWAG_48	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14160.1	000000	TM	61	PBI_121Q_270	Escherichia phage 121Q	GCA_000926855.1
AIT13979.1	000000	TM	50	PBI_121Q_82	Escherichia phage 121Q	GCA_000926855.1
BBM61799.1	000000	TM	62	EO157G_2100	Escherichia phage SP27	GCA_008033345.1
BBM62112.1	000000	TM	83	EO157G_5230	Escherichia phage SP27	GCA_008033345.1
QBO63797.1	000000	TM	218	Goslar_00004	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63807.1	000000	TM	129	Goslar_00014	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QGH72031.1	000000	TM	208	N1M2_168	Klebsiella phage N1M2	GCA_010092605.1
AFA44675.1	000000	TM	86	RaK2_00402	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44735.1	000000	TM	103	RaK2_00462	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57840.1	000000	TM	191	SEA_PAULODIABOLI_106	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72671.1	000000	TM	93	-	Myoviridae sp.	GCA_003657725.1
AXH72703.1	000000	TM	122	-	Myoviridae sp.	GCA_003657725.1
AXH72745.1	000000	TM	81	-	Myoviridae sp.	GCA_003657725.1
AXH72508.1	000000	TM	180	-	Myoviridae sp.	GCA_003657725.1
AXH72713.1	000000	TM	84	-	Myoviridae sp.	GCA_003657725.1
AXH72717.1	000000	TM	85	-	Myoviridae sp.	GCA_003657725.1
AXH72464.1	000000	TM	94	-	Myoviridae sp.	GCA_003657725.1
AXH72387.1	000000	TM	87	-	Myoviridae sp.	GCA_003657725.1
AXH72711.1	000000	TM	107	-	Myoviridae sp.	GCA_003657725.1
AXH72380.1	000000	TM	157	-	Myoviridae sp.	GCA_003657725.1
AXH72714.1	000000	TM	96	-	Myoviridae sp.	GCA_003657725.1
AXH72706.1	000000	TM	95	-	Myoviridae sp.	GCA_003657725.1
QIG65771.1	000000	TM	131	phiOC_p106	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65833.1	000000	TM	74	phiOC_p168	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65972.1	000000	TM	90	phiOC_p330	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66033.1	000000	TM	92	phiOC_p391	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66034.1	000000	TM	45	phiOC_p392	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66041.1	000000	TM	117	phiOC_p399	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM44104.1	000000	TM	53	CBB_541	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38293.1	000000	TM	135	BN7874_124	Phage NCTB	GCA_900092385.1
AIR93527.1	000000	TM	381	AVU42_gp190	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93628.1	000000	TM	63	AVU42_gp099	Prochlorococcus phage P-TIM68	GCA_001503075.1
QMP24132.1	000000	TM	195	-	Proteus phage 10	GCA_014071245.1
QMP24072.1	000000	TM	65	-	Proteus phage 10	GCA_014071245.1
QMP24067.1	000000	TM	108	-	Proteus phage 10	GCA_014071245.1
ABY62904.1	000000	TM	71	201phi2-1p071	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62996.1	000000	TM	58	201phi2-1p166	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63018.1	000000	TM	39	201phi2-1p188	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63079.1	000000	TM	41	201phi2-1p251	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63081.1	000000	TM	150	201phi2-1p253	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63082.1	000000	TM	86	201phi2-1p254	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27243.1	000000	TM	294	PPEV_gp149	Pseudomonas phage EL	GCA_000866825.1
AFH14605.1	000000	TM	446	Lu11_0073	Pseudomonas phage Lu11	GCA_000897175.1
AFH14813.1	000000	TM	220	Lu11_0276	Pseudomonas phage Lu11	GCA_000897175.1
ARV77351.1	000000	TM	38	NOXIFER_182	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77473.1	000000	TM	246	NOXIFER_308	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89568.1	000000	TM	211	OBP_131	Pseudomonas phage OBP	GCA_000896635.1
QHJ85924.1	000000	TM	109	KKIINIFJ_00012	Pseudomonas phage PN05	GCA_009931935.1
AGS81986.1	000000	TM	211	PaBG_00101	Pseudomonas phage PaBG	GCA_000912555.1
AGS82016.1	000000	TM	296	PaBG_00132	Pseudomonas phage PaBG	GCA_000912555.1
AGS82099.2	000000	TM	292	PaBG_00224	Pseudomonas phage PaBG	GCA_000912555.1
ARV76780.1	000000	TM	59	PHABIO_149	Pseudomonas phage Phabio	GCA_002624965.1
ARV76781.1	000000	TM	54	PHABIO_150	Pseudomonas phage Phabio	GCA_002624965.1
ARV76874.1	000000	TM	156	PHABIO_243	Pseudomonas phage Phabio	GCA_002624965.1
ARV76980.1	000000	TM	238	PHABIO_349	Pseudomonas phage Phabio	GCA_002624965.1
ARV77066.1	000000	TM	49	PHABIO_435	Pseudomonas phage Phabio	GCA_002624965.1
AEH03536.1	000000	TM	118	112	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02643.1	000000	TM	55	PSA21_115	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02647.1	000000	TM	61	PSA21_119	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02667.1	000000	TM	108	PSA21_140	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02755.1	000000	TM	57	PSA21_229	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02837.1	000000	TM	97	PSA21_311	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02573.1	000000	TM	115	PSA21_43	Pseudomonas phage Psa21	GCA_004340405.1
QCG75918.1	000000	TM	35	EST35_0034	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75953.1	000000	TM	78	EST35_0071	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75974.1	000000	TM	40	EST35_0092	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75991.1	000000	TM	58	EST35_0109	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76166.1	000000	TM	166	EST35_0285	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76214.1	000000	TM	102	EST35_0333	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76215.1	000000	TM	178	EST35_0334	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76234.1	000000	TM	42	EST35_0354	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76298.1	000000	TM	58	EST35_0430	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76304.1	000000	TM	110	EST35_0436	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76306.1	000000	TM	119	EST35_0438	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM42019.1	000000	TM	92	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
BAU71409.1	000000	TM	160	-	Ralstonia phage RSL2	GCA_001503055.1
BAG41695.1	000000	TM	66	RSL1_ORF247	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41542.1	000000	TM	51	RSL1_ORF097	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41477.1	000000	TM	99	RSL1_ORF032	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44294.1	000000	TM	158	PBI_SCTP2_279	Salicola phage SCTP-2	GCA_002625545.1
ASV44295.1	000000	TM	55	PBI_SCTP2_280	Salicola phage SCTP-2	GCA_002625545.1
ASV44314.1	000000	TM	72	PBI_SCTP2_299	Salicola phage SCTP-2	GCA_002625545.1
ASV44393.1	000000	TM	42	PBI_SCTP2_378	Salicola phage SCTP-2	GCA_002625545.1
ASV44394.1	000000	TM	45	PBI_SCTP2_379	Salicola phage SCTP-2	GCA_002625545.1
ASV44053.1	000000	TM	79	PBI_SCTP2_38	Salicola phage SCTP-2	GCA_002625545.1
ASV44461.1	000000	TM	190	PBI_SCTP2_446	Salicola phage SCTP-2	GCA_002625545.1
QCW18662.1	000000	TM	84	7t3_0141	Salmonella phage 7t3	GCA_006083215.1
QCW18813.1	000000	TM	51	7t3_0292	Salmonella phage 7t3	GCA_006083215.1
QCW18541.1	000000	TM	31	7t3_08	Salmonella phage 7t3	GCA_006083215.1
AXF51136.1	000000	TM	30	MLDJOKPK_00287	Salmonella phage SPAsTU	GCA_003183805.1
AQW88889.1	000000	TM	78	BF_0364	Serratia phage BF	GCA_002619745.1
QDB71038.1	000000	TM	90	CPT_Moabite_006	Serratia phage Moabite	GCA_006384735.1
QDB71243.1	000000	TM	192	CPT_Moabite_213	Serratia phage Moabite	GCA_006384735.1
AIF27791.1	000000	TM	60	SmphiM12_498	Sinorhizobium phage phiM12	GCA_001023565.1
AIF27788.1	000000	TM	51	SmphiM12_502	Sinorhizobium phage phiM12	GCA_001023565.1
AIF27790.1	000000	TM	42	SmphiM12_503	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13650.1	000000	TM	191	PHIN3_387	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28201.1	000000	TM	66	PAU_203	Sphingomonas phage PAU	GCA_000902455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFF28289.1	000000	TM	140	PAU_292	Sphingomonas phage PAU	GCA_000902455.1
AFF28044.1	000000	TM	63	PAU_46	Sphingomonas phage PAU	GCA_000902455.1
AIX30493.1	000000	TM	140	Syn7803US37_16	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30516.1	000000	TM	136	Syn7803US37_39	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30533.1	000000	TM	95	Syn7803US37_56	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30547.1	000000	TM	181	Syn7803US37_70	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76281.1	000000	TM	77	PBI_BELLAMY_245	Synechococcus phage Bellamy	GCA_002627525.1
AXQ70491.1	000000	TM	42	HOU04_gp092	Synechococcus phage S-T4	GCA_003443335.1
QJT70137.1	000000	TM	57	SynMITS9220M01_124	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BAV39205.1	000000	TM	240	BPT24_080	Tenacibaculum phage pT24	GCA_002611925.1
BAV39206.1	000000	TM	254	BPT24_081	Tenacibaculum phage pT24	GCA_002611925.1
BAX25554.1	000000	TM	135	BPT24_106	Tenacibaculum phage pT24	GCA_002611925.1
BAV39237.1	000000	TM	129	BPT24_112	Tenacibaculum phage pT24	GCA_002611925.1
BAV39405.1	000000	TM	45	HYP10_gp240	Tenacibaculum phage pT24	GCA_002611925.1
AXH70878.1	000000	TM	85	-	Vibrio phage BONAISHI	GCA_003441475.1
QIW90716.1	000000	TM	164	GCAPEGMB_00397	Vibrio phage V07	GCA_012361095.1
BAW98335.1	000000	TM	45	FDH33_gp126	Vibrio phage pTD1	GCA_002618825.1
BAW98266.1	000000	TM	156	FDH33_gp057	Vibrio phage pTD1	GCA_002618825.1
AQT28050.1	000000	TM	414	pVa21_109	Vibrio phage pVa-21	GCA_002619305.1
ALP47328.1	000000	TM	45	phiGrn1_0033	Vibrio phage phi-Grn1	GCA_002757115.1
ALY07079.1	000000	TM	127	VmeM32_00090	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21048.1	000000	TM	41	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65575.1	000000	TM	75	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96263.1	000000	TM	38	Xoosp13_76	Xanthomonas phage Xoo-sp13	GCA_013364725.1
CCE26117.1	000000	TM	165	g093	Yersinia phage phiR1-37	GCA_000895615.1
CCE26215.1	000000	TM	440	g191	Yersinia phage phiR1-37	GCA_000895615.1
CCE26241.1	000000	TM	133	g218	Yersinia phage phiR1-37	GCA_000895615.1
CCE26277.1	000000	TM	121	g254	Yersinia phage phiR1-37	GCA_000895615.1
CCE26377.1	000000	TM	85	g354	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000097	000000	TM	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000476	000000	TM	228	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000693	000000	TM	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000241	000000	TM	61	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDH83530.1	000000	SIG+TM+TM	82	H1O15_gp258	Achromobacter phage Motura	GCA_006964305.1
AND75353.1	000000	SIG+TM+TM	165	ME3_192	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QDB70368.1	000000	SIG+TM+TM	96	CF8_0200	Aeromonas phage CF8	GCA_006384595.2
QGY75130.1	000000	SIG+TM+TM	107	CF8_0201	Aeromonas phage CF8	GCA_006384595.2
AUZ95069.1	000000	SIG+TM+TM	296	FDI40_gp300	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95135.1	000000	SIG+TM+TM	110	FDI40_gp376	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83679.1	000000	SIG+TM+TM	100	0306phi8-36p121	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44806.1	000000	SIG+TM+TM	90	SP15_007A	Bacillus phage SP-15	GCA_001754685.1
AMM44815.1	000000	SIG+TM+TM	159	SP15_016	Bacillus phage SP-15	GCA_001754685.1
AEO93295.1	000000	SIG+TM+TM	173	G_24	Bacillus virus G	GCA_000917535.1
AEO93521.1	000000	SIG+TM+TM	161	G_262	Bacillus virus G	GCA_000917535.1
BAE47803.1	000000	SIG+TM+TM	107	CST105	Clostridium phage c-st	GCA_000865225.1
BAE47819.1	000000	SIG+TM+TM	209	CST121	Clostridium phage c-st	GCA_000865225.1
BAE47896.1	000000	SIG+TM+TM	183	CST198	Clostridium phage c-st	GCA_000865225.1
AIA64873.1	000000	SIG+TM+TM	123	S13_074	Cronobacter phage S13	GCA_001503575.1
AGH57008.1	000000	SIG+TM+TM	836	CPXG_00205	Cyanophage P-RSM6	GCA_000906155.1
AGH07628.1	000000	SIG+TM+TM	95	CYVG_00185	Cyanophage S-SSM6a	GCA_002710385.1
QAY00831.1	000000	SIG+TM+TM	87	Ecwhy1_559	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00836.1	000000	SIG+TM+TM	78	Ecwhy1_564	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC35229.1	000000	SIG+TM+TM	247	ACQ29_gp549	Escherichia phage PBECO4	GCA_001041035.1
ARM70948.1	000000	SIG+TM+TM	163	phiC120_c243	Escherichia phage phiC120	GCA_002621185.1
AFA44513.1	000000	SIG+TM+TM	142	RaK2_00240	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44553.1	000000	SIG+TM+TM	107	RaK2_00280	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44566.1	000000	SIG+TM+TM	89	RaK2_00293	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44587.1	000000	SIG+TM+TM	117	RaK2_00314	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44589.1	000000	SIG+TM+TM	114	RaK2_00316	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57839.1	000000	SIG+TM+TM	151	SEA_PAULODIABOLI_105	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72741.1	000000	SIG+TM+TM	118	-	Myoviridae sp.	GCA_003657725.1
AXH72431.1	000000	SIG+TM+TM	105	-	Myoviridae sp.	GCA_003657725.1
AXH72486.1	000000	SIG+TM+TM	158	-	Myoviridae sp.	GCA_003657725.1
AXH72617.1	000000	SIG+TM+TM	158	-	Myoviridae sp.	GCA_003657725.1
AXH72721.1	000000	SIG+TM+TM	95	-	Myoviridae sp.	GCA_003657725.1
QHJ79066.1	000000	SIG+TM+TM	112	-	Myoviridae sp.	GCA_012593985.1
QIG66053.1	000000	SIG+TM+TM	125	phiOC_p411	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QMP24039.1	000000	SIG+TM+TM	170	-	Proteus phage 10	GCA_014071245.1
AFH14844.1	000000	SIG+TM+TM	98	Lu11_0306	Pseudomonas phage Lu11	GCA_000897175.1
QCG75920.1	000000	SIG+TM+TM	73	EST35_0037	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76257.1	000000	SIG+TM+TM	109	EST35_0377	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44039.1	000000	SIG+TM+TM	374	PBI_SCTP2_24	Salicola phage SCTP-2	GCA_002625545.1
QFP93227.1	000000	SIG+TM+TM	124	-	Serratia phage PCH45	GCA_009187865.1
QFP93223.1	000000	SIG+TM+TM	128	-	Serratia phage PCH45	GCA_009187865.1
QFP93241.1	000000	SIG+TM+TM	109	-	Serratia phage PCH45	GCA_009187865.1
AFF28175.1	000000	SIG+TM+TM	183	PAU_177	Sphingomonas phage PAU	GCA_000902455.1
AFF28256.1	000000	SIG+TM+TM	174	PAU_258	Sphingomonas phage PAU	GCA_000902455.1
AXH70869.1	000000	SIG+TM+TM	181	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70868.1	000000	SIG+TM+TM	90	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71001.1	000000	SIG+TM+TM	128	-	Vibrio phage BONAISHI	GCA_003441475.1
QIW90735.1	000000	SIG+TM+TM	95	GCAPEGMB_00416	Vibrio phage V07	GCA_012361095.1
QIW90740.1	000000	SIG+TM+TM	110	GCAPEGMB_00421	Vibrio phage V07	GCA_012361095.1
QNI21241.1	000000	SIG+TM+TM	136	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65588.1	000000	SIG+TM+TM	107	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96294.1	000000	SIG+TM+TM	110	Xoosp13_107	Xanthomonas phage Xoo-sp13	GCA_013364725.1
CCE26177.1	000000	SIG+TM+TM	103	g153	Yersinia phage phiR1-37	GCA_000895615.1
CCE26329.1	000000	SIG+TM+TM	75	g306	Yersinia phage phiR1-37	GCA_000895615.1
QDH83726.1	000000	TM+TM	132	H1O15_gp127	Achromobacter phage Motura	GCA_006964305.1
AND75276.1	000000	TM+TM	99	ME3_115	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AAQ17783.1	000000	TM+TM	72	Aeh1fORF02c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95247.1	000000	TM+TM	237	FDI40_gp488	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83790.1	000000	TM+TM	145	0305phi8-36p232	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44958.1	000000	TM+TM	87	SP15_160	Bacillus phage SP-15	GCA_001754685.1
AMM45111.1	000000	TM+TM	110	SP15_303	Bacillus phage SP-15	GCA_001754685.1
AEO93503.1	000000	TM+TM	63	G_244	Bacillus virus G	GCA_000917535.1
AEO93781.1	000000	TM+TM	110	G_523	Bacillus virus G	GCA_000917535.1
CCH63463.1	000000	TM+TM	102	CP21_001	Campylobacter virus CP21	GCA_000902535.1
BAE47821.1	000000	TM+TM	160	CST123	Clostridium phage c-st	GCA_000865225.1
QBZ70717.1	000000	TM+TM	126	pETSU_136	Edwardsiella virus pEt-SU	GCA_004800915.1
AXF51350.1	000000	TM+TM	117	WELLINGTON_224	Erwinia phage Wellington	GCA_003344985.1
AQT28704.1	000000	TM+TM	141	YOLOSWAG_226	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QGH72046.1	000000	TM+TM	75	N1M2_183	Klebsiella phage N1M2	GCA_010092605.1
AFA44774.1	000000	TM+TM	88	RaK2_00501	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57987.1	000000	TM+TM	123	SEA_PAULODIABOLI_303	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72510.1	000000	TM+TM	129	-	Myoviridae sp.	GCA_003657725.1
AXH72499.1	000000	TM+TM	157	-	Myoviridae sp.	GCA_003657725.1
QIG65776.1	000000	TM+TM	110	phiOC_p111	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AIR93563.1	000000	TM+TM	82	psaK	Prochlorococcus phage P-TIM68	GCA_001503075.1
ABY62845.1	000000	TM+TM	91	201phi2-1p011	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63092.1	000000	TM+TM	89	201phi2-1p264	Pseudomonas phage 201phi2-1	GCA_000875305.1
AEV89672.1	000000	TM+TM	91	OBP_235	Pseudomonas phage OBP	GCA_000896635.1
QHJ86162.1	000000	TM+TM	193	KKIINIFJ_00252	Pseudomonas phage PN05	GCA_009931935.1
ARV77057.1	000000	TM+TM	97	PHABIO_426	Pseudomonas phage Phabio	GCA_002624965.1
QCG76053.1	000000	TM+TM	87	EST35_0172	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76316.1	000000	TM+TM	97	EST35_0448	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAG41450.1	000000	TM+TM	74	RSL1_ORF005	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44199.1	000000	TM+TM	401	PBI_SCTP2_184	Salicola phage SCTP-2	GCA_002625545.1
ASV44315.1	000000	TM+TM	142	PBI_SCTP2_300	Salicola phage SCTP-2	GCA_002625545.1
ASV44398.1	000000	TM+TM	130	PBI_SCTP2_383	Salicola phage SCTP-2	GCA_002625545.1
ASV44423.1	000000	TM+TM	85	PBI_SCTP2_408	Salicola phage SCTP-2	GCA_002625545.1
QFP93232.1	000000	TM+TM	117	-	Serratia phage PCH45	GCA_009187865.1
AFF28041.1	000000	TM+TM	109	PAU_43	Sphingomonas phage PAU	GCA_000902455.1
AIX30606.1	000000	TM+TM	203	Syn7803US37_129	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30628.1	000000	TM+TM	97	Syn7803US37_151	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30546.1	000000	TM+TM	169	Syn7803US37_69	Synechococcus phage ACG-2014f	GCA_002594065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH70914.1	000000	TM+TM	121	-	Vibrio phage BONAISHI	GCA_003441475.1
QAU04478.1	000000	TM+TM	252	ValB1MD_091	Vibrio phage ValB1MD	GCA_004138815.1
AQT27963.1	000000	TM+TM	171	pVa21_021	Vibrio phage pVa-21	GCA_002619305.1
ALY07108.1	000000	TM+TM	564	VmeM32_00121	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07228.1	000000	TM+TM	82	VmeM32_00242	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21118.1	000000	TM+TM	138	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21068.1	000000	TM+TM	63	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26330.1	000000	TM+TM	200	g307	Yersinia phage phiR1-37	GCA_000895615.1
CCE26340.1	000000	TM+TM	70	g317	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000267	000000	TM+TM	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000469	000000	TM+TM	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000829	000000	TM+TM	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000410	000000	TM+TM	962	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AND75165.1	000000	SIG+TM+TM+TM	145	ME3_4	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AUZ95128.1	000000	SIG+TM+TM+TM	188	FDI40_gp369	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95129.1	000000	SIG+TM+TM+TM	183	FDI40_gp370	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95131.1	000000	SIG+TM+TM+TM	203	FDI40_gp372	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83762.1	000000	SIG+TM+TM+TM	171	0305phi8-36p204	Bacillus phage 0305phi8-36	GCA_000871045.1
ALN97720.1	000000	SIG+TM+TM+TM	133	Bp8pS_041	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93319.1	000000	SIG+TM+TM+TM	137	G_48	Bacillus virus G	GCA_000917535.1
AQT28669.1	000000	SIG+TM+TM+TM	110	YOLOSWAG_190	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
QBO63893.1	000000	SIG+TM+TM+TM	123	Goslar_00100	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QIG57905.1	000000	SIG+TM+TM+TM	159	SEA_PAULODIABOLI_220	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72596.1	000000	SIG+TM+TM+TM	165	-	Myoviridae sp.	GCA_003657725.1
CAG27176.1	000000	SIG+TM+TM+TM	118	PPEV_gp082	Pseudomonas phage EL	GCA_000866825.1
ASV44226.1	000000	SIG+TM+TM+TM	122	PBI_SCTP2_211	Salicola phage SCTP-2	GCA_002625545.1
ASV44525.1	000000	SIG+TM+TM+TM	130	PBI_SCTP2_510	Salicola phage SCTP-2	GCA_002625545.1
QFP93238.1	000000	SIG+TM+TM+TM	112	-	Serratia phage PCH45	GCA_009187865.1
AFF28102.1	000000	SIG+TM+TM+TM	194	PAU_104	Sphingomonas phage PAU	GCA_000902455.1
BAV39140.1	000000	SIG+TM+TM+TM	186	BPT24_018	Tenacibaculum phage pT24	GCA_002611925.1
AXH71033.1	000000	SIG+TM+TM+TM	127	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70866.1	000000	SIG+TM+TM+TM	134	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70865.1	000000	SIG+TM+TM+TM	107	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21240.1	000000	SIG+TM+TM+TM	135	-	Vibrio phage vB_pir03	GCA_014319855.1
CCE26313.1	000000	SIG+TM+TM+TM	116	g290	Yersinia phage phiR1-37	GCA_000895615.1
QDH83696.1	000000	TM+TM+TM	133	H1O15_gp265	Achromobacter phage Motura	GCA_006964305.1
ADQ53174.1	000000	TM+TM+TM	141	65p166	Aeromonas virus 65	GCA_000893255.1
AUZ94979.1	000000	TM+TM+TM	845	FDI40_gp197	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94975.1	000000	TM+TM+TM	152	FDI40_gp193	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95293.1	000000	TM+TM+TM	170	FDI40_gp534	Agrobacterium phage Atu_ph07	GCA_002628245.1
AFU86735.1	000000	TM+TM+TM	107	CcrRogue_gp253	Caulobacter virus Rogue	GCA_000900555.1
AXH72906.1	000000	TM+TM+TM	230	-	Myoviridae sp.	GCA_003657725.1
AXH72649.1	000000	TM+TM+TM	154	-	Myoviridae sp.	GCA_003657725.1
QMP24073.1	000000	TM+TM+TM	130	-	Proteus phage 10	GCA_014071245.1
QCG75966.1	000000	TM+TM+TM	114	EST35_0084	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ASV44468.1	000000	TM+TM+TM	284	PBI_SCTP2_453	Salicola phage SCTP-2	GCA_002625545.1
QKE54443.1	000000	TM+TM+TM	209	ACSA002_1290	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AFF28011.1	000000	TM+TM+TM	127	PAU_13	Sphingomonas phage PAU	GCA_000902455.1
AIX30487.1	000000	TM+TM+TM	644	Syn7803US37_10	Synechococcus phage ACG-2014f	GCA_002594065.1
ASR76081.1	000000	TM+TM+TM	130	PBI_BELLAMY_36	Synechococcus phage Bellamy	GCA_002627525.1
BAV39125.1	000000	TM+TM+TM	172	BPT24_003	Tenacibaculum phage pT24	GCA_002611925.1
ABS83644.1	000000	HTH	143	0305phi8-36p084	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93333.1	000000	HTH	72	G_62	Bacillus virus G	GCA_000917535.1
BAE47837.1	000000	HTH	69	CST139	Clostridium phage c-st	GCA_000865225.1
BAE47848.1	000000	HTH	184	CST150	Clostridium phage c-st	GCA_000865225.1
AFH14855.1	000000	HTH	108	Lu11_0317	Pseudomonas phage Lu11	GCA_000897175.1
QHJ86076.1	000000	HTH	82	KKIINIFJ_00164	Pseudomonas phage PN05	GCA_009931935.1
BAG41762.2	000000	HTH	340	RSL1_ORF315	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41461.1	000000	HTH	117	RSL1_ORF016	Ralstonia phage phiRSL1	GCA_000879455.1
QDB71095.1	000000	HTH	247	CPT_Moabite_063	Serratia phage Moabite	GCA_006384735.1
BAV39221.1	000000	HTH	86	BPT24_096	Tenacibaculum phage pT24	GCA_002611925.1
AQT27948.1	000000	HTH	152	pVa21_006	Vibrio phage pVa-21	GCA_002619305.1
CCE26331.1	000000	HTH	130	g308	Yersinia phage phiR1-37	GCA_000895615.1
CCE26332.1	000000	HTH	104	g309	Yersinia phage phiR1-37	GCA_000895615.1
AXH72520.1	000000	TM+TM+TM+TM	164	-	Myoviridae sp.	GCA_003657725.1
AXH72616.1	000000	TM+TM+TM+TM	167	-	Myoviridae sp.	GCA_003657725.1
ASV44131.1	000000	TM+TM+TM+TM	306	PBI_SCTP2_116	Salicola phage SCTP-2	GCA_002625545.1
ASV44196.1	000000	TM+TM+TM+TM	190	PBI_SCTP2_181	Salicola phage SCTP-2	GCA_002625545.1
ASV44550.1	000000	TM+TM+TM+TM	145	PBI_SCTP2_535	Salicola phage SCTP-2	GCA_002625545.1
AXH70864.1	000000	TM+TM+TM+TM	138	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21116.1	000000	TM+TM+TM+TM	140	-	Vibrio phage vB_pir03	GCA_014319855.1
prev15ph1000000027	000000	TM+TM+TM+TM	420	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ94965.1	000000	35exo	190	FDI40_gp183	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93427.1	000000	35exo	377	G_167	Bacillus virus G	GCA_000917535.1
AEO93651.1	000000	35exo	211	G_392	Bacillus virus G	GCA_000917535.1
QIG57964.1	000000	35exo	169	SEA_PAULODIABOLI_280	Microbacterium phage PauloDiaboli	GCA_011067425.1
QHJ86001.1	000000	35exo	211	KKIINIFJ_00089	Pseudomonas phage PN05	GCA_009931935.1
QCG76063.1	000000	35exo	176	EST35_0182	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AFF28165.1	000000	35exo	226	PAU_167	Sphingomonas phage PAU	GCA_000902455.1
BBA65603.1	000000	35exo	111	-	Xanthomonas phage XacN1	GCA_003173815.1
AMM44889.1	000000	HD	220	SP15_090	Bacillus phage SP-15	GCA_001754685.1
AEO93563.1	000000	HD	237	G_304	Bacillus virus G	GCA_000917535.1
QIG57955.1	000000	HD	255	SEA_PAULODIABOLI_271	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG65836.1	000000	HD	257	phiOC_p171	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
SBV38224.1	000000	HD	213	BN7874_055	Phage NCTB	GCA_900092385.1
QHJ86040.1	000000	HD	198	KKIINIFJ_00128	Pseudomonas phage PN05	GCA_009931935.1
QHJ86157.1	000000	HD	72	KKIINIFJ_00247	Pseudomonas phage PN05	GCA_009931935.1
QCG76084.1	000000	HD	498	EST35_0203	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AUZ95381.1	000000	HNH	166	FDI40_gp622	Agrobacterium phage Atu_ph07	GCA_002628245.1
QBQ74585.1	000000	HNH	236	BcepSauron_205	Burkholderia phage BcepSauron	GCA_005394215.1
AXQ70050.1	000000	HNH	155	CcrSC_gp468	Caulobacter phage CcrSC	GCA_003443315.1
BAE47841.1	000000	HNH	450	CST143	Clostridium phage c-st	GCA_000865225.1
AQT28581.1	000000	HNH	285	YOLOSWAG_99	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
ASV44553.1	000000	HNH	269	PBI_SCTP2_538	Salicola phage SCTP-2	GCA_002625545.1
CAG27251.1	000000	GDSL	480	PPEV_gp157	Pseudomonas phage EL	GCA_000866825.1
QHJ85983.1	000000	GDSL	484	KKIINIFJ_00071	Pseudomonas phage PN05	GCA_009931935.1
QHJ86120.1	000000	GDSL	439	KKIINIFJ_00209	Pseudomonas phage PN05	GCA_009931935.1
QCG76291.1	000000	GDSL	212	EST35_0423	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QDJ96366.1	000000	GDSL	1752	Xoosp13_179	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ADQ53034.1	000000	Caudo_TAP	141	PX29p317	Aeromonas phage PX29	GCA_000920195.1
QBO63882.1	000000	Caudo_TAP	138	Goslar_00089	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QHJ86108.1	000000	Caudo_TAP	142	KKIINIFJ_00197	Pseudomonas phage PN05	GCA_009931935.1
AQT28063.1	000000	Caudo_TAP	131	pVa21_122	Vibrio phage pVa-21	GCA_002619305.1
CCE26320.1	000000	Caudo_TAP	228	g297	Yersinia phage phiR1-37	GCA_000895615.1
AEO93274.1	000000	HTH	208	G_3	Bacillus virus G	GCA_000917535.1
BAE47779.1	000000	HTH	179	CST081	Clostridium phage c-st	GCA_000865225.1
BAE47828.1	000000	HTH	1662	CST130	Clostridium phage c-st	GCA_000865225.1
QGH71995.1	000000	HTH	95	N1M2_132	Klebsiella phage N1M2	GCA_010092605.1
AUZ95022.1	000000	IG	338	FDI40_gp240	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83756.1	000000	IG	135	0305phi8-36p198	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83757.1	000000	IG	486	0305phi8-36p199	Bacillus phage 0305phi8-36	GCA_000871045.1
QKE54581.1	000000	IG	355	ACSA002_2650	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AQT28133.1	000000	IG	134	pVa21_192	Vibrio phage pVa-21	GCA_002619305.1
AUZ94911.1	000000	Glutaredoxin	72	FDI40_gp114	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95042.1	000000	Glutaredoxin	85	FDI40_gp266	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93351.1	000000	Glutaredoxin	76	G_80	Bacillus virus G	GCA_000917535.1
BAE47772.1	000000	Glutaredoxin	71	CST074	Clostridium phage c-st	GCA_000865225.1
QIG57904.1	000000	Glutaredoxin	84	SEA_PAULODIABOLI_218	Microbacterium phage PauloDiaboli	GCA_011067425.1
BAG41730.1	000000	-	114	RSL1_ORF283	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41681.1	000000	Sulfotransfer	285	RSL1_ORF232	Ralstonia phage phiRSL1	GCA_000879455.1
AIX30707.1	000000	Sulfotransfer	207	Syn7803US37_230	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30711.1	000000	Sulfotransfer	205	Syn7803US37_234	Synechococcus phage ACG-2014f	GCA_002594065.1
AXQ70461.1	000000	Sulfotransfer	241	HOU04_gp062	Synechococcus phage S-T4	GCA_003443335.1
AXH72895.1	000000	DUF2786	229	-	Myoviridae sp.	GCA_003657725.1
QHJ86048.1	000000	DUF2786	234	KKIINIFJ_00136	Pseudomonas phage PN05	GCA_009931935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFF28064.1	000000	DUF2786	266	PAU_66	Sphingomonas phage PAU	GCA_000902455.1
BAV39381.1	000000	DUF2786	270	BPT24_263	Tenacibaculum phage pT24	GCA_002611925.1
ABS83598.1	000000	LAGLIDADG_3	261	0305phi8-36p036	Bacillus phage 0305phi8-36	GCA_000871045.1
AFU86543.1	000000	LAGLIDADG_3	146	CcrRogue_gp061	Caulobacter virus Rogue	GCA_000900555.1
prev15ph1000000191	000000	LAGLIDADG_3	388	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000210	000000	LAGLIDADG_3	313	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
CCH63486.1	000000	RADICAL-SAM	87	CP21_024	Campylobacter virus CP21	GCA_000902535.1
CCH63489.1	000000	RADICAL-SAM	295	CP21_027	Campylobacter virus CP21	GCA_000902535.1
CCH63572.1	000000	RADICAL-SAM	115	CP21_110	Campylobacter virus CP21	GCA_000902535.1
CCH63613.1	000000	RADICAL-SAM	367	CP21_151	Campylobacter virus CP21	GCA_000902535.1
BAE47783.1	000000	Peptidase_M27+Toxin_R_bind_N+NTNH_C	1196	CST085	Clostridium phage c-st	GCA_000865225.1
CCH63691.1	000000	SidE	140	CP21_230	Campylobacter virus CP21	GCA_000902535.1
BAE47747.1	000000	SidE	210	CST049	Clostridium phage c-st	GCA_000865225.1
ASV44037.1	000000	SidE	377	PBI_SCTP2_22	Salicola phage SCTP-2	GCA_002625545.1
QDB71271.1	000000	SidE	164	CPT_Moabite_241	Serratia phage Moabite	GCA_006384735.1
CCH63530.1	000000	GspA-ATPase	180	CP21_068	Campylobacter virus CP21	GCA_000902535.1
AIA65024.1	000000	GspA-ATPase	136	S13_227	Cronobacter phage S13	GCA_001503575.1
QHJ85913.1	000000	GspA-ATPase	156	KKIINIFJ_00001	Pseudomonas phage PN05	GCA_009931935.1
AXH70996.1	000000	GspA-ATPase	227	-	Vibrio phage BONAISHI	GCA_003441475.1
SBV38323.1	000000	SspB	115	BN7874_154	Phage NCTB	GCA_900092385.1
ABY63173.1	000000	SspB	373	201phi2-1p347	Pseudomonas phage 201phi2-1	GCA_000875305.1
ARV77411.1	000000	SspB	143	NOXIFER_246	Pseudomonas phage Noxifer	GCA_002625005.1
QBJ02825.1	000000	SspB	248	PSA21_299	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02631.1	000000	phiKZ_IP	366	PSA21_103	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02634.1	000000	phiKZ_IP	793	PSA21_106	Pseudomonas phage Psa21	GCA_004340405.1
AXH70845.1	000000	phiKZ_IP	464	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21095.1	000000	phiKZ_IP	414	-	Vibrio phage vB_pir03	GCA_014319855.1
QDH83461.1	000000	Phage_gp49_66	100	H1O15_gp053	Achromobacter phage Motura	GCA_006964305.1
AGX01825.1	000000	Phage_gp49_66	103	CF95_gp103	Erwinia phage PhiEaH1	GCA_000914555.1
AGS81951.1	000000	Phage_gp49_66	86	PaBG_00067	Pseudomonas phage PaBG	GCA_000912555.1
AQT27972.1	000000	Phage_gp49_66	226	pVa21_030	Vibrio phage pVa-21	GCA_002619305.1
BAE47754.1	000000	Sak4	324	CST056	Clostridium phage c-st	GCA_000865225.1
QIG57846.1	000000	Sak4	264	SEA_PAULODIABOLI_112	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIW90786.1	000000	Sak4	247	GCAPEGMB_00468	Vibrio phage V07	GCA_012361095.1
AEH03456.1	000000	HEPN	143	029	Pseudomonas phage PhiPA3	GCA_001502095.1
AQT28036.1	000000	HEPN	507	pVa21_095	Vibrio phage pVa-21	GCA_002619305.1
QNI21173.1	000000	HEPN	220	-	Vibrio phage vB_pir03	GCA_014319855.1
AUZ95056.1	000000	RyR	217	FDI40_gp284	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAG41736.1	000000	RyR	452	RSL1_ORF290	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44297.1	000000	RyR	255	PBI_SCTP2_282	Salicola phage SCTP-2	GCA_002625545.1
AEO93350.1	000000	HDRnase	159	G_79	Bacillus virus G	GCA_000917535.1
BAE47751.1	000000	HDRnase	187	CST053	Clostridium phage c-st	GCA_000865225.1
AEO93330.1	000000	DUF2829	90	G_59	Bacillus virus G	GCA_000917535.1
AFH14704.1	000000	DUF2829	178	Lu11_0169	Pseudomonas phage Lu11	GCA_000897175.1
AGS82045.1	000000	DUF2829	216	PaBG_00163	Pseudomonas phage PaBG	GCA_000912555.1
CCH63697.1	000000	SIG	180	CP21_237	Campylobacter virus CP21	GCA_000902535.1
AND75466.1	000000	2OG-FeII_Oxy_5	253	ME3_305	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AGH26172.1	000000	2OG-FeII_Oxy_5	169	CPMG_00071	Prochlorococcus phage MED4-213	GCA_000904535.1
ASR76125.1	000000	2OG-FeII_Oxy_5	152	PBI_BELLAMY_80	Synechococcus phage Bellamy	GCA_002627525.1
QDH83393.1	000000	PSBP	135	H1O15_gp069	Achromobacter phage Motura	GCA_006964305.1
QBJ02818.1	000000	PSBP	145	PSA21_292	Pseudomonas phage Psa21	GCA_004340405.1
QKE54426.1	000000	PSBP	213	ACSA002_1120	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QDH83398.1	000000	Classical-AAA	194	H1O15_gp064	Achromobacter phage Motura	GCA_006964305.1
AEO93484.1	000000	Classical-AAA	261	G_225	Bacillus virus G	GCA_000917535.1
QHJ86041.1	000000	Classical-AAA	191	KKIINIFJ_00129	Pseudomonas phage PN05	GCA_009931935.1
QDJ97224.1	000000	RING	101	D6_0064	Aeromonas phage D6	GCA_007051205.2
AEO93279.1	000000	RING	130	G_8	Bacillus virus G	GCA_000917535.1
AXH72485.1	000000	RING	115	-	Myoviridae sp.	GCA_003657725.1
QDH83690.1	000000	SIG+TM+TM+TM+TM	170	H1O15_gp271	Achromobacter phage Motura	GCA_006964305.1
AEO93770.1	000000	SIG+TM+TM+TM+TM	175	G_512	Bacillus virus G	GCA_000917535.1
QCG76146.1	000000	SIG+TM+TM+TM+TM	214	EST35_0265	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AEO93336.1	000000	SIG+Band_7	318	G_65	Bacillus virus G	GCA_000917535.1
QHJ86100.1	000000	SIG+Band_7	449	KKIINIFJ_00189	Pseudomonas phage PN05	GCA_009931935.1
AXH71014.1	000000	SIG+Band_7	289	-	Vibrio phage BONAISHI	GCA_003441475.1
AEO93479.1	000000	MerR-HTH	98	G_220	Bacillus virus G	GCA_000917535.1
ARM70910.1	000000	MerR-HTH	316	phiC120_c205	Escherichia phage phiC120	GCA_002621185.1
QBJ02856.1	000000	MerR-HTH	153	PSA21_330	Pseudomonas phage Psa21	GCA_004340405.1
AMM44900.1	000000	Thioredoxin	142	SP15_101	Bacillus phage SP-15	GCA_001754685.1
AQT28723.1	000000	Thioredoxin	149	YOLOSWAG_249	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AFF28242.1	000000	Thioredoxin	88	PAU_244	Sphingomonas phage PAU	GCA_000902455.1
BAE47888.1	000000	MarR-HTH	81	CST190	Clostridium phage c-st	GCA_000865225.1
SBV38234.1	000000	MarR-HTH	142	BN7874_065	Phage NCTB	GCA_900092385.1
QHJ86065.1	000000	MarR-HTH	90	KKIINIFJ_00153	Pseudomonas phage PN05	GCA_009931935.1
QDB70442.1	000000	Beta-helix	586	CF8_0030	Aeromonas phage CF8	GCA_006384595.2
QIG65996.1	000000	Beta-helix	860	phiOC_p354	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QDJ96360.1	000000	Beta-helix	728	Xoosp13_173	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AGH26195.1	000000	VanY	627	CPMG_00094	Prochlorococcus phage MED4-213	GCA_000904535.1
QAU04561.1	000000	VanY	878	ValB1MD_278	Vibrio phage ValB1MD	GCA_004138815.1
AUZ94973.1	000000	A18	762	FDI40_gp191	Agrobacterium phage Atu_ph07	GCA_002628245.1
AMM44887.1	000000	A18	522	SP15_088	Bacillus phage SP-15	GCA_001754685.1
QHJ86117.1	000000	A18	412	KKIINIFJ_00206	Pseudomonas phage PN05	GCA_009931935.1
AGH07728.1	000000	Mtd_N	152	CYVG_00285	Cyanophage S-SSM6a	GCA_002710385.1
AXH72780.1	000000	Mtd_N	702	-	Myoviridae sp.	GCA_003657725.1
QCG76122.1	000000	Mtd_N	399	EST35_0241	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
CCH63493.1	000000	GT	59	CP21_031	Campylobacter virus CP21	GCA_000902535.1
AIR93522.1	000000	GT	533	AVU42_gp185	Prochlorococcus phage P-TIM68	GCA_001503075.1
QAU04528.1	000000	GT	333	ValB1MD_211	Vibrio phage ValB1MD	GCA_004138815.1
AXQ68593.1	000000	CR-HNH3	37	CcrPW_gp054	Caulobacter phage CcrPW	GCA_003443275.1
ARM70837.1	000000	CR-HNH3	248	phiC120_c131	Escherichia phage phiC120	GCA_002621185.1
BBA65605.1	000000	CR-HNH3	113	-	Xanthomonas phage XacN1	GCA_003173815.1
AGH07734.1	000000	Phage_tail_APC	261	CYVG_00291	Cyanophage S-SSM6a	GCA_002710385.1
QCW22988.1	000000	Phage_tail_APC	107	-	Synechococcus phage S-B05	GCA_006083695.1
AQT28061.1	000000	Phage_tail_APC	142	pVa21_120	Vibrio phage pVa-21	GCA_002619305.1
CCH63531.1	000000	-	258	CP21_069	Campylobacter virus CP21	GCA_000902535.1
AND75170.1	000000	HINT	431	ME3_9	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
SBV38304.1	000000	HINT	153	BN7874_135	Phage NCTB	GCA_900092385.1
ASV44019.1	000000	HINT	937	PBI_SCTP2_4	Salicola phage SCTP-2	GCA_002625545.1
ABS83668.1	000000	CHTH	114	0305phi8-36p110	Bacillus phage 0305phi8-36	GCA_000871045.1
AXG67302.1	000000	CHTH	150	AD1_258	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AFH14552.1	000000	CHTH	172	Lu11_0021	Pseudomonas phage Lu11	GCA_000897175.1
CCE26321.1	000000	SIG+Collar	704	g298	Yersinia phage phiR1-37	GCA_000895615.1
ARV77349.1	000000	SIG+DUF3268	113	NOXIFER_180	Pseudomonas phage Noxifer	GCA_002625005.1
prevph1000000477	000000	SIG+DUF3268	139	-	Prevotella_phage_Lak-B8	GCA_004379655.1
SBV38541.1	000000	Tox-PLA2	210	BN7874_297	Phage NCTB	GCA_900092385.1
QHJ86186.1	000000	Tox-PLA2	151	KKIINIFJ_00276	Pseudomonas phage PN05	GCA_009931935.1
BAE47853.1	000000	PG-binding	309	CST155	Clostridium phage c-st	GCA_000865225.1
AFF28259.1	000000	PG-binding	251	PAU_261	Sphingomonas phage PAU	GCA_000902455.1
ALN97800.1	000000	SIG+LysM	104	Bp8pS_121	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93276.1	000000	SIG+LysM	365	G_5	Bacillus virus G	GCA_000917535.1
ABS83722.1	000000	VWA	1062	0305phi8-36p164	Bacillus phage 0305phi8-36	GCA_000871045.1
AXH72676.1	000000	VWA	152	-	Myoviridae sp.	GCA_003657725.1
ARM70890.1	000000	DUF5484	44	phiC120_c185	Escherichia phage phiC120	GCA_002621185.1
AQW88532.1	000000	DUF5484	44	BF_0007	Serratia phage BF	GCA_002619745.1
ALN97730.1	000000	VgrG	162	Bp8pS_051	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
CCE26308.1	000000	VgrG	288	g285	Yersinia phage phiR1-37	GCA_000895615.1
AGS82116.1	000000	SIG+zf-TFIIB	79	PaBG_00242	Pseudomonas phage PaBG	GCA_000912555.1
QNI21014.1	000000	SIG+zf-TFIIB	53	-	Vibrio phage vB_pir03	GCA_014319855.1
AUZ95421.1	000000	WYL	96	FDI40_gp664	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83614.1	000000	WYL	166	0305phi8-36p053	Bacillus phage 0305phi8-36	GCA_000871045.1
QFR59289.1	000000	ADA-DBD	224	PS2_0148	Aeromonas phage PS2	GCA_009388305.2
AEO93850.1	000000	ADA-DBD	59	G_605	Bacillus virus G	GCA_000917535.1
ABS83712.1	000000	ANTHRAXPAG-N	1212	0305phi8-36p154	Bacillus phage 0305phi8-36	GCA_000871045.1
AUZ94978.1	000000	COOHNH2ligase	500	FDI40_gp196	Agrobacterium phage Atu_ph07	GCA_002628245.1
QIW90805.1	000000	COOHNH2ligase	282	GCAPEGMB_00487	Vibrio phage V07	GCA_012361095.1
AEO93640.1	000000	SIG+HNH	135	G_381	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH07661.1	000000	SIG+HNH	505	CYVG_00218	Cyanophage S-SSM6a	GCA_002710385.1
AMM44967.1	000000	DUF1653	121	SP15_169	Bacillus phage SP-15	GCA_001754685.1
QFP93235.1	000000	DUF1653	115	-	Serratia phage PCH45	GCA_009187865.1
ABS83604.1	000000	UDG	205	0305phi8-36p043	Bacillus phage 0305phi8-36	GCA_000871045.1
AMM44899.1	000000	UDG	192	SP15_100	Bacillus phage SP-15	GCA_001754685.1
QAY01413.1	000000	DUF4314	66	ASwh1_354	Aeromonas phage Aswh_1	GCA_004146945.1
AMM45108.1	000000	DUF4314	70	SP15_300	Bacillus phage SP-15	GCA_001754685.1
CCH63515.1	000000	YopX	163	CP21_053	Campylobacter virus CP21	GCA_000902535.1
ASV44407.1	000000	YopX	124	PBI_SCTP2_392	Salicola phage SCTP-2	GCA_002625545.1
ARM70799.1	000000	ILEI	374	phiC120_c93	Escherichia phage phiC120	GCA_002621185.1
ASV44152.1	000000	ILEI	532	PBI_SCTP2_137	Salicola phage SCTP-2	GCA_002625545.1
QDH50531.1	000000	URI	169	-	Synechococcus phage S-B43	GCA_006869725.1
ALP47356.1	000000	URI	552	phiST2_0371	Vibrio phage phi-ST2	GCA_002757135.1
AXH71029.1	000000	RHS	292	-	Vibrio phage BONAISHI	GCA_003441475.1
QNI21276.1	000000	RHS	272	-	Vibrio phage vB_pir03	GCA_014319855.1
QKE54529.1	000000	BRCT	92	ACSA002_2130	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QNI21037.1	000000	BRCT	319	-	Vibrio phage vB_pir03	GCA_014319855.1
AIR93515.1	000000	Glyco_trans_1_2	315	AVU42_gp178	Prochlorococcus phage P-TIM68	GCA_001503075.1
AXQ70510.1	000000	Glyco_trans_1_2	292	HOU04_gp111	Synechococcus phage S-T4	GCA_003443335.1
ALN97836.1	000000	-	38	Bp8pS_157	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ABS83761.1	000000	TM+TM+TM+TM+TM+TM+TM	286	0305phi8-36p203	Bacillus phage 0305phi8-36	GCA_000871045.1
ASV44347.1	000000	TM+TM+TM+TM+TM+TM+TM	223	PBI_SCTP2_332	Salicola phage SCTP-2	GCA_002625545.1
AUZ95018.1	000000	Isochorismatase	202	FDI40_gp236	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93534.1	000000	Isochorismatase	180	G_275	Bacillus virus G	GCA_000917535.1
BAG41544.1	000000	Lar_restr_allev	225	RSL1_ORF099	Ralstonia phage phiRSL1	GCA_000879455.1
QDJ96262.1	000000	Lar_restr_allev	69	Xoosp13_75	Xanthomonas phage Xoo-sp13	GCA_013364725.1
BAV39385.1	000000	SIG+TM+TM+TM+TM+TM+TM	308	BPT24_268	Tenacibaculum phage pT24	GCA_002611925.1
prevph1000000734	000000	SIG+TM+TM+TM+TM+TM+TM	301	-	Prevotella_phage_Lak-B8	GCA_004379655.1
BAE47883.1	000000	ParB	359	CST185	Clostridium phage c-st	GCA_000865225.1
AGH26294.1	000000	ParB	345	CPMG_00194	Prochlorococcus phage MED4-213	GCA_000904535.1
ABS83709.1	000000	Baseplate_J	273	0305phi8-36p151	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93448.1	000000	Baseplate_J	619	G_188	Bacillus virus G	GCA_000917535.1
CCH63474.1	000000	MA	374	CP21_012	Campylobacter virus CP21	GCA_000902535.1
AIA64931.1	000000	Ruc-ZnR	62	S13_132	Cronobacter phage S13	GCA_001503575.1
BBA65439.1	000000	Ruc-ZnR	61	-	Xanthomonas phage XacN1	GCA_003173815.1
AGX01843.1	000000	DUF4262	176	CF95_gp121	Erwinia phage PhiEaH1	GCA_000914555.1
ARV77435.1	000000	DUF4262	229	NOXIFER_270	Pseudomonas phage Noxifer	GCA_002625005.1
BAG41765.1	000000	HIN-HTH	84	RSL1_ORF318	Ralstonia phage phiRSL1	GCA_000879455.1
QIW90809.1	000000	HIN-HTH	137	GCAPEGMB_00491	Vibrio phage V07	GCA_012361095.1
CCH63466.1	000000	ROT	148	CP21_004	Campylobacter virus CP21	GCA_000902535.1
ASV44259.1	000000	ROT	844	PBI_SCTP2_244	Salicola phage SCTP-2	GCA_002625545.1
ASV44018.1	000000	ABhydrolase	192	PBI_SCTP2_3	Salicola phage SCTP-2	GCA_002625545.1
BBA65501.1	000000	ABhydrolase	230	-	Xanthomonas phage XacN1	GCA_003173815.1
QIG65893.1	000000	GNTR-HTH	119	phiOC_p230	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIW90769.1	000000	GNTR-HTH	70	GCAPEGMB_00450	Vibrio phage V07	GCA_012361095.1
QIG57786.1	000000	ParA-Soj-PloopNTPase	98	SEA_PAULODIABOLI_51	Microbacterium phage PauloDiaboli	GCA_011067425.1
BAG41687.1	000000	ParA-Soj-PloopNTPase	231	RSL1_ORF238	Ralstonia phage phiRSL1	GCA_000879455.1
AEO93515.1	000000	PDDEXK_1	270	G_256	Bacillus virus G	GCA_000917535.1
QIG57847.1	000000	PDDEXK_1	311	SEA_PAULODIABOLI_113	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72912.1	000000	SIG+PAS	182	-	Myoviridae sp.	GCA_003657725.1
QHJ85923.1	000000	SIG+PAS	199	KKIINIFJ_00011	Pseudomonas phage PN05	GCA_009931935.1
prevph1000000293	000000	POLYSACPOLYMERASE	82	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000227	000000	POLYSACPOLYMERASE	736	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
CCE26318.1	000000	SIG+KELCH	1372	g295	Yersinia phage phiR1-37	GCA_000895615.1
CCE26319.1	000000	SIG+KELCH	928	g296	Yersinia phage phiR1-37	GCA_000895615.1
CCH63690.1	000000	DUF4376	208	CP21_228	Campylobacter virus CP21	GCA_000902535.1
BAG41643.1	000000	DUF4376	258	RSL1_ORF194	Ralstonia phage phiRSL1	GCA_000879455.1
AMM45067.1	000000	Peptidase-S8	375	SP15_260	Bacillus phage SP-15	GCA_001754685.1
AGH26119.1	000000	Peptidase-S8	1840	CPMG_00018	Prochlorococcus phage MED4-213	GCA_000904535.1
AEO93886.1	000000	VATC	137	G_643	Bacillus virus G	GCA_000917535.1
BAG41491.1	000000	VATC	97	RSL1_ORF046	Ralstonia phage phiRSL1	GCA_000879455.1
QHJ86089.1	000000	DUF4815	496	KKIINIFJ_00177	Pseudomonas phage PN05	GCA_009931935.1
QHJ86150.1	000000	DUF4815	552	KKIINIFJ_00239	Pseudomonas phage PN05	GCA_009931935.1
ABS83758.1	000000	Replic_Relax	283	0305phi8-36p200	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93286.1	000000	MuF	458	G_15	Bacillus virus G	GCA_000917535.1
QIW90744.1	000000	MuF	387	GCAPEGMB_00425	Vibrio phage V07	GCA_012361095.1
AGH26259.1	000000	Asp_Arg_Hydrox	164	CPMG_00158	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26276.1	000000	Asp_Arg_Hydrox	234	CPMG_00176	Prochlorococcus phage MED4-213	GCA_000904535.1
ARM70744.1	000000	DUF2685	55	phiC120_c37	Escherichia phage phiC120	GCA_002621185.1
ALY07013.1	000000	DUF2685	55	VmeM32_00019	Vibrio phage vB_VmeM-32	GCA_002608825.1
AXH70857.1	000000	Med15	981	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70822.1	000000	Med15	601	-	Vibrio phage BONAISHI	GCA_003441475.1
AMM44943.1	000000	SSB	137	SP15_145	Bacillus phage SP-15	GCA_001754685.1
CCE26292.1	000000	SSB	110	g269	Yersinia phage phiR1-37	GCA_000895615.1
AKF13422.1	000000	NACHT	53	PHIN3_159	Sinorhizobium phage phiN3	GCA_001501175.1
BBA65569.1	000000	NACHT	100	-	Xanthomonas phage XacN1	GCA_003173815.1
AXH72898.1	000000	PP-binding	105	-	Myoviridae sp.	GCA_003657725.1
AGH26188.1	000000	PP-binding	155	CPMG_00087	Prochlorococcus phage MED4-213	GCA_000904535.1
SBV38300.1	000000	Calx-beta	853	BN7874_131	Phage NCTB	GCA_900092385.1
AFH14773.1	000000	Calx-beta	1216	Lu11_0237	Pseudomonas phage Lu11	GCA_000897175.1
QDH83699.1	000000	DUF1737	67	H1O15_gp262	Achromobacter phage Motura	GCA_006964305.1
QDH83722.1	000000	DUF1737	59	H1O15_gp105	Achromobacter phage Motura	GCA_006964305.1
BAG41464.1	000000	SIG+aGPT-PPlase	333	RSL1_ORF019	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41680.1	000000	SIG+aGPT-PPlase	348	RSL1_ORF231	Ralstonia phage phiRSL1	GCA_000879455.1
QHJ86088.1	000000	FN3	276	KKIINIFJ_00176	Pseudomonas phage PN05	GCA_009931935.1
QIW90761.1	000000	FN3	1024	GCAPEGMB_00442	Vibrio phage V07	GCA_012361095.1
AMM44810.1	000000	DSBH	226	SP15_011	Bacillus phage SP-15	GCA_001754685.1
AJK27620.1	000000	DSBH	165	PTIM40_207	Cyanophage P-TIM40	GCA_001470935.1
AEO93543.1	000000	SIG+ParBC	144	G_284	Bacillus virus G	GCA_000917535.1
AEO93328.1	000000	SIG+ParBC	202	G_57	Bacillus virus G	GCA_000917535.1
AEO93413.1	000000	TM+TM+TM+TM+TM+TM	319	G_153	Bacillus virus G	GCA_000917535.1
QIG57831.1	000000	TM+TM+TM+TM+TM+TM	1474	SEA_PAULODIABOLI_97	Microbacterium phage PauloDiaboli	GCA_011067425.1
AIR93525.1	000000	adh_short	214	AVU42_gp188	Prochlorococcus phage P-TIM68	GCA_001503075.1
QKE54367.1	000000	adh_short	108	ACSA002_0530	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AEO93771.1	000000	GGACT	138	G_513	Bacillus virus G	GCA_000917535.1
AEO93772.1	000000	GGACT	148	G_514	Bacillus virus G	GCA_000917535.1
ARV77330.1	000000	XIS-HTH	82	NOXIFER_161	Pseudomonas phage Noxifer	GCA_002625005.1
QKE54359.1	000000	XIS-HTH	65	ACSA002_0450	Salmonella phage vB_SalM_SA002	GCA_014131285.1
AGH56812.1	000000	TET-JBP	189	CPXG_00009	Cyanophage P-RSM6	GCA_000906155.1
AIX30527.1	000000	TET-JBP	67	Syn7803US37_50	Synechococcus phage ACG-2014f	GCA_002594065.1
BAQ02656.1	000000	HicB_lk_antitox	96	AVU38_gp128	Ralstonia phage RSL2	GCA_001503055.1
CCE26307.1	000000	HicB_lk_antitox	98	g284	Yersinia phage phiR1-37	GCA_000895615.1
AFF28058.1	000000	SEC-C	195	PAU_60	Sphingomonas phage PAU	GCA_000902455.1
AQT28103.1	000000	SEC-C	53	pVa21_162	Vibrio phage pVa-21	GCA_002619305.1
AEO93555.1	000000	SIG+WYL	203	G_296	Bacillus virus G	GCA_000917535.1
BAE47702.1	000000	YkyB	210	CST004	Clostridium phage c-st	GCA_000865225.1
ARM70748.1	000000	SIG+T4_baseplate	208	phiC120_c41	Escherichia phage phiC120	GCA_002621185.1
AMM44813.1	000000	Putative_PNPOx	151	SP15_014	Bacillus phage SP-15	GCA_001754685.1
AEO93570.1	000000	Pkinase	353	G_311	Bacillus virus G	GCA_000917535.1
QDH83433.1	000000	GATase_7+Asn_synthase	426	H1O15_gp025	Achromobacter phage Motura	GCA_006964305.1
ASR76263.1	000000	UDPG_MGDP_dh_N+UDPG_MGDP_dh	412	PBI_BELLAMY_227	Synechococcus phage Bellamy	GCA_002627525.1
CCH63527.1	000000	PELOTA	312	CP21_065	Campylobacter virus CP21	GCA_000902535.1
QMV29151.1	000000	SIG+TF-AF0608	117	AP1_0450	Aeromonas phage AP1	GCA_014183665.1
AEO93447.1	000000	IONCHANNEL	301	G_187	Bacillus virus G	GCA_000917535.1
CCE26113.1	000000	Peptidase_M15_3	364	g089	Yersinia phage phiR1-37	GCA_000895615.1
ARM70903.1	000000	Inhibitor_I24	137	phiC120_c198	Escherichia phage phiC120	GCA_002621185.1
QIG57872.1	000000	Glyco_transf_7C	233	SEA_PAULODIABOLI_180	Microbacterium phage PauloDiaboli	GCA_011067425.1
QHJ86033.1	000000	N-OB	99	KKIINIFJ_00121	Pseudomonas phage PN05	GCA_009931935.1
BAG41480.1	000000	Helicase_C	320	RSL1_ORF035	Ralstonia phage phiRSL1	GCA_000879455.1
CCH63488.1	000000	Radical_SAM	66	CP21_026	Campylobacter virus CP21	GCA_000902535.1
ABS83739.1	000000	AEPrimase+PriCT1	350	0305phi8-36p181	Bacillus phage 0305phi8-36	GCA_000871045.1
QHJ86081.1	000000	Imm-Cdil	115	KKIINIFJ_00169	Pseudomonas phage PN05	GCA_009931935.1
AMM43704.1	000000	OST-HTH	66	CBB_139	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AEO93641.1	000000	Guanylate_kin	274	G_382	Bacillus virus G	GCA_000917535.1
ABY63086.1	000000	7TMR-DISMED1	178	201phi2-1p258	Pseudomonas phage 201phi2-1	GCA_000875305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW90812.1	000000	MazG-Phage	148	GCAPEGMB_00494	Vibrio phage V07	GCA_012361095.1
QIG65738.1	000000	SIG+TM+TM+Rick-17kDa-Anti+TM	632	phiOC_p073	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AQT28021.1	000000	sinutoxin	209	pVa21_080	Vibrio phage pVa-21	GCA_002619305.1
AGH26156.1	000000	DUF1281_C	174	CPMG_00055	Prochlorococcus phage MED4-213	GCA_000904535.1
AXH72897.1	000000	DAGKIN	258	-	Myoviridae sp.	GCA_003657725.1
AEO93416.1	000000	VirD4-TraG	825	G_156	Bacillus virus G	GCA_000917535.1
ARV77086.1	000000	Peptidase_S49	60	PHABIO_458	Pseudomonas phage Phabio	GCA_002624965.1
AEO93827.1	000000	KOW	200	G_582	Bacillus virus G	GCA_000917535.1
QIG57833.1	000000	FN3+FN3	744	SEA_PAULODIABOLI_99	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57845.1	000000	DUF669	237	SEA_PAULODIABOLI_111	Microbacterium phage PauloDiaboli	GCA_011067425.1
AKF13652.1	000000	SIG+DivIVA	463	PHIN3_389	Sinorhizobium phage phiN3	GCA_001501175.1
AGX01933.1	000000	MED23	135	CF95_gp211	Erwinia phage PhiEaH1	GCA_000914555.1
CCH63522.1	000000	SIG+IZUMO	230	CP21_060	Campylobacter virus CP21	GCA_000902535.1
BAE47865.1	000000	SIG+MED6	525	CST167	Clostridium phage c-st	GCA_000865225.1
AXQ69083.1	000000	SIG+35exo	241	CcrBL9_gp059c	Caulobacter phage CcrBL9	GCA_003443295.1
prev15ph1000000490	000000	TMs	1987	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ARV77225.1	000000	SIG+NMT1_3	294	NOXIFER_54	Pseudomonas phage Noxifer	GCA_002625005.1
QIW90793.1	000000	HTH_17	105	GCAPEGMB_00475	Vibrio phage V07	GCA_012361095.1
AXH72899.1	000000	SAP-LEM-HEH	94	-	Myoviridae sp.	GCA_003657725.1
AXH72879.1	000000	Haem_oxygenas_2	489	-	Myoviridae sp.	GCA_003657725.1
QBX06584.1	000000	SIG+FIS-HTH	302	BcepSaruman_171	Burkholderia phage BcepSaruman	GCA_004771375.1
BAG41728.1	000000	Atg14	166	RSL1_ORF281	Ralstonia phage phiRSL1	GCA_000879455.1
QIW90825.1	000000	DUF5309	347	GCAPEGMB_00510	Vibrio phage V07	GCA_012361095.1
SBV38193.1	000000	SIG+DraT-ART	208	BN7874_024	Phage NCTB	GCA_900092385.1
prevph1000000735	000000	SIG+TM+TM+TM+TM+TM+TM+TM	284	-	Prevotella_phage_Lak-B8	GCA_004379655.1
ASV44265.1	000000	CUB	284	PBI_SCTP2_250	Salicola phage SCTP-2	GCA_002625545.1
BBA65538.1	000000	SIG+LD-peptidase	115	-	Xanthomonas phage XacN1	GCA_003173815.1
SBV38321.1	000000	XpaC	82	BN7874_152	Phage NCTB	GCA_900092385.1
QBJ02552.1	000000	CW-binding-EndolysinC	196	PSA21_22	Pseudomonas phage Psa21	GCA_004340405.1
QBO63831.1	000000	Androgen_recep	852	Goslar_00038	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
AEO93663.1	000000	SIG+Cu-amine-oxidN1	301	G_405	Bacillus virus G	GCA_000917535.1
ARM70739.1	000000	DUF2774	64	phiC120_c32	Escherichia phage phiC120	GCA_002621185.1
AIX30495.1	000000	Glycos_transf_1	363	Syn7803US37_18	Synechococcus phage ACG-2014f	GCA_002594065.1
QIW90759.1	000000	DUF1833	165	GCAPEGMB_00440	Vibrio phage V07	GCA_012361095.1
BAE47826.1	000000	Prophage_tail	741	CST128	Clostridium phage c-st	GCA_000865225.1
SBV38292.1	000000	SIG+Apolipoprotein	239	BN7874_123	Phage NCTB	GCA_900092385.1
QBJ02547.1	000000	RPN10	125	PSA21_17	Pseudomonas phage Psa21	GCA_004340405.1
AFH14557.1	000000	Collagen	176	Lu11_0026	Pseudomonas phage Lu11	GCA_000897175.1
AUZ95123.1	000000	BTV_NS2	40	FDI40_gp364	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEO93681.1	000000	AHD3	460	G_423	Bacillus virus G	GCA_000917535.1
AXH72401.1	000000	ZNR	152	-	Myoviridae sp.	GCA_003657725.1
AEO93923.1	000000	APG7N	486	G_680	Bacillus virus G	GCA_000917535.1
AMM45078.1	000000	DUF3626	763	SP15_271	Bacillus phage SP-15	GCA_001754685.1
ALN97799.1	000000	Imm38	173	Bp8pS_120	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEH03674.1	000000	SIG+SEA	116	251	Pseudomonas phage PhiPA3	GCA_001502095.1
BBA65601.1	000000	PAP_central	55	-	Xanthomonas phage XacN1	GCA_003173815.1
QIG66040.1	000000	SIG+DUF1127	44	phiOC_p398	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
SBV38531.1	000000	ICLR-HTH	211	BN7874_291	Phage NCTB	GCA_900092385.1
ABS83676.1	000000	SNF5	431	0306phi8-36p118	Bacillus phage 0305phi8-36	GCA_000871045.1
QAU04517.1	000000	SIG+CR-Trypsin3	219	ValB1MD_186	Vibrio phage ValB1MD	GCA_004138815.1
ARM70887.1	000000	DUF5495	75	phiC120_c182	Escherichia phage phiC120	GCA_002621185.1
AFF28128.1	000000	DUF3553	47	PAU_130	Sphingomonas phage PAU	GCA_000902455.1
QKE54358.1	000000	YXWGXW	261	ACSA002_0440	Salmonella phage vB_SalM_SA002	GCA_014131285.1
BAE47886.1	000000	XIS-HTH+GASH	239	CST188	Clostridium phage c-st	GCA_000865225.1
QBJ02929.1	000000	Alginate_lyase2	224	PSA21_405	Pseudomonas phage Psa21	GCA_004340405.1
AEO93583.1	000000	CCDC158+DUF2325	441	G_324	Bacillus virus G	GCA_000917535.1
QIG65867.1	000000	DUF2312	85	phiOC_p202	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
BAE47827.1	000000	Sipho_tail	264	CST129	Clostridium phage c-st	GCA_000865225.1
QHJ86154.1	000000	aGPT-PPIase	339	KKIINIFJ_00243	Pseudomonas phage PN05	GCA_009931935.1
QIW90739.1	000000	Amidase_2	145	GCAPEGMB_00420	Vibrio phage V07	GCA_012361095.1
QIG57828.1	000000	HK97-gp10_like	136	SEA_PAULODIABOLI_94	Microbacterium phage PauloDiaboli	GCA_011067425.1
AMM44992.1	000000	VirB11	142	SP15_192	Bacillus phage SP-15	GCA_001754685.1
AXH72810.1	000000	Na	386	-	Myoviridae sp.	GCA_003657725.1
ARV77481.1	000000	Cornase	104	NOXIFER_316	Pseudomonas phage Noxifer	GCA_002625005.1
QKN85958.1	000000	HslUClpX-AAA	75	ACEC001_1200	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
AEO93410.1	000000	VirB2	154	G_150	Bacillus virus G	GCA_000917535.1
QFP93213.1	000000	SIG+Ntox26	134	-	Serratia phage PCH45	GCA_009187865.1
ASR76246.1	000000	DUF563	370	PBI_BELLAMY_210	Synechococcus phage Bellamy	GCA_002627525.1
ARM70866.1	000000	Peptidase_U32	386	phiC120_c160	Escherichia phage phiC120	GCA_002621185.1
BAV39356.1	000000	SBE2	266	BPT24_236	Tenacibaculum phage pT24	GCA_002611925.1
AEO93602.1	000000	SUKH-SYD	123	G_343	Bacillus virus G	GCA_000917535.1
ARM70933.1	000000	REGB_T4	152	phiC120_c228	Escherichia phage phiC120	GCA_002621185.1
ASV44066.1	000000	LPD4	278	PBI_SCTP2_51	Salicola phage SCTP-2	GCA_002625545.1
QDH83658.1	000000	DUF1289	61	H1O15_gp092	Achromobacter phage Motura	GCA_006964305.1
QNI21081.1	000000	Phage_TAC_2	224	-	Vibrio phage vB_pir03	GCA_014319855.1
ASV44040.1	000000	Imm-Barstar	158	PBI_SCTP2_25	Salicola phage SCTP-2	GCA_002625545.1
AQT27954.1	000000	DUF3584	355	pVa21_012	Vibrio phage pVa-21	GCA_002619305.1
AEO93512.1	000000	HIRAN	118	G_253	Bacillus virus G	GCA_000917535.1
ABY62889.1	000000	PDZ	57	201phi2-1p056	Pseudomonas phage 201phi2-1	GCA_000875305.1
AXH72869.1	000000	tRNA-synt_1+Anticodon_1+zf-FPG_IleRS	908	-	Myoviridae sp.	GCA_003657725.1
ABS83740.1	000000	SIG+DnaB	346	0305phi8-36p182	Bacillus phage 0305phi8-36	GCA_000871045.1
prev15ph1000000360	000000	SIG+TM+Adenovirusportal	879	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AEO93916.1	000000	DUF4815+Cellulase+Polysacc_deac_1	1025	G_673	Bacillus virus G	GCA_000917535.1
AFN37547.1	000000	PDDEXK_5	149	pp2_314	Vibriophage phi-pp2	GCA_002630725.1
ABS83714.1	000000	CCDC14	204	0305phi8-36p156	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93527.1	000000	RIFIN	342	G_268	Bacillus virus G	GCA_000917535.1
QIW90802.1	000000	Peptidase_C26	230	GCAPEGMB_00484	Vibrio phage V07	GCA_012361095.1
ARV77344.1	000000	Cornifin+phiKZ_IP	712	NOXIFER_175	Pseudomonas phage Noxifer	GCA_002625005.1
AAX78588.1	000000	LAGLIDADG_3+HTH_38	185	RB43ORF066w	Escherichia virus RB43	GCA_000863505.1
QHJ85944.1	000000	cpYpsA+cpYpsA	179	KKIINIFJ_00032	Pseudomonas phage PN05	GCA_009931935.1
ARM70787.1	000000	DUF5496	84	phiC120_c81	Escherichia phage phiC120	GCA_002621185.1
AEO93478.1	000000	DUF1256	188	G_219	Bacillus virus G	GCA_000917535.1
AUZ94833.1	000000	SIG+Cadherin_3	352	FDI40_gp021	Agrobacterium phage Atu_ph07	GCA_002628245.1
QKE11219.1	000000	SIG+Calx-beta	1217	PaBG_00248	Pseudomonas phage PaBG	GCA_000912555.1
AMM44809.1	000000	dNK	223	SP15_010	Bacillus phage SP-15	GCA_001754685.1
ALN97835.1	000000	LAGLIDADG_2	229	Bp8pS_156	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
BAE47722.1	000000	Bro-N	240	CST024	Clostridium phage c-st	GCA_000865225.1
ABS83725.1	000000	IG+IG	591	0305phi8-36p167	Bacillus phage 0305phi8-36	GCA_000871045.1
QIG57871.1	000000	Glycos_transf_2	206	SEA_PAULODIABOLI_179	Microbacterium phage PauloDiaboli	GCA_011067425.1
SBV38206.1	000000	GlnE	109	BN7874_037	Phage NCTB	GCA_900092385.1
QIW90727.1	000000	DEOR-HTH	87	GCAPEGMB_00408	Vibrio phage V07	GCA_012361095.1
ASV44150.1	000000	Tox-ABHYDROLASE3	149	PBI_SCTP2_135	Salicola phage SCTP-2	GCA_002625545.1
AFF28196.1	000000	MED6	107	PAU_198	Sphingomonas phage PAU	GCA_000902455.1
AGN30171.1	000000	DUF5591	226	VPFG_00169	Vibrio phage nt-1	GCA_000910195.2
ABS83766.1	000000	SIG+PADR-HTH	143	0305phi8-36p208	Bacillus phage 0305phi8-36	GCA_000871045.1
prev15ph1000000481	000000	Apolipoprotein+Apolipoprotein+CCDC158	1202	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
AUZ94854.1	000000	InPase	306	FDI40_gp042	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARM70969.1	000000	IPI_T4	95	phiC120_c264	Escherichia phage phiC120	GCA_002621185.1
QBX06649.1	000000	Uri-nuclease	357	BcepSaruman_236	Burkholderia phage BcepSaruman	GCA_004771375.1
AMM44821.1	000000	HINT+fvmX2	539	SP15_022	Bacillus phage SP-15	GCA_001754685.1
ASV44457.1	000000	BetaPropeller	3456	PBI_SCTP2_442	Salicola phage SCTP-2	GCA_002625545.1
AXQ68640.1	000000	Kdo_hydroxy	286	CcrPW_gp101	Caulobacter phage CcrPW	GCA_003443275.1
BAE47802.1	000000	SIG+Phage_int_SAM_1+Phage_integrase	317	CST104	Clostridium phage c-st	GCA_000865225.1
ABS83645.1	000000	NHase_beta	137	0305phi8-36p085	Bacillus phage 0305phi8-36	GCA_000871045.1
BAG41698.1	000000	SIG+PYRIN	143	RSL1_ORF250	Ralstonia phage phiRSL1	GCA_000879455.1
AGH07713.1	000000	DUF4581	54	CYVG_00270	Cyanophage S-SSM6a	GCA_002710385.1
ABS83721.1	000000	SIG+LEVANB+FN3+FN3+BactIG	2143	0305phi8-36p163	Bacillus phage 0305phi8-36	GCA_000871045.1
AND75456.1	000000	PLDc_2	198	ME3_295	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QMP24206.1	000000	GbpC	360	-	Proteus phage 10	GCA_014071245.1
AGS82160.1	000000	SIG+Tox-MPTasemisc	279	PaBG_00287	Pseudomonas phage PaBG	GCA_000912555.1
QIG57931.1	000000	Stealth_CR2	231	SEA_PAULODIABOLI_246	Microbacterium phage PauloDiaboli	GCA_011067425.1
ASV44168.1	000000	APATPase	276	PBI_SCTP2_153	Salicola phage SCTP-2	GCA_002625545.1
AEO93469.1	000000	HIN-HTH+HIN-HTH	128	G_210	Bacillus virus G	GCA_000917535.1
AEO93662.1	000000	YtxC	288	G_404	Bacillus virus G	GCA_000917535.1
AXH72891.1	000000	Inhibitor_I42	90	-	Myoviridae sp.	GCA_003657725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAE47892.1	000000	BirA-HTH	205	CST194	Clostridium phage c-st	GCA_000865225.1
QIW90728.1	000000	LPD27	91	GCAPEGMB_00409	Vibrio phage V07	GCA_012361095.1
AXH72882.1	000000	LRP-HTH	158	-	Myoviridae sp.	GCA_003657725.1
QCG76069.1	000000	Peptidase_M3	673	EST35_0188	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AEO93483.1	000000	CRP-HTH	676	G_224	Bacillus virus G	GCA_000917535.1
AXH72639.1	000000	SIG+RnasePH	112	-	Myoviridae sp.	GCA_003657725.1
BAE47851.1	000000	AntA	65	CST153	Clostridium phage c-st	GCA_000865225.1
BAV39170.1	000000	SIG+Cytadhesin_P30	106	BPT24_047	Tenacibaculum phage pT24	GCA_002611925.1
QCW22981.1	000000	C1q	226	-	Synechococcus phage S-B05	GCA_006083695.1
QIG57842.1	000000	WhiB	189	SEA_PAULODIABOLI_108	Microbacterium phage PauloDiaboli	GCA_011067425.1
prevph1000000110	000000	RFC-AAA	118	-	Prevotella_phage_Lak-B8	GCA_004379655.1
AEO93401.1	000000	PEP-utilisers	365	G_139	Bacillus virus G	GCA_000917535.1
AFF28026.1	000000	tRNA_synt_2f	187	PAU_28	Sphingomonas phage PAU	GCA_000902455.1
AUZ94991.1	000000	DUF2164	79	FDI40_gp209	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIR93565.1	000000	PSI_PsaE	67	psaE	Prochlorococcus phage P-TIM68	GCA_001503075.1
AEO93628.1	000000	ASRAH	798	G_369	Bacillus virus G	GCA_000917535.1
QDH83537.1	000000	FAM176	98	H1O15_gp251	Achromobacter phage Motura	GCA_006964305.1
QMP24037.1	000000	VMAP-M0	125	-	Proteus phage 10	GCA_014071245.1
AEO93488.1	000000	CHC2+CLOSTRIPAIN	210	G_229	Bacillus virus G	GCA_000917535.1
AEO93332.1	000000	DUF2639	45	G_61	Bacillus virus G	GCA_000917535.1
AXH72863.1	000000	OmpA-beta-barrel+OmpA	342	-	Myoviridae sp.	GCA_003657725.1
QIG57821.1	000000	Pyocin_S	1543	SEA_PAULODIABOLI_87	Microbacterium phage PauloDiaboli	GCA_011067425.1
ABS83779.1	000000	DUF2584	137	0305phi8-36p221	Bacillus phage 0305phi8-36	GCA_000871045.1
AEO93623.1	000000	DISCOIDIN+SUN	667	G_364	Bacillus virus G	GCA_000917535.1
AQT28139.1	000000	SIG+Tox-HNH-DHNNK	233	pVa21_198	Vibrio phage pVa-21	GCA_002619305.1
QKE54639.1	000000	Bul1_C	131	ACSA002_3220	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ARV76787.1	000000	Ter-PxG	87	PHABIO_156	Pseudomonas phage Phabio	GCA_002624965.1
AKF13648.1	000000	SGS	200	PHIN3_385	Sinorhizobium phage phiN3	GCA_001501175.1
AMM44823.1	000000	SIG+HINT	158	SP15_024	Bacillus phage SP-15	GCA_001754685.1
ASV44378.1	000000	SH3_15	86	PBI_SCTP2_363	Salicola phage SCTP-2	GCA_002625545.1
BAE47882.1	000000	ORF6C	198	CST184	Clostridium phage c-st	GCA_000865225.1
AXH70835.1	000000	SLATT	128	-	Vibrio phage BONAISHI	GCA_003441475.1
AMM44804.1	000000	DUF2034	158	SP15_006	Bacillus phage SP-15	GCA_001754685.1
prevph1000000718	000000	R3H-2OGFEDO	64	-	Prevotella_phage_Lak-B8	GCA_004379655.1
CCH63609.1	000000	UDPG_MGDP_dh	256	CP21_147	Campylobacter virus CP21	GCA_000902535.1
QBO63833.1	000000	MIP-T3	478	Goslar_00040	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
ARM70860.1	000000	Phage_head_chap	113	phiC120_c154	Escherichia phage phiC120	GCA_002621185.1
AFH14884.1	000000	SIG+PP-binding	140	Lu11_0346	Pseudomonas phage Lu11	GCA_000897175.1
CCE26269.1	000000	VMAP-M17	190	g246	Yersinia phage phiR1-37	GCA_000895615.1
AMM44956.1	000000	SFII-RAD3	678	SP15_158	Bacillus phage SP-15	GCA_001754685.1
ABY63155.1	000000	Ntox1	139	201phi2-1p330	Pseudomonas phage 201phi2-1	GCA_000875305.1
AXH72865.1	000000	GatB_Yqey	168	-	Myoviridae sp.	GCA_003657725.1
QBO63839.1	000000	HKD	189	Goslar_00046	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
BAE47789.1	000000	SIG+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	394	CST091	Clostridium phage c-st	GCA_000865225.1
AGS82026.1	000000	Cupin	161	PaBG_00143	Pseudomonas phage PaBG	GCA_000912555.1
AEO93500.1	000000	SUKH-SMI1	148	G_241	Bacillus virus G	GCA_000917535.1
AFH14702.1	000000	SIG+DUF1289	71	Lu11_0167A	Pseudomonas phage Lu11	GCA_000897175.1
BAE47716.1	000000	Cas_Cas6	251	CST018	Clostridium phage c-st	GCA_000865225.1
AEO93525.1	000000	SIG+SASP	76	G_266	Bacillus virus G	GCA_000917535.1
AND75212.1	000000	Big_6+Big_6	544	ME3_51	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QNI21268.1	000000	SIG+KAP-NTPase	126	-	Vibrio phage vB_pir03	GCA_014319855.1
ARM70885.1	000000	DUF5491	71	phiC120_c180	Escherichia phage phiC120	GCA_002621185.1
AND75291.1	000000	UbE1	350	ME3_130	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
BBA65345.1	000000	PNKP_ligase	404	-	Xanthomonas phage XacN1	GCA_003173815.1
AEO93473.1	000000	SIG+CACHE+TM	346	G_214	Bacillus virus G	GCA_000917535.1
AXH70921.1	000000	SIG+DASH_Hsk3	275	-	Vibrio phage BONAISHI	GCA_003441475.1
AEO93599.1	000000	Toast-rack	244	G_340	Bacillus virus G	GCA_000917535.1
AEO93841.1	000000	ClpABN-AAA	412	G_596	Bacillus virus G	GCA_000917535.1
CCE26251.1	000000	PBPI	100	g228	Yersinia phage phiR1-37	GCA_000895615.1
AGH07645.1	000000	SIG+Mt_ATP-synt_D	548	CYVG_00202	Cyanophage S-SSM6a	GCA_002710385.1
AJK27448.1	000000	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	1031	PTIM40_21	Cyanophage P-TIM40	GCA_001470935.1
ABS83813.1	000000	BirA-HTH+REase	266	0305phi8-36p029	Bacillus phage 0305phi8-36	GCA_000871045.1
CAG27194.1	000000	DUF4774	327	PPEV_gp100	Pseudomonas phage EL	GCA_000866825.1
BAG41641.1	000000	Pectate_lyase_3	679	RSL1_ORF192	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72949.1	000000	CbiX	91	RSL1_ORF321	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44163.1	000000	Tox-ABHYDROLASE2	270	PBI_SCTP2_148	Salicola phage SCTP-2	GCA_002625545.1
ABS83737.1	000000	RAD52	232	0305phi8-36p179	Bacillus phage 0305phi8-36	GCA_000871045.1
prev15ph1000000575	000000	SFI-ATPase	200	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
ABS83690.1	000000	GH43_C2	369	0305phi8-36p132	Bacillus phage 0305phi8-36	GCA_000871045.1
QCG75957.1	000000	PCNA	99	EST35_0075	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QIW90804.1	000000	GATase_6	450	GCAPEGMB_00486	Vibrio phage V07	GCA_012361095.1
AGH56934.1	000000	SET	99	CPXG_00131	Cyanophage P-RSM6	GCA_000906155.1
QDJ96574.1	000000	Nop53	144	Xoosp13_388	Xanthomonas phage Xoo-sp13	GCA_013364725.1
AQT28733.1	000000	SIG+YadA_anchor	742	YOLOSWAG_260	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AXH72871.1	000000	ADP	292	-	Myoviridae sp.	GCA_003657725.1
AGS81901.1	000000	DUF2226	91	PaBG_00017	Pseudomonas phage PaBG	GCA_000912555.1
AGH26154.1	000000	DUF3574	99	CPMG_00053	Prochlorococcus phage MED4-213	GCA_000904535.1
ASV44058.1	000000	DS	70	PBI_SCTP2_43	Salicola phage SCTP-2	GCA_002625545.1
ARV77326.1	000000	UBP12+TM+TM	153	NOXIFER_157	Pseudomonas phage Noxifer	GCA_002625005.1
ABS83613.1	000000	PBPB	95	0305phi8-36p052	Bacillus phage 0305phi8-36	GCA_000871045.1
AXH72892.1	000000	GCV_H	124	-	Myoviridae sp.	GCA_003657725.1
AEO93810.1	000000	ArsC	132	G_564	Bacillus virus G	GCA_000917535.1
QCG76201.1	000000	SIG+Epimerase	172	EST35_0320	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
ALY07217.1	000000	PTR+PTR	591	VmeM32_00231	Vibrio phage vB_VmeM-32	GCA_002608825.1
QIG65758.1	000000	DUF331	65	phiOC_p093	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGH26233.1	000000	GTF2I	51	CPMG_00132	Prochlorococcus phage MED4-213	GCA_000904535.1
BAE47791.1	000000	Nuc_deoxyrib_tr	221	CST093	Clostridium phage c-st	GCA_000865225.1
BBA65476.1	000000	Glyco_transf_9	222	-	Xanthomonas phage XacN1	GCA_003173815.1
CCE26124.1	000000	HAM	358	g100	Yersinia phage phiR1-37	GCA_000895615.1
QDB70422.1	000000	Tail_spike_N	661	CF8_0009	Aeromonas phage CF8	GCA_006384595.2
QFP93243.1	000000	SIG+HTH	109	-	Serratia phage PCH45	GCA_009187865.1
AEO93605.1	000000	SIG+Ferretin	239	G_346	Bacillus virus G	GCA_000917535.1
QGH72094.1	000000	Antibiotic-GNAT	177	N1M2_231	Klebsiella phage N1M2	GCA_010092605.1
ARM70889.1	000000	TF2SDOMAIN2	66	phiC120_c184	Escherichia phage phiC120	GCA_002621185.1
AAX44656.1	000000	Chloroa_b-bind	34	PSSM2_279	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGX01813.1	000000	IES3	66	CF95_gp091	Erwinia phage PhiEaH1	GCA_000914555.1
ASV44057.1	000000	PspC	93	PBI_SCTP2_42	Salicola phage SCTP-2	GCA_002625545.1
QIG57993.1	000000	YAEB	84	SEA_PAULODIABOLI_309	Microbacterium phage PauloDiaboli	GCA_011067425.1
AGH07719.1	000000	T4_gp9_10	340	CYVG_00276	Cyanophage S-SSM6a	GCA_002710385.1
QHJ86115.1	000000	DegT_DnrJ_EryC1	338	KKIINIFJ_00204	Pseudomonas phage PN05	GCA_009931935.1
AEO93604.1	000000	LSDAT	139	G_345	Bacillus virus G	GCA_000917535.1
QHJ86104.1	000000	DUF4795	109	KKIINIFJ_00193	Pseudomonas phage PN05	GCA_009931935.1
AFU88285.1	000000	GAGA	71	CcrColossus_gp415	Caulobacter phage CcrColossus	GCA_000899635.1
BAE47871.1	000000	Mbetalac	231	CST173	Clostridium phage c-st	GCA_000865225.1
QFP93151.1	000000	NCD2	216	-	Serratia phage PCH45	GCA_009187865.1
AXH72878.1	000000	tRNA-synt_1f	511	-	Myoviridae sp.	GCA_003657725.1
QCG75944.1	000000	VMAP-M16	113	EST35_0061	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QIW90857.1	000000	SIG+Herpes_UL32	906	GCAPEGMB_00542	Vibrio phage V07	GCA_012361095.1
ARM70752.1	000000	MA+TM	514	phiC120_c46	Escherichia phage phiC120	GCA_002621185.1
ABS83781.1	000000	TIR	148	0305phi8-36p223	Bacillus phage 0305phi8-36	GCA_000871045.1
QAU04455.1	000000	Adenylsucc_synt	370	ValB1MD_039	Vibrio phage ValB1MD	GCA_004138815.1
BAV39220.1	000000	MazG	225	BPT24_095	Tenacibaculum phage pT24	GCA_002611925.1
AEO93658.1	000000	CR-REase11	100	G_399	Bacillus virus G	GCA_000917535.1
ARV76741.1	000000	TIMbarrel	118	PHABIO_110	Pseudomonas phage Phabio	GCA_002624965.1
AFF28269.1	000000	RmlD_sub_bind	436	PAU_271	Sphingomonas phage PAU	GCA_000902455.1
ALY07056.1	000000	Amidase_3	179	VmeM32_00065	Vibrio phage vB_VmeM-32	GCA_002608825.1
QIG57819.1	000000	DUF4407	1913	SEA_PAULODIABOLI_85	Microbacterium phage PauloDiaboli	GCA_011067425.1
AGS82024.1	000000	TET-TPase	307	PaBG_00141	Pseudomonas phage PaBG	GCA_000912555.1
BAG41478.1	000000	S4	57	RSL1_ORF033	Ralstonia phage phiRSL1	GCA_000879455.1
CCE26317.1	000000	SIG+KELCH+KELCH	1302	g294	Yersinia phage phiR1-37	GCA_000895615.1
ALY07022.1	000000	FGase	233	VmeM32_00028	Vibrio phage vB_VmeM-32	GCA_002608825.1
AGS82166.1	000000	GTP_EFTU	267	PaBG_00294	Pseudomonas phage PaBG	GCA_000912555.1
ARM70846.1	000000	Soc	78	phiC120_c140	Escherichia phage phiC120	GCA_002621185.1
ARM70811.1	000000	MotA_activ+MotCF	210	phiC120_c105	Escherichia phage phiC120	GCA_002621185.1
AEO93783.1	000000	ZDNA-HTH	215	G_525	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARV77077.1	000000	WSLR	119	PHABIO_446	Pseudomonas phage Phabio	GCA_002624965.1
AEO93457.1	000000	PTS-HPr	84	G_197	Bacillus virus G	GCA_000917535.1
BAE47877.1	000000	RDRP	558	CST179	Clostridium phage c-st	GCA_000865225.1
AEO93296.1	000000	SIG+Phage_holin_6_1	118	G_25	Bacillus virus G	GCA_000917535.1
QNI21246.1	000000	PIN	325	-	Vibrio phage vB_pir03	GCA_014319855.1
QHJ86058.1	000000	DUF5427	321	KKIINIFJ_00146	Pseudomonas phage PN05	GCA_009931935.1
AGX01761.1	000000	SUFU	162	CF95_gp039	Erwinia phage PhiEaH1	GCA_000914555.1
AFH14689.1	000000	DUF4775	370	Lu11_0155	Pseudomonas phage Lu11	GCA_000897175.1
AND75284.1	000000	His_Phos_1	194	ME3_123	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QMV29170.1	000000	P22_portal	70	AP1_0473	Aeromonas phage AP1	GCA_014183365.1
AXH72876.1	000000	tRNA-synt_1b	334	-	Myoviridae sp.	GCA_003657725.1
CCE26120.1	000000	RVT	690	g096	Yersinia phage phiR1-37	GCA_000895615.1
AGS82142.1	000000	NEC	223	PaBG_00269	Pseudomonas phage PaBG	GCA_000912555.1
CCH63503.1	000000	TPP_enzyme_C	192	CP21_041	Campylobacter virus CP21	GCA_000902535.1
AXH72408.1	000000	NanE	141	-	Myoviridae sp.	GCA_003657725.1
AEO93815.1	000000	SIG+PspA	315	G_569	Bacillus virus G	GCA_000917535.1
AND75224.1	000000	SIG+Tox-HNH	150	ME3_63	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
CAG27257.1	000000	SIG+Arc	115	PPEV_gp163	Pseudomonas phage EL	GCA_000866825.1
BAE47781.1	000000	Botulinum_HA-17	146	CST083	Clostridium phage c-st	GCA_000865225.1
QIW90808.1	000000	DADA-Ligase	375	GCAPEGMB_00490	Vibrio phage V07	GCA_012361095.1
BAW98366.1	000000	CarboxypepD-reg-IG	756	FDH33_gp157	Vibrio phage pTD1	GCA_002618825.1
QNI21105.1	000000	SIG+GrpE	355	-	Vibrio phage vB_pir03	GCA_014319855.1
BAE47769.1	000000	SIG+Nucleoporin_FG2	140	CST071	Clostridium phage c-st	GCA_000865225.1
AGS81907.1	000000	DUF3962	102	PaBG_00023	Pseudomonas phage PaBG	GCA_000912555.1
QCG75940.1	000000	Ead_Ea22	199	EST35_0057	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AEO93461.1	000000	CR-ATPase9	186	G_202	Bacillus virus G	GCA_000917535.1
AFA44800.1	000000	Beta_helix	584	RaK2_00529	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
ABS83685.1	000000	Big_5	331	0305phi8-36p127	Bacillus phage 0305phi8-36	GCA_000871045.1
ASV44318.1	000000	YodL	122	PBI_SCTP2_303	Salicola phage SCTP-2	GCA_002625545.1
AUZ94834.1	000000	Cadherin_3	888	FDI40_gp022	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIX30709.1	000000	sf-sug	262	Syn7803US37_232	Synechococcus phage ACG-2014f	GCA_002594065.1
AGH56841.1	000000	Imm70	392	CPXG_00038	Cyanophage P-RSM6	GCA_000906155.1
ARV76941.1	000000	SIG+PSBP	58	PHABIO_310	Pseudomonas phage Phabio	GCA_002624965.1
BBA65530.1	000000	SERAprotease	226	-	Xanthomonas phage XacN1	GCA_003173815.1
AEO93326.1	000000	SIG+PgpA	175	G_55	Bacillus virus G	GCA_000917535.1
CCH63694.1	000000	Ferretin	143	CP21_234	Campylobacter virus CP21	GCA_000902535.1
ARM70856.1	000000	Dmd	62	phiC120_c150	Escherichia phage phiC120	GCA_002621185.1
CCH63656.1	000000	Herpes_ori_bp	342	CP21_194	Campylobacter virus CP21	GCA_000902535.1
QDB70433.1	000000	PEP-utilisers-N	130	CF8_0021	Aeromonas phage CF8	GCA_006384595.2
AIR93560.1	000000	Ferredoxin-RRM	81	psaC	Prochlorococcus phage P-TIM68	GCA_001503075.1
QHJ86181.1	000000	PRELI	116	KKIINIFJ_00271	Pseudomonas phage PN05	GCA_009931935.1
QAU04445.1	000000	Peptidase_S49_N+Peptidase_S49	303	ValB1MD_010	Vibrio phage ValB1MD	GCA_004138815.1
QIW90860.1	000000	VGCC_alpha2	293	GCAPEGMB_00545	Vibrio phage V07	GCA_012361095.1
QNI21038.1	000000	PT-COG5412	152	-	Vibrio phage vB_pir03	GCA_014319855.1
QHJ85986.1	000000	Alginate_lyase2+FAP	392	KKIINIFJ_00074	Pseudomonas phage PN05	GCA_009931935.1
AND75289.1	000000	PcfJ	549	ME3_128	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXH72904.1	000000	FG-GAP_2+Gly_rich	5045	-	Myoviridae sp.	GCA_003657725.1
BBA65339.1	000000	RHOD-CDC25	94	-	Xanthomonas phage XacN1	GCA_003173815.1
BAV39147.1	000000	ADK+DUF5051	389	BPT24_025	Tenacibaculum phage pT24	GCA_002611925.1
QCG76243.1	000000	ADH_N	300	EST35_0363	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAE47782.1	000000	RicinB_lectin_2	286	CST084	Clostridium phage c-st	GCA_000865225.1
AGH07553.1	000000	SIG+DSBH	199	CYVG_00109	Cyanophage S-SSM6a	GCA_002710385.1
AMO43223.1	000000	RE_MjaI	172	R1080702_218	Cyanophage S-RIM32	GCA_001754165.1
BAE47711.1	000000	BZIP	496	CST013	Clostridium phage c-st	GCA_000865225.1
QDB70431.1	000000	End_N_terminal	318	CF8_0019	Aeromonas phage CF8	GCA_006384595.2
ABS83600.1	000000	DNA_pol3_beta_2+DNA_pol3_beta_3	361	0305phi8-36p039	Bacillus phage 0305phi8-36	GCA_000871045.1
ARM70751.1	000000	Phage_hub_GP28	156	phiC120_c45	Escherichia phage phiC120	GCA_002621185.1
AGS82111.1	000000	HTH_43	182	PaBG_00237	Pseudomonas phage PaBG	GCA_000912555.1
AUZ94898.1	000000	N6_Mtase	73	FDI40_gp094	Agrobacterium phage Atu_ph07	GCA_002628245.1
BAE47758.1	000000	SIG+PDDEXK_1	384	CST060	Clostridium phage c-st	GCA_000865225.1
ARM70891.1	000000	DUF5499	97	phiC120_c186	Escherichia phage phiC120	GCA_002621185.1
QHJ86091.1	000000	TUDOR	142	KKIINIFJ_00179	Pseudomonas phage PN05	GCA_009931935.1
QDJ96278.1	000000	D6	39	Xoosp13_91	Xanthomonas phage Xoo-sp13	GCA_013364725.1
ABS83724.1	000000	SIG+FN3+APATPase	406	0305phi8-36p166	Bacillus phage 0305phi8-36	GCA_000871045.1
ARM70959.1	000000	Phage_FRD3	75	phiC120_c254	Escherichia phage phiC120	GCA_002621185.1
BAG41678.1	000000	Nmad1	232	RSL1_ORF229	Ralstonia phage phiRSL1	GCA_000879455.1
ARM70759.1	000000	DUF3045	89	phiC120_c53	Escherichia phage phiC120	GCA_002621185.1
QHJ85934.1	000000	Beta-helix+GDSL	1571	KKIINIFJ_00022	Pseudomonas phage PN05	GCA_009931935.1
ARM70771.1	000000	DAHP_synth_1	330	phiC120_c65	Escherichia phage phiC120	GCA_002621185.1
AXQ70560.1	000000	Fe_bilin_red	54	HOU04_gp161	Synechococcus phage S-T4	GCA_003443335.1
AEO93445.1	000000	LysM+LysM+LysM	840	G_185	Bacillus virus G	GCA_000917535.1
QDH83666.1	000000	DUF4140	55	H1O15_gp084	Achromobacter phage Motura	GCA_006964305.1
QIG57881.1	000000	PG-binding+PG-binding+PG-binding+PG-binding	613	SEA_PAULODIABOLI_193	Microbacterium phage PauloDiaboli	GCA_011067425.1
BAV39179.1	000000	SIG+UPF0227	185	BPT24_056	Tenacibaculum phage pT24	GCA_002611925.1
QIG58032.1	000000	eIF-5_eIF-2B	39	SEA_PAULODIABOLI_348	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72850.1	000000	Peptidase_M29	410	-	Myoviridae sp.	GCA_003657725.1
BAE47723.1	000000	P22_AR_N	305	CST025	Clostridium phage c-st	GCA_000865225.1
AGH26145.1	000000	ACPS	152	CPMG_00044	Prochlorococcus phage MED4-213	GCA_000904535.1
AXH72880.1	000000	EMAP	370	-	Myoviridae sp.	GCA_003657725.1
AXQ70528.1	000000	DUF5585	482	HOU04_gp129	Synechococcus phage S-T4	GCA_003443335.1
ABS83788.1	000000	SIG+ZDNA-HTH	124	0305phi8-36p230	Bacillus phage 0305phi8-36	GCA_000871045.1
BAE47725.1	000000	PemK_toxin	220	CST027	Clostridium phage c-st	GCA_000865225.1
AGH07638.1	000000	SIG+NESP55	565	CYVG_00195	Cyanophage S-SSM6a	GCA_002710385.1
QIG57975.1	000000	DUF5580	151	SEA_PAULODIABOLI_291	Microbacterium phage PauloDiaboli	GCA_011067425.1
ASV44455.1	000000	CITB-HTH	109	PBI_SCTP2_440	Salicola phage SCTP-2	GCA_002625545.1
AIX30729.1	000000	N_methyl	126	Syn7803US37_252	Synechococcus phage ACG-2014f	GCA_002594065.1
QBZ70706.1	000000	IMP	108	pETSU_125	Edwardsiella virus pEt-SU	GCA_004800915.1
ARM70879.1	000000	DUF5487	79	phiC120_c174	Escherichia phage phiC120	GCA_002621185.1
AEO93922.1	000000	TRPR-HTH	98	G_679	Bacillus virus G	GCA_000917535.1
QHJ85964.1	000000	VgrG+Immank	218	KKIINIFJ_00052	Pseudomonas phage PN05	GCA_009931935.1
QHJ86119.1	000000	HHH_8	113	KKIINIFJ_00208	Pseudomonas phage PN05	GCA_009931935.1
QIW90792.1	000000	primpol+OTU	793	GCAPEGMB_00474	Vibrio phage V07	GCA_012361095.1
BAV39354.1	000000	DUF4494	145	BPT24_234	Tenacibaculum phage pT24	GCA_002611925.1
QIW90807.1	000000	SIG+COOHNH2ligase	281	GCAPEGMB_00489	Vibrio phage V07	GCA_012361095.1
SBV38198.1	000000	HemS	91	BN7874_029	Phage NCTB	GCA_900092385.1
AFF28095.1	000000	TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM	1096	PAU_97	Sphingomonas phage PAU	GCA_000902455.1
AMM44863.1	000000	Drf_FH1	4401	SP15_064	Bacillus phage SP-15	GCA_001754685.1
AMM45075.1	000000	SIG+EIF4E-T	71	SP15_268	Bacillus phage SP-15	GCA_001754685.1
BAE47756.1	000000	DnaB	498	CST058	Clostridium phage c-st	GCA_000865225.1
QIG65963.1	000000	Ax_dynein_light	191	phiOC_p321	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ARM70791.1	000000	E2F	130	phiC120_c85	Escherichia phage phiC120	GCA_002621185.1
QIG65822.1	000000	RAG1	146	phiOC_p157	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIW90862.1	000000	Phage_endo_I	135	GCAPEGMB_00547	Vibrio phage V07	GCA_012361095.1
AGS82154.1	000000	O6MGT-HTH	116	PaBG_00281	Pseudomonas phage PaBG	GCA_000912555.1
BAE47889.1	000000	SIG+TM+REase	210	CST191	Clostridium phage c-st	GCA_000865225.1
AXH72844.1	000000	D5ATPase	510	-	Myoviridae sp.	GCA_003657725.1
AEO93331.1	000000	SIG+TM+TM+TM+TM+TM	237	G_60	Bacillus virus G	GCA_000917535.1
CCH63548.1	000000	PIG-L	190	CP21_086	Campylobacter virus CP21	GCA_000902535.1
AFH14856.1	000000	DUF1413	121	Lu11_0318	Pseudomonas phage Lu11	GCA_000897175.1
AMM44991.1	000000	SfsA_N+SfsA	241	SP15_191	Bacillus phage SP-15	GCA_001754685.1
AXH72719.1	000000	Tox-DDRGK	140	-	Myoviridae sp.	GCA_003657725.1
QMV29146.1	000000	Phage-tail-tape	100	AP1_0445	Aeromonas phage AP1	GCA_014183365.1
AXH72874.1	000000	SIG+OprB	375	-	Myoviridae sp.	GCA_003657725.1
SBV38333.1	000000	HDOD	282	BN7874_164	Phage NCTB	GCA_900092385.1
AMM44839.1	000000	Phage_tail_S	167	SP15_040	Bacillus phage SP-15	GCA_001754685.1
AIA64996.1	000000	LysM	99	S13_199	Cronobacter phage S13	GCA_001503575.1
BAX25552.1	000000	Ribopeptidemod-ATPgrasp	319	BPT24_063	Tenacibaculum phage pT24	GCA_002611925.1
AFA44579.1	000000	Rio2_N	116	RaK2_00306	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57838.1	000000	Primpol+PriCT1+D5N+D5ATPase	881	SEA_PAULODIABOLI_104	Microbacterium phage PauloDiaboli	GCA_011067425.1
ASR76063.1	000000	WXG	625	PBI_BELLAMY_16	Synechococcus phage Bellamy	GCA_002627525.1
BAG41754.2	000000	SIG+DEATH	192	RSL1_ORF308	Ralstonia phage phiRSL1	GCA_000879455.1
AGN30212.1	000000	Tox-HNH	235	VPFG_00212	Vibrio phage nt-1	GCA_000910195.2
SBV38433.1	000000	Phytase-like	1330	BN7874_240	Phage NCTB	GCA_900092385.1
AFH14555.1	000000	LYTTR	170	Lu11_0024	Pseudomonas phage Lu11	GCA_000897175.1
ABS83780.1	000000	SIG+MED27	89	0305phi8-36p222	Bacillus phage 0305phi8-36	GCA_000871045.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ95045.1	000000	MCP-N	87	FDI40_gp270	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIR93488.1	000000	SIG+2OG-FeII_Oxy_5	231	AVU42_gp151	Prochlorococcus phage P-TIM68	GCA_001503075.1
QDH83647.1	000000	PARM	543	H1O15_gp141	Achromobacter phage Motura	GCA_006964305.1
BAE47891.1	000000	FTSK	621	CST193	Clostridium phage c-st	GCA_000865225.1
QHJ78858.1	000000	GP38	180	-	Myoviridae sp.	GCA_012593985.1
AEO93415.1	000000	SIG+VirB4-FtsK	549	G_155	Bacillus virus G	GCA_000917535.1
ABS83659.1	000000	SIG+RDRP	1218	0305phi8-36p099	Bacillus phage 0305phi8-36	GCA_000871045.1
AGX01849.1	000000	ABC-ATPase	154	CF95_gp127	Erwinia phage PhiEaH1	GCA_000914555.1
QGH72036.1	000000	SIG+Tox-EndoU	94	N1M2_173	Klebsiella phage N1M2	GCA_010092605.1
AFN39149.1	000000	LpxC	88	CC2_114	Aeromonas phage CC2	GCA_000903495.1
AND75439.1	000000	CAD	119	ME3_278	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
BAE47780.1	000000	Clenterotox+HA70_C	623	CST082	Clostridium phage c-st	GCA_000865225.1
QIW90743.1	000000	DUF4055	526	GCAPEGMB_00424	Vibrio phage V07	GCA_012361095.1
BAE47757.1	000000	Toprim_2	325	CST059	Clostridium phage c-st	GCA_000865225.1
ARM70862.1	000000	sGTP-MglA	182	phiC120_c156	Escherichia phage phiC120	GCA_002621185.1
AMR59879.1	000000	CPSF73-100_C	57	SEGD1_232	Enterobacteria phage SEGD1	GCA_002601865.1
ARM70854.1	000000	Imm_superinfect	82	phiC120_c148	Escherichia phage phiC120	GCA_002621185.1
QDH50677.1	000000	WEMBL	643	-	Synechococcus phage S-B43	GCA_006869725.1
BAV39189.1	000000	DUF2362	116	BPT24_066	Tenacibaculum phage pT24	GCA_002611925.1
AUZ95444.1	000000	HxxxH	235	FDI40_gp705	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGH26206.1	000000	NdhS	65	CPMG_00105	Prochlorococcus phage MED4-213	GCA_000904535.1
AEO93618.1	000000	DUF2460	96	G_359	Bacillus virus G	GCA_000917535.1
AEO93798.1	000000	ParBC	130	G_541	Bacillus virus G	GCA_000917535.1
AUZ94990.1	000000	Radial_spoke_3	272	FDI40_gp208	Agrobacterium phage Atu_ph07	GCA_002628245.1
AND75277.1	000000	Fer2_BFD	57	ME3_116	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QIG57922.1	000000	SIG+PhoD	913	SEA_PAULODIABOLI_237	Microbacterium phage PauloDiaboli	GCA_011067425.1
CCH63704.1	000000	DUF4501	78	CP21_244	Campylobacter virus CP21	GCA_000902535.1
AND75256.1	000000	PBFP24	121	ME3_95	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AXH72509.1	000000	SIG+RRF	190	-	Myoviridae sp.	GCA_003657725.1
CCH63491.1	000000	ParB-HTH	311	CP21_029	Campylobacter virus CP21	GCA_000902535.1
AFF28072.1	000000	PIWI	150	PAU_74	Sphingomonas phage PAU	GCA_000902455.1
AUZ94832.1	000000	Cadherin-Repeats	1168	FDI40_gp020	Agrobacterium phage Atu_ph07	GCA_002628245.1
AND75435.1	000000	Chromo-N	1183	ME3_274	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QCG75913.1	000000	DUF4366	47	EST35_0029	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
prevph1000000292	000000	SIG+Glyco_tranf_2_4	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
ARM70882.1	000000	DUF5486	57	phiC120_c177	Escherichia phage phiC120	GCA_002621185.1
CCH63558.1	000000	SIG+PTR	1283	CP21_096	Campylobacter virus CP21	GCA_000902535.1
SBV38223.1	000000	TBOX	208	BN7874_054	Phage NCTB	GCA_900092385.1
ASV44183.1	000000	PARP	154	PBI_SCTP2_168	Salicola phage SCTP-2	GCA_002625545.1
AFF28134.1	000000	HU-CCDC81	180	PAU_136	Sphingomonas phage PAU	GCA_000902455.1
AUZ95258.1	000000	DUF1127	47	FDI40_gp499	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXH72903.1	000000	SIG+SpoIID	219	-	Myoviridae sp.	GCA_003657725.1
AXH72622.1	000000	WCAK	119	-	Myoviridae sp.	GCA_003657725.1
AGX01936.1	000000	DUF4074	346	CF95_gp214	Erwinia phage PhiEaH1	GCA_000914555.1
CCH63650.1	000000	A32	182	CP21_188	Campylobacter virus CP21	GCA_000902535.1
QIG65898.1	000000	PspA_IM30	136	phiOC_p237	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QAU04457.1	000000	YqeY	140	ValB1MD_043	Vibrio phage ValB1MD	GCA_004138815.1
AMM44949.1	000000	Glyphos_transf	355	SP15_151	Bacillus phage SP-15	GCA_001754685.1
ABS83703.1	000000	TM+Thermonuclease	1930	0305phi8-36p145	Bacillus phage 0305phi8-36	GCA_000871045.1
SBV38458.1	000000	baeRF1	306	BN7874_255	Phage NCTB	GCA_900092385.1
AIX30488.1	000000	SIG+PTSEIIA1	653	Syn7803US37_11	Synechococcus phage ACG-2014f	GCA_002594065.1
QDB70354.1	000000	Phage_Arf	172	CF8_0185	Aeromonas phage CF8	GCA_006384595.2
SBV38409.1	000000	DarA-C	156	BN7874_225	Phage NCTB	GCA_900092385.1
ARM70855.1	000000	SIG+DUF5481	122	phiC120_c149	Escherichia phage phiC120	GCA_002621185.1
QIG65952.1	000000	SIG+MIP-T3	55	phiOC_p310	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
ASV44504.1	000000	CheW	139	PBI_SCTP2_489	Salicola phage SCTP-2	GCA_002625545.1
AUZ94885.1	000000	DUF3450	127	FDI40_gp076	Agrobacterium phage Atu_ph07	GCA_002628245.1
AGH07667.1	000000	SlyX	99	CYVG_00224	Cyanophage S-SSM6a	GCA_002710385.1
BBA65332.1	000000	PCYCGC	65	-	Xanthomonas phage XacN1	GCA_003173815.1
AUZ95334.1	000000	BetaPropeller+BetaPropeller	1438	FDI40_gp575	Agrobacterium phage Atu_ph07	GCA_002628245.1
AIA64856.1	000000	SIG+Chelatase-AAA	283	S13_057	Cronobacter phage S13	GCA_001503575.1
QAU04542.1	000000	T4_neck-protein	228	ValB1MD_255	Vibrio phage ValB1MD	GCA_004138815.1
AEV89647.1	000000	Ferredoxin-betagrasp	84	OBP_210	Pseudomonas phage OBP	GCA_000896635.1
ARM70877.1	000000	Gp45_2	62	phiC120_c172	Escherichia phage phiC120	GCA_002621185.1
AMM44870.1	000000	SIG+NHase_beta	110	SP15_071	Bacillus phage SP-15	GCA_001754685.1
AMM44917.1	000000	N-OB+HDRnase	314	SP15_119	Bacillus phage SP-15	GCA_001754685.1
AMM45101.1	000000	S-l_SbsC_C	163	SP15_293	Bacillus phage SP-15	GCA_001754685.1
BBA65309.1	000000	Imm49	216	-	Xanthomonas phage XacN1	GCA_003173815.1
CCH63549.1	000000	Polysacc_deac_1	181	CP21_087	Campylobacter virus CP21	GCA_000902535.1
AGH56864.1	000000	CCDC106	73	CPXG_00061	Cyanophage P-RSM6	GCA_000906155.1
QHJ86036.1	000000	Glyco_transf_4+Glycos_transf_1	478	KKIINIFJ_00124	Pseudomonas phage PN05	GCA_009931935.1
ASV44180.1	000000	SIG+DUF4376	141	PBI_SCTP2_165	Salicola phage SCTP-2	GCA_002625545.1
AND75243.1	000000	RNA-Helicase	227	ME3_82	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
BAE47807.1	000000	SIG+SUN	230	CST109	Clostridium phage c-st	GCA_000865225.1
AGS82095.1	000000	DUF3138	309	PaBG_00220	Pseudomonas phage PaBG	GCA_000912555.1
AIT14205.1	000000	SIG+HU-IHF	82	PBI_121Q_315	Escherichia phage 121Q	GCA_000926855.1
AMM44913.1	000000	Zw10	78	SP15_115	Bacillus phage SP-15	GCA_001754685.1
QIG65681.1	000000	Pep_deformylase	164	phiOC_p015	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AGS81905.1	000000	GlobuloviralATPase	151	PaBG_00021	Pseudomonas phage PaBG	GCA_000912555.1
AMM44959.1	000000	SIG+FTSK	544	SP15_161	Bacillus phage SP-15	GCA_001754685.1
QIG65791.1	000000	Apolipoprotein	104	phiOC_p126	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AEO93825.1	000000	SIG+CRP-HTH	136	G_580	Bacillus virus G	GCA_000917535.1
AJT60932.1	000000	Ub-RnfH	79	AVU32_gp091	Vibrio phage ValKK3	GCA_001501635.1
SBV38355.1	000000	ISOCOT	338	BN7874_186	Phage NCTB	GCA_900092385.1
QIW90755.1	000000	TM+Phage-tail-tape	812	GCAPEGMB_00436	Vibrio phage V07	GCA_012361095.1
ASV44111.1	000000	NIF	190	PBI_SCTP2_96	Salicola phage SCTP-2	GCA_002625545.1
AUZ95375.1	000000	DUF4175	300	FDI40_gp616	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEH03732.1	000000	Peptidase_M20	189	309	Pseudomonas phage PhiPA3	GCA_001502095.1
AEO93573.1	000000	SWIRM	181	G_314	Bacillus virus G	GCA_000917535.1
AGH26257.1	000000	DNAglycofused-2OGFEDO	254	CPMG_00156	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26266.1	000000	GDC-P+Beta_elim_lyase	914	CPMG_00165	Prochlorococcus phage MED4-213	GCA_000904535.1
ARM70876.1	000000	Phage_RpbA	138	phiC120_c171	Escherichia phage phiC120	GCA_002621185.1
AMM44981.1	000000	Fer4_13	76	SP15_183	Bacillus phage SP-15	GCA_001754685.1
AEO93930.1	000000	SIG+Spc7	133	G_687	Bacillus virus G	GCA_000917535.1
ARM70971.1	000000	GP57	76	phiC120_c266	Escherichia phage phiC120	GCA_002621185.1
ALY07064.1	000000	Vps54_N	189	VmeM32_00073	Vibrio phage vB_VmeM-32	GCA_002608825.1
QDH83396.1	000000	zf-C2H2_jaz	266	H1O15_gp066	Achromobacter phage Motura	GCA_006964305.1
QCG76142.1	000000	Sod_Fe_N+Sod_Fe_C	182	EST35_0261	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AMM45109.1	000000	ZZ-like	146	SP15_301	Bacillus phage SP-15	GCA_001754685.1
ASR76196.1	000000	TANGO2	46	PBI_BELLAMY_151	Synechococcus phage Bellamy	GCA_002627525.1
AEO93885.1	000000	PolB	101	G_642	Bacillus virus G	GCA_000917535.1
AIR93490.1	000000	Glycolytic	354	AVU42_gp153	Prochlorococcus phage P-TIM68	GCA_001503075.1
QBO63804.1	000000	SIG+Ad_Cy_reg	270	Goslar_00011	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QIG57816.1	000000	Phage_portal	578	SEA_PAULODIABOLI_82	Microbacterium phage PauloDiaboli	GCA_011067425.1
QCG76030.1	000000	CEND1	798	EST35_0148	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76051.1	000000	SIG+HCR	136	EST35_0170	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
BAE47864.1	000000	HOOK	523	CST166	Clostridium phage c-st	GCA_000865225.1
ARV76676.1	000000	Imm60	278	PHABIO_45	Pseudomonas phage Phabio	GCA_002624965.1
ARV77438.1	000000	SIG+FlgT_C	93	NOXIFER_273	Pseudomonas phage Noxifer	GCA_002625005.1
BAV39138.1	000000	SIG+Tox-PLA2+TM	202	BPT24_016	Tenacibaculum phage pT24	GCA_002611925.1
AEO93905.1	000000	SIG+OrfB_IS605+OrfB_Zn_ribbon	399	G_662	Bacillus virus G	GCA_000917535.1
ARM70755.1	000000	DUF5498	97	phiC120_c49	Escherichia phage phiC120	GCA_002621185.1
QCW23090.1	000000	SprA_N+AdoMet_dc	1070	-	Synechococcus phage S-B05	GCA_006083695.1
AEO93408.1	000000	Replic_Relax	274	G_146	Bacillus virus G	GCA_000917535.1
AXQ69853.1	000000	RMF	44	CcrSC_gp271c	Caulobacter phage CcrSC	GCA_003443315.1
BAG41637.1	000000	Phage_head_fibr	1091	RSL1_ORF188	Ralstonia phage phiRSL1	GCA_000879455.1
AIX30757.1	000000	BACTERIALFRINGE	205	Syn7803US37_280	Synechococcus phage ACG-2014f	GCA_002594065.1
AUZ94861.1	000000	PAS+PAS+PAS	536	FDI40_gp049	Agrobacterium phage Atu_ph07	GCA_002628245.1
AEV89463.1	000000	SIG+Glyco_tranf_2_5	149	OBP_026	Pseudomonas phage OBP	GCA_000896635.1
QBJ02907.1	000000	VioE	69	PSA21_381	Pseudomonas phage Psa21	GCA_004340405.1
QIW90754.1	000000	Phage_TAC_4	135	GCAPEGMB_00435	Vibrio phage V07	GCA_012361095.1
AMM44947.1	000000	GT4	394	SP15_149	Bacillus phage SP-15	GCA_001754685.1
ARM70833.1	000000	motB	164	phiC120_c127	Escherichia phage phiC120	GCA_002621185.1
QNI21263.1	000000	Asp_Glu_race	394	-	Vibrio phage vB_pir03	GCA_014319855.1
AMM44925.1	000000	SIG+Nuc_deoxyrib_tr	316	SP15_127	Bacillus phage SP-15	GCA_001754685.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ95203.1	000000	DIT1_PvcA	87	FDI40_gp444	Agrobacterium phage Atu_ph07	GCA_002628245.1
AXQ69501.1	000000	HTH_38	93	CcrBL9_gp477	Caulobacter phage CcrBL9	GCA_003443295.1
QKE54360.1	000000	RPN13	231	ACSA002_0460	Salmonella phage vB_SalM_SA002	GCA_014131285.1
CCE26155.1	000000	HU-IHF	120	g131	Yersinia phage phiR1-37	GCA_000895615.1
prev15ph1000000021	000000	Flg_new	1335	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QDB70482.1	000000	DUF4503	86	CF8_0071	Aeromonas phage CF8	GCA_006384595.2
AUZ94922.1	000000	STAT	50	FDI40_gp130	Agrobacterium phage Atu_ph07	GCA_002628245.1
CCH63593.1	000000	DO-GTPase2	79	CP21_131	Campylobacter virus CP21	GCA_000902535.1
AMM44968.1	000000	PilZ	117	SP15_170	Bacillus phage SP-15	GCA_001754685.1
AEO93756.1	000000	ResQ-YqkK	69	G_498	Bacillus virus G	GCA_000917535.1
AGH26171.1	000000	ivWA	82	CPMG_00070	Prochlorococcus phage MED4-213	GCA_000904535.1
QDJ96255.1	000000	FtsK+HerA	454	Xoosp13_68	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QHJ78987.1	000000	DUF5320	120	-	Myoviridae sp.	GCA_012593985.1
AEO93373.1	000000	SIG+Tox-ParB	129	G_111	Bacillus virus G	GCA_000917535.1
AIR93564.1	000000	PsaD	155	psaD	Prochlorococcus phage P-TIM68	GCA_001503075.1
QCG76164.1	000000	Redoxin	111	EST35_0283	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
AGS82031.1	000000	Tox-ART-HYD3	121	PaBG_00149	Pseudomonas phage PaBG	GCA_000912555.1
BAE47816.1	000000	D5N	451	CST118	Clostridium phage c-st	GCA_000865225.1
AFF28121.1	000000	PP2A	229	PAU_123	Sphingomonas phage PAU	GCA_000902455.1
AXQ70437.1	000000	Tail-fiber	722	HOU04_gp038	Synechococcus phage S-T4	GCA_003443335.1
QBJ02699.1	000000	DUF2967	385	PSA21_172	Pseudomonas phage Psa21	GCA_004340405.1
AGH26210.1	000000	TauD	90	CPMG_00109	Prochlorococcus phage MED4-213	GCA_000904535.1
ASR76064.1	000000	GLYCO+ANTHRAXPAG-N	1993	PBI_BELLAMY_17	Synechococcus phage Bellamy	GCA_002627525.1
ARM70815.1	000000	Phage_T4_Ndd	148	phiC120_c109	Escherichia phage phiC120	GCA_002621185.1
AMO43145.1	000000	RimK-ATPgrasp+ATPgraspC	292	R1080702_136	Cyanophage S-RIM32	GCA_001754165.1
AEO93603.1	000000	FAD-NAD-dep-oxidoreductase	315	G_344	Bacillus virus G	GCA_000917535.1
BAE47764.1	000000	DUF1852	177	CST066	Clostridium phage c-st	GCA_000865225.1
AFC21978.1	000000	RNASE-EG	394	GAP32_518	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AMM44927.1	000000	adh_short_C2	214	SP15_129	Bacillus phage SP-15	GCA_001754685.1
AFH14808.1	000000	SpermGS-ATPgrasp	462	Lu11_0271	Pseudomonas phage Lu11	GCA_000897175.1
AMM45092.1	000000	SIG+SpoIIID	94	SP15_284	Bacillus phage SP-15	GCA_001754685.1
QDJ96398.1	000000	Fzo_mitofusin	99	Xoosp13_212	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SBV38334.1	000000	Paralemmin	90	BN7874_165	Phage NCTB	GCA_900092385.1
AGS82139.2	000000	SIG+Ribonuc_P_40	627	PaBG_00265	Pseudomonas phage PaBG	GCA_000912555.1
AEO93636.1	000000	gp32	212	G_377	Bacillus virus G	GCA_000917535.1
AMM44953.1	000000	PGM_PMM_I+PGM_PMM_II+PGM_PMM_III+PGM_PMM_IV	476	SP15_155	Bacillus phage SP-15	GCA_001754685.1
ASV44083.1	000000	SIG+IPI_T4	92	PBI_SCTP2_68	Salicola phage SCTP-2	GCA_002625545.1
AEO93540.1	000000	CTP_transf_like	212	G_281	Bacillus virus G	GCA_000917535.1
AEO93687.1	000000	Phage_XkdX	46	G_429	Bacillus virus G	GCA_000917535.1
QHJ86066.1	000000	SIG+MlaC	204	KKIINIFJ_00154	Pseudomonas phage PN05	GCA_009931935.1
AEO93926.1	000000	Abhydrolase_2	119	G_683	Bacillus virus G	GCA_000917535.1
AUZ95419.1	000000	Peptidase-M15	55	FDI40_gp662	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABY62888.1	000000	ComEA-HHH	86	201phi2-1p055	Pseudomonas phage 201phi2-1	GCA_000875305.1
ASV44156.1	000000	BetaPropeller+BetaPropeller+VWA+VWA	3096	PBI_SCTP2_141	Salicola phage SCTP-2	GCA_002625545.1
QIW90752.1	000000	DUF4128	246	GCAPEGMB_00433	Vibrio phage V07	GCA_012361095.1
QIG57994.1	000000	SIG+PG-binding	244	SEA_PAULODIABOLI_310	Microbacterium phage PauloDiaboli	GCA_011067425.1
CCE26248.1	000000	SIG+Flu_PA	243	g225	Yersinia phage phiR1-37	GCA_000895615.1
AFH14545.1	000000	KORA	99	Lu11_0014	Pseudomonas phage Lu11	GCA_000897175.1
AAQ17940.1	000000	-	34	Aeh1ORF275c	Aeromonas virus Aeh1	GCA_000843245.1
QDH83684.1	000000	-	44	H1O15_gp277	Achromobacter phage Motura	GCA_006964305.1
QDH83525.1	000000	-	65	H1O15_gp281	Achromobacter phage Motura	GCA_006964305.1
QDH83526.1	000000	-	65	H1O15_gp280	Achromobacter phage Motura	GCA_006964305.1
QDH83621.1	000000	-	65	H1O15_gp167	Achromobacter phage Motura	GCA_006964305.1
QDH83584.1	000000	-	31	H1O15_gp204	Achromobacter phage Motura	GCA_006964305.1
QDH83591.1	000000	-	150	H1O15_gp197	Achromobacter phage Motura	GCA_006964305.1
QDH83451.1	000000	-	83	H1O15_gp043	Achromobacter phage Motura	GCA_006964305.1
QDH83426.1	000000	-	121	H1O15_gp018	Achromobacter phage Motura	GCA_006964305.1
QDH83394.1	000000	-	135	H1O15_gp068	Achromobacter phage Motura	GCA_006964305.1
QDH83597.1	000000	-	89	H1O15_gp191	Achromobacter phage Motura	GCA_006964305.1
QDH83490.1	000000	-	162	H1O15_gp316	Achromobacter phage Motura	GCA_006964305.1
QDH83617.1	000000	-	86	H1O15_gp171	Achromobacter phage Motura	GCA_006964305.1
QDH83612.1	000000	-	113	H1O15_gp176	Achromobacter phage Motura	GCA_006964305.1
QDH83538.1	000000	-	112	H1O15_gp250	Achromobacter phage Motura	GCA_006964305.1
QDH83509.1	000000	-	133	H1O15_gp297	Achromobacter phage Motura	GCA_006964305.1
QDH83422.1	000000	-	133	H1O15_gp013	Achromobacter phage Motura	GCA_006964305.1
QDH83630.1	000000	-	173	H1O15_gp158	Achromobacter phage Motura	GCA_006964305.1
QDH83454.1	000000	-	170	H1O15_gp046	Achromobacter phage Motura	GCA_006964305.1
QDH83573.1	000000	-	131	H1O15_gp215	Achromobacter phage Motura	GCA_006964305.1
QDH83541.1	000000	-	106	H1O15_gp247	Achromobacter phage Motura	GCA_006964305.1
QDH83497.1	000000	-	104	H1O15_gp309	Achromobacter phage Motura	GCA_006964305.1
QDH83391.1	000000	-	67	H1O15_gp071	Achromobacter phage Motura	GCA_006964305.1
QDH83528.1	000000	-	101	H1O15_gp014	Achromobacter phage Motura	GCA_006964305.1
QDH83618.1	000000	-	92	H1O15_gp170	Achromobacter phage Motura	GCA_006964305.1
QDH83456.1	000000	-	423	H1O15_gp048	Achromobacter phage Motura	GCA_006964305.1
QDH83714.1	000000	-	600	H1O15_gp113	Achromobacter phage Motura	GCA_006964305.1
QDH83557.1	000000	-	115	H1O15_gp231	Achromobacter phage Motura	GCA_006964305.1
QDH83668.1	000000	-	115	H1O15_gp082	Achromobacter phage Motura	GCA_006964305.1
QDH83544.1	000000	-	54	H1O15_gp244	Achromobacter phage Motura	GCA_006964305.1
QDH83502.1	000000	-	252	H1O15_gp304	Achromobacter phage Motura	GCA_006964305.1
QDH83619.1	000000	-	208	H1O15_gp169	Achromobacter phage Motura	GCA_006964305.1
QDH83566.1	000000	-	117	H1O15_gp222	Achromobacter phage Motura	GCA_006964305.1
QDH83542.1	000000	-	100	H1O15_gp246	Achromobacter phage Motura	GCA_006964305.1
QDH83488.1	000000	-	100	H1O15_gp318	Achromobacter phage Motura	GCA_006964305.1
QDH83669.1	000000	-	119	H1O15_gp081	Achromobacter phage Motura	GCA_006964305.1
QDH83513.1	000000	-	132	H1O15_gp293	Achromobacter phage Motura	GCA_006964305.1
QDH83514.1	000000	-	51	H1O15_gp292	Achromobacter phage Motura	GCA_006964305.1
QDH83700.1	000000	-	58	H1O15_gp261	Achromobacter phage Motura	GCA_006964305.1
QDH83649.1	000000	-	75	H1O15_gp101	Achromobacter phage Motura	GCA_006964305.1
QDH83715.1	000000	-	75	H1O15_gp112	Achromobacter phage Motura	GCA_006964305.1
QDH83534.1	000000	-	79	H1O15_gp254	Achromobacter phage Motura	GCA_006964305.1
QDH83452.1	000000	-	85	H1O15_gp044	Achromobacter phage Motura	GCA_006964305.1
QDH83511.1	000000	-	109	H1O15_gp295	Achromobacter phage Motura	GCA_006964305.1
QDH83470.1	000000	-	109	H1O15_gp336	Achromobacter phage Motura	GCA_006964305.1
QDH83629.1	000000	-	142	H1O15_gp159	Achromobacter phage Motura	GCA_006964305.1
QDH83664.1	000000	-	94	H1O15_gp086	Achromobacter phage Motura	GCA_006964305.1
QDH83397.1	000000	-	195	H1O15_gp065	Achromobacter phage Motura	GCA_006964305.1
QDH83574.1	000000	-	81	H1O15_gp214	Achromobacter phage Motura	GCA_006964305.1
QDH83512.1	000000	-	352	H1O15_gp294	Achromobacter phage Motura	GCA_006964305.1
QDH83492.1	000000	-	212	H1O15_gp314	Achromobacter phage Motura	GCA_006964305.1
QDH83554.1	000000	-	124	H1O15_gp234	Achromobacter phage Motura	GCA_006964305.1
QDH83593.1	000000	-	422	H1O15_gp195	Achromobacter phage Motura	GCA_006964305.1
QDH83460.1	000000	-	571	H1O15_gp052	Achromobacter phage Motura	GCA_006964305.1
QDH83540.1	000000	-	184	H1O15_gp248	Achromobacter phage Motura	GCA_006964305.1
QDH83489.1	000000	-	185	H1O15_gp317	Achromobacter phage Motura	GCA_006964305.1
QDH83570.1	000000	-	228	H1O15_gp218	Achromobacter phage Motura	GCA_006964305.1
AND75266.1	000000	-	174	ME3_105	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75287.1	000000	-	91	ME3_126	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75305.1	000000	-	105	ME3_144	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75313.1	000000	-	45	ME3_152	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75314.1	000000	-	108	ME3_153	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75320.1	000000	-	109	ME3_159	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75322.1	000000	-	92	ME3_161	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75324.1	000000	-	99	ME3_163	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75328.1	000000	-	102	ME3_167	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75333.1	000000	-	94	ME3_172	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75335.1	000000	-	110	ME3_174	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75341.1	000000	-	120	ME3_180	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75342.1	000000	-	82	ME3_181	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75344.1	000000	-	67	ME3_183	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75349.1	000000	-	34	ME3_188	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75352.1	000000	-	146	ME3_191	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75354.1	000000	-	40	ME3_193	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75361.1	000000	-	141	ME3_200	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75362.1	000000	-	55	ME3_201	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75365.1	000000	-	213	ME3_204	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AND75371.1	000000	-	167	ME3_210	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75381.1	000000	-	115	ME3_220	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75382.1	000000	-	113	ME3_221	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75383.1	000000	-	115	ME3_222	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75384.1	000000	-	107	ME3_223	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75385.1	000000	-	119	ME3_224	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75387.1	000000	-	111	ME3_226	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75388.1	000000	-	106	ME3_227	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75389.1	000000	-	63	ME3_228	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75390.1	000000	-	113	ME3_229	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75398.1	000000	-	62	ME3_237	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75399.1	000000	-	229	ME3_238	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75400.1	000000	-	136	ME3_239	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75403.1	000000	-	136	ME3_242	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75404.1	000000	-	70	ME3_243	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75406.1	000000	-	217	ME3_245	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75407.1	000000	-	197	ME3_246	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75186.1	000000	-	95	ME3_25	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75415.1	000000	-	58	ME3_254	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75418.1	000000	-	120	ME3_257	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75421.1	000000	-	44	ME3_260	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75431.1	000000	-	127	ME3_270	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75433.1	000000	-	125	ME3_272	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75464.1	000000	-	61	ME3_303	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75465.1	000000	-	53	ME3_304	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75475.1	000000	-	108	ME3_314	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75476.1	000000	-	119	ME3_315	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75477.1	000000	-	108	ME3_316	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75482.1	000000	-	132	ME3_321	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75484.1	000000	-	103	ME3_323	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75197.1	000000	-	1603	ME3_36	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75254.1	000000	-	78	ME3_93	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75257.1	000000	-	183	ME3_96	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
QMV29144.1	000000	-	62	AP1_0441	Aeromonas phage AP1	GCA_014183365.1
QMV29150.1	000000	-	66	AP1_0449	Aeromonas phage AP1	GCA_014183365.1
QMV29156.1	000000	-	261	AP1_0455	Aeromonas phage AP1	GCA_014183365.1
QMV29158.1	000000	-	183	AP1_0457	Aeromonas phage AP1	GCA_014183365.1
QMV29165.1	000000	-	102	AP1_0467	Aeromonas phage AP1	GCA_014183365.1
AUE22611.1	000000	-	48	Ah1_00070	Aeromonas phage Ah1	GCA_002957415.1
AUE22612.1	000000	-	52	Ah1_00071	Aeromonas phage Ah1	GCA_002957415.1
AUE22636.1	000000	-	32	Ah1_00095	Aeromonas phage Ah1	GCA_002957415.1
AUE22685.1	000000	-	29	Ah1_00144	Aeromonas phage Ah1	GCA_002957415.1
QAX98363.1	000000	-	157	ASfcp2_17	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98372.1	000000	-	33	ASfcp2_26	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98599.1	000000	-	37	ASfcp2_266	Aeromonas phage AsFcp_2	GCA_004146885.1
QAY01189.1	000000	-	105	ASwh1_124	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01192.1	000000	-	111	ASwh1_127	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01084.1	000000	-	52	ASwh1_16	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01085.1	000000	-	46	ASwh1_17	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01270.1	000000	-	102	ASwh1_207	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01333.1	000000	-	64	ASwh1_272	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01372.1	000000	-	70	ASwh1_312	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01397.1	000000	-	141	ASwh1_338	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01414.1	000000	-	171	ASwh1_355	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01461.1	000000	-	181	ASwh1_402	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01125.1	000000	-	104	ASwh1_58	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01143.1	000000	-	216	ASwh1_77	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01161.1	000000	-	125	ASwh1_95	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01164.1	000000	-	71	ASwh1_98	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39173.1	000000	-	90	CC2_024	Aeromonas phage CC2	GCA_000903495.1
QDB70428.1	000000	-	227	CF8_0015	Aeromonas phage CF8	GCA_006384595.2
QGY75116.1	000000	-	42	CF8_0016	Aeromonas phage CF8	GCA_006384595.2
QDB70449.1	000000	-	102	CF8_0037	Aeromonas phage CF8	GCA_006384595.2
QGY75119.1	000000	-	63	CF8_0058	Aeromonas phage CF8	GCA_006384595.2
QDB70316.1	000000	-	113	CF8_0148	Aeromonas phage CF8	GCA_006384595.2
QDB70338.1	000000	-	284	CF8_0169	Aeromonas phage CF8	GCA_006384595.2
QDB70339.1	000000	-	272	CF8_0170	Aeromonas phage CF8	GCA_006384595.2
QDB70340.1	000000	-	136	CF8_0171	Aeromonas phage CF8	GCA_006384595.2
QDB70341.1	000000	-	182	CF8_0172	Aeromonas phage CF8	GCA_006384595.2
QGY75129.1	000000	-	39	CF8_0188	Aeromonas phage CF8	GCA_006384595.2
QDB70408.1	000000	-	182	CF8_0239	Aeromonas phage CF8	GCA_006384595.2
QDB70409.1	000000	-	53	CF8_0240	Aeromonas phage CF8	GCA_006384595.2
QDB70410.1	000000	-	74	CF8_0241	Aeromonas phage CF8	GCA_006384595.2
QDJ97184.2	000000	-	60	D6_0008	Aeromonas phage D6	GCA_007051205.2
QDJ97169.1	000000	-	235	D6_0010	Aeromonas phage D6	GCA_007051205.2
QDJ97210.1	000000	-	49	D6_0050	Aeromonas phage D6	GCA_007051205.2
QDJ97283.1	000000	-	99	D6_0123	Aeromonas phage D6	GCA_007051205.2
QDJ97299.1	000000	-	55	D6_0139	Aeromonas phage D6	GCA_007051205.2
QDJ97330.1	000000	-	64	D6_0171	Aeromonas phage D6	GCA_007051205.2
QDJ97365.1	000000	-	30	D6_0206	Aeromonas phage D6	GCA_007051205.2
QDJ97415.1	000000	-	44	D6_0256	Aeromonas phage D6	GCA_007051205.2
QNH80854.1	000000	-	62	D6_0258	Aeromonas phage D6	GCA_007051205.2
QDJ96783.1	000000	-	73	PS1_0024	Aeromonas phage PS1	GCA_007051165.2
QDJ96889.1	000000	-	38	PS1_0130	Aeromonas phage PS1	GCA_007051165.2
ADQ52757.1	000000	-	31	PX29p038	Aeromonas phage PX29	GCA_000920195.1
ADQ52820.1	000000	-	57	PX29p101	Aeromonas phage PX29	GCA_000920195.1
ADM79878.1	000000	-	99	phiAS5_ORF0035	Aeromonas phage phiAS5	GCA_000887715.1
ADM79924.1	000000	-	108	phiAS5_ORF0081	Aeromonas phage phiAS5	GCA_000887715.1
ADM80051.1	000000	-	42	phiAS5_ORF0208	Aeromonas phage phiAS5	GCA_000887715.1
ADM80077.1	000000	-	58	phiAS5_ORF0234	Aeromonas phage phiAS5	GCA_000887715.1
ADM80081.1	000000	-	48	phiAS5_ORF0238	Aeromonas phage phiAS5	GCA_000887715.1
ADM80087.1	000000	-	91	phiAS5_ORF0244	Aeromonas phage phiAS5	GCA_000887715.1
ADM80096.1	000000	-	43	phiAS5_ORF0253	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53057.1	000000	-	38	65p047	Aeromonas virus 65	GCA_000893255.1
ADQ53087.1	000000	-	39	65p077	Aeromonas virus 65	GCA_000893255.1
ADQ53143.1	000000	-	66	65p135	Aeromonas virus 65	GCA_000893255.1
ADQ53274.1	000000	-	46	65p266	Aeromonas virus 65	GCA_000893255.1
ADQ53280.1	000000	-	66	65p272	Aeromonas virus 65	GCA_000893255.1
ADQ53294.1	000000	-	46	65p286	Aeromonas virus 65	GCA_000893255.1
ADQ53305.1	000000	-	32	65p297	Aeromonas virus 65	GCA_000893255.1
ADQ53326.1	000000	-	65	65p318	Aeromonas virus 65	GCA_000893255.1
ADQ53327.1	000000	-	68	65p319	Aeromonas virus 65	GCA_000893255.1
ADQ53386.1	000000	-	29	65p379	Aeromonas virus 65	GCA_000893255.1
AAQ17699.1	000000	-	28	Aeh1ORF040c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17729.1	000000	-	46	Aeh1ORF069c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17769.1	000000	-	242	Aeh1ORF108c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17775.1	000000	-	173	Aeh1ORF113c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17825.1	000000	-	73	Aeh1ORF159c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17960.1	000000	-	83	Aeh1ORF291c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17999.1	000000	-	55	Aeh1fORF03c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17935.1	000000	-	34	Aeh1hmmORF04c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17948.1	000000	-	51	Aeh1hmmORF05c	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95365.1	000000	-	72	FDI40_gp606	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95328.1	000000	-	116	FDI40_gp569	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95315.1	000000	-	116	FDI40_gp556	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94939.1	000000	-	83	FDI40_gp157	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95218.1	000000	-	56	FDI40_gp459	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95232.1	000000	-	193	FDI40_gp473	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95374.1	000000	-	91	FDI40_gp615	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94936.1	000000	-	38	FDI40_gp154	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95065.1	000000	-	50	FDI40_gp296	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95195.1	000000	-	58	FDI40_gp436	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95270.1	000000	-	281	FDI40_gp511	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95172.1	000000	-	80	FDI40_gp413	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95369.1	000000	-	80	FDI40_gp610	Agrobacterium phage Atu_ph07	GCA_002628245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ94952.1	000000	-	296	FDI40_gp170	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95252.1	000000	-	543	FDI40_gp493	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95423.1	000000	-	39	FDI40_gp666	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95116.1	000000	-	113	FDI40_gp357	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95021.1	000000	-	143	FDI40_gp239	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94928.1	000000	-	164	FDI40_gp139	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95355.1	000000	-	89	FDI40_gp596	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95125.1	000000	-	86	FDI40_gp366	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94933.1	000000	-	57	FDI40_gp151	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94983.1	000000	-	57	FDI40_gp201	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94976.1	000000	-	37	FDI40_gp194	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44702.1	000000	-	101	FDI40_gp096	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95337.1	000000	-	180	FDI40_gp578	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95201.1	000000	-	105	FDI40_gp442	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94988.1	000000	-	218	FDI40_gp206	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95284.1	000000	-	74	FDI40_gp525	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95273.1	000000	-	63	FDI40_gp514	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95408.1	000000	-	66	FDI40_gp649	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95245.1	000000	-	127	FDI40_gp486	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95187.1	000000	-	41	FDI40_gp428	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94853.1	000000	-	94	FDI40_gp041	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94888.1	000000	-	140	FDI40_gp081	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94895.1	000000	-	107	FDI40_gp089	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95431.1	000000	-	154	FDI40_gp682	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95295.1	000000	-	79	FDI40_gp536	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95338.1	000000	-	187	FDI40_gp579	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95063.1	000000	-	109	FDI40_gp294	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95061.1	000000	-	119	FDI40_gp291	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95428.1	000000	-	238	FDI40_gp675	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95166.1	000000	-	342	FDI40_gp407	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95225.1	000000	-	470	FDI40_gp466	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94850.1	000000	-	141	FDI40_gp038	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95190.1	000000	-	46	FDI40_gp431	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94974.1	000000	-	46	FDI40_gp192	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94905.1	000000	-	78	FDI40_gp104	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95367.1	000000	-	71	FDI40_gp608	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95336.1	000000	-	142	FDI40_gp577	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95238.1	000000	-	99	FDI40_gp479	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83579.1	000000	-	62	0305phi8-36p014	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83584.1	000000	-	104	0305phi8-36p019	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83599.1	000000	-	228	0305phi8-36p038	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83606.1	000000	-	81	0305phi8-36p045	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83608.1	000000	-	125	0305phi8-36p047	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83615.1	000000	-	113	0305phi8-36p055	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83620.1	000000	-	142	0305phi8-36p060	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83625.1	000000	-	46	0305phi8-36p065	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83636.1	000000	-	165	0305phi8-36p076	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83660.1	000000	-	69	0305phi8-36p100	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83667.1	000000	-	89	0305phi8-36p109	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83669.1	000000	-	59	0305phi8-36p111	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83696.1	000000	-	226	0305phi8-36p138	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83728.1	000000	-	53	0305phi8-36p170	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83731.1	000000	-	686	0305phi8-36p173	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83735.1	000000	-	94	0305phi8-36p177	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83741.1	000000	-	74	0305phi8-36p183	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83743.1	000000	-	87	0305phi8-36p185	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83745.1	000000	-	89	0305phi8-36p187	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83747.1	000000	-	109	0305phi8-36p189	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83759.1	000000	-	802	0305phi8-36p201	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83760.1	000000	-	39	0305phi8-36p202	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83776.1	000000	-	62	0305phi8-36p218	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83786.1	000000	-	179	0305phi8-36p228	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83811.1	000000	-	54	0305phi8-36p242	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01227.1	000000	-	50	AR9_g143	Bacillus phage AR9	GCA_001743835.1
AMS01290.1	000000	-	47	AR9_g206	Bacillus phage AR9	GCA_001743835.1
AMM44802.1	000000	-	71	SP15_004	Bacillus phage SP-15	GCA_001754685.1
AMM44841.1	000000	-	76	SP15_042	Bacillus phage SP-15	GCA_001754685.1
AMM44847.1	000000	-	168	SP15_048	Bacillus phage SP-15	GCA_001754685.1
AMM44853.1	000000	-	476	SP15_054	Bacillus phage SP-15	GCA_001754685.1
AMM44866.1	000000	-	166	SP15_067	Bacillus phage SP-15	GCA_001754685.1
AMM44868.1	000000	-	86	SP15_069	Bacillus phage SP-15	GCA_001754685.1
AMM44869.1	000000	-	142	SP15_070	Bacillus phage SP-15	GCA_001754685.1
AMM44910.1	000000	-	71	SP15_112	Bacillus phage SP-15	GCA_001754685.1
AMM44915.1	000000	-	85	SP15_117	Bacillus phage SP-15	GCA_001754685.1
AMM44918.1	000000	-	139	SP15_120	Bacillus phage SP-15	GCA_001754685.1
AMM44921.1	000000	-	177	SP15_123	Bacillus phage SP-15	GCA_001754685.1
AMM44972.1	000000	-	71	SP15_174	Bacillus phage SP-15	GCA_001754685.1
AMM44973.1	000000	-	71	SP15_175	Bacillus phage SP-15	GCA_001754685.1
AMM44976.1	000000	-	137	SP15_178	Bacillus phage SP-15	GCA_001754685.1
AMM44978.1	000000	-	87	SP15_180	Bacillus phage SP-15	GCA_001754685.1
AMM44979.1	000000	-	119	SP15_181	Bacillus phage SP-15	GCA_001754685.1
AMM44986.1	000000	-	118	SP15_186	Bacillus phage SP-15	GCA_001754685.1
AMM45022.1	000000	-	93	SP15_221	Bacillus phage SP-15	GCA_001754685.1
AMM45032.1	000000	-	67	SP15_230	Bacillus phage SP-15	GCA_001754685.1
AMM45034.1	000000	-	53	SP15_231A	Bacillus phage SP-15	GCA_001754685.1
AMM45044.1	000000	-	33	SP15_239B	Bacillus phage SP-15	GCA_001754685.1
AMM45046.1	000000	-	205	SP15_241	Bacillus phage SP-15	GCA_001754685.1
AMM45049.1	000000	-	97	SP15_244	Bacillus phage SP-15	GCA_001754685.1
AMM45055.1	000000	-	161	SP15_250	Bacillus phage SP-15	GCA_001754685.1
AMM45056.1	000000	-	27	SP15_250A	Bacillus phage SP-15	GCA_001754685.1
AMM45057.1	000000	-	87	SP15_251	Bacillus phage SP-15	GCA_001754685.1
AMM45074.1	000000	-	129	SP15_267	Bacillus phage SP-15	GCA_001754685.1
AMM45083.1	000000	-	309	SP15_275	Bacillus phage SP-15	GCA_001754685.1
AMM45107.1	000000	-	110	SP15_299	Bacillus phage SP-15	GCA_001754685.1
AMM45114.1	000000	-	79	SP15_306	Bacillus phage SP-15	GCA_001754685.1
AMM45115.1	000000	-	28	SP15_307	Bacillus phage SP-15	GCA_001754685.1
ALN97686.1	000000	-	214	Bp8pS_007	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97696.1	000000	-	100	Bp8pS_017	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97711.1	000000	-	36	Bp8pS_032	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97712.1	000000	-	40	Bp8pS_033	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97713.1	000000	-	36	Bp8pS_034	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97714.1	000000	-	33	Bp8pS_035	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97715.1	000000	-	114	Bp8pS_036	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97716.1	000000	-	151	Bp8pS_037	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97717.1	000000	-	165	Bp8pS_038	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97721.1	000000	-	61	Bp8pS_042	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97764.1	000000	-	148	Bp8pS_085	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97773.1	000000	-	103	Bp8pS_094	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97794.1	000000	-	143	Bp8pS_115	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97795.1	000000	-	60	Bp8pS_116	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97797.1	000000	-	117	Bp8pS_118	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97839.1	000000	-	37	Bp8pS_160	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97859.1	000000	-	223	Bp8pS_180	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97861.1	000000	-	260	Bp8pS_182	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97889.1	000000	-	30	Bp8pS_210	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97938.1	000000	-	121	Bp8pS_259	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97939.1	000000	-	82	Bp8pS_260	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97941.1	000000	-	31	Bp8pS_262	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97985.1	000000	-	89	Bp8pS_306	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97992.1	000000	-	226	Bp8pS_313	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93281.1	000000	-	72	G_10	Bacillus virus G	GCA_000917535.1
AEO93282.1	000000	-	393	G_11	Bacillus virus G	GCA_000917535.1
AEO93284.1	000000	-	88	G_13	Bacillus virus G	GCA_000917535.1
AEO93412.1	000000	-	49	G_152	Bacillus virus G	GCA_000917535.1
AEO93424.1	000000	-	73	G_164	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEO93432.1	000000	-	67	G_172	Bacillus virus G	GCA_000917535.1
AEO93434.1	000000	-	289	G_174	Bacillus virus G	GCA_000917535.1
AEO93289.1	000000	-	81	G_18	Bacillus virus G	GCA_000917535.1
AEO93453.1	000000	-	242	G_193	Bacillus virus G	GCA_000917535.1
AEO93454.1	000000	-	90	G_194	Bacillus virus G	GCA_000917535.1
AEO93940.1	000000	-	55	G_198	Bacillus virus G	GCA_000917535.1
AEO93291.1	000000	-	162	G_20	Bacillus virus G	GCA_000917535.1
AEO93465.1	000000	-	203	G_206	Bacillus virus G	GCA_000917535.1
AEO93494.1	000000	-	144	G_235	Bacillus virus G	GCA_000917535.1
AEO93505.1	000000	-	191	G_246	Bacillus virus G	GCA_000917535.1
AEO93506.1	000000	-	246	G_247	Bacillus virus G	GCA_000917535.1
AEO93522.1	000000	-	143	G_263	Bacillus virus G	GCA_000917535.1
AEO93530.1	000000	-	88	G_271	Bacillus virus G	GCA_000917535.1
AEO93535.1	000000	-	120	G_276	Bacillus virus G	GCA_000917535.1
AEO93592.1	000000	-	94	G_333	Bacillus virus G	GCA_000917535.1
AEO93596.1	000000	-	151	G_337	Bacillus virus G	GCA_000917535.1
AEO93646.1	000000	-	253	G_387	Bacillus virus G	GCA_000917535.1
AEO93653.1	000000	-	83	G_394	Bacillus virus G	GCA_000917535.1
AEO93667.1	000000	-	227	G_409	Bacillus virus G	GCA_000917535.1
AEO93676.1	000000	-	135	G_418	Bacillus virus G	GCA_000917535.1
AEO93679.1	000000	-	371	G_421	Bacillus virus G	GCA_000917535.1
AEO93689.1	000000	-	1013	G_431	Bacillus virus G	GCA_000917535.1
AEO93697.1	000000	-	97	G_439	Bacillus virus G	GCA_000917535.1
AEO93704.1	000000	-	109	G_446	Bacillus virus G	GCA_000917535.1
AEO93745.1	000000	-	113	G_487	Bacillus virus G	GCA_000917535.1
AEO93759.1	000000	-	112	G_501	Bacillus virus G	GCA_000917535.1
AEO93776.1	000000	-	192	G_518	Bacillus virus G	GCA_000917535.1
AEO93779.1	000000	-	107	G_521	Bacillus virus G	GCA_000917535.1
AEO93793.1	000000	-	56	G_535	Bacillus virus G	GCA_000917535.1
AEO93796.1	000000	-	276	G_539	Bacillus virus G	GCA_000917535.1
AEO93327.1	000000	-	151	G_56	Bacillus virus G	GCA_000917535.1
AEO93811.1	000000	-	79	G_565	Bacillus virus G	GCA_000917535.1
AEO93817.1	000000	-	125	G_571	Bacillus virus G	GCA_000917535.1
AEO93943.1	000000	-	33	G_575	Bacillus virus G	GCA_000917535.1
AEO93832.1	000000	-	102	G_587	Bacillus virus G	GCA_000917535.1
AEO93858.1	000000	-	106	G_613	Bacillus virus G	GCA_000917535.1
AEO93877.1	000000	-	132	G_632	Bacillus virus G	GCA_000917535.1
AEO93878.1	000000	-	175	G_633	Bacillus virus G	GCA_000917535.1
AEO93944.1	000000	-	29	G_634	Bacillus virus G	GCA_000917535.1
AEO93881.1	000000	-	65	G_637	Bacillus virus G	GCA_000917535.1
AEO93884.1	000000	-	72	G_641	Bacillus virus G	GCA_000917535.1
AEO93893.1	000000	-	154	G_650	Bacillus virus G	GCA_000917535.1
AEO93894.1	000000	-	126	G_651	Bacillus virus G	GCA_000917535.1
AEO93907.1	000000	-	104	G_664	Bacillus virus G	GCA_000917535.1
AEO93915.1	000000	-	83	G_672	Bacillus virus G	GCA_000917535.1
AEO93934.1	000000	-	255	G_691	Bacillus virus G	GCA_000917535.1
AEO93357.1	000000	-	103	G_89	Bacillus virus G	GCA_000917535.1
AEO93358.1	000000	-	40	G_90	Bacillus virus G	GCA_000917535.1
AEO93361.1	000000	-	108	G_99	Bacillus virus G	GCA_000917535.1
ASU00056.1	000000	-	39	PBI_PBS1_234	Bacillus virus PBS1	GCA_002601325.1
ASU00084.1	000000	-	40	PBI_PBS1_262	Bacillus virus PBS1	GCA_002601325.1
AST99853.1	000000	-	59	PBI_PBS1_31	Bacillus virus PBS1	GCA_002601325.1
ASU00133.1	000000	-	65	PBI_PBS1_311	Bacillus virus PBS1	GCA_002601325.1
AST99830.1	000000	-	39	PBI_PBS1_8	Bacillus virus PBS1	GCA_002601325.1
AST99916.1	000000	-	133	PBI_PBS1_94	Bacillus virus PBS1	GCA_002601325.1
QIG63351.1	000000	-	37	DAC16_118	Bacteroides phage DAC16	GCA_013387695.1
QIG63288.1	000000	-	91	DAC16_55	Bacteroides phage DAC16	GCA_013387695.1
QIG63293.1	000000	-	28	DAC16_60	Bacteroides phage DAC16	GCA_013387695.1
QIG63552.1	000000	-	27	DAC19_61	Bacteroides phage DAC19	GCA_013387715.1
QIG63813.1	000000	-	27	DAC20_60	Bacteroides phage DAC20	GCA_013387725.1
QIG64122.1	000000	-	54	DAC22_108	Bacteroides phage DAC22	GCA_013387735.1
QIG64075.1	000000	-	27	DAC22_61	Bacteroides phage DAC22	GCA_013387735.1
QIG64112.1	000000	-	70	DAC22_98	Bacteroides phage DAC22	GCA_013387735.1
QIG64436.1	000000	-	64	DAC23_161	Bacteroides phage DAC23	GCA_013387745.1
QIG64338.1	000000	-	27	DAC23_60	Bacteroides phage DAC23	GCA_013387745.1
QBX06425.1	000000	-	76	BcepSaruman_012	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06449.1	000000	-	118	BcepSaruman_036	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06687.1	000000	-	184	BcepSaruman_274	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74384.1	000000	-	43	BcepSauron_004	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74629.1	000000	-	45	BcepSauron_249	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74702.1	000000	-	100	BcepSauron_322	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63464.1	000000	-	179	CP21_002	Campylobacter virus CP21	GCA_000902535.1
CCH63483.1	000000	-	137	CP21_021	Campylobacter virus CP21	GCA_000902535.1
CCH63485.1	000000	-	150	CP21_023	Campylobacter virus CP21	GCA_000902535.1
CCH63501.1	000000	-	141	CP21_039	Campylobacter virus CP21	GCA_000902535.1
CCH63545.1	000000	-	219	CP21_083	Campylobacter virus CP21	GCA_000902535.1
CCH63560.1	000000	-	87	CP21_098	Campylobacter virus CP21	GCA_000902535.1
CCH63584.1	000000	-	53	CP21_122	Campylobacter virus CP21	GCA_000902535.1
CCH63591.1	000000	-	139	CP21_129	Campylobacter virus CP21	GCA_000902535.1
CCH63608.1	000000	-	87	CP21_146	Campylobacter virus CP21	GCA_000902535.1
CCH63612.1	000000	-	93	CP21_150	Campylobacter virus CP21	GCA_000902535.1
CCH63617.1	000000	-	34	CP21_155	Campylobacter virus CP21	GCA_000902535.1
CCH63621.1	000000	-	56	CP21_159	Campylobacter virus CP21	GCA_000902535.1
CCH63636.1	000000	-	60	CP21_174	Campylobacter virus CP21	GCA_000902535.1
CCH63638.1	000000	-	109	CP21_176	Campylobacter virus CP21	GCA_000902535.1
CCH63640.1	000000	-	50	CP21_178	Campylobacter virus CP21	GCA_000902535.1
CCH63669.1	000000	-	37	CP21_207	Campylobacter virus CP21	GCA_000902535.1
CCH63673.1	000000	-	83	CP21_211	Campylobacter virus CP21	GCA_000902535.1
CCH63698.1	000000	-	106	CP21_238	Campylobacter virus CP21	GCA_000902535.1
CCH63712.1	000000	-	97	CP21_252	Campylobacter virus CP21	GCA_000902535.1
CCH63716.1	000000	-	92	CP21_256	Campylobacter virus CP21	GCA_000902535.1
ARB15345.1	000000	-	266	Ccr34_gp103	Caulobacter phage Ccr34	GCA_002619525.1
AXQ68394.1	000000	-	47	CcrBL10_gp190c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69096.1	000000	-	68	CcrBL9_gp072c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69264.1	000000	-	78	CcrBL9_gp240c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69335.1	000000	-	110	CcrBL9_gp311	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69390.1	000000	-	37	CcrBL9_gp366c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69418.1	000000	-	53	CcrBL9_gp394	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69425.1	000000	-	90	CcrBL9_gp401	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69429.1	000000	-	189	CcrBL9_gp405	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69430.1	000000	-	131	CcrBL9_gp406	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69508.1	000000	-	93	CcrBL9_gp484	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69522.1	000000	-	38	CcrBL9_gp498	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69524.1	000000	-	65	CcrBL9_gp500	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87916.1	000000	-	48	CcrColossus_gp046	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87983.1	000000	-	22	CcrColossus_gp113	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88019.1	000000	-	53	CcrColossus_gp149	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88064.1	000000	-	245	CcrColossus_gp194	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88080.1	000000	-	80	CcrColossus_gp210	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88211.1	000000	-	141	CcrColossus_gp341	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88233.1	000000	-	55	CcrColossus_gp363	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88254.1	000000	-	92	CcrColossus_gp384	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88256.1	000000	-	58	CcrColossus_gp386	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88271.1	000000	-	96	CcrColossus_gp401	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88304.1	000000	-	37	CcrColossus_gp434	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88309.1	000000	-	142	CcrColossus_gp439	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68617.1	000000	-	46	CcrPW_gp078	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68774.1	000000	-	82	CcrPW_gp235	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68788.1	000000	-	42	CcrPW_gp249c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68807.1	000000	-	88	CcrPW_gp268	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68920.1	000000	-	105	CcrPW_gp381c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68930.1	000000	-	92	CcrPW_gp391c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68939.1	000000	-	107	CcrPW_gp400	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68970.1	000000	-	64	CcrPW_gp431c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69805.1	000000	-	67	CcrSC_gp223c	Caulobacter phage CcrSC	GCA_003443315.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXQ69851.1	000000	-	98	CcrSC_gp269c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69918.1	000000	-	87	CcrSC_gp336	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70051.1	000000	-	371	CcrSC_gp469	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70075.1	000000	-	42	CcrSC_gp493	Caulobacter phage CcrSC	GCA_003443315.1
AFU87194.1	000000	-	25	CcrMagneto_gp024	Caulobacter virus Magneto	GCA_000903095.1
AFU87490.1	000000	-	129	CcrMagneto_gp320	Caulobacter virus Magneto	GCA_000903095.1
AFU86504.1	000000	-	27	CcrRogue_gp022	Caulobacter virus Rogue	GCA_000900555.1
AFU86527.1	000000	-	64	CcrRogue_gp045	Caulobacter virus Rogue	GCA_000900555.1
AFU86682.1	000000	-	61	CcrRogue_gp200	Caulobacter virus Rogue	GCA_000900555.1
AFU86767.1	000000	-	125	CcrRogue_gp285	Caulobacter virus Rogue	GCA_000900555.1
AFU86783.1	000000	-	98	CcrRogue_gp301	Caulobacter virus Rogue	GCA_000900555.1
AFU86797.1	000000	-	69	CcrRogue_gp315	Caulobacter virus Rogue	GCA_000900555.1
ANS06191.1	000000	-	39	ABCD_0099	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47720.1	000000	-	87	CST022	Clostridium phage c-st	GCA_000865225.1
BAE47728.1	000000	-	368	CST030	Clostridium phage c-st	GCA_000865225.1
BAE47729.1	000000	-	123	CST031	Clostridium phage c-st	GCA_000865225.1
BAE47746.1	000000	-	55	CST048	Clostridium phage c-st	GCA_000865225.1
BAE47765.1	000000	-	99	CST067	Clostridium phage c-st	GCA_000865225.1
BAE47770.1	000000	-	248	CST072	Clostridium phage c-st	GCA_000865225.1
BAE47787.1	000000	-	28	CST089	Clostridium phage c-st	GCA_000865225.1
BAE47795.1	000000	-	74	CST097	Clostridium phage c-st	GCA_000865225.1
BAE47810.1	000000	-	58	CST112	Clostridium phage c-st	GCA_000865225.1
BAE47820.1	000000	-	99	CST122	Clostridium phage c-st	GCA_000865225.1
BAE47823.1	000000	-	105	CST125	Clostridium phage c-st	GCA_000865225.1
BAE47824.1	000000	-	320	CST126	Clostridium phage c-st	GCA_000865225.1
BAE47834.1	000000	-	180	CST136	Clostridium phage c-st	GCA_000865225.1
BAE47849.1	000000	-	51	CST151	Clostridium phage c-st	GCA_000865225.1
BAE47852.1	000000	-	128	CST154	Clostridium phage c-st	GCA_000865225.1
BAE47867.1	000000	-	274	CST169	Clostridium phage c-st	GCA_000865225.1
BAE47893.1	000000	-	109	CST195	Clostridium phage c-st	GCA_000865225.1
BAE47894.1	000000	-	62	CST196	Clostridium phage c-st	GCA_000865225.1
AIA64802.1	000000	-	68	S13_003	Cronobacter phage S13	GCA_001503575.1
AIA64864.1	000000	-	88	S13_065	Cronobacter phage S13	GCA_001503575.1
AIA64909.1	000000	-	70	S13_110	Cronobacter phage S13	GCA_001503575.1
AIA64916.1	000000	-	57	S13_117	Cronobacter phage S13	GCA_001503575.1
AIA64925.1	000000	-	89	S13_126	Cronobacter phage S13	GCA_001503575.1
AIA64939.1	000000	-	71	S13_140	Cronobacter phage S13	GCA_001503575.1
AIA64941.1	000000	-	91	S13_142	Cronobacter phage S13	GCA_001503575.1
AIA64950.1	000000	-	68	S13_151	Cronobacter phage S13	GCA_001503575.1
AIA64988.1	000000	-	68	S13_191	Cronobacter phage S13	GCA_001503575.1
AIA65008.1	000000	-	110	S13_211	Cronobacter phage S13	GCA_001503575.1
AIA65011.1	000000	-	119	S13_214	Cronobacter phage S13	GCA_001503575.1
AFC21476.1	000000	-	95	GAP32_028	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21492.1	000000	-	116	GAP32_045	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21544.1	000000	-	101	GAP32_096	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21863.1	000000	-	68	GAP32_410	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21885.1	000000	-	39	GAP32_431A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21920.1	000000	-	64	GAP32_462A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97035.1	000000	-	60	E_026	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97109.1	000000	-	80	E_101	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97125.1	000000	-	46	E_117	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97151.1	000000	-	71	E_143	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97152.1	000000	-	95	E_144	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97264.1	000000	-	108	E_256	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56827.1	000000	-	75	CPXG_00024	Cyanophage P-RSM6	GCA_000906155.1
AGH56830.1	000000	-	74	CPXG_00027	Cyanophage P-RSM6	GCA_000906155.1
AGH56858.1	000000	-	57	CPXG_00055	Cyanophage P-RSM6	GCA_000906155.1
AGH56884.1	000000	-	52	CPXG_00081	Cyanophage P-RSM6	GCA_000906155.1
AGH56895.1	000000	-	84	CPXG_00092	Cyanophage P-RSM6	GCA_000906155.1
AGH56962.1	000000	-	59	CPXG_00159	Cyanophage P-RSM6	GCA_000906155.1
AGH56969.1	000000	-	379	CPXG_00166	Cyanophage P-RSM6	GCA_000906155.1
AGH56974.1	000000	-	116	CPXG_00171	Cyanophage P-RSM6	GCA_000906155.1
AJK27547.1	000000	-	60	PTIM40_120	Cyanophage P-TIM40	GCA_001470935.1
AJK27555.1	000000	-	38	PTIM40_128	Cyanophage P-TIM40	GCA_001470935.1
AJK27582.1	000000	-	47	PTIM40_155	Cyanophage P-TIM40	GCA_001470935.1
AJK27622.1	000000	-	32	PTIM40_210	Cyanophage P-TIM40	GCA_001470935.1
AJK27656.1	000000	-	50	PTIM40_217	Cyanophage P-TIM40	GCA_001470935.1
AJK27451.1	000000	-	27	PTIM40_24	Cyanophage P-TIM40	GCA_001470935.1
AJK27452.1	000000	-	46	PTIM40_25	Cyanophage P-TIM40	GCA_001470935.1
AJK27457.1	000000	-	46	PTIM40_30	Cyanophage P-TIM40	GCA_001470935.1
AJK27514.1	000000	-	52	PTIM40_87	Cyanophage P-TIM40	GCA_001470935.1
AJK27660.1	000000	-	37	PTIM40_215	Cyanophage P-TIM40	GCA_001470935.1
AMO43071.1	000000	-	73	R1080702_062	Cyanophage S-RIM32	GCA_001754165.1
AMO43083.1	000000	-	51	R1080702_074	Cyanophage S-RIM32	GCA_001754165.1
AMO43120.1	000000	-	37	R1080702_111	Cyanophage S-RIM32	GCA_001754165.1
AMO43174.1	000000	-	58	R1080702_165	Cyanophage S-RIM32	GCA_001754165.1
AMO43201.1	000000	-	44	R1080702_192	Cyanophage S-RIM32	GCA_001754165.1
AGH07566.1	000000	-	195	CYVG_00122	Cyanophage S-SSM6a	GCA_002710385.1
AGH07608.1	000000	-	100	CYVG_00165	Cyanophage S-SSM6a	GCA_002710385.1
AGH07639.1	000000	-	595	CYVG_00196	Cyanophage S-SSM6a	GCA_002710385.1
AGH07702.1	000000	-	64	CYVG_00259	Cyanophage S-SSM6a	GCA_002710385.1
AGH07715.1	000000	-	57	CYVG_00272	Cyanophage S-SSM6a	GCA_002710385.1
AGH07720.1	000000	-	3001	CYVG_00277	Cyanophage S-SSM6a	GCA_002710385.1
AGG54396.1	000000	-	60	CYWG_00112	Cyanophage S-SSM6b	GCA_002710425.1
AXG67070.1	000000	-	127	AD1_026	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67308.1	000000	-	69	AD1_264	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG66661.1	000000	-	69	JA13_258	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66662.1	000000	-	68	JA13_259	Dickeya phage vB_DsoM_JA13	GCA_003568455.1
AXG66981.1	000000	-	105	JA29_255	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
QBZ70588.1	000000	-	51	pETSU_007	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70651.1	000000	-	193	pETSU_070	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70674.1	000000	-	108	pETSU_093	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70722.1	000000	-	95	pETSU_141	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70727.1	000000	-	56	pETSU_146	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70743.1	000000	-	56	pETSU_162	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70747.1	000000	-	129	pETSU_166	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70803.1	000000	-	212	pETSU_222	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70818.1	000000	-	41	pETSU_237	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70823.1	000000	-	264	pETSU_242	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70825.1	000000	-	124	pETSU_244	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70826.1	000000	-	116	pETSU_245	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70831.1	000000	-	47	pETSU_250	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70835.1	000000	-	113	pETSU_254	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70841.1	000000	-	231	pETSU_260	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70854.1	000000	-	596	pETSU_273	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59659.1	000000	-	38	SEGD1_008	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59674.1	000000	-	92	SEGD1_023	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59723.1	000000	-	93	SEGD1_074	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59737.1	000000	-	84	SEGD1_088	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59774.1	000000	-	42	SEGD1_127	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59817.1	000000	-	70	SEGD1_170	Enterobacteria phage SEGD1	GCA_002601865.1
ANZ49749.1	000000	-	244	MACHINA_111	Erwinia phage Machina	GCA_002758035.1
AGX01727.1	000000	-	172	CF95_gp005	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01841.1	000000	-	53	CF95_gp119	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01848.1	000000	-	111	CF95_gp126	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01886.1	000000	-	126	CF95_gp163	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01887.1	000000	-	139	CF95_gp164	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01878.1	000000	-	157	CF95_gp156	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01853.1	000000	-	165	CF95_gp131	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01851.1	000000	-	79	CF95_gp129	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01866.1	000000	-	98	CF95_gp144	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01903.1	000000	-	211	CF95_gp181	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01777.1	000000	-	107	CF95_gp055	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01776.1	000000	-	123	CF95_gp054	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01782.1	000000	-	142	CF95_gp060	Erwinia phage PhiEaH1	GCA_000914555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGX01753.1	000000	-	163	CF95_gp031	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01826.1	000000	-	172	CF95_gp104	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01810.1	000000	-	180	CF95_gp088	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01774.1	000000	-	186	CF95_gp052	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01819.1	000000	-	191	CF95_gp097	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01775.1	000000	-	192	CF95_gp053	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01773.1	000000	-	206	CF95_gp051	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01772.1	000000	-	209	CF95_gp050	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01963.1	000000	-	176	CF95_gp241	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01942.1	000000	-	304	CF95_gp218	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01931.1	000000	-	59	CF95_gp209	Erwinia phage PhiEaH1	GCA_000914555.1
AFQ96728.1	000000	-	39	G173_gp183	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96595.1	000000	-	77	G173_gp050	Erwinia phage phiEaH2	GCA_000902915.1
AWY08463.1	000000	-	207	Alexandra_198	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08526.1	000000	-	90	Alexandra_269	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08542.1	000000	-	52	Alexandra_286	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08624.1	000000	-	98	Alexandra_343	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08329.1	000000	-	55	Alexandra_49	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08339.1	000000	-	102	Alexandra_59	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08598.1	000000	-	66	Alexandra_86	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48199.1	000000	-	46	ASESINO_186	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48223.1	000000	-	34	ASESINO_210	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48301.1	000000	-	72	ASESINO_288	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48470.1	000000	-	37	CAITLIN_175	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48323.1	000000	-	94	CAITLIN_28	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48370.1	000000	-	63	CAITLIN_75	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48774.1	000000	-	34	CHRISDB_212	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49213.1	000000	-	61	HUXLEY_131	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ANZ49507.1	000000	-	75	KWAN_155	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ50041.1	000000	-	66	PARSHIK_132	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50319.1	000000	-	37	PHOBOS_129	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50373.1	000000	-	33	PHOBOS_183	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50636.1	000000	-	35	STRATTON_211	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARW58692.1	000000	-	65	Y3_052	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58697.1	000000	-	149	Y3_057	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58704.1	000000	-	39	Y3_064	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58857.1	000000	-	165	Y3_217	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58888.1	000000	-	40	Y3_248	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58911.1	000000	-	73	Y3_271	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58934.1	000000	-	356	Y3_294	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58938.1	000000	-	60	Y3_298	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58946.1	000000	-	110	Y3_306	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28590.1	000000	-	53	YOLOSWAG_108	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28591.1	000000	-	64	YOLOSWAG_109	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28668.1	000000	-	39	YOLOSWAG_189	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28680.1	000000	-	107	YOLOSWAG_202	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28686.1	000000	-	59	YOLOSWAG_208	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28690.1	000000	-	325	YOLOSWAG_212	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28691.1	000000	-	552	YOLOSWAG_213	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28707.1	000000	-	55	YOLOSWAG_229	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28709.1	000000	-	158	YOLOSWAG_231	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28729.1	000000	-	79	YOLOSWAG_255	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28730.1	000000	-	60	YOLOSWAG_256	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28735.1	000000	-	69	YOLOSWAG_262	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28737.1	000000	-	108	YOLOSWAG_264	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28742.1	000000	-	57	YOLOSWAG_269	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28756.1	000000	-	302	YOLOSWAG_285	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28757.1	000000	-	117	YOLOSWAG_286	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28821.1	000000	-	65	YOLOSWAG_310	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28519.1	000000	-	146	YOLOSWAG_34	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28522.1	000000	-	113	YOLOSWAG_37	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28530.1	000000	-	42	YOLOSWAG_45	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28534.1	000000	-	56	YOLOSWAG_50	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28535.1	000000	-	63	YOLOSWAG_51	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28538.1	000000	-	173	YOLOSWAG_54	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28548.1	000000	-	238	YOLOSWAG_65	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28567.1	000000	-	363	YOLOSWAG_84	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14023.1	000000	-	27	PBI_121Q_129	Escherichia phage 121Q	GCA_000926855.1
AIT14028.1	000000	-	100	PBI_121Q_137	Escherichia phage 121Q	GCA_000926855.1
AIT14035.1	000000	-	35	PBI_121Q_145	Escherichia phage 121Q	GCA_000926855.1
AIT14254.1	000000	-	41	PBI_121Q_364	Escherichia phage 121Q	GCA_000926855.1
AIT14375.1	000000	-	59	PBI_121Q_485	Escherichia phage 121Q	GCA_000926855.1
AIT14437.1	000000	-	72	PBI_121Q_547	Escherichia phage 121Q	GCA_000926855.1
QAY00525.1	000000	-	123	Ecwhy1_246	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00315.1	000000	-	61	Ecwhy1_33	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00830.1	000000	-	98	Ecwhy1_558	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00832.1	000000	-	37	Ecwhy1_560	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34973.1	000000	-	39	ACQ29_gp293	Escherichia phage PBECO4	GCA_001041035.1
AGC34958.1	000000	-	77	ACQ29_gp278	Escherichia phage PBECO4	GCA_001041035.1
AGC35231.1	000000	-	348	ACQ29_gp551	Escherichia phage PBECO4	GCA_001041035.1
AGC34911.1	000000	-	121	ACQ29_gp231	Escherichia phage PBECO4	GCA_001041035.1
BBM61910.1	000000	-	66	EO157G_3210	Escherichia phage SP27	GCA_008033345.1
AXC36641.1	000000	-	101	-	Escherichia phage UB	GCA_003341455.1
AXC36642.1	000000	-	63	-	Escherichia phage UB	GCA_003341455.1
ARM70813.1	000000	-	46	phiC120_c107	Escherichia phage phiC120	GCA_002621185.1
ARM70814.1	000000	-	48	phiC120_c108	Escherichia phage phiC120	GCA_002621185.1
ARM70817.1	000000	-	87	phiC120_c111	Escherichia phage phiC120	GCA_002621185.1
ARM70823.1	000000	-	366	phiC120_c117	Escherichia phage phiC120	GCA_002621185.1
ARM70829.1	000000	-	75	phiC120_c123	Escherichia phage phiC120	GCA_002621185.1
ARM70843.1	000000	-	59	phiC120_c137	Escherichia phage phiC120	GCA_002621185.1
ARM70845.1	000000	-	75	phiC120_c139	Escherichia phage phiC120	GCA_002621185.1
ARM70848.1	000000	-	65	phiC120_c142	Escherichia phage phiC120	GCA_002621185.1
ARM70853.1	000000	-	97	phiC120_c147	Escherichia phage phiC120	GCA_002621185.1
ARM70869.1	000000	-	47	phiC120_c164	Escherichia phage phiC120	GCA_002621185.1
ARM70883.1	000000	-	68	phiC120_c178	Escherichia phage phiC120	GCA_002621185.1
ARM70897.1	000000	-	71	phiC120_c192	Escherichia phage phiC120	GCA_002621185.1
ARM70904.1	000000	-	56	phiC120_c199	Escherichia phage phiC120	GCA_002621185.1
ARM70921.1	000000	-	36	phiC120_c216	Escherichia phage phiC120	GCA_002621185.1
ARM70924.1	000000	-	80	phiC120_c219	Escherichia phage phiC120	GCA_002621185.1
ARM70928.1	000000	-	68	phiC120_c223	Escherichia phage phiC120	GCA_002621185.1
ARM70931.1	000000	-	112	phiC120_c226	Escherichia phage phiC120	GCA_002621185.1
ARM70950.1	000000	-	101	phiC120_c245	Escherichia phage phiC120	GCA_002621185.1
ARM70968.1	000000	-	61	phiC120_c263	Escherichia phage phiC120	GCA_002621185.1
ARM70735.1	000000	-	89	phiC120_c28	Escherichia phage phiC120	GCA_002621185.1
ARM70766.1	000000	-	58	phiC120_c60	Escherichia phage phiC120	GCA_002621185.1
ARM70781.1	000000	-	118	phiC120_c75	Escherichia phage phiC120	GCA_002621185.1
QKN85840.1	000000	-	60	ACEC001_0040	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85857.1	000000	-	55	ACEC001_0195	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85978.1	000000	-	44	ACEC001_1395	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86031.1	000000	-	35	ACEC001_1895	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61724.1	000000	-	37	G17_00235	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO63794.1	000000	-	233	Goslar_00001	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63795.1	000000	-	137	Goslar_00002	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63796.1	000000	-	175	Goslar_00003	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63799.1	000000	-	38	Goslar_00006	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63812.1	000000	-	91	Goslar_00019	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63840.1	000000	-	62	Goslar_00047	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63846.1	000000	-	1125	Goslar_00053	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63864.1	000000	-	149	Goslar_00071	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63873.1	000000	-	157	Goslar_00080	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63887.1	000000	-	192	Goslar_00094	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63894.1	000000	-	63	Goslar_00101	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63896.1	000000	-	116	Goslar_00103	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63897.1	000000	-	140	Goslar_00104	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63898.1	000000	-	105	Goslar_00105	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBO63921.1	000000	-	38	Goslar_00128	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63923.1	000000	-	84	Goslar_00130	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63929.1	000000	-	105	Goslar_00136	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63932.1	000000	-	48	Goslar_00139	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63938.1	000000	-	75	Goslar_00145	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63947.1	000000	-	173	Goslar_00154	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63972.1	000000	-	260	Goslar_00179	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63973.1	000000	-	135	Goslar_00180	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63975.1	000000	-	154	Goslar_00182	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63976.1	000000	-	278	Goslar_00183	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63985.1	000000	-	132	Goslar_00193	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63987.1	000000	-	164	Goslar_00195	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63990.1	000000	-	325	Goslar_00198	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63991.1	000000	-	106	Goslar_00199	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63996.1	000000	-	99	Goslar_00204	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64019.1	000000	-	77	Goslar_00227	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64027.1	000000	-	171	Goslar_00236	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64030.1	000000	-	235	Goslar_00239	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64038.1	000000	-	183	Goslar_00247	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13769.1	000000	-	50	vBEcoMphAPEC6_gp140c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13886.1	000000	-	45	vBEcoMphAPEC6_gp261c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13946.1	000000	-	37	vBEcoMphAPEC6_gp322c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF14143.1	000000	-	29	vBEcoMphAPEC6_gp520c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
AAX78605.1	000000	-	31	RB43ORF083w	Escherichia virus RB43	GCA_000863505.1
AAX78646.1	000000	-	63	RB43ORF124c	Escherichia virus RB43	GCA_000863505.1
AAX78694.1	000000	-	57	RB43ORF172c	Escherichia virus RB43	GCA_000863505.1
AAX78766.1	000000	-	45	RB43ORF244w	Escherichia virus RB43	GCA_000863505.1
QGH71873.1	000000	-	126	N1M2_10	Klebsiella phage N1M2	GCA_010092605.1
QGH71966.1	000000	-	129	N1M2_103	Klebsiella phage N1M2	GCA_010092605.1
QGH71989.1	000000	-	107	N1M2_126	Klebsiella phage N1M2	GCA_010092605.1
QGH71999.1	000000	-	230	N1M2_136	Klebsiella phage N1M2	GCA_010092605.1
QGH72001.1	000000	-	95	N1M2_138	Klebsiella phage N1M2	GCA_010092605.1
QGH72007.1	000000	-	94	N1M2_144	Klebsiella phage N1M2	GCA_010092605.1
QGH72015.1	000000	-	79	N1M2_152	Klebsiella phage N1M2	GCA_010092605.1
QGH72034.1	000000	-	95	N1M2_171	Klebsiella phage N1M2	GCA_010092605.1
QGH72038.1	000000	-	54	N1M2_175	Klebsiella phage N1M2	GCA_010092605.1
QGH72115.1	000000	-	170	N1M2_252	Klebsiella phage N1M2	GCA_010092605.1
QGH71866.1	000000	-	210	N1M2_3	Klebsiella phage N1M2	GCA_010092605.1
QGH71867.1	000000	-	83	N1M2_4	Klebsiella phage N1M2	GCA_010092605.1
QGH71870.1	000000	-	87	N1M2_7	Klebsiella phage N1M2	GCA_010092605.1
AFA44287.1	000000	-	217	RaK2_00014	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44296.1	000000	-	154	RaK2_00023	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44350.1	000000	-	57	RaK2_00077	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44478.1	000000	-	103	RaK2_00205	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44490.1	000000	-	47	RaK2_00217	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44493.1	000000	-	61	RaK2_00220	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44494.1	000000	-	66	RaK2_00221	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44496.1	000000	-	138	RaK2_00223	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44519.1	000000	-	66	RaK2_00246	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44522.1	000000	-	54	RaK2_00249	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44542.1	000000	-	176	RaK2_00269	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44573.1	000000	-	71	RaK2_00300	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44574.1	000000	-	52	RaK2_00301	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44576.1	000000	-	95	RaK2_00303	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44596.1	000000	-	50	RaK2_00323	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44604.1	000000	-	71	RaK2_00331	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44608.1	000000	-	90	RaK2_00335	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44623.1	000000	-	88	RaK2_00350	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44628.1	000000	-	140	RaK2_00355	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44650.1	000000	-	88	RaK2_00377	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44656.1	000000	-	111	RaK2_00383	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44657.1	000000	-	184	RaK2_00384	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44658.1	000000	-	111	RaK2_00385	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44670.1	000000	-	111	RaK2_00397	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44679.1	000000	-	98	RaK2_00406	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44684.1	000000	-	90	RaK2_00411	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44725.1	000000	-	107	RaK2_00452	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44731.1	000000	-	68	RaK2_00458	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44733.1	000000	-	53	RaK2_00460	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44738.1	000000	-	57	RaK2_00465	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44753.1	000000	-	98	RaK2_00480	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44785.1	000000	-	74	RaK2_00512	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44799.1	000000	-	1113	RaK2_00528	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44805.1	000000	-	688	RaK2_00534	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57834.1	000000	-	1247	SEA_PAULODIABOLI_100	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57835.1	000000	-	486	SEA_PAULODIABOLI_101	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57861.1	000000	-	58	SEA_PAULODIABOLI_145	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57863.1	000000	-	39	SEA_PAULODIABOLI_164	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57885.1	000000	-	45	SEA_PAULODIABOLI_198	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57921.1	000000	-	116	SEA_PAULODIABOLI_236	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57936.1	000000	-	65	SEA_PAULODIABOLI_251	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57939.1	000000	-	122	SEA_PAULODIABOLI_254	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57940.1	000000	-	78	SEA_PAULODIABOLI_255	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57941.1	000000	-	36	SEA_PAULODIABOLI_256	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57950.1	000000	-	64	SEA_PAULODIABOLI_266	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57961.1	000000	-	174	SEA_PAULODIABOLI_277	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57963.1	000000	-	78	SEA_PAULODIABOLI_279	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57965.1	000000	-	83	SEA_PAULODIABOLI_281	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57970.1	000000	-	144	SEA_PAULODIABOLI_286	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57971.1	000000	-	65	SEA_PAULODIABOLI_287	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57974.1	000000	-	86	SEA_PAULODIABOLI_290	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57991.1	000000	-	68	SEA_PAULODIABOLI_307	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57999.1	000000	-	59	SEA_PAULODIABOLI_315	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58003.1	000000	-	63	SEA_PAULODIABOLI_319	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58005.1	000000	-	151	SEA_PAULODIABOLI_321	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58009.1	000000	-	110	SEA_PAULODIABOLI_325	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58019.1	000000	-	89	SEA_PAULODIABOLI_335	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58020.1	000000	-	69	SEA_PAULODIABOLI_336	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58022.1	000000	-	122	SEA_PAULODIABOLI_338	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58023.1	000000	-	40	SEA_PAULODIABOLI_339	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58026.1	000000	-	112	SEA_PAULODIABOLI_342	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58030.1	000000	-	89	SEA_PAULODIABOLI_346	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58035.1	000000	-	60	SEA_PAULODIABOLI_351	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57787.1	000000	-	74	SEA_PAULODIABOLI_52	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57789.1	000000	-	115	SEA_PAULODIABOLI_54	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57793.1	000000	-	107	SEA_PAULODIABOLI_58	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57794.1	000000	-	118	SEA_PAULODIABOLI_59	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57804.1	000000	-	51	SEA_PAULODIABOLI_69	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72535.1	000000	-	101	-	Myoviridae sp.	GCA_003657725.1
AXH72799.1	000000	-	417	-	Myoviridae sp.	GCA_003657725.1
AXH72402.1	000000	-	93	-	Myoviridae sp.	GCA_003657725.1
AXH72708.1	000000	-	91	-	Myoviridae sp.	GCA_003657725.1
AXH72601.1	000000	-	102	-	Myoviridae sp.	GCA_003657725.1
AXH72762.1	000000	-	150	-	Myoviridae sp.	GCA_003657725.1
AXH72608.1	000000	-	134	-	Myoviridae sp.	GCA_003657725.1
AXH72449.1	000000	-	134	-	Myoviridae sp.	GCA_003657725.1
AXH72582.1	000000	-	122	-	Myoviridae sp.	GCA_003657725.1
AXH72750.1	000000	-	280	-	Myoviridae sp.	GCA_003657725.1
AXH72716.1	000000	-	80	-	Myoviridae sp.	GCA_003657725.1
AXH72621.1	000000	-	80	-	Myoviridae sp.	GCA_003657725.1
AXH72393.1	000000	-	92	-	Myoviridae sp.	GCA_003657725.1
AXH72490.1	000000	-	83	-	Myoviridae sp.	GCA_003657725.1
AXH72792.1	000000	-	129	-	Myoviridae sp.	GCA_003657725.1
AXH72698.1	000000	-	160	-	Myoviridae sp.	GCA_003657725.1
AXH72516.1	000000	-	148	-	Myoviridae sp.	GCA_003657725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH72517.1	000000	-	156	-	Myoviridae sp.	GCA_003657725.1
AXH72425.1	000000	-	143	-	Myoviridae sp.	GCA_003657725.1
AXH72555.1	000000	-	111	-	Myoviridae sp.	GCA_003657725.1
AXH72567.1	000000	-	106	-	Myoviridae sp.	GCA_003657725.1
AXH72553.1	000000	-	121	-	Myoviridae sp.	GCA_003657725.1
AXH72515.1	000000	-	172	-	Myoviridae sp.	GCA_003657725.1
AXH72752.1	000000	-	81	-	Myoviridae sp.	GCA_003657725.1
AXH72518.1	000000	-	171	-	Myoviridae sp.	GCA_003657725.1
AXH72647.1	000000	-	171	-	Myoviridae sp.	GCA_003657725.1
AXH72428.1	000000	-	265	-	Myoviridae sp.	GCA_003657725.1
AXH72604.1	000000	-	146	-	Myoviridae sp.	GCA_003657725.1
AXH72548.1	000000	-	135	-	Myoviridae sp.	GCA_003657725.1
AXH72418.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72688.1	000000	-	198	-	Myoviridae sp.	GCA_003657725.1
AXH72661.1	000000	-	85	-	Myoviridae sp.	GCA_003657725.1
AXH72528.1	000000	-	120	-	Myoviridae sp.	GCA_003657725.1
AXH72686.1	000000	-	120	-	Myoviridae sp.	GCA_003657725.1
AXH72532.1	000000	-	94	-	Myoviridae sp.	GCA_003657725.1
AXH72747.1	000000	-	131	-	Myoviridae sp.	GCA_003657725.1
AXH72433.1	000000	-	87	-	Myoviridae sp.	GCA_003657725.1
AXH72656.1	000000	-	87	-	Myoviridae sp.	GCA_003657725.1
AXH72559.1	000000	-	108	-	Myoviridae sp.	GCA_003657725.1
AXH72396.1	000000	-	108	-	Myoviridae sp.	GCA_003657725.1
AXH72514.1	000000	-	363	-	Myoviridae sp.	GCA_003657725.1
AXH72477.1	000000	-	107	-	Myoviridae sp.	GCA_003657725.1
AXH72585.1	000000	-	126	-	Myoviridae sp.	GCA_003657725.1
AXH72580.1	000000	-	157	-	Myoviridae sp.	GCA_003657725.1
AXH72683.1	000000	-	90	-	Myoviridae sp.	GCA_003657725.1
AXH72513.1	000000	-	1079	-	Myoviridae sp.	GCA_003657725.1
AXH72797.1	000000	-	1084	-	Myoviridae sp.	GCA_003657725.1
AXH72450.1	000000	-	109	-	Myoviridae sp.	GCA_003657725.1
AXH72495.1	000000	-	119	-	Myoviridae sp.	GCA_003657725.1
AXH72466.1	000000	-	96	-	Myoviridae sp.	GCA_003657725.1
AXH72488.1	000000	-	96	-	Myoviridae sp.	GCA_003657725.1
AXH72744.1	000000	-	96	-	Myoviridae sp.	GCA_003657725.1
AXH72502.1	000000	-	125	-	Myoviridae sp.	GCA_003657725.1
AXH72655.1	000000	-	530	-	Myoviridae sp.	GCA_003657725.1
AXH72538.1	000000	-	99	-	Myoviridae sp.	GCA_003657725.1
QHJ78957.1	000000	-	52	-	Myoviridae sp.	GCA_012593985.1
QHJ79035.1	000000	-	76	-	Myoviridae sp.	GCA_012593985.1
QHJ78991.1	000000	-	408	-	Myoviridae sp.	GCA_012593985.1
QHJ79078.1	000000	-	111	-	Myoviridae sp.	GCA_012593985.1
QHJ78983.1	000000	-	101	-	Myoviridae sp.	GCA_012593985.1
QHJ79020.1	000000	-	110	-	Myoviridae sp.	GCA_012593985.1
QHJ78982.1	000000	-	134	-	Myoviridae sp.	GCA_012593985.1
QHJ78989.1	000000	-	220	-	Myoviridae sp.	GCA_012593985.1
QHJ78961.1	000000	-	51	-	Myoviridae sp.	GCA_012593985.1
QHJ78944.1	000000	-	71	-	Myoviridae sp.	GCA_012593985.1
QHJ78846.1	000000	-	71	-	Myoviridae sp.	GCA_012593985.1
QHJ78936.1	000000	-	98	-	Myoviridae sp.	GCA_012593985.1
QHJ78995.1	000000	-	126	-	Myoviridae sp.	GCA_012593985.1
QHJ79019.1	000000	-	69	-	Myoviridae sp.	GCA_012593985.1
QHJ78906.1	000000	-	116	-	Myoviridae sp.	GCA_012593985.1
QIG65689.1	000000	-	194	phiOC_p023	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65692.1	000000	-	168	phiOC_p026	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65708.1	000000	-	54	phiOC_p042	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65724.1	000000	-	150	phiOC_p059	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65740.1	000000	-	37	phiOC_p075	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65741.1	000000	-	96	phiOC_p076	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65742.1	000000	-	52	phiOC_p077	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65743.1	000000	-	68	phiOC_p078	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65745.1	000000	-	76	phiOC_p080	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65747.1	000000	-	43	phiOC_p082	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65748.1	000000	-	44	phiOC_p083	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65777.1	000000	-	31	phiOC_p112	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65780.1	000000	-	81	phiOC_p115	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65800.1	000000	-	119	phiOC_p135	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65806.1	000000	-	122	phiOC_p141	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65816.1	000000	-	68	phiOC_p151	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65817.1	000000	-	61	phiOC_p152	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65823.1	000000	-	153	phiOC_p158	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65824.1	000000	-	90	phiOC_p159	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65825.1	000000	-	146	phiOC_p160	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65830.1	000000	-	151	phiOC_p165	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65838.1	000000	-	38	phiOC_p173	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65842.1	000000	-	73	phiOC_p177	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65849.1	000000	-	40	phiOC_p184	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65855.1	000000	-	150	phiOC_p190	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65856.1	000000	-	163	phiOC_p191	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65858.1	000000	-	147	phiOC_p193	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65863.1	000000	-	51	phiOC_p198	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65865.1	000000	-	29	phiOC_p200	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65869.1	000000	-	60	phiOC_p204	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65873.1	000000	-	54	phiOC_p208	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65884.1	000000	-	29	phiOC_p219	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65889.1	000000	-	110	phiOC_p224	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65919.1	000000	-	111	phiOC_p272	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65920.1	000000	-	96	phiOC_p273	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65925.1	000000	-	40	phiOC_p283	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65926.1	000000	-	30	phiOC_p284	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65927.1	000000	-	93	phiOC_p285	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65928.1	000000	-	31	phiOC_p286	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65941.1	000000	-	62	phiOC_p299	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65949.1	000000	-	217	phiOC_p307	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65953.1	000000	-	34	phiOC_p311	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65956.1	000000	-	61	phiOC_p314	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65973.1	000000	-	70	phiOC_p331	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65975.1	000000	-	67	phiOC_p333	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65982.1	000000	-	103	phiOC_p340	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65983.1	000000	-	77	phiOC_p341	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66013.1	000000	-	77	phiOC_p371	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66017.1	000000	-	51	phiOC_p375	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66018.1	000000	-	66	phiOC_p376	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66028.1	000000	-	120	phiOC_p386	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66031.1	000000	-	39	phiOC_p389	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66032.1	000000	-	35	phiOC_p390	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66039.1	000000	-	55	phiOC_p397	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66050.1	000000	-	99	phiOC_p408	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66051.1	000000	-	121	phiOC_p409	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66052.1	000000	-	193	phiOC_p410	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43977.1	000000	-	38	CBB_414	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43981.1	000000	-	66	CBB_418	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43986.1	000000	-	71	CBB_423	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44005.1	000000	-	54	CBB_442	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44012.1	000000	-	107	CBB_449	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44037.1	000000	-	47	CBB_474	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38191.1	000000	-	181	BN7874_022	Phage NCTB	GCA_900092385.1
SBV38208.1	000000	-	265	BN7874_039	Phage NCTB	GCA_900092385.1
SBV38210.1	000000	-	67	BN7874_041	Phage NCTB	GCA_900092385.1
SBV38213.1	000000	-	94	BN7874_044	Phage NCTB	GCA_900092385.1
SBV38219.1	000000	-	107	BN7874_050	Phage NCTB	GCA_900092385.1
SBV38220.1	000000	-	103	BN7874_051	Phage NCTB	GCA_900092385.1
SBV38226.1	000000	-	148	BN7874_057	Phage NCTB	GCA_900092385.1
SBV38278.1	000000	-	258	BN7874_109	Phage NCTB	GCA_900092385.1
SBV38284.1	000000	-	111	BN7874_115	Phage NCTB	GCA_900092385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SBV38313.1	000000	-	331	BN7874_144	Phage NCTB	GCA_900092385.1
SBV38327.1	000000	-	366	BN7874_158	Phage NCTB	GCA_900092385.1
SBV38330.1	000000	-	149	BN7874_161	Phage NCTB	GCA_900092385.1
SBV38348.1	000000	-	395	BN7874_179	Phage NCTB	GCA_900092385.1
SBV38351.1	000000	-	123	BN7874_182	Phage NCTB	GCA_900092385.1
SBV38352.1	000000	-	175	BN7874_183	Phage NCTB	GCA_900092385.1
SBV38372.1	000000	-	76	BN7874_201	Phage NCTB	GCA_900092385.1
SBV38408.1	000000	-	394	BN7874_224	Phage NCTB	GCA_900092385.1
SBV38442.1	000000	-	143	BN7874_245	Phage NCTB	GCA_900092385.1
SBV38502.1	000000	-	42	BN7874_282	Phage NCTB	GCA_900092385.1
SBV38508.1	000000	-	182	BN7874_284	Phage NCTB	GCA_900092385.1
QGZ14437.1	000000	-	89	HWC77_gp074	Photobacterium phage PDCC-1	GCA_009800445.1
AGH26162.1	000000	-	63	CPMG_00061	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26165.1	000000	-	54	CPMG_00064	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26170.1	000000	-	87	CPMG_00069	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26176.1	000000	-	165	CPMG_00075	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26189.1	000000	-	71	CPMG_00088	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26229.1	000000	-	86	CPMG_00128	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26263.1	000000	-	58	CPMG_00162	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26271.1	000000	-	230	CPMG_00171	Prochlorococcus phage MED4-213	GCA_000904535.1
ADK66273.1	000000	-	39	PSSM2_277.1	Prochlorococcus phage P-SSM2	GCA_000859585.1
ADK66274.1	000000	-	37	PSSM2_279.1	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44663.1	000000	-	24	PSSM2_286	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44665.1	000000	-	28	PSSM2_288	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44652.1	000000	-	37	PSSM2_275	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12345.1	000000	-	65	PRTG_00192	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93624.1	000000	-	85	AVU42_gp079	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93493.1	000000	-	478	AVU42_gp156	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93549.1	000000	-	36	AVU42_gp210	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93550.1	000000	-	76	AVU42_gp212	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93614.1	000000	-	48	AVU42_gp069	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93523.1	000000	-	218	AVU42_gp186	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93596.1	000000	-	78	AVU42_gp046	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93474.1	000000	-	169	AVU42_gp137	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93511.1	000000	-	133	AVU42_gp174	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99175.1	000000	-	51	Syn1_074	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99184.1	000000	-	29	Syn1_083	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99251.1	000000	-	41	Syn1_150	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99303.1	000000	-	29	Syn1_206	Prochlorococcus phage Syn1	GCA_000892495.1
QMP24155.1	000000	-	50	-	Proteus phage 10	GCA_014071245.1
QMP24064.1	000000	-	168	-	Proteus phage 10	GCA_014071245.1
QMP24044.1	000000	-	180	-	Proteus phage 10	GCA_014071245.1
QMP24175.1	000000	-	112	-	Proteus phage 10	GCA_014071245.1
QMP24087.1	000000	-	53	-	Proteus phage 10	GCA_014071245.1
QMP24045.1	000000	-	153	-	Proteus phage 10	GCA_014071245.1
QMP24223.1	000000	-	140	-	Proteus phage 10	GCA_014071245.1
QMP24153.1	000000	-	90	-	Proteus phage 10	GCA_014071245.1
QMP24007.1	000000	-	147	-	Proteus phage 10	GCA_014071245.1
QMP24108.1	000000	-	99	-	Proteus phage 10	GCA_014071245.1
QMP24050.1	000000	-	128	-	Proteus phage 10	GCA_014071245.1
QMP24023.1	000000	-	132	-	Proteus phage 10	GCA_014071245.1
QMP24168.1	000000	-	96	-	Proteus phage 10	GCA_014071245.1
QMP24204.1	000000	-	346	-	Proteus phage 10	GCA_014071245.1
ABY62858.1	000000	-	51	201phi2-1p024	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62859.1	000000	-	53	201phi2-1p025	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62878.1	000000	-	121	201phi2-1p045	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62883.1	000000	-	91	201phi2-1p050	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62885.1	000000	-	88	201phi2-1p052	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62896.1	000000	-	69	201phi2-1p063	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62897.1	000000	-	60	201phi2-1p064	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62898.1	000000	-	57	201phi2-1p065	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62902.1	000000	-	89	201phi2-1p069	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62903.1	000000	-	84	201phi2-1p070	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62909.1	000000	-	125	201phi2-1p076	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62922.1	000000	-	146	201phi2-1p089	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62923.1	000000	-	100	201phi2-1p090	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62943.1	000000	-	67	201phi2-1p111	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62965.1	000000	-	70	201phi2-1p133	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62966.1	000000	-	68	201phi2-1p134	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62999.1	000000	-	111	201phi2-1p169	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63000.1	000000	-	49	201phi2-1p170	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63001.1	000000	-	90	201phi2-1p171	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63002.1	000000	-	89	201phi2-1p172	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63008.1	000000	-	117	201phi2-1p178	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63009.1	000000	-	103	201phi2-1p179	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63010.1	000000	-	108	201phi2-1p180	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63020.1	000000	-	122	201phi2-1p190	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63037.1	000000	-	92	201phi2-1p208	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63080.1	000000	-	108	201phi2-1p252	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63090.1	000000	-	38	201phi2-1p262	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63098.1	000000	-	86	201phi2-1p270	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63105.1	000000	-	162	201phi2-1p278	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63115.1	000000	-	121	201phi2-1p289	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63116.1	000000	-	139	201phi2-1p290	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63127.1	000000	-	97	201phi2-1p301	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63138.1	000000	-	183	201phi2-1p312	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63296.1	000000	-	66	201phi2-1p316	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63142.1	000000	-	144	201phi2-1p317	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63143.1	000000	-	171	201phi2-1p318	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63151.1	000000	-	135	201phi2-1p326	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63159.1	000000	-	368	201phi2-1p334	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63172.1	000000	-	66	201phi2-1p346	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63188.1	000000	-	36	201phi2-1p363	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63189.1	000000	-	140	201phi2-1p364	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63192.1	000000	-	113	201phi2-1p367	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63206.1	000000	-	160	201phi2-1p381	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63211.1	000000	-	112	201phi2-1p386	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63213.1	000000	-	36	201phi2-1p388	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63215.1	000000	-	114	201phi2-1p390	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63217.1	000000	-	128	201phi2-1p393	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63238.1	000000	-	62	201phi2-1p414	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63243.1	000000	-	294	201phi2-1p419	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63244.1	000000	-	272	201phi2-1p420	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63253.1	000000	-	134	201phi2-1p430	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63254.1	000000	-	81	201phi2-1p431	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63282.1	000000	-	110	201phi2-1p459	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27230.1	000000	-	148	PPEV_gp136	Pseudomonas phage EL	GCA_000866825.1
CAG27233.1	000000	-	156	PPEV_gp139	Pseudomonas phage EL	GCA_000866825.1
CAG27256.1	000000	-	135	PPEV_gp162	Pseudomonas phage EL	GCA_000866825.1
CAG27184.1	000000	-	154	PPEV_gp090	Pseudomonas phage EL	GCA_000866825.1
CAG27112.1	000000	-	119	PPEV_gp018	Pseudomonas phage EL	GCA_000866825.1
CAG27098.1	000000	-	134	PPEV_gp004	Pseudomonas phage EL	GCA_000866825.1
CAG27096.1	000000	-	151	PPEV_gp002	Pseudomonas phage EL	GCA_000866825.1
CAG27232.1	000000	-	181	PPEV_gp138	Pseudomonas phage EL	GCA_000866825.1
CAG27253.1	000000	-	58	PPEV_gp159	Pseudomonas phage EL	GCA_000866825.1
CAG27136.1	000000	-	126	PPEV_gp042	Pseudomonas phage EL	GCA_000866825.1
CAG27135.1	000000	-	141	PPEV_gp041	Pseudomonas phage EL	GCA_000866825.1
CAG27168.1	000000	-	142	PPEV_gp074	Pseudomonas phage EL	GCA_000866825.1
CAG27238.1	000000	-	86	PPEV_gp144	Pseudomonas phage EL	GCA_000866825.1
CAG27242.1	000000	-	186	PPEV_gp148	Pseudomonas phage EL	GCA_000866825.1
CAG27196.1	000000	-	201	PPEV_gp102	Pseudomonas phage EL	GCA_000866825.1
AFH14533.1	000000	-	87	Lu11_0002	Pseudomonas phage Lu11	GCA_000897175.1
AFH14534.1	000000	-	127	Lu11_0003	Pseudomonas phage Lu11	GCA_000897175.1
AFH14537.1	000000	-	201	Lu11_0006	Pseudomonas phage Lu11	GCA_000897175.1
AFH14539.1	000000	-	124	Lu11_0008	Pseudomonas phage Lu11	GCA_000897175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFH14542.1	000000	-	116	Lu11_0011	Pseudomonas phage Lu11	GCA_000897175.1
AFH14544.1	000000	-	131	Lu11_0013	Pseudomonas phage Lu11	GCA_000897175.1
AFH14548.1	000000	-	137	Lu11_0017	Pseudomonas phage Lu11	GCA_000897175.1
AFH14553.1	000000	-	172	Lu11_0022	Pseudomonas phage Lu11	GCA_000897175.1
AFH14558.1	000000	-	91	Lu11_0027	Pseudomonas phage Lu11	GCA_000897175.1
AFH14559.1	000000	-	291	Lu11_0028	Pseudomonas phage Lu11	GCA_000897175.1
AFH14560.1	000000	-	132	Lu11_0029	Pseudomonas phage Lu11	GCA_000897175.1
AFH14577.1	000000	-	64	Lu11_0046	Pseudomonas phage Lu11	GCA_000897175.1
AFH14578.1	000000	-	57	Lu11_0047	Pseudomonas phage Lu11	GCA_000897175.1
AFH14599.1	000000	-	120	Lu11_0068	Pseudomonas phage Lu11	GCA_000897175.1
AFH14618.1	000000	-	82	Lu11_0086	Pseudomonas phage Lu11	GCA_000897175.1
AFH14621.1	000000	-	135	Lu11_0089	Pseudomonas phage Lu11	GCA_000897175.1
AFH14640.1	000000	-	401	Lu11_0108	Pseudomonas phage Lu11	GCA_000897175.1
AFH14653.1	000000	-	102	Lu11_0121	Pseudomonas phage Lu11	GCA_000897175.1
AFH14655.1	000000	-	98	Lu11_0123	Pseudomonas phage Lu11	GCA_000897175.1
AFH14687.1	000000	-	68	Lu11_0153A	Pseudomonas phage Lu11	GCA_000897175.1
AFH14691.1	000000	-	92	Lu11_0157	Pseudomonas phage Lu11	GCA_000897175.1
AFH14703.1	000000	-	54	Lu11_0168	Pseudomonas phage Lu11	GCA_000897175.1
AFH14711.1	000000	-	36	Lu11_0175A	Pseudomonas phage Lu11	GCA_000897175.1
AFH14713.1	000000	-	81	Lu11_0176A	Pseudomonas phage Lu11	GCA_000897175.1
AFH14750.1	000000	-	146	Lu11_0213	Pseudomonas phage Lu11	GCA_000897175.1
AFH14751.1	000000	-	157	Lu11_0214	Pseudomonas phage Lu11	GCA_000897175.1
AFH14765.1	000000	-	507	Lu11_0228	Pseudomonas phage Lu11	GCA_000897175.1
AFH14788.1	000000	-	88	Lu11_0252	Pseudomonas phage Lu11	GCA_000897175.1
AFH14792.1	000000	-	148	Lu11_0256	Pseudomonas phage Lu11	GCA_000897175.1
AFH14793.1	000000	-	188	Lu11_0257	Pseudomonas phage Lu11	GCA_000897175.1
AFH14804.1	000000	-	44	Lu11_0267	Pseudomonas phage Lu11	GCA_000897175.1
AFH14805.1	000000	-	143	Lu11_0268	Pseudomonas phage Lu11	GCA_000897175.1
AFH14806.1	000000	-	104	Lu11_0269	Pseudomonas phage Lu11	GCA_000897175.1
AFH14809.1	000000	-	223	Lu11_0272	Pseudomonas phage Lu11	GCA_000897175.1
AFH14811.1	000000	-	278	Lu11_0274	Pseudomonas phage Lu11	GCA_000897175.1
AFH14825.1	000000	-	56	Lu11_0287	Pseudomonas phage Lu11	GCA_000897175.1
AFH14832.1	000000	-	144	Lu11_0294	Pseudomonas phage Lu11	GCA_000897175.1
AFH14842.1	000000	-	578	Lu11_0304	Pseudomonas phage Lu11	GCA_000897175.1
AFH14843.1	000000	-	266	Lu11_0305	Pseudomonas phage Lu11	GCA_000897175.1
AFH14848.1	000000	-	117	Lu11_0310	Pseudomonas phage Lu11	GCA_000897175.1
AFH14849.1	000000	-	110	Lu11_0311	Pseudomonas phage Lu11	GCA_000897175.1
AFH14854.1	000000	-	37	Lu11_0316	Pseudomonas phage Lu11	GCA_000897175.1
AFH14864.1	000000	-	58	Lu11_0326	Pseudomonas phage Lu11	GCA_000897175.1
AFH14869.1	000000	-	122	Lu11_0331	Pseudomonas phage Lu11	GCA_000897175.1
AFH14875.1	000000	-	74	Lu11_0337	Pseudomonas phage Lu11	GCA_000897175.1
AFH14886.1	000000	-	86	Lu11_0348	Pseudomonas phage Lu11	GCA_000897175.1
AFH14892.1	000000	-	119	Lu11_0354	Pseudomonas phage Lu11	GCA_000897175.1
AFH14895.1	000000	-	109	Lu11_0357	Pseudomonas phage Lu11	GCA_000897175.1
AFH14897.1	000000	-	69	Lu11_0359	Pseudomonas phage Lu11	GCA_000897175.1
AFH14900.1	000000	-	185	Lu11_0362	Pseudomonas phage Lu11	GCA_000897175.1
AFH14908.1	000000	-	64	Lu11_0370	Pseudomonas phage Lu11	GCA_000897175.1
AFH14911.1	000000	-	51	Lu11_0373	Pseudomonas phage Lu11	GCA_000897175.1
AFH14912.1	000000	-	226	Lu11_0374	Pseudomonas phage Lu11	GCA_000897175.1
AFH14915.1	000000	-	170	Lu11_0377	Pseudomonas phage Lu11	GCA_000897175.1
AFH14916.1	000000	-	68	Lu11_0378	Pseudomonas phage Lu11	GCA_000897175.1
AFH14921.1	000000	-	41	Lu11_0383	Pseudomonas phage Lu11	GCA_000897175.1
ARV77271.1	000000	-	125	NOXIFER_102	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77277.1	000000	-	284	NOXIFER_108	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77279.1	000000	-	61	NOXIFER_110	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77281.1	000000	-	109	NOXIFER_112	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77292.1	000000	-	148	NOXIFER_123	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77332.1	000000	-	143	NOXIFER_163	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77339.1	000000	-	131	NOXIFER_170	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77346.1	000000	-	320	NOXIFER_177	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77348.1	000000	-	128	NOXIFER_179	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77355.1	000000	-	177	NOXIFER_186	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77368.1	000000	-	82	NOXIFER_199	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77377.1	000000	-	56	NOXIFER_211	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77386.1	000000	-	147	NOXIFER_221	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77391.1	000000	-	58	NOXIFER_226	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77400.1	000000	-	156	NOXIFER_235	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77195.1	000000	-	88	NOXIFER_24	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77408.1	000000	-	258	NOXIFER_243	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77422.1	000000	-	131	NOXIFER_257	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77430.1	000000	-	166	NOXIFER_265	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77441.1	000000	-	76	NOXIFER_276	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77444.1	000000	-	232	NOXIFER_279	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77451.1	000000	-	87	NOXIFER_286	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77452.1	000000	-	91	NOXIFER_287	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77454.1	000000	-	169	NOXIFER_289	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77456.1	000000	-	86	NOXIFER_291	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77472.1	000000	-	89	NOXIFER_307	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77475.1	000000	-	142	NOXIFER_310	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77478.1	000000	-	68	NOXIFER_313	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77491.1	000000	-	171	NOXIFER_326	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77206.1	000000	-	111	NOXIFER_35	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77209.1	000000	-	136	NOXIFER_38	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77176.1	000000	-	151	NOXIFER_5	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89460.1	000000	-	123	OBP_023	Pseudomonas phage OBP	GCA_000896635.1
AEV89469.1	000000	-	229	OBP_032	Pseudomonas phage OBP	GCA_000896635.1
AEV89505.1	000000	-	63	OBP_068	Pseudomonas phage OBP	GCA_000896635.1
AEV89525.1	000000	-	151	OBP_088	Pseudomonas phage OBP	GCA_000896635.1
AEV89567.1	000000	-	197	OBP_130	Pseudomonas phage OBP	GCA_000896635.1
AEV89593.1	000000	-	206	OBP_156	Pseudomonas phage OBP	GCA_000896635.1
AEV89613.1	000000	-	48	OBP_176	Pseudomonas phage OBP	GCA_000896635.1
AEV89614.1	000000	-	107	OBP_177	Pseudomonas phage OBP	GCA_000896635.1
AEV89619.1	000000	-	150	OBP_182	Pseudomonas phage OBP	GCA_000896635.1
AEV89635.1	000000	-	70	OBP_198	Pseudomonas phage OBP	GCA_000896635.1
AEV89642.1	000000	-	939	OBP_205	Pseudomonas phage OBP	GCA_000896635.1
AEV89643.1	000000	-	1859	OBP_206	Pseudomonas phage OBP	GCA_000896635.1
AEV89659.1	000000	-	151	OBP_222	Pseudomonas phage OBP	GCA_000896635.1
AEV89667.1	000000	-	69	OBP_230	Pseudomonas phage OBP	GCA_000896635.1
AEV89668.1	000000	-	73	OBP_231	Pseudomonas phage OBP	GCA_000896635.1
AEV89675.1	000000	-	58	OBP_238	Pseudomonas phage OBP	GCA_000896635.1
AEV89684.1	000000	-	94	OBP_247	Pseudomonas phage OBP	GCA_000896635.1
AEV89688.1	000000	-	96	OBP_251	Pseudomonas phage OBP	GCA_000896635.1
AEV89731.1	000000	-	310	OBP_294	Pseudomonas phage OBP	GCA_000896635.1
AEV89741.1	000000	-	161	OBP_304	Pseudomonas phage OBP	GCA_000896635.1
AEV89742.1	000000	-	197	OBP_305	Pseudomonas phage OBP	GCA_000896635.1
QBX32538.1	000000	-	218	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32338.1	000000	-	75	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ85921.1	000000	-	113	KKIINIFJ_00009	Pseudomonas phage PN05	GCA_009931935.1
QHJ85922.1	000000	-	170	KKIINIFJ_00010	Pseudomonas phage PN05	GCA_009931935.1
QHJ85930.1	000000	-	334	KKIINIFJ_00018	Pseudomonas phage PN05	GCA_009931935.1
QHJ85942.1	000000	-	76	KKIINIFJ_00030	Pseudomonas phage PN05	GCA_009931935.1
QHJ85943.1	000000	-	107	KKIINIFJ_00031	Pseudomonas phage PN05	GCA_009931935.1
QHJ85948.1	000000	-	130	KKIINIFJ_00036	Pseudomonas phage PN05	GCA_009931935.1
QHJ85950.1	000000	-	128	KKIINIFJ_00038	Pseudomonas phage PN05	GCA_009931935.1
QHJ85951.1	000000	-	68	KKIINIFJ_00039	Pseudomonas phage PN05	GCA_009931935.1
QHJ85954.1	000000	-	164	KKIINIFJ_00042	Pseudomonas phage PN05	GCA_009931935.1
QHJ85955.1	000000	-	58	KKIINIFJ_00043	Pseudomonas phage PN05	GCA_009931935.1
QHJ85960.1	000000	-	94	KKIINIFJ_00048	Pseudomonas phage PN05	GCA_009931935.1
QHJ85996.1	000000	-	114	KKIINIFJ_00084	Pseudomonas phage PN05	GCA_009931935.1
QHJ86000.1	000000	-	88	KKIINIFJ_00088	Pseudomonas phage PN05	GCA_009931935.1
QHJ86043.1	000000	-	150	KKIINIFJ_00131	Pseudomonas phage PN05	GCA_009931935.1
QHJ86047.1	000000	-	86	KKIINIFJ_00135	Pseudomonas phage PN05	GCA_009931935.1
QHJ86052.1	000000	-	344	KKIINIFJ_00140	Pseudomonas phage PN05	GCA_009931935.1
QHJ86053.1	000000	-	86	KKIINIFJ_00141	Pseudomonas phage PN05	GCA_009931935.1
QHJ86072.1	000000	-	88	KKIINIFJ_00160	Pseudomonas phage PN05	GCA_009931935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QHJ86075.1	000000	-	78	KKIINIFJ_00163	Pseudomonas phage PN05	GCA_009931935.1
QHJ86102.1	000000	-	65	KKIINIFJ_00191	Pseudomonas phage PN05	GCA_009931935.1
QHJ86121.1	000000	-	55	KKIINIFJ_00210	Pseudomonas phage PN05	GCA_009931935.1
QHJ86129.1	000000	-	55	KKIINIFJ_00218	Pseudomonas phage PN05	GCA_009931935.1
QHJ86144.1	000000	-	81	KKIINIFJ_00233	Pseudomonas phage PN05	GCA_009931935.1
QHJ86151.1	000000	-	47	KKIINIFJ_00240	Pseudomonas phage PN05	GCA_009931935.1
QHJ86182.1	000000	-	152	KKIINIFJ_00272	Pseudomonas phage PN05	GCA_009931935.1
QHJ86187.1	000000	-	62	KKIINIFJ_00277	Pseudomonas phage PN05	GCA_009931935.1
QHJ86196.1	000000	-	43	KKIINIFJ_00286	Pseudomonas phage PN05	GCA_009931935.1
AGS81885.1	000000	-	244	PaBG_00001	Pseudomonas phage PaBG	GCA_000912555.1
AGS81886.1	000000	-	91	PaBG_00002	Pseudomonas phage PaBG	GCA_000912555.1
AGS81893.1	000000	-	168	PaBG_00009	Pseudomonas phage PaBG	GCA_000912555.1
AGS81895.1	000000	-	75	PaBG_00011	Pseudomonas phage PaBG	GCA_000912555.1
AGS81900.2	000000	-	336	PaBG_00016	Pseudomonas phage PaBG	GCA_000912555.1
AGS81906.1	000000	-	155	PaBG_00022	Pseudomonas phage PaBG	GCA_000912555.1
AGS81913.1	000000	-	96	PaBG_00029	Pseudomonas phage PaBG	GCA_000912555.1
AGS81915.1	000000	-	177	PaBG_00031	Pseudomonas phage PaBG	GCA_000912555.1
AGS81918.1	000000	-	129	PaBG_00034	Pseudomonas phage PaBG	GCA_000912555.1
AGS81938.1	000000	-	87	PaBG_00053	Pseudomonas phage PaBG	GCA_000912555.1
AGS81942.1	000000	-	80	PaBG_00058	Pseudomonas phage PaBG	GCA_000912555.1
AGS81946.1	000000	-	181	PaBG_00062	Pseudomonas phage PaBG	GCA_000912555.1
AGS81963.1	000000	-	157	PaBG_00079	Pseudomonas phage PaBG	GCA_000912555.1
AGS81967.1	000000	-	320	PaBG_00083	Pseudomonas phage PaBG	GCA_000912555.1
AGS82017.1	000000	-	120	PaBG_00134	Pseudomonas phage PaBG	GCA_000912555.1
AGS82021.1	000000	-	137	PaBG_00138	Pseudomonas phage PaBG	GCA_000912555.1
AGS82022.1	000000	-	73	PaBG_00139	Pseudomonas phage PaBG	GCA_000912555.1
AGS82023.1	000000	-	269	PaBG_00140	Pseudomonas phage PaBG	GCA_000912555.1
AGS82043.1	000000	-	113	PaBG_00161	Pseudomonas phage PaBG	GCA_000912555.1
AGS82047.1	000000	-	65	PaBG_00170	Pseudomonas phage PaBG	GCA_000912555.1
AGS82079.1	000000	-	169	PaBG_00204	Pseudomonas phage PaBG	GCA_000912555.1
AGS82104.1	000000	-	139	PaBG_00229	Pseudomonas phage PaBG	GCA_000912555.1
AGS82105.2	000000	-	40	PaBG_00231	Pseudomonas phage PaBG	GCA_000912555.1
QKE11220.1	000000	-	56	PaBG_00249	Pseudomonas phage PaBG	GCA_000912555.1
AGS82129.1	000000	-	94	PaBG_00254	Pseudomonas phage PaBG	GCA_000912555.1
AGS82137.1	000000	-	175	PaBG_00263	Pseudomonas phage PaBG	GCA_000912555.1
AGS82138.1	000000	-	587	PaBG_00264	Pseudomonas phage PaBG	GCA_000912555.1
QKE11223.1	000000	-	131	PaBG_00267	Pseudomonas phage PaBG	GCA_000912555.1
AGS82146.1	000000	-	98	PaBG_00273	Pseudomonas phage PaBG	GCA_000912555.1
AGS82151.1	000000	-	188	PaBG_00278	Pseudomonas phage PaBG	GCA_000912555.1
AGS82158.1	000000	-	98	PaBG_00285	Pseudomonas phage PaBG	GCA_000912555.1
QKE11226.1	000000	-	85	PaBG_00293	Pseudomonas phage PaBG	GCA_000912555.1
AGS82170.1	000000	-	300	PaBG_00299	Pseudomonas phage PaBG	GCA_000912555.1
AGS82172.1	000000	-	85	PaBG_00301	Pseudomonas phage PaBG	GCA_000912555.1
AGS82178.1	000000	-	145	PaBG_00307	Pseudomonas phage PaBG	GCA_000912555.1
AGS82181.2	000000	-	130	PaBG_00310	Pseudomonas phage PaBG	GCA_000912555.1
AGS82183.1	000000	-	173	PaBG_00312	Pseudomonas phage PaBG	GCA_000912555.1
AGS82189.1	000000	-	173	PaBG_00318	Pseudomonas phage PaBG	GCA_000912555.1
ARV76746.1	000000	-	69	PHABIO_115	Pseudomonas phage Phabio	GCA_002624965.1
ARV76748.1	000000	-	51	PHABIO_117	Pseudomonas phage Phabio	GCA_002624965.1
ARV76749.1	000000	-	79	PHABIO_118	Pseudomonas phage Phabio	GCA_002624965.1
ARV76644.1	000000	-	69	PHABIO_13	Pseudomonas phage Phabio	GCA_002624965.1
ARV76646.1	000000	-	63	PHABIO_15	Pseudomonas phage Phabio	GCA_002624965.1
ARV76784.1	000000	-	107	PHABIO_153	Pseudomonas phage Phabio	GCA_002624965.1
ARV76785.1	000000	-	48	PHABIO_154	Pseudomonas phage Phabio	GCA_002624965.1
ARV76786.1	000000	-	87	PHABIO_155	Pseudomonas phage Phabio	GCA_002624965.1
ARV76790.1	000000	-	61	PHABIO_159	Pseudomonas phage Phabio	GCA_002624965.1
ARV76798.1	000000	-	37	PHABIO_167	Pseudomonas phage Phabio	GCA_002624965.1
ARV76803.1	000000	-	79	PHABIO_172	Pseudomonas phage Phabio	GCA_002624965.1
ARV76828.1	000000	-	113	PHABIO_197	Pseudomonas phage Phabio	GCA_002624965.1
ARV76870.1	000000	-	44	PHABIO_239	Pseudomonas phage Phabio	GCA_002624965.1
ARV76873.1	000000	-	44	PHABIO_242	Pseudomonas phage Phabio	GCA_002624965.1
ARV76898.1	000000	-	105	PHABIO_267	Pseudomonas phage Phabio	GCA_002624965.1
ARV76900.1	000000	-	170	PHABIO_269	Pseudomonas phage Phabio	GCA_002624965.1
ARV76901.1	000000	-	150	PHABIO_270	Pseudomonas phage Phabio	GCA_002624965.1
ARV76916.1	000000	-	139	PHABIO_285	Pseudomonas phage Phabio	GCA_002624965.1
ARV76660.1	000000	-	62	PHABIO_29	Pseudomonas phage Phabio	GCA_002624965.1
ARV76929.1	000000	-	41	PHABIO_298	Pseudomonas phage Phabio	GCA_002624965.1
ARV76946.1	000000	-	86	PHABIO_315	Pseudomonas phage Phabio	GCA_002624965.1
ARV76954.1	000000	-	132	PHABIO_323	Pseudomonas phage Phabio	GCA_002624965.1
ARV76956.1	000000	-	52	PHABIO_325	Pseudomonas phage Phabio	GCA_002624965.1
ARV76965.1	000000	-	76	PHABIO_334	Pseudomonas phage Phabio	GCA_002624965.1
ARV76968.1	000000	-	94	PHABIO_337	Pseudomonas phage Phabio	GCA_002624965.1
ARV76981.1	000000	-	56	PHABIO_350	Pseudomonas phage Phabio	GCA_002624965.1
ARV76989.1	000000	-	94	PHABIO_358	Pseudomonas phage Phabio	GCA_002624965.1
ARV76994.1	000000	-	51	PHABIO_363	Pseudomonas phage Phabio	GCA_002624965.1
ARV76995.1	000000	-	160	PHABIO_364	Pseudomonas phage Phabio	GCA_002624965.1
ARV77005.1	000000	-	169	PHABIO_374	Pseudomonas phage Phabio	GCA_002624965.1
ARV77008.1	000000	-	59	PHABIO_377	Pseudomonas phage Phabio	GCA_002624965.1
ARV77009.1	000000	-	102	PHABIO_378	Pseudomonas phage Phabio	GCA_002624965.1
ARV77019.1	000000	-	110	PHABIO_388	Pseudomonas phage Phabio	GCA_002624965.1
ARV77028.1	000000	-	63	PHABIO_397	Pseudomonas phage Phabio	GCA_002624965.1
ARV76671.1	000000	-	116	PHABIO_40	Pseudomonas phage Phabio	GCA_002624965.1
ARV76672.1	000000	-	81	PHABIO_41	Pseudomonas phage Phabio	GCA_002624965.1
ARV77042.1	000000	-	99	PHABIO_411	Pseudomonas phage Phabio	GCA_002624965.1
ARV77051.1	000000	-	78	PHABIO_420	Pseudomonas phage Phabio	GCA_002624965.1
ARV77061.1	000000	-	67	PHABIO_430	Pseudomonas phage Phabio	GCA_002624965.1
ARV77087.1	000000	-	60	PHABIO_459	Pseudomonas phage Phabio	GCA_002624965.1
ARV77090.1	000000	-	158	PHABIO_462	Pseudomonas phage Phabio	GCA_002624965.1
ARV77094.1	000000	-	115	PHABIO_466	Pseudomonas phage Phabio	GCA_002624965.1
ARV77095.1	000000	-	31	PHABIO_467	Pseudomonas phage Phabio	GCA_002624965.1
ARV76683.1	000000	-	88	PHABIO_52	Pseudomonas phage Phabio	GCA_002624965.1
ARV76684.1	000000	-	87	PHABIO_53	Pseudomonas phage Phabio	GCA_002624965.1
ARV76686.1	000000	-	82	PHABIO_55	Pseudomonas phage Phabio	GCA_002624965.1
ARV76637.1	000000	-	37	PHABIO_6	Pseudomonas phage Phabio	GCA_002624965.1
ARV76726.1	000000	-	105	PHABIO_95	Pseudomonas phage Phabio	GCA_002624965.1
AEH03463.1	000000	-	191	036	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03533.1	000000	-	109	109	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03534.1	000000	-	100	110	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03614.1	000000	-	70	191	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03615.1	000000	-	97	192	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03668.1	000000	-	144	245	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03681.1	000000	-	105	258	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03683.1	000000	-	172	260	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03689.1	000000	-	98	266	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03710.1	000000	-	70	287	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03715.1	000000	-	120	292	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03740.1	000000	-	125	317	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03748.1	000000	-	139	325	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03759.1	000000	-	145	336	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03766.1	000000	-	121	343	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03772.1	000000	-	107	349	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02644.1	000000	-	40	PSA21_116	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02645.1	000000	-	101	PSA21_117	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02646.1	000000	-	125	PSA21_118	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02649.1	000000	-	37	PSA21_121	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02650.1	000000	-	56	PSA21_122	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02653.1	000000	-	91	PSA21_125	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02656.1	000000	-	56	PSA21_128	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02658.1	000000	-	65	PSA21_131	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02659.1	000000	-	40	PSA21_132	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02661.1	000000	-	58	PSA21_134	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02662.1	000000	-	94	PSA21_135	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02663.1	000000	-	111	PSA21_136	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02665.1	000000	-	187	PSA21_138	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02673.1	000000	-	179	PSA21_146	Pseudomonas phage Psa21	GCA_004340405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBJ02676.1	000000	-	151	PSA21_149	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02545.1	000000	-	109	PSA21_15	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02677.1	000000	-	92	PSA21_150	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02687.1	000000	-	186	PSA21_160	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02704.1	000000	-	145	PSA21_178	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02754.1	000000	-	74	PSA21_228	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02553.1	000000	-	163	PSA21_23	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02756.1	000000	-	55	PSA21_230	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02763.1	000000	-	126	PSA21_237	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02774.1	000000	-	131	PSA21_248	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02776.1	000000	-	355	PSA21_250	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02788.1	000000	-	127	PSA21_262	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02807.1	000000	-	184	PSA21_281	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02814.1	000000	-	303	PSA21_288	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02815.1	000000	-	95	PSA21_289	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02824.1	000000	-	57	PSA21_298	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02833.1	000000	-	67	PSA21_307	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02840.1	000000	-	38	PSA21_314	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02843.1	000000	-	117	PSA21_317	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02844.1	000000	-	93	PSA21_318	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02845.1	000000	-	110	PSA21_319	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02846.1	000000	-	85	PSA21_320	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02847.1	000000	-	82	PSA21_321	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02850.1	000000	-	89	PSA21_324	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02855.1	000000	-	161	PSA21_329	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02857.1	000000	-	125	PSA21_331	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02859.1	000000	-	150	PSA21_333	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02860.1	000000	-	202	PSA21_334	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02865.1	000000	-	94	PSA21_339	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02868.1	000000	-	93	PSA21_342	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02870.1	000000	-	114	PSA21_344	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02875.1	000000	-	152	PSA21_349	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02890.1	000000	-	137	PSA21_364	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02908.1	000000	-	92	PSA21_382	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02937.1	000000	-	55	PSA21_418	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02941.1	000000	-	53	PSA21_423	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02576.1	000000	-	49	PSA21_46	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02535.1	000000	-	100	PSA21_5	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02583.1	000000	-	82	PSA21_53	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02588.1	000000	-	127	PSA21_59	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02607.1	000000	-	69	PSA21_78	Pseudomonas phage Psa21	GCA_004340405.1
QCG75889.1	000000	-	91	EST35_0005	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75890.1	000000	-	87	EST35_0006	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75906.1	000000	-	44	EST35_0022	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75907.1	000000	-	48	EST35_0023	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75910.1	000000	-	44	EST35_0026	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75914.1	000000	-	56	EST35_0030	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75916.1	000000	-	62	EST35_0032	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75927.1	000000	-	43	EST35_0044	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75931.1	000000	-	65	EST35_0048	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75933.1	000000	-	194	EST35_0050	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75934.1	000000	-	182	EST35_0051	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75945.1	000000	-	110	EST35_0062	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75948.1	000000	-	97	EST35_0065	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75949.1	000000	-	96	EST35_0066	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75951.1	000000	-	55	EST35_0069	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75952.1	000000	-	91	EST35_0070	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75956.1	000000	-	64	EST35_0074	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75958.1	000000	-	39	EST35_0076	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75965.1	000000	-	36	EST35_0083	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75978.1	000000	-	123	EST35_0096	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75982.1	000000	-	77	EST35_0100	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75994.1	000000	-	76	EST35_0112	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76061.1	000000	-	187	EST35_0180	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76065.1	000000	-	95	EST35_0184	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76066.1	000000	-	143	EST35_0185	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76071.1	000000	-	63	EST35_0190	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76108.1	000000	-	399	EST35_0227	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76117.1	000000	-	151	EST35_0236	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76127.1	000000	-	74	EST35_0246	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76160.1	000000	-	145	EST35_0279	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76173.1	000000	-	120	EST35_0292	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76185.1	000000	-	211	EST35_0304	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76204.1	000000	-	139	EST35_0323	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76210.1	000000	-	66	EST35_0329	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76213.1	000000	-	124	EST35_0332	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76218.1	000000	-	152	EST35_0337	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76219.1	000000	-	117	EST35_0338	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76228.1	000000	-	75	EST35_0347	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76232.1	000000	-	319	EST35_0351	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76237.1	000000	-	69	EST35_0357	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76240.1	000000	-	185	EST35_0360	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76259.1	000000	-	87	EST35_0379	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76270.1	000000	-	102	EST35_0390	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76293.1	000000	-	81	EST35_0425	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76294.1	000000	-	62	EST35_0426	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76297.1	000000	-	73	EST35_0429	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76302.1	000000	-	39	EST35_0434	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76314.1	000000	-	48	EST35_0446	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76322.1	000000	-	78	EST35_0454	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM42062.1	000000	-	37	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26318.1	000000	-	36	PHIKZ072.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26349.1	000000	-	23	PHIKZ232.1	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19005.1	000000	-	550	FDH28_gp031	Ralstonia phage RP12	GCA_002617345.1
BAS04816.1	000000	-	59	AVU11_gp024	Ralstonia phage RSF1	GCA_001500875.1
BAU71419.1	000000	-	36	AVU11_agp28	Ralstonia phage RSF1	GCA_001500875.1
BAQ02587.2	000000	-	42	-	Ralstonia phage RSL2	GCA_001503055.1
BAU71411.1	000000	-	67	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02673.2	000000	-	199	-	Ralstonia phage RSL2	GCA_001503055.1
BAG41469.1	000000	-	151	RSL1_ORF024	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41449.1	000000	-	54	RSL1_ORF004	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41507.1	000000	-	123	RSL1_ORF061	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41499.1	000000	-	166	RSL1_ORF053	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41506.1	000000	-	96	RSL1_ORF060	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41785.1	000000	-	105	RSL1_ORF337	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41789.1	000000	-	355	RSL1_ORF341	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72951.1	000000	-	77	RSL1_ORF343	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41787.2	000000	-	99	RSL1_ORF339	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41568.1	000000	-	103	RSL1_ORF123	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41572.1	000000	-	110	RSL1_ORF127	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41715.1	000000	-	115	RSL1_ORF268	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72950.1	000000	-	119	RSL1_ORF328	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41756.1	000000	-	122	RSL1_ORF309	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41622.1	000000	-	123	RSL1_ORF174	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41564.1	000000	-	130	RSL1_ORF119	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41720.1	000000	-	151	RSL1_ORF273	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41566.1	000000	-	164	RSL1_ORF121	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41620.1	000000	-	196	RSL1_ORF172	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41732.1	000000	-	198	RSL1_ORF285	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41733.1	000000	-	224	RSL1_ORF286	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41750.1	000000	-	40	RSL1_ORF304	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41688.1	000000	-	40	RSL1_ORF239	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41685.1	000000	-	477	RSL1_ORF236	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41763.1	000000	-	50	RSL1_ORF316	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41708.1	000000	-	57	RSL1_ORF261	Ralstonia phage phiRSL1	GCA_000879455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAG41594.1	000000	-	71	RSL1_ORF148	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41713.1	000000	-	72	RSL1_ORF266	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41725.1	000000	-	75	RSL1_ORF278	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41639.1	000000	-	78	RSL1_ORF190	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41612.1	000000	-	79	RSL1_ORF165	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41734.1	000000	-	83	RSL1_ORF288	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41772.2	000000	-	95	RSL1_ORF325	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41517.1	000000	-	124	RSL1_ORF071	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41526.1	000000	-	126	RSL1_ORF080	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41522.1	000000	-	142	RSL1_ORF076	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41545.1	000000	-	58	RSL1_ORF100	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41535.1	000000	-	69	RSL1_ORF090	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41543.1	000000	-	99	RSL1_ORF098	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41484.1	000000	-	132	RSL1_ORF039	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41459.1	000000	-	142	RSL1_ORF014	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44146.1	000000	-	297	PBI_SCTP2_131	Salicola phage SCTP-2	GCA_002625545.1
ASV44165.1	000000	-	492	PBI_SCTP2_150	Salicola phage SCTP-2	GCA_002625545.1
ASV44179.1	000000	-	146	PBI_SCTP2_164	Salicola phage SCTP-2	GCA_002625545.1
ASV44033.1	000000	-	233	PBI_SCTP2_18	Salicola phage SCTP-2	GCA_002625545.1
ASV44263.1	000000	-	68	PBI_SCTP2_248	Salicola phage SCTP-2	GCA_002625545.1
ASV44269.1	000000	-	116	PBI_SCTP2_254	Salicola phage SCTP-2	GCA_002625545.1
ASV44270.1	000000	-	120	PBI_SCTP2_255	Salicola phage SCTP-2	GCA_002625545.1
ASV44273.1	000000	-	104	PBI_SCTP2_258	Salicola phage SCTP-2	GCA_002625545.1
ASV44284.1	000000	-	99	PBI_SCTP2_269	Salicola phage SCTP-2	GCA_002625545.1
ASV44317.1	000000	-	145	PBI_SCTP2_302	Salicola phage SCTP-2	GCA_002625545.1
ASV44322.1	000000	-	79	PBI_SCTP2_307	Salicola phage SCTP-2	GCA_002625545.1
ASV44329.1	000000	-	46	PBI_SCTP2_314	Salicola phage SCTP-2	GCA_002625545.1
ASV44337.1	000000	-	99	PBI_SCTP2_322	Salicola phage SCTP-2	GCA_002625545.1
ASV44348.1	000000	-	206	PBI_SCTP2_333	Salicola phage SCTP-2	GCA_002625545.1
ASV44350.1	000000	-	44	PBI_SCTP2_335	Salicola phage SCTP-2	GCA_002625545.1
ASV44366.1	000000	-	43	PBI_SCTP2_351	Salicola phage SCTP-2	GCA_002625545.1
ASV44376.1	000000	-	65	PBI_SCTP2_361	Salicola phage SCTP-2	GCA_002625545.1
ASV44383.1	000000	-	72	PBI_SCTP2_368	Salicola phage SCTP-2	GCA_002625545.1
ASV44388.1	000000	-	65	PBI_SCTP2_373	Salicola phage SCTP-2	GCA_002625545.1
ASV44392.1	000000	-	120	PBI_SCTP2_377	Salicola phage SCTP-2	GCA_002625545.1
ASV44397.1	000000	-	58	PBI_SCTP2_382	Salicola phage SCTP-2	GCA_002625545.1
ASV44408.1	000000	-	99	PBI_SCTP2_393	Salicola phage SCTP-2	GCA_002625545.1
ASV44435.1	000000	-	47	PBI_SCTP2_420	Salicola phage SCTP-2	GCA_002625545.1
ASV44445.1	000000	-	210	PBI_SCTP2_430	Salicola phage SCTP-2	GCA_002625545.1
ASV44447.1	000000	-	149	PBI_SCTP2_432	Salicola phage SCTP-2	GCA_002625545.1
ASV44448.1	000000	-	115	PBI_SCTP2_433	Salicola phage SCTP-2	GCA_002625545.1
ASV44475.1	000000	-	380	PBI_SCTP2_460	Salicola phage SCTP-2	GCA_002625545.1
ASV44481.1	000000	-	136	PBI_SCTP2_466	Salicola phage SCTP-2	GCA_002625545.1
ASV44486.1	000000	-	126	PBI_SCTP2_471	Salicola phage SCTP-2	GCA_002625545.1
ASV44529.1	000000	-	43	PBI_SCTP2_514	Salicola phage SCTP-2	GCA_002625545.1
ASV44538.1	000000	-	142	PBI_SCTP2_523	Salicola phage SCTP-2	GCA_002625545.1
ASV44539.1	000000	-	175	PBI_SCTP2_524	Salicola phage SCTP-2	GCA_002625545.1
ASV44541.1	000000	-	21	PBI_SCTP2_526	Salicola phage SCTP-2	GCA_002625545.1
ASV44094.1	000000	-	79	PBI_SCTP2_79	Salicola phage SCTP-2	GCA_002625545.1
ASV44100.1	000000	-	79	PBI_SCTP2_85	Salicola phage SCTP-2	GCA_002625545.1
ASV44101.1	000000	-	804	PBI_SCTP2_86	Salicola phage SCTP-2	GCA_002625545.1
QCW18659.1	000000	-	31	7t3_0138	Salmonella phage 7t3	GCA_006083215.1
QCW18665.1	000000	-	46	7t3_0144	Salmonella phage 7t3	GCA_006083215.1
QCW18667.1	000000	-	34	7t3_0146	Salmonella phage 7t3	GCA_006083215.1
QCW18545.1	000000	-	33	7t3_015	Salmonella phage 7t3	GCA_006083215.1
QCW18674.1	000000	-	35	7t3_0153	Salmonella phage 7t3	GCA_006083215.1
QCW18675.1	000000	-	35	7t3_0154	Salmonella phage 7t3	GCA_006083215.1
QCW18685.1	000000	-	40	7t3_0164	Salmonella phage 7t3	GCA_006083215.1
QCW18700.1	000000	-	36	7t3_0179	Salmonella phage 7t3	GCA_006083215.1
QCW18724.1	000000	-	29	7t3_0203	Salmonella phage 7t3	GCA_006083215.1
QCW18547.1	000000	-	34	7t3_022	Salmonella phage 7t3	GCA_006083215.1
QCW18764.1	000000	-	47	7t3_0243	Salmonella phage 7t3	GCA_006083215.1
QCW18766.1	000000	-	34	7t3_0245	Salmonella phage 7t3	GCA_006083215.1
QCW18774.1	000000	-	68	7t3_0253	Salmonella phage 7t3	GCA_006083215.1
QCW18831.1	000000	-	45	7t3_0310	Salmonella phage 7t3	GCA_006083215.1
QCW18896.1	000000	-	38	7t3_0375	Salmonella phage 7t3	GCA_006083215.1
QCW18563.1	000000	-	65	7t3_040	Salmonella phage 7t3	GCA_006083215.1
QCW18932.1	000000	-	30	7t3_0411	Salmonella phage 7t3	GCA_006083215.1
QCW18965.1	000000	-	37	7t3_0444	Salmonella phage 7t3	GCA_006083215.1
QCW18967.1	000000	-	55	7t3_0446	Salmonella phage 7t3	GCA_006083215.1
QCW18968.1	000000	-	36	7t3_0447	Salmonella phage 7t3	GCA_006083215.1
QCW19071.1	000000	-	36	7t3_0551	Salmonella phage 7t3	GCA_006083215.1
QCW19085.1	000000	-	29	7t3_0566	Salmonella phage 7t3	GCA_006083215.1
QCW18600.1	000000	-	73	7t3_079	Salmonella phage 7t3	GCA_006083215.1
QCW18601.1	000000	-	46	7t3_080	Salmonella phage 7t3	GCA_006083215.1
QCW18602.1	000000	-	33	7t3_081	Salmonella phage 7t3	GCA_006083215.1
AXF51062.1	000000	-	70	MLDJOKPK_00032	Salmonella phage SPAsTU	GCA_003183805.1
AXF51125.1	000000	-	33	MLDJOKPK_00249	Salmonella phage SPAsTU	GCA_003183805.1
QKE54338.1	000000	-	586	ACSA002_0240	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54339.1	000000	-	126	ACSA002_0250	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54341.1	000000	-	101	ACSA002_0270	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54378.1	000000	-	79	ACSA002_0640	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54383.1	000000	-	177	ACSA002_0690	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54384.1	000000	-	168	ACSA002_0700	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54385.1	000000	-	163	ACSA002_0710	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54386.1	000000	-	89	ACSA002_0720	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54393.1	000000	-	52	ACSA002_0790	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54402.1	000000	-	243	ACSA002_0880	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54404.1	000000	-	66	ACSA002_0900	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54432.1	000000	-	126	ACSA002_1180	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54437.1	000000	-	395	ACSA002_1230	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54439.1	000000	-	60	ACSA002_1250	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54440.1	000000	-	43	ACSA002_1260	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54446.1	000000	-	40	ACSA002_1320	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54447.1	000000	-	154	ACSA002_1330	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54466.1	000000	-	61	ACSA002_1520	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54483.1	000000	-	227	ACSA002_1690	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54501.1	000000	-	228	ACSA002_1870	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54507.1	000000	-	247	ACSA002_1930	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54525.1	000000	-	71	ACSA002_2090	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54549.1	000000	-	196	ACSA002_2330	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54556.1	000000	-	160	ACSA002_2400	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54558.1	000000	-	69	ACSA002_2420	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54560.1	000000	-	69	ACSA002_2440	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54568.1	000000	-	89	ACSA002_2520	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54583.1	000000	-	97	ACSA002_2670	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54584.1	000000	-	118	ACSA002_2680	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54640.1	000000	-	95	ACSA002_3230	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65386.1	000000	-	88	2050HW_00051	Serratia phage 2050HW	GCA_002628125.1
ATA65417.1	000000	-	42	2050HW_00082	Serratia phage 2050HW	GCA_002628125.1
ATA65420.1	000000	-	47	2050HW_00085	Serratia phage 2050HW	GCA_002628125.1
ATA65452.1	000000	-	389	2050HW_00117	Serratia phage 2050HW	GCA_002628125.1
ATA65493.1	000000	-	34	2050HW_00158	Serratia phage 2050HW	GCA_002628125.1
ATA65513.1	000000	-	40	2050HW_00178	Serratia phage 2050HW	GCA_002628125.1
AQW88870.1	000000	-	56	BF_0345	Serratia phage BF	GCA_002619745.1
AQW88938.1	000000	-	38	BF_0413	Serratia phage BF	GCA_002619745.1
AQW88943.1	000000	-	60	BF_0418	Serratia phage BF	GCA_002619745.1
AQW89006.1	000000	-	62	BF_0481	Serratia phage BF	GCA_002619745.1
QDB71057.1	000000	-	32	CPT_Moabite_025	Serratia phage Moabite	GCA_006384735.1
QDB71107.1	000000	-	43	CPT_Moabite_075	Serratia phage Moabite	GCA_006384735.1
QDB71173.1	000000	-	79	CPT_Moabite_143	Serratia phage Moabite	GCA_006384735.1
QDB71272.1	000000	-	30	CPT_Moabite_242	Serratia phage Moabite	GCA_006384735.1
QDB71337.1	000000	-	40	CPT_Moabite_307	Serratia phage Moabite	GCA_006384735.1
QDB71357.1	000000	-	103	CPT_Moabite_327	Serratia phage Moabite	GCA_006384735.1
QFP93239.1	000000	-	113	-	Serratia phage PCH45	GCA_009187865.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QFP93237.1	000000	-	112	-	Serratia phage PCH45	GCA_009187865.1
QFP93186.1	000000	-	168	-	Serratia phage PCH45	GCA_009187865.1
QFP93184.1	000000	-	170	-	Serratia phage PCH45	GCA_009187865.1
QFP93247.1	000000	-	104	-	Serratia phage PCH45	GCA_009187865.1
QFP93163.1	000000	-	196	-	Serratia phage PCH45	GCA_009187865.1
QFP93263.1	000000	-	65	-	Serratia phage PCH45	GCA_009187865.1
QFP93205.1	000000	-	144	-	Serratia phage PCH45	GCA_009187865.1
QFP93226.1	000000	-	121	-	Serratia phage PCH45	GCA_009187865.1
QFP93208.1	000000	-	140	-	Serratia phage PCH45	GCA_009187865.1
QFP93125.1	000000	-	261	-	Serratia phage PCH45	GCA_009187865.1
QFP93191.1	000000	-	165	-	Serratia phage PCH45	GCA_009187865.1
QFP93182.1	000000	-	174	-	Serratia phage PCH45	GCA_009187865.1
QFP93224.1	000000	-	126	-	Serratia phage PCH45	GCA_009187865.1
QFP93188.1	000000	-	169	-	Serratia phage PCH45	GCA_009187865.1
AGR47736.1	000000	-	162	SmphiM12_104	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47780.1	000000	-	138	SmphiM12_148	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47908.1	000000	-	161	SmphiM12_276	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47976.1	000000	-	95	SmphiM12_344	Sinorhizobium phage phiM12	GCA_001023565.1
AIF27787.1	000000	-	46	SmphiM12_351	Sinorhizobium phage phiM12	GCA_001023565.1
AKF13440.1	000000	-	121	PHIN3_177	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13523.1	000000	-	78	PHIN3_260	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13293.1	000000	-	77	PHIN3_28	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13565.1	000000	-	47	PHIN3_302	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13566.1	000000	-	33	PHIN3_303	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13636.1	000000	-	35	PHIN3_373	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13640.1	000000	-	159	PHIN3_377	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13641.1	000000	-	122	PHIN3_378	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13643.1	000000	-	74	PHIN3_380	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28099.1	000000	-	205	PAU_101	Sphingomonas phage PAU	GCA_000902455.1
AFF28009.1	000000	-	135	PAU_11	Sphingomonas phage PAU	GCA_000902455.1
AFF28158.1	000000	-	84	PAU_160	Sphingomonas phage PAU	GCA_000902455.1
AFF28160.1	000000	-	152	PAU_162	Sphingomonas phage PAU	GCA_000902455.1
AFF28176.1	000000	-	211	PAU_178	Sphingomonas phage PAU	GCA_000902455.1
AFF28182.1	000000	-	180	PAU_184	Sphingomonas phage PAU	GCA_000902455.1
AFF28195.1	000000	-	408	PAU_197	Sphingomonas phage PAU	GCA_000902455.1
AFF28202.1	000000	-	182	PAU_204	Sphingomonas phage PAU	GCA_000902455.1
AFF28203.1	000000	-	82	PAU_205	Sphingomonas phage PAU	GCA_000902455.1
AFF28208.1	000000	-	169	PAU_210	Sphingomonas phage PAU	GCA_000902455.1
AFF28227.1	000000	-	138	PAU_229	Sphingomonas phage PAU	GCA_000902455.1
AFF28021.1	000000	-	161	PAU_23	Sphingomonas phage PAU	GCA_000902455.1
AFF28229.1	000000	-	81	PAU_231	Sphingomonas phage PAU	GCA_000902455.1
AFF28231.1	000000	-	128	PAU_233	Sphingomonas phage PAU	GCA_000902455.1
AFF28232.1	000000	-	46	PAU_234	Sphingomonas phage PAU	GCA_000902455.1
AFF28233.1	000000	-	67	PAU_235	Sphingomonas phage PAU	GCA_000902455.1
AFF28255.1	000000	-	669	PAU_257	Sphingomonas phage PAU	GCA_000902455.1
AFF28278.1	000000	-	284	PAU_280	Sphingomonas phage PAU	GCA_000902455.1
AFF28282.1	000000	-	116	PAU_284	Sphingomonas phage PAU	GCA_000902455.1
AFF28300.1	000000	-	58	PAU_290	Sphingomonas phage PAU	GCA_000902455.1
AFF28288.1	000000	-	157	PAU_291	Sphingomonas phage PAU	GCA_000902455.1
AFF28294.1	000000	-	92	PAU_297	Sphingomonas phage PAU	GCA_000902455.1
AFF28030.1	000000	-	98	PAU_32	Sphingomonas phage PAU	GCA_000902455.1
AFF28033.1	000000	-	266	PAU_35	Sphingomonas phage PAU	GCA_000902455.1
AFF28046.1	000000	-	81	PAU_48	Sphingomonas phage PAU	GCA_000902455.1
AFF28060.1	000000	-	75	PAU_62	Sphingomonas phage PAU	GCA_000902455.1
AFF28068.1	000000	-	178	PAU_70	Sphingomonas phage PAU	GCA_000902455.1
AFF28079.1	000000	-	250	PAU_81	Sphingomonas phage PAU	GCA_000902455.1
AFF28080.1	000000	-	98	PAU_82	Sphingomonas phage PAU	GCA_000902455.1
AFF28083.1	000000	-	134	PAU_85	Sphingomonas phage PAU	GCA_000902455.1
QJD53892.1	000000	-	105	SEA_KELA_332	Streptomyces phage Kela	GCA_012934305.1
QJD53605.1	000000	-	28	SEA_KELA_34	Streptomyces phage Kela	GCA_012934305.1
QBZ72014.1	000000	-	29	SEA_KRADAL_116	Streptomyces phage Kradal	GCA_004799925.1
QBZ72092.1	000000	-	38	SEA_KRADAL_206	Streptomyces phage Kradal	GCA_004799925.1
QBZ72159.1	000000	-	52	SEA_KRADAL_273	Streptomyces phage Kradal	GCA_004799925.1
AIX30632.1	000000	-	42	Syn7803US37_155	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30649.1	000000	-	71	Syn7803US37_172	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30659.1	000000	-	44	Syn7803US37_182	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30667.1	000000	-	892	Syn7803US37_190	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30674.1	000000	-	57	Syn7803US37_197	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30693.1	000000	-	53	Syn7803US37_216	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30695.1	000000	-	63	Syn7803US37_218	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30499.1	000000	-	702	Syn7803US37_22	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30500.1	000000	-	116	Syn7803US37_23	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30726.1	000000	-	40	Syn7803US37_249	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30730.1	000000	-	187	Syn7803US37_253	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30736.1	000000	-	68	Syn7803US37_259	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30740.1	000000	-	75	Syn7803US37_263	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30745.1	000000	-	3967	Syn7803US37_268	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30517.1	000000	-	72	Syn7803US37_40	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30520.1	000000	-	73	Syn7803US37_43	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30532.1	000000	-	58	Syn7803US37_55	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30536.1	000000	-	116	Syn7803US37_59	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30537.1	000000	-	88	Syn7803US37_60	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30538.1	000000	-	37	Syn7803US37_61	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30543.1	000000	-	83	Syn7803US37_66	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30545.1	000000	-	45	Syn7803US37_68	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30559.1	000000	-	69	Syn7803US37_82	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30560.1	000000	-	48	Syn7803US37_83	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30562.1	000000	-	93	Syn7803US37_85	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30567.1	000000	-	111	Syn7803US37_90	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30572.1	000000	-	105	Syn7803US37_95	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54470.1	000000	-	52	b3_0227	Synechococcus phage B3	GCA_009745215.1
QGT54494.1	000000	-	38	b3_0252	Synechococcus phage B3	GCA_009745215.1
ASR76179.1	000000	-	61	PBI_BELLAMY_134	Synechococcus phage Bellamy	GCA_002627525.1
ASR76102.1	000000	-	39	PBI_BELLAMY_57	Synechococcus phage Bellamy	GCA_002627525.1
ASR76104.1	000000	-	59	PBI_BELLAMY_59	Synechococcus phage Bellamy	GCA_002627525.1
ASR76143.1	000000	-	43	PBI_BELLAMY_98	Synechococcus phage Bellamy	GCA_002627525.1
QCW22859.1	000000	-	67	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22858.1	000000	-	196	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23042.1	000000	-	90	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23007.1	000000	-	63	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50599.1	000000	-	56	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50522.1	000000	-	38	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50507.1	000000	-	38	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50597.1	000000	-	405	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50706.1	000000	-	47	-	Synechococcus phage S-B43	GCA_006869725.1
AXQ70484.1	000000	-	58	HOU04_gp085	Synechococcus phage S-T4	GCA_003443335.1
AXQ70600.1	000000	-	63	HOU04_gp201	Synechococcus phage S-T4	GCA_003443335.1
AXQ70509.1	000000	-	302	HOU04_gp110	Synechococcus phage S-T4	GCA_003443335.1
QJT70077.1	000000	-	53	SynMITS9220M01_064	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70121.1	000000	-	71	SynMITS9220M01_108	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70178.1	000000	-	95	SynMITS9220M01_166	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70210.1	000000	-	315	SynMITS9220M01_204	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70226.1	000000	-	84	SynMITS9220M01_220	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70244.1	000000	-	65	SynMITS9220M01_238	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BAV39131.1	000000	-	74	BPT24_009	Tenacibaculum phage pT24	GCA_002611925.1
BAV39142.1	000000	-	51	BPT24_020	Tenacibaculum phage pT24	GCA_002611925.1
BAV39143.1	000000	-	54	BPT24_021	Tenacibaculum phage pT24	GCA_002611925.1
BAV39155.1	000000	-	296	BPT24_033	Tenacibaculum phage pT24	GCA_002611925.1
BAV39166.1	000000	-	190	BPT24_043	Tenacibaculum phage pT24	GCA_002611925.1
BAV39167.1	000000	-	297	BPT24_044	Tenacibaculum phage pT24	GCA_002611925.1
BAV39173.1	000000	-	36	BPT24_050	Tenacibaculum phage pT24	GCA_002611925.1
BAV39177.1	000000	-	132	BPT24_054	Tenacibaculum phage pT24	GCA_002611925.1
BAV39183.1	000000	-	41	BPT24_060	Tenacibaculum phage pT24	GCA_002611925.1
BAV39198.1	000000	-	189	BPT24_075	Tenacibaculum phage pT24	GCA_002611925.1
BAV39208.1	000000	-	488	BPT24_083	Tenacibaculum phage pT24	GCA_002611925.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAV39212.1	000000	-	216	BPT24_087	Tenacibaculum phage pT24	GCA_002611925.1
BAV39225.1	000000	-	655	BPT24_100	Tenacibaculum phage pT24	GCA_002611925.1
BAV39242.1	000000	-	127	BPT24_117	Tenacibaculum phage pT24	GCA_002611925.1
BAV39245.1	000000	-	127	BPT24_120	Tenacibaculum phage pT24	GCA_002611925.1
BAV39248.1	000000	-	348	BPT24_123	Tenacibaculum phage pT24	GCA_002611925.1
BAV39274.1	000000	-	88	BPT24_148	Tenacibaculum phage pT24	GCA_002611925.1
BAV39277.1	000000	-	90	BPT24_151	Tenacibaculum phage pT24	GCA_002611925.1
BAV39349.1	000000	-	150	BPT24_225	Tenacibaculum phage pT24	GCA_002611925.1
BAV39358.1	000000	-	76	BPT24_238	Tenacibaculum phage pT24	GCA_002611925.1
BAV39369.1	000000	-	111	BPT24_249	Tenacibaculum phage pT24	GCA_002611925.1
BAV39371.1	000000	-	61	BPT24_251	Tenacibaculum phage pT24	GCA_002611925.1
BAV39372.1	000000	-	263	BPT24_253	Tenacibaculum phage pT24	GCA_002611925.1
BAV39378.1	000000	-	116	BPT24_260	Tenacibaculum phage pT24	GCA_002611925.1
BAV39384.1	000000	-	97	BPT24_266	Tenacibaculum phage pT24	GCA_002611925.1
BAV39391.1	000000	-	129	BPT24_274	Tenacibaculum phage pT24	GCA_002611925.1
BAV39402.1	000000	-	70	BPT24_285	Tenacibaculum phage pT24	GCA_002611925.1
BAV39406.1	000000	-	199	BPT24_288	Tenacibaculum phage pT24	GCA_002611925.1
BAV39407.1	000000	-	102	BPT24_289	Tenacibaculum phage pT24	GCA_002611925.1
BAV39411.1	000000	-	194	BPT24_293	Tenacibaculum phage pT24	GCA_002611925.1
BAX25568.1	000000	-	128	BPT24_295	Tenacibaculum phage pT24	GCA_002611925.1
AXH70773.1	000000	-	101	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70981.1	000000	-	101	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70951.1	000000	-	93	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70965.1	000000	-	147	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70867.1	000000	-	147	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71032.1	000000	-	50	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70875.1	000000	-	134	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70793.1	000000	-	80	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70796.1	000000	-	58	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70749.1	000000	-	148	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70772.1	000000	-	111	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70873.1	000000	-	121	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70950.1	000000	-	104	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70760.1	000000	-	171	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70797.1	000000	-	112	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70897.1	000000	-	213	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71016.1	000000	-	137	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70898.1	000000	-	244	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70948.1	000000	-	382	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70768.1	000000	-	61	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70896.1	000000	-	361	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70798.1	000000	-	140	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70983.1	000000	-	154	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70801.1	000000	-	165	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71015.1	000000	-	98	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70932.1	000000	-	451	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70962.1	000000	-	125	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70929.1	000000	-	254	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70990.1	000000	-	744	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70980.1	000000	-	117	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70963.1	000000	-	132	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70750.1	000000	-	132	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70961.1	000000	-	142	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70795.1	000000	-	163	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70938.1	000000	-	228	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71012.1	000000	-	228	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70874.1	000000	-	346	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64271.1	000000	-	36	KVP40.0202	Vibrio phage KVP40	GCA_000843785.1
AAQ64378.1	000000	-	89	KVP40.0309	Vibrio phage KVP40	GCA_000843785.1
AAQ64389.1	000000	-	73	KVP40.0319	Vibrio phage KVP40	GCA_000843785.1
AAQ64438.1	000000	-	39	KVP40.0370	Vibrio phage KVP40	GCA_000843785.1
QIW90717.1	000000	-	89	GCAPEGMB_00398	Vibrio phage V07	GCA_012361095.1
QIW90718.1	000000	-	152	GCAPEGMB_00399	Vibrio phage V07	GCA_012361095.1
QIW90723.1	000000	-	86	GCAPEGMB_00404	Vibrio phage V07	GCA_012361095.1
QIW90741.1	000000	-	136	GCAPEGMB_00422	Vibrio phage V07	GCA_012361095.1
QIW90773.1	000000	-	41	GCAPEGMB_00454	Vibrio phage V07	GCA_012361095.1
QIW90780.1	000000	-	192	GCAPEGMB_00462	Vibrio phage V07	GCA_012361095.1
QIW90787.1	000000	-	144	GCAPEGMB_00469	Vibrio phage V07	GCA_012361095.1
QIW90795.1	000000	-	62	GCAPEGMB_00477	Vibrio phage V07	GCA_012361095.1
QIW90800.1	000000	-	71	GCAPEGMB_00482	Vibrio phage V07	GCA_012361095.1
QIW90841.1	000000	-	41	GCAPEGMB_00526	Vibrio phage V07	GCA_012361095.1
QIW90856.1	000000	-	59	GCAPEGMB_00541	Vibrio phage V07	GCA_012361095.1
QHJ74496.1	000000	-	42	VH12019_00176	Vibrio phage VH1_2019	GCA_009931825.1
QAU04466.1	000000	-	128	ValB1MD_063	Vibrio phage ValB1MD	GCA_004138815.1
QAU04469.1	000000	-	183	ValB1MD_068	Vibrio phage ValB1MD	GCA_004138815.1
AGN30064.1	000000	-	82	VPFG_00061	Vibrio phage nt-1	GCA_000910195.2
AGN30143.1	000000	-	50	VPFG_00141	Vibrio phage nt-1	GCA_000910195.2
AGN30222.1	000000	-	64	VPFG_00222	Vibrio phage nt-1	GCA_000910195.2
AIE13770.1	000000	-	29	-	Vibrio phage nt-1	GCA_000910195.2
AGN30223.1	000000	-	53	VPFG_00223	Vibrio phage nt-1	GCA_000910195.2
AGN30224.1	000000	-	59	VPFG_00224	Vibrio phage nt-1	GCA_000910195.2
AGN30228.1	000000	-	138	VPFG_00229	Vibrio phage nt-1	GCA_000910195.2
AGN30241.1	000000	-	63	VPFG_00242	Vibrio phage nt-1	GCA_000910195.2
AGN30283.1	000000	-	58	VPFG_00284	Vibrio phage nt-1	GCA_000910195.2
AIE13775.1	000000	-	57	-	Vibrio phage nt-1	GCA_000910195.2
AIE13777.1	000000	-	48	-	Vibrio phage nt-1	GCA_000910195.2
AGN30310.2	000000	-	173	VPFG_00311	Vibrio phage nt-1	GCA_000910195.2
AGN30315.1	000000	-	144	VPFG_00317	Vibrio phage nt-1	GCA_000910195.2
AIE13780.1	000000	-	37	-	Vibrio phage nt-1	GCA_000910195.2
BAW98393.1	000000	-	172	FDH33_gp184	Vibrio phage pTD1	GCA_002618825.1
BAW98353.1	000000	-	244	FDH33_gp144	Vibrio phage pTD1	GCA_002618825.1
AQT27947.1	000000	-	276	pVa21_005	Vibrio phage pVa-21	GCA_002619305.1
AQT27952.1	000000	-	187	pVa21_010	Vibrio phage pVa-21	GCA_002619305.1
AQT27957.1	000000	-	261	pVa21_015	Vibrio phage pVa-21	GCA_002619305.1
AQT27975.1	000000	-	78	pVa21_033	Vibrio phage pVa-21	GCA_002619305.1
AQT27981.1	000000	-	92	pVa21_039	Vibrio phage pVa-21	GCA_002619305.1
AQT27994.1	000000	-	153	pVa21_052	Vibrio phage pVa-21	GCA_002619305.1
AQT27995.1	000000	-	203	pVa21_053	Vibrio phage pVa-21	GCA_002619305.1
AQT27996.1	000000	-	201	pVa21_054	Vibrio phage pVa-21	GCA_002619305.1
AQT28012.1	000000	-	180	pVa21_071	Vibrio phage pVa-21	GCA_002619305.1
AQT28023.1	000000	-	67	pVa21_082	Vibrio phage pVa-21	GCA_002619305.1
AQT28035.1	000000	-	271	pVa21_094	Vibrio phage pVa-21	GCA_002619305.1
AQT28056.1	000000	-	509	pVa21_115	Vibrio phage pVa-21	GCA_002619305.1
AQT28057.1	000000	-	268	pVa21_116	Vibrio phage pVa-21	GCA_002619305.1
AQT28070.1	000000	-	271	pVa21_129	Vibrio phage pVa-21	GCA_002619305.1
AQT28078.1	000000	-	99	pVa21_137	Vibrio phage pVa-21	GCA_002619305.1
AQT28084.1	000000	-	95	pVa21_143	Vibrio phage pVa-21	GCA_002619305.1
AQT28093.1	000000	-	171	pVa21_152	Vibrio phage pVa-21	GCA_002619305.1
AQT28109.1	000000	-	64	pVa21_168	Vibrio phage pVa-21	GCA_002619305.1
AQT28116.1	000000	-	92	pVa21_175	Vibrio phage pVa-21	GCA_002619305.1
AQT28142.1	000000	-	123	pVa21_201	Vibrio phage pVa-21	GCA_002619305.1
AQT28167.1	000000	-	154	pVa21_226	Vibrio phage pVa-21	GCA_002619305.1
ALP47716.1	000000	-	42	phiST2_0355	Vibrio phage phi-ST2	GCA_002757135.1
ALY07009.1	000000	-	137	VmeM32_00015	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07027.1	000000	-	114	VmeM32_00033	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07032.1	000000	-	522	VmeM32_00041	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07035.1	000000	-	59	VmeM32_00044	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07037.1	000000	-	68	VmeM32_00046	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07038.1	000000	-	82	VmeM32_00047	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07039.1	000000	-	77	VmeM32_00048	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07044.1	000000	-	66	VmeM32_00053	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07052.1	000000	-	69	VmeM32_00061	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07065.1	000000	-	113	VmeM32_00074	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07066.1	000000	-	113	VmeM32_00075	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07076.1	000000	-	37	VmeM32_00085	Vibrio phage vB_VmeM-32	GCA_002608825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALY07078.1	000000	-	378	VmeM32_00088	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07128.1	000000	-	65	VmeM32_00141	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07144.1	000000	-	76	VmeM32_00158	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07155.1	000000	-	57	VmeM32_00169	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07157.1	000000	-	138	VmeM32_00171	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07173.1	000000	-	84	VmeM32_00187	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07194.1	000000	-	92	VmeM32_00208	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07207.1	000000	-	80	VmeM32_00221	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21235.1	000000	-	32	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21104.1	000000	-	33	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20998.1	000000	-	33	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20993.1	000000	-	35	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20990.1	000000	-	106	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21274.1	000000	-	198	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21203.1	000000	-	231	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21058.1	000000	-	168	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21221.1	000000	-	213	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21247.1	000000	-	118	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21251.1	000000	-	118	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20960.1	000000	-	118	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21239.1	000000	-	484	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21082.1	000000	-	131	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21185.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21028.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21025.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21024.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21010.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21117.1	000000	-	44	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21259.1	000000	-	45	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21078.1	000000	-	45	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21184.1	000000	-	177	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21160.1	000000	-	139	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21249.1	000000	-	80	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21217.1	000000	-	171	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21267.1	000000	-	161	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21166.1	000000	-	299	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21212.1	000000	-	353	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21127.1	000000	-	710	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21102.1	000000	-	145	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20971.1	000000	-	364	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21204.1	000000	-	307	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21015.1	000000	-	101	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20988.1	000000	-	88	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21245.1	000000	-	337	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21244.1	000000	-	107	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21218.1	000000	-	267	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21165.1	000000	-	90	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21260.1	000000	-	99	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21175.1	000000	-	99	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21250.1	000000	-	114	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21016.1	000000	-	120	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21034.1	000000	-	127	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21119.1	000000	-	166	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21252.1	000000	-	219	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21214.1	000000	-	242	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21237.1	000000	-	244	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21248.1	000000	-	340	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21033.1	000000	-	93	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21213.1	000000	-	49	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21032.1	000000	-	49	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21017.1	000000	-	116	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21009.1	000000	-	516	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21198.1	000000	-	422	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21257.1	000000	-	216	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21128.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21049.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21012.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21101.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21004.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20994.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21023.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21169.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
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QNI21152.1	000000	-	169	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21131.1	000000	-	169	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21164.1	000000	-	223	-	Vibrio phage vB_pir03	GCA_014319855.1
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AFN37492.1	000000	-	380	pp2_259	Vibriophage phi-pp2	GCA_002630725.1
BBA65581.1	000000	-	150	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65556.1	000000	-	88	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65311.1	000000	-	88	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65457.1	000000	-	39	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65461.1	000000	-	53	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65431.1	000000	-	68	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65596.1	000000	-	178	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65509.1	000000	-	115	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65306.1	000000	-	106	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65410.1	000000	-	130	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65340.1	000000	-	144	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65308.1	000000	-	57	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65452.1	000000	-	71	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65503.1	000000	-	72	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65548.1	000000	-	86	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96297.1	000000	-	123	Xoosp13_110	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96199.1	000000	-	148	Xoosp13_12	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96325.1	000000	-	47	Xoosp13_138	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96334.1	000000	-	37	Xoosp13_147	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96342.1	000000	-	66	Xoosp13_155	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96344.1	000000	-	246	Xoosp13_157	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96346.1	000000	-	80	Xoosp13_159	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96377.1	000000	-	50	Xoosp13_191	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96379.1	000000	-	171	Xoosp13_193	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96189.1	000000	-	73	Xoosp13_2	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96433.1	000000	-	223	Xoosp13_247	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96449.1	000000	-	63	Xoosp13_263	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96469.1	000000	-	103	Xoosp13_283	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96219.1	000000	-	48	Xoosp13_32	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96506.1	000000	-	191	Xoosp13_320	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96538.1	000000	-	83	Xoosp13_352	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96571.1	000000	-	75	Xoosp13_385	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96226.1	000000	-	62	Xoosp13_39	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96231.1	000000	-	38	Xoosp13_44	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96234.1	000000	-	65	Xoosp13_47	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96192.1	000000	-	37	Xoosp13_5	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96261.1	000000	-	134	Xoosp13_74	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96282.1	000000	-	49	Xoosp13_95	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK59076.1	000000	-	75	g268	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58302.1	000000	-	111	g025	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58624.1	000000	-	23	g347	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26026.1	000000	-	83	g002	Yersinia phage phiR1-37	GCA_000895615.1
CCE26027.1	000000	-	82	g003	Yersinia phage phiR1-37	GCA_000895615.1
CCE26028.1	000000	-	72	g004	Yersinia phage phiR1-37	GCA_000895615.1
CCE26030.1	000000	-	117	g006	Yersinia phage phiR1-37	GCA_000895615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
CCE26032.1	000000	-	62	g008	Yersinia phage phiR1-37	GCA_000895615.1
CCE26034.1	000000	-	68	g010	Yersinia phage phiR1-37	GCA_000895615.1
CCE26035.1	000000	-	69	g011	Yersinia phage phiR1-37	GCA_000895615.1
CCE26037.1	000000	-	81	g013	Yersinia phage phiR1-37	GCA_000895615.1
CCE26040.1	000000	-	85	g016	Yersinia phage phiR1-37	GCA_000895615.1
CCE26044.1	000000	-	78	g020	Yersinia phage phiR1-37	GCA_000895615.1
CCE26046.1	000000	-	85	g022	Yersinia phage phiR1-37	GCA_000895615.1
CCE26050.1	000000	-	101	g026	Yersinia phage phiR1-37	GCA_000895615.1
CCE26054.1	000000	-	119	g030	Yersinia phage phiR1-37	GCA_000895615.1
CCE26064.1	000000	-	88	g040	Yersinia phage phiR1-37	GCA_000895615.1
CCE26067.1	000000	-	83	g043	Yersinia phage phiR1-37	GCA_000895615.1
CCE26086.1	000000	-	52	g062	Yersinia phage phiR1-37	GCA_000895615.1
CCE26090.1	000000	-	118	g066	Yersinia phage phiR1-37	GCA_000895615.1
CCE26091.1	000000	-	30	g067	Yersinia phage phiR1-37	GCA_000895615.1
CCE26095.1	000000	-	58	g071	Yersinia phage phiR1-37	GCA_000895615.1
CCE26099.1	000000	-	102	g075	Yersinia phage phiR1-37	GCA_000895615.1
CCE26100.1	000000	-	121	g076	Yersinia phage phiR1-37	GCA_000895615.1
CCE26132.1	000000	-	95	g108	Yersinia phage phiR1-37	GCA_000895615.1
CCE26133.1	000000	-	69	g109	Yersinia phage phiR1-37	GCA_000895615.1
CCE26140.1	000000	-	52	g116	Yersinia phage phiR1-37	GCA_000895615.1
CCE26144.1	000000	-	124	g120	Yersinia phage phiR1-37	GCA_000895615.1
CCE26148.1	000000	-	261	g124	Yersinia phage phiR1-37	GCA_000895615.1
CCE26156.1	000000	-	94	g132	Yersinia phage phiR1-37	GCA_000895615.1
CCE26162.1	000000	-	137	g138	Yersinia phage phiR1-37	GCA_000895615.1
CCE26180.1	000000	-	148	g156	Yersinia phage phiR1-37	GCA_000895615.1
CCE26189.1	000000	-	32	g165	Yersinia phage phiR1-37	GCA_000895615.1
CCE26208.1	000000	-	106	g184	Yersinia phage phiR1-37	GCA_000895615.1
CCE26212.1	000000	-	28	g188	Yersinia phage phiR1-37	GCA_000895615.1
CCE26229.1	000000	-	324	g206	Yersinia phage phiR1-37	GCA_000895615.1
CCE26239.1	000000	-	126	g216	Yersinia phage phiR1-37	GCA_000895615.1
CCE26240.1	000000	-	30	g217	Yersinia phage phiR1-37	GCA_000895615.1
CCE26258.1	000000	-	120	g235	Yersinia phage phiR1-37	GCA_000895615.1
CCE26259.1	000000	-	140	g236	Yersinia phage phiR1-37	GCA_000895615.1
CCE26281.1	000000	-	124	g258	Yersinia phage phiR1-37	GCA_000895615.1
CCE26300.1	000000	-	121	g277	Yersinia phage phiR1-37	GCA_000895615.1
CCE26311.1	000000	-	37	g288	Yersinia phage phiR1-37	GCA_000895615.1
CCE26312.1	000000	-	251	g289	Yersinia phage phiR1-37	GCA_000895615.1
CCE26323.1	000000	-	731	g300	Yersinia phage phiR1-37	GCA_000895615.1
CCE26338.1	000000	-	37	g315	Yersinia phage phiR1-37	GCA_000895615.1
CCE26342.1	000000	-	115	g319	Yersinia phage phiR1-37	GCA_000895615.1
CCE26351.1	000000	-	311	g328	Yersinia phage phiR1-37	GCA_000895615.1
CCE26355.1	000000	-	308	g332	Yersinia phage phiR1-37	GCA_000895615.1
CCE26378.1	000000	-	82	g355	Yersinia phage phiR1-37	GCA_000895615.1
CCE26381.1	000000	-	78	g358	Yersinia phage phiR1-37	GCA_000895615.1
CCE26385.1	000000	-	85	g362	Yersinia phage phiR1-37	GCA_000895615.1
CCE26386.1	000000	-	84	g363	Yersinia phage phiR1-37	GCA_000895615.1
CCE26024.1	000000	-	61	g367	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000024	000000	-	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000030	000000	-	44	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000079	000000	-	217	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000089	000000	-	114	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000125	000000	-	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000193	000000	-	84	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000222	000000	-	57	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000263	000000	-	58	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000316	000000	-	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000389	000000	-	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000397	000000	-	74	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000400	000000	-	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000404	000000	-	30	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000406	000000	-	41	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000413	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000465	000000	-	44	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000468	000000	-	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000509	000000	-	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000531	000000	-	73	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000560	000000	-	145	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000563	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000581	000000	-	291	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000582	000000	-	175	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000584	000000	-	54	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000593	000000	-	106	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000604	000000	-	62	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000648	000000	-	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000649	000000	-	42	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000675	000000	-	382	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000724	000000	-	146	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000736	000000	-	64	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000737	000000	-	38	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000799	000000	-	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000836	000000	-	75	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000022	000000	-	357	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000084	000000	-	66	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000137	000000	-	129	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000156	000000	-	318	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000319	000000	-	254	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000326	000000	-	505	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000356	000000	-	1351	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000380	000000	-	395	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000401	000000	-	237	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000415	000000	-	2444	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
QHJ86077.1	000000	-	376	KKIINIFJ_00165	Pseudomonas phage PN05	GCA_009931935.1
QHJ86141.1	000000	-	145	KKIINIFJ_00230	Pseudomonas phage PN05	GCA_009931935.1
AUZ94838.1	000000	-	101	FDI40_gp026	Agrobacterium phage Atu_ph07	GCA_002628245.1
ARV77252.1	000000	-	149	NOXIFER_81	Pseudomonas phage Noxifer	GCA_002625005.1
QDH83524.1	000000	-	56	H1O15_gp282	Achromobacter phage Motura	GCA_006964305.1
QDH83516.1	000000	-	52	H1O15_gp290	Achromobacter phage Motura	GCA_006964305.1
QDH83463.1	000000	-	72	H1O15_gp343	Achromobacter phage Motura	GCA_006964305.1
QDH83506.1	000000	-	73	H1O15_gp300	Achromobacter phage Motura	GCA_006964305.1
QDH83568.1	000000	-	150	H1O15_gp220	Achromobacter phage Motura	GCA_006964305.1
QDH83562.1	000000	-	83	H1O15_gp226	Achromobacter phage Motura	GCA_006964305.1
QDH83616.1	000000	-	375	H1O15_gp172	Achromobacter phage Motura	GCA_006964305.1
QDH83389.1	000000	-	76	H1O15_gp074	Achromobacter phage Motura	GCA_006964305.1
QDH83485.1	000000	-	76	H1O15_gp321	Achromobacter phage Motura	GCA_006964305.1
QDH83402.1	000000	-	64	H1O15_gp060	Achromobacter phage Motura	GCA_006964305.1
QDH83646.1	000000	-	64	H1O15_gp142	Achromobacter phage Motura	GCA_006964305.1
QDH83693.1	000000	-	64	H1O15_gp268	Achromobacter phage Motura	GCA_006964305.1
QDH83415.1	000000	-	121	H1O15_gp006	Achromobacter phage Motura	GCA_006964305.1
QDH83723.1	000000	-	121	H1O15_gp103	Achromobacter phage Motura	GCA_006964305.1
QDH83670.1	000000	-	121	H1O15_gp080	Achromobacter phage Motura	GCA_006964305.1
QDH83572.1	000000	-	121	H1O15_gp216	Achromobacter phage Motura	GCA_006964305.1
QDH83549.1	000000	-	121	H1O15_gp239	Achromobacter phage Motura	GCA_006964305.1
QDH83387.1	000000	-	89	H1O15_gp076	Achromobacter phage Motura	GCA_006964305.1
QDH83691.1	000000	-	86	H1O15_gp270	Achromobacter phage Motura	GCA_006964305.1
QDH83425.1	000000	-	113	H1O15_gp017	Achromobacter phage Motura	GCA_006964305.1
QDH83585.1	000000	-	113	H1O15_gp203	Achromobacter phage Motura	GCA_006964305.1
QDH83624.1	000000	-	113	H1O15_gp164	Achromobacter phage Motura	GCA_006964305.1
QDH83563.1	000000	-	136	H1O15_gp225	Achromobacter phage Motura	GCA_006964305.1
QDH83655.1	000000	-	177	H1O15_gp095	Achromobacter phage Motura	GCA_006964305.1
QDH83413.1	000000	-	80	H1O15_gp004	Achromobacter phage Motura	GCA_006964305.1
QDH83567.1	000000	-	137	H1O15_gp221	Achromobacter phage Motura	GCA_006964305.1
QDH83555.1	000000	-	137	H1O15_gp233	Achromobacter phage Motura	GCA_006964305.1
QDH83711.1	000000	-	146	H1O15_gp117	Achromobacter phage Motura	GCA_006964305.1
QDH83718.1	000000	-	103	H1O15_gp109	Achromobacter phage Motura	GCA_006964305.1
QDH83515.1	000000	-	103	H1O15_gp291	Achromobacter phage Motura	GCA_006964305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDH83671.1	000000	-	123	H1O15_gp079	Achromobacter phage Motura	GCA_006964305.1
QDH83560.1	000000	-	148	H1O15_gp228	Achromobacter phage Motura	GCA_006964305.1
QDH83660.1	000000	-	170	H1O15_gp090	Achromobacter phage Motura	GCA_006964305.1
QDH83388.1	000000	-	143	H1O15_gp075	Achromobacter phage Motura	GCA_006964305.1
QDH83423.1	000000	-	309	H1O15_gp015	Achromobacter phage Motura	GCA_006964305.1
QDH83633.1	000000	-	379	H1O15_gp155	Achromobacter phage Motura	GCA_006964305.1
QDH83587.1	000000	-	106	H1O15_gp201	Achromobacter phage Motura	GCA_006964305.1
QDH83728.1	000000	-	106	H1O15_gp104	Achromobacter phage Motura	GCA_006964305.1
QDH83444.1	000000	-	106	H1O15_gp036	Achromobacter phage Motura	GCA_006964305.1
QDH83556.1	000000	-	160	H1O15_gp232	Achromobacter phage Motura	GCA_006964305.1
QDH83583.1	000000	-	160	H1O15_gp205	Achromobacter phage Motura	GCA_006964305.1
QDH83550.1	000000	-	305	H1O15_gp238	Achromobacter phage Motura	GCA_006964305.1
QDH83651.1	000000	-	111	H1O15_gp099	Achromobacter phage Motura	GCA_006964305.1
QDH83721.1	000000	-	145	H1O15_gp106	Achromobacter phage Motura	GCA_006964305.1
QDH83427.1	000000	-	189	H1O15_gp019	Achromobacter phage Motura	GCA_006964305.1
QDH83724.1	000000	-	104	H1O15_gp102	Achromobacter phage Motura	GCA_006964305.1
QDH83571.1	000000	-	67	H1O15_gp217	Achromobacter phage Motura	GCA_006964305.1
QDH83404.1	000000	-	67	H1O15_gp058	Achromobacter phage Motura	GCA_006964305.1
QDH83704.1	000000	-	196	H1O15_gp124	Achromobacter phage Motura	GCA_006964305.1
QDH83546.1	000000	-	101	H1O15_gp242	Achromobacter phage Motura	GCA_006964305.1
QDH83577.1	000000	-	101	H1O15_gp211	Achromobacter phage Motura	GCA_006964305.1
QDH83504.1	000000	-	82	H1O15_gp302	Achromobacter phage Motura	GCA_006964305.1
QDH83565.1	000000	-	82	H1O15_gp223	Achromobacter phage Motura	GCA_006964305.1
QDH83663.1	000000	-	82	H1O15_gp087	Achromobacter phage Motura	GCA_006964305.1
QDH83453.1	000000	-	153	H1O15_gp045	Achromobacter phage Motura	GCA_006964305.1
QDH83707.1	000000	-	683	H1O15_gp121	Achromobacter phage Motura	GCA_006964305.1
QDH83547.1	000000	-	402	H1O15_gp241	Achromobacter phage Motura	GCA_006964305.1
QDH83662.1	000000	-	68	H1O15_gp088	Achromobacter phage Motura	GCA_006964305.1
QDH83576.1	000000	-	68	H1O15_gp212	Achromobacter phage Motura	GCA_006964305.1
QDH83493.1	000000	-	68	H1O15_gp313	Achromobacter phage Motura	GCA_006964305.1
QDH83494.1	000000	-	90	H1O15_gp312	Achromobacter phage Motura	GCA_006964305.1
QDH83720.1	000000	-	90	H1O15_gp107	Achromobacter phage Motura	GCA_006964305.1
QDH83491.1	000000	-	90	H1O15_gp315	Achromobacter phage Motura	GCA_006964305.1
QDH83441.1	000000	-	96	H1O15_gp033	Achromobacter phage Motura	GCA_006964305.1
QDH83468.1	000000	-	100	H1O15_gp338	Achromobacter phage Motura	GCA_006964305.1
QDH83517.1	000000	-	110	H1O15_gp289	Achromobacter phage Motura	GCA_006964305.1
QDH83437.1	000000	-	119	H1O15_gp029	Achromobacter phage Motura	GCA_006964305.1
QDH83701.1	000000	-	119	H1O15_gp260	Achromobacter phage Motura	GCA_006964305.1
QDH83503.1	000000	-	119	H1O15_gp303	Achromobacter phage Motura	GCA_006964305.1
QDH83462.1	000000	-	125	H1O15_gp344	Achromobacter phage Motura	GCA_006964305.1
QDH83661.1	000000	-	125	H1O15_gp089	Achromobacter phage Motura	GCA_006964305.1
QDH83399.1	000000	-	127	H1O15_gp063	Achromobacter phage Motura	GCA_006964305.1
QDH83604.1	000000	-	129	H1O15_gp184	Achromobacter phage Motura	GCA_006964305.1
QDH83628.1	000000	-	134	H1O15_gp160	Achromobacter phage Motura	GCA_006964305.1
QDH83551.1	000000	-	138	H1O15_gp237	Achromobacter phage Motura	GCA_006964305.1
QDH83634.1	000000	-	138	H1O15_gp154	Achromobacter phage Motura	GCA_006964305.1
QDH83543.1	000000	-	157	H1O15_gp245	Achromobacter phage Motura	GCA_006964305.1
QDH83505.1	000000	-	166	H1O15_gp301	Achromobacter phage Motura	GCA_006964305.1
QDH83586.1	000000	-	166	H1O15_gp202	Achromobacter phage Motura	GCA_006964305.1
QDH83626.1	000000	-	174	H1O15_gp162	Achromobacter phage Motura	GCA_006964305.1
QDH83507.1	000000	-	176	H1O15_gp299	Achromobacter phage Motura	GCA_006964305.1
QDH83682.1	000000	-	176	H1O15_gp129	Achromobacter phage Motura	GCA_006964305.1
QDH83564.1	000000	-	176	H1O15_gp224	Achromobacter phage Motura	GCA_006964305.1
QDH83650.1	000000	-	182	H1O15_gp100	Achromobacter phage Motura	GCA_006964305.1
QDH83615.1	000000	-	182	H1O15_gp173	Achromobacter phage Motura	GCA_006964305.1
QDH83623.1	000000	-	241	H1O15_gp165	Achromobacter phage Motura	GCA_006964305.1
QDH83712.1	000000	-	312	H1O15_gp115	Achromobacter phage Motura	GCA_006964305.1
QDH83501.1	000000	-	70	H1O15_gp305	Achromobacter phage Motura	GCA_006964305.1
QDH83536.1	000000	-	70	H1O15_gp252	Achromobacter phage Motura	GCA_006964305.1
QDH83466.1	000000	-	71	H1O15_gp340	Achromobacter phage Motura	GCA_006964305.1
QDH83580.1	000000	-	71	H1O15_gp208	Achromobacter phage Motura	GCA_006964305.1
QDH83548.1	000000	-	74	H1O15_gp240	Achromobacter phage Motura	GCA_006964305.1
QDH83659.1	000000	-	75	H1O15_gp091	Achromobacter phage Motura	GCA_006964305.1
QDH83521.1	000000	-	75	H1O15_gp285	Achromobacter phage Motura	GCA_006964305.1
QDH83465.1	000000	-	75	H1O15_gp341	Achromobacter phage Motura	GCA_006964305.1
QDH83625.1	000000	-	78	H1O15_gp163	Achromobacter phage Motura	GCA_006964305.1
QDH83558.1	000000	-	78	H1O15_gp230	Achromobacter phage Motura	GCA_006964305.1
QDH83581.1	000000	-	79	H1O15_gp207	Achromobacter phage Motura	GCA_006964305.1
QDH83386.1	000000	-	84	H1O15_gp077	Achromobacter phage Motura	GCA_006964305.1
QDH83703.1	000000	-	84	H1O15_gp125	Achromobacter phage Motura	GCA_006964305.1
QDH83627.1	000000	-	84	H1O15_gp161	Achromobacter phage Motura	GCA_006964305.1
QDH83458.1	000000	-	85	H1O15_gp050	Achromobacter phage Motura	GCA_006964305.1
QDH83539.1	000000	-	85	H1O15_gp249	Achromobacter phage Motura	GCA_006964305.1
QDH83553.1	000000	-	91	H1O15_gp235	Achromobacter phage Motura	GCA_006964305.1
QDH83689.1	000000	-	91	H1O15_gp272	Achromobacter phage Motura	GCA_006964305.1
QDH83532.1	000000	-	91	H1O15_gp256	Achromobacter phage Motura	GCA_006964305.1
QDH83639.1	000000	-	97	H1O15_gp149	Achromobacter phage Motura	GCA_006964305.1
QDH83401.1	000000	-	98	H1O15_gp061	Achromobacter phage Motura	GCA_006964305.1
QDH83518.1	000000	-	98	H1O15_gp288	Achromobacter phage Motura	GCA_006964305.1
QDH83520.1	000000	-	98	H1O15_gp286	Achromobacter phage Motura	GCA_006964305.1
QDH83412.1	000000	-	108	H1O15_gp003	Achromobacter phage Motura	GCA_006964305.1
QDH83667.1	000000	-	126	H1O15_gp083	Achromobacter phage Motura	GCA_006964305.1
QDH83695.1	000000	-	141	H1O15_gp266	Achromobacter phage Motura	GCA_006964305.1
QDH83474.1	000000	-	69	H1O15_gp332	Achromobacter phage Motura	GCA_006964305.1
QDH83403.1	000000	-	69	H1O15_gp059	Achromobacter phage Motura	GCA_006964305.1
QDH83657.1	000000	-	87	H1O15_gp093	Achromobacter phage Motura	GCA_006964305.1
QDH83482.1	000000	-	94	H1O15_gp324	Achromobacter phage Motura	GCA_006964305.1
QDH83594.1	000000	-	213	H1O15_gp194	Achromobacter phage Motura	GCA_006964305.1
QDH83620.1	000000	-	81	H1O15_gp168	Achromobacter phage Motura	GCA_006964305.1
QDH83439.1	000000	-	81	H1O15_gp031	Achromobacter phage Motura	GCA_006964305.1
QDH83579.1	000000	-	81	H1O15_gp209	Achromobacter phage Motura	GCA_006964305.1
QDH83716.1	000000	-	63	H1O15_gp111	Achromobacter phage Motura	GCA_006964305.1
QDH83654.1	000000	-	124	H1O15_gp096	Achromobacter phage Motura	GCA_006964305.1
QDH83719.1	000000	-	116	H1O15_gp108	Achromobacter phage Motura	GCA_006964305.1
QDH83390.1	000000	-	116	H1O15_gp073	Achromobacter phage Motura	GCA_006964305.1
QDH83692.1	000000	-	593	H1O15_gp269	Achromobacter phage Motura	GCA_006964305.1
QDH83635.1	000000	-	508	H1O15_gp153	Achromobacter phage Motura	GCA_006964305.1
QDH83697.1	000000	-	185	H1O15_gp264	Achromobacter phage Motura	GCA_006964305.1
QDH83717.1	000000	-	199	H1O15_gp110	Achromobacter phage Motura	GCA_006964305.1
QDH83588.1	000000	-	201	H1O15_gp200	Achromobacter phage Motura	GCA_006964305.1
QDH83435.1	000000	-	201	H1O15_gp027	Achromobacter phage Motura	GCA_006964305.1
QDH83698.1	000000	-	202	H1O15_gp263	Achromobacter phage Motura	GCA_006964305.1
QDH83533.1	000000	-	206	H1O15_gp255	Achromobacter phage Motura	GCA_006964305.1
QDH83595.1	000000	-	300	H1O15_gp193	Achromobacter phage Motura	GCA_006964305.1
QDH83705.1	000000	-	718	H1O15_gp123	Achromobacter phage Motura	GCA_006964305.1
AND75162.1	000000	-	58	ME3_1	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75270.1	000000	-	65	ME3_109	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75172.1	000000	-	529	ME3_11	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75271.1	000000	-	198	ME3_110	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75273.1	000000	-	258	ME3_112	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75275.1	000000	-	133	ME3_114	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75281.1	000000	-	83	ME3_120	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75282.1	000000	-	111	ME3_121	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75283.1	000000	-	94	ME3_122	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75285.1	000000	-	210	ME3_124	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75290.1	000000	-	72	ME3_129	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75292.1	000000	-	216	ME3_131	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75293.1	000000	-	47	ME3_132	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75294.1	000000	-	147	ME3_133	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75295.1	000000	-	136	ME3_134	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75296.1	000000	-	144	ME3_135	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75297.1	000000	-	294	ME3_136	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75298.1	000000	-	101	ME3_137	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75299.1	000000	-	146	ME3_138	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75300.1	000000	-	63	ME3_139	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AND75175.1	000000	-	136	ME3_14	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75301.1	000000	-	334	ME3_140	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75303.1	000000	-	80	ME3_142	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75304.1	000000	-	132	ME3_143	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75306.1	000000	-	168	ME3_145	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75307.1	000000	-	66	ME3_146	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75309.1	000000	-	143	ME3_148	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75310.1	000000	-	68	ME3_149	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75176.1	000000	-	226	ME3_15	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75311.1	000000	-	32	ME3_150	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75312.1	000000	-	123	ME3_151	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75315.1	000000	-	72	ME3_154	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75316.1	000000	-	99	ME3_155	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75317.1	000000	-	66	ME3_156	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75318.1	000000	-	48	ME3_157	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75319.1	000000	-	85	ME3_158	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75177.1	000000	-	84	ME3_16	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75321.1	000000	-	141	ME3_160	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75326.1	000000	-	102	ME3_165	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75329.1	000000	-	122	ME3_168	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75330.1	000000	-	79	ME3_169	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75178.1	000000	-	168	ME3_17	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75331.1	000000	-	96	ME3_170	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75334.1	000000	-	150	ME3_173	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75336.1	000000	-	88	ME3_175	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75337.1	000000	-	317	ME3_176	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75339.1	000000	-	102	ME3_178	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75179.1	000000	-	554	ME3_18	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75343.1	000000	-	59	ME3_182	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75346.1	000000	-	88	ME3_185	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75348.1	000000	-	63	ME3_187	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75350.1	000000	-	111	ME3_189	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75351.1	000000	-	80	ME3_190	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75359.1	000000	-	59	ME3_198	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75360.1	000000	-	76	ME3_199	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75181.1	000000	-	593	ME3_20	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75363.1	000000	-	88	ME3_202	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75367.1	000000	-	131	ME3_206	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75368.1	000000	-	64	ME3_207	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75370.1	000000	-	115	ME3_209	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75182.1	000000	-	300	ME3_21	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75372.1	000000	-	31	ME3_211	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75373.1	000000	-	133	ME3_212	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75378.1	000000	-	124	ME3_217	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75379.1	000000	-	87	ME3_218	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75380.1	000000	-	108	ME3_219	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75386.1	000000	-	119	ME3_225	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75184.1	000000	-	76	ME3_23	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75392.1	000000	-	104	ME3_231	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75395.1	000000	-	202	ME3_234	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75396.1	000000	-	32	ME3_235	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75185.1	000000	-	350	ME3_24	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75402.1	000000	-	112	ME3_241	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75408.1	000000	-	103	ME3_247	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75410.1	000000	-	70	ME3_249	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75411.1	000000	-	133	ME3_250	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75412.1	000000	-	85	ME3_251	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75413.1	000000	-	129	ME3_252	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75417.1	000000	-	124	ME3_256	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75419.1	000000	-	130	ME3_258	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75187.1	000000	-	235	ME3_26	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75423.1	000000	-	128	ME3_262	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75424.1	000000	-	72	ME3_263	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75425.1	000000	-	136	ME3_264	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75429.1	000000	-	134	ME3_268	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75188.1	000000	-	168	ME3_27	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75432.1	000000	-	256	ME3_271	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75436.1	000000	-	46	ME3_275	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75437.1	000000	-	78	ME3_276	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75438.1	000000	-	27	ME3_277	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75440.1	000000	-	92	ME3_279	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75189.1	000000	-	227	ME3_28	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75443.1	000000	-	62	ME3_282	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75446.1	000000	-	67	ME3_285	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75450.1	000000	-	99	ME3_289	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75452.1	000000	-	116	ME3_291	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75455.1	000000	-	320	ME3_294	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75458.1	000000	-	213	ME3_297	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75460.1	000000	-	212	ME3_299	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75191.1	000000	-	228	ME3_30	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75462.1	000000	-	102	ME3_301	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75467.1	000000	-	72	ME3_306	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75468.1	000000	-	333	ME3_307	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75470.1	000000	-	798	ME3_309	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75192.1	000000	-	244	ME3_31	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75471.1	000000	-	75	ME3_310	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75473.1	000000	-	61	ME3_312	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75474.1	000000	-	55	ME3_313	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75479.1	000000	-	76	ME3_318	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75480.1	000000	-	165	ME3_319	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75193.1	000000	-	191	ME3_32	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75481.1	000000	-	184	ME3_320	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75483.1	000000	-	465	ME3_322	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75485.1	000000	-	134	ME3_324	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75486.1	000000	-	118	ME3_325	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75487.1	000000	-	69	ME3_326	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75195.1	000000	-	176	ME3_34	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75196.1	000000	-	1263	ME3_35	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75199.1	000000	-	261	ME3_38	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75200.1	000000	-	104	ME3_39	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75201.1	000000	-	130	ME3_40	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75202.1	000000	-	394	ME3_41	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75203.1	000000	-	700	ME3_42	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75204.1	000000	-	61	ME3_43	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75205.1	000000	-	208	ME3_44	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75206.1	000000	-	376	ME3_45	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75207.1	000000	-	1180	ME3_46	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75208.1	000000	-	397	ME3_47	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75209.1	000000	-	408	ME3_48	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75210.1	000000	-	713	ME3_49	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75211.1	000000	-	238	ME3_50	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75213.1	000000	-	199	ME3_52	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75214.1	000000	-	520	ME3_53	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75215.1	000000	-	149	ME3_54	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75216.1	000000	-	231	ME3_55	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75217.1	000000	-	88	ME3_56	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75220.1	000000	-	189	ME3_59	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75167.1	000000	-	126	ME3_6	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75225.1	000000	-	36	ME3_64	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75226.1	000000	-	203	ME3_65	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75230.1	000000	-	112	ME3_69	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75231.1	000000	-	279	ME3_70	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75232.1	000000	-	301	ME3_71	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75233.1	000000	-	156	ME3_72	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75234.1	000000	-	153	ME3_73	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AND75237.1	000000	-	364	ME3_76	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75239.1	000000	-	47	ME3_78	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75240.1	000000	-	187	ME3_79	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75244.1	000000	-	31	ME3_83	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75245.1	000000	-	120	ME3_84	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75250.1	000000	-	46	ME3_89	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75251.1	000000	-	168	ME3_90	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75252.1	000000	-	93	ME3_91	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75253.1	000000	-	45	ME3_92	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75255.1	000000	-	234	ME3_94	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75258.1	000000	-	56	ME3_97	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
AND75260.1	000000	-	136	ME3_99	Acinetobacter phage vB_AbaM_ME3	GCA_002609765.1
APU01520.1	000000	-	39	-	Aeromonas phage 65.2	GCA_002618145.1
APU01588.1	000000	-	116	-	Aeromonas phage 65.2	GCA_002618145.1
QMV29001.1	000000	-	31	AP1_0294	Aeromonas phage AP1	GCA_014183365.1
QMV29090.1	000000	-	41	AP1_0383	Aeromonas phage AP1	GCA_014183365.1
QMV29105.1	000000	-	263	AP1_0398	Aeromonas phage AP1	GCA_014183365.1
QMV29107.1	000000	-	38	AP1_0400	Aeromonas phage AP1	GCA_014183365.1
QMV29123.1	000000	-	40	AP1_0420	Aeromonas phage AP1	GCA_014183365.1
QMV29130.1	000000	-	249	AP1_0427	Aeromonas phage AP1	GCA_014183365.1
QMV29136.1	000000	-	132	AP1_0433	Aeromonas phage AP1	GCA_014183365.1
QMV29137.1	000000	-	124	AP1_0434	Aeromonas phage AP1	GCA_014183365.1
QMV29143.1	000000	-	43	AP1_0440	Aeromonas phage AP1	GCA_014183365.1
QMV29147.1	000000	-	112	AP1_0446	Aeromonas phage AP1	GCA_014183365.1
QMV29149.1	000000	-	101	AP1_0448	Aeromonas phage AP1	GCA_014183365.1
QMV29153.1	000000	-	99	AP1_0452	Aeromonas phage AP1	GCA_014183365.1
QMV29154.1	000000	-	254	AP1_0453	Aeromonas phage AP1	GCA_014183365.1
QMV29160.1	000000	-	291	AP1_0462	Aeromonas phage AP1	GCA_014183365.1
QMV29162.1	000000	-	191	AP1_0464	Aeromonas phage AP1	GCA_014183365.1
QMV29163.1	000000	-	50	AP1_0465	Aeromonas phage AP1	GCA_014183365.1
QMV29164.1	000000	-	40	AP1_0466	Aeromonas phage AP1	GCA_014183365.1
QMV29167.1	000000	-	44	AP1_0470	Aeromonas phage AP1	GCA_014183365.1
QMV29168.1	000000	-	58	AP1_0471	Aeromonas phage AP1	GCA_014183365.1
ATI17577.1	000000	-	216	-	Aeromonas phage AS-szw	GCA_002743635.1
AUE22570.1	000000	-	114	Ah1_00029	Aeromonas phage Ah1	GCA_002957415.1
AUE22600.1	000000	-	34	Ah1_00059	Aeromonas phage Ah1	GCA_002957415.1
AUE22637.1	000000	-	50	Ah1_00096	Aeromonas phage Ah1	GCA_002957415.1
AUE22654.1	000000	-	88	Ah1_00113	Aeromonas phage Ah1	GCA_002957415.1
AUE22706.1	000000	-	32	Ah1_00180	Aeromonas phage Ah1	GCA_002957415.1
AUE22784.1	000000	-	39	Ah1_00266	Aeromonas phage Ah1	GCA_002957415.1
AUE22743.1	000000	-	163	Ah1_00225	Aeromonas phage Ah1	GCA_002957415.1
QAX98356.1	000000	-	350	ASfcp2_10	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX98357.1	000000	-	135	ASfcp2_11	Aeromonas phage AsFcp_2	GCA_004146885.1
QAX97820.1	000000	-	105	ASswx1_176	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97823.1	000000	-	49	ASswx1_179	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97961.1	000000	-	112	ASswx1_319	Aeromonas phage Asswx_1	GCA_004146865.1
QAX98036.1	000000	-	104	ASswx1_396	Aeromonas phage Asswx_1	GCA_004146865.1
QAX97702.1	000000	-	175	ASswx1_56	Aeromonas phage Asswx_1	GCA_004146865.1
QAY01078.1	000000	-	84	ASwh1_10	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01178.1	000000	-	67	ASwh1_112	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01183.1	000000	-	60	ASwh1_118	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01080.1	000000	-	70	ASwh1_12	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01186.1	000000	-	95	ASwh1_121	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01196.1	000000	-	93	ASwh1_131	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01197.1	000000	-	48	ASwh1_132	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01210.1	000000	-	124	ASwh1_145	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01211.1	000000	-	57	ASwh1_146	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01224.1	000000	-	81	ASwh1_159	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01233.1	000000	-	91	ASwh1_168	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01244.1	000000	-	117	ASwh1_179	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01086.1	000000	-	63	ASwh1_18	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01251.1	000000	-	40	ASwh1_186	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01087.1	000000	-	96	ASwh1_19	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01261.1	000000	-	63	ASwh1_197	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01267.1	000000	-	64	ASwh1_204	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01089.1	000000	-	76	ASwh1_21	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01276.1	000000	-	67	ASwh1_213	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01279.1	000000	-	70	ASwh1_216	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01091.1	000000	-	102	ASwh1_23	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01323.1	000000	-	99	ASwh1_261	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01325.1	000000	-	63	ASwh1_263	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01331.1	000000	-	115	ASwh1_270	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01332.1	000000	-	72	ASwh1_271	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01342.1	000000	-	162	ASwh1_281	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01352.1	000000	-	59	ASwh1_292	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01100.1	000000	-	82	ASwh1_32	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01381.1	000000	-	98	ASwh1_321	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01383.1	000000	-	83	ASwh1_323	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01390.1	000000	-	151	ASwh1_331	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01391.1	000000	-	90	ASwh1_332	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01102.1	000000	-	165	ASwh1_34	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01405.1	000000	-	94	ASwh1_346	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01423.1	000000	-	64	ASwh1_364	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01424.1	000000	-	51	ASwh1_365	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01427.1	000000	-	68	ASwh1_368	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01428.1	000000	-	66	ASwh1_369	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01105.1	000000	-	83	ASwh1_37	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01434.1	000000	-	88	ASwh1_375	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01446.1	000000	-	90	ASwh1_387	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01450.1	000000	-	50	ASwh1_391	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01072.1	000000	-	94	ASwh1_4	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01460.1	000000	-	109	ASwh1_401	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01467.1	000000	-	70	ASwh1_408	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01471.1	000000	-	80	ASwh1_412	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01111.1	000000	-	72	ASwh1_43	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01112.1	000000	-	60	ASwh1_44	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01113.1	000000	-	63	ASwh1_45	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01114.1	000000	-	94	ASwh1_46	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01115.1	000000	-	72	ASwh1_47	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01118.1	000000	-	120	ASwh1_51	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01149.1	000000	-	68	ASwh1_83	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01150.1	000000	-	131	ASwh1_84	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01151.1	000000	-	101	ASwh1_85	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01152.1	000000	-	112	ASwh1_86	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01077.1	000000	-	79	ASwh1_9	Aeromonas phage Aswh_1	GCA_004146945.1
QAY01162.1	000000	-	82	ASwh1_96	Aeromonas phage Aswh_1	GCA_004146945.1
AFN39171.1	000000	-	94	CC2_020	Aeromonas phage CC2	GCA_000903495.1
AFN39204.1	000000	-	131	CC2_069	Aeromonas phage CC2	GCA_000903495.1
AFN39205.1	000000	-	119	CC2_070	Aeromonas phage CC2	GCA_000903495.1
AFN39229.1	000000	-	78	CC2_135	Aeromonas phage CC2	GCA_000903495.1
AFN39234.1	000000	-	51	CC2_145	Aeromonas phage CC2	GCA_000903495.1
AFN39155.1	000000	-	134	CC2_248	Aeromonas phage CC2	GCA_000903495.1
AFN39158.1	000000	-	45	CC2_356	Aeromonas phage CC2	GCA_000903495.1
QDB70419.1	000000	-	150	CF8_0006	Aeromonas phage CF8	GCA_006384595.2
QGY75115.1	000000	-	83	CF8_0007	Aeromonas phage CF8	GCA_006384595.2
QDB70430.1	000000	-	174	CF8_0018	Aeromonas phage CF8	GCA_006384595.2
QDB70434.1	000000	-	167	CF8_0022	Aeromonas phage CF8	GCA_006384595.2
QGY75117.1	000000	-	117	CF8_0023	Aeromonas phage CF8	GCA_006384595.2
QDB70436.1	000000	-	188	CF8_0024	Aeromonas phage CF8	GCA_006384595.2
QDB70440.1	000000	-	107	CF8_0028	Aeromonas phage CF8	GCA_006384595.2
QDB70441.1	000000	-	94	CF8_0029	Aeromonas phage CF8	GCA_006384595.2
QDB70277.2	000000	-	249	CF8_0033	Aeromonas phage CF8	GCA_006384595.2
QDB70447.1	000000	-	162	CF8_0035	Aeromonas phage CF8	GCA_006384595.2
QDB70450.1	000000	-	102	CF8_0038	Aeromonas phage CF8	GCA_006384595.2
QDB70451.1	000000	-	387	CF8_0039	Aeromonas phage CF8	GCA_006384595.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGY75120.1	000000	-	42	CF8_0064	Aeromonas phage CF8	GCA_006384595.2
QDB70247.1	000000	-	231	CF8_0079	Aeromonas phage CF8	GCA_006384595.2
QDB70257.1	000000	-	197	CF8_0089	Aeromonas phage CF8	GCA_006384595.2
QDB70288.1	000000	-	149	CF8_0120	Aeromonas phage CF8	GCA_006384595.2
QDB70307.1	000000	-	67	CF8_0139	Aeromonas phage CF8	GCA_006384595.2
QDB70309.1	000000	-	105	CF8_0141	Aeromonas phage CF8	GCA_006384595.2
QDB70311.1	000000	-	242	CF8_0143	Aeromonas phage CF8	GCA_006384595.2
QDB70318.1	000000	-	407	CF8_0149	Aeromonas phage CF8	GCA_006384595.2
QDB70323.1	000000	-	188	CF8_0153	Aeromonas phage CF8	GCA_006384595.2
QDB70324.1	000000	-	141	CF8_0154	Aeromonas phage CF8	GCA_006384595.2
QDB70325.1	000000	-	117	CF8_0155	Aeromonas phage CF8	GCA_006384595.2
QDB70327.1	000000	-	112	CF8_0157	Aeromonas phage CF8	GCA_006384595.2
QDB70330.1	000000	-	767	CF8_0160	Aeromonas phage CF8	GCA_006384595.2
QDB70332.1	000000	-	197	CF8_0162	Aeromonas phage CF8	GCA_006384595.2
QDB70334.1	000000	-	144	CF8_0164	Aeromonas phage CF8	GCA_006384595.2
QDB70346.1	000000	-	120	CF8_0177	Aeromonas phage CF8	GCA_006384595.2
QDB70349.1	000000	-	139	CF8_0180	Aeromonas phage CF8	GCA_006384595.2
QDB70350.1	000000	-	234	CF8_0181	Aeromonas phage CF8	GCA_006384595.2
QDB70353.1	000000	-	163	CF8_0184	Aeromonas phage CF8	GCA_006384595.2
QDB70357.1	000000	-	129	CF8_0189	Aeromonas phage CF8	GCA_006384595.2
QDB70360.1	000000	-	210	CF8_0192	Aeromonas phage CF8	GCA_006384595.2
QDJ97433.1	000000	-	40	D6_0006	Aeromonas phage D6	GCA_007051205.2
QDJ97168.1	000000	-	66	D6_0009	Aeromonas phage D6	GCA_007051205.2
QNH80836.1	000000	-	136	D6_0027	Aeromonas phage D6	GCA_007051205.2
QNH80838.1	000000	-	275	D6_0030	Aeromonas phage D6	GCA_007051205.2
QDJ97222.1	000000	-	60	D6_0062	Aeromonas phage D6	GCA_007051205.2
QDJ97223.1	000000	-	59	D6_0063	Aeromonas phage D6	GCA_007051205.2
QDJ97236.1	000000	-	43	D6_0076	Aeromonas phage D6	GCA_007051205.2
QDJ97284.1	000000	-	55	D6_0124	Aeromonas phage D6	GCA_007051205.2
QDJ97287.1	000000	-	104	D6_0127	Aeromonas phage D6	GCA_007051205.2
QDJ97288.1	000000	-	91	D6_0128	Aeromonas phage D6	GCA_007051205.2
QDJ97289.1	000000	-	114	D6_0129	Aeromonas phage D6	GCA_007051205.2
QDJ97293.1	000000	-	78	D6_0133	Aeromonas phage D6	GCA_007051205.2
QDJ97295.1	000000	-	211	D6_0135	Aeromonas phage D6	GCA_007051205.2
QDJ97314.1	000000	-	50	D6_0154	Aeromonas phage D6	GCA_007051205.2
QNH80846.1	000000	-	64	D6_0163	Aeromonas phage D6	GCA_007051205.2
QNH80848.1	000000	-	88	D6_0168	Aeromonas phage D6	GCA_007051205.2
QDJ97405.1	000000	-	48	D6_0246	Aeromonas phage D6	GCA_007051205.2
QNH80855.1	000000	-	112	D6_0260	Aeromonas phage D6	GCA_007051205.2
QDJ97420.1	000000	-	104	D6_0261	Aeromonas phage D6	GCA_007051205.2
QDJ97421.1	000000	-	89	D6_0262	Aeromonas phage D6	GCA_007051205.2
QDH47200.1	000000	-	131	LAh10_195	Aeromonas phage LAh10	GCA_006863975.1
QDH47232.1	000000	-	106	LAh10_69	Aeromonas phage LAh10	GCA_006863975.1
QDH47057.1	000000	-	447	LAh10_84	Aeromonas phage LAh10	GCA_006863975.1
QDJ96683.1	000000	-	131	PS1_0172	Aeromonas phage PS1	GCA_007051165.2
QFR59285.1	000000	-	106	PS2_0144	Aeromonas phage PS2	GCA_009388305.2
QFR59286.1	000000	-	204	PS2_0145	Aeromonas phage PS2	GCA_009388305.2
QFR59288.1	000000	-	228	PS2_0147	Aeromonas phage PS2	GCA_009388305.2
ADQ52740.1	000000	-	29	PX29p021	Aeromonas phage PX29	GCA_000920195.1
ADM79866.1	000000	-	60	phiAS5_ORF0023	Aeromonas phage phiAS5	GCA_000887715.1
ADM79868.1	000000	-	61	phiAS5_ORF0025	Aeromonas phage phiAS5	GCA_000887715.1
ADM79876.1	000000	-	108	phiAS5_ORF0033	Aeromonas phage phiAS5	GCA_000887715.1
ADM79914.1	000000	-	219	phiAS5_ORF0071	Aeromonas phage phiAS5	GCA_000887715.1
ADM79918.1	000000	-	64	phiAS5_ORF0075	Aeromonas phage phiAS5	GCA_000887715.1
ADM79928.1	000000	-	42	phiAS5_ORF0085	Aeromonas phage phiAS5	GCA_000887715.1
ADM79933.1	000000	-	84	phiAS5_ORF0090	Aeromonas phage phiAS5	GCA_000887715.1
ADM79997.1	000000	-	141	phiAS5_ORF0154	Aeromonas phage phiAS5	GCA_000887715.1
ADM79998.1	000000	-	38	phiAS5_ORF0155	Aeromonas phage phiAS5	GCA_000887715.1
ADM79999.1	000000	-	224	phiAS5_ORF0156	Aeromonas phage phiAS5	GCA_000887715.1
ADM80022.1	000000	-	105	phiAS5_ORF0179	Aeromonas phage phiAS5	GCA_000887715.1
ADM80043.1	000000	-	96	phiAS5_ORF0200	Aeromonas phage phiAS5	GCA_000887715.1
ADM80048.1	000000	-	38	phiAS5_ORF0205	Aeromonas phage phiAS5	GCA_000887715.1
ADM80062.1	000000	-	258	phiAS5_ORF0219	Aeromonas phage phiAS5	GCA_000887715.1
ADM80117.1	000000	-	51	phiAS5_ORF0274	Aeromonas phage phiAS5	GCA_000887715.1
ADM80128.1	000000	-	77	phiAS5_ORF0285	Aeromonas phage phiAS5	GCA_000887715.1
ADM80151.1	000000	-	54	phiAS5_ORF0308	Aeromonas phage phiAS5	GCA_000887715.1
ADM80156.1	000000	-	180	phiAS5_ORF0313	Aeromonas phage phiAS5	GCA_000887715.1
ADQ53092.1	000000	-	29	65p082	Aeromonas virus 65	GCA_000893255.1
ADQ53127.1	000000	-	26	65p119	Aeromonas virus 65	GCA_000893255.1
ADQ53133.1	000000	-	64	65p125	Aeromonas virus 65	GCA_000893255.1
ADQ53212.1	000000	-	74	65p204	Aeromonas virus 65	GCA_000893255.1
ADQ53287.1	000000	-	32	65p279	Aeromonas virus 65	GCA_000893255.1
ADQ53307.1	000000	-	17	65p299	Aeromonas virus 65	GCA_000893255.1
ADQ53372.1	000000	-	41	65p364	Aeromonas virus 65	GCA_000893255.1
ADQ53387.1	000000	-	55	65p380	Aeromonas virus 65	GCA_000893255.1
ADQ53388.1	000000	-	25	65p381	Aeromonas virus 65	GCA_000893255.1
AAQ17684.1	000000	-	773	Aeh1ORF027c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17685.1	000000	-	95	Aeh1ORF028c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17697.1	000000	-	77	Aeh1ORF038c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17838.1	000000	-	110	Aeh1ORF172c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17714.1	000000	-	60	Aeh1fORF01c	Aeromonas virus Aeh1	GCA_000843245.1
AAQ17899.1	000000	-	69	rnlB-A	Aeromonas virus Aeh1	GCA_000843245.1
AUZ95281.1	000000	-	77	FDI40_gp522	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95175.1	000000	-	72	FDI40_gp416	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95392.1	000000	-	72	FDI40_gp633	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95347.1	000000	-	72	FDI40_gp588	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94894.1	000000	-	72	FDI40_gp087	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95277.1	000000	-	116	FDI40_gp518	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95351.1	000000	-	116	FDI40_gp592	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94914.1	000000	-	131	FDI40_gp117	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94828.1	000000	-	101	FDI40_gp016	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95109.1	000000	-	101	FDI40_gp350	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95302.1	000000	-	101	FDI40_gp543	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95228.1	000000	-	42	FDI40_gp469	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94961.1	000000	-	42	FDI40_gp179	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95091.1	000000	-	133	FDI40_gp332	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95417.1	000000	-	73	FDI40_gp660	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94938.1	000000	-	73	FDI40_gp156	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95227.1	000000	-	73	FDI40_gp468	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94818.1	000000	-	73	FDI40_gp006	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95043.1	000000	-	73	FDI40_gp268	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95319.1	000000	-	73	FDI40_gp560	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95031.1	000000	-	73	FDI40_gp251	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95356.1	000000	-	73	FDI40_gp597	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95433.1	000000	-	40	FDI40_gp687	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95110.1	000000	-	65	FDI40_gp351	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94849.1	000000	-	65	FDI40_gp037	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95105.1	000000	-	83	FDI40_gp346	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94880.1	000000	-	83	FDI40_gp068	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94837.1	000000	-	83	FDI40_gp025	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95174.1	000000	-	83	FDI40_gp415	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94819.1	000000	-	83	FDI40_gp007	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95341.1	000000	-	93	FDI40_gp582	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95405.1	000000	-	93	FDI40_gp646	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95094.1	000000	-	93	FDI40_gp335	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95104.1	000000	-	93	FDI40_gp345	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95249.1	000000	-	147	FDI40_gp490	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94927.1	000000	-	147	FDI40_gp138	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94884.1	000000	-	155	FDI40_gp075	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95342.1	000000	-	155	FDI40_gp583	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95426.1	000000	-	194	FDI40_gp672	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95176.1	000000	-	91	FDI40_gp417	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95348.1	000000	-	91	FDI40_gp589	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95255.1	000000	-	91	FDI40_gp496	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95401.1	000000	-	102	FDI40_gp642	Agrobacterium phage Atu_ph07	GCA_002628245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ94881.1	000000	-	102	FDI40_gp069	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95037.1	000000	-	102	FDI40_gp258	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95229.1	000000	-	130	FDI40_gp470	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95194.1	000000	-	130	FDI40_gp435	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95052.1	000000	-	134	FDI40_gp280	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95387.1	000000	-	134	FDI40_gp628	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95078.1	000000	-	134	FDI40_gp315	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95312.1	000000	-	129	FDI40_gp553	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94822.1	000000	-	129	FDI40_gp010	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95200.1	000000	-	129	FDI40_gp441	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95143.1	000000	-	60	FDI40_gp384	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95141.1	000000	-	60	FDI40_gp382	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95177.1	000000	-	60	FDI40_gp418	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95077.1	000000	-	60	FDI40_gp313	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94956.1	000000	-	60	FDI40_gp174	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95306.1	000000	-	60	FDI40_gp547	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95121.1	000000	-	52	FDI40_gp362	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95288.1	000000	-	52	FDI40_gp529	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94994.1	000000	-	38	FDI40_gp212	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95441.1	000000	-	38	FDI40_gp702	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95191.1	000000	-	38	FDI40_gp432	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95030.1	000000	-	88	FDI40_gp249	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95015.1	000000	-	88	FDI40_gp233	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95117.1	000000	-	88	FDI40_gp358	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95184.1	000000	-	88	FDI40_gp425	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95349.1	000000	-	88	FDI40_gp590	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95359.1	000000	-	88	FDI40_gp600	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94941.1	000000	-	58	FDI40_gp159	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95382.1	000000	-	58	FDI40_gp623	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95434.1	000000	-	58	FDI40_gp688	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95124.1	000000	-	58	FDI40_gp365	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95090.1	000000	-	48	FDI40_gp331	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95320.1	000000	-	159	FDI40_gp561	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94972.1	000000	-	370	FDI40_gp190	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94935.1	000000	-	80	FDI40_gp153	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94907.1	000000	-	863	FDI40_gp108	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94843.1	000000	-	429	FDI40_gp031	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94877.1	000000	-	277	FDI40_gp065	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94878.1	000000	-	324	FDI40_gp066	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95235.1	000000	-	437	FDI40_gp476	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95012.1	000000	-	397	FDI40_gp230	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95100.1	000000	-	39	FDI40_gp341	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95267.1	000000	-	39	FDI40_gp508	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94899.1	000000	-	160	FDI40_gp095	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95327.1	000000	-	160	FDI40_gp568	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94970.1	000000	-	160	FDI40_gp188	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95402.1	000000	-	114	FDI40_gp643	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95221.1	000000	-	113	FDI40_gp462	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94908.1	000000	-	113	FDI40_gp111	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94993.1	000000	-	82	FDI40_gp211	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95370.1	000000	-	82	FDI40_gp611	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95180.1	000000	-	82	FDI40_gp421	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95339.1	000000	-	82	FDI40_gp580	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94863.1	000000	-	82	FDI40_gp051	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94930.1	000000	-	82	FDI40_gp146	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95144.1	000000	-	82	FDI40_gp385	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95169.1	000000	-	82	FDI40_gp410	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95296.1	000000	-	82	FDI40_gp537	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95350.1	000000	-	139	FDI40_gp591	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95390.1	000000	-	156	FDI40_gp631	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95060.1	000000	-	110	FDI40_gp289	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95411.1	000000	-	110	FDI40_gp652	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95067.1	000000	-	110	FDI40_gp298	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95010.1	000000	-	110	FDI40_gp228	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95256.1	000000	-	110	FDI40_gp497	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95034.1	000000	-	110	FDI40_gp255	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95108.1	000000	-	110	FDI40_gp349	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95246.1	000000	-	110	FDI40_gp487	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95305.1	000000	-	110	FDI40_gp546	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95299.1	000000	-	110	FDI40_gp540	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95322.1	000000	-	111	FDI40_gp563	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95102.1	000000	-	111	FDI40_gp343	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95323.1	000000	-	111	FDI40_gp564	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95164.1	000000	-	106	FDI40_gp405	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95096.1	000000	-	106	FDI40_gp337	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95304.1	000000	-	106	FDI40_gp545	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94945.1	000000	-	106	FDI40_gp163	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94921.1	000000	-	106	FDI40_gp129	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95016.1	000000	-	215	-	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95280.1	000000	-	153	FDI40_gp521	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95253.1	000000	-	153	FDI40_gp494	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95282.1	000000	-	153	FDI40_gp523	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95193.1	000000	-	145	FDI40_gp434	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94968.1	000000	-	76	FDI40_gp186	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95215.1	000000	-	76	FDI40_gp456	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94966.1	000000	-	232	FDI40_gp184	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95377.1	000000	-	97	FDI40_gp618	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94906.1	000000	-	97	FDI40_gp105	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95286.1	000000	-	81	FDI40_gp527	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94987.1	000000	-	250	FDI40_gp205	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95287.1	000000	-	89	FDI40_gp528	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94897.1	000000	-	89	FDI40_gp093	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95309.1	000000	-	89	FDI40_gp550	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95198.1	000000	-	89	FDI40_gp439	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95150.1	000000	-	89	FDI40_gp391	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95424.1	000000	-	89	FDI40_gp667	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95362.1	000000	-	246	FDI40_gp603	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95297.1	000000	-	86	FDI40_gp538	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95379.1	000000	-	86	FDI40_gp620	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94967.1	000000	-	86	FDI40_gp185	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95271.1	000000	-	86	FDI40_gp512	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95324.1	000000	-	86	FDI40_gp565	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94864.1	000000	-	86	FDI40_gp052	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95139.1	000000	-	86	FDI40_gp380	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95103.1	000000	-	86	FDI40_gp344	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95206.1	000000	-	86	FDI40_gp447	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95076.1	000000	-	104	FDI40_gp311	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94821.1	000000	-	104	FDI40_gp009	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95168.1	000000	-	104	FDI40_gp409	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95352.1	000000	-	64	FDI40_gp593	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95260.1	000000	-	64	FDI40_gp501	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95113.1	000000	-	64	FDI40_gp354	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95186.1	000000	-	64	FDI40_gp427	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95413.1	000000	-	64	FDI40_gp654	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94913.1	000000	-	64	FDI40_gp116	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95376.1	000000	-	118	FDI40_gp617	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94831.1	000000	-	118	FDI40_gp019	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95274.1	000000	-	118	FDI40_gp515	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95029.1	000000	-	115	FDI40_gp248	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95307.1	000000	-	115	FDI40_gp548	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95014.1	000000	-	115	FDI40_gp232	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95165.1	000000	-	115	FDI40_gp406	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94845.1	000000	-	330	FDI40_gp033	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94917.1	000000	-	57	FDI40_gp120	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95262.1	000000	-	57	FDI40_gp503	Agrobacterium phage Atu_ph07	GCA_002628245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ94844.1	000000	-	308	FDI40_gp032	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94835.1	000000	-	167	FDI40_gp023	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95138.1	000000	-	167	FDI40_gp379	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95269.1	000000	-	151	FDI40_gp510	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94925.1	000000	-	151	FDI40_gp136	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95222.1	000000	-	151	FDI40_gp463	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95344.1	000000	-	112	FDI40_gp585	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95291.1	000000	-	112	FDI40_gp532	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95162.1	000000	-	112	FDI40_gp403	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94949.1	000000	-	112	FDI40_gp167	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95436.1	000000	-	112	FDI40_gp690	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95161.1	000000	-	112	FDI40_gp402	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95197.1	000000	-	112	FDI40_gp438	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94926.1	000000	-	158	FDI40_gp137	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95407.1	000000	-	168	FDI40_gp648	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95111.1	000000	-	37	FDI40_gp352	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95226.1	000000	-	49	FDI40_gp467	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94841.1	000000	-	49	FDI40_gp029	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95378.1	000000	-	49	FDI40_gp619	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95066.1	000000	-	49	FDI40_gp297	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95097.1	000000	-	105	FDI40_gp338	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95285.1	000000	-	105	FDI40_gp526	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44704.1	000000	-	105	FDI40_gp100	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95122.1	000000	-	105	FDI40_gp363	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95093.1	000000	-	105	FDI40_gp334	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95254.1	000000	-	105	FDI40_gp495	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95272.1	000000	-	105	FDI40_gp513	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94839.1	000000	-	124	FDI40_gp027	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95340.1	000000	-	53	FDI40_gp581	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95038.1	000000	-	53	FDI40_gp259	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94896.1	000000	-	62	FDI40_gp091	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95217.1	000000	-	62	FDI40_gp458	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94825.1	000000	-	74	FDI40_gp013	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95112.1	000000	-	63	FDI40_gp353	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94840.1	000000	-	63	FDI40_gp028	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94969.1	000000	-	63	FDI40_gp187	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95289.1	000000	-	63	FDI40_gp530	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95366.1	000000	-	179	FDI40_gp607	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95011.1	000000	-	92	FDI40_gp229	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95137.1	000000	-	92	FDI40_gp378	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95266.1	000000	-	92	FDI40_gp507	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95243.1	000000	-	144	FDI40_gp484	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95257.1	000000	-	326	FDI40_gp498	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95354.1	000000	-	67	FDI40_gp595	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95237.1	000000	-	67	FDI40_gp478	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94942.1	000000	-	67	FDI40_gp160	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95292.1	000000	-	66	FDI40_gp533	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95439.1	000000	-	66	FDI40_gp700	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95000.1	000000	-	66	FDI40_gp218	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95182.1	000000	-	66	FDI40_gp423	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95155.1	000000	-	66	FDI40_gp396	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95008.1	000000	-	66	FDI40_gp226	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95005.1	000000	-	66	FDI40_gp223	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95290.1	000000	-	66	FDI40_gp531	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95159.1	000000	-	66	FDI40_gp400	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95321.1	000000	-	123	FDI40_gp562	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95239.1	000000	-	123	FDI40_gp480	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94859.1	000000	-	122	FDI40_gp047	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95303.1	000000	-	278	FDI40_gp544	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95058.1	000000	-	367	FDI40_gp286	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95317.1	000000	-	61	FDI40_gp558	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95294.1	000000	-	61	FDI40_gp535	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94904.1	000000	-	61	FDI40_gp103	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95399.1	000000	-	61	FDI40_gp640	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95230.1	000000	-	61	FDI40_gp471	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95234.1	000000	-	283	FDI40_gp475	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94857.1	000000	-	230	FDI40_gp045	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95157.1	000000	-	54	FDI40_gp398	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95004.1	000000	-	69	FDI40_gp222	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95409.1	000000	-	69	FDI40_gp650	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95318.1	000000	-	41	FDI40_gp559	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95120.1	000000	-	41	FDI40_gp361	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95443.1	000000	-	41	FDI40_gp704	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95209.1	000000	-	47	FDI40_gp450	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95265.1	000000	-	47	FDI40_gp506	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95151.1	000000	-	47	FDI40_gp392	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95119.1	000000	-	500	FDI40_gp360	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95087.1	000000	-	876	FDI40_gp328	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95331.1	000000	-	85	FDI40_gp572	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94836.1	000000	-	120	FDI40_gp024	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95160.1	000000	-	59	FDI40_gp401	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94912.1	000000	-	59	FDI40_gp115	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95196.1	000000	-	59	FDI40_gp437	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94901.1	000000	-	68	FDI40_gp099	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95371.1	000000	-	68	FDI40_gp612	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95214.1	000000	-	68	FDI40_gp455	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95071.1	000000	-	68	FDI40_gp304	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94943.1	000000	-	68	FDI40_gp161	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95040.1	000000	-	94	FDI40_gp262	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95047.1	000000	-	94	FDI40_gp273	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95442.1	000000	-	94	FDI40_gp703	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95279.1	000000	-	87	FDI40_gp520	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94955.1	000000	-	87	FDI40_gp173	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95326.1	000000	-	87	FDI40_gp567	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95384.1	000000	-	108	FDI40_gp625	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94944.1	000000	-	108	FDI40_gp162	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95343.1	000000	-	108	FDI40_gp584	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95403.1	000000	-	108	FDI40_gp644	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94889.1	000000	-	334	FDI40_gp082	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95170.1	000000	-	335	FDI40_gp411	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95033.1	000000	-	173	FDI40_gp254	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95364.1	000000	-	140	FDI40_gp605	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94932.1	000000	-	234	FDI40_gp150	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95445.1	000000	-	263	FDI40_gp706	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95095.1	000000	-	107	FDI40_gp336	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95263.1	000000	-	107	FDI40_gp504	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95070.1	000000	-	107	FDI40_gp302	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95202.1	000000	-	107	FDI40_gp443	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95372.1	000000	-	107	FDI40_gp613	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95101.1	000000	-	107	FDI40_gp342	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95142.1	000000	-	126	FDI40_gp383	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95373.1	000000	-	126	FDI40_gp614	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95039.1	000000	-	154	FDI40_gp260	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95148.1	000000	-	157	FDI40_gp389	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95051.1	000000	-	165	FDI40_gp278	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94890.1	000000	-	181	FDI40_gp083	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95406.1	000000	-	181	FDI40_gp647	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94826.1	000000	-	208	FDI40_gp014	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95248.1	000000	-	249	FDI40_gp489	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95080.1	000000	-	55	FDI40_gp318	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95192.1	000000	-	55	FDI40_gp433	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95163.1	000000	-	79	FDI40_gp404	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94992.1	000000	-	79	FDI40_gp210	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95250.1	000000	-	79	FDI40_gp491	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95098.1	000000	-	79	FDI40_gp339	Agrobacterium phage Atu_ph07	GCA_002628245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AUZ94915.1	000000	-	79	FDI40_gp118	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95437.1	000000	-	79	FDI40_gp692	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94923.1	000000	-	90	FDI40_gp131	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95028.1	000000	-	90	FDI40_gp247	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95283.1	000000	-	90	FDI40_gp524	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95276.1	000000	-	98	FDI40_gp517	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95430.1	000000	-	98	FDI40_gp681	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95179.1	000000	-	98	FDI40_gp420	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95107.1	000000	-	98	FDI40_gp348	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95325.1	000000	-	98	FDI40_gp566	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95429.1	000000	-	109	FDI40_gp679	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95264.1	000000	-	109	FDI40_gp505	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94998.1	000000	-	119	FDI40_gp216	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95314.1	000000	-	119	FDI40_gp555	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44748.1	000000	-	119	FDI40_gp659	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95026.1	000000	-	119	FDI40_gp244	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95275.1	000000	-	128	FDI40_gp516	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95416.1	000000	-	128	FDI40_gp657	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95212.1	000000	-	128	FDI40_gp453	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94851.1	000000	-	128	FDI40_gp039	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95358.1	000000	-	174	FDI40_gp599	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95048.1	000000	-	174	FDI40_gp274	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95353.1	000000	-	219	FDI40_gp594	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94879.1	000000	-	239	FDI40_gp067	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95414.1	000000	-	70	FDI40_gp655	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94848.1	000000	-	70	FDI40_gp036	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95115.1	000000	-	70	FDI40_gp356	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94957.1	000000	-	96	FDI40_gp175	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94903.1	000000	-	96	FDI40_gp102	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95027.1	000000	-	125	FDI40_gp245	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94929.1	000000	-	141	FDI40_gp144	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95332.1	000000	-	1383	FDI40_gp573	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95236.1	000000	-	195	FDI40_gp477	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95023.1	000000	-	401	FDI40_gp241	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94909.1	000000	-	744	FDI40_gp112	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94858.1	000000	-	75	FDI40_gp046	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95147.1	000000	-	75	FDI40_gp388	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95391.1	000000	-	75	FDI40_gp632	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94823.1	000000	-	75	FDI40_gp011	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95183.1	000000	-	75	FDI40_gp424	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94985.1	000000	-	75	FDI40_gp203	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95178.1	000000	-	46	FDI40_gp419	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95181.1	000000	-	46	FDI40_gp422	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94916.1	000000	-	103	FDI40_gp119	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95188.1	000000	-	103	FDI40_gp429	Agrobacterium phage Atu_ph07	GCA_002628245.1
ASV44699.1	000000	-	103	FDI40_gp088	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95308.1	000000	-	103	FDI40_gp549	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94940.1	000000	-	78	FDI40_gp158	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95073.1	000000	-	256	FDI40_gp307	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95361.1	000000	-	166	FDI40_gp602	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95118.1	000000	-	71	FDI40_gp359	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95145.1	000000	-	71	FDI40_gp386	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95329.1	000000	-	71	FDI40_gp570	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95173.1	000000	-	71	FDI40_gp414	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95149.1	000000	-	100	FDI40_gp390	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94902.1	000000	-	100	FDI40_gp101	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95432.1	000000	-	117	FDI40_gp683	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94984.1	000000	-	117	FDI40_gp202	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95205.1	000000	-	117	FDI40_gp446	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95013.1	000000	-	117	FDI40_gp231	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95171.1	000000	-	221	FDI40_gp412	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95074.1	000000	-	223	FDI40_gp308	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94852.1	000000	-	132	FDI40_gp040	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94931.1	000000	-	132	FDI40_gp147	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95360.1	000000	-	138	FDI40_gp601	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95357.1	000000	-	142	FDI40_gp598	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95398.1	000000	-	142	FDI40_gp639	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95126.1	000000	-	163	FDI40_gp367	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95311.1	000000	-	183	FDI40_gp552	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95079.1	000000	-	184	FDI40_gp317	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95223.1	000000	-	186	FDI40_gp464	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95451.1	000000	-	199	FDI40_gp712	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95298.1	000000	-	200	FDI40_gp539	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95450.1	000000	-	202	FDI40_gp711	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95233.1	000000	-	203	FDI40_gp474	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95363.1	000000	-	228	FDI40_gp604	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95114.1	000000	-	99	FDI40_gp355	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94892.1	000000	-	99	FDI40_gp085	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95278.1	000000	-	99	FDI40_gp519	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95099.1	000000	-	99	FDI40_gp340	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95089.1	000000	-	99	FDI40_gp330	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95106.1	000000	-	99	FDI40_gp347	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95092.1	000000	-	99	FDI40_gp333	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95453.1	000000	-	95	FDI40_gp714	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95412.1	000000	-	95	FDI40_gp653	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95068.1	000000	-	95	FDI40_gp299	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ94948.1	000000	-	300	FDI40_gp166	Agrobacterium phage Atu_ph07	GCA_002628245.1
AUZ95082.1	000000	-	301	FDI40_gp322	Agrobacterium phage Atu_ph07	GCA_002628245.1
ABS83568.1	000000	-	136	0305phi8-36p003	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83569.1	000000	-	143	0305phi8-36p004	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83571.1	000000	-	238	0305phi8-36p006	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83572.1	000000	-	92	0305phi8-36p007	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83576.1	000000	-	120	0305phi8-36p011	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83577.1	000000	-	79	0305phi8-36p012	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83578.1	000000	-	67	0305phi8-36p013	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83582.1	000000	-	101	0305phi8-36p017	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83583.1	000000	-	216	0305phi8-36p018	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83586.1	000000	-	160	0305phi8-36p021	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83587.1	000000	-	203	0305phi8-36p022	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83589.1	000000	-	41	0305phi8-36p024	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83590.1	000000	-	72	0305phi8-36p025	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83591.1	000000	-	82	0305phi8-36p026	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83592.1	000000	-	131	0305phi8-36p027	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83594.1	000000	-	94	0305phi8-36p031	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83597.1	000000	-	66	0305phi8-36p034	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83601.1	000000	-	165	0305phi8-36p040	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83603.1	000000	-	148	0305phi8-36p042	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83607.1	000000	-	318	0305phi8-36p046	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83609.1	000000	-	176	0305phi8-36p048	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83610.1	000000	-	138	0305phi8-36p049	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83611.1	000000	-	82	0305phi8-36p050	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83612.1	000000	-	124	0305phi8-36p051	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83812.1	000000	-	156	0305phi8-36p054	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83616.1	000000	-	155	0305phi8-36p056	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83617.1	000000	-	254	0305phi8-36p057	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83618.1	000000	-	51	0305phi8-36p058	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83619.1	000000	-	92	0305phi8-36p059	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83624.1	000000	-	85	0305phi8-36p064	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83627.1	000000	-	222	0305phi8-36p067	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83628.1	000000	-	163	0305phi8-36p068	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83632.1	000000	-	56	0305phi8-36p072	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83633.1	000000	-	130	0305phi8-36p073	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83634.1	000000	-	69	0305phi8-36p074	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83635.1	000000	-	65	0305phi8-36p075	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83637.1	000000	-	212	0305phi8-36p077	Bacillus phage 0305phi8-36	GCA_000871045.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ABS83638.1	000000	-	132	0305phi8-36p078	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83640.1	000000	-	183	0305phi8-36p080	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83643.1	000000	-	97	0305phi8-36p083	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83646.1	000000	-	97	0305phi8-36p086	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83647.1	000000	-	132	0305phi8-36p087	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83648.1	000000	-	154	0305phi8-36p088	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83649.1	000000	-	185	0305phi8-36p089	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83650.1	000000	-	130	0305phi8-36p090	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83652.1	000000	-	119	0305phi8-36p092	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83653.1	000000	-	155	0305phi8-36p093	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83654.1	000000	-	127	0305phi8-36p094	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83655.1	000000	-	61	0305phi8-36p095	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83656.1	000000	-	42	0305phi8-36p096	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83658.1	000000	-	82	0305phi8-36p098	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83666.1	000000	-	204	0305phi8-36p108	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83670.1	000000	-	242	0305phi8-36p112	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83671.1	000000	-	194	0305phi8-36p113	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83672.1	000000	-	248	0305phi8-36p114	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83673.1	000000	-	159	0305phi8-36p115	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83674.1	000000	-	181	0306phi8-36p116	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83677.1	000000	-	401	0306phi8-36p119	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83678.1	000000	-	74	0306phi8-36p120	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83682.1	000000	-	364	0306phi8-36p124	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83684.1	000000	-	168	0305phi8-36p126	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83686.1	000000	-	143	0305phi8-36p128	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83687.1	000000	-	989	0305phi8-36p129	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83688.1	000000	-	1073	0305phi8-36p130	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83689.1	000000	-	119	0305phi8-36p131	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83691.1	000000	-	900	0305phi8-36p133	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83692.1	000000	-	123	0305phi8-36p134	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83693.1	000000	-	288	0305phi8-36p135	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83694.1	000000	-	177	0305phi8-36p136	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83698.1	000000	-	260	0305phi8-36p140	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83699.1	000000	-	502	0305phi8-36p141	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83704.1	000000	-	2537	0305phi8-36p146	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83706.1	000000	-	127	0305phi8-36p148	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83707.1	000000	-	187	0305phi8-36p149	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83708.1	000000	-	141	0305phi8-36p150	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83710.1	000000	-	265	0305phi8-36p152	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83711.1	000000	-	383	0305phi8-36p153	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83713.1	000000	-	936	0305phi8-36p155	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83715.1	000000	-	127	0305phi8-36p157	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83716.1	000000	-	293	0305phi8-36p158	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83717.1	000000	-	270	0305phi8-36p159	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83718.1	000000	-	267	0305phi8-36p160	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83719.1	000000	-	114	0305phi8-36p161	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83720.1	000000	-	372	0305phi8-36p162	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83723.1	000000	-	421	0305phi8-36p165	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83726.1	000000	-	693	0305phi8-36p168	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83727.1	000000	-	160	0305phi8-36p169	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83729.1	000000	-	755	0305phi8-36p171	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83730.1	000000	-	591	0305phi8-36p172	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83732.1	000000	-	82	0305phi8-36p174	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83733.1	000000	-	398	0305phi8-36p175	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83736.1	000000	-	62	0305phi8-36p178	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83738.1	000000	-	229	0305phi8-36p180	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83742.1	000000	-	97	0305phi8-36p184	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83744.1	000000	-	100	0305phi8-36p186	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83746.1	000000	-	70	0305phi8-36p188	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83748.1	000000	-	269	0305phi8-36p190	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83749.1	000000	-	45	0305phi8-36p191	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83751.1	000000	-	287	0305phi8-36p193	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83753.1	000000	-	102	0305phi8-36p195	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83755.1	000000	-	78	0305phi8-36p197	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83764.1	000000	-	88	0305phi8-36p206	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83770.1	000000	-	49	0305phi8-36p212	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83772.1	000000	-	176	0305phi8-36p214	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83774.1	000000	-	104	0305phi8-36p216	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83775.1	000000	-	87	0305phi8-36p217	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83777.1	000000	-	323	0305phi8-36p219	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83778.1	000000	-	232	0305phi8-36p220	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83784.1	000000	-	62	0305phi8-36p226	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83785.1	000000	-	206	0305phi8-36p227	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83787.1	000000	-	195	0305phi8-36p229	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83789.1	000000	-	181	0305phi8-36p231	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83791.1	000000	-	380	0305phi8-36p233	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83793.1	000000	-	107	0305phi8-36p235	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83796.1	000000	-	111	0305phi8-36p238	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83809.1	000000	-	40	0305phi8-36p243	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83810.1	000000	-	43	0305phi8-36p244	Bacillus phage 0305phi8-36	GCA_000871045.1
ABS83641.1	000000	-	70	0305phi8-36p081	Bacillus phage 0305phi8-36	GCA_000871045.1
AMS01125.1	000000	-	88	AR9_g040	Bacillus phage AR9	GCA_001743835.1
AMS01130.1	000000	-	160	AR9_g045	Bacillus phage AR9	GCA_001743835.1
AMS01155.1	000000	-	91	AR9_g071	Bacillus phage AR9	GCA_001743835.1
AMS01206.1	000000	-	39	AR9_g122	Bacillus phage AR9	GCA_001743835.1
AMS01346.1	000000	-	90	AR9_g262	Bacillus phage AR9	GCA_001743835.1
AMS01347.1	000000	-	179	AR9_g263	Bacillus phage AR9	GCA_001743835.1
AMM44801.1	000000	-	151	SP15_003	Bacillus phage SP-15	GCA_001754685.1
AMM44803.1	000000	-	121	SP15_005	Bacillus phage SP-15	GCA_001754685.1
AMM44805.1	000000	-	144	SP15_007	Bacillus phage SP-15	GCA_001754685.1
AMM44807.1	000000	-	213	SP15_008	Bacillus phage SP-15	GCA_001754685.1
AMM44811.1	000000	-	73	SP15_012	Bacillus phage SP-15	GCA_001754685.1
AMM44812.1	000000	-	247	SP15_013	Bacillus phage SP-15	GCA_001754685.1
AMM44816.1	000000	-	53	SP15_017	Bacillus phage SP-15	GCA_001754685.1
AMM44817.1	000000	-	120	SP15_018	Bacillus phage SP-15	GCA_001754685.1
AMM44819.1	000000	-	92	SP15_020	Bacillus phage SP-15	GCA_001754685.1
AMM44820.1	000000	-	95	SP15_021	Bacillus phage SP-15	GCA_001754685.1
AMM44824.1	000000	-	230	SP15_025	Bacillus phage SP-15	GCA_001754685.1
AMM44825.1	000000	-	488	SP15_026	Bacillus phage SP-15	GCA_001754685.1
AMM44827.1	000000	-	152	SP15_028	Bacillus phage SP-15	GCA_001754685.1
AMM44835.1	000000	-	218	SP15_036	Bacillus phage SP-15	GCA_001754685.1
AMM44836.1	000000	-	338	SP15_037	Bacillus phage SP-15	GCA_001754685.1
AMM44837.1	000000	-	184	SP15_038	Bacillus phage SP-15	GCA_001754685.1
AMM44838.1	000000	-	174	SP15_039	Bacillus phage SP-15	GCA_001754685.1
AMM44840.1	000000	-	199	SP15_041	Bacillus phage SP-15	GCA_001754685.1
AMM44844.1	000000	-	246	SP15_045	Bacillus phage SP-15	GCA_001754685.1
AMM44845.1	000000	-	39	SP15_046	Bacillus phage SP-15	GCA_001754685.1
AMM44846.1	000000	-	1198	SP15_047	Bacillus phage SP-15	GCA_001754685.1
AMM44849.1	000000	-	382	SP15_050	Bacillus phage SP-15	GCA_001754685.1
AMM44854.1	000000	-	250	SP15_055	Bacillus phage SP-15	GCA_001754685.1
AMM44855.1	000000	-	556	SP15_056	Bacillus phage SP-15	GCA_001754685.1
AMM44856.1	000000	-	51	SP15_057	Bacillus phage SP-15	GCA_001754685.1
AMM44857.1	000000	-	168	SP15_058	Bacillus phage SP-15	GCA_001754685.1
AMM44864.1	000000	-	121	SP15_065	Bacillus phage SP-15	GCA_001754685.1
AMM44871.1	000000	-	132	SP15_072	Bacillus phage SP-15	GCA_001754685.1
AMM44873.1	000000	-	58	SP15_074	Bacillus phage SP-15	GCA_001754685.1
AMM44874.1	000000	-	94	SP15_075	Bacillus phage SP-15	GCA_001754685.1
AMM44875.1	000000	-	91	SP15_076	Bacillus phage SP-15	GCA_001754685.1
AMM44876.1	000000	-	82	SP15_077	Bacillus phage SP-15	GCA_001754685.1
AMM44878.1	000000	-	127	SP15_079	Bacillus phage SP-15	GCA_001754685.1
AMM44880.1	000000	-	118	SP15_081	Bacillus phage SP-15	GCA_001754685.1
AMM44882.1	000000	-	195	SP15_083	Bacillus phage SP-15	GCA_001754685.1
AMM44883.1	000000	-	82	SP15_084	Bacillus phage SP-15	GCA_001754685.1
AMM44884.1	000000	-	153	SP15_085	Bacillus phage SP-15	GCA_001754685.1
AMM44885.1	000000	-	356	SP15_086	Bacillus phage SP-15	GCA_001754685.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMM44886.1	000000	-	183	SP15_087	Bacillus phage SP-15	GCA_001754685.1
AMM44894.1	000000	-	270	SP15_095	Bacillus phage SP-15	GCA_001754685.1
AMM44895.1	000000	-	128	SP15_096	Bacillus phage SP-15	GCA_001754685.1
AMM44896.1	000000	-	80	SP15_097	Bacillus phage SP-15	GCA_001754685.1
AMM44897.1	000000	-	99	SP15_098	Bacillus phage SP-15	GCA_001754685.1
AMM44901.1	000000	-	45	SP15_102	Bacillus phage SP-15	GCA_001754685.1
AMM44904.1	000000	-	161	SP15_105	Bacillus phage SP-15	GCA_001754685.1
AMM44905.1	000000	-	79	SP15_106	Bacillus phage SP-15	GCA_001754685.1
AMM44907.1	000000	-	154	SP15_108	Bacillus phage SP-15	GCA_001754685.1
AMM44911.1	000000	-	97	SP15_113	Bacillus phage SP-15	GCA_001754685.1
AMM44916.1	000000	-	95	SP15_118	Bacillus phage SP-15	GCA_001754685.1
AMM44919.1	000000	-	79	SP15_121	Bacillus phage SP-15	GCA_001754685.1
AMM44920.1	000000	-	124	SP15_122	Bacillus phage SP-15	GCA_001754685.1
AMM44922.1	000000	-	74	SP15_124	Bacillus phage SP-15	GCA_001754685.1
AMM44923.1	000000	-	161	SP15_125	Bacillus phage SP-15	GCA_001754685.1
AMM44924.1	000000	-	107	SP15_126	Bacillus phage SP-15	GCA_001754685.1
AMM44926.1	000000	-	62	SP15_128	Bacillus phage SP-15	GCA_001754685.1
AMM44930.1	000000	-	174	SP15_132	Bacillus phage SP-15	GCA_001754685.1
AMM44931.1	000000	-	74	SP15_133	Bacillus phage SP-15	GCA_001754685.1
AMM44932.1	000000	-	201	SP15_134	Bacillus phage SP-15	GCA_001754685.1
AMM44936.1	000000	-	82	SP15_138	Bacillus phage SP-15	GCA_001754685.1
AMM44937.1	000000	-	225	SP15_139	Bacillus phage SP-15	GCA_001754685.1
AMM44938.1	000000	-	139	SP15_140	Bacillus phage SP-15	GCA_001754685.1
AMM44939.1	000000	-	190	SP15_141	Bacillus phage SP-15	GCA_001754685.1
AMM44940.1	000000	-	104	SP15_142	Bacillus phage SP-15	GCA_001754685.1
AMM44942.1	000000	-	118	SP15_144	Bacillus phage SP-15	GCA_001754685.1
AMM44950.1	000000	-	383	SP15_152	Bacillus phage SP-15	GCA_001754685.1
AMM44951.1	000000	-	380	SP15_153	Bacillus phage SP-15	GCA_001754685.1
AMM44952.1	000000	-	130	SP15_154	Bacillus phage SP-15	GCA_001754685.1
AMM44957.1	000000	-	43	SP15_159	Bacillus phage SP-15	GCA_001754685.1
AMM44960.1	000000	-	119	SP15_162	Bacillus phage SP-15	GCA_001754685.1
AMM44961.1	000000	-	132	SP15_163	Bacillus phage SP-15	GCA_001754685.1
AMM44962.1	000000	-	81	SP15_164	Bacillus phage SP-15	GCA_001754685.1
AMM44964.1	000000	-	106	SP15_166	Bacillus phage SP-15	GCA_001754685.1
AMM44966.1	000000	-	152	SP15_168	Bacillus phage SP-15	GCA_001754685.1
AMM44969.1	000000	-	244	SP15_171	Bacillus phage SP-15	GCA_001754685.1
AMM44970.1	000000	-	102	SP15_172	Bacillus phage SP-15	GCA_001754685.1
AMM44971.1	000000	-	80	SP15_173	Bacillus phage SP-15	GCA_001754685.1
AMM44975.1	000000	-	99	SP15_177	Bacillus phage SP-15	GCA_001754685.1
AMM44977.1	000000	-	119	SP15_179	Bacillus phage SP-15	GCA_001754685.1
AMM44980.1	000000	-	83	SP15_182	Bacillus phage SP-15	GCA_001754685.1
AMM44982.1	000000	-	125	SP15_184	Bacillus phage SP-15	GCA_001754685.1
AMM44983.1	000000	-	51	SP15_184A	Bacillus phage SP-15	GCA_001754685.1
AMM44985.1	000000	-	96	SP15_185	Bacillus phage SP-15	GCA_001754685.1
AMM44987.1	000000	-	80	SP15_187	Bacillus phage SP-15	GCA_001754685.1
AMM44988.1	000000	-	89	SP15_188	Bacillus phage SP-15	GCA_001754685.1
AMM44989.1	000000	-	83	SP15_189	Bacillus phage SP-15	GCA_001754685.1
AMM44990.1	000000	-	77	SP15_190	Bacillus phage SP-15	GCA_001754685.1
AMM44993.1	000000	-	104	SP15_193	Bacillus phage SP-15	GCA_001754685.1
AMM44994.1	000000	-	368	SP15_194	Bacillus phage SP-15	GCA_001754685.1
AMM44996.1	000000	-	68	SP15_196	Bacillus phage SP-15	GCA_001754685.1
AMM44997.1	000000	-	134	SP15_197	Bacillus phage SP-15	GCA_001754685.1
AMM44999.1	000000	-	127	SP15_199	Bacillus phage SP-15	GCA_001754685.1
AMM45000.1	000000	-	56	SP15_200	Bacillus phage SP-15	GCA_001754685.1
AMM45001.1	000000	-	96	SP15_201	Bacillus phage SP-15	GCA_001754685.1
AMM45002.1	000000	-	156	SP15_202	Bacillus phage SP-15	GCA_001754685.1
AMM45003.1	000000	-	319	SP15_203	Bacillus phage SP-15	GCA_001754685.1
AMM45004.1	000000	-	104	SP15_204	Bacillus phage SP-15	GCA_001754685.1
AMM45005.1	000000	-	164	SP15_205	Bacillus phage SP-15	GCA_001754685.1
AMM45006.1	000000	-	76	SP15_206	Bacillus phage SP-15	GCA_001754685.1
AMM45007.1	000000	-	67	SP15_207	Bacillus phage SP-15	GCA_001754685.1
AMM45008.1	000000	-	83	SP15_208	Bacillus phage SP-15	GCA_001754685.1
AMM45009.1	000000	-	99	SP15_209	Bacillus phage SP-15	GCA_001754685.1
AMM45010.1	000000	-	121	SP15_210	Bacillus phage SP-15	GCA_001754685.1
AMM45012.1	000000	-	119	SP15_212	Bacillus phage SP-15	GCA_001754685.1
AMM45013.1	000000	-	70	SP15_213	Bacillus phage SP-15	GCA_001754685.1
AMM45014.1	000000	-	108	SP15_214	Bacillus phage SP-15	GCA_001754685.1
AMM45015.1	000000	-	113	SP15_215	Bacillus phage SP-15	GCA_001754685.1
AMM45021.1	000000	-	179	SP15_220	Bacillus phage SP-15	GCA_001754685.1
AMM45023.1	000000	-	152	SP15_222	Bacillus phage SP-15	GCA_001754685.1
AMM45024.1	000000	-	160	SP15_223	Bacillus phage SP-15	GCA_001754685.1
AMM45026.1	000000	-	58	SP15_224A	Bacillus phage SP-15	GCA_001754685.1
AMM45027.1	000000	-	156	SP15_225	Bacillus phage SP-15	GCA_001754685.1
AMM45028.1	000000	-	93	SP15_226	Bacillus phage SP-15	GCA_001754685.1
AMM45029.1	000000	-	58	SP15_227	Bacillus phage SP-15	GCA_001754685.1
AMM45030.1	000000	-	100	SP15_228	Bacillus phage SP-15	GCA_001754685.1
AMM45031.1	000000	-	87	SP15_229	Bacillus phage SP-15	GCA_001754685.1
AMM45033.1	000000	-	68	SP15_231	Bacillus phage SP-15	GCA_001754685.1
AMM45035.1	000000	-	140	SP15_232	Bacillus phage SP-15	GCA_001754685.1
AMM45037.1	000000	-	118	SP15_234	Bacillus phage SP-15	GCA_001754685.1
AMM45038.1	000000	-	340	SP15_235	Bacillus phage SP-15	GCA_001754685.1
AMM45039.1	000000	-	69	SP15_236	Bacillus phage SP-15	GCA_001754685.1
AMM45040.1	000000	-	145	SP15_237	Bacillus phage SP-15	GCA_001754685.1
AMM45041.1	000000	-	92	SP15_238	Bacillus phage SP-15	GCA_001754685.1
AMM45042.1	000000	-	145	SP15_239	Bacillus phage SP-15	GCA_001754685.1
AMM45045.1	000000	-	97	SP15_240	Bacillus phage SP-15	GCA_001754685.1
AMM45047.1	000000	-	300	SP15_242	Bacillus phage SP-15	GCA_001754685.1
AMM45048.1	000000	-	177	SP15_243	Bacillus phage SP-15	GCA_001754685.1
AMM45050.1	000000	-	61	SP15_245	Bacillus phage SP-15	GCA_001754685.1
AMM45051.1	000000	-	153	SP15_246	Bacillus phage SP-15	GCA_001754685.1
AMM45052.1	000000	-	88	SP15_247	Bacillus phage SP-15	GCA_001754685.1
AMM45054.1	000000	-	94	SP15_249	Bacillus phage SP-15	GCA_001754685.1
AMM45058.1	000000	-	182	SP15_252	Bacillus phage SP-15	GCA_001754685.1
AMM45059.1	000000	-	107	SP15_253	Bacillus phage SP-15	GCA_001754685.1
AMM45060.1	000000	-	59	SP15_253A	Bacillus phage SP-15	GCA_001754685.1
AMM45061.1	000000	-	78	SP15_254	Bacillus phage SP-15	GCA_001754685.1
AMM45062.1	000000	-	242	SP15_255	Bacillus phage SP-15	GCA_001754685.1
AMM45063.1	000000	-	137	SP15_256	Bacillus phage SP-15	GCA_001754685.1
AMM45064.1	000000	-	69	SP15_257	Bacillus phage SP-15	GCA_001754685.1
AMM45065.1	000000	-	469	SP15_258	Bacillus phage SP-15	GCA_001754685.1
AMM45066.1	000000	-	475	SP15_259	Bacillus phage SP-15	GCA_001754685.1
AMM45068.1	000000	-	205	SP15_261	Bacillus phage SP-15	GCA_001754685.1
AMM45069.1	000000	-	48	SP15_262	Bacillus phage SP-15	GCA_001754685.1
AMM45070.1	000000	-	90	SP15_263	Bacillus phage SP-15	GCA_001754685.1
AMM45071.1	000000	-	105	SP15_264	Bacillus phage SP-15	GCA_001754685.1
AMM45072.1	000000	-	102	SP15_265	Bacillus phage SP-15	GCA_001754685.1
AMM45076.1	000000	-	273	SP15_269	Bacillus phage SP-15	GCA_001754685.1
AMM45077.1	000000	-	80	SP15_270	Bacillus phage SP-15	GCA_001754685.1
AMM45079.1	000000	-	42	SP15_271A	Bacillus phage SP-15	GCA_001754685.1
AMM45080.1	000000	-	99	SP15_272	Bacillus phage SP-15	GCA_001754685.1
AMM45081.1	000000	-	212	SP15_273	Bacillus phage SP-15	GCA_001754685.1
AMM45082.1	000000	-	108	SP15_274	Bacillus phage SP-15	GCA_001754685.1
AMM45084.1	000000	-	218	SP15_276	Bacillus phage SP-15	GCA_001754685.1
AMM45085.1	000000	-	102	SP15_277	Bacillus phage SP-15	GCA_001754685.1
AMM45086.1	000000	-	378	SP15_278	Bacillus phage SP-15	GCA_001754685.1
AMM45087.1	000000	-	189	SP15_279	Bacillus phage SP-15	GCA_001754685.1
AMM45089.1	000000	-	267	SP15_281	Bacillus phage SP-15	GCA_001754685.1
AMM45091.1	000000	-	74	SP15_283	Bacillus phage SP-15	GCA_001754685.1
AMM45093.1	000000	-	361	SP15_285	Bacillus phage SP-15	GCA_001754685.1
AMM45094.1	000000	-	300	SP15_286	Bacillus phage SP-15	GCA_001754685.1
AMM45095.1	000000	-	212	SP15_287	Bacillus phage SP-15	GCA_001754685.1
AMM45097.1	000000	-	183	SP15_289	Bacillus phage SP-15	GCA_001754685.1
AMM45098.1	000000	-	122	SP15_290	Bacillus phage SP-15	GCA_001754685.1
AMM45099.1	000000	-	126	SP15_291	Bacillus phage SP-15	GCA_001754685.1
AMM45100.1	000000	-	57	SP15_292	Bacillus phage SP-15	GCA_001754685.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AMM45102.1	000000	-	105	SP15_294	Bacillus phage SP-15	GCA_001754685.1
AMM45103.1	000000	-	55	SP15_295	Bacillus phage SP-15	GCA_001754685.1
AMM45104.1	000000	-	72	SP15_296	Bacillus phage SP-15	GCA_001754685.1
AMM45105.1	000000	-	72	SP15_297	Bacillus phage SP-15	GCA_001754685.1
AMM45110.1	000000	-	135	SP15_302	Bacillus phage SP-15	GCA_001754685.1
AMM45113.1	000000	-	100	SP15_305	Bacillus phage SP-15	GCA_001754685.1
ALN97680.1	000000	-	90	Bp8pS_001	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97682.1	000000	-	76	Bp8pS_003	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97685.1	000000	-	37	Bp8pS_006	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97694.1	000000	-	54	Bp8pS_015	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97695.1	000000	-	83	Bp8pS_016	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97708.1	000000	-	61	Bp8pS_029	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97718.1	000000	-	106	Bp8pS_039	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97727.1	000000	-	109	Bp8pS_048	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97740.1	000000	-	161	Bp8pS_061	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97747.1	000000	-	56	Bp8pS_068	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97748.1	000000	-	272	Bp8pS_069	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97752.1	000000	-	96	Bp8pS_073	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97753.1	000000	-	99	Bp8pS_074	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97754.1	000000	-	155	Bp8pS_075	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97758.1	000000	-	400	Bp8pS_079	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97765.1	000000	-	208	Bp8pS_086	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97766.1	000000	-	85	Bp8pS_087	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97768.1	000000	-	360	Bp8pS_089	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97769.1	000000	-	345	Bp8pS_090	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97771.1	000000	-	99	Bp8pS_092	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97774.1	000000	-	121	Bp8pS_095	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97775.1	000000	-	64	Bp8pS_096	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97776.1	000000	-	54	Bp8pS_097	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97777.1	000000	-	129	Bp8pS_098	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97786.1	000000	-	139	Bp8pS_107	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97787.1	000000	-	143	Bp8pS_108	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97789.1	000000	-	136	Bp8pS_110	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97796.1	000000	-	122	Bp8pS_117	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97798.1	000000	-	126	Bp8pS_119	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97823.1	000000	-	236	Bp8pS_144	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97830.1	000000	-	149	Bp8pS_151	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97838.1	000000	-	154	Bp8pS_159	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97840.1	000000	-	126	Bp8pS_161	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97843.1	000000	-	91	Bp8pS_164	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97844.1	000000	-	160	Bp8pS_165	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97845.1	000000	-	166	Bp8pS_166	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97850.1	000000	-	175	Bp8pS_171	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97854.1	000000	-	65	Bp8pS_175	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97866.1	000000	-	38	Bp8pS_187	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97869.1	000000	-	123	Bp8pS_190	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97874.1	000000	-	217	Bp8pS_195	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97894.1	000000	-	66	Bp8pS_215	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97899.1	000000	-	238	Bp8pS_220	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97908.1	000000	-	110	Bp8pS_229	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97909.1	000000	-	115	Bp8pS_230	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97910.1	000000	-	88	Bp8pS_231	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97911.1	000000	-	150	Bp8pS_232	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97912.1	000000	-	275	Bp8pS_233	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97922.1	000000	-	110	Bp8pS_243	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97923.1	000000	-	69	Bp8pS_244	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97926.1	000000	-	112	Bp8pS_247	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97928.1	000000	-	106	Bp8pS_249	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97930.1	000000	-	85	Bp8pS_251	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97952.1	000000	-	258	Bp8pS_273	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97964.1	000000	-	46	Bp8pS_285	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97968.1	000000	-	117	Bp8pS_289	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97979.1	000000	-	218	Bp8pS_300	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97980.1	000000	-	100	Bp8pS_301	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97981.1	000000	-	203	Bp8pS_302	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97983.1	000000	-	225	Bp8pS_304	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97987.1	000000	-	214	Bp8pS_308	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97988.1	000000	-	73	Bp8pS_309	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97989.1	000000	-	49	Bp8pS_310	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97990.1	000000	-	132	Bp8pS_311	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97991.1	000000	-	125	Bp8pS_312	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
ALN97993.1	000000	-	104	Bp8pS_314	Bacillus phage vB_BpuM-BpSp	GCA_002607645.1
AEO93362.1	000000	-	131	G_100	Bacillus virus G	GCA_000917535.1
AEO93363.1	000000	-	61	G_101	Bacillus virus G	GCA_000917535.1
AEO93369.1	000000	-	96	G_107	Bacillus virus G	GCA_000917535.1
AEO93370.1	000000	-	180	G_108	Bacillus virus G	GCA_000917535.1
AEO93372.1	000000	-	123	G_110	Bacillus virus G	GCA_000917535.1
AEO93374.1	000000	-	62	G_112	Bacillus virus G	GCA_000917535.1
AEO93375.1	000000	-	95	G_113	Bacillus virus G	GCA_000917535.1
AEO93377.1	000000	-	76	G_115	Bacillus virus G	GCA_000917535.1
AEO93379.1	000000	-	67	G_117	Bacillus virus G	GCA_000917535.1
AEO93381.1	000000	-	78	G_119	Bacillus virus G	GCA_000917535.1
AEO93283.1	000000	-	118	G_12	Bacillus virus G	GCA_000917535.1
AEO93383.1	000000	-	84	G_121	Bacillus virus G	GCA_000917535.1
AEO93388.1	000000	-	119	G_126	Bacillus virus G	GCA_000917535.1
AEO93389.1	000000	-	107	G_127	Bacillus virus G	GCA_000917535.1
AEO93391.1	000000	-	158	G_129	Bacillus virus G	GCA_000917535.1
AEO93392.1	000000	-	100	G_130	Bacillus virus G	GCA_000917535.1
AEO93393.1	000000	-	111	G_131	Bacillus virus G	GCA_000917535.1
AEO93394.1	000000	-	158	G_132	Bacillus virus G	GCA_000917535.1
AEO93395.1	000000	-	117	G_133	Bacillus virus G	GCA_000917535.1
AEO93396.1	000000	-	81	G_134	Bacillus virus G	GCA_000917535.1
AEO93399.1	000000	-	98	G_137	Bacillus virus G	GCA_000917535.1
AEO93285.1	000000	-	648	G_14	Bacillus virus G	GCA_000917535.1
AEO93402.1	000000	-	138	G_140	Bacillus virus G	GCA_000917535.1
AEO93405.1	000000	-	48	G_143	Bacillus virus G	GCA_000917535.1
AEO93946.1	000000	-	55	G_147	Bacillus virus G	GCA_000917535.1
AEO93409.1	000000	-	152	G_149	Bacillus virus G	GCA_000917535.1
AEO93414.1	000000	-	125	G_154	Bacillus virus G	GCA_000917535.1
AEO93418.1	000000	-	170	G_158	Bacillus virus G	GCA_000917535.1
AEO93419.1	000000	-	419	G_159	Bacillus virus G	GCA_000917535.1
AEO93287.1	000000	-	124	G_16	Bacillus virus G	GCA_000917535.1
AEO93420.1	000000	-	382	G_160	Bacillus virus G	GCA_000917535.1
AEO93421.1	000000	-	47	G_161	Bacillus virus G	GCA_000917535.1
AEO93423.1	000000	-	152	G_163	Bacillus virus G	GCA_000917535.1
AEO93425.1	000000	-	179	G_165	Bacillus virus G	GCA_000917535.1
AEO93428.1	000000	-	111	G_168	Bacillus virus G	GCA_000917535.1
AEO93429.1	000000	-	118	G_169	Bacillus virus G	GCA_000917535.1
AEO93288.1	000000	-	104	G_17	Bacillus virus G	GCA_000917535.1
AEO93430.1	000000	-	334	G_170	Bacillus virus G	GCA_000917535.1
AEO93433.1	000000	-	180	G_173	Bacillus virus G	GCA_000917535.1
AEO93435.1	000000	-	283	G_175	Bacillus virus G	GCA_000917535.1
AEO93436.1	000000	-	114	G_176	Bacillus virus G	GCA_000917535.1
AEO93437.1	000000	-	187	G_177	Bacillus virus G	GCA_000917535.1
AEO93444.1	000000	-	484	G_184	Bacillus virus G	GCA_000917535.1
AEO93446.1	000000	-	334	G_186	Bacillus virus G	GCA_000917535.1
AEO93450.1	000000	-	197	G_190	Bacillus virus G	GCA_000917535.1
AEO93451.1	000000	-	68	G_191	Bacillus virus G	GCA_000917535.1
AEO93452.1	000000	-	68	G_192	Bacillus virus G	GCA_000917535.1
AEO93456.1	000000	-	56	G_196	Bacillus virus G	GCA_000917535.1
AEO93459.1	000000	-	139	G_200	Bacillus virus G	GCA_000917535.1
AEO93460.1	000000	-	110	G_201	Bacillus virus G	GCA_000917535.1
AEO93462.1	000000	-	216	G_203	Bacillus virus G	GCA_000917535.1
AEO93463.1	000000	-	117	G_204	Bacillus virus G	GCA_000917535.1
AEO93466.1	000000	-	79	G_207	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEO93292.1	000000	-	486	G_21	Bacillus virus G	GCA_000917535.1
AEO93472.1	000000	-	64	G_213	Bacillus virus G	GCA_000917535.1
AEO93475.1	000000	-	85	G_216	Bacillus virus G	GCA_000917535.1
AEO93476.1	000000	-	129	G_217	Bacillus virus G	GCA_000917535.1
AEO93481.1	000000	-	73	G_222	Bacillus virus G	GCA_000917535.1
AEO93486.1	000000	-	166	G_227	Bacillus virus G	GCA_000917535.1
AEO93487.1	000000	-	104	G_228	Bacillus virus G	GCA_000917535.1
AEO93489.1	000000	-	100	G_230	Bacillus virus G	GCA_000917535.1
AEO93490.1	000000	-	135	G_231	Bacillus virus G	GCA_000917535.1
AEO93491.1	000000	-	55	G_232	Bacillus virus G	GCA_000917535.1
AEO93496.1	000000	-	81	G_237	Bacillus virus G	GCA_000917535.1
AEO93497.1	000000	-	245	G_238	Bacillus virus G	GCA_000917535.1
AEO93507.1	000000	-	137	G_248	Bacillus virus G	GCA_000917535.1
AEO93514.1	000000	-	611	G_255	Bacillus virus G	GCA_000917535.1
AEO93518.1	000000	-	185	G_259	Bacillus virus G	GCA_000917535.1
AEO93297.1	000000	-	165	G_26	Bacillus virus G	GCA_000917535.1
AEO93520.1	000000	-	213	G_261	Bacillus virus G	GCA_000917535.1
AEO93528.1	000000	-	74	G_269	Bacillus virus G	GCA_000917535.1
AEO93529.1	000000	-	149	G_270	Bacillus virus G	GCA_000917535.1
AEO93531.1	000000	-	151	G_272	Bacillus virus G	GCA_000917535.1
AEO93537.1	000000	-	116	G_278	Bacillus virus G	GCA_000917535.1
AEO93538.1	000000	-	129	G_279	Bacillus virus G	GCA_000917535.1
AEO93299.1	000000	-	310	G_28	Bacillus virus G	GCA_000917535.1
AEO93541.1	000000	-	102	G_282	Bacillus virus G	GCA_000917535.1
AEO93547.1	000000	-	105	G_288	Bacillus virus G	GCA_000917535.1
AEO93548.1	000000	-	252	G_289	Bacillus virus G	GCA_000917535.1
AEO93549.1	000000	-	79	G_290	Bacillus virus G	GCA_000917535.1
AEO93550.1	000000	-	84	G_291	Bacillus virus G	GCA_000917535.1
AEO93554.1	000000	-	69	G_295	Bacillus virus G	GCA_000917535.1
AEO93556.1	000000	-	65	G_297	Bacillus virus G	GCA_000917535.1
AEO93557.1	000000	-	102	G_298	Bacillus virus G	GCA_000917535.1
AEO93301.1	000000	-	110	G_30	Bacillus virus G	GCA_000917535.1
AEO93561.1	000000	-	136	G_302	Bacillus virus G	GCA_000917535.1
AEO93562.1	000000	-	138	G_303	Bacillus virus G	GCA_000917535.1
AEO93566.1	000000	-	168	G_307	Bacillus virus G	GCA_000917535.1
AEO93567.1	000000	-	138	G_308	Bacillus virus G	GCA_000917535.1
AEO93302.1	000000	-	105	G_31	Bacillus virus G	GCA_000917535.1
AEO93571.1	000000	-	112	G_312	Bacillus virus G	GCA_000917535.1
AEO93575.1	000000	-	164	G_316	Bacillus virus G	GCA_000917535.1
AEO93577.1	000000	-	142	G_318	Bacillus virus G	GCA_000917535.1
AEO93579.1	000000	-	118	G_320	Bacillus virus G	GCA_000917535.1
AEO93581.1	000000	-	137	G_322	Bacillus virus G	GCA_000917535.1
AEO93582.1	000000	-	79	G_323	Bacillus virus G	GCA_000917535.1
AEO93585.1	000000	-	131	G_326	Bacillus virus G	GCA_000917535.1
AEO93586.1	000000	-	87	G_327	Bacillus virus G	GCA_000917535.1
AEO93591.1	000000	-	207	G_332	Bacillus virus G	GCA_000917535.1
AEO93594.1	000000	-	48	G_335	Bacillus virus G	GCA_000917535.1
AEO93597.1	000000	-	292	G_338	Bacillus virus G	GCA_000917535.1
AEO93601.1	000000	-	295	G_342	Bacillus virus G	GCA_000917535.1
AEO93610.1	000000	-	150	G_351	Bacillus virus G	GCA_000917535.1
AEO93616.1	000000	-	67	G_357	Bacillus virus G	GCA_000917535.1
AEO93307.1	000000	-	102	G_36	Bacillus virus G	GCA_000917535.1
AEO93619.1	000000	-	191	G_360	Bacillus virus G	GCA_000917535.1
AEO93626.1	000000	-	580	G_367	Bacillus virus G	GCA_000917535.1
AEO93308.1	000000	-	92	G_37	Bacillus virus G	GCA_000917535.1
AEO93629.1	000000	-	87	G_370	Bacillus virus G	GCA_000917535.1
AEO93633.1	000000	-	96	G_374	Bacillus virus G	GCA_000917535.1
AEO93635.1	000000	-	212	G_376	Bacillus virus G	GCA_000917535.1
AEO93642.1	000000	-	110	G_383	Bacillus virus G	GCA_000917535.1
AEO93643.1	000000	-	99	G_384	Bacillus virus G	GCA_000917535.1
AEO93644.1	000000	-	95	G_385	Bacillus virus G	GCA_000917535.1
AEO93645.1	000000	-	434	G_386	Bacillus virus G	GCA_000917535.1
AEO93648.1	000000	-	210	G_389	Bacillus virus G	GCA_000917535.1
AEO93310.1	000000	-	346	G_39	Bacillus virus G	GCA_000917535.1
AEO93649.1	000000	-	220	G_390	Bacillus virus G	GCA_000917535.1
AEO93650.1	000000	-	150	G_391	Bacillus virus G	GCA_000917535.1
AEO93652.1	000000	-	61	G_393	Bacillus virus G	GCA_000917535.1
AEO93654.1	000000	-	95	G_395	Bacillus virus G	GCA_000917535.1
AEO93655.1	000000	-	76	G_396	Bacillus virus G	GCA_000917535.1
AEO93656.1	000000	-	96	G_397	Bacillus virus G	GCA_000917535.1
AEO93657.1	000000	-	59	G_398	Bacillus virus G	GCA_000917535.1
AEO93275.1	000000	-	267	G_4	Bacillus virus G	GCA_000917535.1
AEO93311.1	000000	-	85	G_40	Bacillus virus G	GCA_000917535.1
AEO93661.1	000000	-	65	G_403	Bacillus virus G	GCA_000917535.1
AEO93664.1	000000	-	48	G_406	Bacillus virus G	GCA_000917535.1
AEO93666.1	000000	-	128	G_408	Bacillus virus G	GCA_000917535.1
AEO93312.1	000000	-	119	G_41	Bacillus virus G	GCA_000917535.1
AEO93668.1	000000	-	104	G_410	Bacillus virus G	GCA_000917535.1
AEO93669.1	000000	-	72	G_411	Bacillus virus G	GCA_000917535.1
AEO93671.1	000000	-	74	G_413	Bacillus virus G	GCA_000917535.1
AEO93673.1	000000	-	62	G_415	Bacillus virus G	GCA_000917535.1
AEO93313.1	000000	-	152	G_42	Bacillus virus G	GCA_000917535.1
AEO93680.1	000000	-	113	G_422	Bacillus virus G	GCA_000917535.1
AEO93686.1	000000	-	178	G_428	Bacillus virus G	GCA_000917535.1
AEO93314.1	000000	-	217	G_43	Bacillus virus G	GCA_000917535.1
AEO93688.1	000000	-	120	G_430	Bacillus virus G	GCA_000917535.1
AEO93690.1	000000	-	115	G_432	Bacillus virus G	GCA_000917535.1
AEO93691.1	000000	-	117	G_433	Bacillus virus G	GCA_000917535.1
AEO93692.1	000000	-	237	G_434	Bacillus virus G	GCA_000917535.1
AEO93693.1	000000	-	173	G_435	Bacillus virus G	GCA_000917535.1
AEO93694.1	000000	-	85	G_436	Bacillus virus G	GCA_000917535.1
AEO93696.1	000000	-	78	G_438	Bacillus virus G	GCA_000917535.1
AEO93315.1	000000	-	173	G_44	Bacillus virus G	GCA_000917535.1
AEO93698.1	000000	-	72	G_440	Bacillus virus G	GCA_000917535.1
AEO93700.1	000000	-	68	G_442	Bacillus virus G	GCA_000917535.1
AEO93703.1	000000	-	104	G_445	Bacillus virus G	GCA_000917535.1
AEO93316.1	000000	-	130	G_45	Bacillus virus G	GCA_000917535.1
AEO93710.1	000000	-	104	G_452	Bacillus virus G	GCA_000917535.1
AEO93318.1	000000	-	65	G_47	Bacillus virus G	GCA_000917535.1
AEO93733.1	000000	-	122	G_475	Bacillus virus G	GCA_000917535.1
AEO93734.1	000000	-	86	G_476	Bacillus virus G	GCA_000917535.1
AEO93735.1	000000	-	103	G_477	Bacillus virus G	GCA_000917535.1
AEO93739.1	000000	-	107	G_481	Bacillus virus G	GCA_000917535.1
AEO93740.1	000000	-	83	G_482	Bacillus virus G	GCA_000917535.1
AEO93741.1	000000	-	95	G_483	Bacillus virus G	GCA_000917535.1
AEO93742.1	000000	-	107	G_484	Bacillus virus G	GCA_000917535.1
AEO93743.1	000000	-	146	G_485	Bacillus virus G	GCA_000917535.1
AEO93744.1	000000	-	139	G_486	Bacillus virus G	GCA_000917535.1
AEO93746.1	000000	-	151	G_488	Bacillus virus G	GCA_000917535.1
AEO93747.1	000000	-	138	G_489	Bacillus virus G	GCA_000917535.1
AEO93320.1	000000	-	63	G_49	Bacillus virus G	GCA_000917535.1
AEO93748.1	000000	-	145	G_490	Bacillus virus G	GCA_000917535.1
AEO93749.1	000000	-	158	G_491	Bacillus virus G	GCA_000917535.1
AEO93750.1	000000	-	158	G_492	Bacillus virus G	GCA_000917535.1
AEO93751.1	000000	-	155	G_493	Bacillus virus G	GCA_000917535.1
AEO93752.1	000000	-	144	G_494	Bacillus virus G	GCA_000917535.1
AEO93753.1	000000	-	138	G_495	Bacillus virus G	GCA_000917535.1
AEO93754.1	000000	-	87	G_496	Bacillus virus G	GCA_000917535.1
AEO93755.1	000000	-	140	G_497	Bacillus virus G	GCA_000917535.1
AEO93757.1	000000	-	191	G_499	Bacillus virus G	GCA_000917535.1
AEO93321.1	000000	-	139	G_50	Bacillus virus G	GCA_000917535.1
AEO93758.1	000000	-	110	G_500	Bacillus virus G	GCA_000917535.1
AEO93760.1	000000	-	227	G_502	Bacillus virus G	GCA_000917535.1
AEO93761.1	000000	-	260	G_503	Bacillus virus G	GCA_000917535.1
AEO93763.1	000000	-	129	G_505	Bacillus virus G	GCA_000917535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEO93765.1	000000	-	168	G_507	Bacillus virus G	GCA_000917535.1
AEO93322.1	000000	-	110	G_51	Bacillus virus G	GCA_000917535.1
AEO93768.1	000000	-	292	G_510	Bacillus virus G	GCA_000917535.1
AEO93773.1	000000	-	96	G_515	Bacillus virus G	GCA_000917535.1
AEO93774.1	000000	-	98	G_516	Bacillus virus G	GCA_000917535.1
AEO93775.1	000000	-	185	G_517	Bacillus virus G	GCA_000917535.1
AEO93777.1	000000	-	138	G_519	Bacillus virus G	GCA_000917535.1
AEO93323.1	000000	-	76	G_52	Bacillus virus G	GCA_000917535.1
AEO93778.1	000000	-	144	G_520	Bacillus virus G	GCA_000917535.1
AEO93784.1	000000	-	107	G_526	Bacillus virus G	GCA_000917535.1
AEO93786.1	000000	-	50	G_528	Bacillus virus G	GCA_000917535.1
AEO93787.1	000000	-	104	G_529	Bacillus virus G	GCA_000917535.1
AEO93791.1	000000	-	63	G_533	Bacillus virus G	GCA_000917535.1
AEO93792.1	000000	-	147	G_534	Bacillus virus G	GCA_000917535.1
AEO93794.1	000000	-	77	G_537	Bacillus virus G	GCA_000917535.1
AEO93325.1	000000	-	296	G_54	Bacillus virus G	GCA_000917535.1
AEO93799.1	000000	-	168	G_542	Bacillus virus G	GCA_000917535.1
AEO93800.1	000000	-	86	G_544	Bacillus virus G	GCA_000917535.1
AEO93802.1	000000	-	109	G_550	Bacillus virus G	GCA_000917535.1
AEO93942.1	000000	-	18	G_554	Bacillus virus G	GCA_000917535.1
AEO93807.1	000000	-	92	G_561	Bacillus virus G	GCA_000917535.1
AEO93813.1	000000	-	103	G_567	Bacillus virus G	GCA_000917535.1
AEO93818.1	000000	-	90	G_572	Bacillus virus G	GCA_000917535.1
AEO93819.1	000000	-	125	G_573	Bacillus virus G	GCA_000917535.1
AEO93823.1	000000	-	158	G_578	Bacillus virus G	GCA_000917535.1
AEO93824.1	000000	-	390	G_579	Bacillus virus G	GCA_000917535.1
AEO93329.1	000000	-	270	G_58	Bacillus virus G	GCA_000917535.1
AEO93826.1	000000	-	160	G_581	Bacillus virus G	GCA_000917535.1
AEO93828.1	000000	-	215	G_583	Bacillus virus G	GCA_000917535.1
AEO93829.1	000000	-	256	G_584	Bacillus virus G	GCA_000917535.1
AEO93830.1	000000	-	118	G_585	Bacillus virus G	GCA_000917535.1
AEO93834.1	000000	-	311	G_589	Bacillus virus G	GCA_000917535.1
AEO93835.1	000000	-	67	G_590	Bacillus virus G	GCA_000917535.1
AEO93836.1	000000	-	148	G_591	Bacillus virus G	GCA_000917535.1
AEO93837.1	000000	-	106	G_592	Bacillus virus G	GCA_000917535.1
AEO93838.1	000000	-	137	G_593	Bacillus virus G	GCA_000917535.1
AEO93842.1	000000	-	114	G_597	Bacillus virus G	GCA_000917535.1
AEO93844.1	000000	-	117	G_599	Bacillus virus G	GCA_000917535.1
AEO93277.1	000000	-	68	G_6	Bacillus virus G	GCA_000917535.1
AEO93845.1	000000	-	60	G_600	Bacillus virus G	GCA_000917535.1
AEO93846.1	000000	-	97	G_601	Bacillus virus G	GCA_000917535.1
AEO93847.1	000000	-	138	G_602	Bacillus virus G	GCA_000917535.1
AEO93848.1	000000	-	107	G_603	Bacillus virus G	GCA_000917535.1
AEO93849.1	000000	-	124	G_604	Bacillus virus G	GCA_000917535.1
AEO93851.1	000000	-	84	G_606	Bacillus virus G	GCA_000917535.1
AEO93852.1	000000	-	117	G_607	Bacillus virus G	GCA_000917535.1
AEO93854.1	000000	-	74	G_609	Bacillus virus G	GCA_000917535.1
AEO93855.1	000000	-	215	G_610	Bacillus virus G	GCA_000917535.1
AEO93857.1	000000	-	155	G_612	Bacillus virus G	GCA_000917535.1
AEO93859.1	000000	-	238	G_614	Bacillus virus G	GCA_000917535.1
AEO93860.1	000000	-	129	G_615	Bacillus virus G	GCA_000917535.1
AEO93861.1	000000	-	72	G_616	Bacillus virus G	GCA_000917535.1
AEO93862.1	000000	-	109	G_617	Bacillus virus G	GCA_000917535.1
AEO93863.1	000000	-	71	G_618	Bacillus virus G	GCA_000917535.1
AEO93864.1	000000	-	167	G_619	Bacillus virus G	GCA_000917535.1
AEO93865.1	000000	-	56	G_620	Bacillus virus G	GCA_000917535.1
AEO93866.1	000000	-	111	G_621	Bacillus virus G	GCA_000917535.1
AEO93867.1	000000	-	81	G_622	Bacillus virus G	GCA_000917535.1
AEO93868.1	000000	-	64	G_623	Bacillus virus G	GCA_000917535.1
AEO93869.1	000000	-	50	G_624	Bacillus virus G	GCA_000917535.1
AEO93870.1	000000	-	87	G_625	Bacillus virus G	GCA_000917535.1
AEO93334.1	000000	-	186	G_63	Bacillus virus G	GCA_000917535.1
AEO93875.1	000000	-	107	G_630	Bacillus virus G	GCA_000917535.1
AEO93879.1	000000	-	82	G_635	Bacillus virus G	GCA_000917535.1
AEO93880.1	000000	-	151	G_636	Bacillus virus G	GCA_000917535.1
AEO93882.1	000000	-	151	G_638	Bacillus virus G	GCA_000917535.1
AEO93883.1	000000	-	164	G_639	Bacillus virus G	GCA_000917535.1
AEO93887.1	000000	-	112	G_644	Bacillus virus G	GCA_000917535.1
AEO93888.1	000000	-	134	G_645	Bacillus virus G	GCA_000917535.1
AEO93889.1	000000	-	95	G_646	Bacillus virus G	GCA_000917535.1
AEO93890.1	000000	-	53	G_647	Bacillus virus G	GCA_000917535.1
AEO93891.1	000000	-	85	G_648	Bacillus virus G	GCA_000917535.1
AEO93892.1	000000	-	124	G_649	Bacillus virus G	GCA_000917535.1
AEO93896.1	000000	-	51	G_653	Bacillus virus G	GCA_000917535.1
AEO93898.1	000000	-	72	G_655	Bacillus virus G	GCA_000917535.1
AEO93899.1	000000	-	213	G_656	Bacillus virus G	GCA_000917535.1
AEO93901.1	000000	-	155	G_658	Bacillus virus G	GCA_000917535.1
AEO93902.1	000000	-	62	G_659	Bacillus virus G	GCA_000917535.1
AEO93904.1	000000	-	62	G_661	Bacillus virus G	GCA_000917535.1
AEO93909.1	000000	-	123	G_666	Bacillus virus G	GCA_000917535.1
AEO93910.1	000000	-	117	G_667	Bacillus virus G	GCA_000917535.1
AEO93911.1	000000	-	97	G_668	Bacillus virus G	GCA_000917535.1
AEO93912.1	000000	-	45	G_669	Bacillus virus G	GCA_000917535.1
AEO93338.1	000000	-	130	G_67	Bacillus virus G	GCA_000917535.1
AEO93913.1	000000	-	119	G_670	Bacillus virus G	GCA_000917535.1
AEO93914.1	000000	-	134	G_671	Bacillus virus G	GCA_000917535.1
AEO93917.1	000000	-	139	G_674	Bacillus virus G	GCA_000917535.1
AEO93919.1	000000	-	81	G_676	Bacillus virus G	GCA_000917535.1
AEO93920.1	000000	-	121	G_677	Bacillus virus G	GCA_000917535.1
AEO93339.1	000000	-	86	G_68	Bacillus virus G	GCA_000917535.1
AEO93924.1	000000	-	652	G_681	Bacillus virus G	GCA_000917535.1
AEO93925.1	000000	-	88	G_682	Bacillus virus G	GCA_000917535.1
AEO93927.1	000000	-	82	G_684	Bacillus virus G	GCA_000917535.1
AEO93928.1	000000	-	167	G_685	Bacillus virus G	GCA_000917535.1
AEO93929.1	000000	-	69	G_686	Bacillus virus G	GCA_000917535.1
AEO93931.1	000000	-	101	G_688	Bacillus virus G	GCA_000917535.1
AEO93932.1	000000	-	230	G_689	Bacillus virus G	GCA_000917535.1
AEO93935.1	000000	-	229	G_692	Bacillus virus G	GCA_000917535.1
AEO93936.1	000000	-	98	G_693	Bacillus virus G	GCA_000917535.1
AEO93278.1	000000	-	930	G_7	Bacillus virus G	GCA_000917535.1
AEO93343.1	000000	-	121	G_72	Bacillus virus G	GCA_000917535.1
AEO93345.1	000000	-	89	G_74	Bacillus virus G	GCA_000917535.1
AEO93346.1	000000	-	86	G_75	Bacillus virus G	GCA_000917535.1
AEO93347.1	000000	-	133	G_76	Bacillus virus G	GCA_000917535.1
AEO93348.1	000000	-	70	G_77	Bacillus virus G	GCA_000917535.1
AEO93349.1	000000	-	233	G_78	Bacillus virus G	GCA_000917535.1
AEO93938.1	000000	-	44	G_86	Bacillus virus G	GCA_000917535.1
AEO93280.1	000000	-	135	G_9	Bacillus virus G	GCA_000917535.1
AEO93359.1	000000	-	67	G_95	Bacillus virus G	GCA_000917535.1
AEO93360.1	000000	-	101	G_97	Bacillus virus G	GCA_000917535.1
AST99961.1	000000	-	48	PBI_PBS1_140	Bacillus virus PBS1	GCA_002601325.1
AST99978.1	000000	-	84	PBI_PBS1_157	Bacillus virus PBS1	GCA_002601325.1
AST99983.1	000000	-	54	PBI_PBS1_162	Bacillus virus PBS1	GCA_002601325.1
ASU00038.1	000000	-	49	PBI_PBS1_216	Bacillus virus PBS1	GCA_002601325.1
ASU00039.1	000000	-	44	PBI_PBS1_217	Bacillus virus PBS1	GCA_002601325.1
ASU00049.1	000000	-	30	PBI_PBS1_227	Bacillus virus PBS1	GCA_002601325.1
ASU00053.1	000000	-	31	PBI_PBS1_231	Bacillus virus PBS1	GCA_002601325.1
ASU00055.1	000000	-	57	PBI_PBS1_233	Bacillus virus PBS1	GCA_002601325.1
ASU00077.1	000000	-	116	PBI_PBS1_255	Bacillus virus PBS1	GCA_002601325.1
ASU00100.1	000000	-	152	PBI_PBS1_278	Bacillus virus PBS1	GCA_002601325.1
ASU00104.1	000000	-	48	PBI_PBS1_282	Bacillus virus PBS1	GCA_002601325.1
AST99854.1	000000	-	54	PBI_PBS1_32	Bacillus virus PBS1	GCA_002601325.1
AST99887.1	000000	-	42	PBI_PBS1_65	Bacillus virus PBS1	GCA_002601325.1
AST99920.1	000000	-	129	PBI_PBS1_98	Bacillus virus PBS1	GCA_002601325.1
QIG63378.1	000000	-	15	DAC16_145	Bacteroides phage DAC16	GCA_013387695.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG63260.1	000000	-	46	DAC16_27	Bacteroides phage DAC16	GCA_013387695.1
QIG63267.1	000000	-	34	DAC16_34	Bacteroides phage DAC16	GCA_013387695.1
QIG63281.1	000000	-	21	DAC16_48	Bacteroides phage DAC16	GCA_013387695.1
QIG63529.1	000000	-	21	DAC19_38	Bacteroides phage DAC19	GCA_013387715.1
QIG63543.1	000000	-	21	DAC19_52	Bacteroides phage DAC19	GCA_013387715.1
QIG63791.1	000000	-	21	DAC20_38	Bacteroides phage DAC20	GCA_013387725.1
QIG63804.1	000000	-	21	DAC20_51	Bacteroides phage DAC20	GCA_013387725.1
QIG64123.1	000000	-	107	DAC22_109	Bacteroides phage DAC22	GCA_013387735.1
QIG64168.1	000000	-	23	DAC22_154	Bacteroides phage DAC22	GCA_013387735.1
QIG64052.1	000000	-	23	DAC22_38	Bacteroides phage DAC22	GCA_013387735.1
QIG64065.1	000000	-	21	DAC22_51	Bacteroides phage DAC22	GCA_013387735.1
QIG64068.1	000000	-	130	DAC22_54	Bacteroides phage DAC22	GCA_013387735.1
QIG64522.1	000000	-	60	DAC23_248	Bacteroides phage DAC23	GCA_013387745.1
QIG64326.1	000000	-	21	DAC23_48	Bacteroides phage DAC23	GCA_013387745.1
QBX06445.1	000000	-	62	BcepSaruman_032	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06468.1	000000	-	63	BcepSaruman_055	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06482.1	000000	-	106	BcepSaruman_069	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06565.1	000000	-	64	BcepSaruman_152	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06608.1	000000	-	121	BcepSaruman_195	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06703.1	000000	-	58	BcepSaruman_290	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06730.1	000000	-	56	BcepSaruman_317	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06733.1	000000	-	167	BcepSaruman_320	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06793.1	000000	-	54	BcepSaruman_380	Burkholderia phage BcepSaruman	GCA_004771375.1
QBX06799.1	000000	-	124	BcepSaruman_386	Burkholderia phage BcepSaruman	GCA_004771375.1
QBQ74402.1	000000	-	109	BcepSauron_022	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74414.1	000000	-	87	BcepSauron_034	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74421.1	000000	-	176	BcepSauron_041	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74449.1	000000	-	74	BcepSauron_069	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74518.1	000000	-	69	BcepSauron_138	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74528.1	000000	-	98	BcepSauron_148	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74569.1	000000	-	129	BcepSauron_189	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74574.1	000000	-	59	BcepSauron_194	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74586.1	000000	-	79	BcepSauron_206	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74596.1	000000	-	135	BcepSauron_216	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74695.1	000000	-	89	BcepSauron_315	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74699.1	000000	-	129	BcepSauron_319	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74724.1	000000	-	106	BcepSauron_344	Burkholderia phage BcepSauron	GCA_005394215.1
QBQ74763.1	000000	-	214	BcepSauron_383	Burkholderia phage BcepSauron	GCA_005394215.1
CCH63467.1	000000	-	53	CP21_005	Campylobacter virus CP21	GCA_000902535.1
CCH63468.1	000000	-	239	CP21_006	Campylobacter virus CP21	GCA_000902535.1
CCH63469.1	000000	-	119	CP21_007	Campylobacter virus CP21	GCA_000902535.1
CCH63470.1	000000	-	420	CP21_008	Campylobacter virus CP21	GCA_000902535.1
CCH63472.1	000000	-	107	CP21_010	Campylobacter virus CP21	GCA_000902535.1
CCH63473.1	000000	-	49	CP21_011	Campylobacter virus CP21	GCA_000902535.1
CCH63479.1	000000	-	77	CP21_017	Campylobacter virus CP21	GCA_000902535.1
CCH63480.1	000000	-	149	CP21_018	Campylobacter virus CP21	GCA_000902535.1
CCH63482.1	000000	-	98	CP21_020	Campylobacter virus CP21	GCA_000902535.1
CCH63487.1	000000	-	132	CP21_025	Campylobacter virus CP21	GCA_000902535.1
CCH63490.1	000000	-	212	CP21_028	Campylobacter virus CP21	GCA_000902535.1
CCH63492.1	000000	-	185	CP21_030	Campylobacter virus CP21	GCA_000902535.1
CCH63497.1	000000	-	41	CP21_035	Campylobacter virus CP21	GCA_000902535.1
CCH63499.1	000000	-	83	CP21_037	Campylobacter virus CP21	GCA_000902535.1
CCH63504.1	000000	-	121	CP21_042	Campylobacter virus CP21	GCA_000902535.1
CCH63506.1	000000	-	69	CP21_044	Campylobacter virus CP21	GCA_000902535.1
CCH63507.1	000000	-	173	CP21_045	Campylobacter virus CP21	GCA_000902535.1
CCH63510.1	000000	-	160	CP21_048	Campylobacter virus CP21	GCA_000902535.1
CCH63511.1	000000	-	94	CP21_049	Campylobacter virus CP21	GCA_000902535.1
CCH63512.1	000000	-	56	CP21_050	Campylobacter virus CP21	GCA_000902535.1
CCH63514.1	000000	-	246	CP21_052	Campylobacter virus CP21	GCA_000902535.1
CCH63516.1	000000	-	93	CP21_054	Campylobacter virus CP21	GCA_000902535.1
CCH63517.1	000000	-	134	CP21_055	Campylobacter virus CP21	GCA_000902535.1
CCH63518.1	000000	-	70	CP21_056	Campylobacter virus CP21	GCA_000902535.1
CCH63520.1	000000	-	42	CP21_058	Campylobacter virus CP21	GCA_000902535.1
CCH63523.1	000000	-	49	CP21_061	Campylobacter virus CP21	GCA_000902535.1
CCH63526.1	000000	-	85	CP21_064	Campylobacter virus CP21	GCA_000902535.1
CCH63535.1	000000	-	94	CP21_073	Campylobacter virus CP21	GCA_000902535.1
CCH63539.1	000000	-	163	CP21_077	Campylobacter virus CP21	GCA_000902535.1
CCH63543.1	000000	-	84	CP21_081	Campylobacter virus CP21	GCA_000902535.1
CCH63546.1	000000	-	293	CP21_084	Campylobacter virus CP21	GCA_000902535.1
CCH63551.1	000000	-	75	CP21_089	Campylobacter virus CP21	GCA_000902535.1
CCH63553.1	000000	-	78	CP21_091	Campylobacter virus CP21	GCA_000902535.1
CCH63554.1	000000	-	382	CP21_092	Campylobacter virus CP21	GCA_000902535.1
CCH63555.1	000000	-	37	CP21_093	Campylobacter virus CP21	GCA_000902535.1
CCH63556.1	000000	-	99	CP21_094	Campylobacter virus CP21	GCA_000902535.1
CCH63557.1	000000	-	486	CP21_095	Campylobacter virus CP21	GCA_000902535.1
CCH63559.1	000000	-	78	CP21_097	Campylobacter virus CP21	GCA_000902535.1
CCH63561.1	000000	-	325	CP21_099	Campylobacter virus CP21	GCA_000902535.1
CCH63567.1	000000	-	534	CP21_105	Campylobacter virus CP21	GCA_000902535.1
CCH63569.1	000000	-	106	CP21_107	Campylobacter virus CP21	GCA_000902535.1
CCH63571.1	000000	-	113	CP21_109	Campylobacter virus CP21	GCA_000902535.1
CCH63573.1	000000	-	283	CP21_111	Campylobacter virus CP21	GCA_000902535.1
CCH63574.1	000000	-	63	CP21_112	Campylobacter virus CP21	GCA_000902535.1
CCH63578.1	000000	-	163	CP21_116	Campylobacter virus CP21	GCA_000902535.1
CCH63580.1	000000	-	139	CP21_118	Campylobacter virus CP21	GCA_000902535.1
CCH63581.1	000000	-	451	CP21_119	Campylobacter virus CP21	GCA_000902535.1
CCH63582.1	000000	-	157	CP21_120	Campylobacter virus CP21	GCA_000902535.1
CCH63583.1	000000	-	72	CP21_121	Campylobacter virus CP21	GCA_000902535.1
CCH63586.1	000000	-	68	CP21_124	Campylobacter virus CP21	GCA_000902535.1
CCH63590.1	000000	-	195	CP21_128	Campylobacter virus CP21	GCA_000902535.1
CCH63594.1	000000	-	111	CP21_132	Campylobacter virus CP21	GCA_000902535.1
CCH63596.1	000000	-	80	CP21_134	Campylobacter virus CP21	GCA_000902535.1
CCH63602.1	000000	-	182	CP21_140	Campylobacter virus CP21	GCA_000902535.1
CCH63603.1	000000	-	137	CP21_141	Campylobacter virus CP21	GCA_000902535.1
CCH63605.1	000000	-	230	CP21_143	Campylobacter virus CP21	GCA_000902535.1
CCH63606.1	000000	-	72	CP21_144	Campylobacter virus CP21	GCA_000902535.1
CCH63610.1	000000	-	125	CP21_148	Campylobacter virus CP21	GCA_000902535.1
CCH63611.1	000000	-	282	CP21_149	Campylobacter virus CP21	GCA_000902535.1
CCH63616.1	000000	-	42	CP21_154	Campylobacter virus CP21	GCA_000902535.1
CCH63619.1	000000	-	60	CP21_157	Campylobacter virus CP21	GCA_000902535.1
CCH63623.1	000000	-	75	CP21_161	Campylobacter virus CP21	GCA_000902535.1
CCH63624.1	000000	-	53	CP21_162	Campylobacter virus CP21	GCA_000902535.1
CCH63631.1	000000	-	41	CP21_169	Campylobacter virus CP21	GCA_000902535.1
CCH63632.1	000000	-	34	CP21_170	Campylobacter virus CP21	GCA_000902535.1
CCH63637.1	000000	-	99	CP21_175	Campylobacter virus CP21	GCA_000902535.1
CCH63643.1	000000	-	52	CP21_181	Campylobacter virus CP21	GCA_000902535.1
CCH63646.1	000000	-	158	CP21_184	Campylobacter virus CP21	GCA_000902535.1
CCH63647.1	000000	-	616	CP21_185	Campylobacter virus CP21	GCA_000902535.1
CCH63652.1	000000	-	61	CP21_190	Campylobacter virus CP21	GCA_000902535.1
CCH63655.1	000000	-	48	CP21_193	Campylobacter virus CP21	GCA_000902535.1
CCH63661.1	000000	-	208	CP21_199	Campylobacter virus CP21	GCA_000902535.1
CCH63662.1	000000	-	70	CP21_200	Campylobacter virus CP21	GCA_000902535.1
CCH63665.1	000000	-	55	CP21_203	Campylobacter virus CP21	GCA_000902535.1
CCH63666.1	000000	-	133	CP21_204	Campylobacter virus CP21	GCA_000902535.1
CCH63671.1	000000	-	48	CP21_209	Campylobacter virus CP21	GCA_000902535.1
CCH63672.1	000000	-	36	CP21_210	Campylobacter virus CP21	GCA_000902535.1
CCH63674.1	000000	-	202	CP21_212	Campylobacter virus CP21	GCA_000902535.1
CCH63675.1	000000	-	61	CP21_213	Campylobacter virus CP21	GCA_000902535.1
CCH63676.1	000000	-	80	CP21_214	Campylobacter virus CP21	GCA_000902535.1
CCH63677.1	000000	-	336	CP21_215	Campylobacter virus CP21	GCA_000902535.1
CCH63678.1	000000	-	276	CP21_216	Campylobacter virus CP21	GCA_000902535.1
CCH63679.1	000000	-	55	CP21_217	Campylobacter virus CP21	GCA_000902535.1
CCH63680.1	000000	-	144	CP21_218	Campylobacter virus CP21	GCA_000902535.1
CCH63682.1	000000	-	272	CP21_220	Campylobacter virus CP21	GCA_000902535.1
CCH63684.1	000000	-	152	CP21_222	Campylobacter virus CP21	GCA_000902535.1
CCH63686.1	000000	-	87	CP21_224	Campylobacter virus CP21	GCA_000902535.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
CCH63687.1	000000	-	266	CP21_225	Campylobacter virus CP21	GCA_000902535.1
CCH63688.1	000000	-	131	CP21_226	Campylobacter virus CP21	GCA_000902535.1
CCH63689.1	000000	-	108	CP21_227	Campylobacter virus CP21	GCA_000902535.1
CCH63696.1	000000	-	103	CP21_236	Campylobacter virus CP21	GCA_000902535.1
CCH63700.1	000000	-	44	CP21_240	Campylobacter virus CP21	GCA_000902535.1
CCH63701.1	000000	-	77	CP21_241	Campylobacter virus CP21	GCA_000902535.1
CCH63702.1	000000	-	66	CP21_242	Campylobacter virus CP21	GCA_000902535.1
CCH63713.1	000000	-	55	CP21_253	Campylobacter virus CP21	GCA_000902535.1
CCH63715.1	000000	-	107	CP21_255	Campylobacter virus CP21	GCA_000902535.1
CCH63717.1	000000	-	242	CP21_257	Campylobacter virus CP21	GCA_000902535.1
CCH63718.1	000000	-	74	CP21_258	Campylobacter virus CP21	GCA_000902535.1
CCH63719.1	000000	-	34	CP21_259	Campylobacter virus CP21	GCA_000902535.1
ARB14752.1	000000	-	65	Ccr29_gp196	Caulobacter phage Ccr29	GCA_002619485.1
ARB15586.1	000000	-	105	Ccr34_gp077	Caulobacter phage Ccr34	GCA_002619525.1
AXQ68240.1	000000	-	78	CcrBL10_gp036	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68242.1	000000	-	114	CcrBL10_gp038	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68289.1	000000	-	41	CcrBL10_gp085c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68329.1	000000	-	82	CcrBL10_gp125c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68357.1	000000	-	80	CcrBL10_gp153c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68375.1	000000	-	106	CcrBL10_gp171c	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68457.1	000000	-	82	CcrBL10_gp253	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68474.1	000000	-	112	CcrBL10_gp270	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ68480.1	000000	-	103	CcrBL10_gp276	Caulobacter phage CcrBL10	GCA_003443255.1
AXQ69071.1	000000	-	87	CcrBL9_gp047c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69078.1	000000	-	124	CcrBL9_gp054c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69082.1	000000	-	83	CcrBL9_gp058c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69084.1	000000	-	95	CcrBL9_gp060c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69098.1	000000	-	120	CcrBL9_gp074c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69105.1	000000	-	54	CcrBL9_gp081c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69172.1	000000	-	50	CcrBL9_gp148	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69256.1	000000	-	136	CcrBL9_gp232c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69343.1	000000	-	247	CcrBL9_gp319	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69395.1	000000	-	100	CcrBL9_gp371	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69398.1	000000	-	81	CcrBL9_gp374	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69406.1	000000	-	123	CcrBL9_gp382	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69411.1	000000	-	158	CcrBL9_gp387	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69416.1	000000	-	63	CcrBL9_gp392	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69437.1	000000	-	64	CcrBL9_gp413	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69443.1	000000	-	48	CcrBL9_gp419	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69453.1	000000	-	93	CcrBL9_gp429	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69485.1	000000	-	245	CcrBL9_gp461	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69500.1	000000	-	61	CcrBL9_gp476	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69504.1	000000	-	105	CcrBL9_gp480	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69512.1	000000	-	221	CcrBL9_gp488	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69516.1	000000	-	77	CcrBL9_gp492c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69517.1	000000	-	65	CcrBL9_gp493c	Caulobacter phage CcrBL9	GCA_003443295.1
AXQ69540.1	000000	-	37	CcrBL9_gp516c	Caulobacter phage CcrBL9	GCA_003443295.1
AFU87872.1	000000	-	108	CcrColossus_gp002	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87877.1	000000	-	95	CcrColossus_gp007	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87880.1	000000	-	144	CcrColossus_gp010	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87881.1	000000	-	46	CcrColossus_gp011	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87888.1	000000	-	165	CcrColossus_gp018	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87909.1	000000	-	131	CcrColossus_gp039	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87936.1	000000	-	106	CcrColossus_gp066	Caulobacter phage CcrColossus	GCA_000899635.1
AFU87964.1	000000	-	101	CcrColossus_gp094	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88033.1	000000	-	69	CcrColossus_gp163	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88097.1	000000	-	78	CcrColossus_gp227	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88130.1	000000	-	88	CcrColossus_gp260	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88134.1	000000	-	130	CcrColossus_gp264	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88192.1	000000	-	132	CcrColossus_gp322	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88213.1	000000	-	63	CcrColossus_gp343	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88220.1	000000	-	54	CcrColossus_gp350	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88238.1	000000	-	68	CcrColossus_gp368	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88245.1	000000	-	127	CcrColossus_gp375	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88258.1	000000	-	77	CcrColossus_gp388	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88264.1	000000	-	78	CcrColossus_gp394	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88265.1	000000	-	98	CcrColossus_gp395	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88279.1	000000	-	67	CcrColossus_gp409	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88283.1	000000	-	65	CcrColossus_gp413	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88288.1	000000	-	59	CcrColossus_gp418	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88289.1	000000	-	83	CcrColossus_gp419	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88293.1	000000	-	101	CcrColossus_gp423	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88296.1	000000	-	71	CcrColossus_gp426	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88306.1	000000	-	81	CcrColossus_gp436	Caulobacter phage CcrColossus	GCA_000899635.1
AFU88307.1	000000	-	85	CcrColossus_gp437	Caulobacter phage CcrColossus	GCA_000899635.1
AXQ68579.1	000000	-	56	CcrPW_gp040	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68608.1	000000	-	98	CcrPW_gp069	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68631.1	000000	-	54	CcrPW_gp092c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68686.1	000000	-	42	CcrPW_gp147	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68696.1	000000	-	67	CcrPW_gp157c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68710.1	000000	-	197	CcrPW_gp171	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68727.1	000000	-	43	CcrPW_gp188	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68834.1	000000	-	38	CcrPW_gp295	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68843.1	000000	-	180	CcrPW_gp304c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68867.1	000000	-	139	CcrPW_gp328	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68888.1	000000	-	99	CcrPW_gp349	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68897.1	000000	-	126	CcrPW_gp358	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68932.1	000000	-	103	CcrPW_gp393c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68937.1	000000	-	146	CcrPW_gp398	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68942.1	000000	-	71	CcrPW_gp403	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68944.1	000000	-	129	CcrPW_gp405	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68947.1	000000	-	139	CcrPW_gp408	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68961.1	000000	-	211	CcrPW_gp422c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68967.1	000000	-	85	CcrPW_gp428c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ68969.1	000000	-	89	CcrPW_gp430c	Caulobacter phage CcrPW	GCA_003443275.1
AXQ69631.1	000000	-	64	CcrSC_gp049c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69641.1	000000	-	124	CcrSC_gp059c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69651.1	000000	-	127	CcrSC_gp069c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69709.1	000000	-	245	CcrSC_gp127	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69762.1	000000	-	43	CcrSC_gp180c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69808.1	000000	-	44	CcrSC_gp226c	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69829.1	000000	-	39	CcrSC_gp247	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69871.1	000000	-	63	CcrSC_gp289	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69893.1	000000	-	81	CcrSC_gp311	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69967.1	000000	-	40	CcrSC_gp385	Caulobacter phage CcrSC	GCA_003443315.1
AXQ69968.1	000000	-	55	CcrSC_gp386	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70046.1	000000	-	112	CcrSC_gp464	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70048.1	000000	-	168	CcrSC_gp466	Caulobacter phage CcrSC	GCA_003443315.1
AXQ70060.1	000000	-	76	CcrSC_gp478	Caulobacter phage CcrSC	GCA_003443315.1
AFU87543.1	000000	-	102	CcrKarma_gp026	Caulobacter virus Karma	GCA_000901575.1
AFU87389.1	000000	-	89	CcrMagneto_gp219	Caulobacter virus Magneto	GCA_000903095.1
AFU87410.1	000000	-	66	CcrMagneto_gp240	Caulobacter virus Magneto	GCA_000903095.1
AFU86522.1	000000	-	94	CcrRogue_gp040	Caulobacter virus Rogue	GCA_000900555.1
AFU86607.1	000000	-	137	CcrRogue_gp125	Caulobacter virus Rogue	GCA_000900555.1
AFU86658.1	000000	-	43	CcrRogue_gp176	Caulobacter virus Rogue	GCA_000900555.1
AFU86665.1	000000	-	55	CcrRogue_gp183	Caulobacter virus Rogue	GCA_000900555.1
AFU86666.1	000000	-	77	CcrRogue_gp184	Caulobacter virus Rogue	GCA_000900555.1
AFU86680.1	000000	-	59	CcrRogue_gp198	Caulobacter virus Rogue	GCA_000900555.1
AFU86766.1	000000	-	68	CcrRogue_gp284	Caulobacter virus Rogue	GCA_000900555.1
AFU86768.1	000000	-	130	CcrRogue_gp286	Caulobacter virus Rogue	GCA_000900555.1
AFU86804.1	000000	-	117	CcrRogue_gp322	Caulobacter virus Rogue	GCA_000900555.1
AFU88354.1	000000	-	66	CcrSwift_gp036	Caulobacter virus Swift	GCA_000899655.1
ANS06148.1	000000	-	79	ABCD_0076	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS06193.1	000000	-	37	ABCD_0077	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS06159.1	000000	-	72	ABCD_0091	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANS06137.1	000000	-	84	ABCD_0096	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
ANS06170.1	000000	-	66	ABCD_0165	Citrobacter phage vB_CfrM_CfP1	GCA_001744555.1
BAE47700.1	000000	-	65	CST002	Clostridium phage c-st	GCA_000865225.1
BAE47701.1	000000	-	97	CST003	Clostridium phage c-st	GCA_000865225.1
BAE47708.1	000000	-	38	CST010	Clostridium phage c-st	GCA_000865225.1
BAE47712.1	000000	-	79	CST014	Clostridium phage c-st	GCA_000865225.1
BAE47713.1	000000	-	410	CST015	Clostridium phage c-st	GCA_000865225.1
BAE47714.1	000000	-	255	CST016	Clostridium phage c-st	GCA_000865225.1
BAE47715.1	000000	-	214	CST017	Clostridium phage c-st	GCA_000865225.1
BAE47717.1	000000	-	227	CST019	Clostridium phage c-st	GCA_000865225.1
BAE47721.1	000000	-	345	CST023	Clostridium phage c-st	GCA_000865225.1
BAE47724.1	000000	-	53	CST026	Clostridium phage c-st	GCA_000865225.1
BAE47726.1	000000	-	218	CST028	Clostridium phage c-st	GCA_000865225.1
BAE47727.1	000000	-	466	CST029	Clostridium phage c-st	GCA_000865225.1
BAE47731.1	000000	-	60	CST033	Clostridium phage c-st	GCA_000865225.1
BAE47732.1	000000	-	60	CST034	Clostridium phage c-st	GCA_000865225.1
BAE47733.1	000000	-	45	CST035	Clostridium phage c-st	GCA_000865225.1
BAE47734.1	000000	-	62	CST036	Clostridium phage c-st	GCA_000865225.1
BAE47735.1	000000	-	163	CST037	Clostridium phage c-st	GCA_000865225.1
BAE47736.1	000000	-	131	CST038	Clostridium phage c-st	GCA_000865225.1
BAE47737.1	000000	-	777	CST039	Clostridium phage c-st	GCA_000865225.1
BAE47739.1	000000	-	90	CST041	Clostridium phage c-st	GCA_000865225.1
BAE47741.1	000000	-	196	CST043	Clostridium phage c-st	GCA_000865225.1
BAE47745.1	000000	-	170	CST047	Clostridium phage c-st	GCA_000865225.1
BAE47748.1	000000	-	70	CST050	Clostridium phage c-st	GCA_000865225.1
BAE47749.1	000000	-	61	CST051	Clostridium phage c-st	GCA_000865225.1
BAE47750.1	000000	-	95	CST052	Clostridium phage c-st	GCA_000865225.1
BAE47752.1	000000	-	77	CST054	Clostridium phage c-st	GCA_000865225.1
BAE47753.1	000000	-	408	CST055	Clostridium phage c-st	GCA_000865225.1
BAE47755.1	000000	-	148	CST057	Clostridium phage c-st	GCA_000865225.1
BAE47761.1	000000	-	74	CST063	Clostridium phage c-st	GCA_000865225.1
BAE47763.1	000000	-	43	CST065	Clostridium phage c-st	GCA_000865225.1
BAE47766.1	000000	-	134	CST068	Clostridium phage c-st	GCA_000865225.1
BAE47768.1	000000	-	126	CST070	Clostridium phage c-st	GCA_000865225.1
BAE47771.1	000000	-	76	CST073	Clostridium phage c-st	GCA_000865225.1
BAE47775.1	000000	-	63	CST077	Clostridium phage c-st	GCA_000865225.1
BAE47777.1	000000	-	59	CST079	Clostridium phage c-st	GCA_000865225.1
BAE47778.1	000000	-	121	CST080	Clostridium phage c-st	GCA_000865225.1
BAE47785.1	000000	-	181	CST087	Clostridium phage c-st	GCA_000865225.1
BAE47788.1	000000	-	171	CST090	Clostridium phage c-st	GCA_000865225.1
BAE47790.1	000000	-	116	CST092	Clostridium phage c-st	GCA_000865225.1
BAE47792.1	000000	-	183	CST094	Clostridium phage c-st	GCA_000865225.1
BAE47794.1	000000	-	80	CST096	Clostridium phage c-st	GCA_000865225.1
BAE47796.1	000000	-	180	CST098	Clostridium phage c-st	GCA_000865225.1
BAE47809.1	000000	-	182	CST111	Clostridium phage c-st	GCA_000865225.1
BAE47812.1	000000	-	421	CST114	Clostridium phage c-st	GCA_000865225.1
BAE47817.1	000000	-	57	CST119	Clostridium phage c-st	GCA_000865225.1
BAE47825.1	000000	-	544	CST127	Clostridium phage c-st	GCA_000865225.1
BAE47832.1	000000	-	124	CST134	Clostridium phage c-st	GCA_000865225.1
BAE47833.1	000000	-	187	CST135	Clostridium phage c-st	GCA_000865225.1
BAE47835.1	000000	-	65	CST137	Clostridium phage c-st	GCA_000865225.1
BAE47836.1	000000	-	100	CST138	Clostridium phage c-st	GCA_000865225.1
BAE47838.1	000000	-	129	CST140	Clostridium phage c-st	GCA_000865225.1
BAE47839.1	000000	-	89	CST141	Clostridium phage c-st	GCA_000865225.1
BAE47842.1	000000	-	132	CST144	Clostridium phage c-st	GCA_000865225.1
BAE47843.1	000000	-	63	CST145	Clostridium phage c-st	GCA_000865225.1
BAE47847.1	000000	-	131	CST149	Clostridium phage c-st	GCA_000865225.1
BAE47850.1	000000	-	266	CST152	Clostridium phage c-st	GCA_000865225.1
BAE47854.1	000000	-	96	CST156	Clostridium phage c-st	GCA_000865225.1
BAE47855.1	000000	-	254	CST157	Clostridium phage c-st	GCA_000865225.1
BAE47856.1	000000	-	279	CST158	Clostridium phage c-st	GCA_000865225.1
BAE47857.1	000000	-	175	CST159	Clostridium phage c-st	GCA_000865225.1
BAE47858.1	000000	-	204	CST160	Clostridium phage c-st	GCA_000865225.1
BAE47859.1	000000	-	397	CST161	Clostridium phage c-st	GCA_000865225.1
BAE47860.1	000000	-	138	CST162	Clostridium phage c-st	GCA_000865225.1
BAE47861.1	000000	-	175	CST163	Clostridium phage c-st	GCA_000865225.1
BAE47862.1	000000	-	350	CST164	Clostridium phage c-st	GCA_000865225.1
BAE47863.1	000000	-	200	CST165	Clostridium phage c-st	GCA_000865225.1
BAE47875.1	000000	-	276	CST177	Clostridium phage c-st	GCA_000865225.1
BAE47876.1	000000	-	354	CST178	Clostridium phage c-st	GCA_000865225.1
BAE47878.1	000000	-	104	CST180	Clostridium phage c-st	GCA_000865225.1
BAE47884.1	000000	-	250	CST186	Clostridium phage c-st	GCA_000865225.1
BAE47895.1	000000	-	103	CST197	Clostridium phage c-st	GCA_000865225.1
AFO71325.1	000000	-	144	CR5_105	Cronobacter phage CR5	GCA_000910235.1
AFO71377.1	000000	-	70	CR5_157	Cronobacter phage CR5	GCA_000910235.1
AIA64804.1	000000	-	72	S13_005	Cronobacter phage S13	GCA_001503575.1
AIA64823.1	000000	-	113	S13_024	Cronobacter phage S13	GCA_001503575.1
AIA64834.1	000000	-	95	S13_035	Cronobacter phage S13	GCA_001503575.1
AIA64844.1	000000	-	81	S13_045	Cronobacter phage S13	GCA_001503575.1
AIA64851.1	000000	-	79	S13_052	Cronobacter phage S13	GCA_001503575.1
AIA64860.1	000000	-	121	S13_061	Cronobacter phage S13	GCA_001503575.1
AIA64862.1	000000	-	71	S13_063	Cronobacter phage S13	GCA_001503575.1
AIA64865.1	000000	-	84	S13_066	Cronobacter phage S13	GCA_001503575.1
AIA64871.1	000000	-	77	S13_072	Cronobacter phage S13	GCA_001503575.1
AIA64904.1	000000	-	107	S13_105	Cronobacter phage S13	GCA_001503575.1
AIA64905.1	000000	-	76	S13_106	Cronobacter phage S13	GCA_001503575.1
AIA64906.1	000000	-	158	S13_107	Cronobacter phage S13	GCA_001503575.1
AIA64907.1	000000	-	61	S13_108	Cronobacter phage S13	GCA_001503575.1
AIA64911.1	000000	-	95	S13_112	Cronobacter phage S13	GCA_001503575.1
AIA64912.1	000000	-	74	S13_113	Cronobacter phage S13	GCA_001503575.1
AIA64914.1	000000	-	81	S13_115	Cronobacter phage S13	GCA_001503575.1
AIA64917.1	000000	-	58	S13_118	Cronobacter phage S13	GCA_001503575.1
AIA64928.1	000000	-	81	S13_129	Cronobacter phage S13	GCA_001503575.1
AIA64929.1	000000	-	217	S13_130	Cronobacter phage S13	GCA_001503575.1
AIA64930.1	000000	-	230	S13_131	Cronobacter phage S13	GCA_001503575.1
AIA64932.1	000000	-	99	S13_133	Cronobacter phage S13	GCA_001503575.1
AIA64933.1	000000	-	84	S13_134	Cronobacter phage S13	GCA_001503575.1
AIA64936.1	000000	-	89	S13_137	Cronobacter phage S13	GCA_001503575.1
AIA64937.1	000000	-	74	S13_138	Cronobacter phage S13	GCA_001503575.1
AIA64940.1	000000	-	74	S13_141	Cronobacter phage S13	GCA_001503575.1
AIA64944.1	000000	-	108	S13_145	Cronobacter phage S13	GCA_001503575.1
AIA64946.1	000000	-	87	S13_147	Cronobacter phage S13	GCA_001503575.1
AIA64949.1	000000	-	89	S13_150	Cronobacter phage S13	GCA_001503575.1
AIA64951.1	000000	-	80	S13_152	Cronobacter phage S13	GCA_001503575.1
AIA64954.1	000000	-	97	S13_155	Cronobacter phage S13	GCA_001503575.1
AIA64971.1	000000	-	51	S13_172	Cronobacter phage S13	GCA_001503575.1
AIA64976.1	000000	-	20	S13_178	Cronobacter phage S13	GCA_001503575.1
AIA64977.1	000000	-	68	S13_179	Cronobacter phage S13	GCA_001503575.1
AIA64978.1	000000	-	84	S13_180	Cronobacter phage S13	GCA_001503575.1
AIA64979.1	000000	-	128	S13_182	Cronobacter phage S13	GCA_001503575.1
AIA64986.1	000000	-	156	S13_189	Cronobacter phage S13	GCA_001503575.1
AIA64991.1	000000	-	250	S13_194	Cronobacter phage S13	GCA_001503575.1
AIA65010.1	000000	-	93	S13_213	Cronobacter phage S13	GCA_001503575.1
AIA65031.1	000000	-	88	S13_234	Cronobacter phage S13	GCA_001503575.1
AIA65060.1	000000	-	76	S13_263	Cronobacter phage S13	GCA_001503575.1
AIA65063.1	000000	-	71	S13_266	Cronobacter phage S13	GCA_001503575.1
AFC21450.1	000000	-	45	GAP32_003	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21451.1	000000	-	57	GAP32_004	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21460.1	000000	-	118	GAP32_013	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21463.1	000000	-	69	GAP32_016	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21472.1	000000	-	66	GAP32_024	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21494.1	000000	-	97	GAP32_047	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21520.1	000000	-	49	GAP32_072	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21521.1	000000	-	49	GAP32_073	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21587.1	000000	-	96	GAP32_137	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFC21818.1	000000	-	43	GAP32_367A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21833.1	000000	-	42	GAP32_381	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21835.1	000000	-	117	GAP32_383	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21838.1	000000	-	89	GAP32_386	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21866.1	000000	-	64	GAP32_413	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21867.1	000000	-	150	GAP32_414	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21892.1	000000	-	44	GAP32_438	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21894.1	000000	-	52	GAP32_439A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21899.1	000000	-	72	GAP32_444	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21904.1	000000	-	136	GAP32_449	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21906.1	000000	-	66	GAP32_450	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21909.1	000000	-	150	GAP32_453	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21946.1	000000	-	55	GAP32_487A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21963.1	000000	-	37	GAP32_503A	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21973.1	000000	-	58	GAP32_513	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AFC21977.1	000000	-	152	GAP32_517	Cronobacter phage vB_CsaM_GAP32	GCA_000898015.1
AON97022.1	000000	-	50	E_013	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97023.1	000000	-	70	E_014	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97038.1	000000	-	73	E_029	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97060.1	000000	-	44	E_051	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97083.1	000000	-	59	E_074	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97095.1	000000	-	66	E_087	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97099.1	000000	-	82	E_091	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97132.1	000000	-	77	E_124	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97171.1	000000	-	76	E_163	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97181.1	000000	-	82	E_173	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97236.1	000000	-	45	E_228	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97249.1	000000	-	121	E_241	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97273.1	000000	-	53	E_265	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AON97288.1	000000	-	75	E_280	Cronobacter phage vB_CsaM_leE	GCA_002611805.1
AGH56815.1	000000	-	82	CPXG_00012	Cyanophage P-RSM6	GCA_000906155.1
AGH56817.1	000000	-	78	CPXG_00014	Cyanophage P-RSM6	GCA_000906155.1
AGH56826.1	000000	-	55	CPXG_00023	Cyanophage P-RSM6	GCA_000906155.1
AGH56840.1	000000	-	61	CPXG_00037	Cyanophage P-RSM6	GCA_000906155.1
AGH56842.1	000000	-	83	CPXG_00039	Cyanophage P-RSM6	GCA_000906155.1
AGH56847.1	000000	-	57	CPXG_00044	Cyanophage P-RSM6	GCA_000906155.1
AGH56856.1	000000	-	80	CPXG_00053	Cyanophage P-RSM6	GCA_000906155.1
AGH56857.1	000000	-	103	CPXG_00054	Cyanophage P-RSM6	GCA_000906155.1
AGH56880.1	000000	-	55	CPXG_00077	Cyanophage P-RSM6	GCA_000906155.1
AGH56892.1	000000	-	76	CPXG_00089	Cyanophage P-RSM6	GCA_000906155.1
AGH56940.1	000000	-	53	CPXG_00137	Cyanophage P-RSM6	GCA_000906155.1
AGH56948.1	000000	-	52	CPXG_00145	Cyanophage P-RSM6	GCA_000906155.1
AGH56950.1	000000	-	56	CPXG_00147	Cyanophage P-RSM6	GCA_000906155.1
AGH56953.1	000000	-	50	CPXG_00150	Cyanophage P-RSM6	GCA_000906155.1
AGH56954.1	000000	-	64	CPXG_00151	Cyanophage P-RSM6	GCA_000906155.1
AGH56955.1	000000	-	59	CPXG_00152	Cyanophage P-RSM6	GCA_000906155.1
AGH56958.1	000000	-	50	CPXG_00155	Cyanophage P-RSM6	GCA_000906155.1
AGH56960.1	000000	-	69	CPXG_00157	Cyanophage P-RSM6	GCA_000906155.1
AGH56961.1	000000	-	56	CPXG_00158	Cyanophage P-RSM6	GCA_000906155.1
AGH56963.1	000000	-	57	CPXG_00160	Cyanophage P-RSM6	GCA_000906155.1
AGH56964.1	000000	-	66	CPXG_00161	Cyanophage P-RSM6	GCA_000906155.1
AGH56965.1	000000	-	55	CPXG_00162	Cyanophage P-RSM6	GCA_000906155.1
AGH56966.1	000000	-	88	CPXG_00163	Cyanophage P-RSM6	GCA_000906155.1
AGH56967.1	000000	-	62	CPXG_00164	Cyanophage P-RSM6	GCA_000906155.1
AGH56970.1	000000	-	71	CPXG_00167	Cyanophage P-RSM6	GCA_000906155.1
AGH56975.1	000000	-	58	CPXG_00172	Cyanophage P-RSM6	GCA_000906155.1
AGH56979.1	000000	-	58	CPXG_00176	Cyanophage P-RSM6	GCA_000906155.1
AGH56985.1	000000	-	187	CPXG_00182	Cyanophage P-RSM6	GCA_000906155.1
AGH57001.1	000000	-	65	CPXG_00198	Cyanophage P-RSM6	GCA_000906155.1
AJK27438.1	000000	-	77	PTIM40_11	Cyanophage P-TIM40	GCA_001470935.1
AJK27546.1	000000	-	46	PTIM40_119	Cyanophage P-TIM40	GCA_001470935.1
AJK27565.1	000000	-	50	PTIM40_138	Cyanophage P-TIM40	GCA_001470935.1
AJK27594.1	000000	-	35	PTIM40_167	Cyanophage P-TIM40	GCA_001470935.1
AJK27598.1	000000	-	23	PTIM40_171	Cyanophage P-TIM40	GCA_001470935.1
AJK27599.1	000000	-	53	PTIM40_172	Cyanophage P-TIM40	GCA_001470935.1
AJK27606.1	000000	-	140	PTIM40_185	Cyanophage P-TIM40	GCA_001470935.1
AJK27614.1	000000	-	58	PTIM40_200	Cyanophage P-TIM40	GCA_001470935.1
AJK27616.1	000000	-	42	PTIM40_202	Cyanophage P-TIM40	GCA_001470935.1
AJK27626.1	000000	-	56	PTIM40_219	Cyanophage P-TIM40	GCA_001470935.1
AJK27627.1	000000	-	91	PTIM40_220	Cyanophage P-TIM40	GCA_001470935.1
AJK27629.1	000000	-	39	PTIM40_223	Cyanophage P-TIM40	GCA_001470935.1
AJK27468.1	000000	-	111	PTIM40_41	Cyanophage P-TIM40	GCA_001470935.1
AJK27476.1	000000	-	122	PTIM40_49	Cyanophage P-TIM40	GCA_001470935.1
AJK27482.1	000000	-	64	PTIM40_55	Cyanophage P-TIM40	GCA_001470935.1
AJK27486.1	000000	-	206	PTIM40_59	Cyanophage P-TIM40	GCA_001470935.1
AJK27487.1	000000	-	72	PTIM40_61	Cyanophage P-TIM40	GCA_001470935.1
AJK27492.1	000000	-	72	PTIM40_65	Cyanophage P-TIM40	GCA_001470935.1
AJK27494.1	000000	-	77	PTIM40_67	Cyanophage P-TIM40	GCA_001470935.1
AJK27495.1	000000	-	106	PTIM40_68	Cyanophage P-TIM40	GCA_001470935.1
AJK27498.1	000000	-	90	PTIM40_71	Cyanophage P-TIM40	GCA_001470935.1
AJK27500.1	000000	-	70	PTIM40_73	Cyanophage P-TIM40	GCA_001470935.1
AJK27502.1	000000	-	38	PTIM40_75	Cyanophage P-TIM40	GCA_001470935.1
AJK27506.1	000000	-	66	PTIM40_79	Cyanophage P-TIM40	GCA_001470935.1
AJK27435.1	000000	-	48	PTIM40_8	Cyanophage P-TIM40	GCA_001470935.1
AJK27509.1	000000	-	50	PTIM40_82	Cyanophage P-TIM40	GCA_001470935.1
AJK27511.1	000000	-	52	PTIM40_84	Cyanophage P-TIM40	GCA_001470935.1
AJK27523.1	000000	-	45	PTIM40_96	Cyanophage P-TIM40	GCA_001470935.1
AMO43017.1	000000	-	41	R1080702_002	Cyanophage S-RIM32	GCA_001754165.1
AMO43032.1	000000	-	52	R1080702_017	Cyanophage S-RIM32	GCA_001754165.1
AMO43037.1	000000	-	88	R1080702_023	Cyanophage S-RIM32	GCA_001754165.1
AMO43064.1	000000	-	191	R1080702_055	Cyanophage S-RIM32	GCA_001754165.1
AMO43065.1	000000	-	73	R1080702_056	Cyanophage S-RIM32	GCA_001754165.1
AMO43066.1	000000	-	60	R1080702_057	Cyanophage S-RIM32	GCA_001754165.1
AMO43067.1	000000	-	92	R1080702_058	Cyanophage S-RIM32	GCA_001754165.1
AMO43068.1	000000	-	45	R1080702_059	Cyanophage S-RIM32	GCA_001754165.1
AMO43070.1	000000	-	70	R1080702_061	Cyanophage S-RIM32	GCA_001754165.1
AMO43078.1	000000	-	38	R1080702_069	Cyanophage S-RIM32	GCA_001754165.1
AMO43079.1	000000	-	37	R1080702_070	Cyanophage S-RIM32	GCA_001754165.1
AMO43080.1	000000	-	80	R1080702_071	Cyanophage S-RIM32	GCA_001754165.1
AMO43082.1	000000	-	51	R1080702_073	Cyanophage S-RIM32	GCA_001754165.1
AMO43087.1	000000	-	76	R1080702_078	Cyanophage S-RIM32	GCA_001754165.1
AMO43091.1	000000	-	55	R1080702_082	Cyanophage S-RIM32	GCA_001754165.1
AMO43094.1	000000	-	37	R1080702_085	Cyanophage S-RIM32	GCA_001754165.1
AMO43096.1	000000	-	39	R1080702_087	Cyanophage S-RIM32	GCA_001754165.1
AMO43098.1	000000	-	48	R1080702_089	Cyanophage S-RIM32	GCA_001754165.1
AMO43121.1	000000	-	40	R1080702_112	Cyanophage S-RIM32	GCA_001754165.1
AMO43131.1	000000	-	50	R1080702_122	Cyanophage S-RIM32	GCA_001754165.1
AMO43143.1	000000	-	45	R1080702_134	Cyanophage S-RIM32	GCA_001754165.1
AMO43207.1	000000	-	96	R1080702_200	Cyanophage S-RIM32	GCA_001754165.1
AMO43235.1	000000	-	48	R1080702_230	Cyanophage S-RIM32	GCA_001754165.1
AMO43236.1	000000	-	41	R1080702_231	Cyanophage S-RIM32	GCA_001754165.1
AMO43238.1	000000	-	40	R1080702_233	Cyanophage S-RIM32	GCA_001754165.1
AGH07452.1	000000	-	83	CYVG_00008	Cyanophage S-SSM6a	GCA_002710385.1
AGH07470.1	000000	-	50	CYVG_00026	Cyanophage S-SSM6a	GCA_002710385.1
AGH07474.1	000000	-	80	CYVG_00030	Cyanophage S-SSM6a	GCA_002710385.1
AGH07478.1	000000	-	104	CYVG_00034	Cyanophage S-SSM6a	GCA_002710385.1
AGH07485.1	000000	-	78	CYVG_00041	Cyanophage S-SSM6a	GCA_002710385.1
AGH07498.1	000000	-	54	CYVG_00054	Cyanophage S-SSM6a	GCA_002710385.1
AGH07508.1	000000	-	383	CYVG_00064	Cyanophage S-SSM6a	GCA_002710385.1
AGH07509.1	000000	-	173	CYVG_00065	Cyanophage S-SSM6a	GCA_002710385.1
AGH07511.1	000000	-	83	CYVG_00067	Cyanophage S-SSM6a	GCA_002710385.1
AGH07525.1	000000	-	57	CYVG_00081	Cyanophage S-SSM6a	GCA_002710385.1
AGH07531.1	000000	-	102	CYVG_00087	Cyanophage S-SSM6a	GCA_002710385.1
AGH07542.1	000000	-	200	CYVG_00098	Cyanophage S-SSM6a	GCA_002710385.1
AGH07552.1	000000	-	55	CYVG_00108	Cyanophage S-SSM6a	GCA_002710385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGH07560.1	000000	-	80	CYVG_00116	Cyanophage S-SSM6a	GCA_002710385.1
AGH07563.1	000000	-	68	CYVG_00119	Cyanophage S-SSM6a	GCA_002710385.1
AGH07569.1	000000	-	270	CYVG_00125	Cyanophage S-SSM6a	GCA_002710385.1
AGH07576.1	000000	-	168	CYVG_00132	Cyanophage S-SSM6a	GCA_002710385.1
AGH07586.1	000000	-	148	CYVG_00142	Cyanophage S-SSM6a	GCA_002710385.1
AGH07587.1	000000	-	49	CYVG_00143	Cyanophage S-SSM6a	GCA_002710385.1
AGH07594.1	000000	-	90	CYVG_00150	Cyanophage S-SSM6a	GCA_002710385.1
AGH07600.1	000000	-	64	CYVG_00156	Cyanophage S-SSM6a	GCA_002710385.1
AGH07601.1	000000	-	49	CYVG_00157	Cyanophage S-SSM6a	GCA_002710385.1
AGH07606.1	000000	-	79	CYVG_00162	Cyanophage S-SSM6a	GCA_002710385.1
AGH07613.1	000000	-	131	CYVG_00170	Cyanophage S-SSM6a	GCA_002710385.1
AGH07615.1	000000	-	53	CYVG_00172	Cyanophage S-SSM6a	GCA_002710385.1
AGH07622.1	000000	-	49	CYVG_00179	Cyanophage S-SSM6a	GCA_002710385.1
AGH07643.1	000000	-	191	CYVG_00200	Cyanophage S-SSM6a	GCA_002710385.1
AGH07649.1	000000	-	100	CYVG_00206	Cyanophage S-SSM6a	GCA_002710385.1
AGH07651.1	000000	-	53	CYVG_00208	Cyanophage S-SSM6a	GCA_002710385.1
AGH07652.1	000000	-	62	CYVG_00209	Cyanophage S-SSM6a	GCA_002710385.1
AGH07653.1	000000	-	233	CYVG_00210	Cyanophage S-SSM6a	GCA_002710385.1
AGH07655.1	000000	-	71	CYVG_00212	Cyanophage S-SSM6a	GCA_002710385.1
AGH07656.1	000000	-	255	CYVG_00213	Cyanophage S-SSM6a	GCA_002710385.1
AGH07658.1	000000	-	309	CYVG_00215	Cyanophage S-SSM6a	GCA_002710385.1
AGH07660.1	000000	-	54	CYVG_00217	Cyanophage S-SSM6a	GCA_002710385.1
AGH07668.1	000000	-	72	CYVG_00225	Cyanophage S-SSM6a	GCA_002710385.1
AGH07670.1	000000	-	82	CYVG_00227	Cyanophage S-SSM6a	GCA_002710385.1
AGH07672.1	000000	-	63	CYVG_00229	Cyanophage S-SSM6a	GCA_002710385.1
AGH07674.1	000000	-	60	CYVG_00231	Cyanophage S-SSM6a	GCA_002710385.1
AGH07675.1	000000	-	65	CYVG_00232	Cyanophage S-SSM6a	GCA_002710385.1
AGH07679.1	000000	-	57	CYVG_00236	Cyanophage S-SSM6a	GCA_002710385.1
AGH07680.1	000000	-	67	CYVG_00237	Cyanophage S-SSM6a	GCA_002710385.1
AGH07682.1	000000	-	77	CYVG_00239	Cyanophage S-SSM6a	GCA_002710385.1
AGH07686.1	000000	-	57	CYVG_00243	Cyanophage S-SSM6a	GCA_002710385.1
AGH07687.1	000000	-	63	CYVG_00244	Cyanophage S-SSM6a	GCA_002710385.1
AGH07688.1	000000	-	57	CYVG_00245	Cyanophage S-SSM6a	GCA_002710385.1
AGH07689.1	000000	-	90	CYVG_00246	Cyanophage S-SSM6a	GCA_002710385.1
AGH07690.1	000000	-	54	CYVG_00247	Cyanophage S-SSM6a	GCA_002710385.1
AGH07691.1	000000	-	71	CYVG_00248	Cyanophage S-SSM6a	GCA_002710385.1
AGH07693.1	000000	-	86	CYVG_00250	Cyanophage S-SSM6a	GCA_002710385.1
AGH07695.1	000000	-	83	CYVG_00252	Cyanophage S-SSM6a	GCA_002710385.1
AGH07697.1	000000	-	113	CYVG_00254	Cyanophage S-SSM6a	GCA_002710385.1
AGH07699.1	000000	-	54	CYVG_00256	Cyanophage S-SSM6a	GCA_002710385.1
AGH07700.1	000000	-	53	CYVG_00257	Cyanophage S-SSM6a	GCA_002710385.1
AGH07701.1	000000	-	82	CYVG_00258	Cyanophage S-SSM6a	GCA_002710385.1
AGH07704.1	000000	-	70	CYVG_00261	Cyanophage S-SSM6a	GCA_002710385.1
AGH07705.1	000000	-	61	CYVG_00262	Cyanophage S-SSM6a	GCA_002710385.1
AGH07709.1	000000	-	168	CYVG_00266	Cyanophage S-SSM6a	GCA_002710385.1
AGH07710.1	000000	-	55	CYVG_00267	Cyanophage S-SSM6a	GCA_002710385.1
AGH07711.1	000000	-	55	CYVG_00268	Cyanophage S-SSM6a	GCA_002710385.1
AGH07714.1	000000	-	50	CYVG_00271	Cyanophage S-SSM6a	GCA_002710385.1
AGH07725.1	000000	-	224	CYVG_00282	Cyanophage S-SSM6a	GCA_002710385.1
AGH07726.1	000000	-	335	CYVG_00283	Cyanophage S-SSM6a	GCA_002710385.1
AGH07727.1	000000	-	1552	CYVG_00284	Cyanophage S-SSM6a	GCA_002710385.1
AGH07730.1	000000	-	1477	CYVG_00287	Cyanophage S-SSM6a	GCA_002710385.1
AGH07744.1	000000	-	51	CYVG_00301	Cyanophage S-SSM6a	GCA_002710385.1
AGH07748.1	000000	-	26	CYVG_00305	Cyanophage S-SSM6a	GCA_002710385.1
AGG54305.1	000000	-	111	CYWG_00021	Cyanophage S-SSM6b	GCA_002710425.1
AGG54310.1	000000	-	46	CYWG_00026	Cyanophage S-SSM6b	GCA_002710425.1
AGG54311.1	000000	-	66	CYWG_00027	Cyanophage S-SSM6b	GCA_002710425.1
AGG54317.1	000000	-	60	CYWG_00033	Cyanophage S-SSM6b	GCA_002710425.1
AGG54321.1	000000	-	96	CYWG_00037	Cyanophage S-SSM6b	GCA_002710425.1
AGG54322.1	000000	-	57	CYWG_00038	Cyanophage S-SSM6b	GCA_002710425.1
AGG54328.1	000000	-	74	CYWG_00044	Cyanophage S-SSM6b	GCA_002710425.1
AGG54329.1	000000	-	52	CYWG_00045	Cyanophage S-SSM6b	GCA_002710425.1
AGG54330.1	000000	-	84	CYWG_00046	Cyanophage S-SSM6b	GCA_002710425.1
AGG54332.1	000000	-	94	CYWG_00048	Cyanophage S-SSM6b	GCA_002710425.1
AGG54338.1	000000	-	66	CYWG_00054	Cyanophage S-SSM6b	GCA_002710425.1
AGG54339.1	000000	-	50	CYWG_00055	Cyanophage S-SSM6b	GCA_002710425.1
AGG54340.1	000000	-	58	CYWG_00056	Cyanophage S-SSM6b	GCA_002710425.1
AGG54351.1	000000	-	199	CYWG_00067	Cyanophage S-SSM6b	GCA_002710425.1
AGG54352.1	000000	-	150	CYWG_00068	Cyanophage S-SSM6b	GCA_002710425.1
AGG54353.1	000000	-	77	CYWG_00069	Cyanophage S-SSM6b	GCA_002710425.1
AGG54375.1	000000	-	84	CYWG_00091	Cyanophage S-SSM6b	GCA_002710425.1
AGG54386.1	000000	-	96	CYWG_00102	Cyanophage S-SSM6b	GCA_002710425.1
AGG54387.1	000000	-	1101	CYWG_00103	Cyanophage S-SSM6b	GCA_002710425.1
AGG54391.1	000000	-	141	CYWG_00107	Cyanophage S-SSM6b	GCA_002710425.1
AGG54395.1	000000	-	62	CYWG_00111	Cyanophage S-SSM6b	GCA_002710425.1
AGG54401.1	000000	-	99	CYWG_00117	Cyanophage S-SSM6b	GCA_002710425.1
AGG54409.1	000000	-	54	CYWG_00125	Cyanophage S-SSM6b	GCA_002710425.1
AGG54415.1	000000	-	63	CYWG_00131	Cyanophage S-SSM6b	GCA_002710425.1
AGG54420.1	000000	-	58	CYWG_00136	Cyanophage S-SSM6b	GCA_002710425.1
AGG54439.1	000000	-	62	CYWG_00155	Cyanophage S-SSM6b	GCA_002710425.1
AGG54474.1	000000	-	43	CYWG_00190	Cyanophage S-SSM6b	GCA_002710425.1
AGG54478.1	000000	-	66	CYWG_00194	Cyanophage S-SSM6b	GCA_002710425.1
AXG67072.1	000000	-	103	AD1_028	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67156.1	000000	-	41	AD1_112	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67206.1	000000	-	120	AD1_162	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67230.1	000000	-	251	AD1_186	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67266.1	000000	-	59	AD1_222	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67352.1	000000	-	71	AD1_308	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AXG67355.1	000000	-	50	AD1_311	Dickeya phage vB_DsoM_AD1	GCA_003568515.1
AYD80117.1	000000	-	31	JA11_312	Dickeya phage vB_DsoM_JA11	GCA_003613635.1
AXG66790.1	000000	-	76	JA29_064	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG66994.1	000000	-	136	JA29_268	Dickeya phage vB_DsoM_JA29	GCA_003568475.1
AXG67576.1	000000	-	58	JA33_202	Dickeya phage vB_DsoM_JA33	GCA_003568495.1
QBZ70585.1	000000	-	40	pETSU_004	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70601.1	000000	-	159	pETSU_020	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70603.1	000000	-	213	pETSU_022	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70648.1	000000	-	125	pETSU_067	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70649.1	000000	-	111	pETSU_068	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70650.1	000000	-	124	pETSU_069	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70672.1	000000	-	105	pETSU_091	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70675.1	000000	-	195	pETSU_094	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70681.1	000000	-	218	pETSU_100	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70683.1	000000	-	222	pETSU_102	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70686.1	000000	-	79	pETSU_105	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70692.1	000000	-	154	pETSU_111	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70693.1	000000	-	246	pETSU_112	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70694.1	000000	-	140	pETSU_113	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70697.1	000000	-	94	pETSU_116	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70698.1	000000	-	352	pETSU_117	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70699.1	000000	-	68	pETSU_118	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70702.1	000000	-	176	pETSU_121	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70708.1	000000	-	108	pETSU_127	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70710.1	000000	-	126	pETSU_129	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70713.1	000000	-	3124	pETSU_132	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70715.1	000000	-	1488	pETSU_134	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70724.1	000000	-	97	pETSU_143	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70726.1	000000	-	116	pETSU_145	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70729.1	000000	-	147	pETSU_148	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70732.1	000000	-	139	pETSU_151	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70733.1	000000	-	124	pETSU_152	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70738.1	000000	-	122	pETSU_157	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70741.1	000000	-	90	pETSU_160	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70748.1	000000	-	63	pETSU_167	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70765.1	000000	-	66	pETSU_184	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70788.1	000000	-	326	pETSU_207	Edwardsiella virus pEt-SU	GCA_004800915.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBZ70791.1	000000	-	111	pETSU_210	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70793.1	000000	-	421	pETSU_212	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70797.1	000000	-	117	pETSU_215	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70800.1	000000	-	131	pETSU_219	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70820.1	000000	-	169	pETSU_238	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70829.1	000000	-	183	pETSU_248	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70833.1	000000	-	55	pETSU_252	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70834.1	000000	-	205	pETSU_253	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70836.1	000000	-	109	pETSU_255	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70837.1	000000	-	142	pETSU_256	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70839.1	000000	-	94	pETSU_258	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70840.1	000000	-	120	pETSU_259	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70842.1	000000	-	201	pETSU_261	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70844.1	000000	-	269	pETSU_263	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70848.1	000000	-	235	pETSU_267	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70849.1	000000	-	93	pETSU_268	Edwardsiella virus pEt-SU	GCA_004800915.1
QBZ70855.1	000000	-	152	pETSU_274	Edwardsiella virus pEt-SU	GCA_004800915.1
AMR59658.1	000000	-	41	SEGD1_007	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59673.1	000000	-	238	SEGD1_022	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59682.1	000000	-	105	SEGD1_033	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59732.1	000000	-	177	SEGD1_083	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59736.1	000000	-	62	SEGD1_087	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59850.1	000000	-	49	SEGD1_203	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59851.1	000000	-	40	SEGD1_204	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59872.1	000000	-	38	SEGD1_225	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59890.1	000000	-	112	SEGD1_243	Enterobacteria phage SEGD1	GCA_002601865.1
AMR59918.1	000000	-	42	SEGD1_271	Enterobacteria phage SEGD1	GCA_002601865.1
QBP07588.1	000000	-	132	DERBICUS_162	Erwinia phage Derbicus	GCA_004521655.1
AHI60265.1	000000	-	43	Ea357_114	Erwinia phage Ea35-70	GCA_000914635.1
AGX01732.1	000000	-	110	CF95_gp010	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01723.1	000000	-	81	CF95_gp001	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01840.1	000000	-	114	CF95_gp118	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01842.1	000000	-	140	CF95_gp120	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01844.1	000000	-	264	CF95_gp122	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01885.1	000000	-	107	CF95_gp162	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01872.1	000000	-	129	CF95_gp150	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01850.1	000000	-	149	CF95_gp128	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01873.1	000000	-	150	CF95_gp151	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01847.1	000000	-	150	CF95_gp125	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01874.1	000000	-	158	CF95_gp152	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01880.1	000000	-	168	CF95_gp158	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01892.1	000000	-	176	CF95_gp170	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01855.1	000000	-	180	CF95_gp133	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01856.1	000000	-	198	CF95_gp134	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01883.1	000000	-	208	CF95_gp160	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01863.1	000000	-	249	CF95_gp141	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01871.1	000000	-	255	CF95_gp149	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01882.1	000000	-	288	CF95_gp159	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01884.1	000000	-	55	CF95_gp161	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01852.1	000000	-	66	CF95_gp130	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01876.1	000000	-	79	CF95_gp154	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01875.1	000000	-	84	CF95_gp153	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01846.1	000000	-	88	-	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01877.1	000000	-	90	CF95_gp155	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01733.1	000000	-	99	CF95_gp011	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01833.1	000000	-	103	CF95_gp111	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01832.1	000000	-	152	CF95_gp110	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01830.1	000000	-	35	CF95_gp108	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01908.1	000000	-	100	CF95_gp186	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01905.1	000000	-	117	CF95_gp183	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01907.1	000000	-	169	CF95_gp185	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01904.1	000000	-	223	CF95_gp182	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01755.1	000000	-	104	CF95_gp033	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01769.1	000000	-	111	CF95_gp047	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01759.1	000000	-	114	CF95_gp037	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01815.1	000000	-	118	CF95_gp093	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01771.1	000000	-	122	CF95_gp049	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01752.1	000000	-	123	CF95_gp030	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01748.1	000000	-	127	CF95_gp026	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01749.1	000000	-	132	CF95_gp027	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01788.1	000000	-	133	CF95_gp066	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01789.1	000000	-	135	CF95_gp067	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01780.1	000000	-	138	CF95_gp058	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01751.1	000000	-	138	CF95_gp029	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01818.1	000000	-	140	CF95_gp096	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01750.1	000000	-	142	CF95_gp028	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01816.1	000000	-	144	CF95_gp094	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01754.1	000000	-	151	CF95_gp032	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01828.1	000000	-	163	CF95_gp106	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01778.1	000000	-	203	CF95_gp056	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01768.1	000000	-	214	CF95_gp046	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01784.1	000000	-	215	CF95_gp062	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01792.1	000000	-	224	CF95_gp070	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01787.1	000000	-	229	CF95_gp065	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01827.1	000000	-	246	CF95_gp105	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01814.1	000000	-	291	CF95_gp092	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01785.1	000000	-	343	CF95_gp063	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01791.1	000000	-	345	CF95_gp069	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01817.1	000000	-	37	CF95_gp095	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01820.1	000000	-	56	CF95_gp098	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01824.1	000000	-	69	CF95_gp102	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01779.1	000000	-	73	CF95_gp057	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01823.1	000000	-	76	CF95_gp101	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01812.1	000000	-	81	CF95_gp090	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01783.1	000000	-	99	CF95_gp061	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01932.1	000000	-	217	CF95_gp210	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01955.1	000000	-	344	CF95_gp233	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01945.1	000000	-	517	CF95_gp223	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01934.1	000000	-	720	CF95_gp212	Erwinia phage PhiEaH1	GCA_000914555.1
AGX01913.1	000000	-	893	CF95_gp191	Erwinia phage PhiEaH1	GCA_000914555.1
AXF51367.1	000000	-	158	WELLINGTON_241	Erwinia phage Wellington	GCA_003344985.1
AXF51384.1	000000	-	131	WELLINGTON_258	Erwinia phage Wellington	GCA_003344985.1
AXF51403.1	000000	-	119	WELLINGTON_277	Erwinia phage Wellington	GCA_003344985.1
AXF51428.1	000000	-	111	WELLINGTON_290	Erwinia phage Wellington	GCA_003344985.1
AFQ96729.1	000000	-	42	G173_gp184	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96633.1	000000	-	44	G173_gp088	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96762.1	000000	-	47	G173_gp217	Erwinia phage phiEaH2	GCA_000902915.1
AFQ96805.1	000000	-	37	G173_gp260	Erwinia phage phiEaH2	GCA_000902915.1
AWY08617.1	000000	-	120	Alexandra_167	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08606.1	000000	-	289	Alexandra_192	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08460.1	000000	-	288	Alexandra_194	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08607.1	000000	-	283	Alexandra_196	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08486.1	000000	-	165	Alexandra_223	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08513.1	000000	-	122	Alexandra_256	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08529.1	000000	-	95	Alexandra_272	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08540.1	000000	-	133	Alexandra_284	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08547.1	000000	-	109	Alexandra_291	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08549.1	000000	-	136	Alexandra_293	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08587.1	000000	-	41	Alexandra_338	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08335.1	000000	-	61	Alexandra_55	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
AWY08626.1	000000	-	35	Alexandra_69	Erwinia phage vB_EamM_Alexandra	GCA_003308555.1
ANZ48132.1	000000	-	139	ASESINO_119	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48164.1	000000	-	129	ASESINO_151	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48188.1	000000	-	22	ASESINO_175	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48027.1	000000	-	39	ASESINO_2	Erwinia phage vB_EamM_Asesino	GCA_001744335.2

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ANZ48033.1	000000	-	53	ASESINO_20	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48224.1	000000	-	37	ASESINO_211	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48302.1	000000	-	57	ASESINO_289	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48032.1	000000	-	61	ASESINO_9	Erwinia phage vB_EamM_Asesino	GCA_001744335.2
ANZ48402.1	000000	-	244	CAITLIN_107	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48404.1	000000	-	244	CAITLIN_109	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48406.1	000000	-	100	CAITLIN_111	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48431.1	000000	-	120	CAITLIN_136	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48439.1	000000	-	165	CAITLIN_144	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48441.1	000000	-	224	CAITLIN_146	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48471.1	000000	-	72	CAITLIN_176	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48500.1	000000	-	60	CAITLIN_205	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48502.1	000000	-	35	CAITLIN_207	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48521.1	000000	-	167	CAITLIN_226	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48556.1	000000	-	53	CAITLIN_261	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48572.1	000000	-	213	CAITLIN_277	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48573.1	000000	-	180	CAITLIN_278	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48363.1	000000	-	96	CAITLIN_68	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48372.1	000000	-	94	CAITLIN_77	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48382.1	000000	-	88	CAITLIN_87	Erwinia phage vB_EamM_Caitlin	GCA_001744955.1
ANZ48675.1	000000	-	122	CHRISDB_113	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48678.1	000000	-	69	CHRISDB_116	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48690.1	000000	-	110	CHRISDB_128	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48706.1	000000	-	118	CHRISDB_144	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48708.1	000000	-	113	CHRISDB_146	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48779.1	000000	-	101	CHRISDB_217	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48814.1	000000	-	80	CHRISDB_252	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48818.1	000000	-	69	CHRISDB_256	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48837.1	000000	-	93	CHRISDB_275	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48849.1	000000	-	72	CHRISDB_287	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48636.1	000000	-	148	CHRISDB_74	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48579.1	000000	-	53	CHRISDB_8	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48642.1	000000	-	61	CHRISDB_80	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48645.1	000000	-	76	CHRISDB_83	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ48580.1	000000	-	69	CHRISDB_9	Erwinia phage vB_EamM_ChrisDB	GCA_001743655.1
ANZ49028.1	000000	-	27	EARLPHILLIPIV_179	Erwinia phage vB_EamM_EarlPhillipIV	GCA_001744975.1
ANZ49099.1	000000	-	40	HUXLEY_10	Erwinia phage vB_EamM_Huxley	GCA_001745635.1
ASU03788.1	000000	-	162	JOAD_127	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ASU03730.1	000000	-	96	JOAD_185	Erwinia phage vB_EamM_Joad	GCA_002629065.1
ANZ49482.1	000000	-	259	KWAN_130	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49591.1	000000	-	164	KWAN_239	Erwinia phage vB_EamM_Kwan	GCA_001744315.1
ANZ49922.1	000000	-	50	PARSHIK_4	Erwinia phage vB_EamM_Parshik	GCA_002758055.1
ANZ50347.1	000000	-	196	PHOBOS_157	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50366.1	000000	-	319	PHOBOS_176	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50210.1	000000	-	151	PHOBOS_20	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50436.1	000000	-	68	PHOBOS_246	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50236.1	000000	-	62	PHOBOS_46	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ANZ50251.1	000000	-	169	PHOBOS_61	Erwinia phage vB_EamM_Phobos	GCA_001743635.1
ASB43075.1	000000	-	38	SIMMY50_207	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANH51470.1	000000	-	56	SIMMY50_8	Erwinia phage vB_EamM_Simmy50	GCA_002624365.1
ANZ50573.1	000000	-	135	STRATTON_148	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50444.1	000000	-	113	STRATTON_19	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50637.1	000000	-	89	STRATTON_212	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50643.1	000000	-	100	STRATTON_218	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50712.1	000000	-	61	STRATTON_287	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50713.1	000000	-	96	STRATTON_288	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ANZ50507.1	000000	-	71	STRATTON_82	Erwinia phage vB_EamM_Stratton	GCA_002600675.1
ARW58649.1	000000	-	40	Y3_009	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58659.1	000000	-	49	Y3_019	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58668.1	000000	-	139	Y3_028	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58676.1	000000	-	225	Y3_036	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58679.1	000000	-	153	Y3_039	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58693.1	000000	-	40	Y3_053	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58804.1	000000	-	96	Y3_164	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58806.1	000000	-	171	Y3_166	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58807.1	000000	-	94	Y3_167	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58829.1	000000	-	280	Y3_189	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58830.1	000000	-	311	Y3_190	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58840.1	000000	-	82	Y3_200	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58847.1	000000	-	45	Y3_207	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58875.1	000000	-	111	Y3_235	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58884.1	000000	-	125	Y3_244	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58890.1	000000	-	186	Y3_250	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58891.1	000000	-	212	Y3_251	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58893.1	000000	-	218	Y3_253	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58896.1	000000	-	113	Y3_256	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58908.1	000000	-	66	Y3_268	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58924.1	000000	-	238	Y3_284	Erwinia phage vB_EamM_Y3	GCA_002955045.1
ARW58968.1	000000	-	100	Y3_328	Erwinia phage vB_EamM_Y3	GCA_002955045.1
AQT28593.1	000000	-	136	YOLOSWAG_111	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28600.1	000000	-	217	YOLOSWAG_119	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28601.1	000000	-	231	YOLOSWAG_120	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28604.1	000000	-	83	YOLOSWAG_123	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28642.1	000000	-	146	YOLOSWAG_162	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28505.1	000000	-	44	YOLOSWAG_18	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28663.1	000000	-	294	YOLOSWAG_184	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28664.1	000000	-	293	YOLOSWAG_185	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28671.1	000000	-	101	YOLOSWAG_192	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28672.1	000000	-	100	YOLOSWAG_193	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28674.1	000000	-	62	YOLOSWAG_195	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28818.1	000000	-	62	YOLOSWAG_199	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28681.1	000000	-	54	YOLOSWAG_203	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28683.1	000000	-	125	YOLOSWAG_205	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28687.1	000000	-	176	YOLOSWAG_209	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28688.1	000000	-	48	YOLOSWAG_210	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28695.1	000000	-	99	YOLOSWAG_217	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28509.1	000000	-	83	YOLOSWAG_22	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28706.1	000000	-	125	YOLOSWAG_228	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28716.1	000000	-	243	YOLOSWAG_239	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28718.1	000000	-	219	YOLOSWAG_242	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28808.1	000000	-	110	YOLOSWAG_244	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28721.1	000000	-	80	YOLOSWAG_246	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28819.1	000000	-	55	YOLOSWAG_247	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28722.1	000000	-	85	YOLOSWAG_248	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28724.1	000000	-	121	YOLOSWAG_250	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28725.1	000000	-	134	YOLOSWAG_251	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28726.1	000000	-	158	YOLOSWAG_252	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28727.1	000000	-	219	YOLOSWAG_253	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28728.1	000000	-	113	YOLOSWAG_254	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28741.1	000000	-	124	YOLOSWAG_268	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28802.1	000000	-	104	YOLOSWAG_27	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28744.1	000000	-	127	YOLOSWAG_271	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28810.1	000000	-	180	YOLOSWAG_272	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28745.1	000000	-	290	YOLOSWAG_273	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28747.1	000000	-	104	YOLOSWAG_275	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28749.1	000000	-	80	YOLOSWAG_277	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28752.1	000000	-	96	YOLOSWAG_280	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28820.1	000000	-	66	YOLOSWAG_281	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28758.1	000000	-	329	YOLOSWAG_287	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28759.1	000000	-	214	YOLOSWAG_288	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28514.1	000000	-	139	YOLOSWAG_29	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28761.1	000000	-	192	YOLOSWAG_291	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28763.1	000000	-	59	YOLOSWAG_293	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28769.1	000000	-	203	YOLOSWAG_299	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28515.1	000000	-	106	YOLOSWAG_30	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQT28770.1	000000	-	146	YOLOSWAG_300	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28771.1	000000	-	146	YOLOSWAG_301	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28772.1	000000	-	104	YOLOSWAG_302	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28773.1	000000	-	476	YOLOSWAG_303	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28774.1	000000	-	94	YOLOSWAG_304	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28775.1	000000	-	337	YOLOSWAG_305	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28777.1	000000	-	143	YOLOSWAG_307	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28788.1	000000	-	294	YOLOSWAG_319	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28812.1	000000	-	165	YOLOSWAG_323	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28794.1	000000	-	73	YOLOSWAG_326	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28795.1	000000	-	84	YOLOSWAG_327	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28518.1	000000	-	159	YOLOSWAG_33	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28525.1	000000	-	304	YOLOSWAG_40	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28814.1	000000	-	69	YOLOSWAG_46	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28531.1	000000	-	98	YOLOSWAG_47	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28537.1	000000	-	124	YOLOSWAG_53	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28539.1	000000	-	83	YOLOSWAG_55	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28540.1	000000	-	153	YOLOSWAG_56	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28541.1	000000	-	84	YOLOSWAG_57	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28542.1	000000	-	100	YOLOSWAG_59	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28543.1	000000	-	104	YOLOSWAG_60	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28544.1	000000	-	205	YOLOSWAG_61	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28545.1	000000	-	124	YOLOSWAG_62	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28546.1	000000	-	165	YOLOSWAG_63	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28547.1	000000	-	220	YOLOSWAG_64	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AQT28496.1	000000	-	44	YOLOSWAG_9	Erwinia phage vB_EamM_Yoloswag	GCA_002619345.1
AIT14012.1	000000	-	20	PBI_121Q_115	Escherichia phage 121Q	GCA_000926855.1
AIT14013.1	000000	-	32	PBI_121Q_116	Escherichia phage 121Q	GCA_000926855.1
AIT14014.1	000000	-	53	PBI_121Q_117	Escherichia phage 121Q	GCA_000926855.1
AIT14130.1	000000	-	68	PBI_121Q_240	Escherichia phage 121Q	GCA_000926855.1
AIT14362.1	000000	-	43	PBI_121Q_472	Escherichia phage 121Q	GCA_000926855.1
QAY00592.1	000000	-	131	Ecwhy1_315	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00601.1	000000	-	71	Ecwhy1_324	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00621.1	000000	-	87	Ecwhy1_346	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00698.1	000000	-	58	Ecwhy1_423	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00702.1	000000	-	74	Ecwhy1_427	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00802.1	000000	-	374	Ecwhy1_529	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00813.1	000000	-	245	Ecwhy1_540	Escherichia phage Ecwhy_1	GCA_004146585.1
QAY00815.1	000000	-	89	Ecwhy1_542	Escherichia phage Ecwhy_1	GCA_004146585.1
AGC34927.1	000000	-	54	ACQ29_gp247	Escherichia phage PBECO4	GCA_001041035.1
AGC35230.1	000000	-	96	ACQ29_gp550	Escherichia phage PBECO4	GCA_001041035.1
AXC36613.1	000000	-	50	-	Escherichia phage UB	GCA_003341455.1
ARM70762.1	000000	-	72	phiC120_C56	Escherichia phage phiC120	GCA_002621185.1
ARM70708.1	000000	-	34	phiC120_c1	Escherichia phage phiC120	GCA_002621185.1
ARM70806.1	000000	-	95	phiC120_c100	Escherichia phage phiC120	GCA_002621185.1
ARM70807.1	000000	-	75	phiC120_c101	Escherichia phage phiC120	GCA_002621185.1
ARM70808.1	000000	-	93	phiC120_c102	Escherichia phage phiC120	GCA_002621185.1
ARM70810.1	000000	-	114	phiC120_c104	Escherichia phage phiC120	GCA_002621185.1
ARM70816.1	000000	-	66	phiC120_c110	Escherichia phage phiC120	GCA_002621185.1
ARM70818.1	000000	-	158	phiC120_c112	Escherichia phage phiC120	GCA_002621185.1
ARM70819.1	000000	-	95	phiC120_c113	Escherichia phage phiC120	GCA_002621185.1
ARM70822.1	000000	-	66	phiC120_c116	Escherichia phage phiC120	GCA_002621185.1
ARM70826.1	000000	-	141	phiC120_c120	Escherichia phage phiC120	GCA_002621185.1
ARM70828.1	000000	-	137	phiC120_c122	Escherichia phage phiC120	GCA_002621185.1
ARM70830.1	000000	-	174	phiC120_c124	Escherichia phage phiC120	GCA_002621185.1
ARM70836.1	000000	-	103	phiC120_c130	Escherichia phage phiC120	GCA_002621185.1
ARM70839.1	000000	-	44	phiC120_c133	Escherichia phage phiC120	GCA_002621185.1
ARM70840.1	000000	-	54	phiC120_c134	Escherichia phage phiC120	GCA_002621185.1
ARM70841.1	000000	-	59	phiC120_c135	Escherichia phage phiC120	GCA_002621185.1
ARM70842.1	000000	-	154	phiC120_c136	Escherichia phage phiC120	GCA_002621185.1
ARM70844.1	000000	-	78	phiC120_c138	Escherichia phage phiC120	GCA_002621185.1
ARM70851.1	000000	-	65	phiC120_c145	Escherichia phage phiC120	GCA_002621185.1
ARM70852.1	000000	-	216	phiC120_c146	Escherichia phage phiC120	GCA_002621185.1
ARM70858.1	000000	-	124	phiC120_c152	Escherichia phage phiC120	GCA_002621185.1
ARM70863.1	000000	-	299	phiC120_c157	Escherichia phage phiC120	GCA_002621185.1
ARM70865.1	000000	-	79	phiC120_c159	Escherichia phage phiC120	GCA_002621185.1
ARM70880.1	000000	-	85	phiC120_c175	Escherichia phage phiC120	GCA_002621185.1
ARM70892.1	000000	-	82	phiC120_c187	Escherichia phage phiC120	GCA_002621185.1
ARM70893.1	000000	-	60	phiC120_c188	Escherichia phage phiC120	GCA_002621185.1
ARM70894.1	000000	-	38	phiC120_c189	Escherichia phage phiC120	GCA_002621185.1
ARM70896.1	000000	-	105	phiC120_c191	Escherichia phage phiC120	GCA_002621185.1
ARM70898.1	000000	-	33	phiC120_c193	Escherichia phage phiC120	GCA_002621185.1
ARM70902.1	000000	-	59	phiC120_c197	Escherichia phage phiC120	GCA_002621185.1
ARM70905.1	000000	-	118	phiC120_c200	Escherichia phage phiC120	GCA_002621185.1
ARM70906.1	000000	-	98	phiC120_c201	Escherichia phage phiC120	GCA_002621185.1
ARM70909.1	000000	-	101	phiC120_c204	Escherichia phage phiC120	GCA_002621185.1
ARM70911.1	000000	-	319	phiC120_c206	Escherichia phage phiC120	GCA_002621185.1
ARM70912.1	000000	-	331	phiC120_c207	Escherichia phage phiC120	GCA_002621185.1
ARM70914.1	000000	-	91	phiC120_c209	Escherichia phage phiC120	GCA_002621185.1
ARM70916.1	000000	-	72	phiC120_c211	Escherichia phage phiC120	GCA_002621185.1
ARM70919.1	000000	-	176	phiC120_c214	Escherichia phage phiC120	GCA_002621185.1
ARM70920.1	000000	-	59	phiC120_c215	Escherichia phage phiC120	GCA_002621185.1
ARM70922.1	000000	-	68	phiC120_c217	Escherichia phage phiC120	GCA_002621185.1
ARM70923.1	000000	-	59	phiC120_c218	Escherichia phage phiC120	GCA_002621185.1
ARM70925.1	000000	-	70	phiC120_c220	Escherichia phage phiC120	GCA_002621185.1
ARM70927.1	000000	-	60	phiC120_c222	Escherichia phage phiC120	GCA_002621185.1
ARM70929.1	000000	-	70	phiC120_c224	Escherichia phage phiC120	GCA_002621185.1
ARM70934.1	000000	-	71	phiC120_c229	Escherichia phage phiC120	GCA_002621185.1
ARM70936.1	000000	-	74	phiC120_c231	Escherichia phage phiC120	GCA_002621185.1
ARM70938.1	000000	-	102	phiC120_c233	Escherichia phage phiC120	GCA_002621185.1
ARM70940.1	000000	-	109	phiC120_c235	Escherichia phage phiC120	GCA_002621185.1
ARM70941.1	000000	-	192	phiC120_c236	Escherichia phage phiC120	GCA_002621185.1
ARM70942.1	000000	-	86	phiC120_c237	Escherichia phage phiC120	GCA_002621185.1
ARM70944.1	000000	-	93	phiC120_c239	Escherichia phage phiC120	GCA_002621185.1
ARM70952.1	000000	-	79	phiC120_c247	Escherichia phage phiC120	GCA_002621185.1
ARM70953.1	000000	-	65	phiC120_c248	Escherichia phage phiC120	GCA_002621185.1
ARM70954.1	000000	-	90	phiC120_c249	Escherichia phage phiC120	GCA_002621185.1
ARM70957.1	000000	-	198	phiC120_c252	Escherichia phage phiC120	GCA_002621185.1
ARM70960.1	000000	-	167	phiC120_c255	Escherichia phage phiC120	GCA_002621185.1
ARM70961.1	000000	-	87	phiC120_c256	Escherichia phage phiC120	GCA_002621185.1
ARM70962.1	000000	-	187	phiC120_c257	Escherichia phage phiC120	GCA_002621185.1
ARM70963.1	000000	-	154	phiC120_c258	Escherichia phage phiC120	GCA_002621185.1
ARM70964.1	000000	-	114	phiC120_c259	Escherichia phage phiC120	GCA_002621185.1
ARM70966.1	000000	-	96	phiC120_c261	Escherichia phage phiC120	GCA_002621185.1
ARM70738.1	000000	-	83	phiC120_c31	Escherichia phage phiC120	GCA_002621185.1
ARM70745.1	000000	-	74	phiC120_c38	Escherichia phage phiC120	GCA_002621185.1
ARM70757.1	000000	-	62	phiC120_c51	Escherichia phage phiC120	GCA_002621185.1
ARM70763.1	000000	-	95	phiC120_c57	Escherichia phage phiC120	GCA_002621185.1
ARM70767.1	000000	-	82	phiC120_c61	Escherichia phage phiC120	GCA_002621185.1
ARM70772.1	000000	-	78	phiC120_c66	Escherichia phage phiC120	GCA_002621185.1
ARM70773.1	000000	-	91	phiC120_c67	Escherichia phage phiC120	GCA_002621185.1
ARM70774.1	000000	-	71	phiC120_c68	Escherichia phage phiC120	GCA_002621185.1
ARM70777.1	000000	-	63	phiC120_c71	Escherichia phage phiC120	GCA_002621185.1
ARM70778.1	000000	-	99	phiC120_c72	Escherichia phage phiC120	GCA_002621185.1
ARM70779.1	000000	-	74	phiC120_c73	Escherichia phage phiC120	GCA_002621185.1
ARM70792.1	000000	-	83	phiC120_c86	Escherichia phage phiC120	GCA_002621185.1
ARM70805.1	000000	-	53	phiC120_c99	Escherichia phage phiC120	GCA_002621185.1
QKN85841.1	000000	-	62	ACEC001_0045	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85972.1	000000	-	52	ACEC001_1340	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN85995.1	000000	-	50	ACEC001_1555	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QKN86032.1	000000	-	106	ACEC001_1897	Escherichia phage vB_EcoM_EC001	GCA_014131305.1
QBO61664.1	000000	-	25	G17_00168	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO61725.1	000000	-	57	G17_00236	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO62050.1	000000	-	29	G17_00561	Escherichia phage vB_EcoM_G17	GCA_004521135.1
QBO63798.1	000000	-	273	Goslar_00005	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBO63800.1	000000	-	102	Goslar_00007	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63808.1	000000	-	120	Goslar_00015	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63809.1	000000	-	141	Goslar_00016	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63810.1	000000	-	147	Goslar_00017	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63811.1	000000	-	135	Goslar_00018	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63813.1	000000	-	99	Goslar_00020	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63814.1	000000	-	260	Goslar_00021	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63819.1	000000	-	867	Goslar_00026	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63820.1	000000	-	161	Goslar_00027	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63830.1	000000	-	91	Goslar_00037	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63835.1	000000	-	206	Goslar_00042	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63837.1	000000	-	108	Goslar_00044	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63838.1	000000	-	133	Goslar_00045	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63842.1	000000	-	201	Goslar_00049	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63845.1	000000	-	127	Goslar_00052	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63847.1	000000	-	368	Goslar_00054	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63848.1	000000	-	433	Goslar_00055	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63851.1	000000	-	440	Goslar_00058	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63857.1	000000	-	930	Goslar_00064	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63858.1	000000	-	934	Goslar_00065	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63859.1	000000	-	146	Goslar_00066	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63863.1	000000	-	161	Goslar_00070	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63865.1	000000	-	161	Goslar_00072	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63866.1	000000	-	163	Goslar_00073	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63867.1	000000	-	200	Goslar_00074	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63868.1	000000	-	141	Goslar_00075	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63869.1	000000	-	133	Goslar_00076	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63870.1	000000	-	212	Goslar_00077	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63872.1	000000	-	290	Goslar_00079	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63877.1	000000	-	124	Goslar_00084	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63879.1	000000	-	870	Goslar_00086	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63888.1	000000	-	249	Goslar_00095	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63890.1	000000	-	85	Goslar_00097	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63892.1	000000	-	103	Goslar_00099	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63895.1	000000	-	69	Goslar_00102	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63899.1	000000	-	317	Goslar_00106	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63900.1	000000	-	148	Goslar_00107	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63901.1	000000	-	138	Goslar_00108	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63902.1	000000	-	199	Goslar_00109	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63903.1	000000	-	223	Goslar_00110	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63905.1	000000	-	142	Goslar_00112	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63913.1	000000	-	235	Goslar_00120	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63916.1	000000	-	202	Goslar_00123	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63917.1	000000	-	106	Goslar_00124	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63918.1	000000	-	138	Goslar_00125	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63919.1	000000	-	325	Goslar_00126	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63920.1	000000	-	88	Goslar_00127	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63922.1	000000	-	124	Goslar_00129	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63925.1	000000	-	93	Goslar_00132	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63926.1	000000	-	99	Goslar_00133	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63927.1	000000	-	108	Goslar_00134	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63928.1	000000	-	214	Goslar_00135	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63930.1	000000	-	65	Goslar_00137	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63931.1	000000	-	67	Goslar_00138	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63933.1	000000	-	97	Goslar_00140	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63935.1	000000	-	67	Goslar_00142	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63939.1	000000	-	104	Goslar_00146	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63941.1	000000	-	111	Goslar_00148	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63942.1	000000	-	198	Goslar_00149	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63943.1	000000	-	100	Goslar_00150	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63944.1	000000	-	280	Goslar_00151	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63945.1	000000	-	318	Goslar_00152	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63946.1	000000	-	87	Goslar_00153	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63948.1	000000	-	144	Goslar_00155	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63949.1	000000	-	91	Goslar_00156	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63951.1	000000	-	160	Goslar_00158	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63955.1	000000	-	112	Goslar_00162	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63959.1	000000	-	161	Goslar_00166	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63960.1	000000	-	31	Goslar_00167	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63961.1	000000	-	120	Goslar_00168	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63962.1	000000	-	116	Goslar_00169	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63963.1	000000	-	136	Goslar_00170	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63974.1	000000	-	149	Goslar_00181	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63981.1	000000	-	631	Goslar_00189	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63986.1	000000	-	160	Goslar_00194	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63988.1	000000	-	161	Goslar_00196	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63989.1	000000	-	98	Goslar_00197	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63992.1	000000	-	66	Goslar_00200	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63995.1	000000	-	178	Goslar_00203	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63997.1	000000	-	124	Goslar_00205	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63998.1	000000	-	274	Goslar_00206	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO63999.1	000000	-	345	Goslar_00207	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64000.1	000000	-	117	Goslar_00208	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64001.1	000000	-	199	Goslar_00209	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64002.1	000000	-	174	Goslar_00210	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64011.1	000000	-	179	Goslar_00219	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64013.1	000000	-	159	Goslar_00221	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64014.1	000000	-	266	Goslar_00222	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64018.1	000000	-	507	Goslar_00226	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64025.1	000000	-	355	Goslar_00234	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64026.1	000000	-	170	Goslar_00235	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64028.1	000000	-	209	Goslar_00237	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64033.1	000000	-	106	Goslar_00242	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64035.1	000000	-	280	Goslar_00244	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QBO64036.1	000000	-	143	Goslar_00245	Escherichia phage vB_EcoM_Goslar	GCA_004521275.1
QDF13639.1	000000	-	35	vBEcoMphAPEC6_gp008	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13754.1	000000	-	25	vBEcoMphAPEC6_gp125c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13824.1	000000	-	35	vBEcoMphAPEC6_gp195c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13850.1	000000	-	49	vBEcoMphAPEC6_gp221c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
QDF13930.1	000000	-	55	vBEcoMphAPEC6_gp305c	Escherichia phage vB_EcoM_phAPEC6	GCA_006529615.1
SCA80150.1	000000	-	54	PSLUR01_00173	Escherichia phage vB_Eco_slurp01	GCA_900094095.1
AAX78528.1	000000	-	69	RB43ORF006c	Escherichia virus RB43	GCA_000863505.1
AAX78626.1	000000	-	105	RB43ORF104w	Escherichia virus RB43	GCA_000863505.1
AAX78636.1	000000	-	92	RB43ORF114c	Escherichia virus RB43	GCA_000863505.1
AAX78648.1	000000	-	156	RB43ORF126c	Escherichia virus RB43	GCA_000863505.1
AAX78657.1	000000	-	32	RB43ORF135c	Escherichia virus RB43	GCA_000863505.1
AAX78668.1	000000	-	61	RB43ORF146c	Escherichia virus RB43	GCA_000863505.1
AAX78670.1	000000	-	30	RB43ORF148c	Escherichia virus RB43	GCA_000863505.1
AAX78690.1	000000	-	58	RB43ORF168c	Escherichia virus RB43	GCA_000863505.1
AAX78695.1	000000	-	66	RB43ORF173c	Escherichia virus RB43	GCA_000863505.1
AAX78697.1	000000	-	53	RB43ORF175c	Escherichia virus RB43	GCA_000863505.1
AAX78701.1	000000	-	61	RB43ORF179c	Escherichia virus RB43	GCA_000863505.1
AAX78715.1	000000	-	24	RB43ORF193c	Escherichia virus RB43	GCA_000863505.1
AAX78753.1	000000	-	28	RB43ORF231w	Escherichia virus RB43	GCA_000863505.1
AAX78760.1	000000	-	47	RB43ORF238w	Escherichia virus RB43	GCA_000863505.1
AAX78784.1	000000	-	77	RB43ORF262w	Escherichia virus RB43	GCA_000863505.1
AAX78789.1	000000	-	65	RB43ORF267w	Escherichia virus RB43	GCA_000863505.1
AAX78811.1	000000	-	55	RB43ORF289c	Escherichia virus RB43	GCA_000863505.1
QGH71864.1	000000	-	124	N1M2_1	Klebsiella phage N1M2	GCA_010092605.1
QGH71967.1	000000	-	220	N1M2_104	Klebsiella phage N1M2	GCA_010092605.1
QGH71874.1	000000	-	118	N1M2_11	Klebsiella phage N1M2	GCA_010092605.1
QGH71987.1	000000	-	240	N1M2_124	Klebsiella phage N1M2	GCA_010092605.1
QGH71990.1	000000	-	191	N1M2_127	Klebsiella phage N1M2	GCA_010092605.1
QGH71876.1	000000	-	89	N1M2_13	Klebsiella phage N1M2	GCA_010092605.1
QGH71993.1	000000	-	437	N1M2_130	Klebsiella phage N1M2	GCA_010092605.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QGH72000.1	000000	-	253	N1M2_137	Klebsiella phage N1M2	GCA_010092605.1
QGH72002.1	000000	-	140	N1M2_139	Klebsiella phage N1M2	GCA_010092605.1
QGH72005.1	000000	-	119	N1M2_142	Klebsiella phage N1M2	GCA_010092605.1
QGH72008.1	000000	-	152	N1M2_145	Klebsiella phage N1M2	GCA_010092605.1
QGH72009.1	000000	-	72	N1M2_146	Klebsiella phage N1M2	GCA_010092605.1
QGH72012.1	000000	-	104	N1M2_149	Klebsiella phage N1M2	GCA_010092605.1
QGH72013.1	000000	-	161	N1M2_150	Klebsiella phage N1M2	GCA_010092605.1
QGH72019.1	000000	-	108	N1M2_156	Klebsiella phage N1M2	GCA_010092605.1
QGH72020.1	000000	-	435	N1M2_157	Klebsiella phage N1M2	GCA_010092605.1
QGH72022.1	000000	-	62	N1M2_159	Klebsiella phage N1M2	GCA_010092605.1
QGH72023.1	000000	-	722	N1M2_160	Klebsiella phage N1M2	GCA_010092605.1
QGH72024.1	000000	-	1338	N1M2_161	Klebsiella phage N1M2	GCA_010092605.1
QGH72026.1	000000	-	938	N1M2_163	Klebsiella phage N1M2	GCA_010092605.1
QGH72027.1	000000	-	221	N1M2_164	Klebsiella phage N1M2	GCA_010092605.1
QGH71880.1	000000	-	234	N1M2_17	Klebsiella phage N1M2	GCA_010092605.1
QGH72037.1	000000	-	70	N1M2_174	Klebsiella phage N1M2	GCA_010092605.1
QGH71881.1	000000	-	153	N1M2_18	Klebsiella phage N1M2	GCA_010092605.1
QGH72044.1	000000	-	134	N1M2_181	Klebsiella phage N1M2	GCA_010092605.1
QGH72049.1	000000	-	299	N1M2_186	Klebsiella phage N1M2	GCA_010092605.1
QGH72054.1	000000	-	29	N1M2_191	Klebsiella phage N1M2	GCA_010092605.1
QGH71886.1	000000	-	583	N1M2_23	Klebsiella phage N1M2	GCA_010092605.1
QGH72096.1	000000	-	150	N1M2_233	Klebsiella phage N1M2	GCA_010092605.1
QGH72098.1	000000	-	133	N1M2_235	Klebsiella phage N1M2	GCA_010092605.1
QGH71887.1	000000	-	146	N1M2_24	Klebsiella phage N1M2	GCA_010092605.1
QGH71916.1	000000	-	99	N1M2_53	Klebsiella phage N1M2	GCA_010092605.1
QGH71933.1	000000	-	171	N1M2_70	Klebsiella phage N1M2	GCA_010092605.1
QGH71935.1	000000	-	179	N1M2_72	Klebsiella phage N1M2	GCA_010092605.1
QGH71871.1	000000	-	119	N1M2_8	Klebsiella phage N1M2	GCA_010092605.1
QGH71872.1	000000	-	84	N1M2_9	Klebsiella phage N1M2	GCA_010092605.1
AFA44277.1	000000	-	154	RaK2_00004	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44293.1	000000	-	56	RaK2_00020	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44299.1	000000	-	159	RaK2_00026	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44303.1	000000	-	150	RaK2_00030	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44347.1	000000	-	140	RaK2_00074	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44348.1	000000	-	152	RaK2_00075	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44349.1	000000	-	69	RaK2_00076	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44370.1	000000	-	244	RaK2_00097	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44374.1	000000	-	90	RaK2_00101	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44403.1	000000	-	127	RaK2_00130	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44462.1	000000	-	124	RaK2_00189	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44464.1	000000	-	154	RaK2_00191	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44466.1	000000	-	184	RaK2_00193	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44468.1	000000	-	69	RaK2_00195	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44470.1	000000	-	95	RaK2_00197	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44473.1	000000	-	79	RaK2_00200	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44474.1	000000	-	80	RaK2_00201	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44476.1	000000	-	118	RaK2_00203	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44482.1	000000	-	98	RaK2_00209	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44485.1	000000	-	81	RaK2_00212	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44486.1	000000	-	132	RaK2_00213	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44495.1	000000	-	59	RaK2_00222	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44497.1	000000	-	50	RaK2_00224	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44500.1	000000	-	128	RaK2_00227	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44501.1	000000	-	138	RaK2_00228	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44508.1	000000	-	85	RaK2_00235	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44509.1	000000	-	80	RaK2_00236	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44514.1	000000	-	100	RaK2_00241	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44518.1	000000	-	68	RaK2_00245	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44520.1	000000	-	60	RaK2_00247	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44521.1	000000	-	296	RaK2_00248	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44528.1	000000	-	50	RaK2_00255	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44529.1	000000	-	81	RaK2_00256	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44531.1	000000	-	64	RaK2_00258	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44532.1	000000	-	68	RaK2_00259	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44533.1	000000	-	60	RaK2_00260	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44534.1	000000	-	87	RaK2_00261	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44541.1	000000	-	103	RaK2_00268	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44545.1	000000	-	162	RaK2_00272	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44549.1	000000	-	130	RaK2_00276	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44550.1	000000	-	78	RaK2_00277	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44552.1	000000	-	140	RaK2_00279	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44554.1	000000	-	124	RaK2_00281	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44555.1	000000	-	84	RaK2_00282	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44557.1	000000	-	127	RaK2_00284	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44558.1	000000	-	90	RaK2_00285	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44567.1	000000	-	173	RaK2_00294	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44568.1	000000	-	64	RaK2_00295	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44569.1	000000	-	59	RaK2_00296	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44570.1	000000	-	97	RaK2_00297	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44572.1	000000	-	64	RaK2_00299	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44575.1	000000	-	195	RaK2_00302	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44577.1	000000	-	48	RaK2_00304	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44581.1	000000	-	104	RaK2_00308	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44592.1	000000	-	68	RaK2_00319	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44593.1	000000	-	147	RaK2_00320	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44594.1	000000	-	200	RaK2_00321	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44595.1	000000	-	185	RaK2_00322	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44597.1	000000	-	56	RaK2_00324	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44598.1	000000	-	75	RaK2_00325	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44603.1	000000	-	67	RaK2_00330	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44606.1	000000	-	157	RaK2_00333	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44612.1	000000	-	101	RaK2_00339	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44614.1	000000	-	62	RaK2_00341	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44616.1	000000	-	76	RaK2_00343	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44618.1	000000	-	96	RaK2_00345	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44621.1	000000	-	83	RaK2_00348	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44625.1	000000	-	121	RaK2_00352	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44630.1	000000	-	120	RaK2_00357	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44632.1	000000	-	93	RaK2_00359	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44633.1	000000	-	98	RaK2_00360	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44635.1	000000	-	121	RaK2_00362	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44636.1	000000	-	149	RaK2_00363	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44637.1	000000	-	175	RaK2_00364	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44638.1	000000	-	214	RaK2_00365	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44642.1	000000	-	84	RaK2_00369	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44643.1	000000	-	57	RaK2_00370	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44644.1	000000	-	60	RaK2_00371	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44645.1	000000	-	115	RaK2_00372	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44646.1	000000	-	83	RaK2_00373	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44647.1	000000	-	55	RaK2_00374	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44651.1	000000	-	142	RaK2_00378	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44655.1	000000	-	58	RaK2_00382	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44659.1	000000	-	85	RaK2_00386	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44660.1	000000	-	79	RaK2_00387	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44661.1	000000	-	109	RaK2_00388	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44662.1	000000	-	59	RaK2_00389	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44663.1	000000	-	67	RaK2_00390	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44664.1	000000	-	112	RaK2_00391	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44667.1	000000	-	101	RaK2_00394	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44668.1	000000	-	94	RaK2_00395	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44669.1	000000	-	67	RaK2_00396	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44672.1	000000	-	61	RaK2_00399	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44673.1	000000	-	58	RaK2_00400	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44674.1	000000	-	63	RaK2_00401	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44676.1	000000	-	86	RaK2_00403	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFA44677.1	000000	-	105	RaK2_00404	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44678.1	000000	-	108	RaK2_00405	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44680.1	000000	-	69	RaK2_00407	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44681.1	000000	-	64	RaK2_00408	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44682.1	000000	-	60	RaK2_00409	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44683.1	000000	-	69	RaK2_00410	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44685.1	000000	-	124	RaK2_00412	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44686.1	000000	-	132	RaK2_00413	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44687.1	000000	-	64	RaK2_00414	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44688.1	000000	-	140	RaK2_00415	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44689.1	000000	-	131	RaK2_00416	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44690.1	000000	-	178	RaK2_00417	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44691.1	000000	-	173	RaK2_00418	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44694.1	000000	-	200	RaK2_00421	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44695.1	000000	-	165	RaK2_00422	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44696.1	000000	-	193	RaK2_00423	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44698.1	000000	-	187	RaK2_00425	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44699.1	000000	-	194	RaK2_00426	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44700.1	000000	-	192	RaK2_00427	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44701.1	000000	-	203	RaK2_00428	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44702.1	000000	-	187	RaK2_00429	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44704.1	000000	-	197	RaK2_00431	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44705.1	000000	-	208	RaK2_00432	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44706.1	000000	-	171	RaK2_00433	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44707.1	000000	-	194	RaK2_00434	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44709.1	000000	-	183	RaK2_00436	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44711.1	000000	-	159	RaK2_00438	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44714.1	000000	-	297	RaK2_00441	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44723.1	000000	-	86	RaK2_00450	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44726.1	000000	-	110	RaK2_00453	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44728.1	000000	-	89	RaK2_00455	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44729.1	000000	-	89	RaK2_00456	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44734.1	000000	-	94	RaK2_00461	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44736.1	000000	-	90	RaK2_00463	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44740.1	000000	-	88	RaK2_00467	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44741.1	000000	-	88	RaK2_00468	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44742.1	000000	-	85	RaK2_00469	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44744.1	000000	-	88	RaK2_00471	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44745.1	000000	-	100	RaK2_00472	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44746.1	000000	-	97	RaK2_00473	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44747.1	000000	-	91	RaK2_00474	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44748.1	000000	-	52	RaK2_00475	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44749.1	000000	-	61	RaK2_00476	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44750.1	000000	-	49	RaK2_00477	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44751.1	000000	-	99	RaK2_00478	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44752.1	000000	-	86	RaK2_00479	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44754.1	000000	-	77	RaK2_00481	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44757.1	000000	-	223	RaK2_00484	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44760.1	000000	-	131	RaK2_00487	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44766.1	000000	-	182	RaK2_00493	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44787.1	000000	-	400	RaK2_00514	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44788.1	000000	-	72	RaK2_00515	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44796.1	000000	-	570	RaK2_00525	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44797.1	000000	-	580	RaK2_00526	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
AFA44798.1	000000	-	715	RaK2_00527	Klebsiella phage vB_KleM_RaK2	GCA_000903335.1
QIG57836.1	000000	-	70	SEA_PAULODIABOLI_102	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57837.1	000000	-	156	SEA_PAULODIABOLI_103	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57843.1	000000	-	105	SEA_PAULODIABOLI_109	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57844.1	000000	-	141	SEA_PAULODIABOLI_110	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57850.1	000000	-	155	SEA_PAULODIABOLI_116	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57852.1	000000	-	86	SEA_PAULODIABOLI_118	Microbacterium phage PauloDiaboli	GCA_011067425.1
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QIG57854.1	000000	-	57	SEA_PAULODIABOLI_131	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57856.1	000000	-	264	SEA_PAULODIABOLI_138	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58082.1	000000	-	96	SEA_PAULODIABOLI_139	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57857.1	000000	-	129	SEA_PAULODIABOLI_140	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57859.1	000000	-	60	SEA_PAULODIABOLI_142	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57865.1	000000	-	72	SEA_PAULODIABOLI_170	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57867.1	000000	-	93	SEA_PAULODIABOLI_172	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57868.1	000000	-	121	SEA_PAULODIABOLI_173	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57869.1	000000	-	95	SEA_PAULODIABOLI_174	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58083.1	000000	-	23	SEA_PAULODIABOLI_175	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57870.1	000000	-	229	SEA_PAULODIABOLI_176	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57874.1	000000	-	78	SEA_PAULODIABOLI_183	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57875.1	000000	-	138	SEA_PAULODIABOLI_184	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57876.1	000000	-	112	SEA_PAULODIABOLI_185	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57878.1	000000	-	62	SEA_PAULODIABOLI_190	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57879.1	000000	-	42	SEA_PAULODIABOLI_191	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57880.1	000000	-	56	SEA_PAULODIABOLI_192	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57883.1	000000	-	107	SEA_PAULODIABOLI_195	Microbacterium phage PauloDiaboli	GCA_011067425.1
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QIG57886.1	000000	-	64	SEA_PAULODIABOLI_199	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57887.1	000000	-	58	SEA_PAULODIABOLI_200	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57890.1	000000	-	87	SEA_PAULODIABOLI_203	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57891.1	000000	-	117	SEA_PAULODIABOLI_204	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58085.1	000000	-	90	SEA_PAULODIABOLI_205	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57892.1	000000	-	148	SEA_PAULODIABOLI_206	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57893.1	000000	-	55	SEA_PAULODIABOLI_207	Microbacterium phage PauloDiaboli	GCA_011067425.1
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QIG57896.1	000000	-	102	SEA_PAULODIABOLI_210	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57897.1	000000	-	58	SEA_PAULODIABOLI_211	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57899.1	000000	-	79	SEA_PAULODIABOLI_213	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57900.1	000000	-	63	SEA_PAULODIABOLI_214	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57901.1	000000	-	105	SEA_PAULODIABOLI_215	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58086.1	000000	-	58	SEA_PAULODIABOLI_219	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57906.1	000000	-	86	SEA_PAULODIABOLI_221	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57907.1	000000	-	161	SEA_PAULODIABOLI_222	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57908.1	000000	-	69	SEA_PAULODIABOLI_223	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57909.1	000000	-	130	SEA_PAULODIABOLI_224	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57910.1	000000	-	76	SEA_PAULODIABOLI_225	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57915.1	000000	-	206	SEA_PAULODIABOLI_230	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57917.1	000000	-	194	SEA_PAULODIABOLI_232	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57918.1	000000	-	37	SEA_PAULODIABOLI_233	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57919.1	000000	-	229	SEA_PAULODIABOLI_234	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57923.1	000000	-	74	SEA_PAULODIABOLI_238	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57925.1	000000	-	212	SEA_PAULODIABOLI_240	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57926.1	000000	-	128	SEA_PAULODIABOLI_241	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57927.1	000000	-	145	SEA_PAULODIABOLI_242	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57932.1	000000	-	69	SEA_PAULODIABOLI_247	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57934.1	000000	-	131	SEA_PAULODIABOLI_249	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57937.1	000000	-	54	SEA_PAULODIABOLI_252	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57942.1	000000	-	67	SEA_PAULODIABOLI_257	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57943.1	000000	-	58	SEA_PAULODIABOLI_258	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57944.1	000000	-	57	SEA_PAULODIABOLI_259	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58087.1	000000	-	64	SEA_PAULODIABOLI_260	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57945.1	000000	-	51	SEA_PAULODIABOLI_261	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57947.1	000000	-	57	SEA_PAULODIABOLI_263	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57951.1	000000	-	254	SEA_PAULODIABOLI_267	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57960.1	000000	-	71	SEA_PAULODIABOLI_276	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57968.1	000000	-	92	SEA_PAULODIABOLI_284	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57969.1	000000	-	110	SEA_PAULODIABOLI_285	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57972.1	000000	-	153	SEA_PAULODIABOLI_288	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57973.1	000000	-	65	SEA_PAULODIABOLI_289	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57976.1	000000	-	121	SEA_PAULODIABOLI_292	Microbacterium phage PauloDiaboli	GCA_011067425.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG57977.1	000000	-	85	SEA_PAULODIABOLI_293	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57978.1	000000	-	110	SEA_PAULODIABOLI_294	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57980.1	000000	-	191	SEA_PAULODIABOLI_296	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57984.1	000000	-	120	SEA_PAULODIABOLI_300	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57985.1	000000	-	81	SEA_PAULODIABOLI_301	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57995.1	000000	-	193	SEA_PAULODIABOLI_311	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57996.1	000000	-	106	SEA_PAULODIABOLI_312	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57997.1	000000	-	72	SEA_PAULODIABOLI_313	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57998.1	000000	-	76	SEA_PAULODIABOLI_314	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58000.1	000000	-	89	SEA_PAULODIABOLI_316	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58001.1	000000	-	140	SEA_PAULODIABOLI_317	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58002.1	000000	-	575	SEA_PAULODIABOLI_318	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58004.1	000000	-	130	SEA_PAULODIABOLI_320	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58006.1	000000	-	54	SEA_PAULODIABOLI_322	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58007.1	000000	-	56	SEA_PAULODIABOLI_323	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58008.1	000000	-	103	SEA_PAULODIABOLI_324	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58010.1	000000	-	124	SEA_PAULODIABOLI_326	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58011.1	000000	-	130	SEA_PAULODIABOLI_327	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58012.1	000000	-	96	SEA_PAULODIABOLI_328	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58013.1	000000	-	124	SEA_PAULODIABOLI_329	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58014.1	000000	-	106	SEA_PAULODIABOLI_330	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58015.1	000000	-	101	SEA_PAULODIABOLI_331	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58016.1	000000	-	146	SEA_PAULODIABOLI_332	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58017.1	000000	-	182	SEA_PAULODIABOLI_333	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58018.1	000000	-	134	SEA_PAULODIABOLI_334	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58021.1	000000	-	92	SEA_PAULODIABOLI_337	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58024.1	000000	-	68	SEA_PAULODIABOLI_340	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58025.1	000000	-	78	SEA_PAULODIABOLI_341	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58027.1	000000	-	80	SEA_PAULODIABOLI_343	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58028.1	000000	-	110	SEA_PAULODIABOLI_344	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58029.1	000000	-	61	SEA_PAULODIABOLI_345	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58031.1	000000	-	60	SEA_PAULODIABOLI_347	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58033.1	000000	-	51	SEA_PAULODIABOLI_349	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58037.1	000000	-	62	SEA_PAULODIABOLI_353	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58039.1	000000	-	79	SEA_PAULODIABOLI_355	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57777.1	000000	-	51	SEA_PAULODIABOLI_42	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57779.1	000000	-	59	SEA_PAULODIABOLI_44	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57780.1	000000	-	90	SEA_PAULODIABOLI_45	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57781.1	000000	-	66	SEA_PAULODIABOLI_46	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57782.1	000000	-	71	SEA_PAULODIABOLI_47	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57783.1	000000	-	119	SEA_PAULODIABOLI_48	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57784.1	000000	-	125	SEA_PAULODIABOLI_49	Microbacterium phage PauloDiaboli	GCA_011067425.1
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QIG57790.1	000000	-	43	SEA_PAULODIABOLI_55	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57791.1	000000	-	88	SEA_PAULODIABOLI_56	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57792.1	000000	-	79	SEA_PAULODIABOLI_57	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57795.1	000000	-	81	SEA_PAULODIABOLI_60	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57796.1	000000	-	99	SEA_PAULODIABOLI_61	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57797.1	000000	-	67	SEA_PAULODIABOLI_62	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57798.1	000000	-	70	SEA_PAULODIABOLI_63	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57799.1	000000	-	61	SEA_PAULODIABOLI_64	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57800.1	000000	-	193	SEA_PAULODIABOLI_65	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57801.1	000000	-	54	SEA_PAULODIABOLI_66	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57802.1	000000	-	30	SEA_PAULODIABOLI_67	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57803.1	000000	-	133	SEA_PAULODIABOLI_68	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57805.1	000000	-	55	SEA_PAULODIABOLI_70	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57806.1	000000	-	69	SEA_PAULODIABOLI_71	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57808.1	000000	-	165	SEA_PAULODIABOLI_73	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG58081.1	000000	-	34	SEA_PAULODIABOLI_74	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57809.1	000000	-	125	SEA_PAULODIABOLI_75	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57810.1	000000	-	67	SEA_PAULODIABOLI_76	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57811.1	000000	-	85	SEA_PAULODIABOLI_77	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57817.1	000000	-	97	SEA_PAULODIABOLI_83	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57818.1	000000	-	611	SEA_PAULODIABOLI_84	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57820.1	000000	-	189	SEA_PAULODIABOLI_86	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57822.1	000000	-	669	SEA_PAULODIABOLI_88	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57823.1	000000	-	293	SEA_PAULODIABOLI_89	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57824.1	000000	-	346	SEA_PAULODIABOLI_90	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57825.1	000000	-	253	SEA_PAULODIABOLI_91	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57826.1	000000	-	95	SEA_PAULODIABOLI_92	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57827.1	000000	-	174	SEA_PAULODIABOLI_93	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57829.1	000000	-	110	SEA_PAULODIABOLI_95	Microbacterium phage PauloDiaboli	GCA_011067425.1
QIG57830.1	000000	-	149	SEA_PAULODIABOLI_96	Microbacterium phage PauloDiaboli	GCA_011067425.1
AXH72595.1	000000	-	116	-	Myoviridae sp.	GCA_003657725.1
AXH72653.1	000000	-	116	-	Myoviridae sp.	GCA_003657725.1
AXH72504.1	000000	-	116	-	Myoviridae sp.	GCA_003657725.1
AXH72404.1	000000	-	116	-	Myoviridae sp.	GCA_003657725.1
AXH72648.1	000000	-	101	-	Myoviridae sp.	GCA_003657725.1
AXH72501.1	000000	-	101	-	Myoviridae sp.	GCA_003657725.1
AXH72573.1	000000	-	93	-	Myoviridae sp.	GCA_003657725.1
AXH72557.1	000000	-	93	-	Myoviridae sp.	GCA_003657725.1
AXH72395.1	000000	-	197	-	Myoviridae sp.	GCA_003657725.1
AXH72500.1	000000	-	197	-	Myoviridae sp.	GCA_003657725.1
AXH72519.1	000000	-	577	-	Myoviridae sp.	GCA_003657725.1
AXH72565.1	000000	-	155	-	Myoviridae sp.	GCA_003657725.1
AXH72400.1	000000	-	328	-	Myoviridae sp.	GCA_003657725.1
AXH72544.1	000000	-	252	-	Myoviridae sp.	GCA_003657725.1
AXH72412.1	000000	-	193	-	Myoviridae sp.	GCA_003657725.1
AXH72568.1	000000	-	193	-	Myoviridae sp.	GCA_003657725.1
AXH72457.1	000000	-	91	-	Myoviridae sp.	GCA_003657725.1
AXH72384.1	000000	-	91	-	Myoviridae sp.	GCA_003657725.1
AXH72417.1	000000	-	102	-	Myoviridae sp.	GCA_003657725.1
AXH72467.1	000000	-	102	-	Myoviridae sp.	GCA_003657725.1
AXH72615.1	000000	-	102	-	Myoviridae sp.	GCA_003657725.1
AXH72498.1	000000	-	130	-	Myoviridae sp.	GCA_003657725.1
AXH72397.1	000000	-	130	-	Myoviridae sp.	GCA_003657725.1
AXH72643.1	000000	-	127	-	Myoviridae sp.	GCA_003657725.1
AXH72669.1	000000	-	103	-	Myoviridae sp.	GCA_003657725.1
AXH72506.1	000000	-	134	-	Myoviridae sp.	GCA_003657725.1
AXH72447.1	000000	-	88	-	Myoviridae sp.	GCA_003657725.1
AXH72684.1	000000	-	88	-	Myoviridae sp.	GCA_003657725.1
AXH72739.1	000000	-	122	-	Myoviridae sp.	GCA_003657725.1
AXH72455.1	000000	-	122	-	Myoviridae sp.	GCA_003657725.1
AXH72795.1	000000	-	122	-	Myoviridae sp.	GCA_003657725.1
AXH72432.1	000000	-	122	-	Myoviridae sp.	GCA_003657725.1
AXH72660.1	000000	-	133	-	Myoviridae sp.	GCA_003657725.1
AXH72530.1	000000	-	133	-	Myoviridae sp.	GCA_003657725.1
AXH72624.1	000000	-	280	-	Myoviridae sp.	GCA_003657725.1
AXH72654.1	000000	-	80	-	Myoviridae sp.	GCA_003657725.1
AXH72641.1	000000	-	80	-	Myoviridae sp.	GCA_003657725.1
AXH72666.1	000000	-	80	-	Myoviridae sp.	GCA_003657725.1
AXH72772.1	000000	-	456	-	Myoviridae sp.	GCA_003657725.1
AXH72577.1	000000	-	309	-	Myoviridae sp.	GCA_003657725.1
AXH72779.1	000000	-	396	-	Myoviridae sp.	GCA_003657725.1
AXH72562.1	000000	-	445	-	Myoviridae sp.	GCA_003657725.1
AXH72426.1	000000	-	92	-	Myoviridae sp.	GCA_003657725.1
AXH72440.1	000000	-	97	-	Myoviridae sp.	GCA_003657725.1
AXH72674.1	000000	-	144	-	Myoviridae sp.	GCA_003657725.1
AXH72638.1	000000	-	144	-	Myoviridae sp.	GCA_003657725.1
AXH72381.1	000000	-	160	-	Myoviridae sp.	GCA_003657725.1
AXH72763.1	000000	-	1316	-	Myoviridae sp.	GCA_003657725.1
AXH72908.1	000000	-	298	-	Myoviridae sp.	GCA_003657725.1
AXH72769.1	000000	-	114	-	Myoviridae sp.	GCA_003657725.1
AXH72547.1	000000	-	114	-	Myoviridae sp.	GCA_003657725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH72794.1	000000	-	114	-	Myoviridae sp.	GCA_003657725.1
AXH72667.1	000000	-	148	-	Myoviridae sp.	GCA_003657725.1
AXH72448.1	000000	-	148	-	Myoviridae sp.	GCA_003657725.1
AXH72700.1	000000	-	113	-	Myoviridae sp.	GCA_003657725.1
AXH72460.1	000000	-	113	-	Myoviridae sp.	GCA_003657725.1
AXH72473.1	000000	-	113	-	Myoviridae sp.	GCA_003657725.1
AXH72732.1	000000	-	113	-	Myoviridae sp.	GCA_003657725.1
AXH72783.1	000000	-	113	-	Myoviridae sp.	GCA_003657725.1
AXH72527.1	000000	-	82	-	Myoviridae sp.	GCA_003657725.1
AXH72521.1	000000	-	139	-	Myoviridae sp.	GCA_003657725.1
AXH72507.1	000000	-	139	-	Myoviridae sp.	GCA_003657725.1
AXH72662.1	000000	-	110	-	Myoviridae sp.	GCA_003657725.1
AXH72386.1	000000	-	111	-	Myoviridae sp.	GCA_003657725.1
AXH72525.1	000000	-	106	-	Myoviridae sp.	GCA_003657725.1
AXH72606.1	000000	-	106	-	Myoviridae sp.	GCA_003657725.1
AXH72789.1	000000	-	121	-	Myoviridae sp.	GCA_003657725.1
AXH72640.1	000000	-	121	-	Myoviridae sp.	GCA_003657725.1
AXH72434.1	000000	-	121	-	Myoviridae sp.	GCA_003657725.1
AXH72610.1	000000	-	121	-	Myoviridae sp.	GCA_003657725.1
AXH72790.1	000000	-	215	-	Myoviridae sp.	GCA_003657725.1
AXH72709.1	000000	-	164	-	Myoviridae sp.	GCA_003657725.1
AXH72505.1	000000	-	164	-	Myoviridae sp.	GCA_003657725.1
AXH72586.1	000000	-	172	-	Myoviridae sp.	GCA_003657725.1
AXH72413.1	000000	-	172	-	Myoviridae sp.	GCA_003657725.1
AXH72756.1	000000	-	172	-	Myoviridae sp.	GCA_003657725.1
AXH72588.1	000000	-	172	-	Myoviridae sp.	GCA_003657725.1
AXH72576.1	000000	-	153	-	Myoviridae sp.	GCA_003657725.1
AXH72632.1	000000	-	153	-	Myoviridae sp.	GCA_003657725.1
AXH72644.1	000000	-	153	-	Myoviridae sp.	GCA_003657725.1
AXH72766.1	000000	-	153	-	Myoviridae sp.	GCA_003657725.1
AXH72651.1	000000	-	145	-	Myoviridae sp.	GCA_003657725.1
AXH72458.1	000000	-	145	-	Myoviridae sp.	GCA_003657725.1
AXH72456.1	000000	-	81	-	Myoviridae sp.	GCA_003657725.1
AXH72445.1	000000	-	188	-	Myoviridae sp.	GCA_003657725.1
AXH72788.1	000000	-	189	-	Myoviridae sp.	GCA_003657725.1
AXH72682.1	000000	-	89	-	Myoviridae sp.	GCA_003657725.1
AXH72626.1	000000	-	89	-	Myoviridae sp.	GCA_003657725.1
AXH72612.1	000000	-	86	-	Myoviridae sp.	GCA_003657725.1
AXH72590.1	000000	-	104	-	Myoviridae sp.	GCA_003657725.1
AXH72749.1	000000	-	152	-	Myoviridae sp.	GCA_003657725.1
AXH72391.1	000000	-	152	-	Myoviridae sp.	GCA_003657725.1
AXH72470.1	000000	-	149	-	Myoviridae sp.	GCA_003657725.1
AXH72614.1	000000	-	149	-	Myoviridae sp.	GCA_003657725.1
AXH72398.1	000000	-	149	-	Myoviridae sp.	GCA_003657725.1
AXH72526.1	000000	-	118	-	Myoviridae sp.	GCA_003657725.1
AXH72421.1	000000	-	118	-	Myoviridae sp.	GCA_003657725.1
AXH72594.1	000000	-	118	-	Myoviridae sp.	GCA_003657725.1
AXH72475.1	000000	-	118	-	Myoviridae sp.	GCA_003657725.1
AXH72452.1	000000	-	118	-	Myoviridae sp.	GCA_003657725.1
AXH72523.1	000000	-	115	-	Myoviridae sp.	GCA_003657725.1
AXH72681.1	000000	-	115	-	Myoviridae sp.	GCA_003657725.1
AXH72630.1	000000	-	115	-	Myoviridae sp.	GCA_003657725.1
AXH72537.1	000000	-	115	-	Myoviridae sp.	GCA_003657725.1
AXH72482.1	000000	-	115	-	Myoviridae sp.	GCA_003657725.1
AXH72603.1	000000	-	115	-	Myoviridae sp.	GCA_003657725.1
AXH72734.1	000000	-	171	-	Myoviridae sp.	GCA_003657725.1
AXH72720.1	000000	-	171	-	Myoviridae sp.	GCA_003657725.1
AXH72551.1	000000	-	171	-	Myoviridae sp.	GCA_003657725.1
AXH72782.1	000000	-	307	-	Myoviridae sp.	GCA_003657725.1
AXH72531.1	000000	-	112	-	Myoviridae sp.	GCA_003657725.1
AXH72422.1	000000	-	112	-	Myoviridae sp.	GCA_003657725.1
AXH72755.1	000000	-	146	-	Myoviridae sp.	GCA_003657725.1
AXH72599.1	000000	-	146	-	Myoviridae sp.	GCA_003657725.1
AXH72459.1	000000	-	168	-	Myoviridae sp.	GCA_003657725.1
AXH72392.1	000000	-	137	-	Myoviridae sp.	GCA_003657725.1
AXH72390.1	000000	-	137	-	Myoviridae sp.	GCA_003657725.1
AXH72524.1	000000	-	137	-	Myoviridae sp.	GCA_003657725.1
AXH72410.1	000000	-	137	-	Myoviridae sp.	GCA_003657725.1
AXH72746.1	000000	-	170	-	Myoviridae sp.	GCA_003657725.1
AXH72479.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72463.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72569.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72451.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72489.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72554.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72549.1	000000	-	105	-	Myoviridae sp.	GCA_003657725.1
AXH72631.1	000000	-	217	-	Myoviridae sp.	GCA_003657725.1
AXH72593.1	000000	-	124	-	Myoviridae sp.	GCA_003657725.1
AXH72670.1	000000	-	84	-	Myoviridae sp.	GCA_003657725.1
AXH72699.1	000000	-	84	-	Myoviridae sp.	GCA_003657725.1
AXH72492.1	000000	-	123	-	Myoviridae sp.	GCA_003657725.1
AXH72414.1	000000	-	123	-	Myoviridae sp.	GCA_003657725.1
AXH72419.1	000000	-	123	-	Myoviridae sp.	GCA_003657725.1
AXH72791.1	000000	-	433	-	Myoviridae sp.	GCA_003657725.1
AXH72740.1	000000	-	85	-	Myoviridae sp.	GCA_003657725.1
AXH72694.1	000000	-	85	-	Myoviridae sp.	GCA_003657725.1
AXH72415.1	000000	-	85	-	Myoviridae sp.	GCA_003657725.1
AXH72657.1	000000	-	85	-	Myoviridae sp.	GCA_003657725.1
AXH72597.1	000000	-	120	-	Myoviridae sp.	GCA_003657725.1
AXH72728.1	000000	-	751	-	Myoviridae sp.	GCA_003657725.1
AXH72751.1	000000	-	774	-	Myoviridae sp.	GCA_003657725.1
AXH72407.1	000000	-	94	-	Myoviridae sp.	GCA_003657725.1
AXH72591.1	000000	-	94	-	Myoviridae sp.	GCA_003657725.1
AXH72735.1	000000	-	131	-	Myoviridae sp.	GCA_003657725.1
AXH72668.1	000000	-	87	-	Myoviridae sp.	GCA_003657725.1
AXH72718.1	000000	-	87	-	Myoviridae sp.	GCA_003657725.1
AXH72581.1	000000	-	87	-	Myoviridae sp.	GCA_003657725.1
AXH72642.1	000000	-	87	-	Myoviridae sp.	GCA_003657725.1
AXH72441.1	000000	-	108	-	Myoviridae sp.	GCA_003657725.1
AXH72444.1	000000	-	108	-	Myoviridae sp.	GCA_003657725.1
AXH72778.1	000000	-	214	-	Myoviridae sp.	GCA_003657725.1
AXH72774.1	000000	-	359	-	Myoviridae sp.	GCA_003657725.1
AXH72558.1	000000	-	140	-	Myoviridae sp.	GCA_003657725.1
AXH72480.1	000000	-	140	-	Myoviridae sp.	GCA_003657725.1
AXH72503.1	000000	-	235	-	Myoviridae sp.	GCA_003657725.1
AXH72775.1	000000	-	235	-	Myoviridae sp.	GCA_003657725.1
AXH72663.1	000000	-	107	-	Myoviridae sp.	GCA_003657725.1
AXH72411.1	000000	-	107	-	Myoviridae sp.	GCA_003657725.1
AXH72399.1	000000	-	154	-	Myoviridae sp.	GCA_003657725.1
AXH72472.1	000000	-	154	-	Myoviridae sp.	GCA_003657725.1
AXH72659.1	000000	-	165	-	Myoviridae sp.	GCA_003657725.1
AXH72429.1	000000	-	207	-	Myoviridae sp.	GCA_003657725.1
AXH72522.1	000000	-	90	-	Myoviridae sp.	GCA_003657725.1
AXH72771.1	000000	-	90	-	Myoviridae sp.	GCA_003657725.1
AXH72742.1	000000	-	90	-	Myoviridae sp.	GCA_003657725.1
AXH72652.1	000000	-	98	-	Myoviridae sp.	GCA_003657725.1
AXH72692.1	000000	-	98	-	Myoviridae sp.	GCA_003657725.1
AXH72611.1	000000	-	98	-	Myoviridae sp.	GCA_003657725.1
AXH72578.1	000000	-	98	-	Myoviridae sp.	GCA_003657725.1
AXH72493.1	000000	-	109	-	Myoviridae sp.	GCA_003657725.1
AXH72625.1	000000	-	109	-	Myoviridae sp.	GCA_003657725.1
AXH72389.1	000000	-	109	-	Myoviridae sp.	GCA_003657725.1
AXH72598.1	000000	-	109	-	Myoviridae sp.	GCA_003657725.1
AXH72385.1	000000	-	109	-	Myoviridae sp.	GCA_003657725.1
AXH72388.1	000000	-	119	-	Myoviridae sp.	GCA_003657725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXH72556.1	000000	-	119	-	Myoviridae sp.	GCA_003657725.1
AXH72483.1	000000	-	119	-	Myoviridae sp.	GCA_003657725.1
AXH72476.1	000000	-	128	-	Myoviridae sp.	GCA_003657725.1
AXH72469.1	000000	-	128	-	Myoviridae sp.	GCA_003657725.1
AXH72511.1	000000	-	128	-	Myoviridae sp.	GCA_003657725.1
AXH72443.1	000000	-	128	-	Myoviridae sp.	GCA_003657725.1
AXH72438.1	000000	-	174	-	Myoviridae sp.	GCA_003657725.1
AXH72618.1	000000	-	238	-	Myoviridae sp.	GCA_003657725.1
AXH72793.1	000000	-	243	-	Myoviridae sp.	GCA_003657725.1
AXH72690.1	000000	-	96	-	Myoviridae sp.	GCA_003657725.1
AXH72634.1	000000	-	971	-	Myoviridae sp.	GCA_003657725.1
AXH72650.1	000000	-	125	-	Myoviridae sp.	GCA_003657725.1
AXH72748.1	000000	-	400	-	Myoviridae sp.	GCA_003657725.1
AXH72442.1	000000	-	414	-	Myoviridae sp.	GCA_003657725.1
AXH72754.1	000000	-	286	-	Myoviridae sp.	GCA_003657725.1
AXH72730.1	000000	-	216	-	Myoviridae sp.	GCA_003657725.1
AXH72786.1	000000	-	311	-	Myoviridae sp.	GCA_003657725.1
AXH72753.1	000000	-	256	-	Myoviridae sp.	GCA_003657725.1
AXH72574.1	000000	-	100	-	Myoviridae sp.	GCA_003657725.1
AXH72552.1	000000	-	100	-	Myoviridae sp.	GCA_003657725.1
AXH72607.1	000000	-	100	-	Myoviridae sp.	GCA_003657725.1
AXH72403.1	000000	-	169	-	Myoviridae sp.	GCA_003657725.1
AXH72539.1	000000	-	222	-	Myoviridae sp.	GCA_003657725.1
AXH72785.1	000000	-	138	-	Myoviridae sp.	GCA_003657725.1
AXH72664.1	000000	-	138	-	Myoviridae sp.	GCA_003657725.1
AXH72423.1	000000	-	142	-	Myoviridae sp.	GCA_003657725.1
AXH72534.1	000000	-	182	-	Myoviridae sp.	GCA_003657725.1
AXH72605.1	000000	-	183	-	Myoviridae sp.	GCA_003657725.1
AXH72584.1	000000	-	183	-	Myoviridae sp.	GCA_003657725.1
AXH72465.1	000000	-	186	-	Myoviridae sp.	GCA_003657725.1
AXH72637.1	000000	-	192	-	Myoviridae sp.	GCA_003657725.1
AXH72702.1	000000	-	99	-	Myoviridae sp.	GCA_003657725.1
AXH72416.1	000000	-	99	-	Myoviridae sp.	GCA_003657725.1
AXH72784.1	000000	-	301	-	Myoviridae sp.	GCA_003657725.1
QHJ78841.1	000000	-	56	-	Myoviridae sp.	GCA_012593985.1
QHJ79002.1	000000	-	83	-	Myoviridae sp.	GCA_012593985.1
QHJ78938.1	000000	-	83	-	Myoviridae sp.	GCA_012593985.1
QHJ78828.1	000000	-	83	-	Myoviridae sp.	GCA_012593985.1
QHJ79021.1	000000	-	86	-	Myoviridae sp.	GCA_012593985.1
QHJ78985.1	000000	-	86	-	Myoviridae sp.	GCA_012593985.1
QHJ79006.1	000000	-	168	-	Myoviridae sp.	GCA_012593985.1
QHJ79013.1	000000	-	211	-	Myoviridae sp.	GCA_012593985.1
QHJ78962.1	000000	-	53	-	Myoviridae sp.	GCA_012593985.1
QHJ78814.1	000000	-	64	-	Myoviridae sp.	GCA_012593985.1
QHJ79076.1	000000	-	64	-	Myoviridae sp.	GCA_012593985.1
QHJ79030.1	000000	-	73	-	Myoviridae sp.	GCA_012593985.1
QHJ78901.1	000000	-	80	-	Myoviridae sp.	GCA_012593985.1
QHJ79017.1	000000	-	161	-	Myoviridae sp.	GCA_012593985.1
QHJ78986.1	000000	-	133	-	Myoviridae sp.	GCA_012593985.1
QHJ78862.1	000000	-	47	-	Myoviridae sp.	GCA_012593985.1
QHJ78988.1	000000	-	196	-	Myoviridae sp.	GCA_012593985.1
QHJ79026.1	000000	-	92	-	Myoviridae sp.	GCA_012593985.1
QHJ78904.1	000000	-	92	-	Myoviridae sp.	GCA_012593985.1
QHJ78996.1	000000	-	103	-	Myoviridae sp.	GCA_012593985.1
QHJ78948.1	000000	-	144	-	Myoviridae sp.	GCA_012593985.1
QHJ79028.1	000000	-	88	-	Myoviridae sp.	GCA_012593985.1
QHJ78941.1	000000	-	356	-	Myoviridae sp.	GCA_012593985.1
QHJ79004.1	000000	-	110	-	Myoviridae sp.	GCA_012593985.1
QHJ78981.1	000000	-	114	-	Myoviridae sp.	GCA_012593985.1
QHJ78839.1	000000	-	119	-	Myoviridae sp.	GCA_012593985.1
QHJ79009.1	000000	-	164	-	Myoviridae sp.	GCA_012593985.1
QHJ78859.1	000000	-	55	-	Myoviridae sp.	GCA_012593985.1
QHJ79022.1	000000	-	55	-	Myoviridae sp.	GCA_012593985.1
QHJ78945.1	000000	-	57	-	Myoviridae sp.	GCA_012593985.1
QHJ79007.1	000000	-	60	-	Myoviridae sp.	GCA_012593985.1
QHJ78903.1	000000	-	60	-	Myoviridae sp.	GCA_012593985.1
QHJ79015.1	000000	-	61	-	Myoviridae sp.	GCA_012593985.1
QHJ78870.1	000000	-	61	-	Myoviridae sp.	GCA_012593985.1
QHJ79016.1	000000	-	78	-	Myoviridae sp.	GCA_012593985.1
QHJ79068.1	000000	-	79	-	Myoviridae sp.	GCA_012593985.1
QHJ79003.1	000000	-	79	-	Myoviridae sp.	GCA_012593985.1
QHJ78964.1	000000	-	84	-	Myoviridae sp.	GCA_012593985.1
QHJ79029.1	000000	-	84	-	Myoviridae sp.	GCA_012593985.1
QHJ79072.1	000000	-	84	-	Myoviridae sp.	GCA_012593985.1
QHJ79032.1	000000	-	84	-	Myoviridae sp.	GCA_012593985.1
QHJ79010.1	000000	-	85	-	Myoviridae sp.	GCA_012593985.1
QHJ78998.1	000000	-	85	-	Myoviridae sp.	GCA_012593985.1
QHJ78990.1	000000	-	93	-	Myoviridae sp.	GCA_012593985.1
QHJ78922.1	000000	-	93	-	Myoviridae sp.	GCA_012593985.1
QHJ78993.1	000000	-	98	-	Myoviridae sp.	GCA_012593985.1
QHJ79031.1	000000	-	49	-	Myoviridae sp.	GCA_012593985.1
QHJ78980.1	000000	-	116	-	Myoviridae sp.	GCA_012593985.1
QIG65669.1	000000	-	82	phiOC_p003	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65684.1	000000	-	45	phiOC_p018	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65685.1	000000	-	58	phiOC_p019	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65690.1	000000	-	194	phiOC_p024	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65691.1	000000	-	177	phiOC_p025	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65693.1	000000	-	186	phiOC_p027	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65695.1	000000	-	312	phiOC_p029	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65699.1	000000	-	108	phiOC_p033	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65706.1	000000	-	68	phiOC_p040	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65707.1	000000	-	91	phiOC_p041	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65710.1	000000	-	228	phiOC_p044	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65713.1	000000	-	73	phiOC_p047	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65716.1	000000	-	631	phiOC_p050	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65721.1	000000	-	59	phiOC_p055	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65722.1	000000	-	34	phiOC_p056	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65725.1	000000	-	84	phiOC_p060	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65726.1	000000	-	98	phiOC_p061	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65727.1	000000	-	194	phiOC_p062	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65728.1	000000	-	214	phiOC_p063	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65737.1	000000	-	46	phiOC_p072	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65744.1	000000	-	78	phiOC_p079	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65752.1	000000	-	54	phiOC_p087	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65755.1	000000	-	214	phiOC_p090	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65759.1	000000	-	226	phiOC_p094	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65760.1	000000	-	93	phiOC_p095	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65762.1	000000	-	158	phiOC_p097	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65763.1	000000	-	158	phiOC_p098	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65764.1	000000	-	162	phiOC_p099	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65766.1	000000	-	158	phiOC_p101	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65768.1	000000	-	115	phiOC_p103	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65769.1	000000	-	90	phiOC_p104	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65778.1	000000	-	146	phiOC_p113	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65786.1	000000	-	63	phiOC_p121	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65787.1	000000	-	143	phiOC_p122	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65788.1	000000	-	72	phiOC_p123	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65789.1	000000	-	70	phiOC_p124	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65790.1	000000	-	71	phiOC_p125	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65792.1	000000	-	114	phiOC_p127	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65794.1	000000	-	81	phiOC_p129	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65796.1	000000	-	105	phiOC_p131	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65798.1	000000	-	83	phiOC_p133	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65799.1	000000	-	79	phiOC_p134	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65807.1	000000	-	60	phiOC_p142	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG65809.1	000000	-	95	phiOC_p144	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65811.1	000000	-	49	phiOC_p146	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65813.1	000000	-	109	phiOC_p148	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65814.1	000000	-	74	phiOC_p149	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65815.1	000000	-	139	phiOC_p150	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65819.1	000000	-	135	phiOC_p154	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65820.1	000000	-	80	phiOC_p155	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65821.1	000000	-	185	phiOC_p156	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65826.1	000000	-	127	phiOC_p161	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65827.1	000000	-	48	phiOC_p162	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65828.1	000000	-	167	phiOC_p163	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65835.1	000000	-	61	phiOC_p170	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65839.1	000000	-	59	phiOC_p174	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65840.1	000000	-	165	phiOC_p175	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65843.1	000000	-	118	phiOC_p178	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65845.1	000000	-	88	phiOC_p180	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65846.1	000000	-	55	phiOC_p181	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65847.1	000000	-	147	phiOC_p182	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65848.1	000000	-	83	phiOC_p183	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65851.1	000000	-	103	phiOC_p186	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65852.1	000000	-	55	phiOC_p187	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65859.1	000000	-	145	phiOC_p194	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65860.1	000000	-	125	phiOC_p195	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65862.1	000000	-	96	phiOC_p197	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65864.1	000000	-	112	phiOC_p199	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65866.1	000000	-	134	phiOC_p201	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65870.1	000000	-	112	phiOC_p205	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65872.1	000000	-	213	phiOC_p207	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65874.1	000000	-	110	phiOC_p209	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65875.1	000000	-	146	phiOC_p210	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65876.1	000000	-	81	phiOC_p211	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65877.1	000000	-	78	phiOC_p212	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65880.1	000000	-	94	phiOC_p215	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65881.1	000000	-	109	phiOC_p216	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65882.1	000000	-	181	phiOC_p217	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65883.1	000000	-	165	phiOC_p218	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65885.1	000000	-	90	phiOC_p220	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65886.1	000000	-	167	phiOC_p221	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65887.1	000000	-	148	phiOC_p222	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65888.1	000000	-	50	phiOC_p223	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65890.1	000000	-	362	phiOC_p225	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65891.1	000000	-	313	phiOC_p226	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65892.1	000000	-	127	phiOC_p227	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65896.1	000000	-	62	phiOC_p235	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65897.1	000000	-	70	phiOC_p236	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65899.1	000000	-	152	phiOC_p238	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65900.1	000000	-	106	phiOC_p239	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65904.1	000000	-	572	phiOC_p243	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65905.1	000000	-	52	phiOC_p245	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65906.1	000000	-	49	phiOC_p246	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65907.1	000000	-	183	phiOC_p247	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65908.1	000000	-	65	phiOC_p248	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65909.1	000000	-	72	phiOC_p249	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65910.1	000000	-	84	phiOC_p253	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65912.1	000000	-	84	phiOC_p255	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65913.1	000000	-	43	phiOC_p260	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65915.1	000000	-	164	phiOC_p264	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65916.1	000000	-	138	phiOC_p265	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65917.1	000000	-	64	phiOC_p267	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65921.1	000000	-	37	phiOC_p275	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65922.1	000000	-	31	phiOC_p278	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65923.1	000000	-	29	phiOC_p279	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65924.1	000000	-	29	phiOC_p282	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65929.1	000000	-	36	phiOC_p287	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65930.1	000000	-	29	phiOC_p288	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65931.1	000000	-	66	phiOC_p289	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65932.1	000000	-	204	phiOC_p290	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65934.1	000000	-	72	phiOC_p292	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65935.1	000000	-	169	phiOC_p293	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65936.1	000000	-	164	phiOC_p294	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65937.1	000000	-	81	phiOC_p295	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65938.1	000000	-	59	phiOC_p296	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65939.1	000000	-	55	phiOC_p297	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65940.1	000000	-	91	phiOC_p298	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65942.1	000000	-	87	phiOC_p300	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65943.1	000000	-	270	phiOC_p301	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65944.1	000000	-	163	phiOC_p302	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65945.1	000000	-	153	phiOC_p303	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65946.1	000000	-	155	phiOC_p304	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65947.1	000000	-	150	phiOC_p305	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65948.1	000000	-	298	phiOC_p306	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65950.1	000000	-	158	phiOC_p308	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65951.1	000000	-	88	phiOC_p309	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65954.1	000000	-	285	phiOC_p312	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65957.1	000000	-	61	phiOC_p315	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65959.1	000000	-	54	phiOC_p317	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65961.1	000000	-	98	phiOC_p319	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65962.1	000000	-	192	phiOC_p320	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65964.1	000000	-	70	phiOC_p322	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65965.1	000000	-	117	phiOC_p323	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65966.1	000000	-	66	phiOC_p324	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65969.1	000000	-	63	phiOC_p327	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65970.1	000000	-	84	phiOC_p328	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65971.1	000000	-	81	phiOC_p329	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65974.1	000000	-	226	phiOC_p332	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65976.1	000000	-	54	phiOC_p334	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65977.1	000000	-	70	phiOC_p335	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65978.1	000000	-	61	phiOC_p336	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65980.1	000000	-	150	phiOC_p338	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65981.1	000000	-	175	phiOC_p339	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65984.1	000000	-	157	phiOC_p342	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65985.1	000000	-	90	phiOC_p343	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65989.1	000000	-	58	phiOC_p347	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65991.1	000000	-	245	phiOC_p349	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65992.1	000000	-	129	phiOC_p350	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65993.1	000000	-	293	phiOC_p351	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65994.1	000000	-	264	phiOC_p352	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65995.1	000000	-	284	phiOC_p353	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65997.1	000000	-	202	phiOC_p355	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG65998.1	000000	-	393	phiOC_p356	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66005.1	000000	-	163	phiOC_p363	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66006.1	000000	-	130	phiOC_p364	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66007.1	000000	-	177	phiOC_p365	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66008.1	000000	-	162	phiOC_p366	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66009.1	000000	-	178	phiOC_p367	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66011.1	000000	-	185	phiOC_p369	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66014.1	000000	-	73	phiOC_p372	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66015.1	000000	-	104	phiOC_p373	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66016.1	000000	-	57	phiOC_p374	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66019.1	000000	-	67	phiOC_p377	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66020.1	000000	-	67	phiOC_p378	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66030.1	000000	-	292	phiOC_p388	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66037.1	000000	-	83	phiOC_p395	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66038.1	000000	-	79	phiOC_p396	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66042.1	000000	-	97	phiOC_p400	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIG66044.1	000000	-	135	phiOC_p402	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66045.1	000000	-	62	phiOC_p403	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66046.1	000000	-	61	phiOC_p404	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66048.1	000000	-	122	phiOC_p406	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66055.1	000000	-	144	phiOC_p413	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
QIG66056.1	000000	-	65	phiOC_p414	Ochrobactrum phage vB_OspM_OC	GCA_011067635.1
AMM43566.1	000000	-	55	CBB_1	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43755.1	000000	-	47	CBB_190	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43913.1	000000	-	79	CBB_350	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43918.1	000000	-	116	CBB_355	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43926.1	000000	-	103	CBB_363	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43928.1	000000	-	67	CBB_365	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43930.1	000000	-	101	CBB_367	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43976.1	000000	-	67	CBB_413	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43989.1	000000	-	70	CBB_426	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43995.1	000000	-	100	CBB_432	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44021.1	000000	-	103	CBB_458	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44028.1	000000	-	127	CBB_465	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44046.1	000000	-	47	CBB_483	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44055.1	000000	-	65	CBB_492	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44056.1	000000	-	73	CBB_493	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44073.1	000000	-	63	CBB_510	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM44080.1	000000	-	98	CBB_517	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
AMM43641.1	000000	-	52	CBB_76	Pectinobacterium phage vB_PcaM_CBB	GCA_002609265.1
SBV38171.1	000000	-	89	BN7874_002	Phage NCTB	GCA_900092385.1
SBV38173.1	000000	-	253	BN7874_004	Phage NCTB	GCA_900092385.1
SBV38178.1	000000	-	164	BN7874_009	Phage NCTB	GCA_900092385.1
SBV38179.1	000000	-	108	BN7874_010	Phage NCTB	GCA_900092385.1
SBV38181.1	000000	-	59	BN7874_012	Phage NCTB	GCA_900092385.1
SBV38185.1	000000	-	88	BN7874_016	Phage NCTB	GCA_900092385.1
SBV38186.1	000000	-	39	BN7874_017	Phage NCTB	GCA_900092385.1
SBV38187.1	000000	-	195	BN7874_018	Phage NCTB	GCA_900092385.1
SBV38192.1	000000	-	132	BN7874_023	Phage NCTB	GCA_900092385.1
SBV38194.1	000000	-	288	BN7874_025	Phage NCTB	GCA_900092385.1
SBV38195.1	000000	-	209	BN7874_026	Phage NCTB	GCA_900092385.1
SBV38196.1	000000	-	111	BN7874_027	Phage NCTB	GCA_900092385.1
SBV38199.1	000000	-	109	BN7874_030	Phage NCTB	GCA_900092385.1
SBV38200.1	000000	-	82	BN7874_031	Phage NCTB	GCA_900092385.1
SBV38201.1	000000	-	198	BN7874_032	Phage NCTB	GCA_900092385.1
SBV38202.1	000000	-	243	BN7874_033	Phage NCTB	GCA_900092385.1
SBV38205.1	000000	-	67	BN7874_036	Phage NCTB	GCA_900092385.1
SBV38207.1	000000	-	114	BN7874_038	Phage NCTB	GCA_900092385.1
SBV38209.1	000000	-	202	BN7874_040	Phage NCTB	GCA_900092385.1
SBV38211.1	000000	-	119	BN7874_042	Phage NCTB	GCA_900092385.1
SBV38214.1	000000	-	396	BN7874_045	Phage NCTB	GCA_900092385.1
SBV38215.1	000000	-	102	BN7874_046	Phage NCTB	GCA_900092385.1
SBV38216.1	000000	-	238	BN7874_047	Phage NCTB	GCA_900092385.1
SBV38217.1	000000	-	185	BN7874_048	Phage NCTB	GCA_900092385.1
SBV38218.1	000000	-	51	BN7874_049	Phage NCTB	GCA_900092385.1
SBV38221.1	000000	-	120	BN7874_052	Phage NCTB	GCA_900092385.1
SBV38225.1	000000	-	97	BN7874_056	Phage NCTB	GCA_900092385.1
SBV38227.1	000000	-	62	BN7874_058	Phage NCTB	GCA_900092385.1
SBV38228.1	000000	-	266	BN7874_059	Phage NCTB	GCA_900092385.1
SBV38229.1	000000	-	121	BN7874_060	Phage NCTB	GCA_900092385.1
SBV38230.1	000000	-	134	BN7874_061	Phage NCTB	GCA_900092385.1
SBV38231.1	000000	-	417	BN7874_062	Phage NCTB	GCA_900092385.1
SBV38233.1	000000	-	86	BN7874_064	Phage NCTB	GCA_900092385.1
SBV38235.1	000000	-	125	BN7874_066	Phage NCTB	GCA_900092385.1
SBV38236.1	000000	-	183	BN7874_067	Phage NCTB	GCA_900092385.1
SBV38237.1	000000	-	131	BN7874_068	Phage NCTB	GCA_900092385.1
SBV38238.1	000000	-	174	BN7874_069	Phage NCTB	GCA_900092385.1
SBV38240.1	000000	-	89	BN7874_071	Phage NCTB	GCA_900092385.1
SBV38241.1	000000	-	70	BN7874_072	Phage NCTB	GCA_900092385.1
SBV38243.1	000000	-	129	BN7874_074	Phage NCTB	GCA_900092385.1
SBV38244.1	000000	-	455	BN7874_075	Phage NCTB	GCA_900092385.1
SBV38245.1	000000	-	420	BN7874_076	Phage NCTB	GCA_900092385.1
SBV38249.1	000000	-	197	BN7874_080	Phage NCTB	GCA_900092385.1
SBV38250.1	000000	-	122	BN7874_081	Phage NCTB	GCA_900092385.1
SBV38252.1	000000	-	112	BN7874_083	Phage NCTB	GCA_900092385.1
SBV38253.1	000000	-	163	BN7874_084	Phage NCTB	GCA_900092385.1
SBV38254.1	000000	-	114	BN7874_085	Phage NCTB	GCA_900092385.1
SBV38256.1	000000	-	460	BN7874_087	Phage NCTB	GCA_900092385.1
SBV38260.1	000000	-	161	BN7874_091	Phage NCTB	GCA_900092385.1
SBV38262.1	000000	-	282	BN7874_093	Phage NCTB	GCA_900092385.1
SBV38264.1	000000	-	238	BN7874_095	Phage NCTB	GCA_900092385.1
SBV38266.1	000000	-	317	BN7874_097	Phage NCTB	GCA_900092385.1
SBV38267.1	000000	-	126	BN7874_098	Phage NCTB	GCA_900092385.1
SBV38268.1	000000	-	98	BN7874_099	Phage NCTB	GCA_900092385.1
SBV38270.1	000000	-	102	BN7874_101	Phage NCTB	GCA_900092385.1
SBV38271.1	000000	-	191	BN7874_102	Phage NCTB	GCA_900092385.1
SBV38274.1	000000	-	63	BN7874_105	Phage NCTB	GCA_900092385.1
SBV38276.1	000000	-	218	BN7874_107	Phage NCTB	GCA_900092385.1
SBV38277.1	000000	-	184	BN7874_108	Phage NCTB	GCA_900092385.1
SBV38279.1	000000	-	226	BN7874_110	Phage NCTB	GCA_900092385.1
SBV38280.1	000000	-	208	BN7874_111	Phage NCTB	GCA_900092385.1
SBV38283.1	000000	-	182	BN7874_114	Phage NCTB	GCA_900092385.1
SBV38286.1	000000	-	91	BN7874_117	Phage NCTB	GCA_900092385.1
SBV38296.1	000000	-	161	BN7874_127	Phage NCTB	GCA_900092385.1
SBV38298.1	000000	-	38	BN7874_129	Phage NCTB	GCA_900092385.1
SBV38299.1	000000	-	159	BN7874_130	Phage NCTB	GCA_900092385.1
SBV38307.1	000000	-	1625	BN7874_138	Phage NCTB	GCA_900092385.1
SBV38311.1	000000	-	181	BN7874_142	Phage NCTB	GCA_900092385.1
SBV38312.1	000000	-	102	BN7874_143	Phage NCTB	GCA_900092385.1
SBV38314.1	000000	-	123	BN7874_145	Phage NCTB	GCA_900092385.1
SBV38315.1	000000	-	207	BN7874_146	Phage NCTB	GCA_900092385.1
SBV38316.1	000000	-	85	BN7874_147	Phage NCTB	GCA_900092385.1
SBV38317.1	000000	-	72	BN7874_148	Phage NCTB	GCA_900092385.1
SBV38318.1	000000	-	176	BN7874_149	Phage NCTB	GCA_900092385.1
SBV38319.1	000000	-	300	BN7874_150	Phage NCTB	GCA_900092385.1
SBV38322.1	000000	-	61	BN7874_153	Phage NCTB	GCA_900092385.1
SBV38324.1	000000	-	96	BN7874_155	Phage NCTB	GCA_900092385.1
SBV38329.1	000000	-	243	BN7874_160	Phage NCTB	GCA_900092385.1
SBV38332.1	000000	-	45	BN7874_163	Phage NCTB	GCA_900092385.1
SBV38336.1	000000	-	126	BN7874_167	Phage NCTB	GCA_900092385.1
SBV38337.1	000000	-	188	BN7874_168	Phage NCTB	GCA_900092385.1
SBV38339.1	000000	-	45	BN7874_170	Phage NCTB	GCA_900092385.1
SBV38340.1	000000	-	823	BN7874_171	Phage NCTB	GCA_900092385.1
SBV38341.1	000000	-	224	BN7874_172	Phage NCTB	GCA_900092385.1
SBV38342.1	000000	-	179	BN7874_173	Phage NCTB	GCA_900092385.1
SBV38345.1	000000	-	211	BN7874_176	Phage NCTB	GCA_900092385.1
SBV38346.1	000000	-	86	BN7874_177	Phage NCTB	GCA_900092385.1
SBV38349.1	000000	-	83	BN7874_180	Phage NCTB	GCA_900092385.1
SBV38353.1	000000	-	308	BN7874_184	Phage NCTB	GCA_900092385.1
SBV38354.1	000000	-	153	BN7874_185	Phage NCTB	GCA_900092385.1
SBV38356.1	000000	-	250	BN7874_187	Phage NCTB	GCA_900092385.1
SBV38361.1	000000	-	136	BN7874_192	Phage NCTB	GCA_900092385.1
SBV38362.1	000000	-	151	BN7874_193	Phage NCTB	GCA_900092385.1
SBV38367.1	000000	-	356	BN7874_197	Phage NCTB	GCA_900092385.1
SBV38368.1	000000	-	341	BN7874_198	Phage NCTB	GCA_900092385.1
SBV38373.1	000000	-	175	BN7874_202	Phage NCTB	GCA_900092385.1
SBV38374.1	000000	-	101	BN7874_203	Phage NCTB	GCA_900092385.1
SBV38383.1	000000	-	847	BN7874_209	Phage NCTB	GCA_900092385.1
SBV38393.1	000000	-	105	BN7874_214	Phage NCTB	GCA_900092385.1
SBV38399.1	000000	-	65	BN7874_217	Phage NCTB	GCA_900092385.1
SBV38403.1	000000	-	134	BN7874_219	Phage NCTB	GCA_900092385.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
SBV38407.1	000000	-	591	BN7874_223	Phage NCTB	GCA_900092385.1
SBV38415.1	000000	-	158	BN7874_229	Phage NCTB	GCA_900092385.1
SBV38419.1	000000	-	175	BN7874_231	Phage NCTB	GCA_900092385.1
SBV38421.1	000000	-	107	BN7874_232	Phage NCTB	GCA_900092385.1
SBV38427.1	000000	-	88	BN7874_236	Phage NCTB	GCA_900092385.1
SBV38430.1	000000	-	60	BN7874_238	Phage NCTB	GCA_900092385.1
SBV38456.1	000000	-	262	BN7874_253	Phage NCTB	GCA_900092385.1
SBV38457.1	000000	-	71	BN7874_254	Phage NCTB	GCA_900092385.1
SBV38461.1	000000	-	81	BN7874_258	Phage NCTB	GCA_900092385.1
SBV38468.1	000000	-	46	BN7874_263	Phage NCTB	GCA_900092385.1
SBV38469.1	000000	-	70	BN7874_264	Phage NCTB	GCA_900092385.1
SBV38472.1	000000	-	143	BN7874_266	Phage NCTB	GCA_900092385.1
SBV38476.1	000000	-	116	BN7874_268	Phage NCTB	GCA_900092385.1
SBV38486.1	000000	-	188	BN7874_273	Phage NCTB	GCA_900092385.1
SBV38487.1	000000	-	268	BN7874_274	Phage NCTB	GCA_900092385.1
SBV38511.1	000000	-	216	BN7874_285	Phage NCTB	GCA_900092385.1
SBV38527.1	000000	-	190	BN7874_290	Phage NCTB	GCA_900092385.1
SBV38533.1	000000	-	41	BN7874_292	Phage NCTB	GCA_900092385.1
SBV38534.1	000000	-	47	BN7874_293	Phage NCTB	GCA_900092385.1
SBV38536.1	000000	-	72	BN7874_294	Phage NCTB	GCA_900092385.1
SBV38539.1	000000	-	296	BN7874_296	Phage NCTB	GCA_900092385.1
SBV38548.1	000000	-	127	BN7874_299	Phage NCTB	GCA_900092385.1
SBV38552.1	000000	-	354	BN7874_301	Phage NCTB	GCA_900092385.1
QGZ14428.1	000000	-	62	HWC77_gp065	Photobacterium phage PDCC-1	GCA_009800445.1
AGH26106.1	000000	-	90	CPMG_00005	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26111.1	000000	-	51	CPMG_00010	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26113.1	000000	-	122	CPMG_00012	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26120.1	000000	-	111	CPMG_00019	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26121.1	000000	-	61	CPMG_00020	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26127.1	000000	-	946	CPMG_00026	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26129.1	000000	-	68	CPMG_00028	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26131.1	000000	-	73	CPMG_00030	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26139.1	000000	-	55	CPMG_00038	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26141.1	000000	-	169	CPMG_00040	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26142.1	000000	-	72	CPMG_00041	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26143.1	000000	-	75	CPMG_00042	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26146.1	000000	-	67	CPMG_00045	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26147.1	000000	-	59	CPMG_00046	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26148.1	000000	-	65	CPMG_00047	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26151.1	000000	-	60	CPMG_00050	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26152.1	000000	-	102	CPMG_00051	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26153.1	000000	-	55	CPMG_00052	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26155.1	000000	-	58	CPMG_00054	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26164.1	000000	-	59	CPMG_00063	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26166.1	000000	-	83	CPMG_00065	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26167.1	000000	-	75	CPMG_00066	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26168.1	000000	-	85	CPMG_00067	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26169.1	000000	-	60	CPMG_00068	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26174.1	000000	-	55	CPMG_00073	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26179.1	000000	-	107	CPMG_00078	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26180.1	000000	-	223	CPMG_00079	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26181.1	000000	-	239	CPMG_00080	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26182.1	000000	-	156	CPMG_00081	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26185.1	000000	-	336	CPMG_00084	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26190.1	000000	-	78	CPMG_00089	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26194.1	000000	-	577	CPMG_00093	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26211.1	000000	-	282	CPMG_00110	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26219.1	000000	-	114	CPMG_00118	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26253.1	000000	-	258	CPMG_00152	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26258.1	000000	-	78	CPMG_00157	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26260.1	000000	-	80	CPMG_00159	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26262.1	000000	-	50	CPMG_00161	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26264.1	000000	-	67	CPMG_00163	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26275.1	000000	-	61	CPMG_00175	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26277.1	000000	-	73	CPMG_00177	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26281.1	000000	-	484	CPMG_00181	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26286.1	000000	-	182	CPMG_00186	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26290.1	000000	-	153	CPMG_00190	Prochlorococcus phage MED4-213	GCA_000904535.1
AGH26297.1	000000	-	69	CPMG_00197	Prochlorococcus phage MED4-213	GCA_000904535.1
AAX44449.1	000000	-	42	PSSM2_071	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44447.2	000000	-	56	PSSM2_073.1	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44476.1	000000	-	51	PSSM2_098	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44530.1	000000	-	45	PSSM2_152	Prochlorococcus phage P-SSM2	GCA_000859585.1
AAX44611.1	000000	-	27	PSSM2_234	Prochlorococcus phage P-SSM2	GCA_000859585.1
AGN12169.1	000000	-	64	PRTG_00011	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12170.1	000000	-	59	PRTG_00012	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12176.1	000000	-	59	PRTG_00018	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12198.1	000000	-	50	PRTG_00040	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12278.1	000000	-	49	PRTG_00125	Prochlorococcus phage P-SSM5	GCA_002991095.1
AGN12376.1	000000	-	82	PRTG_00223	Prochlorococcus phage P-SSM5	GCA_002991095.1
AIR93499.1	000000	-	60	AVU42_gp160	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93619.1	000000	-	52	AVU42_gp074	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93537.1	000000	-	52	AVU42_gp200	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93601.1	000000	-	75	AVU42_gp056	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93589.1	000000	-	64	AVU42_gp038	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93448.1	000000	-	64	AVU42_gp110	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93591.1	000000	-	61	AVU42_gp040	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93464.1	000000	-	58	AVU42_gp125	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93416.1	000000	-	77	AVU42_gp034	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93482.1	000000	-	51	AVU42_gp144	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93613.1	000000	-	68	AVU42_gp068	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93617.1	000000	-	62	AVU42_gp072	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93616.1	000000	-	57	AVU42_gp071	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93615.1	000000	-	57	AVU42_gp070	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93608.1	000000	-	57	AVU42_gp063	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93602.1	000000	-	48	AVU42_gp057	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93586.1	000000	-	67	AVU42_gp030	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93598.1	000000	-	53	AVU42_gp048	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93612.1	000000	-	53	AVU42_gp067	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93600.1	000000	-	55	AVU42_gp055	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93509.1	000000	-	101	AVU42_gp171	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93606.1	000000	-	137	AVU42_gp061	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93618.1	000000	-	50	AVU42_gp073	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93594.1	000000	-	96	AVU42_gp043	Prochlorococcus phage P-TIM68	GCA_001503075.1
AIR93524.1	000000	-	268	AVU42_gp187	Prochlorococcus phage P-TIM68	GCA_001503075.1
ADO99104.1	000000	-	41	Syn1_002	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99131.1	000000	-	26	Syn1_030	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99174.1	000000	-	44	Syn1_073	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99178.1	000000	-	69	Syn1_077	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99187.1	000000	-	66	Syn1_086	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99189.1	000000	-	74	Syn1_088	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99283.1	000000	-	40	Syn1_182	Prochlorococcus phage Syn1	GCA_000892495.1
ADO99315.1	000000	-	41	Syn1_218	Prochlorococcus phage Syn1	GCA_000892495.1
QMP24105.1	000000	-	581	-	Proteus phage 10	GCA_014071245.1
QMP24139.1	000000	-	137	-	Proteus phage 10	GCA_014071245.1
QMP24221.1	000000	-	148	-	Proteus phage 10	GCA_014071245.1
QMP24183.1	000000	-	148	-	Proteus phage 10	GCA_014071245.1
QMP24032.1	000000	-	254	-	Proteus phage 10	GCA_014071245.1
QMP24027.1	000000	-	118	-	Proteus phage 10	GCA_014071245.1
QMP24016.1	000000	-	112	-	Proteus phage 10	GCA_014071245.1
QMP24141.1	000000	-	103	-	Proteus phage 10	GCA_014071245.1
QMP24129.1	000000	-	131	-	Proteus phage 10	GCA_014071245.1
QMP24154.1	000000	-	150	-	Proteus phage 10	GCA_014071245.1
QMP24046.1	000000	-	377	-	Proteus phage 10	GCA_014071245.1
QMP24128.1	000000	-	113	-	Proteus phage 10	GCA_014071245.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QMP24208.1	000000	-	371	-	Proteus phage 10	GCA_014071245.1
QMP24170.1	000000	-	323	-	Proteus phage 10	GCA_014071245.1
QMP24062.1	000000	-	144	-	Proteus phage 10	GCA_014071245.1
QMP24126.1	000000	-	139	-	Proteus phage 10	GCA_014071245.1
QMP24207.1	000000	-	347	-	Proteus phage 10	GCA_014071245.1
QMP24019.1	000000	-	135	-	Proteus phage 10	GCA_014071245.1
QMP24070.1	000000	-	173	-	Proteus phage 10	GCA_014071245.1
QMP24017.1	000000	-	171	-	Proteus phage 10	GCA_014071245.1
QMP24182.1	000000	-	232	-	Proteus phage 10	GCA_014071245.1
QMP24014.1	000000	-	65	-	Proteus phage 10	GCA_014071245.1
QMP24106.1	000000	-	309	-	Proteus phage 10	GCA_014071245.1
QMP24200.1	000000	-	446	-	Proteus phage 10	GCA_014071245.1
QMP24124.1	000000	-	160	-	Proteus phage 10	GCA_014071245.1
QMP24190.1	000000	-	160	-	Proteus phage 10	GCA_014071245.1
QMP24123.1	000000	-	161	-	Proteus phage 10	GCA_014071245.1
QMP24028.1	000000	-	145	-	Proteus phage 10	GCA_014071245.1
QMP24220.1	000000	-	104	-	Proteus phage 10	GCA_014071245.1
QMP24130.1	000000	-	104	-	Proteus phage 10	GCA_014071245.1
QMP24209.1	000000	-	365	-	Proteus phage 10	GCA_014071245.1
QMP24066.1	000000	-	47	-	Proteus phage 10	GCA_014071245.1
QMP24034.1	000000	-	295	-	Proteus phage 10	GCA_014071245.1
QMP24135.1	000000	-	502	-	Proteus phage 10	GCA_014071245.1
QMP24181.1	000000	-	235	-	Proteus phage 10	GCA_014071245.1
QMP24022.1	000000	-	154	-	Proteus phage 10	GCA_014071245.1
QMP24051.1	000000	-	110	-	Proteus phage 10	GCA_014071245.1
QMP24060.1	000000	-	110	-	Proteus phage 10	GCA_014071245.1
QMP24151.1	000000	-	114	-	Proteus phage 10	GCA_014071245.1
QMP24055.1	000000	-	119	-	Proteus phage 10	GCA_014071245.1
QMP24137.1	000000	-	120	-	Proteus phage 10	GCA_014071245.1
QMP24121.1	000000	-	120	-	Proteus phage 10	GCA_014071245.1
QMP24048.1	000000	-	122	-	Proteus phage 10	GCA_014071245.1
QMP24059.1	000000	-	125	-	Proteus phage 10	GCA_014071245.1
QMP24150.1	000000	-	125	-	Proteus phage 10	GCA_014071245.1
QMP24140.1	000000	-	127	-	Proteus phage 10	GCA_014071245.1
QMP24120.1	000000	-	130	-	Proteus phage 10	GCA_014071245.1
QMP24049.1	000000	-	130	-	Proteus phage 10	GCA_014071245.1
QMP24069.1	000000	-	132	-	Proteus phage 10	GCA_014071245.1
QMP24033.1	000000	-	192	-	Proteus phage 10	GCA_014071245.1
QMP24029.1	000000	-	192	-	Proteus phage 10	GCA_014071245.1
QMP24222.1	000000	-	59	-	Proteus phage 10	GCA_014071245.1
QMP24052.1	000000	-	60	-	Proteus phage 10	GCA_014071245.1
QMP24125.1	000000	-	78	-	Proteus phage 10	GCA_014071245.1
QMP24006.1	000000	-	84	-	Proteus phage 10	GCA_014071245.1
QMP24071.1	000000	-	91	-	Proteus phage 10	GCA_014071245.1
QMP24047.1	000000	-	97	-	Proteus phage 10	GCA_014071245.1
QMP24018.1	000000	-	97	-	Proteus phage 10	GCA_014071245.1
QMP24074.1	000000	-	69	-	Proteus phage 10	GCA_014071245.1
QMP24026.1	000000	-	69	-	Proteus phage 10	GCA_014071245.1
QMP24103.1	000000	-	87	-	Proteus phage 10	GCA_014071245.1
QMP24088.1	000000	-	94	-	Proteus phage 10	GCA_014071245.1
QMP24152.1	000000	-	159	-	Proteus phage 10	GCA_014071245.1
QMP24024.1	000000	-	401	-	Proteus phage 10	GCA_014071245.1
QMP24217.1	000000	-	529	-	Proteus phage 10	GCA_014071245.1
QMP24205.1	000000	-	63	-	Proteus phage 10	GCA_014071245.1
QMP24025.1	000000	-	186	-	Proteus phage 10	GCA_014071245.1
QMP24148.1	000000	-	201	-	Proteus phage 10	GCA_014071245.1
QMP24107.1	000000	-	206	-	Proteus phage 10	GCA_014071245.1
ABY62841.1	000000	-	164	201phi2-1p007	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62842.1	000000	-	201	201phi2-1p008	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62843.1	000000	-	75	201phi2-1p009	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62846.1	000000	-	63	201phi2-1p012	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62847.1	000000	-	125	201phi2-1p013	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62849.1	000000	-	82	201phi2-1p015	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62850.1	000000	-	46	201phi2-1p016	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62851.1	000000	-	95	201phi2-1p017	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62852.1	000000	-	91	201phi2-1p018	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62854.1	000000	-	53	201phi2-1p020	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62855.1	000000	-	136	201phi2-1p021	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62856.1	000000	-	107	201phi2-1p022	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62857.1	000000	-	85	201phi2-1p023	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62860.1	000000	-	90	201phi2-1p026	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62866.1	000000	-	80	201phi2-1p033	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62870.1	000000	-	100	201phi2-1p037	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62871.1	000000	-	82	201phi2-1p038	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62872.1	000000	-	106	201phi2-1p039	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62873.1	000000	-	97	201phi2-1p040	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62874.1	000000	-	190	201phi2-1p041	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62876.1	000000	-	103	201phi2-1p043	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62877.1	000000	-	124	201phi2-1p044	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62880.1	000000	-	99	201phi2-1p047	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62882.1	000000	-	115	201phi2-1p049	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62884.1	000000	-	122	201phi2-1p051	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62887.1	000000	-	449	201phi2-1p054	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62891.1	000000	-	110	201phi2-1p058	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62893.1	000000	-	94	201phi2-1p060	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62894.1	000000	-	109	201phi2-1p061	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62900.1	000000	-	124	201phi2-1p067	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62901.1	000000	-	90	201phi2-1p068	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62913.1	000000	-	128	201phi2-1p080	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62915.1	000000	-	145	201phi2-1p082	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62917.1	000000	-	125	201phi2-1p084	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62919.1	000000	-	63	201phi2-1p086	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62920.1	000000	-	71	201phi2-1p087	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62921.1	000000	-	594	201phi2-1p088	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62924.1	000000	-	63	201phi2-1p091	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62925.1	000000	-	56	201phi2-1p092	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62926.1	000000	-	121	201phi2-1p093	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62927.1	000000	-	116	201phi2-1p094	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62928.1	000000	-	57	201phi2-1p095	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62929.1	000000	-	111	201phi2-1p096	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62930.1	000000	-	100	201phi2-1p097	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62932.1	000000	-	57	201phi2-1p099	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62933.1	000000	-	76	201phi2-1p100	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62934.1	000000	-	96	201phi2-1p101	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62936.1	000000	-	71	201phi2-1p103	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62940.1	000000	-	142	201phi2-1p108	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62941.1	000000	-	174	201phi2-1p109	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62942.1	000000	-	135	201phi2-1p110	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62944.1	000000	-	117	201phi2-1p112	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62945.1	000000	-	51	201phi2-1p113	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62947.1	000000	-	124	201phi2-1p115	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62948.1	000000	-	156	201phi2-1p116	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62949.1	000000	-	139	201phi2-1p117	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62960.1	000000	-	59	201phi2-1p128	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY62973.1	000000	-	97	201phi2-1p142	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63004.1	000000	-	146	201phi2-1p174	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63005.1	000000	-	317	201phi2-1p175	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63006.1	000000	-	69	201phi2-1p176	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63007.1	000000	-	139	201phi2-1p177	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63011.1	000000	-	97	201phi2-1p181	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63014.1	000000	-	170	201phi2-1p184	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63016.1	000000	-	91	201phi2-1p186	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63017.1	000000	-	166	201phi2-1p187	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63019.1	000000	-	117	201phi2-1p189	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63022.1	000000	-	91	201phi2-1p192	Pseudomonas phage 201phi2-1	GCA_000875305.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ABY63024.1	000000	-	130	201phi2-1p194	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63025.1	000000	-	116	201phi2-1p195	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63026.1	000000	-	133	201phi2-1p196	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63030.1	000000	-	172	201phi2-1p201	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63031.1	000000	-	345	201phi2-1p202	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63034.1	000000	-	109	201phi2-1p205	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63088.1	000000	-	297	201phi2-1p260	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63091.1	000000	-	258	201phi2-1p263	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63094.1	000000	-	129	201phi2-1p266	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63106.1	000000	-	174	201phi2-1p279	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63108.1	000000	-	163	201phi2-1p281	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63111.1	000000	-	127	201phi2-1p284	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63117.1	000000	-	80	201phi2-1p291	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63119.1	000000	-	125	201phi2-1p293	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63120.1	000000	-	157	201phi2-1p294	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63128.1	000000	-	57	201phi2-1p302	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63130.1	000000	-	140	201phi2-1p304	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63131.1	000000	-	241	201phi2-1p305	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63135.1	000000	-	103	201phi2-1p309	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63136.1	000000	-	133	201phi2-1p310	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63137.1	000000	-	304	201phi2-1p311	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63140.1	000000	-	140	201phi2-1p314	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63147.1	000000	-	166	201phi2-1p322	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63148.1	000000	-	124	201phi2-1p323	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63152.1	000000	-	130	201phi2-1p327	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63153.1	000000	-	205	201phi2-1p328	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63154.1	000000	-	113	201phi2-1p329	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63160.1	000000	-	343	201phi2-1p335	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63161.1	000000	-	79	201phi2-1p336	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63164.1	000000	-	82	201phi2-1p339	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63165.1	000000	-	107	201phi2-1p340	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63167.1	000000	-	80	201phi2-1p342	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63170.1	000000	-	77	201phi2-1p344	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63175.1	000000	-	132	201phi2-1p349	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63177.1	000000	-	77	201phi2-1p351	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63178.1	000000	-	197	201phi2-1p352	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63179.1	000000	-	107	201phi2-1p353	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63182.1	000000	-	243	201phi2-1p356	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63183.1	000000	-	93	201phi2-1p357	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63184.1	000000	-	29	201phi2-1p358	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63185.1	000000	-	105	201phi2-1p360	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63190.1	000000	-	193	201phi2-1p365	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63191.1	000000	-	205	201phi2-1p366	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63193.1	000000	-	145	201phi2-1p368	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63196.1	000000	-	74	201phi2-1p371	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63197.1	000000	-	123	201phi2-1p372	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63202.1	000000	-	104	201phi2-1p377	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63203.1	000000	-	158	201phi2-1p378	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63205.1	000000	-	66	201phi2-1p380	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63210.1	000000	-	116	201phi2-1p385	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63214.1	000000	-	80	201phi2-1p389	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63218.1	000000	-	77	201phi2-1p394	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63219.1	000000	-	233	201phi2-1p395	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63221.1	000000	-	89	201phi2-1p397	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63223.1	000000	-	54	201phi2-1p399	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63224.1	000000	-	115	201phi2-1p400	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63226.1	000000	-	64	201phi2-1p402	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63227.1	000000	-	188	201phi2-1p403	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63228.1	000000	-	114	201phi2-1p404	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63229.1	000000	-	182	201phi2-1p405	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63232.1	000000	-	60	201phi2-1p408	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63233.1	000000	-	99	201phi2-1p409	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63234.1	000000	-	275	201phi2-1p410	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63235.1	000000	-	273	201phi2-1p411	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63236.1	000000	-	116	201phi2-1p412	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63237.1	000000	-	94	201phi2-1p413	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63239.1	000000	-	145	201phi2-1p415	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63240.1	000000	-	95	201phi2-1p416	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63242.1	000000	-	298	201phi2-1p418	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63248.1	000000	-	88	201phi2-1p425	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63250.1	000000	-	165	201phi2-1p427	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63251.1	000000	-	143	201phi2-1p428	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63256.1	000000	-	83	201phi2-1p433	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63258.1	000000	-	108	201phi2-1p435	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63260.1	000000	-	118	201phi2-1p437	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63267.1	000000	-	103	201phi2-1p444	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63268.1	000000	-	112	201phi2-1p445	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63269.1	000000	-	172	201phi2-1p446	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63270.1	000000	-	206	201phi2-1p447	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63274.1	000000	-	48	201phi2-1p451	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63276.1	000000	-	70	201phi2-1p453	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63281.1	000000	-	141	201phi2-1p458	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63283.1	000000	-	132	201phi2-1p460	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63284.1	000000	-	121	201phi2-1p461	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63285.1	000000	-	138	201phi2-1p462	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63286.1	000000	-	152	201phi2-1p463	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63287.1	000000	-	98	201phi2-1p464	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63288.1	000000	-	164	201phi2-1p465	Pseudomonas phage 201phi2-1	GCA_000875305.1
ABY63289.1	000000	-	69	201phi2-1p466	Pseudomonas phage 201phi2-1	GCA_000875305.1
CAG27291.1	000000	-	101	PPEV_gp197	Pseudomonas phage EL	GCA_000866825.1
CAG27180.1	000000	-	155	PPEV_gp086	Pseudomonas phage EL	GCA_000866825.1
CAG27236.1	000000	-	159	PPEV_gp142	Pseudomonas phage EL	GCA_000866825.1
CAG27255.1	000000	-	159	PPEV_gp161	Pseudomonas phage EL	GCA_000866825.1
CAG27137.1	000000	-	159	PPEV_gp043	Pseudomonas phage EL	GCA_000866825.1
CAG27190.1	000000	-	80	PPEV_gp096	Pseudomonas phage EL	GCA_000866825.1
CAG27235.1	000000	-	92	PPEV_gp141	Pseudomonas phage EL	GCA_000866825.1
CAG27188.1	000000	-	63	PPEV_gp094	Pseudomonas phage EL	GCA_000866825.1
CAG27217.1	000000	-	435	PPEV_gp123	Pseudomonas phage EL	GCA_000866825.1
CAG27181.1	000000	-	160	PPEV_gp087	Pseudomonas phage EL	GCA_000866825.1
CAG27293.1	000000	-	111	PPEV_gp199	Pseudomonas phage EL	GCA_000866825.1
CAG27185.1	000000	-	121	PPEV_gp091	Pseudomonas phage EL	GCA_000866825.1
CAG27221.1	000000	-	404	PPEV_gp127	Pseudomonas phage EL	GCA_000866825.1
CAG27097.1	000000	-	226	PPEV_gp003	Pseudomonas phage EL	GCA_000866825.1
CAG27227.1	000000	-	89	PPEV_gp133	Pseudomonas phage EL	GCA_000866825.1
CAG27130.1	000000	-	104	PPEV_gp036	Pseudomonas phage EL	GCA_000866825.1
CAG27167.1	000000	-	146	PPEV_gp073	Pseudomonas phage EL	GCA_000866825.1
CAG27270.1	000000	-	137	PPEV_gp176	Pseudomonas phage EL	GCA_000866825.1
CAG27225.1	000000	-	54	PPEV_gp131	Pseudomonas phage EL	GCA_000866825.1
CAG27095.1	000000	-	173	PPEV_gp001	Pseudomonas phage EL	GCA_000866825.1
CAG27182.1	000000	-	107	PPEV_gp088	Pseudomonas phage EL	GCA_000866825.1
CAG27222.1	000000	-	106	PPEV_gp128	Pseudomonas phage EL	GCA_000866825.1
CAG27234.1	000000	-	110	PPEV_gp140	Pseudomonas phage EL	GCA_000866825.1
CAG27187.1	000000	-	113	PPEV_gp093	Pseudomonas phage EL	GCA_000866825.1
CAG27224.1	000000	-	124	PPEV_gp130	Pseudomonas phage EL	GCA_000866825.1
CAG27290.1	000000	-	129	PPEV_gp196	Pseudomonas phage EL	GCA_000866825.1
CAG27199.1	000000	-	132	PPEV_gp105	Pseudomonas phage EL	GCA_000866825.1
CAG27226.1	000000	-	134	PPEV_gp132	Pseudomonas phage EL	GCA_000866825.1
CAG27178.1	000000	-	143	PPEV_gp084	Pseudomonas phage EL	GCA_000866825.1
CAG27215.1	000000	-	164	PPEV_gp121	Pseudomonas phage EL	GCA_000866825.1
CAG27244.1	000000	-	192	PPEV_gp150	Pseudomonas phage EL	GCA_000866825.1
CAG27149.1	000000	-	243	PPEV_gp055	Pseudomonas phage EL	GCA_000866825.1
CAG27158.1	000000	-	312	PPEV_gp064	Pseudomonas phage EL	GCA_000866825.1
CAG27229.1	000000	-	57	PPEV_gp135	Pseudomonas phage EL	GCA_000866825.1
CAG27104.1	000000	-	61	PPEV_gp010	Pseudomonas phage EL	GCA_000866825.1
CAG27258.1	000000	-	66	PPEV_gp164	Pseudomonas phage EL	GCA_000866825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
CAG27289.1	000000	-	71	PPEV_gp195	Pseudomonas phage EL	GCA_000866825.1
CAG27254.1	000000	-	76	PPEV_gp160	Pseudomonas phage EL	GCA_000866825.1
CAG27195.1	000000	-	81	PPEV_gp101	Pseudomonas phage EL	GCA_000866825.1
CAG27166.1	000000	-	81	PPEV_gp072	Pseudomonas phage EL	GCA_000866825.1
CAG27213.1	000000	-	97	PPEV_gp119	Pseudomonas phage EL	GCA_000866825.1
CAG27106.1	000000	-	98	PPEV_gp012	Pseudomonas phage EL	GCA_000866825.1
CAG27191.1	000000	-	98	PPEV_gp097	Pseudomonas phage EL	GCA_000866825.1
CAG27252.1	000000	-	109	PPEV_gp158	Pseudomonas phage EL	GCA_000866825.1
CAG27113.1	000000	-	126	PPEV_gp019	Pseudomonas phage EL	GCA_000866825.1
CAG27228.1	000000	-	69	PPEV_gp134	Pseudomonas phage EL	GCA_000866825.1
CAG27245.1	000000	-	287	PPEV_gp151	Pseudomonas phage EL	GCA_000866825.1
CAG27223.1	000000	-	199	PPEV_gp129	Pseudomonas phage EL	GCA_000866825.1
ANM45045.1	000000	-	93	KTN4_287	Pseudomonas phage KTN4	GCA_002607225.1
AFH14532.1	000000	-	137	Lu11_0001	Pseudomonas phage Lu11	GCA_000897175.1
AFH14535.1	000000	-	177	Lu11_0004	Pseudomonas phage Lu11	GCA_000897175.1
AFH14536.1	000000	-	153	Lu11_0005	Pseudomonas phage Lu11	GCA_000897175.1
AFH14540.1	000000	-	135	Lu11_0009	Pseudomonas phage Lu11	GCA_000897175.1
AFH14541.1	000000	-	135	Lu11_0010	Pseudomonas phage Lu11	GCA_000897175.1
AFH14543.1	000000	-	132	Lu11_0012	Pseudomonas phage Lu11	GCA_000897175.1
AFH14546.1	000000	-	162	Lu11_0015	Pseudomonas phage Lu11	GCA_000897175.1
AFH14547.1	000000	-	126	Lu11_0016	Pseudomonas phage Lu11	GCA_000897175.1
AFH14549.1	000000	-	92	Lu11_0018	Pseudomonas phage Lu11	GCA_000897175.1
AFH14550.1	000000	-	58	Lu11_0019	Pseudomonas phage Lu11	GCA_000897175.1
AFH14551.1	000000	-	126	Lu11_0020	Pseudomonas phage Lu11	GCA_000897175.1
AFH14554.1	000000	-	115	Lu11_0023	Pseudomonas phage Lu11	GCA_000897175.1
AFH14561.1	000000	-	109	Lu11_0030	Pseudomonas phage Lu11	GCA_000897175.1
AFH14562.1	000000	-	121	Lu11_0031	Pseudomonas phage Lu11	GCA_000897175.1
AFH14563.1	000000	-	100	Lu11_0032	Pseudomonas phage Lu11	GCA_000897175.1
AFH14565.1	000000	-	104	Lu11_0034	Pseudomonas phage Lu11	GCA_000897175.1
AFH14566.1	000000	-	103	Lu11_0035	Pseudomonas phage Lu11	GCA_000897175.1
AFH14567.1	000000	-	98	Lu11_0036	Pseudomonas phage Lu11	GCA_000897175.1
AFH14568.1	000000	-	89	Lu11_0037	Pseudomonas phage Lu11	GCA_000897175.1
AFH14570.1	000000	-	233	Lu11_0039	Pseudomonas phage Lu11	GCA_000897175.1
AFH14572.1	000000	-	229	Lu11_0041	Pseudomonas phage Lu11	GCA_000897175.1
AFH14573.1	000000	-	306	Lu11_0042	Pseudomonas phage Lu11	GCA_000897175.1
AFH14574.1	000000	-	103	Lu11_0043	Pseudomonas phage Lu11	GCA_000897175.1
AFH14579.1	000000	-	126	Lu11_0048	Pseudomonas phage Lu11	GCA_000897175.1
AFH14581.1	000000	-	98	Lu11_0050	Pseudomonas phage Lu11	GCA_000897175.1
AFH14582.1	000000	-	77	Lu11_0051	Pseudomonas phage Lu11	GCA_000897175.1
AFH14583.1	000000	-	63	Lu11_0052	Pseudomonas phage Lu11	GCA_000897175.1
AFH14593.1	000000	-	453	Lu11_0062	Pseudomonas phage Lu11	GCA_000897175.1
AFH14595.1	000000	-	177	Lu11_0064	Pseudomonas phage Lu11	GCA_000897175.1
AFH14601.1	000000	-	54	Lu11_0069	Pseudomonas phage Lu11	GCA_000897175.1
AFH14602.1	000000	-	39	Lu11_0070	Pseudomonas phage Lu11	GCA_000897175.1
AFH14607.1	000000	-	100	Lu11_0075	Pseudomonas phage Lu11	GCA_000897175.1
AFH14616.1	000000	-	72	Lu11_0084	Pseudomonas phage Lu11	GCA_000897175.1
AFH14617.1	000000	-	112	Lu11_0085	Pseudomonas phage Lu11	GCA_000897175.1
AFH14619.1	000000	-	71	Lu11_0087	Pseudomonas phage Lu11	GCA_000897175.1
AFH14622.1	000000	-	195	Lu11_0090	Pseudomonas phage Lu11	GCA_000897175.1
AFH14624.1	000000	-	140	Lu11_0092	Pseudomonas phage Lu11	GCA_000897175.1
AFH14627.1	000000	-	90	Lu11_0095	Pseudomonas phage Lu11	GCA_000897175.1
AFH14629.1	000000	-	159	Lu11_0097	Pseudomonas phage Lu11	GCA_000897175.1
AFH14632.1	000000	-	138	Lu11_0100	Pseudomonas phage Lu11	GCA_000897175.1
AFH14637.1	000000	-	287	Lu11_0105	Pseudomonas phage Lu11	GCA_000897175.1
AFH14644.1	000000	-	143	Lu11_0112	Pseudomonas phage Lu11	GCA_000897175.1
AFH14648.1	000000	-	45	Lu11_0116	Pseudomonas phage Lu11	GCA_000897175.1
AFH14649.1	000000	-	93	Lu11_0117	Pseudomonas phage Lu11	GCA_000897175.1
AFH14651.1	000000	-	700	Lu11_0119	Pseudomonas phage Lu11	GCA_000897175.1
AFH14658.1	000000	-	206	Lu11_0126	Pseudomonas phage Lu11	GCA_000897175.1
AFH14659.1	000000	-	216	Lu11_0127	Pseudomonas phage Lu11	GCA_000897175.1
AFH14660.1	000000	-	462	Lu11_0128	Pseudomonas phage Lu11	GCA_000897175.1
AFH14662.1	000000	-	65	Lu11_0129A	Pseudomonas phage Lu11	GCA_000897175.1
AFH14661.1	000000	-	43	Lu11_0129B	Pseudomonas phage Lu11	GCA_000897175.1
AFH14664.1	000000	-	196	Lu11_0130	Pseudomonas phage Lu11	GCA_000897175.1
AFH14665.1	000000	-	161	Lu11_0131	Pseudomonas phage Lu11	GCA_000897175.1
AFH14668.1	000000	-	150	Lu11_0134	Pseudomonas phage Lu11	GCA_000897175.1
AFH14674.1	000000	-	126	Lu11_0141	Pseudomonas phage Lu11	GCA_000897175.1
AFH14675.1	000000	-	104	Lu11_0142	Pseudomonas phage Lu11	GCA_000897175.1
AFH14677.1	000000	-	124	Lu11_0144	Pseudomonas phage Lu11	GCA_000897175.1
AFH14681.1	000000	-	153	Lu11_0148	Pseudomonas phage Lu11	GCA_000897175.1
AFH14682.1	000000	-	76	Lu11_0149	Pseudomonas phage Lu11	GCA_000897175.1
AFH14683.1	000000	-	140	Lu11_0150	Pseudomonas phage Lu11	GCA_000897175.1
AFH14686.1	000000	-	285	Lu11_0153	Pseudomonas phage Lu11	GCA_000897175.1
AFH14690.1	000000	-	164	Lu11_0156	Pseudomonas phage Lu11	GCA_000897175.1
AFH14693.1	000000	-	289	Lu11_0159	Pseudomonas phage Lu11	GCA_000897175.1
AFH14698.1	000000	-	83	Lu11_0164	Pseudomonas phage Lu11	GCA_000897175.1
AFH14701.1	000000	-	150	Lu11_0167	Pseudomonas phage Lu11	GCA_000897175.1
AFH14706.1	000000	-	58	Lu11_0171	Pseudomonas phage Lu11	GCA_000897175.1
AFH14709.1	000000	-	67	Lu11_0174	Pseudomonas phage Lu11	GCA_000897175.1
AFH14710.1	000000	-	186	Lu11_0175	Pseudomonas phage Lu11	GCA_000897175.1
AFH14716.1	000000	-	118	Lu11_0179	Pseudomonas phage Lu11	GCA_000897175.1
AFH14721.1	000000	-	203	Lu11_0184	Pseudomonas phage Lu11	GCA_000897175.1
AFH14723.1	000000	-	97	Lu11_0186	Pseudomonas phage Lu11	GCA_000897175.1
AFH14725.1	000000	-	208	Lu11_0188	Pseudomonas phage Lu11	GCA_000897175.1
AFH14726.1	000000	-	59	Lu11_0189	Pseudomonas phage Lu11	GCA_000897175.1
AFH14727.1	000000	-	105	Lu11_0190	Pseudomonas phage Lu11	GCA_000897175.1
AFH14729.1	000000	-	155	Lu11_0192	Pseudomonas phage Lu11	GCA_000897175.1
AFH14735.1	000000	-	92	Lu11_0198	Pseudomonas phage Lu11	GCA_000897175.1
AFH14736.1	000000	-	128	Lu11_0199	Pseudomonas phage Lu11	GCA_000897175.1
AFH14738.1	000000	-	58	Lu11_0201	Pseudomonas phage Lu11	GCA_000897175.1
AFH14740.1	000000	-	129	Lu11_0203	Pseudomonas phage Lu11	GCA_000897175.1
AFH14747.1	000000	-	142	Lu11_0210	Pseudomonas phage Lu11	GCA_000897175.1
AFH14748.1	000000	-	74	Lu11_0211	Pseudomonas phage Lu11	GCA_000897175.1
AFH14749.1	000000	-	85	Lu11_0212	Pseudomonas phage Lu11	GCA_000897175.1
AFH14753.1	000000	-	93	Lu11_0216	Pseudomonas phage Lu11	GCA_000897175.1
AFH14754.1	000000	-	99	Lu11_0217	Pseudomonas phage Lu11	GCA_000897175.1
AFH14755.1	000000	-	110	Lu11_0218	Pseudomonas phage Lu11	GCA_000897175.1
AFH14756.1	000000	-	239	Lu11_0219	Pseudomonas phage Lu11	GCA_000897175.1
AFH14757.1	000000	-	151	Lu11_0220	Pseudomonas phage Lu11	GCA_000897175.1
AFH14759.1	000000	-	136	Lu11_0222	Pseudomonas phage Lu11	GCA_000897175.1
AFH14766.1	000000	-	74	Lu11_0229	Pseudomonas phage Lu11	GCA_000897175.1
AFH14768.1	000000	-	137	Lu11_0231	Pseudomonas phage Lu11	GCA_000897175.1
AFH14770.1	000000	-	830	Lu11_0233	Pseudomonas phage Lu11	GCA_000897175.1
AFH14775.1	000000	-	1433	Lu11_0239	Pseudomonas phage Lu11	GCA_000897175.1
AFH14779.1	000000	-	365	Lu11_0243	Pseudomonas phage Lu11	GCA_000897175.1
AFH14780.1	000000	-	460	Lu11_0244	Pseudomonas phage Lu11	GCA_000897175.1
AFH14781.1	000000	-	463	Lu11_0245	Pseudomonas phage Lu11	GCA_000897175.1
AFH14787.1	000000	-	57	Lu11_0251	Pseudomonas phage Lu11	GCA_000897175.1
AFH14790.1	000000	-	87	Lu11_0254	Pseudomonas phage Lu11	GCA_000897175.1
AFH14795.1	000000	-	85	Lu11_0259	Pseudomonas phage Lu11	GCA_000897175.1
AFH14797.1	000000	-	344	Lu11_0260	Pseudomonas phage Lu11	GCA_000897175.1
AFH14798.1	000000	-	247	Lu11_0261	Pseudomonas phage Lu11	GCA_000897175.1
AFH14800.1	000000	-	56	Lu11_0263	Pseudomonas phage Lu11	GCA_000897175.1
AFH14801.1	000000	-	284	Lu11_0264	Pseudomonas phage Lu11	GCA_000897175.1
AFH14802.1	000000	-	303	Lu11_0265	Pseudomonas phage Lu11	GCA_000897175.1
AFH14803.1	000000	-	102	Lu11_0266	Pseudomonas phage Lu11	GCA_000897175.1
AFH14810.1	000000	-	118	Lu11_0273	Pseudomonas phage Lu11	GCA_000897175.1
AFH14812.1	000000	-	266	Lu11_0275	Pseudomonas phage Lu11	GCA_000897175.1
AFH14814.1	000000	-	174	Lu11_0277	Pseudomonas phage Lu11	GCA_000897175.1
AFH14816.1	000000	-	104	Lu11_0279	Pseudomonas phage Lu11	GCA_000897175.1
AFH14817.1	000000	-	79	Lu11_0280	Pseudomonas phage Lu11	GCA_000897175.1
AFH14818.1	000000	-	67	Lu11_0281A	Pseudomonas phage Lu11	GCA_000897175.1
AFH14822.1	000000	-	324	Lu11_0284	Pseudomonas phage Lu11	GCA_000897175.1
AFH14823.1	000000	-	80	Lu11_0285	Pseudomonas phage Lu11	GCA_000897175.1
AFH14824.1	000000	-	154	Lu11_0286	Pseudomonas phage Lu11	GCA_000897175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFH14827.1	000000	-	55	Lu11_0289	Pseudomonas phage Lu11	GCA_000897175.1
AFH14828.1	000000	-	72	Lu11_0290	Pseudomonas phage Lu11	GCA_000897175.1
AFH14829.1	000000	-	187	Lu11_0291	Pseudomonas phage Lu11	GCA_000897175.1
AFH14831.1	000000	-	177	Lu11_0293	Pseudomonas phage Lu11	GCA_000897175.1
AFH14833.1	000000	-	228	Lu11_0295	Pseudomonas phage Lu11	GCA_000897175.1
AFH14834.1	000000	-	120	Lu11_0296	Pseudomonas phage Lu11	GCA_000897175.1
AFH14835.1	000000	-	115	Lu11_0297	Pseudomonas phage Lu11	GCA_000897175.1
AFH14837.1	000000	-	255	Lu11_0299	Pseudomonas phage Lu11	GCA_000897175.1
AFH14838.1	000000	-	270	Lu11_0300	Pseudomonas phage Lu11	GCA_000897175.1
AFH14839.1	000000	-	362	Lu11_0301	Pseudomonas phage Lu11	GCA_000897175.1
AFH14840.1	000000	-	114	Lu11_0302	Pseudomonas phage Lu11	GCA_000897175.1
AFH14841.1	000000	-	218	Lu11_0303	Pseudomonas phage Lu11	GCA_000897175.1
AFH14846.1	000000	-	256	Lu11_0308	Pseudomonas phage Lu11	GCA_000897175.1
AFH14850.1	000000	-	157	Lu11_0312	Pseudomonas phage Lu11	GCA_000897175.1
AFH14853.1	000000	-	182	Lu11_0315	Pseudomonas phage Lu11	GCA_000897175.1
AFH14857.1	000000	-	136	Lu11_0319	Pseudomonas phage Lu11	GCA_000897175.1
AFH14858.1	000000	-	175	Lu11_0320	Pseudomonas phage Lu11	GCA_000897175.1
AFH14859.1	000000	-	132	Lu11_0321	Pseudomonas phage Lu11	GCA_000897175.1
AFH14860.1	000000	-	191	Lu11_0322	Pseudomonas phage Lu11	GCA_000897175.1
AFH14861.1	000000	-	112	Lu11_0323	Pseudomonas phage Lu11	GCA_000897175.1
AFH14862.1	000000	-	138	Lu11_0324	Pseudomonas phage Lu11	GCA_000897175.1
AFH14865.1	000000	-	172	Lu11_0327	Pseudomonas phage Lu11	GCA_000897175.1
AFH14867.1	000000	-	276	Lu11_0329	Pseudomonas phage Lu11	GCA_000897175.1
AFH14870.1	000000	-	285	Lu11_0332	Pseudomonas phage Lu11	GCA_000897175.1
AFH14871.1	000000	-	77	Lu11_0333	Pseudomonas phage Lu11	GCA_000897175.1
AFH14874.1	000000	-	165	Lu11_0336	Pseudomonas phage Lu11	GCA_000897175.1
AFH14876.1	000000	-	218	Lu11_0338	Pseudomonas phage Lu11	GCA_000897175.1
AFH14877.1	000000	-	118	Lu11_0339	Pseudomonas phage Lu11	GCA_000897175.1
AFH14878.1	000000	-	116	Lu11_0340	Pseudomonas phage Lu11	GCA_000897175.1
AFH14879.1	000000	-	87	Lu11_0341	Pseudomonas phage Lu11	GCA_000897175.1
AFH14881.1	000000	-	61	Lu11_0343	Pseudomonas phage Lu11	GCA_000897175.1
AFH14883.1	000000	-	79	Lu11_0345	Pseudomonas phage Lu11	GCA_000897175.1
AFH14885.1	000000	-	88	Lu11_0347	Pseudomonas phage Lu11	GCA_000897175.1
AFH14888.1	000000	-	78	Lu11_0350	Pseudomonas phage Lu11	GCA_000897175.1
AFH14891.1	000000	-	88	Lu11_0353	Pseudomonas phage Lu11	GCA_000897175.1
AFH14893.1	000000	-	285	Lu11_0355	Pseudomonas phage Lu11	GCA_000897175.1
AFH14894.1	000000	-	146	Lu11_0356	Pseudomonas phage Lu11	GCA_000897175.1
AFH14898.1	000000	-	226	Lu11_0360	Pseudomonas phage Lu11	GCA_000897175.1
AFH14899.1	000000	-	129	Lu11_0361	Pseudomonas phage Lu11	GCA_000897175.1
AFH14902.1	000000	-	161	Lu11_0364	Pseudomonas phage Lu11	GCA_000897175.1
AFH14904.1	000000	-	130	Lu11_0366	Pseudomonas phage Lu11	GCA_000897175.1
AFH14906.1	000000	-	113	Lu11_0368	Pseudomonas phage Lu11	GCA_000897175.1
AFH14907.1	000000	-	328	Lu11_0369	Pseudomonas phage Lu11	GCA_000897175.1
AFH14909.1	000000	-	241	Lu11_0371	Pseudomonas phage Lu11	GCA_000897175.1
AFH14910.1	000000	-	143	Lu11_0372	Pseudomonas phage Lu11	GCA_000897175.1
AFH14913.1	000000	-	85	Lu11_0375	Pseudomonas phage Lu11	GCA_000897175.1
AFH14914.1	000000	-	94	Lu11_0376	Pseudomonas phage Lu11	GCA_000897175.1
AFH14918.1	000000	-	115	Lu11_0380	Pseudomonas phage Lu11	GCA_000897175.1
AFH14919.1	000000	-	96	Lu11_0381	Pseudomonas phage Lu11	GCA_000897175.1
AFH14920.1	000000	-	118	Lu11_0382	Pseudomonas phage Lu11	GCA_000897175.1
AFH14922.1	000000	-	74	Lu11_0384	Pseudomonas phage Lu11	GCA_000897175.1
ARV77181.1	000000	-	95	NOXIFER_10	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77273.1	000000	-	125	NOXIFER_104	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77278.1	000000	-	125	NOXIFER_109	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77182.1	000000	-	114	NOXIFER_11	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77280.1	000000	-	73	NOXIFER_111	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77282.1	000000	-	119	NOXIFER_113	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77283.1	000000	-	115	NOXIFER_114	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77284.1	000000	-	133	NOXIFER_115	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77287.1	000000	-	353	NOXIFER_118	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77288.1	000000	-	157	NOXIFER_119	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77183.1	000000	-	88	NOXIFER_12	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77293.1	000000	-	406	NOXIFER_124	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77296.1	000000	-	300	NOXIFER_127	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77185.1	000000	-	181	NOXIFER_14	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77186.1	000000	-	425	NOXIFER_15	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77187.1	000000	-	93	NOXIFER_16	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77188.1	000000	-	149	NOXIFER_17	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77347.1	000000	-	39	NOXIFER_178	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77353.1	000000	-	39	NOXIFER_184	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77357.1	000000	-	136	NOXIFER_188	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77358.1	000000	-	88	NOXIFER_189	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77373.1	000000	-	215	NOXIFER_204	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77374.1	000000	-	145	NOXIFER_205	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77378.1	000000	-	94	NOXIFER_212	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77379.1	000000	-	117	NOXIFER_213	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77380.1	000000	-	185	NOXIFER_214	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77381.1	000000	-	93	NOXIFER_215	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77382.1	000000	-	166	NOXIFER_216	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77383.1	000000	-	181	NOXIFER_218	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77384.1	000000	-	248	NOXIFER_219	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77385.1	000000	-	139	NOXIFER_220	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77388.1	000000	-	64	NOXIFER_223	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77389.1	000000	-	44	NOXIFER_224	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77390.1	000000	-	153	NOXIFER_225	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77194.1	000000	-	57	NOXIFER_23	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77399.1	000000	-	61	NOXIFER_234	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77402.1	000000	-	305	NOXIFER_237	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77404.1	000000	-	116	NOXIFER_239	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77406.1	000000	-	130	NOXIFER_241	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77407.1	000000	-	133	NOXIFER_242	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77409.1	000000	-	165	NOXIFER_244	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77414.1	000000	-	106	NOXIFER_249	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77196.1	000000	-	215	NOXIFER_25	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77415.1	000000	-	111	NOXIFER_250	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77416.1	000000	-	106	NOXIFER_251	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77417.1	000000	-	136	NOXIFER_252	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77418.1	000000	-	106	NOXIFER_253	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77420.1	000000	-	75	NOXIFER_255	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77421.1	000000	-	96	NOXIFER_256	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77423.1	000000	-	121	NOXIFER_258	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77424.1	000000	-	215	NOXIFER_259	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77425.1	000000	-	273	NOXIFER_260	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77426.1	000000	-	176	NOXIFER_261	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77427.1	000000	-	405	NOXIFER_262	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77431.1	000000	-	138	NOXIFER_266	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77432.1	000000	-	132	NOXIFER_267	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77434.1	000000	-	164	NOXIFER_269	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77436.1	000000	-	172	NOXIFER_271	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77439.1	000000	-	153	NOXIFER_274	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77440.1	000000	-	145	NOXIFER_275	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77443.1	000000	-	226	NOXIFER_278	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77199.1	000000	-	737	NOXIFER_28	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77445.1	000000	-	177	NOXIFER_280	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77448.1	000000	-	183	NOXIFER_283	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77453.1	000000	-	285	NOXIFER_288	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77200.1	000000	-	81	NOXIFER_29	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77455.1	000000	-	99	NOXIFER_290	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77457.1	000000	-	300	NOXIFER_292	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77458.1	000000	-	276	NOXIFER_293	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77459.1	000000	-	93	NOXIFER_294	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77461.1	000000	-	128	NOXIFER_296	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77462.1	000000	-	130	NOXIFER_297	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77464.1	000000	-	236	NOXIFER_299	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77201.1	000000	-	117	NOXIFER_30	Pseudomonas phage Noxifer	GCA_002625005.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARV77467.1	000000	-	190	NOXIFER_302	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77468.1	000000	-	93	NOXIFER_303	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77469.1	000000	-	166	NOXIFER_304	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77470.1	000000	-	201	NOXIFER_305	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77471.1	000000	-	236	NOXIFER_306	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77474.1	000000	-	171	NOXIFER_309	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77476.1	000000	-	86	NOXIFER_311	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77483.1	000000	-	64	NOXIFER_318	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77484.1	000000	-	208	NOXIFER_319	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77486.1	000000	-	133	NOXIFER_321	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77487.1	000000	-	152	NOXIFER_322	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77488.1	000000	-	149	NOXIFER_323	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77489.1	000000	-	118	NOXIFER_324	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77490.1	000000	-	115	NOXIFER_325	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77493.1	000000	-	330	NOXIFER_328	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77494.1	000000	-	88	NOXIFER_329	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77497.1	000000	-	110	NOXIFER_332	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77498.1	000000	-	68	NOXIFER_333	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77499.1	000000	-	57	NOXIFER_334	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77501.1	000000	-	308	NOXIFER_336	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77207.1	000000	-	365	NOXIFER_36	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77208.1	000000	-	126	NOXIFER_37	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77210.1	000000	-	118	NOXIFER_39	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77175.1	000000	-	215	NOXIFER_4	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77211.1	000000	-	174	NOXIFER_40	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77212.1	000000	-	167	NOXIFER_41	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77213.1	000000	-	147	NOXIFER_42	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77216.1	000000	-	131	NOXIFER_45	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77217.1	000000	-	266	NOXIFER_46	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77218.1	000000	-	265	NOXIFER_47	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77220.1	000000	-	51	NOXIFER_49	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77224.1	000000	-	112	NOXIFER_53	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77227.1	000000	-	161	NOXIFER_56	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77177.1	000000	-	150	NOXIFER_6	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77239.1	000000	-	201	NOXIFER_68	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77240.1	000000	-	160	NOXIFER_69	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77178.1	000000	-	213	NOXIFER_7	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77241.1	000000	-	192	NOXIFER_70	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77242.1	000000	-	41	NOXIFER_71	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77179.1	000000	-	125	NOXIFER_8	Pseudomonas phage Noxifer	GCA_002625005.1
ARV77180.1	000000	-	158	NOXIFER_9	Pseudomonas phage Noxifer	GCA_002625005.1
AEV89448.1	000000	-	136	OBP_011	Pseudomonas phage OBP	GCA_000896635.1
AEV89450.1	000000	-	77	OBP_013	Pseudomonas phage OBP	GCA_000896635.1
AEV89452.1	000000	-	43	OBP_015	Pseudomonas phage OBP	GCA_000896635.1
AEV89455.1	000000	-	288	OBP_018	Pseudomonas phage OBP	GCA_000896635.1
AEV89457.1	000000	-	113	OBP_020	Pseudomonas phage OBP	GCA_000896635.1
AEV89465.1	000000	-	332	OBP_028	Pseudomonas phage OBP	GCA_000896635.1
AEV89466.1	000000	-	180	OBP_029	Pseudomonas phage OBP	GCA_000896635.1
AEV89467.1	000000	-	107	OBP_030	Pseudomonas phage OBP	GCA_000896635.1
AEV89470.1	000000	-	156	OBP_033	Pseudomonas phage OBP	GCA_000896635.1
AEV89472.1	000000	-	216	OBP_035	Pseudomonas phage OBP	GCA_000896635.1
AEV89474.1	000000	-	228	OBP_037	Pseudomonas phage OBP	GCA_000896635.1
AEV89480.1	000000	-	717	OBP_043	Pseudomonas phage OBP	GCA_000896635.1
AEV89481.1	000000	-	148	OBP_044	Pseudomonas phage OBP	GCA_000896635.1
AEV89512.1	000000	-	110	OBP_075	Pseudomonas phage OBP	GCA_000896635.1
AEV89513.1	000000	-	67	OBP_076	Pseudomonas phage OBP	GCA_000896635.1
AEV89520.1	000000	-	156	OBP_083	Pseudomonas phage OBP	GCA_000896635.1
AEV89534.1	000000	-	155	OBP_097	Pseudomonas phage OBP	GCA_000896635.1
AEV89588.1	000000	-	125	OBP_151	Pseudomonas phage OBP	GCA_000896635.1
AEV89591.1	000000	-	145	OBP_154	Pseudomonas phage OBP	GCA_000896635.1
AEV89592.1	000000	-	102	OBP_155	Pseudomonas phage OBP	GCA_000896635.1
AEV89594.1	000000	-	255	OBP_157	Pseudomonas phage OBP	GCA_000896635.1
AEV89596.1	000000	-	50	OBP_159	Pseudomonas phage OBP	GCA_000896635.1
AEV89601.1	000000	-	39	OBP_164	Pseudomonas phage OBP	GCA_000896635.1
AEV89605.1	000000	-	155	OBP_168	Pseudomonas phage OBP	GCA_000896635.1
AEV89610.1	000000	-	201	OBP_173	Pseudomonas phage OBP	GCA_000896635.1
AEV89611.1	000000	-	333	OBP_174	Pseudomonas phage OBP	GCA_000896635.1
AEV89612.1	000000	-	85	OBP_175	Pseudomonas phage OBP	GCA_000896635.1
AEV89616.1	000000	-	223	OBP_179	Pseudomonas phage OBP	GCA_000896635.1
AEV89622.1	000000	-	125	OBP_185	Pseudomonas phage OBP	GCA_000896635.1
AEV89623.1	000000	-	377	OBP_186	Pseudomonas phage OBP	GCA_000896635.1
AEV89624.1	000000	-	267	OBP_187	Pseudomonas phage OBP	GCA_000896635.1
AEV89626.1	000000	-	144	OBP_189	Pseudomonas phage OBP	GCA_000896635.1
AEV89627.1	000000	-	71	OBP_190	Pseudomonas phage OBP	GCA_000896635.1
AEV89628.1	000000	-	67	OBP_191	Pseudomonas phage OBP	GCA_000896635.1
AEV89629.1	000000	-	119	OBP_192	Pseudomonas phage OBP	GCA_000896635.1
AEV89633.1	000000	-	136	OBP_196	Pseudomonas phage OBP	GCA_000896635.1
AEV89638.1	000000	-	161	OBP_201	Pseudomonas phage OBP	GCA_000896635.1
AEV89640.1	000000	-	507	OBP_203	Pseudomonas phage OBP	GCA_000896635.1
AEV89645.1	000000	-	1252	OBP_208	Pseudomonas phage OBP	GCA_000896635.1
AEV89646.1	000000	-	711	OBP_209	Pseudomonas phage OBP	GCA_000896635.1
AEV89658.1	000000	-	72	OBP_221	Pseudomonas phage OBP	GCA_000896635.1
AEV89665.1	000000	-	136	OBP_228	Pseudomonas phage OBP	GCA_000896635.1
AEV89673.1	000000	-	296	OBP_236	Pseudomonas phage OBP	GCA_000896635.1
AEV89690.1	000000	-	50	OBP_253	Pseudomonas phage OBP	GCA_000896635.1
AEV89722.1	000000	-	147	OBP_285	Pseudomonas phage OBP	GCA_000896635.1
AEV89724.1	000000	-	314	OBP_287	Pseudomonas phage OBP	GCA_000896635.1
AEV89725.1	000000	-	301	OBP_288	Pseudomonas phage OBP	GCA_000896635.1
AEV89726.1	000000	-	334	OBP_289	Pseudomonas phage OBP	GCA_000896635.1
AEV89729.1	000000	-	244	OBP_292	Pseudomonas phage OBP	GCA_000896635.1
AEV89730.1	000000	-	117	OBP_293	Pseudomonas phage OBP	GCA_000896635.1
AEV89735.1	000000	-	129	OBP_298	Pseudomonas phage OBP	GCA_000896635.1
QBX32178.1	000000	-	34	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32174.1	000000	-	32	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32239.1	000000	-	76	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32509.1	000000	-	62	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32253.1	000000	-	135	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32298.1	000000	-	159	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32168.1	000000	-	39	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32193.1	000000	-	30	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32502.1	000000	-	47	-	Pseudomonas phage PA1C	GCA_004785505.1
QBX32247.1	000000	-	84	-	Pseudomonas phage PA1C	GCA_004785505.1
QHJ85914.1	000000	-	38	KKIINIFJ_00002	Pseudomonas phage PN05	GCA_009931935.1
QHJ85915.1	000000	-	75	KKIINIFJ_00003	Pseudomonas phage PN05	GCA_009931935.1
QHJ85916.1	000000	-	173	KKIINIFJ_00004	Pseudomonas phage PN05	GCA_009931935.1
QHJ85917.1	000000	-	102	KKIINIFJ_00005	Pseudomonas phage PN05	GCA_009931935.1
QHJ85918.1	000000	-	73	KKIINIFJ_00006	Pseudomonas phage PN05	GCA_009931935.1
QHJ85929.1	000000	-	333	KKIINIFJ_00017	Pseudomonas phage PN05	GCA_009931935.1
QHJ85931.1	000000	-	161	KKIINIFJ_00019	Pseudomonas phage PN05	GCA_009931935.1
QHJ85936.1	000000	-	43	KKIINIFJ_00024	Pseudomonas phage PN05	GCA_009931935.1
QHJ85937.1	000000	-	128	KKIINIFJ_00025	Pseudomonas phage PN05	GCA_009931935.1
QHJ85938.1	000000	-	212	KKIINIFJ_00026	Pseudomonas phage PN05	GCA_009931935.1
QHJ85939.1	000000	-	187	KKIINIFJ_00027	Pseudomonas phage PN05	GCA_009931935.1
QHJ85940.1	000000	-	88	KKIINIFJ_00028	Pseudomonas phage PN05	GCA_009931935.1
QHJ85945.1	000000	-	61	KKIINIFJ_00033	Pseudomonas phage PN05	GCA_009931935.1
QHJ85946.1	000000	-	116	KKIINIFJ_00034	Pseudomonas phage PN05	GCA_009931935.1
QHJ85947.1	000000	-	131	KKIINIFJ_00035	Pseudomonas phage PN05	GCA_009931935.1
QHJ85949.1	000000	-	73	KKIINIFJ_00037	Pseudomonas phage PN05	GCA_009931935.1
QHJ85953.1	000000	-	174	KKIINIFJ_00041	Pseudomonas phage PN05	GCA_009931935.1
QHJ85956.1	000000	-	89	KKIINIFJ_00044	Pseudomonas phage PN05	GCA_009931935.1
QHJ85957.1	000000	-	82	KKIINIFJ_00045	Pseudomonas phage PN05	GCA_009931935.1
QHJ85959.1	000000	-	155	KKIINIFJ_00047	Pseudomonas phage PN05	GCA_009931935.1
QHJ85961.1	000000	-	92	KKIINIFJ_00049	Pseudomonas phage PN05	GCA_009931935.1
QHJ85962.1	000000	-	123	KKIINIFJ_00050	Pseudomonas phage PN05	GCA_009931935.1
QHJ85963.1	000000	-	87	KKIINIFJ_00051	Pseudomonas phage PN05	GCA_009931935.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QHJ85969.1	000000	-	64	KKIINIFJ_00057	Pseudomonas phage PN05	GCA_009931935.1
QHJ85970.1	000000	-	238	KKIINIFJ_00058	Pseudomonas phage PN05	GCA_009931935.1
QHJ85974.1	000000	-	69	KKIINIFJ_00062	Pseudomonas phage PN05	GCA_009931935.1
QHJ85975.1	000000	-	156	KKIINIFJ_00063	Pseudomonas phage PN05	GCA_009931935.1
QHJ85976.1	000000	-	356	KKIINIFJ_00064	Pseudomonas phage PN05	GCA_009931935.1
QHJ85977.1	000000	-	178	KKIINIFJ_00065	Pseudomonas phage PN05	GCA_009931935.1
QHJ85978.1	000000	-	143	KKIINIFJ_00066	Pseudomonas phage PN05	GCA_009931935.1
QHJ85979.1	000000	-	228	KKIINIFJ_00067	Pseudomonas phage PN05	GCA_009931935.1
QHJ85980.1	000000	-	229	KKIINIFJ_00068	Pseudomonas phage PN05	GCA_009931935.1
QHJ85982.1	000000	-	199	KKIINIFJ_00070	Pseudomonas phage PN05	GCA_009931935.1
QHJ85984.1	000000	-	114	KKIINIFJ_00072	Pseudomonas phage PN05	GCA_009931935.1
QHJ85985.1	000000	-	348	KKIINIFJ_00073	Pseudomonas phage PN05	GCA_009931935.1
QHJ85989.1	000000	-	125	KKIINIFJ_00077	Pseudomonas phage PN05	GCA_009931935.1
QHJ85991.1	000000	-	156	KKIINIFJ_00079	Pseudomonas phage PN05	GCA_009931935.1
QHJ85992.1	000000	-	701	KKIINIFJ_00080	Pseudomonas phage PN05	GCA_009931935.1
QHJ85993.1	000000	-	286	KKIINIFJ_00081	Pseudomonas phage PN05	GCA_009931935.1
QHJ85994.1	000000	-	261	KKIINIFJ_00082	Pseudomonas phage PN05	GCA_009931935.1
QHJ85995.1	000000	-	59	KKIINIFJ_00083	Pseudomonas phage PN05	GCA_009931935.1
QHJ85997.1	000000	-	125	KKIINIFJ_00085	Pseudomonas phage PN05	GCA_009931935.1
QHJ85998.1	000000	-	231	KKIINIFJ_00086	Pseudomonas phage PN05	GCA_009931935.1
QHJ85999.1	000000	-	58	KKIINIFJ_00087	Pseudomonas phage PN05	GCA_009931935.1
QHJ86008.1	000000	-	48	KKIINIFJ_00096	Pseudomonas phage PN05	GCA_009931935.1
QHJ86009.1	000000	-	297	KKIINIFJ_00097	Pseudomonas phage PN05	GCA_009931935.1
QHJ86012.1	000000	-	171	KKIINIFJ_00100	Pseudomonas phage PN05	GCA_009931935.1
QHJ86013.1	000000	-	83	KKIINIFJ_00101	Pseudomonas phage PN05	GCA_009931935.1
QHJ86014.1	000000	-	244	KKIINIFJ_00102	Pseudomonas phage PN05	GCA_009931935.1
QHJ86015.1	000000	-	150	KKIINIFJ_00103	Pseudomonas phage PN05	GCA_009931935.1
QHJ86016.1	000000	-	357	KKIINIFJ_00104	Pseudomonas phage PN05	GCA_009931935.1
QHJ86019.1	000000	-	166	KKIINIFJ_00107	Pseudomonas phage PN05	GCA_009931935.1
QHJ86022.1	000000	-	126	KKIINIFJ_00110	Pseudomonas phage PN05	GCA_009931935.1
QHJ86025.1	000000	-	155	KKIINIFJ_00113	Pseudomonas phage PN05	GCA_009931935.1
QHJ86026.1	000000	-	91	KKIINIFJ_00114	Pseudomonas phage PN05	GCA_009931935.1
QHJ86028.1	000000	-	245	KKIINIFJ_00116	Pseudomonas phage PN05	GCA_009931935.1
QHJ86029.1	000000	-	627	KKIINIFJ_00117	Pseudomonas phage PN05	GCA_009931935.1
QHJ86030.1	000000	-	199	KKIINIFJ_00118	Pseudomonas phage PN05	GCA_009931935.1
QHJ86031.1	000000	-	153	KKIINIFJ_00119	Pseudomonas phage PN05	GCA_009931935.1
QHJ86032.1	000000	-	283	KKIINIFJ_00120	Pseudomonas phage PN05	GCA_009931935.1
QHJ86034.1	000000	-	467	KKIINIFJ_00122	Pseudomonas phage PN05	GCA_009931935.1
QHJ86037.1	000000	-	232	KKIINIFJ_00125	Pseudomonas phage PN05	GCA_009931935.1
QHJ86042.1	000000	-	108	KKIINIFJ_00130	Pseudomonas phage PN05	GCA_009931935.1
QHJ86045.1	000000	-	188	KKIINIFJ_00133	Pseudomonas phage PN05	GCA_009931935.1
QHJ86050.1	000000	-	85	KKIINIFJ_00138	Pseudomonas phage PN05	GCA_009931935.1
QHJ86055.1	000000	-	107	KKIINIFJ_00143	Pseudomonas phage PN05	GCA_009931935.1
QHJ86059.1	000000	-	351	KKIINIFJ_00147	Pseudomonas phage PN05	GCA_009931935.1
QHJ86060.1	000000	-	81	KKIINIFJ_00148	Pseudomonas phage PN05	GCA_009931935.1
QHJ86063.1	000000	-	59	KKIINIFJ_00151	Pseudomonas phage PN05	GCA_009931935.1
QHJ86064.1	000000	-	93	KKIINIFJ_00152	Pseudomonas phage PN05	GCA_009931935.1
QHJ86068.1	000000	-	138	KKIINIFJ_00156	Pseudomonas phage PN05	GCA_009931935.1
QHJ86069.1	000000	-	116	KKIINIFJ_00157	Pseudomonas phage PN05	GCA_009931935.1
QHJ86071.1	000000	-	65	KKIINIFJ_00159	Pseudomonas phage PN05	GCA_009931935.1
QHJ86073.1	000000	-	194	KKIINIFJ_00161	Pseudomonas phage PN05	GCA_009931935.1
QHJ86078.1	000000	-	86	KKIINIFJ_00166	Pseudomonas phage PN05	GCA_009931935.1
QHJ86080.1	000000	-	107	KKIINIFJ_00168	Pseudomonas phage PN05	GCA_009931935.1
QHJ86085.1	000000	-	460	KKIINIFJ_00173	Pseudomonas phage PN05	GCA_009931935.1
QHJ86086.1	000000	-	479	KKIINIFJ_00174	Pseudomonas phage PN05	GCA_009931935.1
QHJ86087.1	000000	-	62	KKIINIFJ_00175	Pseudomonas phage PN05	GCA_009931935.1
QHJ86090.1	000000	-	163	KKIINIFJ_00178	Pseudomonas phage PN05	GCA_009931935.1
QHJ86092.1	000000	-	222	KKIINIFJ_00180	Pseudomonas phage PN05	GCA_009931935.1
QHJ86095.1	000000	-	139	KKIINIFJ_00183	Pseudomonas phage PN05	GCA_009931935.1
QHJ86101.1	000000	-	145	KKIINIFJ_00190	Pseudomonas phage PN05	GCA_009931935.1
QHJ86106.1	000000	-	310	KKIINIFJ_00195	Pseudomonas phage PN05	GCA_009931935.1
QHJ86114.1	000000	-	381	KKIINIFJ_00203	Pseudomonas phage PN05	GCA_009931935.1
QHJ86118.1	000000	-	180	KKIINIFJ_00207	Pseudomonas phage PN05	GCA_009931935.1
QHJ86122.1	000000	-	90	KKIINIFJ_00211	Pseudomonas phage PN05	GCA_009931935.1
QHJ86123.1	000000	-	399	KKIINIFJ_00212	Pseudomonas phage PN05	GCA_009931935.1
QHJ86126.1	000000	-	117	KKIINIFJ_00215	Pseudomonas phage PN05	GCA_009931935.1
QHJ86127.1	000000	-	104	KKIINIFJ_00216	Pseudomonas phage PN05	GCA_009931935.1
QHJ86131.1	000000	-	86	KKIINIFJ_00220	Pseudomonas phage PN05	GCA_009931935.1
QHJ86132.1	000000	-	140	KKIINIFJ_00221	Pseudomonas phage PN05	GCA_009931935.1
QHJ86133.1	000000	-	140	KKIINIFJ_00222	Pseudomonas phage PN05	GCA_009931935.1
QHJ86134.1	000000	-	79	KKIINIFJ_00223	Pseudomonas phage PN05	GCA_009931935.1
QHJ86135.1	000000	-	196	KKIINIFJ_00224	Pseudomonas phage PN05	GCA_009931935.1
QHJ86137.1	000000	-	380	KKIINIFJ_00226	Pseudomonas phage PN05	GCA_009931935.1
QHJ86140.1	000000	-	185	KKIINIFJ_00229	Pseudomonas phage PN05	GCA_009931935.1
QHJ86142.1	000000	-	100	KKIINIFJ_00231	Pseudomonas phage PN05	GCA_009931935.1
QHJ86145.1	000000	-	206	KKIINIFJ_00234	Pseudomonas phage PN05	GCA_009931935.1
QHJ86146.1	000000	-	69	KKIINIFJ_00235	Pseudomonas phage PN05	GCA_009931935.1
QHJ86148.1	000000	-	246	KKIINIFJ_00237	Pseudomonas phage PN05	GCA_009931935.1
QHJ86155.1	000000	-	86	KKIINIFJ_00245	Pseudomonas phage PN05	GCA_009931935.1
QHJ86160.1	000000	-	328	KKIINIFJ_00250	Pseudomonas phage PN05	GCA_009931935.1
QHJ86164.1	000000	-	94	KKIINIFJ_00254	Pseudomonas phage PN05	GCA_009931935.1
QHJ86165.1	000000	-	108	KKIINIFJ_00255	Pseudomonas phage PN05	GCA_009931935.1
QHJ86169.1	000000	-	231	KKIINIFJ_00259	Pseudomonas phage PN05	GCA_009931935.1
QHJ86170.1	000000	-	229	KKIINIFJ_00260	Pseudomonas phage PN05	GCA_009931935.1
QHJ86172.1	000000	-	195	KKIINIFJ_00262	Pseudomonas phage PN05	GCA_009931935.1
QHJ86173.1	000000	-	179	KKIINIFJ_00263	Pseudomonas phage PN05	GCA_009931935.1
QHJ86178.1	000000	-	83	KKIINIFJ_00268	Pseudomonas phage PN05	GCA_009931935.1
QHJ86183.1	000000	-	97	KKIINIFJ_00273	Pseudomonas phage PN05	GCA_009931935.1
QHJ86185.1	000000	-	49	KKIINIFJ_00275	Pseudomonas phage PN05	GCA_009931935.1
QHJ86190.1	000000	-	123	KKIINIFJ_00280	Pseudomonas phage PN05	GCA_009931935.1
QHJ86192.1	000000	-	107	KKIINIFJ_00282	Pseudomonas phage PN05	GCA_009931935.1
QHJ86194.1	000000	-	82	KKIINIFJ_00284	Pseudomonas phage PN05	GCA_009931935.1
QHJ86195.1	000000	-	92	KKIINIFJ_00285	Pseudomonas phage PN05	GCA_009931935.1
QHJ86176.1	000000	-	200	KKIINIFJ_00266	Pseudomonas phage PN05	GCA_009931935.1
QKE11200.1	000000	-	187	PaBG_00004	Pseudomonas phage PaBG	GCA_000912555.1
AGS81889.1	000000	-	237	PaBG_00005	Pseudomonas phage PaBG	GCA_000912555.1
AGS81890.1	000000	-	144	PaBG_00006	Pseudomonas phage PaBG	GCA_000912555.1
AGS81891.1	000000	-	200	PaBG_00007	Pseudomonas phage PaBG	GCA_000912555.1
AGS81892.1	000000	-	153	PaBG_00008	Pseudomonas phage PaBG	GCA_000912555.1
AGS81896.1	000000	-	139	PaBG_00012	Pseudomonas phage PaBG	GCA_000912555.1
AGS81898.1	000000	-	149	PaBG_00014	Pseudomonas phage PaBG	GCA_000912555.1
AGS81899.1	000000	-	100	PaBG_00015	Pseudomonas phage PaBG	GCA_000912555.1
AGS81903.1	000000	-	180	PaBG_00019	Pseudomonas phage PaBG	GCA_000912555.1
AGS81909.1	000000	-	114	PaBG_00025	Pseudomonas phage PaBG	GCA_000912555.1
AGS81911.1	000000	-	98	PaBG_00027	Pseudomonas phage PaBG	GCA_000912555.1
AGS81912.1	000000	-	99	PaBG_00028	Pseudomonas phage PaBG	GCA_000912555.1
AGS81916.1	000000	-	166	PaBG_00032	Pseudomonas phage PaBG	GCA_000912555.1
AGS81917.2	000000	-	74	PaBG_00033	Pseudomonas phage PaBG	GCA_000912555.1
AGS81919.2	000000	-	124	PaBG_00035	Pseudomonas phage PaBG	GCA_000912555.1
AGS81921.1	000000	-	147	PaBG_00037	Pseudomonas phage PaBG	GCA_000912555.1
AGS81922.1	000000	-	196	PaBG_00038	Pseudomonas phage PaBG	GCA_000912555.1
AGS81923.1	000000	-	111	PaBG_00039	Pseudomonas phage PaBG	GCA_000912555.1
AGS81925.1	000000	-	151	PaBG_00041	Pseudomonas phage PaBG	GCA_000912555.1
AGS81926.1	000000	-	145	PaBG_00042	Pseudomonas phage PaBG	GCA_000912555.1
AGS81927.2	000000	-	512	PaBG_00043	Pseudomonas phage PaBG	GCA_000912555.1
AGS81931.1	000000	-	139	PaBG_00047	Pseudomonas phage PaBG	GCA_000912555.1
AGS81932.1	000000	-	154	PaBG_00048	Pseudomonas phage PaBG	GCA_000912555.1
AGS81933.1	000000	-	70	PaBG_00049	Pseudomonas phage PaBG	GCA_000912555.1
QKE11201.1	000000	-	153	PaBG_00050	Pseudomonas phage PaBG	GCA_000912555.1
QKE11202.1	000000	-	137	PaBG_00051	Pseudomonas phage PaBG	GCA_000912555.1
QKE11204.1	000000	-	69	PaBG_00054	Pseudomonas phage PaBG	GCA_000912555.1
AGS81939.1	000000	-	87	PaBG_00055	Pseudomonas phage PaBG	GCA_000912555.1
AGS81940.1	000000	-	125	PaBG_00056	Pseudomonas phage PaBG	GCA_000912555.1
AGS81943.1	000000	-	267	PaBG_00059	Pseudomonas phage PaBG	GCA_000912555.1
AGS81945.1	000000	-	93	PaBG_00061	Pseudomonas phage PaBG	GCA_000912555.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AGS81947.1	000000	-	188	PaBG_00063	Pseudomonas phage PaBG	GCA_000912555.1
AGS81948.1	000000	-	108	PaBG_00064	Pseudomonas phage PaBG	GCA_000912555.1
AGS81950.2	000000	-	141	PaBG_00066	Pseudomonas phage PaBG	GCA_000912555.1
AGS81961.1	000000	-	461	PaBG_00077	Pseudomonas phage PaBG	GCA_000912555.1
AGS81970.1	000000	-	320	PaBG_00085	Pseudomonas phage PaBG	GCA_000912555.1
AGS81976.2	000000	-	117	PaBG_00091	Pseudomonas phage PaBG	GCA_000912555.1
AGS81979.1	000000	-	121	PaBG_00094	Pseudomonas phage PaBG	GCA_000912555.1
QKE11205.1	000000	-	60	PaBG_00095	Pseudomonas phage PaBG	GCA_000912555.1
AGS81980.1	000000	-	106	PaBG_00096	Pseudomonas phage PaBG	GCA_000912555.1
AGS81982.1	000000	-	133	PaBG_00098	Pseudomonas phage PaBG	GCA_000912555.1
AGS81985.1	000000	-	70	PaBG_00100	Pseudomonas phage PaBG	GCA_000912555.1
AGS81987.1	000000	-	112	PaBG_00102	Pseudomonas phage PaBG	GCA_000912555.1
QKE11207.1	000000	-	130	PaBG_00103	Pseudomonas phage PaBG	GCA_000912555.1
AGS81990.1	000000	-	87	PaBG_00105	Pseudomonas phage PaBG	GCA_000912555.1
AGS81996.1	000000	-	133	PaBG_00111	Pseudomonas phage PaBG	GCA_000912555.1
AGS82003.1	000000	-	165	PaBG_00119	Pseudomonas phage PaBG	GCA_000912555.1
AGS82005.1	000000	-	241	PaBG_00121	Pseudomonas phage PaBG	GCA_000912555.1
AGS82006.2	000000	-	135	PaBG_00122	Pseudomonas phage PaBG	GCA_000912555.1
AGS82011.1	000000	-	356	PaBG_00127	Pseudomonas phage PaBG	GCA_000912555.1
AGS82013.2	000000	-	114	PaBG_00129	Pseudomonas phage PaBG	GCA_000912555.1
AGS82014.1	000000	-	175	PaBG_00130	Pseudomonas phage PaBG	GCA_000912555.1
QKE11212.1	000000	-	70	PaBG_00135	Pseudomonas phage PaBG	GCA_000912555.1
AGS82025.1	000000	-	52	PaBG_00142	Pseudomonas phage PaBG	GCA_000912555.1
AGS82028.2	000000	-	169	PaBG_00145	Pseudomonas phage PaBG	GCA_000912555.1
AGS82032.1	000000	-	100	PaBG_00150	Pseudomonas phage PaBG	GCA_000912555.1
QKE11214.1	000000	-	83	PaBG_00158	Pseudomonas phage PaBG	GCA_000912555.1
AGS82042.1	000000	-	268	PaBG_00160	Pseudomonas phage PaBG	GCA_000912555.1
AGS82044.1	000000	-	225	PaBG_00162	Pseudomonas phage PaBG	GCA_000912555.1
AGS82049.1	000000	-	156	PaBG_00172	Pseudomonas phage PaBG	GCA_000912555.1
QKE11215.1	000000	-	73	PaBG_00173	Pseudomonas phage PaBG	GCA_000912555.1
AGS82051.1	000000	-	215	PaBG_00175	Pseudomonas phage PaBG	GCA_000912555.1
AGS82057.1	000000	-	203	PaBG_00181	Pseudomonas phage PaBG	GCA_000912555.1
AGS82059.1	000000	-	187	PaBG_00183	Pseudomonas phage PaBG	GCA_000912555.1
AGS82069.1	000000	-	347	PaBG_00193	Pseudomonas phage PaBG	GCA_000912555.1
AGS82076.1	000000	-	126	PaBG_00201	Pseudomonas phage PaBG	GCA_000912555.1
AGS82081.2	000000	-	137	PaBG_00206	Pseudomonas phage PaBG	GCA_000912555.1
AGS82094.1	000000	-	141	PaBG_00219	Pseudomonas phage PaBG	GCA_000912555.1
AGS82096.1	000000	-	116	PaBG_00221	Pseudomonas phage PaBG	GCA_000912555.1
AGS82097.2	000000	-	101	PaBG_00222	Pseudomonas phage PaBG	GCA_000912555.1
QKE11218.1	000000	-	81	PaBG_00230	Pseudomonas phage PaBG	GCA_000912555.1
AGS82107.1	000000	-	87	PaBG_00233	Pseudomonas phage PaBG	GCA_000912555.1
AGS82108.1	000000	-	62	PaBG_00234	Pseudomonas phage PaBG	GCA_000912555.1
AGS82109.1	000000	-	125	PaBG_00235	Pseudomonas phage PaBG	GCA_000912555.1
AGS82118.1	000000	-	163	PaBG_00244	Pseudomonas phage PaBG	GCA_000912555.1
AGS82126.1	000000	-	150	PaBG_00251	Pseudomonas phage PaBG	GCA_000912555.1
QKE11222.1	000000	-	70	PaBG_00259	Pseudomonas phage PaBG	GCA_000912555.1
AGS82140.1	000000	-	595	PaBG_00266	Pseudomonas phage PaBG	GCA_000912555.1
AGS82141.2	000000	-	635	PaBG_00268	Pseudomonas phage PaBG	GCA_000912555.1
AGS82145.1	000000	-	230	PaBG_00272	Pseudomonas phage PaBG	GCA_000912555.1
AGS82153.1	000000	-	84	PaBG_00280	Pseudomonas phage PaBG	GCA_000912555.1
AGS82155.1	000000	-	208	PaBG_00282	Pseudomonas phage PaBG	GCA_000912555.1
AGS82156.1	000000	-	217	PaBG_00283	Pseudomonas phage PaBG	GCA_000912555.1
AGS82157.1	000000	-	171	PaBG_00284	Pseudomonas phage PaBG	GCA_000912555.1
AGS82159.2	000000	-	174	PaBG_00286	Pseudomonas phage PaBG	GCA_000912555.1
AGS82161.1	000000	-	219	PaBG_00288	Pseudomonas phage PaBG	GCA_000912555.1
QKE11224.1	000000	-	136	PaBG_00289	Pseudomonas phage PaBG	GCA_000912555.1
QKE11225.1	000000	-	227	PaBG_00290	Pseudomonas phage PaBG	GCA_000912555.1
AGS82165.1	000000	-	99	PaBG_00292	Pseudomonas phage PaBG	GCA_000912555.1
QKE11227.1	000000	-	106	PaBG_00295	Pseudomonas phage PaBG	GCA_000912555.1
AGS82167.2	000000	-	156	PaBG_00296	Pseudomonas phage PaBG	GCA_000912555.1
AGS82168.1	000000	-	67	PaBG_00297	Pseudomonas phage PaBG	GCA_000912555.1
AGS82169.2	000000	-	100	PaBG_00298	Pseudomonas phage PaBG	GCA_000912555.1
AGS82171.2	000000	-	116	PaBG_00300	Pseudomonas phage PaBG	GCA_000912555.1
AGS82174.2	000000	-	125	PaBG_00303	Pseudomonas phage PaBG	GCA_000912555.1
AGS82175.1	000000	-	277	PaBG_00304	Pseudomonas phage PaBG	GCA_000912555.1
AGS82176.1	000000	-	101	PaBG_00305	Pseudomonas phage PaBG	GCA_000912555.1
AGS82177.1	000000	-	134	PaBG_00306	Pseudomonas phage PaBG	GCA_000912555.1
AGS82182.1	000000	-	117	PaBG_00311	Pseudomonas phage PaBG	GCA_000912555.1
AGS82184.1	000000	-	170	PaBG_00313	Pseudomonas phage PaBG	GCA_000912555.1
AGS82185.2	000000	-	171	PaBG_00314	Pseudomonas phage PaBG	GCA_000912555.1
AGS82190.1	000000	-	307	PaBG_00319	Pseudomonas phage PaBG	GCA_000912555.1
AGS82191.1	000000	-	197	PaBG_00320	Pseudomonas phage PaBG	GCA_000912555.1
QKE11228.1	000000	-	93	PaBG_00322	Pseudomonas phage PaBG	GCA_000912555.1
ARV76739.1	000000	-	23	PHABIO_108	Pseudomonas phage Phabio	GCA_002624965.1
ARV76740.1	000000	-	62	PHABIO_109	Pseudomonas phage Phabio	GCA_002624965.1
ARV76742.1	000000	-	63	PHABIO_111	Pseudomonas phage Phabio	GCA_002624965.1
ARV76643.1	000000	-	92	PHABIO_12	Pseudomonas phage Phabio	GCA_002624965.1
ARV76645.1	000000	-	154	PHABIO_14	Pseudomonas phage Phabio	GCA_002624965.1
ARV76783.1	000000	-	142	PHABIO_152	Pseudomonas phage Phabio	GCA_002624965.1
ARV76791.1	000000	-	146	PHABIO_160	Pseudomonas phage Phabio	GCA_002624965.1
ARV76792.1	000000	-	179	PHABIO_161	Pseudomonas phage Phabio	GCA_002624965.1
ARV76793.1	000000	-	110	PHABIO_162	Pseudomonas phage Phabio	GCA_002624965.1
ARV76795.1	000000	-	168	PHABIO_164	Pseudomonas phage Phabio	GCA_002624965.1
ARV76797.1	000000	-	107	PHABIO_166	Pseudomonas phage Phabio	GCA_002624965.1
ARV76799.1	000000	-	70	PHABIO_168	Pseudomonas phage Phabio	GCA_002624965.1
ARV76800.1	000000	-	60	PHABIO_169	Pseudomonas phage Phabio	GCA_002624965.1
ARV76801.1	000000	-	288	PHABIO_170	Pseudomonas phage Phabio	GCA_002624965.1
ARV76802.1	000000	-	200	PHABIO_171	Pseudomonas phage Phabio	GCA_002624965.1
ARV76804.1	000000	-	117	PHABIO_173	Pseudomonas phage Phabio	GCA_002624965.1
ARV76807.1	000000	-	118	PHABIO_176	Pseudomonas phage Phabio	GCA_002624965.1
ARV76808.1	000000	-	156	PHABIO_177	Pseudomonas phage Phabio	GCA_002624965.1
ARV76809.1	000000	-	86	PHABIO_178	Pseudomonas phage Phabio	GCA_002624965.1
ARV76810.1	000000	-	79	PHABIO_179	Pseudomonas phage Phabio	GCA_002624965.1
ARV76815.1	000000	-	119	PHABIO_184	Pseudomonas phage Phabio	GCA_002624965.1
ARV76819.1	000000	-	135	PHABIO_188	Pseudomonas phage Phabio	GCA_002624965.1
ARV76652.1	000000	-	82	PHABIO_21	Pseudomonas phage Phabio	GCA_002624965.1
ARV76845.1	000000	-	43	PHABIO_214	Pseudomonas phage Phabio	GCA_002624965.1
ARV76654.1	000000	-	100	PHABIO_23	Pseudomonas phage Phabio	GCA_002624965.1
ARV76655.1	000000	-	73	PHABIO_24	Pseudomonas phage Phabio	GCA_002624965.1
ARV76871.1	000000	-	63	PHABIO_240	Pseudomonas phage Phabio	GCA_002624965.1
ARV76872.1	000000	-	66	PHABIO_241	Pseudomonas phage Phabio	GCA_002624965.1
ARV76879.1	000000	-	291	PHABIO_248	Pseudomonas phage Phabio	GCA_002624965.1
ARV76656.1	000000	-	200	PHABIO_25	Pseudomonas phage Phabio	GCA_002624965.1
ARV76881.1	000000	-	49	PHABIO_250	Pseudomonas phage Phabio	GCA_002624965.1
ARV76883.1	000000	-	95	PHABIO_252	Pseudomonas phage Phabio	GCA_002624965.1
ARV76885.1	000000	-	61	PHABIO_254	Pseudomonas phage Phabio	GCA_002624965.1
ARV76886.1	000000	-	95	PHABIO_255	Pseudomonas phage Phabio	GCA_002624965.1
ARV76891.1	000000	-	87	PHABIO_260	Pseudomonas phage Phabio	GCA_002624965.1
ARV76899.1	000000	-	121	PHABIO_268	Pseudomonas phage Phabio	GCA_002624965.1
ARV76658.1	000000	-	101	PHABIO_27	Pseudomonas phage Phabio	GCA_002624965.1
ARV76903.1	000000	-	117	PHABIO_272	Pseudomonas phage Phabio	GCA_002624965.1
ARV76904.1	000000	-	92	PHABIO_273	Pseudomonas phage Phabio	GCA_002624965.1
ARV76908.1	000000	-	116	PHABIO_277	Pseudomonas phage Phabio	GCA_002624965.1
ARV76910.1	000000	-	64	PHABIO_279	Pseudomonas phage Phabio	GCA_002624965.1
ARV76659.1	000000	-	106	PHABIO_28	Pseudomonas phage Phabio	GCA_002624965.1
ARV76911.1	000000	-	227	PHABIO_280	Pseudomonas phage Phabio	GCA_002624965.1
ARV76912.1	000000	-	228	PHABIO_281	Pseudomonas phage Phabio	GCA_002624965.1
ARV76915.1	000000	-	76	PHABIO_284	Pseudomonas phage Phabio	GCA_002624965.1
ARV76917.1	000000	-	78	PHABIO_286	Pseudomonas phage Phabio	GCA_002624965.1
ARV76918.1	000000	-	114	PHABIO_287	Pseudomonas phage Phabio	GCA_002624965.1
ARV76930.1	000000	-	68	PHABIO_299	Pseudomonas phage Phabio	GCA_002624965.1
ARV76661.1	000000	-	110	PHABIO_30	Pseudomonas phage Phabio	GCA_002624965.1
ARV76931.1	000000	-	81	PHABIO_300	Pseudomonas phage Phabio	GCA_002624965.1
ARV76932.1	000000	-	180	PHABIO_301	Pseudomonas phage Phabio	GCA_002624965.1
ARV76933.1	000000	-	82	PHABIO_302	Pseudomonas phage Phabio	GCA_002624965.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ARV76934.1	000000	-	84	PHABIO_303	Pseudomonas phage Phabio	GCA_002624965.1
ARV76935.1	000000	-	92	PHABIO_304	Pseudomonas phage Phabio	GCA_002624965.1
ARV76936.1	000000	-	85	PHABIO_305	Pseudomonas phage Phabio	GCA_002624965.1
ARV76937.1	000000	-	88	PHABIO_306	Pseudomonas phage Phabio	GCA_002624965.1
ARV76940.1	000000	-	96	PHABIO_309	Pseudomonas phage Phabio	GCA_002624965.1
ARV76662.1	000000	-	105	PHABIO_31	Pseudomonas phage Phabio	GCA_002624965.1
ARV76942.1	000000	-	79	PHABIO_311	Pseudomonas phage Phabio	GCA_002624965.1
ARV76944.1	000000	-	113	PHABIO_313	Pseudomonas phage Phabio	GCA_002624965.1
ARV76947.1	000000	-	143	PHABIO_316	Pseudomonas phage Phabio	GCA_002624965.1
ARV76949.1	000000	-	148	PHABIO_318	Pseudomonas phage Phabio	GCA_002624965.1
ARV76950.1	000000	-	139	PHABIO_319	Pseudomonas phage Phabio	GCA_002624965.1
ARV76952.1	000000	-	217	PHABIO_321	Pseudomonas phage Phabio	GCA_002624965.1
ARV76955.1	000000	-	104	PHABIO_324	Pseudomonas phage Phabio	GCA_002624965.1
ARV76957.1	000000	-	123	PHABIO_326	Pseudomonas phage Phabio	GCA_002624965.1
ARV76958.1	000000	-	112	PHABIO_327	Pseudomonas phage Phabio	GCA_002624965.1
ARV76959.1	000000	-	153	PHABIO_328	Pseudomonas phage Phabio	GCA_002624965.1
ARV76664.1	000000	-	97	PHABIO_33	Pseudomonas phage Phabio	GCA_002624965.1
ARV76964.1	000000	-	415	PHABIO_333	Pseudomonas phage Phabio	GCA_002624965.1
ARV76665.1	000000	-	96	PHABIO_34	Pseudomonas phage Phabio	GCA_002624965.1
ARV76971.1	000000	-	117	PHABIO_340	Pseudomonas phage Phabio	GCA_002624965.1
ARV76983.1	000000	-	93	PHABIO_352	Pseudomonas phage Phabio	GCA_002624965.1
ARV76984.1	000000	-	27	PHABIO_353	Pseudomonas phage Phabio	GCA_002624965.1
ARV76985.1	000000	-	18	PHABIO_354	Pseudomonas phage Phabio	GCA_002624965.1
ARV76986.1	000000	-	29	PHABIO_355	Pseudomonas phage Phabio	GCA_002624965.1
ARV76987.1	000000	-	53	PHABIO_356	Pseudomonas phage Phabio	GCA_002624965.1
ARV76988.1	000000	-	62	PHABIO_357	Pseudomonas phage Phabio	GCA_002624965.1
ARV76991.1	000000	-	122	PHABIO_360	Pseudomonas phage Phabio	GCA_002624965.1
ARV76992.1	000000	-	118	PHABIO_361	Pseudomonas phage Phabio	GCA_002624965.1
ARV76996.1	000000	-	134	PHABIO_365	Pseudomonas phage Phabio	GCA_002624965.1
ARV76999.1	000000	-	91	PHABIO_368	Pseudomonas phage Phabio	GCA_002624965.1
ARV77000.1	000000	-	218	PHABIO_369	Pseudomonas phage Phabio	GCA_002624965.1
ARV76668.1	000000	-	145	PHABIO_37	Pseudomonas phage Phabio	GCA_002624965.1
ARV77001.1	000000	-	122	PHABIO_370	Pseudomonas phage Phabio	GCA_002624965.1
ARV77003.1	000000	-	98	PHABIO_372	Pseudomonas phage Phabio	GCA_002624965.1
ARV77006.1	000000	-	192	PHABIO_375	Pseudomonas phage Phabio	GCA_002624965.1
ARV76669.1	000000	-	45	PHABIO_38	Pseudomonas phage Phabio	GCA_002624965.1
ARV77014.1	000000	-	61	PHABIO_383	Pseudomonas phage Phabio	GCA_002624965.1
ARV77015.1	000000	-	150	PHABIO_384	Pseudomonas phage Phabio	GCA_002624965.1
ARV77016.1	000000	-	239	PHABIO_385	Pseudomonas phage Phabio	GCA_002624965.1
ARV77017.1	000000	-	83	PHABIO_386	Pseudomonas phage Phabio	GCA_002624965.1
ARV77018.1	000000	-	114	PHABIO_387	Pseudomonas phage Phabio	GCA_002624965.1
ARV77020.1	000000	-	74	PHABIO_389	Pseudomonas phage Phabio	GCA_002624965.1
ARV77022.1	000000	-	74	PHABIO_391	Pseudomonas phage Phabio	GCA_002624965.1
ARV77023.1	000000	-	229	PHABIO_392	Pseudomonas phage Phabio	GCA_002624965.1
ARV76635.1	000000	-	86	PHABIO_4	Pseudomonas phage Phabio	GCA_002624965.1
ARV77031.1	000000	-	116	PHABIO_400	Pseudomonas phage Phabio	GCA_002624965.1
ARV77032.1	000000	-	179	PHABIO_401	Pseudomonas phage Phabio	GCA_002624965.1
ARV77034.1	000000	-	92	PHABIO_403	Pseudomonas phage Phabio	GCA_002624965.1
ARV77035.1	000000	-	243	PHABIO_404	Pseudomonas phage Phabio	GCA_002624965.1
ARV77036.1	000000	-	245	PHABIO_405	Pseudomonas phage Phabio	GCA_002624965.1
ARV77040.1	000000	-	113	PHABIO_409	Pseudomonas phage Phabio	GCA_002624965.1
ARV77041.1	000000	-	237	PHABIO_410	Pseudomonas phage Phabio	GCA_002624965.1
ARV77043.1	000000	-	144	PHABIO_412	Pseudomonas phage Phabio	GCA_002624965.1
ARV77044.1	000000	-	91	PHABIO_413	Pseudomonas phage Phabio	GCA_002624965.1
ARV77046.1	000000	-	327	PHABIO_415	Pseudomonas phage Phabio	GCA_002624965.1
ARV77048.1	000000	-	184	PHABIO_417	Pseudomonas phage Phabio	GCA_002624965.1
ARV77050.1	000000	-	236	PHABIO_419	Pseudomonas phage Phabio	GCA_002624965.1
ARV76673.1	000000	-	260	PHABIO_42	Pseudomonas phage Phabio	GCA_002624965.1
ARV77052.1	000000	-	262	PHABIO_421	Pseudomonas phage Phabio	GCA_002624965.1
ARV77056.1	000000	-	119	PHABIO_425	Pseudomonas phage Phabio	GCA_002624965.1
ARV76674.1	000000	-	41	PHABIO_43	Pseudomonas phage Phabio	GCA_002624965.1
ARV77062.1	000000	-	66	PHABIO_431	Pseudomonas phage Phabio	GCA_002624965.1
ARV77063.1	000000	-	130	PHABIO_432	Pseudomonas phage Phabio	GCA_002624965.1
ARV77064.1	000000	-	139	PHABIO_433	Pseudomonas phage Phabio	GCA_002624965.1
ARV77067.1	000000	-	128	PHABIO_436	Pseudomonas phage Phabio	GCA_002624965.1
ARV77070.1	000000	-	107	PHABIO_439	Pseudomonas phage Phabio	GCA_002624965.1
ARV77071.1	000000	-	82	PHABIO_440	Pseudomonas phage Phabio	GCA_002624965.1
ARV77072.1	000000	-	123	PHABIO_441	Pseudomonas phage Phabio	GCA_002624965.1
ARV77073.1	000000	-	122	PHABIO_442	Pseudomonas phage Phabio	GCA_002624965.1
ARV77079.1	000000	-	76	PHABIO_450	Pseudomonas phage Phabio	GCA_002624965.1
ARV77080.1	000000	-	58	PHABIO_451	Pseudomonas phage Phabio	GCA_002624965.1
ARV77081.1	000000	-	87	PHABIO_452	Pseudomonas phage Phabio	GCA_002624965.1
ARV77083.1	000000	-	198	PHABIO_455	Pseudomonas phage Phabio	GCA_002624965.1
ARV77088.1	000000	-	65	PHABIO_460	Pseudomonas phage Phabio	GCA_002624965.1
ARV77089.1	000000	-	290	PHABIO_461	Pseudomonas phage Phabio	GCA_002624965.1
ARV77092.1	000000	-	130	PHABIO_464	Pseudomonas phage Phabio	GCA_002624965.1
ARV77093.1	000000	-	127	PHABIO_465	Pseudomonas phage Phabio	GCA_002624965.1
ARV77096.1	000000	-	149	PHABIO_468	Pseudomonas phage Phabio	GCA_002624965.1
ARV76678.1	000000	-	99	PHABIO_47	Pseudomonas phage Phabio	GCA_002624965.1
ARV76636.1	000000	-	143	PHABIO_5	Pseudomonas phage Phabio	GCA_002624965.1
ARV76681.1	000000	-	123	PHABIO_50	Pseudomonas phage Phabio	GCA_002624965.1
ARV76682.1	000000	-	93	PHABIO_51	Pseudomonas phage Phabio	GCA_002624965.1
ARV76685.1	000000	-	51	PHABIO_54	Pseudomonas phage Phabio	GCA_002624965.1
ARV76691.1	000000	-	171	PHABIO_60	Pseudomonas phage Phabio	GCA_002624965.1
ARV76700.1	000000	-	68	PHABIO_69	Pseudomonas phage Phabio	GCA_002624965.1
ARV76701.1	000000	-	130	PHABIO_70	Pseudomonas phage Phabio	GCA_002624965.1
ARV76702.1	000000	-	138	PHABIO_71	Pseudomonas phage Phabio	GCA_002624965.1
ARV76703.1	000000	-	75	PHABIO_72	Pseudomonas phage Phabio	GCA_002624965.1
ARV76704.1	000000	-	132	PHABIO_73	Pseudomonas phage Phabio	GCA_002624965.1
ARV76705.1	000000	-	115	PHABIO_74	Pseudomonas phage Phabio	GCA_002624965.1
ARV76707.1	000000	-	263	PHABIO_76	Pseudomonas phage Phabio	GCA_002624965.1
ARV76708.1	000000	-	86	PHABIO_77	Pseudomonas phage Phabio	GCA_002624965.1
ARV76710.1	000000	-	64	PHABIO_79	Pseudomonas phage Phabio	GCA_002624965.1
ARV76639.1	000000	-	77	PHABIO_8	Pseudomonas phage Phabio	GCA_002624965.1
ARV76712.1	000000	-	69	PHABIO_81	Pseudomonas phage Phabio	GCA_002624965.1
ARV76714.1	000000	-	90	PHABIO_83	Pseudomonas phage Phabio	GCA_002624965.1
ARV76716.1	000000	-	367	PHABIO_85	Pseudomonas phage Phabio	GCA_002624965.1
ARV76717.1	000000	-	244	PHABIO_86	Pseudomonas phage Phabio	GCA_002624965.1
ARV76718.1	000000	-	125	PHABIO_87	Pseudomonas phage Phabio	GCA_002624965.1
ARV76719.1	000000	-	92	PHABIO_88	Pseudomonas phage Phabio	GCA_002624965.1
ARV76720.1	000000	-	104	PHABIO_89	Pseudomonas phage Phabio	GCA_002624965.1
ARV76723.1	000000	-	172	PHABIO_92	Pseudomonas phage Phabio	GCA_002624965.1
ARV76725.1	000000	-	144	PHABIO_94	Pseudomonas phage Phabio	GCA_002624965.1
ARV76728.1	000000	-	130	PHABIO_97	Pseudomonas phage Phabio	GCA_002624965.1
AEH03432.1	000000	-	90	006	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03439.1	000000	-	75	013	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03440.1	000000	-	130	014	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03441.1	000000	-	128	015	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03444.1	000000	-	340	018	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03445.1	000000	-	220	019	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03448.1	000000	-	256	022	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03449.1	000000	-	52	023	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03450.1	000000	-	80	024	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03451.1	000000	-	43	024A	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03453.1	000000	-	238	026	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03454.1	000000	-	109	027	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03458.1	000000	-	121	031	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03459.1	000000	-	87	032	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03462.1	000000	-	80	035	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03467.1	000000	-	137	040	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03468.1	000000	-	88	041	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03475.1	000000	-	115	048	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03477.1	000000	-	156	050	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03479.1	000000	-	550	052	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03520.1	000000	-	321	096	Pseudomonas phage PhiPA3	GCA_001502095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AEH03538.1	000000	-	139	114	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03540.1	000000	-	75	116	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03543.1	000000	-	151	119	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03545.1	000000	-	86	121	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03547.1	000000	-	114	123	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03548.1	000000	-	356	124	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03549.1	000000	-	95	125	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03553.1	000000	-	136	129	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03556.1	000000	-	100	133	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03560.1	000000	-	177	137	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03564.1	000000	-	484	141	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03568.1	000000	-	146	145	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03592.1	000000	-	395	169	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03607.1	000000	-	157	184	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03617.1	000000	-	84	194	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03630.1	000000	-	228	207	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03638.1	000000	-	122	215	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03641.1	000000	-	177	218	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03647.1	000000	-	85	224	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03650.1	000000	-	111	227	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03662.1	000000	-	275	239	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03665.1	000000	-	130	242	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03666.1	000000	-	61	243	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03670.1	000000	-	184	247	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03671.1	000000	-	86	248	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03673.1	000000	-	119	250	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03682.1	000000	-	365	259	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03685.1	000000	-	143	262	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03691.1	000000	-	408	268	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03696.1	000000	-	83	273	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03698.1	000000	-	86	275	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03699.1	000000	-	75	276	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03700.1	000000	-	101	277	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03701.1	000000	-	228	278	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03707.1	000000	-	127	284	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03708.1	000000	-	123	285	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03713.1	000000	-	98	290	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03717.1	000000	-	195	294	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03719.1	000000	-	102	296	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03720.1	000000	-	167	297	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03721.1	000000	-	164	298	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03722.1	000000	-	174	299	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03723.1	000000	-	304	300	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03725.1	000000	-	112	302	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03728.1	000000	-	88	305	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03731.1	000000	-	180	308	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03733.1	000000	-	205	310	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03734.1	000000	-	104	311	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03735.1	000000	-	96	312	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03741.1	000000	-	215	318	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03742.1	000000	-	79	319	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03744.1	000000	-	153	321	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03745.1	000000	-	103	322	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03746.1	000000	-	140	323	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03755.1	000000	-	123	332	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03756.1	000000	-	183	333	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03762.1	000000	-	136	339	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03763.1	000000	-	177	340	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03765.1	000000	-	135	342	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03767.1	000000	-	275	344	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03768.1	000000	-	260	345	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03776.1	000000	-	162	353	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03777.1	000000	-	134	354	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03779.1	000000	-	164	356	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03780.1	000000	-	118	357	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03782.1	000000	-	76	359	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03784.1	000000	-	293	361	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03786.1	000000	-	111	363	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03789.1	000000	-	115	366	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03791.1	000000	-	73	368	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03792.1	000000	-	118	369	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03793.1	000000	-	156	370	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03794.1	000000	-	75	371	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03795.1	000000	-	64	372	Pseudomonas phage PhiPA3	GCA_001502095.1
AEH03797.1	000000	-	73	374	Pseudomonas phage PhiPA3	GCA_001502095.1
QBJ02652.1	000000	-	111	PSA21_124	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02654.1	000000	-	146	PSA21_126	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02655.1	000000	-	82	PSA21_127	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02543.1	000000	-	57	PSA21_13	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02660.1	000000	-	43	PSA21_133	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02664.1	000000	-	127	PSA21_137	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02544.1	000000	-	383	PSA21_14	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02668.1	000000	-	166	PSA21_141	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02670.1	000000	-	96	PSA21_143	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02671.1	000000	-	138	PSA21_144	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02672.1	000000	-	168	PSA21_145	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02675.1	000000	-	129	PSA21_148	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02680.1	000000	-	134	PSA21_153	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02682.1	000000	-	151	PSA21_155	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02684.1	000000	-	95	PSA21_157	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02685.1	000000	-	117	PSA21_158	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02686.1	000000	-	251	PSA21_159	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02688.1	000000	-	129	PSA21_161	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02689.1	000000	-	142	PSA21_162	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02690.1	000000	-	185	PSA21_163	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02691.1	000000	-	132	PSA21_164	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02693.1	000000	-	113	PSA21_166	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02698.1	000000	-	205	PSA21_171	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02701.1	000000	-	126	PSA21_175	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02702.1	000000	-	112	PSA21_176	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02548.1	000000	-	299	PSA21_18	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02550.1	000000	-	138	PSA21_20	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02734.1	000000	-	168	PSA21_208	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02551.1	000000	-	254	PSA21_21	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02747.1	000000	-	387	PSA21_221	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02751.1	000000	-	168	PSA21_225	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02752.1	000000	-	133	PSA21_226	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02753.1	000000	-	71	PSA21_227	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02764.1	000000	-	88	PSA21_238	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02554.1	000000	-	78	PSA21_24	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02767.1	000000	-	60	PSA21_241	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02775.1	000000	-	91	PSA21_249	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02555.1	000000	-	49	PSA21_25	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02778.1	000000	-	142	PSA21_252	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02779.1	000000	-	56	PSA21_253	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02780.1	000000	-	81	PSA21_254	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02781.1	000000	-	113	PSA21_255	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02782.1	000000	-	140	PSA21_256	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02556.1	000000	-	253	PSA21_26	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02786.1	000000	-	147	PSA21_260	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02792.1	000000	-	144	PSA21_266	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02793.1	000000	-	132	PSA21_267	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02798.1	000000	-	167	PSA21_272	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02800.1	000000	-	151	PSA21_274	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02801.1	000000	-	126	PSA21_275	Pseudomonas phage Psa21	GCA_004340405.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QBJ02802.1	000000	-	114	PSA21_276	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02804.1	000000	-	461	PSA21_278	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02805.1	000000	-	113	PSA21_279	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02558.1	000000	-	122	PSA21_28	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02808.1	000000	-	188	PSA21_282	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02810.1	000000	-	165	PSA21_284	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02812.1	000000	-	88	PSA21_286	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02813.1	000000	-	307	PSA21_287	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02816.1	000000	-	120	PSA21_290	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02817.1	000000	-	130	PSA21_291	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02821.1	000000	-	68	PSA21_295	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02822.1	000000	-	156	PSA21_296	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02823.1	000000	-	147	PSA21_297	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02533.1	000000	-	232	PSA21_3	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02560.1	000000	-	165	PSA21_30	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02826.1	000000	-	240	PSA21_300	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02828.1	000000	-	113	PSA21_302	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02831.1	000000	-	194	PSA21_305	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02834.1	000000	-	101	PSA21_308	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02835.1	000000	-	174	PSA21_309	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02839.1	000000	-	104	PSA21_313	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02841.1	000000	-	203	PSA21_315	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02842.1	000000	-	80	PSA21_316	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02562.1	000000	-	83	PSA21_32	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02848.1	000000	-	133	PSA21_322	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02849.1	000000	-	68	PSA21_323	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02851.1	000000	-	124	PSA21_325	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02852.1	000000	-	215	PSA21_326	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02853.1	000000	-	139	PSA21_327	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02854.1	000000	-	141	PSA21_328	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02563.1	000000	-	82	PSA21_33	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02858.1	000000	-	152	PSA21_332	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02861.1	000000	-	111	PSA21_335	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02862.1	000000	-	118	PSA21_336	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02863.1	000000	-	90	PSA21_337	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02864.1	000000	-	140	PSA21_338	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02564.1	000000	-	91	PSA21_34	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02866.1	000000	-	94	PSA21_340	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02867.1	000000	-	77	PSA21_341	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02869.1	000000	-	91	PSA21_343	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02872.1	000000	-	102	PSA21_346	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02873.1	000000	-	77	PSA21_347	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02874.1	000000	-	63	PSA21_348	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02565.1	000000	-	69	PSA21_35	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02876.1	000000	-	116	PSA21_350	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02877.1	000000	-	102	PSA21_351	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02878.1	000000	-	122	PSA21_352	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02880.1	000000	-	131	PSA21_354	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02881.1	000000	-	102	PSA21_355	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02885.1	000000	-	75	PSA21_359	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02886.1	000000	-	242	PSA21_360	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02887.1	000000	-	142	PSA21_361	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02888.1	000000	-	162	PSA21_362	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02893.1	000000	-	116	PSA21_367	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02894.1	000000	-	49	PSA21_368	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02896.1	000000	-	206	PSA21_370	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02897.1	000000	-	84	PSA21_371	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02898.1	000000	-	106	PSA21_372	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02899.1	000000	-	120	PSA21_373	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02900.1	000000	-	98	PSA21_374	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02902.1	000000	-	139	PSA21_376	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02904.1	000000	-	136	PSA21_378	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02905.1	000000	-	119	PSA21_379	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02912.1	000000	-	151	PSA21_386	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02917.1	000000	-	60	PSA21_391	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02919.1	000000	-	169	PSA21_393	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02920.1	000000	-	518	PSA21_394	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02921.1	000000	-	423	PSA21_395	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02923.1	000000	-	221	PSA21_397	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02570.1	000000	-	165	PSA21_40	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02926.1	000000	-	111	PSA21_400	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02931.1	000000	-	63	PSA21_409	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02934.1	000000	-	84	PSA21_412	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02939.1	000000	-	69	PSA21_421	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02944.1	000000	-	602	PSA21_426	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02574.1	000000	-	126	PSA21_44	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02577.1	000000	-	114	PSA21_47	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02580.1	000000	-	96	PSA21_50	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02581.1	000000	-	124	PSA21_51	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02582.1	000000	-	322	PSA21_52	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02585.1	000000	-	558	PSA21_55	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02947.1	000000	-	80	PSA21_57	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02536.1	000000	-	85	PSA21_6	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02590.1	000000	-	98	PSA21_61	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02591.1	000000	-	140	PSA21_62	Pseudomonas phage Psa21	GCA_004340405.1
QBJ02592.1	000000	-	130	PSA21_63	Pseudomonas phage Psa21	GCA_004340405.1
ATN94921.1	000000	-	32	SL2_344	Pseudomonas phage SL2	GCA_002956015.1
QJB22958.1	000000	-	50	fnug_315	Pseudomonas phage fnug	GCA_012837215.1
QCG75885.1	000000	-	83	EST35_0001	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75886.1	000000	-	89	EST35_0002	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75887.1	000000	-	101	EST35_0003	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75888.1	000000	-	94	EST35_0004	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75891.1	000000	-	99	EST35_0007	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75892.1	000000	-	37	EST35_0008	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75893.1	000000	-	104	EST35_0009	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75894.1	000000	-	100	EST35_0010	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75895.1	000000	-	85	EST35_0011	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75896.1	000000	-	45	EST35_0012	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75897.1	000000	-	40	EST35_0013	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75898.1	000000	-	41	EST35_0014	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75899.1	000000	-	44	EST35_0015	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75900.1	000000	-	54	EST35_0016	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75901.1	000000	-	49	EST35_0017	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75902.1	000000	-	44	EST35_0018	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75903.1	000000	-	55	EST35_0019	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75904.1	000000	-	52	EST35_0020	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75905.1	000000	-	45	EST35_0021	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75908.1	000000	-	46	EST35_0024	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75909.1	000000	-	57	EST35_0025	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75911.1	000000	-	50	EST35_0027	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75912.1	000000	-	49	EST35_0028	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75915.1	000000	-	62	EST35_0031	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75917.1	000000	-	94	EST35_0033	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75919.1	000000	-	135	EST35_0035	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75922.1	000000	-	57	EST35_0039	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75923.1	000000	-	55	EST35_0040	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75924.1	000000	-	67	EST35_0041	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75925.1	000000	-	88	EST35_0042	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75926.1	000000	-	44	EST35_0043	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75929.1	000000	-	113	EST35_0046	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75930.1	000000	-	134	EST35_0047	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75932.1	000000	-	85	EST35_0049	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75935.1	000000	-	185	EST35_0052	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75937.1	000000	-	99	EST35_0054	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75938.1	000000	-	178	EST35_0055	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCG75939.1	000000	-	88	EST35_0056	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75941.1	000000	-	107	EST35_0058	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75942.1	000000	-	76	EST35_0059	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75943.1	000000	-	58	EST35_0060	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75946.1	000000	-	74	EST35_0063	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75947.1	000000	-	101	EST35_0064	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75954.1	000000	-	68	EST35_0072	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75955.1	000000	-	67	EST35_0073	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75959.1	000000	-	71	EST35_0077	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75960.1	000000	-	65	EST35_0078	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75961.1	000000	-	150	EST35_0079	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75962.1	000000	-	215	EST35_0080	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75964.1	000000	-	49	EST35_0082	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75967.1	000000	-	38	EST35_0085	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75969.1	000000	-	82	EST35_0087	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75970.1	000000	-	100	EST35_0088	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75971.1	000000	-	101	EST35_0089	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75972.1	000000	-	123	EST35_0090	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75973.1	000000	-	95	EST35_0091	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75975.1	000000	-	60	EST35_0093	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75976.1	000000	-	79	EST35_0094	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75977.1	000000	-	126	EST35_0095	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75979.1	000000	-	105	EST35_0097	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75983.1	000000	-	107	EST35_0101	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75984.1	000000	-	51	EST35_0102	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75985.1	000000	-	69	EST35_0103	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75986.1	000000	-	163	EST35_0104	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75987.1	000000	-	98	EST35_0105	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75988.1	000000	-	54	EST35_0106	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75989.1	000000	-	69	EST35_0107	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75990.1	000000	-	61	EST35_0108	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75992.1	000000	-	63	EST35_0110	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75993.1	000000	-	61	EST35_0111	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75996.1	000000	-	71	EST35_0114	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75997.1	000000	-	71	EST35_0115	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75998.1	000000	-	64	EST35_0116	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG75999.1	000000	-	85	EST35_0117	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76000.1	000000	-	73	EST35_0118	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76001.1	000000	-	79	EST35_0119	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76002.1	000000	-	61	EST35_0120	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76003.1	000000	-	61	EST35_0121	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76004.1	000000	-	325	EST35_0122	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76005.1	000000	-	406	EST35_0123	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76009.1	000000	-	41	EST35_0127	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76010.1	000000	-	3857	EST35_0128	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76013.1	000000	-	80	EST35_0131	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76014.1	000000	-	94	EST35_0132	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76024.1	000000	-	43	EST35_0142	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76025.1	000000	-	38	EST35_0143	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76026.1	000000	-	50	EST35_0144	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76027.1	000000	-	39	EST35_0145	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76028.1	000000	-	150	EST35_0146	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76032.1	000000	-	73	EST35_0150	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76038.1	000000	-	154	EST35_0156	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76042.1	000000	-	202	EST35_0160	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76046.1	000000	-	165	EST35_0164	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76050.1	000000	-	55	EST35_0169	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76052.1	000000	-	76	EST35_0171	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76059.1	000000	-	89	EST35_0178	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76060.1	000000	-	184	EST35_0179	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76064.1	000000	-	59	EST35_0183	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76070.1	000000	-	98	EST35_0189	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76072.1	000000	-	50	EST35_0191	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76080.1	000000	-	151	EST35_0199	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76093.1	000000	-	66	EST35_0212	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76094.1	000000	-	108	EST35_0213	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76097.1	000000	-	83	EST35_0216	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76107.1	000000	-	203	EST35_0226	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76109.1	000000	-	446	EST35_0228	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76110.1	000000	-	339	EST35_0229	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76111.1	000000	-	81	EST35_0230	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76112.1	000000	-	237	EST35_0231	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76113.1	000000	-	143	EST35_0232	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76114.1	000000	-	100	EST35_0233	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76116.1	000000	-	208	EST35_0235	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76119.1	000000	-	104	EST35_0238	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76120.1	000000	-	111	EST35_0239	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76128.1	000000	-	71	EST35_0247	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76133.1	000000	-	103	EST35_0252	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76138.1	000000	-	111	EST35_0257	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76143.1	000000	-	94	EST35_0262	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76144.1	000000	-	97	EST35_0263	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76145.1	000000	-	75	EST35_0264	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76149.1	000000	-	53	EST35_0268	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76150.1	000000	-	169	EST35_0269	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76152.1	000000	-	128	EST35_0271	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76154.1	000000	-	76	EST35_0273	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76155.1	000000	-	85	EST35_0274	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76156.1	000000	-	73	EST35_0275	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76161.1	000000	-	89	EST35_0280	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76162.1	000000	-	86	EST35_0281	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76163.1	000000	-	70	EST35_0282	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76165.1	000000	-	100	EST35_0284	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76167.1	000000	-	98	EST35_0286	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76168.1	000000	-	235	EST35_0287	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76181.1	000000	-	2236	EST35_0300	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76182.1	000000	-	128	EST35_0301	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76186.1	000000	-	894	EST35_0305	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76196.1	000000	-	86	EST35_0315	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76198.1	000000	-	353	EST35_0317	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76199.1	000000	-	125	EST35_0318	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76200.1	000000	-	86	EST35_0319	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76208.1	000000	-	96	EST35_0327	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76209.1	000000	-	181	EST35_0328	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76212.1	000000	-	116	EST35_0331	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76223.1	000000	-	106	EST35_0342	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76224.1	000000	-	79	EST35_0343	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76229.1	000000	-	82	EST35_0348	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76231.1	000000	-	248	EST35_0350	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76233.1	000000	-	297	EST35_0352	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76235.1	000000	-	73	EST35_0355	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76236.1	000000	-	72	EST35_0356	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76238.1	000000	-	65	EST35_0358	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76241.1	000000	-	136	EST35_0361	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76242.1	000000	-	288	EST35_0362	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76244.1	000000	-	168	EST35_0364	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76245.1	000000	-	101	EST35_0365	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76246.1	000000	-	156	EST35_0366	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76247.1	000000	-	79	EST35_0367	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76249.1	000000	-	76	EST35_0369	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76250.1	000000	-	99	EST35_0370	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76251.1	000000	-	119	EST35_0371	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76252.1	000000	-	203	EST35_0372	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76253.1	000000	-	202	EST35_0373	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76254.1	000000	-	159	EST35_0374	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QCG76255.1	000000	-	125	EST35_0375	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76256.1	000000	-	208	EST35_0376	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76262.1	000000	-	64	EST35_0382	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76265.1	000000	-	361	EST35_0385	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76266.1	000000	-	70	EST35_0386	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76267.1	000000	-	108	EST35_0387	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76268.1	000000	-	108	EST35_0388	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76269.1	000000	-	85	EST35_0389	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76272.1	000000	-	64	EST35_0392	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76273.1	000000	-	62	EST35_0399	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76274.1	000000	-	53	EST35_0400	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76275.1	000000	-	49	EST35_0401	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76276.1	000000	-	68	EST35_0402	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76277.1	000000	-	80	EST35_0404	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76278.1	000000	-	110	EST35_0405	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76279.1	000000	-	58	EST35_0409	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76280.1	000000	-	62	EST35_0410	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76281.1	000000	-	55	EST35_0411	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76282.1	000000	-	119	EST35_0412	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76283.1	000000	-	71	EST35_0415	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76284.1	000000	-	67	EST35_0416	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76285.1	000000	-	87	EST35_0417	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76286.1	000000	-	49	EST35_0418	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76287.1	000000	-	116	EST35_0419	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76288.1	000000	-	59	EST35_0420	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76289.1	000000	-	72	EST35_0421	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76295.1	000000	-	37	EST35_0427	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76296.1	000000	-	49	EST35_0428	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76299.1	000000	-	98	EST35_0431	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76303.1	000000	-	115	EST35_0435	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76305.1	000000	-	113	EST35_0437	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76307.1	000000	-	71	EST35_0439	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76308.1	000000	-	107	EST35_0440	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76310.1	000000	-	113	EST35_0442	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76311.1	000000	-	107	EST35_0443	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76312.1	000000	-	97	EST35_0444	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76313.1	000000	-	97	EST35_0445	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76315.1	000000	-	87	EST35_0447	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76317.1	000000	-	93	EST35_0449	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76318.1	000000	-	101	EST35_0450	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76319.1	000000	-	93	EST35_0451	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76321.1	000000	-	83	EST35_0453	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76323.1	000000	-	108	EST35_0455	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76324.1	000000	-	84	EST35_0456	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76325.1	000000	-	93	EST35_0457	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76326.1	000000	-	94	EST35_0458	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76327.1	000000	-	91	EST35_0459	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76328.1	000000	-	93	EST35_0460	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QCG76329.1	000000	-	40	EST35_0461	Pseudomonas phage vB_PaeM_PA5oct	GCA_006516655.1
QEM42082.1	000000	-	39	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM42007.1	000000	-	41	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41811.1	000000	-	38	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM41976.1	000000	-	130	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
QEM42108.1	000000	-	96	-	Pseudomonas phage vB_PaeM_PS119XW	GCA_008375575.1
AGC26306.1	000000	-	42	PHIKZ024.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26336.1	000000	-	20	PHIKZ144.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26305.1	000000	-	46	PHIKZ024.1	Pseudomonas virus phiKZ	GCA_000842965.1
AAL83140.1	000000	-	138	PHIKZ239	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26332.1	000000	-	31	PHIKZ117.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26364.1	000000	-	31	PHIKZ294.1	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26365.1	000000	-	40	PHIKZ294.2	Pseudomonas virus phiKZ	GCA_000842965.1
AGC26317.1	000000	-	56	PHIKZ070.1	Pseudomonas virus phiKZ	GCA_000842965.1
BAW19076.1	000000	-	41	FDH28_gp102	Ralstonia phage RP12	GCA_002617345.1
BAW19028.1	000000	-	268	FDH28_gp054	Ralstonia phage RP12	GCA_002617345.1
BAW19002.1	000000	-	36	FDH28_gp028	Ralstonia phage RP12	GCA_002617345.1
BAW19366.1	000000	-	95	-	Ralstonia phage RP31	GCA_002617365.1
BAW19546.1	000000	-	97	-	Ralstonia phage RP31	GCA_002617365.1
BAW19361.1	000000	-	36	-	Ralstonia phage RP31	GCA_002617365.1
BAS04930.2	000000	-	101	AVU11_gp138	Ralstonia phage RSF1	GCA_001500875.1
BAU71418.1	000000	-	35	AVU11_agp27	Ralstonia phage RSF1	GCA_001500875.1
BAU71420.1	000000	-	39	AVU11_agp35	Ralstonia phage RSF1	GCA_001500875.1
BAS04884.2	000000	-	89	AVU11_gp092	Ralstonia phage RSF1	GCA_001500875.1
BAS04924.1	000000	-	213	AVU11_gp132	Ralstonia phage RSF1	GCA_001500875.1
BAS04868.1	000000	-	54	AVU11_gp076	Ralstonia phage RSF1	GCA_001500875.1
BAS04929.2	000000	-	165	AVU11_agp31	Ralstonia phage RSF1	GCA_001500875.1
BAS04811.2	000000	-	119	AVU11_agp08	Ralstonia phage RSF1	GCA_001500875.1
BAU71415.1	000000	-	51	AVU11_agp02	Ralstonia phage RSF1	GCA_001500875.1
BAS04919.1	000000	-	60	AVU11_gp127	Ralstonia phage RSF1	GCA_001500875.1
BAS04794.2	000000	-	71	AVU11_agp01	Ralstonia phage RSF1	GCA_001500875.1
BAS04921.2	000000	-	75	AVU11_gp129	Ralstonia phage RSF1	GCA_001500875.1
BAS04898.1	000000	-	152	AVU11_gp106	Ralstonia phage RSF1	GCA_001500875.1
BAS04885.2	000000	-	69	AVU11_agp20	Ralstonia phage RSF1	GCA_001500875.1
BAU71417.1	000000	-	36	AVU11_agp22	Ralstonia phage RSF1	GCA_001500875.1
BAS04999.2	000000	-	256	AVU11_gp207	Ralstonia phage RSF1	GCA_001500875.1
BAS04928.1	000000	-	183	AVU11_gp136	Ralstonia phage RSF1	GCA_001500875.1
BAS04894.2	000000	-	201	AVU11_agp23	Ralstonia phage RSF1	GCA_001500875.1
BAS04878.2	000000	-	202	AVU11_gp086	Ralstonia phage RSF1	GCA_001500875.1
BAQ02530.2	000000	-	35	-	Ralstonia phage RSL2	GCA_001503055.1
BAU71413.1	000000	-	48	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02659.2	000000	-	31	-	Ralstonia phage RSL2	GCA_001503055.1
BAU71405.1	000000	-	39	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02624.1	000000	-	172	AVU38_gp096	Ralstonia phage RSL2	GCA_001503055.1
BAQ02648.2	000000	-	102	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02628.1	000000	-	113	AVU38_gp100	Ralstonia phage RSL2	GCA_001503055.1
BAQ02637.2	000000	-	240	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02726.1	000000	-	51	AVU38_gp198	Ralstonia phage RSL2	GCA_001503055.1
BAU71410.1	000000	-	52	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02636.2	000000	-	57	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02583.1	000000	-	71	AVU38_gp055	Ralstonia phage RSL2	GCA_001503055.1
BAQ02728.2	000000	-	75	-	Ralstonia phage RSL2	GCA_001503055.1
BAU71408.1	000000	-	76	-	Ralstonia phage RSL2	GCA_001503055.1
BAQ02581.1	000000	-	91	AVU38_gp053	Ralstonia phage RSL2	GCA_001503055.1
BAG41463.1	000000	-	136	RSL1_ORF018	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41468.1	000000	-	58	RSL1_ORF023	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41492.1	000000	-	162	RSL1_ORF047	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41487.1	000000	-	446	RSL1_ORF042	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41473.1	000000	-	97	RSL1_ORF028	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41474.1	000000	-	121	RSL1_ORF029	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41495.1	000000	-	153	RSL1_ORF049	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41488.1	000000	-	104	RSL1_ORF043	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41482.1	000000	-	118	RSL1_ORF037	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41472.1	000000	-	124	RSL1_ORF027	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41471.1	000000	-	62	RSL1_ORF026	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41458.1	000000	-	84	RSL1_ORF013	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41462.1	000000	-	67	RSL1_ORF017	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41460.1	000000	-	123	RSL1_ORF015	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41485.1	000000	-	69	RSL1_ORF040	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41476.1	000000	-	41	RSL1_ORF031	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41481.1	000000	-	68	RSL1_ORF036	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41470.1	000000	-	178	RSL1_ORF025	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41457.1	000000	-	94	RSL1_ORF012	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41466.2	000000	-	165	RSL1_ORF022	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41501.1	000000	-	147	RSL1_ORF055	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41510.1	000000	-	205	RSL1_ORF064	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41509.1	000000	-	91	RSL1_ORF063	Ralstonia phage phiRSL1	GCA_000879455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAG41786.1	000000	-	115	RSL1_ORF338	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41788.1	000000	-	187	RSL1_ORF340	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41781.1	000000	-	117	RSL1_ORF334	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41768.2	000000	-	100	RSL1_ORF320	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41675.1	000000	-	100	RSL1_ORF225	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41709.1	000000	-	103	RSL1_ORF262	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41584.1	000000	-	103	RSL1_ORF139	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41746.1	000000	-	105	RSL1_ORF300	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72947.1	000000	-	105	RSL1_ORF260	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41735.1	000000	-	105	RSL1_ORF289	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41700.1	000000	-	105	RSL1_ORF252	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41710.1	000000	-	106	RSL1_ORF263	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41749.1	000000	-	109	RSL1_ORF303	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41748.1	000000	-	112	RSL1_ORF302	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41718.1	000000	-	113	RSL1_ORF271	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41769.1	000000	-	114	RSL1_ORF322	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41666.1	000000	-	114	RSL1_ORF217	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41693.1	000000	-	120	RSL1_ORF245	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41559.1	000000	-	125	RSL1_ORF114	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41623.1	000000	-	127	RSL1_ORF175	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41703.1	000000	-	127	RSL1_ORF255	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41731.1	000000	-	128	RSL1_ORF284	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41569.1	000000	-	128	RSL1_ORF124	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41712.1	000000	-	129	RSL1_ORF265	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41692.1	000000	-	130	RSL1_ORF243	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41669.1	000000	-	130	RSL1_ORF220	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72946.1	000000	-	130	RSL1_ORF244	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41711.1	000000	-	132	RSL1_ORF264	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41690.1	000000	-	134	RSL1_ORF241	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41770.1	000000	-	134	RSL1_ORF323	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41691.1	000000	-	138	RSL1_ORF242	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41764.1	000000	-	143	RSL1_ORF317	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41600.1	000000	-	144	RSL1_ORF154	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41555.1	000000	-	153	RSL1_ORF111	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41719.1	000000	-	157	RSL1_ORF272	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72948.1	000000	-	158	RSL1_ORF287	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41609.1	000000	-	161	RSL1_ORF162	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41578.1	000000	-	166	RSL1_ORF133	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41726.1	000000	-	167	RSL1_ORF279	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41721.1	000000	-	174	RSL1_ORF274	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41465.1	000000	-	174	RSL1_ORF021	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41740.1	000000	-	179	RSL1_ORF294	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41744.1	000000	-	181	RSL1_ORF298	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41593.1	000000	-	182	RSL1_ORF147	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41757.1	000000	-	204	RSL1_ORF310	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41774.2	000000	-	220	RSL1_ORF327	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41747.1	000000	-	232	RSL1_ORF301	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41562.1	000000	-	236	RSL1_ORF117	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41707.1	000000	-	244	RSL1_ORF259	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41717.1	000000	-	265	RSL1_ORF270	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41686.1	000000	-	312	RSL1_ORF237	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41586.1	000000	-	343	RSL1_ORF141	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72941.1	000000	-	50	RSL1_ORF020	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41761.2	000000	-	51	RSL1_ORF314	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41738.1	000000	-	51	RSL1_ORF292	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41714.1	000000	-	52	RSL1_ORF267	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41621.1	000000	-	55	RSL1_ORF173	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41616.1	000000	-	57	RSL1_ORF169	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41596.1	000000	-	58	RSL1_ORF150	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41589.2	000000	-	59	RSL1_ORF144	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41727.1	000000	-	60	RSL1_ORF280	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41640.1	000000	-	60	RSL1_ORF191	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41590.1	000000	-	61	RSL1_ORF145	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41771.1	000000	-	65	RSL1_ORF324	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41615.1	000000	-	66	RSL1_ORF168	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41636.1	000000	-	70	RSL1_ORF187	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41598.1	000000	-	70	RSL1_ORF152	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41760.1	000000	-	71	RSL1_ORF313	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41766.1	000000	-	71	RSL1_ORF319	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41724.1	000000	-	74	RSL1_ORF277	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72945.1	000000	-	76	RSL1_ORF227	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41668.2	000000	-	78	RSL1_ORF219	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41571.1	000000	-	78	RSL1_ORF126	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41716.1	000000	-	81	RSL1_ORF269	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41614.1	000000	-	82	RSL1_ORF167	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41588.1	000000	-	84	RSL1_ORF143	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41634.1	000000	-	85	RSL1_ORF185	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41610.1	000000	-	93	RSL1_ORF163	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41753.1	000000	-	93	RSL1_ORF307	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41626.1	000000	-	97	RSL1_ORF178	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41638.1	000000	-	973	RSL1_ORF189	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41611.1	000000	-	98	RSL1_ORF164	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41538.1	000000	-	108	RSL1_ORF093	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72942.1	000000	-	109	RSL1_ORF087	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41514.1	000000	-	115	RSL1_ORF068	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41527.1	000000	-	123	RSL1_ORF081	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41519.1	000000	-	133	RSL1_ORF073	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41539.1	000000	-	143	RSL1_ORF094	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41549.1	000000	-	152	RSL1_ORF105	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41515.1	000000	-	171	RSL1_ORF069	Ralstonia phage phiRSL1	GCA_000879455.1
BAH72943.1	000000	-	49	RSL1_ORF103	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41547.1	000000	-	56	RSL1_ORF102	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41534.1	000000	-	64	RSL1_ORF089	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41520.1	000000	-	74	RSL1_ORF074	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41521.1	000000	-	76	RSL1_ORF075	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41513.1	000000	-	76	RSL1_ORF067	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41531.1	000000	-	78	RSL1_ORF085	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41525.1	000000	-	81	RSL1_ORF079	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41512.1	000000	-	86	RSL1_ORF066	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41533.1	000000	-	87	RSL1_ORF088	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41530.1	000000	-	94	RSL1_ORF084	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41446.1	000000	-	46	RSL1_ORF001	Ralstonia phage phiRSL1	GCA_000879455.1
BAG41479.1	000000	-	345	RSL1_ORF034	Ralstonia phage phiRSL1	GCA_000879455.1
ASV44016.1	000000	-	154	PBI_SCTP2_1	Salicola phage SCTP-2	GCA_002625545.1
ASV44025.1	000000	-	69	PBI_SCTP2_10	Salicola phage SCTP-2	GCA_002625545.1
ASV44115.1	000000	-	73	PBI_SCTP2_100	Salicola phage SCTP-2	GCA_002625545.1
ASV44117.1	000000	-	343	PBI_SCTP2_102	Salicola phage SCTP-2	GCA_002625545.1
ASV44120.1	000000	-	474	PBI_SCTP2_105	Salicola phage SCTP-2	GCA_002625545.1
ASV44121.1	000000	-	173	PBI_SCTP2_106	Salicola phage SCTP-2	GCA_002625545.1
ASV44122.1	000000	-	282	PBI_SCTP2_107	Salicola phage SCTP-2	GCA_002625545.1
ASV44124.1	000000	-	233	PBI_SCTP2_109	Salicola phage SCTP-2	GCA_002625545.1
ASV44026.1	000000	-	56	PBI_SCTP2_11	Salicola phage SCTP-2	GCA_002625545.1
ASV44130.1	000000	-	356	PBI_SCTP2_115	Salicola phage SCTP-2	GCA_002625545.1
ASV44132.1	000000	-	220	PBI_SCTP2_117	Salicola phage SCTP-2	GCA_002625545.1
ASV44134.1	000000	-	349	PBI_SCTP2_119	Salicola phage SCTP-2	GCA_002625545.1
ASV44027.1	000000	-	108	PBI_SCTP2_12	Salicola phage SCTP-2	GCA_002625545.1
ASV44135.1	000000	-	233	PBI_SCTP2_120	Salicola phage SCTP-2	GCA_002625545.1
ASV44136.1	000000	-	85	PBI_SCTP2_121	Salicola phage SCTP-2	GCA_002625545.1
ASV44138.1	000000	-	131	PBI_SCTP2_123	Salicola phage SCTP-2	GCA_002625545.1
ASV44142.1	000000	-	133	PBI_SCTP2_127	Salicola phage SCTP-2	GCA_002625545.1
ASV44144.1	000000	-	114	PBI_SCTP2_129	Salicola phage SCTP-2	GCA_002625545.1
ASV44147.1	000000	-	110	PBI_SCTP2_132	Salicola phage SCTP-2	GCA_002625545.1
ASV44148.1	000000	-	372	PBI_SCTP2_133	Salicola phage SCTP-2	GCA_002625545.1
ASV44149.1	000000	-	112	PBI_SCTP2_134	Salicola phage SCTP-2	GCA_002625545.1
ASV44153.1	000000	-	481	PBI_SCTP2_138	Salicola phage SCTP-2	GCA_002625545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASV44029.1	000000	-	127	PBI_SCTP2_14	Salicola phage SCTP-2	GCA_002625545.1
ASV44159.1	000000	-	167	PBI_SCTP2_144	Salicola phage SCTP-2	GCA_002625545.1
ASV44164.1	000000	-	403	PBI_SCTP2_149	Salicola phage SCTP-2	GCA_002625545.1
ASV44172.1	000000	-	337	PBI_SCTP2_157	Salicola phage SCTP-2	GCA_002625545.1
ASV44174.1	000000	-	158	PBI_SCTP2_159	Salicola phage SCTP-2	GCA_002625545.1
ASV44175.1	000000	-	268	PBI_SCTP2_160	Salicola phage SCTP-2	GCA_002625545.1
ASV44177.1	000000	-	161	PBI_SCTP2_162	Salicola phage SCTP-2	GCA_002625545.1
ASV44178.1	000000	-	187	PBI_SCTP2_163	Salicola phage SCTP-2	GCA_002625545.1
ASV44182.1	000000	-	38	PBI_SCTP2_167	Salicola phage SCTP-2	GCA_002625545.1
ASV44032.1	000000	-	1910	PBI_SCTP2_17	Salicola phage SCTP-2	GCA_002625545.1
ASV44188.1	000000	-	126	PBI_SCTP2_173	Salicola phage SCTP-2	GCA_002625545.1
ASV44190.1	000000	-	78	PBI_SCTP2_175	Salicola phage SCTP-2	GCA_002625545.1
ASV44192.1	000000	-	440	PBI_SCTP2_177	Salicola phage SCTP-2	GCA_002625545.1
ASV44197.1	000000	-	115	PBI_SCTP2_182	Salicola phage SCTP-2	GCA_002625545.1
ASV44198.1	000000	-	299	PBI_SCTP2_183	Salicola phage SCTP-2	GCA_002625545.1
ASV44203.1	000000	-	607	PBI_SCTP2_188	Salicola phage SCTP-2	GCA_002625545.1
ASV44205.1	000000	-	104	PBI_SCTP2_190	Salicola phage SCTP-2	GCA_002625545.1
ASV44213.1	000000	-	154	PBI_SCTP2_198	Salicola phage SCTP-2	GCA_002625545.1
ASV44017.1	000000	-	22	PBI_SCTP2_2	Salicola phage SCTP-2	GCA_002625545.1
ASV44035.1	000000	-	55	PBI_SCTP2_20	Salicola phage SCTP-2	GCA_002625545.1
ASV44215.1	000000	-	130	PBI_SCTP2_200	Salicola phage SCTP-2	GCA_002625545.1
ASV44216.1	000000	-	234	PBI_SCTP2_201	Salicola phage SCTP-2	GCA_002625545.1
ASV44217.1	000000	-	123	PBI_SCTP2_202	Salicola phage SCTP-2	GCA_002625545.1
ASV44222.1	000000	-	99	PBI_SCTP2_207	Salicola phage SCTP-2	GCA_002625545.1
ASV44223.1	000000	-	314	PBI_SCTP2_208	Salicola phage SCTP-2	GCA_002625545.1
ASV44224.1	000000	-	117	PBI_SCTP2_209	Salicola phage SCTP-2	GCA_002625545.1
ASV44036.1	000000	-	68	PBI_SCTP2_21	Salicola phage SCTP-2	GCA_002625545.1
ASV44225.1	000000	-	190	PBI_SCTP2_210	Salicola phage SCTP-2	GCA_002625545.1
ASV44227.1	000000	-	59	PBI_SCTP2_212	Salicola phage SCTP-2	GCA_002625545.1
ASV44230.1	000000	-	87	PBI_SCTP2_215	Salicola phage SCTP-2	GCA_002625545.1
ASV44237.1	000000	-	161	PBI_SCTP2_222	Salicola phage SCTP-2	GCA_002625545.1
ASV44238.1	000000	-	75	PBI_SCTP2_223	Salicola phage SCTP-2	GCA_002625545.1
ASV44038.1	000000	-	288	PBI_SCTP2_23	Salicola phage SCTP-2	GCA_002625545.1
ASV44247.1	000000	-	250	PBI_SCTP2_232	Salicola phage SCTP-2	GCA_002625545.1
ASV44249.1	000000	-	141	PBI_SCTP2_234	Salicola phage SCTP-2	GCA_002625545.1
ASV44250.1	000000	-	152	PBI_SCTP2_235	Salicola phage SCTP-2	GCA_002625545.1
ASV44251.1	000000	-	329	PBI_SCTP2_236	Salicola phage SCTP-2	GCA_002625545.1
ASV44258.1	000000	-	81	PBI_SCTP2_243	Salicola phage SCTP-2	GCA_002625545.1
ASV44260.1	000000	-	110	PBI_SCTP2_245	Salicola phage SCTP-2	GCA_002625545.1
ASV44266.1	000000	-	351	PBI_SCTP2_251	Salicola phage SCTP-2	GCA_002625545.1
ASV44267.1	000000	-	299	PBI_SCTP2_252	Salicola phage SCTP-2	GCA_002625545.1
ASV44268.1	000000	-	127	PBI_SCTP2_253	Salicola phage SCTP-2	GCA_002625545.1
ASV44271.1	000000	-	297	PBI_SCTP2_256	Salicola phage SCTP-2	GCA_002625545.1
ASV44272.1	000000	-	133	PBI_SCTP2_257	Salicola phage SCTP-2	GCA_002625545.1
ASV44274.1	000000	-	90	PBI_SCTP2_259	Salicola phage SCTP-2	GCA_002625545.1
ASV44041.1	000000	-	61	PBI_SCTP2_26	Salicola phage SCTP-2	GCA_002625545.1
ASV44277.1	000000	-	290	PBI_SCTP2_262	Salicola phage SCTP-2	GCA_002625545.1
ASV44278.1	000000	-	178	PBI_SCTP2_263	Salicola phage SCTP-2	GCA_002625545.1
ASV44279.1	000000	-	620	PBI_SCTP2_264	Salicola phage SCTP-2	GCA_002625545.1
ASV44283.1	000000	-	174	PBI_SCTP2_268	Salicola phage SCTP-2	GCA_002625545.1
ASV44285.1	000000	-	203	PBI_SCTP2_270	Salicola phage SCTP-2	GCA_002625545.1
ASV44286.1	000000	-	143	PBI_SCTP2_271	Salicola phage SCTP-2	GCA_002625545.1
ASV44287.1	000000	-	622	PBI_SCTP2_272	Salicola phage SCTP-2	GCA_002625545.1
ASV44289.1	000000	-	301	PBI_SCTP2_274	Salicola phage SCTP-2	GCA_002625545.1
ASV44293.1	000000	-	96	PBI_SCTP2_278	Salicola phage SCTP-2	GCA_002625545.1
ASV44043.1	000000	-	145	PBI_SCTP2_28	Salicola phage SCTP-2	GCA_002625545.1
ASV44296.1	000000	-	216	PBI_SCTP2_281	Salicola phage SCTP-2	GCA_002625545.1
ASV44298.1	000000	-	623	PBI_SCTP2_283	Salicola phage SCTP-2	GCA_002625545.1
ASV44299.1	000000	-	109	PBI_SCTP2_284	Salicola phage SCTP-2	GCA_002625545.1
ASV44300.1	000000	-	93	PBI_SCTP2_285	Salicola phage SCTP-2	GCA_002625545.1
ASV44301.1	000000	-	234	PBI_SCTP2_286	Salicola phage SCTP-2	GCA_002625545.1
ASV44302.1	000000	-	234	PBI_SCTP2_287	Salicola phage SCTP-2	GCA_002625545.1
ASV44303.1	000000	-	261	PBI_SCTP2_288	Salicola phage SCTP-2	GCA_002625545.1
ASV44304.1	000000	-	326	PBI_SCTP2_289	Salicola phage SCTP-2	GCA_002625545.1
ASV44305.1	000000	-	251	PBI_SCTP2_290	Salicola phage SCTP-2	GCA_002625545.1
ASV44310.1	000000	-	147	PBI_SCTP2_295	Salicola phage SCTP-2	GCA_002625545.1
ASV44312.1	000000	-	249	PBI_SCTP2_297	Salicola phage SCTP-2	GCA_002625545.1
ASV44316.1	000000	-	91	PBI_SCTP2_301	Salicola phage SCTP-2	GCA_002625545.1
ASV44319.1	000000	-	169	PBI_SCTP2_304	Salicola phage SCTP-2	GCA_002625545.1
ASV44320.1	000000	-	304	PBI_SCTP2_305	Salicola phage SCTP-2	GCA_002625545.1
ASV44321.1	000000	-	149	PBI_SCTP2_306	Salicola phage SCTP-2	GCA_002625545.1
ASV44046.1	000000	-	735	PBI_SCTP2_31	Salicola phage SCTP-2	GCA_002625545.1
ASV44325.1	000000	-	145	PBI_SCTP2_310	Salicola phage SCTP-2	GCA_002625545.1
ASV44330.1	000000	-	82	PBI_SCTP2_315	Salicola phage SCTP-2	GCA_002625545.1
ASV44331.1	000000	-	131	PBI_SCTP2_316	Salicola phage SCTP-2	GCA_002625545.1
ASV44333.1	000000	-	51	PBI_SCTP2_318	Salicola phage SCTP-2	GCA_002625545.1
ASV44334.1	000000	-	84	PBI_SCTP2_319	Salicola phage SCTP-2	GCA_002625545.1
ASV44047.1	000000	-	64	PBI_SCTP2_32	Salicola phage SCTP-2	GCA_002625545.1
ASV44336.1	000000	-	138	PBI_SCTP2_321	Salicola phage SCTP-2	GCA_002625545.1
ASV44339.1	000000	-	215	PBI_SCTP2_324	Salicola phage SCTP-2	GCA_002625545.1
ASV44342.1	000000	-	77	PBI_SCTP2_327	Salicola phage SCTP-2	GCA_002625545.1
ASV44343.1	000000	-	265	PBI_SCTP2_328	Salicola phage SCTP-2	GCA_002625545.1
ASV44344.1	000000	-	38	PBI_SCTP2_329	Salicola phage SCTP-2	GCA_002625545.1
ASV44048.1	000000	-	193	PBI_SCTP2_33	Salicola phage SCTP-2	GCA_002625545.1
ASV44345.1	000000	-	83	PBI_SCTP2_330	Salicola phage SCTP-2	GCA_002625545.1
ASV44346.1	000000	-	172	PBI_SCTP2_331	Salicola phage SCTP-2	GCA_002625545.1
ASV44349.1	000000	-	154	PBI_SCTP2_334	Salicola phage SCTP-2	GCA_002625545.1
ASV44351.1	000000	-	146	PBI_SCTP2_336	Salicola phage SCTP-2	GCA_002625545.1
ASV44352.1	000000	-	57	PBI_SCTP2_337	Salicola phage SCTP-2	GCA_002625545.1
ASV44353.1	000000	-	53	PBI_SCTP2_338	Salicola phage SCTP-2	GCA_002625545.1
ASV44354.1	000000	-	68	PBI_SCTP2_339	Salicola phage SCTP-2	GCA_002625545.1
ASV44360.1	000000	-	148	PBI_SCTP2_345	Salicola phage SCTP-2	GCA_002625545.1
ASV44361.1	000000	-	88	PBI_SCTP2_346	Salicola phage SCTP-2	GCA_002625545.1
ASV44362.1	000000	-	93	PBI_SCTP2_347	Salicola phage SCTP-2	GCA_002625545.1
ASV44363.1	000000	-	134	PBI_SCTP2_348	Salicola phage SCTP-2	GCA_002625545.1
ASV44364.1	000000	-	68	PBI_SCTP2_349	Salicola phage SCTP-2	GCA_002625545.1
ASV44050.1	000000	-	66	PBI_SCTP2_35	Salicola phage SCTP-2	GCA_002625545.1
ASV44367.1	000000	-	19	PBI_SCTP2_352	Salicola phage SCTP-2	GCA_002625545.1
ASV44368.1	000000	-	73	PBI_SCTP2_353	Salicola phage SCTP-2	GCA_002625545.1
ASV44369.1	000000	-	112	PBI_SCTP2_354	Salicola phage SCTP-2	GCA_002625545.1
ASV44370.1	000000	-	115	PBI_SCTP2_355	Salicola phage SCTP-2	GCA_002625545.1
ASV44371.1	000000	-	115	PBI_SCTP2_356	Salicola phage SCTP-2	GCA_002625545.1
ASV44372.1	000000	-	73	PBI_SCTP2_357	Salicola phage SCTP-2	GCA_002625545.1
ASV44373.1	000000	-	63	PBI_SCTP2_358	Salicola phage SCTP-2	GCA_002625545.1
ASV44374.1	000000	-	77	PBI_SCTP2_359	Salicola phage SCTP-2	GCA_002625545.1
ASV44051.1	000000	-	159	PBI_SCTP2_36	Salicola phage SCTP-2	GCA_002625545.1
ASV44377.1	000000	-	65	PBI_SCTP2_362	Salicola phage SCTP-2	GCA_002625545.1
ASV44379.1	000000	-	37	PBI_SCTP2_364	Salicola phage SCTP-2	GCA_002625545.1
ASV44382.1	000000	-	84	PBI_SCTP2_367	Salicola phage SCTP-2	GCA_002625545.1
ASV44386.1	000000	-	105	PBI_SCTP2_371	Salicola phage SCTP-2	GCA_002625545.1
ASV44387.1	000000	-	114	PBI_SCTP2_372	Salicola phage SCTP-2	GCA_002625545.1
ASV44389.1	000000	-	25	PBI_SCTP2_374	Salicola phage SCTP-2	GCA_002625545.1
ASV44391.1	000000	-	139	PBI_SCTP2_376	Salicola phage SCTP-2	GCA_002625545.1
ASV44396.1	000000	-	82	PBI_SCTP2_381	Salicola phage SCTP-2	GCA_002625545.1
ASV44401.1	000000	-	243	PBI_SCTP2_386	Salicola phage SCTP-2	GCA_002625545.1
ASV44402.1	000000	-	64	PBI_SCTP2_387	Salicola phage SCTP-2	GCA_002625545.1
ASV44403.1	000000	-	44	PBI_SCTP2_388	Salicola phage SCTP-2	GCA_002625545.1
ASV44404.1	000000	-	78	PBI_SCTP2_389	Salicola phage SCTP-2	GCA_002625545.1
ASV44405.1	000000	-	49	PBI_SCTP2_390	Salicola phage SCTP-2	GCA_002625545.1
ASV44406.1	000000	-	44	PBI_SCTP2_391	Salicola phage SCTP-2	GCA_002625545.1
ASV44409.1	000000	-	150	PBI_SCTP2_394	Salicola phage SCTP-2	GCA_002625545.1
ASV44413.1	000000	-	111	PBI_SCTP2_398	Salicola phage SCTP-2	GCA_002625545.1
ASV44055.1	000000	-	378	PBI_SCTP2_40	Salicola phage SCTP-2	GCA_002625545.1
ASV44418.1	000000	-	66	PBI_SCTP2_403	Salicola phage SCTP-2	GCA_002625545.1
ASV44419.1	000000	-	37	PBI_SCTP2_404	Salicola phage SCTP-2	GCA_002625545.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ASV44421.1	000000	-	77	PBI_SCTP2_406	Salicola phage SCTP-2	GCA_002625545.1
ASV44424.1	000000	-	106	PBI_SCTP2_409	Salicola phage SCTP-2	GCA_002625545.1
ASV44426.1	000000	-	37	PBI_SCTP2_411	Salicola phage SCTP-2	GCA_002625545.1
ASV44428.1	000000	-	43	PBI_SCTP2_413	Salicola phage SCTP-2	GCA_002625545.1
ASV44430.1	000000	-	65	PBI_SCTP2_415	Salicola phage SCTP-2	GCA_002625545.1
ASV44431.1	000000	-	67	PBI_SCTP2_416	Salicola phage SCTP-2	GCA_002625545.1
ASV44432.1	000000	-	24	PBI_SCTP2_417	Salicola phage SCTP-2	GCA_002625545.1
ASV44434.1	000000	-	114	PBI_SCTP2_419	Salicola phage SCTP-2	GCA_002625545.1
ASV44437.1	000000	-	39	PBI_SCTP2_422	Salicola phage SCTP-2	GCA_002625545.1
ASV44438.1	000000	-	39	PBI_SCTP2_423	Salicola phage SCTP-2	GCA_002625545.1
ASV44440.1	000000	-	121	PBI_SCTP2_425	Salicola phage SCTP-2	GCA_002625545.1
ASV44059.1	000000	-	248	PBI_SCTP2_44	Salicola phage SCTP-2	GCA_002625545.1
ASV44456.1	000000	-	109	PBI_SCTP2_441	Salicola phage SCTP-2	GCA_002625545.1
ASV44458.1	000000	-	128	PBI_SCTP2_443	Salicola phage SCTP-2	GCA_002625545.1
ASV44459.1	000000	-	466	PBI_SCTP2_444	Salicola phage SCTP-2	GCA_002625545.1
ASV44466.1	000000	-	93	PBI_SCTP2_451	Salicola phage SCTP-2	GCA_002625545.1
ASV44470.1	000000	-	204	PBI_SCTP2_455	Salicola phage SCTP-2	GCA_002625545.1
ASV44471.1	000000	-	90	PBI_SCTP2_456	Salicola phage SCTP-2	GCA_002625545.1
ASV44472.1	000000	-	545	PBI_SCTP2_457	Salicola phage SCTP-2	GCA_002625545.1
ASV44473.1	000000	-	216	PBI_SCTP2_458	Salicola phage SCTP-2	GCA_002625545.1
ASV44477.1	000000	-	250	PBI_SCTP2_462	Salicola phage SCTP-2	GCA_002625545.1
ASV44478.1	000000	-	233	PBI_SCTP2_463	Salicola phage SCTP-2	GCA_002625545.1
ASV44480.1	000000	-	245	PBI_SCTP2_465	Salicola phage SCTP-2	GCA_002625545.1
ASV44482.1	000000	-	277	PBI_SCTP2_467	Salicola phage SCTP-2	GCA_002625545.1
ASV44062.1	000000	-	433	PBI_SCTP2_47	Salicola phage SCTP-2	GCA_002625545.1
ASV44489.1	000000	-	109	PBI_SCTP2_474	Salicola phage SCTP-2	GCA_002625545.1
ASV44490.1	000000	-	538	PBI_SCTP2_475	Salicola phage SCTP-2	GCA_002625545.1
ASV44493.1	000000	-	38	PBI_SCTP2_478	Salicola phage SCTP-2	GCA_002625545.1
ASV44500.1	000000	-	79	PBI_SCTP2_485	Salicola phage SCTP-2	GCA_002625545.1
ASV44503.1	000000	-	81	PBI_SCTP2_488	Salicola phage SCTP-2	GCA_002625545.1
ASV44064.1	000000	-	102	PBI_SCTP2_49	Salicola phage SCTP-2	GCA_002625545.1
ASV44506.1	000000	-	237	PBI_SCTP2_491	Salicola phage SCTP-2	GCA_002625545.1
ASV44507.1	000000	-	75	PBI_SCTP2_492	Salicola phage SCTP-2	GCA_002625545.1
ASV44509.1	000000	-	83	PBI_SCTP2_494	Salicola phage SCTP-2	GCA_002625545.1
ASV44510.1	000000	-	214	PBI_SCTP2_495	Salicola phage SCTP-2	GCA_002625545.1
ASV44511.1	000000	-	83	PBI_SCTP2_496	Salicola phage SCTP-2	GCA_002625545.1
ASV44512.1	000000	-	109	PBI_SCTP2_497	Salicola phage SCTP-2	GCA_002625545.1
ASV44513.1	000000	-	118	PBI_SCTP2_498	Salicola phage SCTP-2	GCA_002625545.1
ASV44514.1	000000	-	120	PBI_SCTP2_499	Salicola phage SCTP-2	GCA_002625545.1
ASV44020.1	000000	-	303	PBI_SCTP2_5	Salicola phage SCTP-2	GCA_002625545.1
ASV44515.1	000000	-	232	PBI_SCTP2_500	Salicola phage SCTP-2	GCA_002625545.1
ASV44516.1	000000	-	128	PBI_SCTP2_501	Salicola phage SCTP-2	GCA_002625545.1
ASV44517.1	000000	-	100	PBI_SCTP2_502	Salicola phage SCTP-2	GCA_002625545.1
ASV44519.1	000000	-	161	PBI_SCTP2_504	Salicola phage SCTP-2	GCA_002625545.1
ASV44520.1	000000	-	253	PBI_SCTP2_505	Salicola phage SCTP-2	GCA_002625545.1
ASV44521.1	000000	-	215	PBI_SCTP2_506	Salicola phage SCTP-2	GCA_002625545.1
ASV44522.1	000000	-	190	PBI_SCTP2_507	Salicola phage SCTP-2	GCA_002625545.1
ASV44523.1	000000	-	140	PBI_SCTP2_508	Salicola phage SCTP-2	GCA_002625545.1
ASV44526.1	000000	-	148	PBI_SCTP2_511	Salicola phage SCTP-2	GCA_002625545.1
ASV44531.1	000000	-	462	PBI_SCTP2_516	Salicola phage SCTP-2	GCA_002625545.1
ASV44535.1	000000	-	217	PBI_SCTP2_520	Salicola phage SCTP-2	GCA_002625545.1
ASV44542.1	000000	-	201	PBI_SCTP2_527	Salicola phage SCTP-2	GCA_002625545.1
ASV44543.1	000000	-	71	PBI_SCTP2_528	Salicola phage SCTP-2	GCA_002625545.1
ASV44544.1	000000	-	764	PBI_SCTP2_529	Salicola phage SCTP-2	GCA_002625545.1
ASV44545.1	000000	-	166	PBI_SCTP2_530	Salicola phage SCTP-2	GCA_002625545.1
ASV44546.1	000000	-	83	PBI_SCTP2_531	Salicola phage SCTP-2	GCA_002625545.1
ASV44547.1	000000	-	156	PBI_SCTP2_532	Salicola phage SCTP-2	GCA_002625545.1
ASV44552.1	000000	-	662	PBI_SCTP2_537	Salicola phage SCTP-2	GCA_002625545.1
ASV44069.1	000000	-	160	PBI_SCTP2_54	Salicola phage SCTP-2	GCA_002625545.1
ASV44556.1	000000	-	408	PBI_SCTP2_541	Salicola phage SCTP-2	GCA_002625545.1
ASV44070.1	000000	-	52	PBI_SCTP2_55	Salicola phage SCTP-2	GCA_002625545.1
ASV44071.1	000000	-	326	PBI_SCTP2_56	Salicola phage SCTP-2	GCA_002625545.1
ASV44074.1	000000	-	232	PBI_SCTP2_59	Salicola phage SCTP-2	GCA_002625545.1
ASV44075.1	000000	-	143	PBI_SCTP2_60	Salicola phage SCTP-2	GCA_002625545.1
ASV44077.1	000000	-	218	PBI_SCTP2_62	Salicola phage SCTP-2	GCA_002625545.1
ASV44078.1	000000	-	137	PBI_SCTP2_63	Salicola phage SCTP-2	GCA_002625545.1
ASV44079.1	000000	-	133	PBI_SCTP2_64	Salicola phage SCTP-2	GCA_002625545.1
ASV44080.1	000000	-	159	PBI_SCTP2_65	Salicola phage SCTP-2	GCA_002625545.1
ASV44081.1	000000	-	497	PBI_SCTP2_66	Salicola phage SCTP-2	GCA_002625545.1
ASV44022.1	000000	-	122	PBI_SCTP2_7	Salicola phage SCTP-2	GCA_002625545.1
ASV44086.1	000000	-	113	PBI_SCTP2_71	Salicola phage SCTP-2	GCA_002625545.1
ASV44091.1	000000	-	89	PBI_SCTP2_76	Salicola phage SCTP-2	GCA_002625545.1
ASV44092.1	000000	-	71	PBI_SCTP2_77	Salicola phage SCTP-2	GCA_002625545.1
ASV44096.1	000000	-	131	PBI_SCTP2_81	Salicola phage SCTP-2	GCA_002625545.1
ASV44102.1	000000	-	64	PBI_SCTP2_87	Salicola phage SCTP-2	GCA_002625545.1
ASV44104.1	000000	-	1074	PBI_SCTP2_89	Salicola phage SCTP-2	GCA_002625545.1
ASV44024.1	000000	-	212	PBI_SCTP2_9	Salicola phage SCTP-2	GCA_002625545.1
ASV44106.1	000000	-	72	PBI_SCTP2_91	Salicola phage SCTP-2	GCA_002625545.1
ASV44112.1	000000	-	138	PBI_SCTP2_97	Salicola phage SCTP-2	GCA_002625545.1
ASV44113.1	000000	-	1012	PBI_SCTP2_98	Salicola phage SCTP-2	GCA_002625545.1
QCW18651.1	000000	-	31	7t3_0130	Salmonella phage 7t3	GCA_006083215.1
QCW18660.1	000000	-	44	7t3_0139	Salmonella phage 7t3	GCA_006083215.1
QCW18661.1	000000	-	29	7t3_0140	Salmonella phage 7t3	GCA_006083215.1
QCW18663.1	000000	-	32	7t3_0142	Salmonella phage 7t3	GCA_006083215.1
QCW18664.1	000000	-	36	7t3_0143	Salmonella phage 7t3	GCA_006083215.1
QCW18666.1	000000	-	31	7t3_0145	Salmonella phage 7t3	GCA_006083215.1
QCW18673.1	000000	-	42	7t3_0152	Salmonella phage 7t3	GCA_006083215.1
QCW18686.1	000000	-	77	7t3_0165	Salmonella phage 7t3	GCA_006083215.1
QCW18693.1	000000	-	59	7t3_0172	Salmonella phage 7t3	GCA_006083215.1
QCW18727.1	000000	-	32	7t3_0206	Salmonella phage 7t3	GCA_006083215.1
QCW18739.1	000000	-	30	7t3_0218	Salmonella phage 7t3	GCA_006083215.1
QCW18765.1	000000	-	44	7t3_0244	Salmonella phage 7t3	GCA_006083215.1
QCW18838.1	000000	-	42	7t3_0317	Salmonella phage 7t3	GCA_006083215.1
QCW18848.1	000000	-	29	7t3_0327	Salmonella phage 7t3	GCA_006083215.1
QCW18870.1	000000	-	56	7t3_0349	Salmonella phage 7t3	GCA_006083215.1
QCW18871.1	000000	-	29	7t3_0350	Salmonella phage 7t3	GCA_006083215.1
QCW18872.1	000000	-	97	7t3_0351	Salmonella phage 7t3	GCA_006083215.1
QCW18929.1	000000	-	32	7t3_0408	Salmonella phage 7t3	GCA_006083215.1
QCW18951.1	000000	-	37	7t3_0430	Salmonella phage 7t3	GCA_006083215.1
QCW18966.1	000000	-	31	7t3_0445	Salmonella phage 7t3	GCA_006083215.1
QCW18978.1	000000	-	41	7t3_0457	Salmonella phage 7t3	GCA_006083215.1
QCW18999.1	000000	-	59	7t3_0479	Salmonella phage 7t3	GCA_006083215.1
QCW19059.1	000000	-	35	7t3_0539	Salmonella phage 7t3	GCA_006083215.1
QCW19070.1	000000	-	52	7t3_0550	Salmonella phage 7t3	GCA_006083215.1
QCW19072.1	000000	-	72	7t3_0552	Salmonella phage 7t3	GCA_006083215.1
QCW19081.1	000000	-	36	7t3_0562	Salmonella phage 7t3	GCA_006083215.1
QCW19086.1	000000	-	36	7t3_0568	Salmonella phage 7t3	GCA_006083215.1
QCW18579.1	000000	-	31	7t3_058	Salmonella phage 7t3	GCA_006083215.1
AZU97954.1	000000	-	97	CPT_Munch_010	Salmonella phage Munch	GCA_004015485.1
AZU98390.1	000000	-	213	CPT_Munch_457	Salmonella phage Munch	GCA_004015485.1
QIG63031.1	000000	-	45	SEPL_418	Salmonella phage SE_PL	GCA_011067555.1
AXF51052.1	000000	-	241	MLDJOKPK_00012	Salmonella phage SPAsTU	GCA_003183805.1
AXF51058.1	000000	-	126	MLDJOKPK_00020	Salmonella phage SPAsTU	GCA_003183805.1
AXF51060.1	000000	-	92	MLDJOKPK_00024	Salmonella phage SPAsTU	GCA_003183805.1
AXF51061.1	000000	-	97	MLDJOKPK_00025	Salmonella phage SPAsTU	GCA_003183805.1
AXF51064.1	000000	-	130	MLDJOKPK_00034	Salmonella phage SPAsTU	GCA_003183805.1
AXF51076.1	000000	-	150	MLDJOKPK_00057	Salmonella phage SPAsTU	GCA_003183805.1
AXF51077.1	000000	-	204	MLDJOKPK_00059	Salmonella phage SPAsTU	GCA_003183805.1
AXF51084.1	000000	-	235	MLDJOKPK_00085	Salmonella phage SPAsTU	GCA_003183805.1
AXF51085.1	000000	-	83	MLDJOKPK_00086	Salmonella phage SPAsTU	GCA_003183805.1
AXF51089.1	000000	-	144	MLDJOKPK_00097	Salmonella phage SPAsTU	GCA_003183805.1
AXF51093.1	000000	-	184	MLDJOKPK_00106	Salmonella phage SPAsTU	GCA_003183805.1
AXF51105.1	000000	-	64	MLDJOKPK_00170	Salmonella phage SPAsTU	GCA_003183805.1
AXF51107.1	000000	-	129	MLDJOKPK_00174	Salmonella phage SPAsTU	GCA_003183805.1
AXF51108.1	000000	-	205	MLDJOKPK_00175	Salmonella phage SPAsTU	GCA_003183805.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AXF51122.1	000000	-	63	MLDJOKPK_00244	Salmonella phage SPAsTU	GCA_003183805.1
AXF51137.1	000000	-	31	MLDJOKPK_00288	Salmonella phage SPAsTU	GCA_003183805.1
AEP83836.1	000000	-	78	SPN3US_0003	Salmonella phage SPN3US	GCA_001042275.1
AEP83970.1	000000	-	143	SPN3US_0137	Salmonella phage SPN3US	GCA_001042275.1
QKE54318.1	000000	-	61	ACSA002_0040	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54319.1	000000	-	107	ACSA002_0050	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54342.1	000000	-	138	ACSA002_0280	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54346.1	000000	-	123	ACSA002_0320	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54347.1	000000	-	198	ACSA002_0330	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54348.1	000000	-	258	ACSA002_0340	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54350.1	000000	-	125	ACSA002_0360	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54351.1	000000	-	188	ACSA002_0370	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54357.1	000000	-	472	ACSA002_0430	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54361.1	000000	-	583	ACSA002_0470	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54363.1	000000	-	161	ACSA002_0490	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54364.1	000000	-	291	ACSA002_0500	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54365.1	000000	-	210	ACSA002_0510	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54366.1	000000	-	137	ACSA002_0520	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54369.1	000000	-	148	ACSA002_0550	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54370.1	000000	-	146	ACSA002_0560	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54372.1	000000	-	224	ACSA002_0580	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54373.1	000000	-	201	ACSA002_0590	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54374.1	000000	-	105	ACSA002_0600	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54376.1	000000	-	98	ACSA002_0620	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54377.1	000000	-	138	ACSA002_0630	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54380.1	000000	-	147	ACSA002_0660	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54382.1	000000	-	156	ACSA002_0680	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54387.1	000000	-	112	ACSA002_0730	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54388.1	000000	-	167	ACSA002_0740	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54394.1	000000	-	152	ACSA002_0800	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54397.1	000000	-	224	ACSA002_0830	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54399.1	000000	-	102	ACSA002_0850	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54403.1	000000	-	183	ACSA002_0890	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54406.1	000000	-	221	ACSA002_0920	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54407.1	000000	-	107	ACSA002_0930	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54408.1	000000	-	255	ACSA002_0940	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54424.1	000000	-	180	ACSA002_1100	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54425.1	000000	-	211	ACSA002_1110	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54445.1	000000	-	64	ACSA002_1310	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54478.1	000000	-	318	ACSA002_1640	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54480.1	000000	-	55	ACSA002_1660	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54482.1	000000	-	329	ACSA002_1680	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54484.1	000000	-	203	ACSA002_1700	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54486.1	000000	-	134	ACSA002_1720	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54502.1	000000	-	91	ACSA002_1880	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54503.1	000000	-	184	ACSA002_1890	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54504.1	000000	-	82	ACSA002_1900	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54505.1	000000	-	134	ACSA002_1910	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54506.1	000000	-	200	ACSA002_1920	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54508.1	000000	-	67	ACSA002_1940	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54510.1	000000	-	54	ACSA002_1960	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54513.1	000000	-	254	ACSA002_1990	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54514.1	000000	-	143	ACSA002_2000	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54515.1	000000	-	85	ACSA002_2010	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54516.1	000000	-	40	ACSA002_2020	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54517.1	000000	-	45	ACSA002_2030	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54518.1	000000	-	334	ACSA002_2040	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54521.1	000000	-	39	ACSA002_2056	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54526.1	000000	-	195	ACSA002_2100	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54527.1	000000	-	95	ACSA002_2110	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54530.1	000000	-	163	ACSA002_2140	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54531.1	000000	-	185	ACSA002_2150	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54532.1	000000	-	223	ACSA002_2160	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54537.1	000000	-	117	ACSA002_2210	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54539.1	000000	-	125	ACSA002_2230	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54541.1	000000	-	141	ACSA002_2250	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54548.1	000000	-	230	ACSA002_2320	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54553.1	000000	-	89	ACSA002_2370	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54554.1	000000	-	64	ACSA002_2380	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54557.1	000000	-	111	ACSA002_2410	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54559.1	000000	-	177	ACSA002_2430	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54577.1	000000	-	151	ACSA002_2610	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54578.1	000000	-	130	ACSA002_2620	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54579.1	000000	-	237	ACSA002_2630	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54580.1	000000	-	226	ACSA002_2640	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54582.1	000000	-	113	ACSA002_2660	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54585.1	000000	-	88	ACSA002_2690	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54586.1	000000	-	196	ACSA002_2700	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54587.1	000000	-	235	ACSA002_2710	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54590.1	000000	-	163	ACSA002_2740	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54591.1	000000	-	108	ACSA002_2750	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54592.1	000000	-	120	ACSA002_2760	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54593.1	000000	-	60	ACSA002_2765	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54595.1	000000	-	112	ACSA002_2780	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54602.1	000000	-	263	ACSA002_2850	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54603.1	000000	-	103	ACSA002_2860	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54604.1	000000	-	115	ACSA002_2870	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54605.1	000000	-	108	ACSA002_2880	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54606.1	000000	-	216	ACSA002_2890	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54607.1	000000	-	169	ACSA002_2900	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54624.1	000000	-	484	ACSA002_3070	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54642.1	000000	-	114	ACSA002_3250	Salmonella phage vB_SalM_SA002	GCA_014131285.1
QKE54644.1	000000	-	151	ACSA002_3270	Salmonella phage vB_SalM_SA002	GCA_014131285.1
ATA65337.1	000000	-	77	2050HW_00002	Serratia phage 2050HW	GCA_002628125.1
ATA65348.1	000000	-	72	2050HW_00013	Serratia phage 2050HW	GCA_002628125.1
ATA65396.1	000000	-	131	2050HW_00061	Serratia phage 2050HW	GCA_002628125.1
ATA65423.1	000000	-	44	2050HW_00088	Serratia phage 2050HW	GCA_002628125.1
ATA65429.1	000000	-	133	2050HW_00094	Serratia phage 2050HW	GCA_002628125.1
ATA65457.1	000000	-	61	2050HW_00122	Serratia phage 2050HW	GCA_002628125.1
ATA65459.1	000000	-	421	2050HW_00124	Serratia phage 2050HW	GCA_002628125.1
ATA65460.1	000000	-	362	2050HW_00125	Serratia phage 2050HW	GCA_002628125.1
ATA65491.1	000000	-	293	2050HW_00156	Serratia phage 2050HW	GCA_002628125.1
ATA65500.1	000000	-	147	2050HW_00165	Serratia phage 2050HW	GCA_002628125.1
ATA65502.1	000000	-	38	2050HW_00167	Serratia phage 2050HW	GCA_002628125.1
ATA65503.1	000000	-	20	2050HW_00168	Serratia phage 2050HW	GCA_002628125.1
ATA65504.1	000000	-	176	2050HW_00169	Serratia phage 2050HW	GCA_002628125.1
ATA65566.1	000000	-	132	2050HW_00231	Serratia phage 2050HW	GCA_002628125.1
ATA65567.1	000000	-	688	2050HW_00232	Serratia phage 2050HW	GCA_002628125.1
ATA65646.1	000000	-	100	2050HW_00311	Serratia phage 2050HW	GCA_002628125.1
ATA65647.1	000000	-	83	2050HW_00312	Serratia phage 2050HW	GCA_002628125.1
ATA65677.1	000000	-	93	2050HW_00342	Serratia phage 2050HW	GCA_002628125.1
AQW88534.1	000000	-	58	BF_0009	Serratia phage BF	GCA_002619745.1
AQW88537.1	000000	-	55	BF_0012	Serratia phage BF	GCA_002619745.1
AQW88540.1	000000	-	82	BF_0015	Serratia phage BF	GCA_002619745.1
AQW88541.1	000000	-	92	BF_0016	Serratia phage BF	GCA_002619745.1
AQW88543.1	000000	-	99	BF_0018	Serratia phage BF	GCA_002619745.1
AQW88557.1	000000	-	47	BF_0032	Serratia phage BF	GCA_002619745.1
AQW88603.1	000000	-	123	BF_0078	Serratia phage BF	GCA_002619745.1
AQW88660.1	000000	-	56	BF_0135	Serratia phage BF	GCA_002619745.1
AQW88661.1	000000	-	169	BF_0136	Serratia phage BF	GCA_002619745.1
AQW88690.1	000000	-	33	BF_0165	Serratia phage BF	GCA_002619745.1
AQW88692.1	000000	-	159	BF_0167	Serratia phage BF	GCA_002619745.1
AQW88695.1	000000	-	78	BF_0170	Serratia phage BF	GCA_002619745.1
AQW88704.1	000000	-	90	BF_0179	Serratia phage BF	GCA_002619745.1
AQW88748.1	000000	-	555	BF_0223	Serratia phage BF	GCA_002619745.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AQW88919.1	000000	-	77	BF_0394	Serratia phage BF	GCA_002619745.1
AQW88937.1	000000	-	51	BF_0412	Serratia phage BF	GCA_002619745.1
AQW88972.1	000000	-	103	BF_0447	Serratia phage BF	GCA_002619745.1
AQW88973.1	000000	-	53	BF_0448	Serratia phage BF	GCA_002619745.1
AQW88991.1	000000	-	101	BF_0466	Serratia phage BF	GCA_002619745.1
AQW89026.1	000000	-	90	BF_0501	Serratia phage BF	GCA_002619745.1
AQW89029.1	000000	-	136	BF_0504	Serratia phage BF	GCA_002619745.1
AQW89030.1	000000	-	122	BF_0505	Serratia phage BF	GCA_002619745.1
AQW89033.1	000000	-	145	BF_0508	Serratia phage BF	GCA_002619745.1
AQW89037.1	000000	-	96	BF_0512	Serratia phage BF	GCA_002619745.1
AQW89064.1	000000	-	160	BF_0539	Serratia phage BF	GCA_002619745.1
AQW89069.1	000000	-	377	BF_0544	Serratia phage BF	GCA_002619745.1
AQW89072.1	000000	-	32	BF_0547	Serratia phage BF	GCA_002619745.1
QDB71036.1	000000	-	35	CPT_Moabite_004	Serratia phage Moabite	GCA_006384735.1
QDB71037.1	000000	-	80	CPT_Moabite_005	Serratia phage Moabite	GCA_006384735.1
QDB71108.1	000000	-	40	CPT_Moabite_078	Serratia phage Moabite	GCA_006384735.1
QDB71109.1	000000	-	54	CPT_Moabite_079	Serratia phage Moabite	GCA_006384735.1
QDB71110.1	000000	-	67	CPT_Moabite_080	Serratia phage Moabite	GCA_006384735.1
QDB71112.1	000000	-	35	CPT_Moabite_082	Serratia phage Moabite	GCA_006384735.1
QDB71113.1	000000	-	34	CPT_Moabite_083	Serratia phage Moabite	GCA_006384735.1
QDB71229.1	000000	-	95	CPT_Moabite_199	Serratia phage Moabite	GCA_006384735.1
QDB71261.1	000000	-	109	CPT_Moabite_231	Serratia phage Moabite	GCA_006384735.1
QDB71267.1	000000	-	58	CPT_Moabite_237	Serratia phage Moabite	GCA_006384735.1
QDB71268.1	000000	-	209	CPT_Moabite_238	Serratia phage Moabite	GCA_006384735.1
QDB71270.1	000000	-	196	CPT_Moabite_240	Serratia phage Moabite	GCA_006384735.1
QDB71334.1	000000	-	56	CPT_Moabite_304	Serratia phage Moabite	GCA_006384735.1
QFP93197.1	000000	-	155	-	Serratia phage PCH45	GCA_009187865.1
QFP93256.1	000000	-	83	-	Serratia phage PCH45	GCA_009187865.1
QFP93119.1	000000	-	283	-	Serratia phage PCH45	GCA_009187865.1
QFP93254.1	000000	-	89	-	Serratia phage PCH45	GCA_009187865.1
QFP93240.1	000000	-	112	-	Serratia phage PCH45	GCA_009187865.1
QFP93214.1	000000	-	136	-	Serratia phage PCH45	GCA_009187865.1
QFP93216.1	000000	-	136	-	Serratia phage PCH45	GCA_009187865.1
QFP93185.1	000000	-	168	-	Serratia phage PCH45	GCA_009187865.1
QFP93201.1	000000	-	146	-	Serratia phage PCH45	GCA_009187865.1
QFP93207.1	000000	-	146	-	Serratia phage PCH45	GCA_009187865.1
QFP93218.1	000000	-	133	-	Serratia phage PCH45	GCA_009187865.1
QFP93190.1	000000	-	161	-	Serratia phage PCH45	GCA_009187865.1
QFP93177.1	000000	-	178	-	Serratia phage PCH45	GCA_009187865.1
QFP93118.1	000000	-	280	-	Serratia phage PCH45	GCA_009187865.1
QFP93092.1	000000	-	380	-	Serratia phage PCH45	GCA_009187865.1
QFP93111.1	000000	-	305	-	Serratia phage PCH45	GCA_009187865.1
QFP93206.1	000000	-	145	-	Serratia phage PCH45	GCA_009187865.1
QFP93140.1	000000	-	226	-	Serratia phage PCH45	GCA_009187865.1
QFP93169.1	000000	-	190	-	Serratia phage PCH45	GCA_009187865.1
QFP93175.1	000000	-	180	-	Serratia phage PCH45	GCA_009187865.1
QFP93112.1	000000	-	299	-	Serratia phage PCH45	GCA_009187865.1
QFP93199.1	000000	-	153	-	Serratia phage PCH45	GCA_009187865.1
QFP93066.1	000000	-	556	-	Serratia phage PCH45	GCA_009187865.1
QFP93044.1	000000	-	887	-	Serratia phage PCH45	GCA_009187865.1
QFP93094.1	000000	-	370	-	Serratia phage PCH45	GCA_009187865.1
QFP93129.1	000000	-	247	-	Serratia phage PCH45	GCA_009187865.1
QFP93250.1	000000	-	92	-	Serratia phage PCH45	GCA_009187865.1
QFP93265.1	000000	-	42	-	Serratia phage PCH45	GCA_009187865.1
QFP93210.1	000000	-	137	-	Serratia phage PCH45	GCA_009187865.1
QFP93212.1	000000	-	137	-	Serratia phage PCH45	GCA_009187865.1
QFP93261.1	000000	-	65	-	Serratia phage PCH45	GCA_009187865.1
QFP93255.1	000000	-	88	-	Serratia phage PCH45	GCA_009187865.1
QFP93258.1	000000	-	77	-	Serratia phage PCH45	GCA_009187865.1
QFP93135.1	000000	-	235	-	Serratia phage PCH45	GCA_009187865.1
QFP93200.1	000000	-	154	-	Serratia phage PCH45	GCA_009187865.1
QFP93189.1	000000	-	165	-	Serratia phage PCH45	GCA_009187865.1
QFP93157.1	000000	-	208	-	Serratia phage PCH45	GCA_009187865.1
QFP93204.1	000000	-	147	-	Serratia phage PCH45	GCA_009187865.1
QFP93170.1	000000	-	188	-	Serratia phage PCH45	GCA_009187865.1
QFP93248.1	000000	-	99	-	Serratia phage PCH45	GCA_009187865.1
QFP93233.1	000000	-	117	-	Serratia phage PCH45	GCA_009187865.1
QFP93244.1	000000	-	110	-	Serratia phage PCH45	GCA_009187865.1
QFP93242.1	000000	-	110	-	Serratia phage PCH45	GCA_009187865.1
QFP93234.1	000000	-	114	-	Serratia phage PCH45	GCA_009187865.1
QFP93229.1	000000	-	120	-	Serratia phage PCH45	GCA_009187865.1
QFP93222.1	000000	-	127	-	Serratia phage PCH45	GCA_009187865.1
QFP93219.1	000000	-	134	-	Serratia phage PCH45	GCA_009187865.1
QFP93215.1	000000	-	134	-	Serratia phage PCH45	GCA_009187865.1
QFP93196.1	000000	-	157	-	Serratia phage PCH45	GCA_009187865.1
QFP93168.1	000000	-	192	-	Serratia phage PCH45	GCA_009187865.1
QFP93134.1	000000	-	239	-	Serratia phage PCH45	GCA_009187865.1
QFP93131.1	000000	-	243	-	Serratia phage PCH45	GCA_009187865.1
QFP93130.1	000000	-	258	-	Serratia phage PCH45	GCA_009187865.1
QFP93102.1	000000	-	340	-	Serratia phage PCH45	GCA_009187865.1
QFP93101.1	000000	-	342	-	Serratia phage PCH45	GCA_009187865.1
QFP93100.1	000000	-	348	-	Serratia phage PCH45	GCA_009187865.1
QFP93260.1	000000	-	70	-	Serratia phage PCH45	GCA_009187865.1
QFP93259.1	000000	-	71	-	Serratia phage PCH45	GCA_009187865.1
QFP93257.1	000000	-	75	-	Serratia phage PCH45	GCA_009187865.1
QFP93253.1	000000	-	91	-	Serratia phage PCH45	GCA_009187865.1
QFP93252.1	000000	-	91	-	Serratia phage PCH45	GCA_009187865.1
QFP93245.1	000000	-	97	-	Serratia phage PCH45	GCA_009187865.1
QFP93117.1	000000	-	279	-	Serratia phage PCH45	GCA_009187865.1
QFP93150.1	000000	-	216	-	Serratia phage PCH45	GCA_009187865.1
QFP93115.1	000000	-	297	-	Serratia phage PCH45	GCA_009187865.1
QFP93192.1	000000	-	163	-	Serratia phage PCH45	GCA_009187865.1
QFP93171.1	000000	-	185	-	Serratia phage PCH45	GCA_009187865.1
QFP93164.1	000000	-	199	-	Serratia phage PCH45	GCA_009187865.1
QFP93160.1	000000	-	200	-	Serratia phage PCH45	GCA_009187865.1
QFP93159.1	000000	-	202	-	Serratia phage PCH45	GCA_009187865.1
QFP93139.1	000000	-	227	-	Serratia phage PCH45	GCA_009187865.1
QFP93246.1	000000	-	96	-	Serratia phage PCH45	GCA_009187865.1
AGR47635.1	000000	-	238	SmphiM12_003	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47669.1	000000	-	84	SmphiM12_037	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47689.1	000000	-	23	SmphiM12_057	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47735.1	000000	-	247	SmphiM12_103	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47740.1	000000	-	126	SmphiM12_108	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47757.1	000000	-	671	SmphiM12_125	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47762.1	000000	-	301	SmphiM12_130	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47763.1	000000	-	377	SmphiM12_131	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47765.1	000000	-	490	SmphiM12_133	Sinorhizobium phage phiM12	GCA_001023565.1
AGR47986.1	000000	-	333	SmphiM12_354	Sinorhizobium phage phiM12	GCA_001023565.1
AIF27781.1	000000	-	67	SmphiM12_497	Sinorhizobium phage phiM12	GCA_001023565.1
AIF27783.1	000000	-	37	SmphiM12_499	Sinorhizobium phage phiM12	GCA_001023565.1
AKF12799.1	000000	-	61	PHIM7_254	Sinorhizobium phage phiM7	GCA_002622405.1
AKF13280.1	000000	-	65	PHIN3_13	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13405.1	000000	-	77	PHIN3_142	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13414.1	000000	-	99	PHIN3_151	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13438.1	000000	-	70	PHIN3_175	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13439.1	000000	-	66	PHIN3_176	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13269.1	000000	-	149	PHIN3_2	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13291.1	000000	-	61	PHIN3_26	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13292.1	000000	-	68	PHIN3_27	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13561.1	000000	-	56	PHIN3_298	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13270.1	000000	-	96	PHIN3_3	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13563.1	000000	-	69	PHIN3_300	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13590.1	000000	-	65	PHIN3_327	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13639.1	000000	-	66	PHIN3_376	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13647.1	000000	-	40	PHIN3_384	Sinorhizobium phage phiN3	GCA_001501175.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AKF13649.1	000000	-	51	PHIN3_386	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13651.1	000000	-	119	PHIN3_388	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13310.1	000000	-	202	PHIN3_45	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13313.1	000000	-	88	PHIN3_48	Sinorhizobium phage phiN3	GCA_001501175.1
AKF13272.1	000000	-	113	PHIN3_5	Sinorhizobium phage phiN3	GCA_001501175.1
AFF28008.1	000000	-	543	PAU_10	Sphingomonas phage PAU	GCA_000902455.1
AFF28098.1	000000	-	131	PAU_100	Sphingomonas phage PAU	GCA_000902455.1
AFF28100.1	000000	-	197	PAU_102	Sphingomonas phage PAU	GCA_000902455.1
AFF28105.1	000000	-	149	PAU_107	Sphingomonas phage PAU	GCA_000902455.1
AFF28106.1	000000	-	180	PAU_108	Sphingomonas phage PAU	GCA_000902455.1
AFF28107.1	000000	-	271	PAU_109	Sphingomonas phage PAU	GCA_000902455.1
AFF28109.1	000000	-	418	PAU_111	Sphingomonas phage PAU	GCA_000902455.1
AFF28111.1	000000	-	80	PAU_113	Sphingomonas phage PAU	GCA_000902455.1
AFF28113.1	000000	-	141	PAU_115	Sphingomonas phage PAU	GCA_000902455.1
AFF28117.1	000000	-	351	PAU_119	Sphingomonas phage PAU	GCA_000902455.1
AFF28010.1	000000	-	156	PAU_12	Sphingomonas phage PAU	GCA_000902455.1
AFF28118.1	000000	-	94	PAU_120	Sphingomonas phage PAU	GCA_000902455.1
AFF28119.1	000000	-	210	PAU_121	Sphingomonas phage PAU	GCA_000902455.1
AFF28120.1	000000	-	72	PAU_122	Sphingomonas phage PAU	GCA_000902455.1
AFF28122.1	000000	-	110	PAU_124	Sphingomonas phage PAU	GCA_000902455.1
AFF28123.1	000000	-	130	PAU_125	Sphingomonas phage PAU	GCA_000902455.1
AFF28124.1	000000	-	101	PAU_126	Sphingomonas phage PAU	GCA_000902455.1
AFF28129.1	000000	-	127	PAU_131	Sphingomonas phage PAU	GCA_000902455.1
AFF28130.1	000000	-	132	PAU_132	Sphingomonas phage PAU	GCA_000902455.1
AFF28131.1	000000	-	221	PAU_133	Sphingomonas phage PAU	GCA_000902455.1
AFF28133.1	000000	-	167	PAU_135	Sphingomonas phage PAU	GCA_000902455.1
AFF28135.1	000000	-	181	PAU_137	Sphingomonas phage PAU	GCA_000902455.1
AFF28136.1	000000	-	206	PAU_138	Sphingomonas phage PAU	GCA_000902455.1
AFF28138.1	000000	-	83	PAU_140	Sphingomonas phage PAU	GCA_000902455.1
AFF28140.1	000000	-	153	PAU_142	Sphingomonas phage PAU	GCA_000902455.1
AFF28141.1	000000	-	91	PAU_143	Sphingomonas phage PAU	GCA_000902455.1
AFF28142.1	000000	-	208	PAU_144	Sphingomonas phage PAU	GCA_000902455.1
AFF28143.1	000000	-	125	PAU_145	Sphingomonas phage PAU	GCA_000902455.1
AFF28144.1	000000	-	123	PAU_146	Sphingomonas phage PAU	GCA_000902455.1
AFF28147.1	000000	-	65	PAU_149	Sphingomonas phage PAU	GCA_000902455.1
AFF28013.1	000000	-	126	PAU_15	Sphingomonas phage PAU	GCA_000902455.1
AFF28148.1	000000	-	156	PAU_150	Sphingomonas phage PAU	GCA_000902455.1
AFF28150.1	000000	-	277	PAU_152	Sphingomonas phage PAU	GCA_000902455.1
AFF28151.1	000000	-	103	PAU_153	Sphingomonas phage PAU	GCA_000902455.1
AFF28152.1	000000	-	140	PAU_154	Sphingomonas phage PAU	GCA_000902455.1
AFF28155.1	000000	-	92	PAU_157	Sphingomonas phage PAU	GCA_000902455.1
AFF28157.1	000000	-	82	PAU_159	Sphingomonas phage PAU	GCA_000902455.1
AFF28014.1	000000	-	117	PAU_16	Sphingomonas phage PAU	GCA_000902455.1
AFF28162.1	000000	-	80	PAU_164	Sphingomonas phage PAU	GCA_000902455.1
AFF28163.1	000000	-	113	PAU_165	Sphingomonas phage PAU	GCA_000902455.1
AFF28164.1	000000	-	61	PAU_166	Sphingomonas phage PAU	GCA_000902455.1
AFF28166.1	000000	-	231	PAU_168	Sphingomonas phage PAU	GCA_000902455.1
AFF28170.1	000000	-	201	PAU_172	Sphingomonas phage PAU	GCA_000902455.1
AFF28173.1	000000	-	155	PAU_175	Sphingomonas phage PAU	GCA_000902455.1
AFF28016.1	000000	-	63	PAU_18	Sphingomonas phage PAU	GCA_000902455.1
AFF28179.1	000000	-	410	PAU_181	Sphingomonas phage PAU	GCA_000902455.1
AFF28181.1	000000	-	397	PAU_183	Sphingomonas phage PAU	GCA_000902455.1
AFF28187.1	000000	-	113	PAU_189	Sphingomonas phage PAU	GCA_000902455.1
AFF28017.1	000000	-	60	PAU_19	Sphingomonas phage PAU	GCA_000902455.1
AFF28188.1	000000	-	220	PAU_190	Sphingomonas phage PAU	GCA_000902455.1
AFF28189.1	000000	-	68	PAU_191	Sphingomonas phage PAU	GCA_000902455.1
AFF28190.1	000000	-	67	PAU_192	Sphingomonas phage PAU	GCA_000902455.1
AFF28191.1	000000	-	175	PAU_193	Sphingomonas phage PAU	GCA_000902455.1
AFF28193.1	000000	-	143	PAU_195	Sphingomonas phage PAU	GCA_000902455.1
AFF28194.1	000000	-	118	PAU_196	Sphingomonas phage PAU	GCA_000902455.1
AFF28197.1	000000	-	182	PAU_199	Sphingomonas phage PAU	GCA_000902455.1
AFF28018.1	000000	-	110	PAU_20	Sphingomonas phage PAU	GCA_000902455.1
AFF28198.1	000000	-	177	PAU_200	Sphingomonas phage PAU	GCA_000902455.1
AFF28199.1	000000	-	104	PAU_201	Sphingomonas phage PAU	GCA_000902455.1
AFF28200.1	000000	-	107	PAU_202	Sphingomonas phage PAU	GCA_000902455.1
AFF28205.1	000000	-	138	PAU_207	Sphingomonas phage PAU	GCA_000902455.1
AFF28206.1	000000	-	181	PAU_208	Sphingomonas phage PAU	GCA_000902455.1
AFF28207.1	000000	-	166	PAU_209	Sphingomonas phage PAU	GCA_000902455.1
AFF28019.1	000000	-	951	PAU_21	Sphingomonas phage PAU	GCA_000902455.1
AFF28209.1	000000	-	272	PAU_211	Sphingomonas phage PAU	GCA_000902455.1
AFF28211.1	000000	-	65	PAU_213	Sphingomonas phage PAU	GCA_000902455.1
AFF28212.1	000000	-	140	PAU_214	Sphingomonas phage PAU	GCA_000902455.1
AFF28214.1	000000	-	329	PAU_216	Sphingomonas phage PAU	GCA_000902455.1
AFF28216.1	000000	-	109	PAU_218	Sphingomonas phage PAU	GCA_000902455.1
AFF28217.1	000000	-	94	PAU_219	Sphingomonas phage PAU	GCA_000902455.1
AFF28020.1	000000	-	300	PAU_22	Sphingomonas phage PAU	GCA_000902455.1
AFF28218.1	000000	-	125	PAU_220	Sphingomonas phage PAU	GCA_000902455.1
AFF28219.1	000000	-	161	PAU_221	Sphingomonas phage PAU	GCA_000902455.1
AFF28220.1	000000	-	173	PAU_222	Sphingomonas phage PAU	GCA_000902455.1
AFF28221.1	000000	-	203	PAU_223	Sphingomonas phage PAU	GCA_000902455.1
AFF28222.1	000000	-	135	PAU_224	Sphingomonas phage PAU	GCA_000902455.1
AFF28223.1	000000	-	128	PAU_225	Sphingomonas phage PAU	GCA_000902455.1
AFF28224.1	000000	-	82	PAU_226	Sphingomonas phage PAU	GCA_000902455.1
AFF28225.1	000000	-	183	PAU_227	Sphingomonas phage PAU	GCA_000902455.1
AFF28226.1	000000	-	158	PAU_228	Sphingomonas phage PAU	GCA_000902455.1
AFF28228.1	000000	-	204	PAU_230	Sphingomonas phage PAU	GCA_000902455.1
AFF28230.1	000000	-	131	PAU_232	Sphingomonas phage PAU	GCA_000902455.1
AFF28234.1	000000	-	114	PAU_236	Sphingomonas phage PAU	GCA_000902455.1
AFF28235.1	000000	-	327	PAU_237	Sphingomonas phage PAU	GCA_000902455.1
AFF28236.1	000000	-	207	PAU_238	Sphingomonas phage PAU	GCA_000902455.1
AFF28022.1	000000	-	91	PAU_24	Sphingomonas phage PAU	GCA_000902455.1
AFF28238.1	000000	-	94	PAU_240	Sphingomonas phage PAU	GCA_000902455.1
AFF28239.1	000000	-	86	PAU_241	Sphingomonas phage PAU	GCA_000902455.1
AFF28240.1	000000	-	87	PAU_242	Sphingomonas phage PAU	GCA_000902455.1
AFF28241.1	000000	-	103	PAU_243	Sphingomonas phage PAU	GCA_000902455.1
AFF28245.1	000000	-	161	PAU_247	Sphingomonas phage PAU	GCA_000902455.1
AFF28246.1	000000	-	234	PAU_248	Sphingomonas phage PAU	GCA_000902455.1
AFF28247.1	000000	-	124	PAU_249	Sphingomonas phage PAU	GCA_000902455.1
AFF28248.1	000000	-	103	PAU_250	Sphingomonas phage PAU	GCA_000902455.1
AFF28249.1	000000	-	115	PAU_251	Sphingomonas phage PAU	GCA_000902455.1
AFF28251.1	000000	-	175	PAU_253	Sphingomonas phage PAU	GCA_000902455.1
AFF28254.1	000000	-	72	PAU_256	Sphingomonas phage PAU	GCA_000902455.1
AFF28024.1	000000	-	134	PAU_26	Sphingomonas phage PAU	GCA_000902455.1
AFF28258.1	000000	-	321	PAU_260	Sphingomonas phage PAU	GCA_000902455.1
AFF28260.1	000000	-	94	PAU_262	Sphingomonas phage PAU	GCA_000902455.1
AFF28265.1	000000	-	384	PAU_267	Sphingomonas phage PAU	GCA_000902455.1
AFF28025.1	000000	-	275	PAU_27	Sphingomonas phage PAU	GCA_000902455.1
AFF28268.1	000000	-	347	PAU_270	Sphingomonas phage PAU	GCA_000902455.1
AFF28270.1	000000	-	136	PAU_272	Sphingomonas phage PAU	GCA_000902455.1
AFF28271.1	000000	-	61	PAU_273	Sphingomonas phage PAU	GCA_000902455.1
AFF28272.1	000000	-	110	PAU_274	Sphingomonas phage PAU	GCA_000902455.1
AFF28273.1	000000	-	161	PAU_275	Sphingomonas phage PAU	GCA_000902455.1
AFF28275.1	000000	-	81	PAU_277	Sphingomonas phage PAU	GCA_000902455.1
AFF28276.1	000000	-	166	PAU_278	Sphingomonas phage PAU	GCA_000902455.1
AFF28277.1	000000	-	152	PAU_279	Sphingomonas phage PAU	GCA_000902455.1
AFF28279.1	000000	-	73	PAU_281	Sphingomonas phage PAU	GCA_000902455.1
AFF28280.1	000000	-	138	PAU_282	Sphingomonas phage PAU	GCA_000902455.1
AFF28281.1	000000	-	90	PAU_283	Sphingomonas phage PAU	GCA_000902455.1
AFF28283.1	000000	-	168	PAU_285	Sphingomonas phage PAU	GCA_000902455.1
AFF28284.1	000000	-	134	PAU_286	Sphingomonas phage PAU	GCA_000902455.1
AFF28291.1	000000	-	113	PAU_294	Sphingomonas phage PAU	GCA_000902455.1
AFF28295.1	000000	-	95	PAU_298	Sphingomonas phage PAU	GCA_000902455.1
AFF28296.1	000000	-	106	PAU_299	Sphingomonas phage PAU	GCA_000902455.1
AFF28028.1	000000	-	82	PAU_30	Sphingomonas phage PAU	GCA_000902455.1
AFF28297.1	000000	-	57	PAU_300	Sphingomonas phage PAU	GCA_000902455.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AFF28298.1	000000	-	70	PAU_301	Sphingomonas phage PAU	GCA_000902455.1
AFF28299.1	000000	-	116	PAU_302	Sphingomonas phage PAU	GCA_000902455.1
AFF28029.1	000000	-	177	PAU_31	Sphingomonas phage PAU	GCA_000902455.1
AFF28031.1	000000	-	204	PAU_33	Sphingomonas phage PAU	GCA_000902455.1
AFF28032.1	000000	-	130	PAU_34	Sphingomonas phage PAU	GCA_000902455.1
AFF28034.1	000000	-	124	PAU_36	Sphingomonas phage PAU	GCA_000902455.1
AFF28036.1	000000	-	131	PAU_38	Sphingomonas phage PAU	GCA_000902455.1
AFF28038.1	000000	-	69	PAU_40	Sphingomonas phage PAU	GCA_000902455.1
AFF28040.1	000000	-	419	PAU_42	Sphingomonas phage PAU	GCA_000902455.1
AFF28042.1	000000	-	269	PAU_44	Sphingomonas phage PAU	GCA_000902455.1
AFF28045.1	000000	-	133	PAU_47	Sphingomonas phage PAU	GCA_000902455.1
AFF28047.1	000000	-	109	PAU_49	Sphingomonas phage PAU	GCA_000902455.1
AFF28048.1	000000	-	60	PAU_50	Sphingomonas phage PAU	GCA_000902455.1
AFF28049.1	000000	-	46	PAU_51	Sphingomonas phage PAU	GCA_000902455.1
AFF28050.1	000000	-	144	PAU_52	Sphingomonas phage PAU	GCA_000902455.1
AFF28052.1	000000	-	74	PAU_54	Sphingomonas phage PAU	GCA_000902455.1
AFF28053.1	000000	-	117	PAU_55	Sphingomonas phage PAU	GCA_000902455.1
AFF28054.1	000000	-	120	PAU_56	Sphingomonas phage PAU	GCA_000902455.1
AFF28055.1	000000	-	75	PAU_57	Sphingomonas phage PAU	GCA_000902455.1
AFF28056.1	000000	-	110	PAU_58	Sphingomonas phage PAU	GCA_000902455.1
AFF28057.1	000000	-	224	PAU_59	Sphingomonas phage PAU	GCA_000902455.1
AFF28059.1	000000	-	202	PAU_61	Sphingomonas phage PAU	GCA_000902455.1
AFF28061.1	000000	-	141	PAU_63	Sphingomonas phage PAU	GCA_000902455.1
AFF28062.1	000000	-	117	PAU_64	Sphingomonas phage PAU	GCA_000902455.1
AFF28063.1	000000	-	119	PAU_65	Sphingomonas phage PAU	GCA_000902455.1
AFF28067.1	000000	-	45	PAU_69	Sphingomonas phage PAU	GCA_000902455.1
AFF28069.1	000000	-	66	PAU_71	Sphingomonas phage PAU	GCA_000902455.1
AFF28070.1	000000	-	468	PAU_72	Sphingomonas phage PAU	GCA_000902455.1
AFF28071.1	000000	-	73	PAU_73	Sphingomonas phage PAU	GCA_000902455.1
AFF28073.1	000000	-	122	PAU_75	Sphingomonas phage PAU	GCA_000902455.1
AFF28075.1	000000	-	123	PAU_77	Sphingomonas phage PAU	GCA_000902455.1
AFF28076.1	000000	-	131	PAU_78	Sphingomonas phage PAU	GCA_000902455.1
AFF28077.1	000000	-	248	PAU_79	Sphingomonas phage PAU	GCA_000902455.1
AFF28078.1	000000	-	265	PAU_80	Sphingomonas phage PAU	GCA_000902455.1
AFF28082.1	000000	-	97	PAU_84	Sphingomonas phage PAU	GCA_000902455.1
AFF28007.1	000000	-	768	PAU_9	Sphingomonas phage PAU	GCA_000902455.1
AFF28089.1	000000	-	366	PAU_91	Sphingomonas phage PAU	GCA_000902455.1
AFF28092.1	000000	-	45	PAU_94	Sphingomonas phage PAU	GCA_000902455.1
AFF28094.1	000000	-	102	PAU_96	Sphingomonas phage PAU	GCA_000902455.1
AFF28097.1	000000	-	1048	PAU_99	Sphingomonas phage PAU	GCA_000902455.1
AYD81352.1	000000	-	90	SEA_JUSTBECAUSE_187	Streptomyces phage JustBecause	GCA_003613775.1
AYD81414.1	000000	-	28	SEA_JUSTBECAUSE_259	Streptomyces phage JustBecause	GCA_003613775.1
AYD81429.1	000000	-	29	SEA_JUSTBECAUSE_274	Streptomyces phage JustBecause	GCA_003613775.1
AYD81444.1	000000	-	72	SEA_JUSTBECAUSE_289	Streptomyces phage JustBecause	GCA_003613775.1
AYD81489.1	000000	-	76	SEA_JUSTBECAUSE_334	Streptomyces phage JustBecause	GCA_003613775.1
QJD53755.1	000000	-	97	SEA_KELA_185	Streptomyces phage Kela	GCA_012934305.1
QJD53814.1	000000	-	143	SEA_KELA_254	Streptomyces phage Kela	GCA_012934305.1
QJD53851.1	000000	-	60	SEA_KELA_291	Streptomyces phage Kela	GCA_012934305.1
QJD53898.1	000000	-	60	SEA_KELA_338	Streptomyces phage Kela	GCA_012934305.1
QBZ72003.1	000000	-	52	SEA_KRADAL_105	Streptomyces phage Kradal	GCA_004799925.1
QBZ72081.1	000000	-	42	SEA_KRADAL_185	Streptomyces phage Kradal	GCA_004799925.1
QBZ71930.1	000000	-	138	SEA_KRADAL_31	Streptomyces phage Kradal	GCA_004799925.1
AXH66275.1	000000	-	40	SEA_SATIS_114	Streptomyces phage Satis	GCA_003366315.1
AXH66409.1	000000	-	26	SEA_SATIS_260	Streptomyces phage Satis	GCA_003366315.1
AXH66422.1	000000	-	41	SEA_SATIS_273	Streptomyces phage Satis	GCA_003366315.1
AXH66192.1	000000	-	33	SEA_SATIS_31	Streptomyces phage Satis	GCA_003366315.1
AIX30579.1	000000	-	160	Syn7803US37_102	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30580.1	000000	-	39	Syn7803US37_103	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30581.1	000000	-	53	Syn7803US37_104	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30582.1	000000	-	77	Syn7803US37_105	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30583.1	000000	-	52	Syn7803US37_106	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30584.1	000000	-	63	Syn7803US37_107	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30585.1	000000	-	54	Syn7803US37_108	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30586.1	000000	-	63	Syn7803US37_109	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30588.1	000000	-	54	Syn7803US37_111	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30589.1	000000	-	43	Syn7803US37_112	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30592.1	000000	-	45	Syn7803US37_115	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30598.1	000000	-	74	Syn7803US37_121	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30600.1	000000	-	85	Syn7803US37_123	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30605.1	000000	-	137	Syn7803US37_128	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30490.1	000000	-	685	Syn7803US37_13	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30608.1	000000	-	403	Syn7803US37_131	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30614.1	000000	-	85	Syn7803US37_137	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30491.1	000000	-	233	Syn7803US37_14	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30618.1	000000	-	119	Syn7803US37_141	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30626.1	000000	-	134	Syn7803US37_149	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30494.1	000000	-	187	Syn7803US37_17	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30648.1	000000	-	52	Syn7803US37_171	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30657.1	000000	-	40	Syn7803US37_180	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30663.1	000000	-	59	Syn7803US37_186	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30664.1	000000	-	433	Syn7803US37_187	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30666.1	000000	-	151	Syn7803US37_189	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30673.1	000000	-	71	Syn7803US37_196	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30677.1	000000	-	61	Syn7803US37_200	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30685.1	000000	-	44	Syn7803US37_208	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30690.1	000000	-	54	Syn7803US37_213	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30699.1	000000	-	98	Syn7803US37_222	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30705.1	000000	-	50	Syn7803US37_228	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30501.1	000000	-	99	Syn7803US37_24	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30717.1	000000	-	771	Syn7803US37_240	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30718.1	000000	-	80	Syn7803US37_241	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30721.1	000000	-	54	Syn7803US37_244	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30722.1	000000	-	192	Syn7803US37_245	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30502.1	000000	-	69	Syn7803US37_25	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30731.1	000000	-	60	Syn7803US37_254	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30737.1	000000	-	162	Syn7803US37_260	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30738.1	000000	-	63	Syn7803US37_261	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30739.1	000000	-	66	Syn7803US37_262	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30741.1	000000	-	58	Syn7803US37_264	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30742.1	000000	-	129	Syn7803US37_265	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30743.1	000000	-	486	Syn7803US37_266	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30747.1	000000	-	1868	Syn7803US37_270	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30750.1	000000	-	124	Syn7803US37_273	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30754.1	000000	-	70	Syn7803US37_277	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30762.1	000000	-	59	Syn7803US37_285	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30507.1	000000	-	79	Syn7803US37_30	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30508.1	000000	-	115	Syn7803US37_31	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30510.1	000000	-	56	Syn7803US37_33	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30511.1	000000	-	42	Syn7803US37_34	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30512.1	000000	-	95	Syn7803US37_35	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30513.1	000000	-	88	Syn7803US37_36	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30514.1	000000	-	84	Syn7803US37_37	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30518.1	000000	-	96	Syn7803US37_41	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30523.1	000000	-	72	Syn7803US37_46	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30526.1	000000	-	59	Syn7803US37_49	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30534.1	000000	-	69	Syn7803US37_57	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30535.1	000000	-	38	Syn7803US37_58	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30539.1	000000	-	63	Syn7803US37_62	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30540.1	000000	-	73	Syn7803US37_63	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30541.1	000000	-	81	Syn7803US37_64	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30542.1	000000	-	80	Syn7803US37_65	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30544.1	000000	-	65	Syn7803US37_67	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30548.1	000000	-	83	Syn7803US37_71	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30552.1	000000	-	63	Syn7803US37_75	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30553.1	000000	-	123	Syn7803US37_76	Synechococcus phage ACG-2014f	GCA_002594065.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
AIX30554.1	000000	-	67	Syn7803US37_77	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30555.1	000000	-	124	Syn7803US37_78	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30557.1	000000	-	50	Syn7803US37_80	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30558.1	000000	-	63	Syn7803US37_81	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30561.1	000000	-	58	Syn7803US37_84	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30563.1	000000	-	52	Syn7803US37_86	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30564.1	000000	-	74	Syn7803US37_87	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30568.1	000000	-	118	Syn7803US37_91	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30570.1	000000	-	65	Syn7803US37_93	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30571.1	000000	-	89	Syn7803US37_94	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30573.1	000000	-	88	Syn7803US37_96	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30574.1	000000	-	57	Syn7803US37_97	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30575.1	000000	-	87	Syn7803US37_98	Synechococcus phage ACG-2014f	GCA_002594065.1
AIX30576.1	000000	-	74	Syn7803US37_99	Synechococcus phage ACG-2014f	GCA_002594065.1
QGT54468.1	000000	-	128	b3_0225	Synechococcus phage B3	GCA_009745215.1
QGT54469.1	000000	-	118	b3_0226	Synechococcus phage B3	GCA_009745215.1
ASR76183.1	000000	-	64	PBI_BELLAMY_138	Synechococcus phage Bellamy	GCA_002627525.1
ASR76192.1	000000	-	49	PBI_BELLAMY_147	Synechococcus phage Bellamy	GCA_002627525.1
ASR76224.1	000000	-	51	PBI_BELLAMY_181	Synechococcus phage Bellamy	GCA_002627525.1
ASR76227.1	000000	-	59	PBI_BELLAMY_188	Synechococcus phage Bellamy	GCA_002627525.1
ASR76232.1	000000	-	38	PBI_BELLAMY_196	Synechococcus phage Bellamy	GCA_002627525.1
ASR76250.1	000000	-	251	PBI_BELLAMY_214	Synechococcus phage Bellamy	GCA_002627525.1
ASR76069.1	000000	-	67	PBI_BELLAMY_22	Synechococcus phage Bellamy	GCA_002627525.1
ASR76260.1	000000	-	285	PBI_BELLAMY_224	Synechococcus phage Bellamy	GCA_002627525.1
ASR76271.1	000000	-	26	PBI_BELLAMY_235	Synechococcus phage Bellamy	GCA_002627525.1
ASR76308.1	000000	-	47	PBI_BELLAMY_272	Synechococcus phage Bellamy	GCA_002627525.1
ASR76079.1	000000	-	144	PBI_BELLAMY_34	Synechococcus phage Bellamy	GCA_002627525.1
ASR76084.1	000000	-	111	PBI_BELLAMY_39	Synechococcus phage Bellamy	GCA_002627525.1
ASR76085.1	000000	-	126	PBI_BELLAMY_40	Synechococcus phage Bellamy	GCA_002627525.1
ASR76101.1	000000	-	51	PBI_BELLAMY_56	Synechococcus phage Bellamy	GCA_002627525.1
ASR76107.1	000000	-	52	PBI_BELLAMY_62	Synechococcus phage Bellamy	GCA_002627525.1
ASR76109.1	000000	-	119	PBI_BELLAMY_64	Synechococcus phage Bellamy	GCA_002627525.1
ASR76111.1	000000	-	49	PBI_BELLAMY_66	Synechococcus phage Bellamy	GCA_002627525.1
ASR76115.1	000000	-	49	PBI_BELLAMY_70	Synechococcus phage Bellamy	GCA_002627525.1
ASR76119.1	000000	-	41	PBI_BELLAMY_74	Synechococcus phage Bellamy	GCA_002627525.1
ASR76121.1	000000	-	77	PBI_BELLAMY_76	Synechococcus phage Bellamy	GCA_002627525.1
ASR76124.1	000000	-	48	PBI_BELLAMY_79	Synechococcus phage Bellamy	GCA_002627525.1
ASR76126.1	000000	-	42	PBI_BELLAMY_81	Synechococcus phage Bellamy	GCA_002627525.1
ASR76129.1	000000	-	79	PBI_BELLAMY_84	Synechococcus phage Bellamy	GCA_002627525.1
ASR76136.1	000000	-	48	PBI_BELLAMY_91	Synechococcus phage Bellamy	GCA_002627525.1
ASR76141.1	000000	-	41	PBI_BELLAMY_96	Synechococcus phage Bellamy	GCA_002627525.1
ASR76144.1	000000	-	38	PBI_BELLAMY_99	Synechococcus phage Bellamy	GCA_002627525.1
QCW22943.1	000000	-	687	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23041.1	000000	-	52	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23057.1	000000	-	45	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23077.1	000000	-	62	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22862.1	000000	-	106	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22856.1	000000	-	53	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22854.1	000000	-	54	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22998.1	000000	-	54	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22861.1	000000	-	47	-	Synechococcus phage S-B05	GCA_006083695.1
QCW23009.1	000000	-	51	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22855.1	000000	-	55	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22853.1	000000	-	59	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22864.1	000000	-	85	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22863.1	000000	-	69	-	Synechococcus phage S-B05	GCA_006083695.1
QCW22987.1	000000	-	195	-	Synechococcus phage S-B05	GCA_006083695.1
QDH50689.1	000000	-	38	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50548.1	000000	-	38	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50606.1	000000	-	72	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50630.1	000000	-	155	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50609.1	000000	-	53	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50634.1	000000	-	838	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50545.1	000000	-	353	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50694.1	000000	-	190	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50601.1	000000	-	115	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50602.1	000000	-	68	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50539.1	000000	-	187	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50604.1	000000	-	58	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50590.1	000000	-	74	-	Synechococcus phage S-B43	GCA_006869725.1
QDH50690.1	000000	-	29	-	Synechococcus phage S-B43	GCA_006869725.1
AOV59891.1	000000	-	48	N231010_192	Synechococcus phage S-CAM4	GCA_002922155.1
AXQ70495.1	000000	-	42	HOU04_gp096	Synechococcus phage S-T4	GCA_003443335.1
AXQ70496.1	000000	-	42	HOU04_gp097	Synechococcus phage S-T4	GCA_003443335.1
AXQ70541.1	000000	-	56	HOU04_gp142	Synechococcus phage S-T4	GCA_003443335.1
AXQ70474.1	000000	-	60	HOU04_gp075	Synechococcus phage S-T4	GCA_003443335.1
AXQ70470.1	000000	-	38	HOU04_gp071	Synechococcus phage S-T4	GCA_003443335.1
AXQ70537.1	000000	-	375	HOU04_gp138	Synechococcus phage S-T4	GCA_003443335.1
AXQ70429.1	000000	-	83	HOU04_gp030	Synechococcus phage S-T4	GCA_003443335.1
AXQ70532.1	000000	-	63	HOU04_gp133	Synechococcus phage S-T4	GCA_003443335.1
AXQ70477.1	000000	-	63	HOU04_gp078	Synechococcus phage S-T4	GCA_003443335.1
AXQ70440.1	000000	-	721	HOU04_gp041	Synechococcus phage S-T4	GCA_003443335.1
AXQ70436.1	000000	-	180	HOU04_gp037	Synechococcus phage S-T4	GCA_003443335.1
AXQ70570.1	000000	-	66	HOU04_gp171	Synechococcus phage S-T4	GCA_003443335.1
AXQ70471.1	000000	-	1267	HOU04_gp072	Synechococcus phage S-T4	GCA_003443335.1
AXQ70481.1	000000	-	45	HOU04_gp082	Synechococcus phage S-T4	GCA_003443335.1
AXQ70475.1	000000	-	68	HOU04_gp076	Synechococcus phage S-T4	GCA_003443335.1
AXQ70519.1	000000	-	255	HOU04_gp120	Synechococcus phage S-T4	GCA_003443335.1
AXQ70486.1	000000	-	46	HOU04_gp087	Synechococcus phage S-T4	GCA_003443335.1
AXQ70553.1	000000	-	132	HOU04_gp154	Synechococcus phage S-T4	GCA_003443335.1
AXQ70516.1	000000	-	209	HOU04_gp117	Synechococcus phage S-T4	GCA_003443335.1
AXQ70434.1	000000	-	228	HOU04_gp035	Synechococcus phage S-T4	GCA_003443335.1
AXQ70428.1	000000	-	346	HOU04_gp029	Synechococcus phage S-T4	GCA_003443335.1
QJT70032.1	000000	-	405	SynMITS9220M01_016	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70036.1	000000	-	259	SynMITS9220M01_020	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70042.1	000000	-	113	SynMITS9220M01_029	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70056.1	000000	-	48	SynMITS9220M01_043	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70060.1	000000	-	48	SynMITS9220M01_047	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70061.1	000000	-	77	SynMITS9220M01_048	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70064.1	000000	-	45	SynMITS9220M01_051	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70067.1	000000	-	341	SynMITS9220M01_054	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70070.1	000000	-	141	SynMITS9220M01_057	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70071.1	000000	-	79	SynMITS9220M01_058	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70079.1	000000	-	50	SynMITS9220M01_066	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70080.1	000000	-	49	SynMITS9220M01_067	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70083.1	000000	-	52	SynMITS9220M01_070	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70090.1	000000	-	92	SynMITS9220M01_077	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70108.1	000000	-	57	SynMITS9220M01_095	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70135.1	000000	-	54	SynMITS9220M01_122	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70142.1	000000	-	128	SynMITS9220M01_129	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70152.1	000000	-	1177	SynMITS9220M01_139	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70156.1	000000	-	265	SynMITS9220M01_143	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70169.1	000000	-	268	SynMITS9220M01_157	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70171.1	000000	-	364	SynMITS9220M01_159	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70173.1	000000	-	65	SynMITS9220M01_161	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70188.1	000000	-	233	SynMITS9220M01_181	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70211.1	000000	-	168	SynMITS9220M01_205	Synechococcus phage SynMITS9220M01	GCA_013187275.1
QJT70215.1	000000	-	233	SynMITS9220M01_209	Synechococcus phage SynMITS9220M01	GCA_013187275.1
BBI90694.1	000000	-	73	HYO65_gp302	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90586.1	000000	-	39	HYO65_gp194	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90465.1	000000	-	122	HYO65_gp073	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90594.1	000000	-	174	HYO65_gp202	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90650.1	000000	-	75	HYO65_gp258	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90605.1	000000	-	69	HYO65_gp213	Tenacibaculum phage PTm1	GCA_009730695.1
BBI90897.1	000000	-	92	-	Tenacibaculum phage PTm5	GCA_009730715.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBI90979.1	000000	-	273	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90784.1	000000	-	68	-	Tenacibaculum phage PTm5	GCA_009730715.1
BBI90749.1	000000	-	40	-	Tenacibaculum phage PTm5	GCA_009730715.1
BAV39123.1	000000	-	134	BPT24_001	Tenacibaculum phage pT24	GCA_002611925.1
BAV39124.1	000000	-	468	BPT24_002	Tenacibaculum phage pT24	GCA_002611925.1
BAX25545.1	000000	-	246	BPT24_004	Tenacibaculum phage pT24	GCA_002611925.1
BAV39129.1	000000	-	35	BPT24_007	Tenacibaculum phage pT24	GCA_002611925.1
BAV39130.1	000000	-	58	BPT24_008	Tenacibaculum phage pT24	GCA_002611925.1
BAV39132.1	000000	-	91	BPT24_010	Tenacibaculum phage pT24	GCA_002611925.1
BAV39133.1	000000	-	197	BPT24_011	Tenacibaculum phage pT24	GCA_002611925.1
BAV39134.1	000000	-	129	BPT24_012	Tenacibaculum phage pT24	GCA_002611925.1
BAV39136.1	000000	-	115	BPT24_014	Tenacibaculum phage pT24	GCA_002611925.1
BAV39137.1	000000	-	137	BPT24_015	Tenacibaculum phage pT24	GCA_002611925.1
BAV39139.1	000000	-	80	BPT24_017	Tenacibaculum phage pT24	GCA_002611925.1
BAV39144.1	000000	-	250	BPT24_022	Tenacibaculum phage pT24	GCA_002611925.1
BAV39145.1	000000	-	99	BPT24_023	Tenacibaculum phage pT24	GCA_002611925.1
BAV39146.1	000000	-	223	BPT24_024	Tenacibaculum phage pT24	GCA_002611925.1
BAV39148.1	000000	-	107	BPT24_026	Tenacibaculum phage pT24	GCA_002611925.1
BAV39149.1	000000	-	38	BPT24_027	Tenacibaculum phage pT24	GCA_002611925.1
BAV39150.1	000000	-	208	BPT24_028	Tenacibaculum phage pT24	GCA_002611925.1
BAV39151.1	000000	-	232	BPT24_029	Tenacibaculum phage pT24	GCA_002611925.1
BAV39153.1	000000	-	173	BPT24_031	Tenacibaculum phage pT24	GCA_002611925.1
BAV39157.1	000000	-	146	BPT24_035	Tenacibaculum phage pT24	GCA_002611925.1
BAV39158.1	000000	-	123	BPT24_036	Tenacibaculum phage pT24	GCA_002611925.1
BAV39162.1	000000	-	81	BPT24_040	Tenacibaculum phage pT24	GCA_002611925.1
BAV39163.1	000000	-	141	BPT24_041	Tenacibaculum phage pT24	GCA_002611925.1
BAV39168.1	000000	-	160	BPT24_045	Tenacibaculum phage pT24	GCA_002611925.1
BAV39169.1	000000	-	140	BPT24_046	Tenacibaculum phage pT24	GCA_002611925.1
BAV39171.1	000000	-	53	BPT24_048	Tenacibaculum phage pT24	GCA_002611925.1
BAV39176.1	000000	-	114	BPT24_053	Tenacibaculum phage pT24	GCA_002611925.1
BAV39178.1	000000	-	165	BPT24_055	Tenacibaculum phage pT24	GCA_002611925.1
BAV39180.1	000000	-	182	BPT24_057	Tenacibaculum phage pT24	GCA_002611925.1
BAV39182.1	000000	-	56	BPT24_059	Tenacibaculum phage pT24	GCA_002611925.1
BAV39185.1	000000	-	237	BPT24_062	Tenacibaculum phage pT24	GCA_002611925.1
BAV39187.1	000000	-	94	BPT24_064	Tenacibaculum phage pT24	GCA_002611925.1
BAV39188.1	000000	-	109	BPT24_065	Tenacibaculum phage pT24	GCA_002611925.1
BAV39191.1	000000	-	73	BPT24_068	Tenacibaculum phage pT24	GCA_002611925.1
BAV39193.1	000000	-	115	BPT24_070	Tenacibaculum phage pT24	GCA_002611925.1
BAV39194.1	000000	-	292	BPT24_071	Tenacibaculum phage pT24	GCA_002611925.1
BAV39196.1	000000	-	75	BPT24_073	Tenacibaculum phage pT24	GCA_002611925.1
BAV39197.1	000000	-	196	BPT24_074	Tenacibaculum phage pT24	GCA_002611925.1
BAV39199.1	000000	-	162	BPT24_076	Tenacibaculum phage pT24	GCA_002611925.1
BAV39204.1	000000	-	95	BPT24_079	Tenacibaculum phage pT24	GCA_002611925.1
BAV39209.1	000000	-	548	BPT24_084	Tenacibaculum phage pT24	GCA_002611925.1
BAV39210.1	000000	-	131	BPT24_085	Tenacibaculum phage pT24	GCA_002611925.1
BAV39211.1	000000	-	149	BPT24_086	Tenacibaculum phage pT24	GCA_002611925.1
BAV39213.1	000000	-	95	BPT24_088	Tenacibaculum phage pT24	GCA_002611925.1
BAV39214.1	000000	-	206	BPT24_089	Tenacibaculum phage pT24	GCA_002611925.1
BAV39215.1	000000	-	51	BPT24_090	Tenacibaculum phage pT24	GCA_002611925.1
BAV39216.1	000000	-	406	BPT24_091	Tenacibaculum phage pT24	GCA_002611925.1
BAV39217.1	000000	-	88	BPT24_092	Tenacibaculum phage pT24	GCA_002611925.1
BAV39218.1	000000	-	146	BPT24_093	Tenacibaculum phage pT24	GCA_002611925.1
BAV39219.1	000000	-	83	BPT24_094	Tenacibaculum phage pT24	GCA_002611925.1
BAX25553.1	000000	-	29	BPT24_099	Tenacibaculum phage pT24	GCA_002611925.1
BAV39226.1	000000	-	113	BPT24_101	Tenacibaculum phage pT24	GCA_002611925.1
BAV39227.1	000000	-	61	BPT24_102	Tenacibaculum phage pT24	GCA_002611925.1
BAV39229.1	000000	-	301	BPT24_104	Tenacibaculum phage pT24	GCA_002611925.1
BAV39230.1	000000	-	230	BPT24_105	Tenacibaculum phage pT24	GCA_002611925.1
BAV39232.1	000000	-	270	BPT24_107	Tenacibaculum phage pT24	GCA_002611925.1
BAV39233.1	000000	-	139	BPT24_108	Tenacibaculum phage pT24	GCA_002611925.1
BAV39241.1	000000	-	126	BPT24_116	Tenacibaculum phage pT24	GCA_002611925.1
BAV39247.1	000000	-	92	BPT24_122	Tenacibaculum phage pT24	GCA_002611925.1
BAV39252.1	000000	-	270	BPT24_127	Tenacibaculum phage pT24	GCA_002611925.1
BAV39253.1	000000	-	267	BPT24_128	Tenacibaculum phage pT24	GCA_002611925.1
BAV39254.1	000000	-	112	BPT24_129	Tenacibaculum phage pT24	GCA_002611925.1
BAV39255.1	000000	-	84	BPT24_130	Tenacibaculum phage pT24	GCA_002611925.1
BAV39256.1	000000	-	73	BPT24_131	Tenacibaculum phage pT24	GCA_002611925.1
BAV39259.1	000000	-	161	BPT24_134	Tenacibaculum phage pT24	GCA_002611925.1
BAV39263.1	000000	-	3229	BPT24_138	Tenacibaculum phage pT24	GCA_002611925.1
BAX25555.1	000000	-	32	BPT24_141	Tenacibaculum phage pT24	GCA_002611925.1
BAV39275.1	000000	-	230	BPT24_149	Tenacibaculum phage pT24	GCA_002611925.1
BAX25558.1	000000	-	187	BPT24_150	Tenacibaculum phage pT24	GCA_002611925.1
BAV39278.1	000000	-	202	BPT24_152	Tenacibaculum phage pT24	GCA_002611925.1
BAX25560.1	000000	-	26	BPT24_158	Tenacibaculum phage pT24	GCA_002611925.1
BAV39290.1	000000	-	112	BPT24_164	Tenacibaculum phage pT24	GCA_002611925.1
BAV39292.1	000000	-	99	BPT24_166	Tenacibaculum phage pT24	GCA_002611925.1
BAV39293.1	000000	-	299	BPT24_167	Tenacibaculum phage pT24	GCA_002611925.1
BAV39295.1	000000	-	936	BPT24_169	Tenacibaculum phage pT24	GCA_002611925.1
BAV39296.1	000000	-	461	BPT24_170	Tenacibaculum phage pT24	GCA_002611925.1
BAV39305.1	000000	-	208	BPT24_180	Tenacibaculum phage pT24	GCA_002611925.1
BAV39308.1	000000	-	106	BPT24_183	Tenacibaculum phage pT24	GCA_002611925.1
BAV39309.1	000000	-	180	BPT24_184	Tenacibaculum phage pT24	GCA_002611925.1
BAV39315.1	000000	-	119	BPT24_190	Tenacibaculum phage pT24	GCA_002611925.1
BAV39317.1	000000	-	237	BPT24_192	Tenacibaculum phage pT24	GCA_002611925.1
BAV39320.1	000000	-	210	BPT24_196	Tenacibaculum phage pT24	GCA_002611925.1
BAV39323.1	000000	-	114	BPT24_199	Tenacibaculum phage pT24	GCA_002611925.1
BAV39324.1	000000	-	100	BPT24_200	Tenacibaculum phage pT24	GCA_002611925.1
BAV39327.1	000000	-	104	BPT24_203	Tenacibaculum phage pT24	GCA_002611925.1
BAV39328.1	000000	-	327	BPT24_204	Tenacibaculum phage pT24	GCA_002611925.1
BAV39329.1	000000	-	114	BPT24_205	Tenacibaculum phage pT24	GCA_002611925.1
BAV39330.1	000000	-	148	BPT24_206	Tenacibaculum phage pT24	GCA_002611925.1
BAV39333.1	000000	-	119	BPT24_209	Tenacibaculum phage pT24	GCA_002611925.1
BAV39335.1	000000	-	127	BPT24_211	Tenacibaculum phage pT24	GCA_002611925.1
BAV39337.1	000000	-	90	BPT24_213	Tenacibaculum phage pT24	GCA_002611925.1
BAV39338.1	000000	-	154	BPT24_214	Tenacibaculum phage pT24	GCA_002611925.1
BAV39339.1	000000	-	48	BPT24_215	Tenacibaculum phage pT24	GCA_002611925.1
BAV39340.1	000000	-	220	BPT24_216	Tenacibaculum phage pT24	GCA_002611925.1
BAV39341.1	000000	-	163	BPT24_217	Tenacibaculum phage pT24	GCA_002611925.1
BAV39342.1	000000	-	179	BPT24_218	Tenacibaculum phage pT24	GCA_002611925.1
BAV39343.1	000000	-	77	BPT24_219	Tenacibaculum phage pT24	GCA_002611925.1
BAV39345.1	000000	-	154	BPT24_221	Tenacibaculum phage pT24	GCA_002611925.1
BAV39346.1	000000	-	229	BPT24_222	Tenacibaculum phage pT24	GCA_002611925.1
BAV39347.1	000000	-	81	BPT24_223	Tenacibaculum phage pT24	GCA_002611925.1
BAX25561.1	000000	-	158	BPT24_224	Tenacibaculum phage pT24	GCA_002611925.1
BAV39350.1	000000	-	204	BPT24_226	Tenacibaculum phage pT24	GCA_002611925.1
BAV39351.1	000000	-	80	BPT24_231	Tenacibaculum phage pT24	GCA_002611925.1
BAV39359.1	000000	-	46	BPT24_239	Tenacibaculum phage pT24	GCA_002611925.1
BAV39360.1	000000	-	69	BPT24_240	Tenacibaculum phage pT24	GCA_002611925.1
BAV39361.1	000000	-	64	BPT24_241	Tenacibaculum phage pT24	GCA_002611925.1
BAV39362.1	000000	-	52	BPT24_242	Tenacibaculum phage pT24	GCA_002611925.1
BAV39367.1	000000	-	68	BPT24_247	Tenacibaculum phage pT24	GCA_002611925.1
BAV39368.1	000000	-	152	BPT24_248	Tenacibaculum phage pT24	GCA_002611925.1
BAV39370.1	000000	-	191	BPT24_250	Tenacibaculum phage pT24	GCA_002611925.1
BAV39373.1	000000	-	144	BPT24_254	Tenacibaculum phage pT24	GCA_002611925.1
BAV39376.1	000000	-	88	BPT24_257	Tenacibaculum phage pT24	GCA_002611925.1
BAV39379.1	000000	-	166	BPT24_261	Tenacibaculum phage pT24	GCA_002611925.1
BAV39386.1	000000	-	146	BPT24_269	Tenacibaculum phage pT24	GCA_002611925.1
BAX25566.1	000000	-	151	BPT24_271	Tenacibaculum phage pT24	GCA_002611925.1
BAV39389.1	000000	-	135	BPT24_272	Tenacibaculum phage pT24	GCA_002611925.1
BAV39390.1	000000	-	118	BPT24_273	Tenacibaculum phage pT24	GCA_002611925.1
BAV39392.1	000000	-	132	BPT24_275	Tenacibaculum phage pT24	GCA_002611925.1
BAV39393.1	000000	-	230	BPT24_276	Tenacibaculum phage pT24	GCA_002611925.1
BAV39394.1	000000	-	73	BPT24_277	Tenacibaculum phage pT24	GCA_002611925.1
BAV39395.1	000000	-	62	BPT24_278	Tenacibaculum phage pT24	GCA_002611925.1
BAV39396.1	000000	-	68	BPT24_279	Tenacibaculum phage pT24	GCA_002611925.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAV39397.1	000000	-	116	BPT24_280	Tenacibaculum phage pT24	GCA_002611925.1
BAV39398.1	000000	-	128	BPT24_281	Tenacibaculum phage pT24	GCA_002611925.1
BAV39399.1	000000	-	201	BPT24_282	Tenacibaculum phage pT24	GCA_002611925.1
BAV39400.1	000000	-	149	BPT24_283	Tenacibaculum phage pT24	GCA_002611925.1
BAV39401.1	000000	-	217	BPT24_284	Tenacibaculum phage pT24	GCA_002611925.1
BAV39404.1	000000	-	142	BPT24_287	Tenacibaculum phage pT24	GCA_002611925.1
BAV39408.1	000000	-	103	BPT24_290	Tenacibaculum phage pT24	GCA_002611925.1
BAV39410.1	000000	-	297	BPT24_292	Tenacibaculum phage pT24	GCA_002611925.1
BAX25567.1	000000	-	327	BPT24_294	Tenacibaculum phage pT24	GCA_002611925.1
BAV39415.1	000000	-	181	BPT24_297	Tenacibaculum phage pT24	GCA_002611925.1
BAV39417.1	000000	-	108	BPT24_299	Tenacibaculum phage pT24	GCA_002611925.1
BAV39418.1	000000	-	93	BPT24_300	Tenacibaculum phage pT24	GCA_002611925.1
QAU04178.1	000000	-	36	HWC03_gp023	Vibrio phage 2 TSL-2019	GCA_006964105.1
AUR81102.1	000000	-	48	Aphrodite1_0181	Vibrio phage Aphrodite1	GCA_002958015.1
AXH71019.1	000000	-	72	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71011.1	000000	-	116	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70787.1	000000	-	101	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70957.1	000000	-	388	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70984.1	000000	-	56	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70935.1	000000	-	197	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70936.1	000000	-	147	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70910.1	000000	-	155	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70959.1	000000	-	210	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71017.1	000000	-	328	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70887.1	000000	-	252	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70776.1	000000	-	150	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70802.1	000000	-	150	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70755.1	000000	-	50	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70942.1	000000	-	43	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70924.1	000000	-	288	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70834.1	000000	-	375	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70945.1	000000	-	371	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70855.1	000000	-	373	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70889.1	000000	-	488	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70888.1	000000	-	490	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71007.1	000000	-	324	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70949.1	000000	-	455	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70883.1	000000	-	535	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70907.1	000000	-	259	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70836.1	000000	-	441	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70792.1	000000	-	64	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70937.1	000000	-	424	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70986.1	000000	-	113	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70899.1	000000	-	156	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70759.1	000000	-	156	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70989.1	000000	-	305	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70940.1	000000	-	143	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70923.1	000000	-	273	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70847.1	000000	-	405	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71024.1	000000	-	164	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70954.1	000000	-	250	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70827.1	000000	-	190	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70993.1	000000	-	104	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70967.1	000000	-	104	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70831.1	000000	-	118	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70844.1	000000	-	167	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70982.1	000000	-	151	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71025.1	000000	-	112	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70757.1	000000	-	146	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70946.1	000000	-	135	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70807.1	000000	-	135	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70912.1	000000	-	137	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71006.1	000000	-	137	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70870.1	000000	-	49	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70902.1	000000	-	105	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70966.1	000000	-	53	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70872.1	000000	-	179	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71009.1	000000	-	179	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70978.1	000000	-	245	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70808.1	000000	-	123	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71026.1	000000	-	123	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71021.1	000000	-	198	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70893.1	000000	-	557	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71037.1	000000	-	230	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70839.1	000000	-	638	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70960.1	000000	-	274	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70925.1	000000	-	120	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70806.1	000000	-	120	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70853.1	000000	-	158	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70805.1	000000	-	131	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70794.1	000000	-	87	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70911.1	000000	-	334	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70895.1	000000	-	362	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70829.1	000000	-	140	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70886.1	000000	-	262	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70871.1	000000	-	154	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70916.1	000000	-	165	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71022.1	000000	-	208	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70919.1	000000	-	204	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70987.1	000000	-	204	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71003.1	000000	-	119	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71020.1	000000	-	175	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70928.1	000000	-	141	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71005.1	000000	-	141	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71038.1	000000	-	2008	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70783.1	000000	-	354	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70894.1	000000	-	354	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71004.1	000000	-	400	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70985.1	000000	-	195	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70892.1	000000	-	413	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70850.1	000000	-	224	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70846.1	000000	-	384	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70944.1	000000	-	386	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70968.1	000000	-	310	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70969.1	000000	-	310	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70964.1	000000	-	311	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70920.1	000000	-	166	-	Vibrio phage BONAISHI	GCA_003441475.1
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AXH70934.1	000000	-	100	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71018.1	000000	-	169	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70774.1	000000	-	223	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71008.1	000000	-	132	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70804.1	000000	-	142	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70988.1	000000	-	183	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70926.1	000000	-	183	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70958.1	000000	-	183	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70931.1	000000	-	183	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70791.1	000000	-	185	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH71028.1	000000	-	185	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70915.1	000000	-	199	-	Vibrio phage BONAISHI	GCA_003441475.1
AXH70789.1	000000	-	200	-	Vibrio phage BONAISHI	GCA_003441475.1
AAQ64310.1	000000	-	41	KVP40.0241	Vibrio phage KVP40	GCA_000843785.1
AAQ64385.1	000000	-	54	KVP40.0315	Vibrio phage KVP40	GCA_000843785.1
QDH47530.1	000000	-	190	HWC35_gp136	Vibrio phage USC-1	GCA_006864065.1
QIW90719.1	000000	-	110	GCAPEGMB_00400	Vibrio phage V07	GCA_012361095.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QIW90720.1	000000	-	128	GCAPEGMB_00401	Vibrio phage V07	GCA_012361095.1
QIW90721.1	000000	-	130	GCAPEGMB_00402	Vibrio phage V07	GCA_012361095.1
QIW90724.1	000000	-	76	GCAPEGMB_00405	Vibrio phage V07	GCA_012361095.1
QIW90725.1	000000	-	60	GCAPEGMB_00406	Vibrio phage V07	GCA_012361095.1
QIW90726.1	000000	-	229	GCAPEGMB_00407	Vibrio phage V07	GCA_012361095.1
QIW90729.1	000000	-	82	GCAPEGMB_00410	Vibrio phage V07	GCA_012361095.1
QIW90730.1	000000	-	64	GCAPEGMB_00411	Vibrio phage V07	GCA_012361095.1
QIW90731.1	000000	-	52	GCAPEGMB_00412	Vibrio phage V07	GCA_012361095.1
QIW90732.1	000000	-	153	GCAPEGMB_00413	Vibrio phage V07	GCA_012361095.1
QIW90733.1	000000	-	139	GCAPEGMB_00414	Vibrio phage V07	GCA_012361095.1
QIW90734.1	000000	-	142	GCAPEGMB_00415	Vibrio phage V07	GCA_012361095.1
QIW90737.1	000000	-	178	GCAPEGMB_00418	Vibrio phage V07	GCA_012361095.1
QIW90746.1	000000	-	238	GCAPEGMB_00427	Vibrio phage V07	GCA_012361095.1
QIW90747.1	000000	-	212	GCAPEGMB_00428	Vibrio phage V07	GCA_012361095.1
QIW90748.1	000000	-	62	GCAPEGMB_00429	Vibrio phage V07	GCA_012361095.1
QIW90749.1	000000	-	176	GCAPEGMB_00430	Vibrio phage V07	GCA_012361095.1
QIW90750.1	000000	-	125	GCAPEGMB_00431	Vibrio phage V07	GCA_012361095.1
QIW90751.1	000000	-	99	GCAPEGMB_00432	Vibrio phage V07	GCA_012361095.1
QIW90756.1	000000	-	124	GCAPEGMB_00437	Vibrio phage V07	GCA_012361095.1
QIW90757.1	000000	-	169	GCAPEGMB_00438	Vibrio phage V07	GCA_012361095.1
QIW90763.1	000000	-	118	GCAPEGMB_00444	Vibrio phage V07	GCA_012361095.1
QIW90765.1	000000	-	170	GCAPEGMB_00446	Vibrio phage V07	GCA_012361095.1
QIW90766.1	000000	-	735	GCAPEGMB_00447	Vibrio phage V07	GCA_012361095.1
QIW90768.1	000000	-	324	GCAPEGMB_00449	Vibrio phage V07	GCA_012361095.1
QIW90771.1	000000	-	100	GCAPEGMB_00452	Vibrio phage V07	GCA_012361095.1
QIW90775.1	000000	-	59	GCAPEGMB_00456	Vibrio phage V07	GCA_012361095.1
QIW90779.1	000000	-	194	GCAPEGMB_00461	Vibrio phage V07	GCA_012361095.1
QIW90781.1	000000	-	70	GCAPEGMB_00463	Vibrio phage V07	GCA_012361095.1
QIW90783.1	000000	-	358	GCAPEGMB_00465	Vibrio phage V07	GCA_012361095.1
QIW90788.1	000000	-	139	GCAPEGMB_00470	Vibrio phage V07	GCA_012361095.1
QIW90790.1	000000	-	101	GCAPEGMB_00472	Vibrio phage V07	GCA_012361095.1
QIW90791.1	000000	-	102	GCAPEGMB_00473	Vibrio phage V07	GCA_012361095.1
QIW90794.1	000000	-	43	GCAPEGMB_00476	Vibrio phage V07	GCA_012361095.1
QIW90796.1	000000	-	103	GCAPEGMB_00478	Vibrio phage V07	GCA_012361095.1
QIW90797.1	000000	-	64	GCAPEGMB_00479	Vibrio phage V07	GCA_012361095.1
QIW90798.1	000000	-	88	GCAPEGMB_00480	Vibrio phage V07	GCA_012361095.1
QIW90801.1	000000	-	494	GCAPEGMB_00483	Vibrio phage V07	GCA_012361095.1
QIW90803.1	000000	-	67	GCAPEGMB_00485	Vibrio phage V07	GCA_012361095.1
QIW90806.1	000000	-	198	GCAPEGMB_00488	Vibrio phage V07	GCA_012361095.1
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QIW90811.1	000000	-	79	GCAPEGMB_00493	Vibrio phage V07	GCA_012361095.1
QIW90813.1	000000	-	119	GCAPEGMB_00495	Vibrio phage V07	GCA_012361095.1
QIW90816.1	000000	-	47	GCAPEGMB_00501	Vibrio phage V07	GCA_012361095.1
QIW90819.1	000000	-	68	GCAPEGMB_00504	Vibrio phage V07	GCA_012361095.1
QIW90820.1	000000	-	120	GCAPEGMB_00505	Vibrio phage V07	GCA_012361095.1
QIW90822.1	000000	-	713	GCAPEGMB_00507	Vibrio phage V07	GCA_012361095.1
QIW90823.1	000000	-	74	GCAPEGMB_00508	Vibrio phage V07	GCA_012361095.1
QIW90826.1	000000	-	101	GCAPEGMB_00511	Vibrio phage V07	GCA_012361095.1
QIW90827.1	000000	-	234	GCAPEGMB_00512	Vibrio phage V07	GCA_012361095.1
QIW90828.1	000000	-	117	GCAPEGMB_00513	Vibrio phage V07	GCA_012361095.1
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QIW90839.1	000000	-	74	GCAPEGMB_00524	Vibrio phage V07	GCA_012361095.1
QIW90840.1	000000	-	249	GCAPEGMB_00525	Vibrio phage V07	GCA_012361095.1
QIW90842.1	000000	-	58	GCAPEGMB_00527	Vibrio phage V07	GCA_012361095.1
QIW90844.1	000000	-	148	GCAPEGMB_00529	Vibrio phage V07	GCA_012361095.1
QIW90846.1	000000	-	209	GCAPEGMB_00531	Vibrio phage V07	GCA_012361095.1
QIW90847.1	000000	-	220	GCAPEGMB_00532	Vibrio phage V07	GCA_012361095.1
QIW90848.1	000000	-	400	GCAPEGMB_00533	Vibrio phage V07	GCA_012361095.1
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QIW90853.1	000000	-	188	GCAPEGMB_00538	Vibrio phage V07	GCA_012361095.1
QIW90854.1	000000	-	81	GCAPEGMB_00539	Vibrio phage V07	GCA_012361095.1
QIW90855.1	000000	-	235	GCAPEGMB_00540	Vibrio phage V07	GCA_012361095.1
QIW90859.1	000000	-	666	GCAPEGMB_00544	Vibrio phage V07	GCA_012361095.1
QIW90861.1	000000	-	73	GCAPEGMB_00546	Vibrio phage V07	GCA_012361095.1
QIW90863.1	000000	-	167	GCAPEGMB_00548	Vibrio phage V07	GCA_012361095.1
QHJ74352.1	000000	-	102	VH12019_00025	Vibrio phage VH1_2019	GCA_009931825.1
QHJ74531.1	000000	-	66	VH12019_00231	Vibrio phage VH1_2019	GCA_009931825.1
QBX05973.1	000000	-	199	ValB1HC_019	Vibrio phage ValB1 HC	GCA_004771355.1
QAU04444.1	000000	-	73	ValB1MD_006	Vibrio phage ValB1MD	GCA_004138815.1
QAU04454.1	000000	-	295	ValB1MD_038	Vibrio phage ValB1MD	GCA_004138815.1
QAU04458.1	000000	-	76	ValB1MD_044	Vibrio phage ValB1MD	GCA_004138815.1
QAU04470.1	000000	-	207	ValB1MD_069	Vibrio phage ValB1MD	GCA_004138815.1
QAU04473.1	000000	-	171	ValB1MD_072	Vibrio phage ValB1MD	GCA_004138815.1
QAU04475.1	000000	-	112	ValB1MD_082	Vibrio phage ValB1MD	GCA_004138815.1
QAU04477.1	000000	-	166	ValB1MD_090	Vibrio phage ValB1MD	GCA_004138815.1
QAU04487.1	000000	-	78	ValB1MD_116	Vibrio phage ValB1MD	GCA_004138815.1
QAU04490.1	000000	-	118	ValB1MD_127	Vibrio phage ValB1MD	GCA_004138815.1
QAU04492.1	000000	-	121	ValB1MD_134	Vibrio phage ValB1MD	GCA_004138815.1
QAU04500.1	000000	-	123	ValB1MD_147	Vibrio phage ValB1MD	GCA_004138815.1
QAU04502.1	000000	-	68	ValB1MD_150	Vibrio phage ValB1MD	GCA_004138815.1
QAU04507.1	000000	-	113	ValB1MD_162	Vibrio phage ValB1MD	GCA_004138815.1
QAU04509.1	000000	-	264	ValB1MD_167	Vibrio phage ValB1MD	GCA_004138815.1
QAU04510.1	000000	-	750	ValB1MD_171	Vibrio phage ValB1MD	GCA_004138815.1
QAU04523.1	000000	-	151	ValB1MD_203	Vibrio phage ValB1MD	GCA_004138815.1
QAU04526.1	000000	-	61	ValB1MD_209	Vibrio phage ValB1MD	GCA_004138815.1
QAU04527.1	000000	-	139	ValB1MD_210	Vibrio phage ValB1MD	GCA_004138815.1
QAU04534.1	000000	-	203	ValB1MD_239	Vibrio phage ValB1MD	GCA_004138815.1
QAU04537.1	000000	-	288	ValB1MD_244	Vibrio phage ValB1MD	GCA_004138815.1
QAU04539.1	000000	-	152	ValB1MD_252	Vibrio phage ValB1MD	GCA_004138815.1
QAU04554.1	000000	-	77	ValB1MD_270	Vibrio phage ValB1MD	GCA_004138815.1
QAU04560.1	000000	-	229	ValB1MD_277	Vibrio phage ValB1MD	GCA_004138815.1
QAU04568.1	000000	-	597	ValB1MD_288	Vibrio phage ValB1MD	GCA_004138815.1
QAU04572.1	000000	-	192	ValB1MD_294	Vibrio phage ValB1MD	GCA_004138815.1
AGN30067.1	000000	-	69	VPFG_00064	Vibrio phage nt-1	GCA_000910195.2
AGN30076.1	000000	-	74	VPFG_00074	Vibrio phage nt-1	GCA_000910195.2
AGN30090.1	000000	-	84	VPFG_00088	Vibrio phage nt-1	GCA_000910195.2
AIE13792.1	000000	-	62	VPFG_p15	Vibrio phage nt-1	GCA_000910195.2
AGN30167.1	000000	-	70	VPFG_00165	Vibrio phage nt-1	GCA_000910195.2
AGN30184.1	000000	-	102	VPFG_00184	Vibrio phage nt-1	GCA_000910195.2
AGN30199.1	000000	-	117	VPFG_00199	Vibrio phage nt-1	GCA_000910195.2
AGN30214.2	000000	-	74	VPFG_00214	Vibrio phage nt-1	GCA_000910195.2
AGN30220.1	000000	-	74	VPFG_00220	Vibrio phage nt-1	GCA_000910195.2
AGN30225.2	000000	-	176	VPFG_00225	Vibrio phage nt-1	GCA_000910195.2
AIE13772.1	000000	-	33	-	Vibrio phage nt-1	GCA_000910195.2
AGN30229.1	000000	-	74	VPFG_00230	Vibrio phage nt-1	GCA_000910195.2
AGN30230.1	000000	-	107	VPFG_00231	Vibrio phage nt-1	GCA_000910195.2
AGN30231.1	000000	-	126	VPFG_00232	Vibrio phage nt-1	GCA_000910195.2
AGN30269.1	000000	-	80	VPFG_00270	Vibrio phage nt-1	GCA_000910195.2
AIE13776.1	000000	-	41	VPFG_p06	Vibrio phage nt-1	GCA_000910195.2
AGN30296.1	000000	-	97	VPFG_00297	Vibrio phage nt-1	GCA_000910195.2
AGN30346.1	000000	-	101	VPFG_00349	Vibrio phage nt-1	GCA_000910195.2
AIE13781.1	000000	-	29	VPFG_p09	Vibrio phage nt-1	GCA_000910195.2
AGN30357.1	000000	-	77	VPFG_00360	Vibrio phage nt-1	GCA_000910195.2
AGN30358.1	000000	-	74	VPFG_00361	Vibrio phage nt-1	GCA_000910195.2
AGN30359.1	000000	-	100	VPFG_00362	Vibrio phage nt-1	GCA_000910195.2
AGN30360.1	000000	-	103	VPFG_00363	Vibrio phage nt-1	GCA_000910195.2
AIE13782.1	000000	-	47	VPFG_p10	Vibrio phage nt-1	GCA_000910195.2
AGN30362.1	000000	-	78	VPFG_00365	Vibrio phage nt-1	GCA_000910195.2
AGN30365.1	000000	-	82	VPFG_00368	Vibrio phage nt-1	GCA_000910195.2
AGN30366.1	000000	-	302	VPFG_00369	Vibrio phage nt-1	GCA_000910195.2
AGN30368.1	000000	-	96	VPFG_00371	Vibrio phage nt-1	GCA_000910195.2
AGN30370.1	000000	-	69	VPFG_00373	Vibrio phage nt-1	GCA_000910195.2
AIE13784.1	000000	-	46	VPFG_p12	Vibrio phage nt-1	GCA_000910195.2
BAW98360.1	000000	-	210	FDH33_gp151	Vibrio phage pTD1	GCA_002618825.1
BAW98346.1	000000	-	38	FDH33_gp137	Vibrio phage pTD1	GCA_002618825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BAW98240.1	000000	-	177	FDH33_gp031	Vibrio phage pTD1	GCA_002618825.1
BAW98217.1	000000	-	505	FDH33_gp008	Vibrio phage pTD1	GCA_002618825.1
BAW98367.1	000000	-	1156	FDH33_gp158	Vibrio phage pTD1	GCA_002618825.1
BAW98279.1	000000	-	802	FDH33_gp070	Vibrio phage pTD1	GCA_002618825.1
BAW98227.1	000000	-	335	FDH33_gp018	Vibrio phage pTD1	GCA_002618825.1
BAW98355.1	000000	-	204	FDH33_gp146	Vibrio phage pTD1	GCA_002618825.1
BAW98243.1	000000	-	341	FDH33_gp034	Vibrio phage pTD1	GCA_002618825.1
BAW98357.1	000000	-	343	FDH33_gp148	Vibrio phage pTD1	GCA_002618825.1
BAW98286.1	000000	-	57	FDH33_gp077	Vibrio phage pTD1	GCA_002618825.1
BAW98285.1	000000	-	81	FDH33_gp076	Vibrio phage pTD1	GCA_002618825.1
BAW98233.1	000000	-	82	FDH33_gp024	Vibrio phage pTD1	GCA_002618825.1
BAW98376.1	000000	-	109	FDH33_gp167	Vibrio phage pTD1	GCA_002618825.1
AQT27949.1	000000	-	146	pVa21_007	Vibrio phage pVa-21	GCA_002619305.1
AQT27950.1	000000	-	184	pVa21_008	Vibrio phage pVa-21	GCA_002619305.1
AQT27956.1	000000	-	620	pVa21_014	Vibrio phage pVa-21	GCA_002619305.1
AQT27964.1	000000	-	97	pVa21_022	Vibrio phage pVa-21	GCA_002619305.1
AQT27965.1	000000	-	145	pVa21_023	Vibrio phage pVa-21	GCA_002619305.1
AQT27966.1	000000	-	85	pVa21_024	Vibrio phage pVa-21	GCA_002619305.1
AQT27967.1	000000	-	157	pVa21_025	Vibrio phage pVa-21	GCA_002619305.1
AQT27969.1	000000	-	73	pVa21_027	Vibrio phage pVa-21	GCA_002619305.1
AQT27973.1	000000	-	439	pVa21_031	Vibrio phage pVa-21	GCA_002619305.1
AQT27974.1	000000	-	176	pVa21_032	Vibrio phage pVa-21	GCA_002619305.1
AQT27976.1	000000	-	209	pVa21_034	Vibrio phage pVa-21	GCA_002619305.1
AQT27979.1	000000	-	170	pVa21_037	Vibrio phage pVa-21	GCA_002619305.1
AQT27980.1	000000	-	63	pVa21_038	Vibrio phage pVa-21	GCA_002619305.1
AQT27982.1	000000	-	122	pVa21_040	Vibrio phage pVa-21	GCA_002619305.1
AQT27983.1	000000	-	85	pVa21_041	Vibrio phage pVa-21	GCA_002619305.1
AQT27984.1	000000	-	236	pVa21_042	Vibrio phage pVa-21	GCA_002619305.1
AQT27985.1	000000	-	136	pVa21_043	Vibrio phage pVa-21	GCA_002619305.1
AQT27986.1	000000	-	99	pVa21_044	Vibrio phage pVa-21	GCA_002619305.1
AQT27987.1	000000	-	114	pVa21_045	Vibrio phage pVa-21	GCA_002619305.1
AQT27990.1	000000	-	106	pVa21_048	Vibrio phage pVa-21	GCA_002619305.1
AQT27993.1	000000	-	90	pVa21_051	Vibrio phage pVa-21	GCA_002619305.1
AQT27998.1	000000	-	49	pVa21_056	Vibrio phage pVa-21	GCA_002619305.1
AQT28000.1	000000	-	111	pVa21_058	Vibrio phage pVa-21	GCA_002619305.1
AQT28001.1	000000	-	95	pVa21_059	Vibrio phage pVa-21	GCA_002619305.1
AQT28002.1	000000	-	254	pVa21_060	Vibrio phage pVa-21	GCA_002619305.1
AQT28004.1	000000	-	128	pVa21_062	Vibrio phage pVa-21	GCA_002619305.1
AQT28005.1	000000	-	82	pVa21_063	Vibrio phage pVa-21	GCA_002619305.1
AQT28006.1	000000	-	96	pVa21_064	Vibrio phage pVa-21	GCA_002619305.1
AQT28008.1	000000	-	163	pVa21_067	Vibrio phage pVa-21	GCA_002619305.1
AQT28011.1	000000	-	109	pVa21_070	Vibrio phage pVa-21	GCA_002619305.1
AQT28013.1	000000	-	165	pVa21_072	Vibrio phage pVa-21	GCA_002619305.1
AQT28014.1	000000	-	105	pVa21_073	Vibrio phage pVa-21	GCA_002619305.1
AQT28015.1	000000	-	260	pVa21_074	Vibrio phage pVa-21	GCA_002619305.1
AQT28016.1	000000	-	439	pVa21_075	Vibrio phage pVa-21	GCA_002619305.1
AQT28017.1	000000	-	222	pVa21_076	Vibrio phage pVa-21	GCA_002619305.1
AQT28019.1	000000	-	57	pVa21_078	Vibrio phage pVa-21	GCA_002619305.1
AQT28020.1	000000	-	168	pVa21_079	Vibrio phage pVa-21	GCA_002619305.1
AQT28022.1	000000	-	219	pVa21_081	Vibrio phage pVa-21	GCA_002619305.1
AQT28024.1	000000	-	179	pVa21_083	Vibrio phage pVa-21	GCA_002619305.1
AQT28025.1	000000	-	174	pVa21_084	Vibrio phage pVa-21	GCA_002619305.1
AQT28027.1	000000	-	74	pVa21_086	Vibrio phage pVa-21	GCA_002619305.1
AQT28028.1	000000	-	127	pVa21_087	Vibrio phage pVa-21	GCA_002619305.1
AQT28029.1	000000	-	400	pVa21_088	Vibrio phage pVa-21	GCA_002619305.1
AQT28030.1	000000	-	534	pVa21_089	Vibrio phage pVa-21	GCA_002619305.1
AQT28031.1	000000	-	54	pVa21_090	Vibrio phage pVa-21	GCA_002619305.1
AQT28032.1	000000	-	102	pVa21_091	Vibrio phage pVa-21	GCA_002619305.1
AQT28033.1	000000	-	220	pVa21_092	Vibrio phage pVa-21	GCA_002619305.1
AQT28034.1	000000	-	186	pVa21_093	Vibrio phage pVa-21	GCA_002619305.1
AQT28038.1	000000	-	566	pVa21_097	Vibrio phage pVa-21	GCA_002619305.1
AQT28040.1	000000	-	273	pVa21_099	Vibrio phage pVa-21	GCA_002619305.1
AQT28042.1	000000	-	102	pVa21_101	Vibrio phage pVa-21	GCA_002619305.1
AQT28043.1	000000	-	136	pVa21_102	Vibrio phage pVa-21	GCA_002619305.1
AQT28044.1	000000	-	131	pVa21_103	Vibrio phage pVa-21	GCA_002619305.1
AQT28045.1	000000	-	71	pVa21_104	Vibrio phage pVa-21	GCA_002619305.1
AQT28047.1	000000	-	185	pVa21_106	Vibrio phage pVa-21	GCA_002619305.1
AQT28048.1	000000	-	195	pVa21_107	Vibrio phage pVa-21	GCA_002619305.1
AQT28049.1	000000	-	86	pVa21_108	Vibrio phage pVa-21	GCA_002619305.1
AQT28052.1	000000	-	77	pVa21_111	Vibrio phage pVa-21	GCA_002619305.1
AQT28053.1	000000	-	148	pVa21_112	Vibrio phage pVa-21	GCA_002619305.1
AQT28054.1	000000	-	43	pVa21_113	Vibrio phage pVa-21	GCA_002619305.1
AQT28055.1	000000	-	401	pVa21_114	Vibrio phage pVa-21	GCA_002619305.1
AQT28058.1	000000	-	744	pVa21_117	Vibrio phage pVa-21	GCA_002619305.1
AQT28059.1	000000	-	50	pVa21_118	Vibrio phage pVa-21	GCA_002619305.1
AQT28071.1	000000	-	92	pVa21_130	Vibrio phage pVa-21	GCA_002619305.1
AQT28073.1	000000	-	130	pVa21_132	Vibrio phage pVa-21	GCA_002619305.1
AQT28082.1	000000	-	154	pVa21_141	Vibrio phage pVa-21	GCA_002619305.1
AQT28083.1	000000	-	94	pVa21_142	Vibrio phage pVa-21	GCA_002619305.1
AQT28085.1	000000	-	61	pVa21_144	Vibrio phage pVa-21	GCA_002619305.1
AQT28086.1	000000	-	137	pVa21_145	Vibrio phage pVa-21	GCA_002619305.1
AQT28087.1	000000	-	168	pVa21_146	Vibrio phage pVa-21	GCA_002619305.1
AQT28088.1	000000	-	287	pVa21_147	Vibrio phage pVa-21	GCA_002619305.1
AQT28090.1	000000	-	102	pVa21_149	Vibrio phage pVa-21	GCA_002619305.1
AQT28096.1	000000	-	60	pVa21_155	Vibrio phage pVa-21	GCA_002619305.1
AQT28099.1	000000	-	229	pVa21_158	Vibrio phage pVa-21	GCA_002619305.1
AQT28104.1	000000	-	174	pVa21_163	Vibrio phage pVa-21	GCA_002619305.1
AQT28110.1	000000	-	485	pVa21_169	Vibrio phage pVa-21	GCA_002619305.1
AQT28115.1	000000	-	145	pVa21_174	Vibrio phage pVa-21	GCA_002619305.1
AQT28117.1	000000	-	96	pVa21_176	Vibrio phage pVa-21	GCA_002619305.1
AQT28118.1	000000	-	69	pVa21_177	Vibrio phage pVa-21	GCA_002619305.1
AQT28119.1	000000	-	67	pVa21_178	Vibrio phage pVa-21	GCA_002619305.1
AQT28120.1	000000	-	60	pVa21_179	Vibrio phage pVa-21	GCA_002619305.1
AQT28127.1	000000	-	117	pVa21_186	Vibrio phage pVa-21	GCA_002619305.1
AQT28128.1	000000	-	186	pVa21_187	Vibrio phage pVa-21	GCA_002619305.1
AQT28130.1	000000	-	177	pVa21_189	Vibrio phage pVa-21	GCA_002619305.1
AQT28135.1	000000	-	95	pVa21_194	Vibrio phage pVa-21	GCA_002619305.1
AQT28137.1	000000	-	141	pVa21_196	Vibrio phage pVa-21	GCA_002619305.1
AQT28138.1	000000	-	75	pVa21_197	Vibrio phage pVa-21	GCA_002619305.1
AQT28141.1	000000	-	224	pVa21_200	Vibrio phage pVa-21	GCA_002619305.1
AQT28143.1	000000	-	145	pVa21_202	Vibrio phage pVa-21	GCA_002619305.1
AQT28144.1	000000	-	229	pVa21_203	Vibrio phage pVa-21	GCA_002619305.1
AQT28145.1	000000	-	99	pVa21_204	Vibrio phage pVa-21	GCA_002619305.1
AQT28149.1	000000	-	619	pVa21_208	Vibrio phage pVa-21	GCA_002619305.1
AQT28153.1	000000	-	203	pVa21_212	Vibrio phage pVa-21	GCA_002619305.1
AQT28171.1	000000	-	227	pVa21_230	Vibrio phage pVa-21	GCA_002619305.1
AQT28173.1	000000	-	422	pVa21_232	Vibrio phage pVa-21	GCA_002619305.1
AQT28175.1	000000	-	139	pVa21_234	Vibrio phage pVa-21	GCA_002619305.1
AQT28176.1	000000	-	530	pVa21_235	Vibrio phage pVa-21	GCA_002619305.1
ALP47152.1	000000	-	130	phiGrn1_0065	Vibrio phage phi-Grn1	GCA_002757115.1
ALP47719.1	000000	-	37	phiST2_0015	Vibrio phage phi-ST2	GCA_002757135.1
ALP47704.1	000000	-	55	phiST2_0159	Vibrio phage phi-ST2	GCA_002757135.1
ALY06999.1	000000	-	274	VmeM32_00003	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07002.1	000000	-	56	VmeM32_00006	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07015.1	000000	-	87	VmeM32_00021	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07020.1	000000	-	91	VmeM32_00026	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07023.1	000000	-	223	VmeM32_00029	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07024.1	000000	-	85	VmeM32_00030	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07025.1	000000	-	100	VmeM32_00031	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07026.1	000000	-	104	VmeM32_00032	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07030.1	000000	-	41	VmeM32_00039	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07031.1	000000	-	62	VmeM32_00040	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07033.1	000000	-	120	VmeM32_00042	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07034.1	000000	-	62	VmeM32_00043	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07036.1	000000	-	82	VmeM32_00045	Vibrio phage vB_VmeM-32	GCA_002608825.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
ALY07040.1	000000	-	87	VmeM32_00049	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07041.1	000000	-	247	VmeM32_00050	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07042.1	000000	-	78	VmeM32_00051	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07046.1	000000	-	70	VmeM32_00055	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07048.1	000000	-	1210	VmeM32_00057	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07053.1	000000	-	169	VmeM32_00062	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07054.1	000000	-	96	VmeM32_00063	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07055.1	000000	-	254	VmeM32_00064	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07059.1	000000	-	115	VmeM32_00068	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07061.1	000000	-	123	VmeM32_00070	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07062.1	000000	-	80	VmeM32_00071	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07067.1	000000	-	126	VmeM32_00076	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07068.1	000000	-	67	VmeM32_00077	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07071.1	000000	-	64	VmeM32_00080	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07081.1	000000	-	133	VmeM32_00092	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07095.1	000000	-	99	VmeM32_00106	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07117.1	000000	-	62	VmeM32_00130	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07118.1	000000	-	74	VmeM32_00131	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07121.1	000000	-	86	VmeM32_00134	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07134.1	000000	-	83	VmeM32_00147	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07136.1	000000	-	69	VmeM32_00149	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07137.1	000000	-	62	VmeM32_00150	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07139.1	000000	-	96	VmeM32_00153	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07143.1	000000	-	694	VmeM32_00157	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07147.1	000000	-	630	VmeM32_00161	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07156.1	000000	-	41	VmeM32_00170	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07159.1	000000	-	71	VmeM32_00173	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07160.1	000000	-	88	VmeM32_00174	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07161.1	000000	-	76	VmeM32_00175	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07163.1	000000	-	73	VmeM32_00177	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07164.1	000000	-	96	VmeM32_00178	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07165.1	000000	-	74	VmeM32_00179	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07166.1	000000	-	78	VmeM32_00180	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07169.1	000000	-	96	VmeM32_00183	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07170.1	000000	-	110	VmeM32_00184	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07171.1	000000	-	152	VmeM32_00185	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07172.1	000000	-	154	VmeM32_00186	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07180.1	000000	-	105	VmeM32_00194	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07181.1	000000	-	77	VmeM32_00195	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07182.1	000000	-	124	VmeM32_00196	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07184.1	000000	-	98	VmeM32_00198	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07186.1	000000	-	130	VmeM32_00200	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07187.1	000000	-	68	VmeM32_00201	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07190.1	000000	-	96	VmeM32_00204	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07198.1	000000	-	99	VmeM32_00212	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07199.1	000000	-	103	VmeM32_00213	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07203.1	000000	-	79	VmeM32_00217	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07208.1	000000	-	84	VmeM32_00222	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07211.1	000000	-	161	VmeM32_00225	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07213.1	000000	-	185	VmeM32_00227	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07214.1	000000	-	181	VmeM32_00228	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07215.1	000000	-	65	VmeM32_00229	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07216.1	000000	-	305	VmeM32_00230	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07218.1	000000	-	306	VmeM32_00232	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07219.1	000000	-	87	VmeM32_00233	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07220.1	000000	-	94	VmeM32_00234	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07223.1	000000	-	89	VmeM32_00237	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07224.1	000000	-	97	VmeM32_00238	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07235.1	000000	-	58	VmeM32_00249	Vibrio phage vB_VmeM-32	GCA_002608825.1
ALY07247.1	000000	-	61	VmeM32_00261	Vibrio phage vB_VmeM-32	GCA_002608825.1
QNI21148.1	000000	-	32	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21006.1	000000	-	106	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21216.1	000000	-	106	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21040.1	000000	-	137	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21229.1	000000	-	146	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21280.1	000000	-	215	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21200.1	000000	-	193	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21180.1	000000	-	195	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21075.1	000000	-	118	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21042.1	000000	-	115	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21176.1	000000	-	150	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21269.1	000000	-	150	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21139.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21031.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21071.1	000000	-	31	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21254.1	000000	-	42	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21098.1	000000	-	226	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20966.1	000000	-	135	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21020.1	000000	-	50	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21055.1	000000	-	50	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21008.1	000000	-	40	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21030.1	000000	-	43	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21022.1	000000	-	44	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20969.1	000000	-	149	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21262.1	000000	-	350	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21052.1	000000	-	45	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21243.1	000000	-	89	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21087.1	000000	-	658	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21136.1	000000	-	272	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21275.1	000000	-	172	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21215.1	000000	-	172	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21207.1	000000	-	53	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21083.1	000000	-	62	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21077.1	000000	-	112	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21238.1	000000	-	112	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21094.1	000000	-	371	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21092.1	000000	-	153	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21201.1	000000	-	177	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21150.1	000000	-	178	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21151.1	000000	-	212	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21255.1	000000	-	246	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21142.1	000000	-	320	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21107.1	000000	-	864	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21093.1	000000	-	433	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21192.1	000000	-	440	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21179.1	000000	-	218	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20981.1	000000	-	65	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21202.1	000000	-	276	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21186.1	000000	-	310	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21146.1	000000	-	548	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21018.1	000000	-	39	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21236.1	000000	-	259	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21171.1	000000	-	160	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21157.1	000000	-	161	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21219.1	000000	-	111	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21256.1	000000	-	104	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20964.1	000000	-	104	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21189.1	000000	-	626	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21067.1	000000	-	638	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20976.1	000000	-	41	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21162.1	000000	-	295	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21161.1	000000	-	369	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21220.1	000000	-	252	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21158.1	000000	-	378	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21137.1	000000	-	124	-	Vibrio phage vB_pir03	GCA_014319855.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QNI20995.1	000000	-	336	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21153.1	000000	-	362	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21168.1	000000	-	165	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21013.1	000000	-	208	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21224.1	000000	-	267	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21178.1	000000	-	90	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21232.1	000000	-	188	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21155.1	000000	-	187	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21205.1	000000	-	187	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21041.1	000000	-	117	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21126.1	000000	-	100	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21199.1	000000	-	100	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21036.1	000000	-	105	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21227.1	000000	-	105	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21144.1	000000	-	110	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21133.1	000000	-	119	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21231.1	000000	-	128	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21057.1	000000	-	128	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20968.1	000000	-	134	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21261.1	000000	-	138	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21163.1	000000	-	157	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21039.1	000000	-	164	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21271.1	000000	-	164	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21223.1	000000	-	166	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21073.1	000000	-	174	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21226.1	000000	-	175	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21209.1	000000	-	239	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20984.1	000000	-	61	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21123.1	000000	-	66	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21272.1	000000	-	66	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21109.1	000000	-	79	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21121.1	000000	-	84	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21182.1	000000	-	93	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21242.1	000000	-	98	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20989.1	000000	-	142	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21122.1	000000	-	152	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21043.1	000000	-	116	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21134.1	000000	-	354	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21264.1	000000	-	738	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21211.1	000000	-	216	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20951.1	000000	-	46	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21187.1	000000	-	214	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21053.1	000000	-	48	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21027.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20982.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21029.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21265.1	000000	-	30	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21011.1	000000	-	36	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20991.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21253.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21026.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20956.1	000000	-	29	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21181.1	000000	-	72	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI20977.1	000000	-	34	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21045.1	000000	-	34	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21019.1	000000	-	63	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21208.1	000000	-	284	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21135.1	000000	-	169	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21174.1	000000	-	163	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21159.1	000000	-	184	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21054.1	000000	-	184	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21206.1	000000	-	200	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21258.1	000000	-	209	-	Vibrio phage vB_pir03	GCA_014319855.1
QNI21167.1	000000	-	302	-	Vibrio phage vB_pir03	GCA_014319855.1
BBA65567.1	000000	-	150	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65363.1	000000	-	88	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65291.1	000000	-	159	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65358.1	000000	-	45	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65297.1	000000	-	177	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65591.1	000000	-	80	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65447.1	000000	-	80	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65519.1	000000	-	1102	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65421.1	000000	-	136	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65592.1	000000	-	63	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65298.1	000000	-	148	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65300.1	000000	-	139	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65579.1	000000	-	111	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65483.1	000000	-	145	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65294.1	000000	-	145	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65419.1	000000	-	89	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65590.1	000000	-	104	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65587.1	000000	-	168	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65458.1	000000	-	135	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65289.1	000000	-	137	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65510.1	000000	-	62	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65328.1	000000	-	1259	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65552.1	000000	-	68	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65357.1	000000	-	68	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65307.1	000000	-	107	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65607.1	000000	-	107	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65432.1	000000	-	147	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65606.1	000000	-	100	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65428.1	000000	-	100	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65286.1	000000	-	102	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65589.1	000000	-	105	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65282.1	000000	-	106	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65459.1	000000	-	113	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65285.1	000000	-	113	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65284.1	000000	-	123	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65288.1	000000	-	128	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65574.1	000000	-	128	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65293.1	000000	-	128	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65292.1	000000	-	128	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65290.1	000000	-	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65564.1	000000	-	129	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65597.1	000000	-	144	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65595.1	000000	-	153	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65454.1	000000	-	158	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65302.1	000000	-	164	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65455.1	000000	-	181	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65299.1	000000	-	198	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65475.1	000000	-	237	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65404.1	000000	-	242	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65360.1	000000	-	55	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65602.1	000000	-	55	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65543.1	000000	-	57	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65604.1	000000	-	58	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65426.1	000000	-	58	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65303.1	000000	-	60	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65344.1	000000	-	61	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65507.1	000000	-	61	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65317.1	000000	-	65	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65558.1	000000	-	72	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65506.1	000000	-	75	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65573.1	000000	-	79	-	Xanthomonas phage XacN1	GCA_003173815.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
BBA65440.1	000000	-	81	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65572.1	000000	-	82	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65566.1	000000	-	83	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65563.1	000000	-	84	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65349.1	000000	-	91	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65295.1	000000	-	108	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65283.1	000000	-	109	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65576.1	000000	-	126	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65287.1	000000	-	133	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65541.1	000000	-	64	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65577.1	000000	-	64	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65425.1	000000	-	86	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65327.1	000000	-	87	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65370.1	000000	-	94	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65565.1	000000	-	94	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65550.1	000000	-	311	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65513.1	000000	-	223	-	Xanthomonas phage XacN1	GCA_003173815.1
BBA65296.1	000000	-	200	-	Xanthomonas phage XacN1	GCA_003173815.1
QDJ96188.1	000000	-	130	Xoosp13_1	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96197.1	000000	-	74	Xoosp13_10	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96287.1	000000	-	126	Xoosp13_100	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96289.1	000000	-	51	Xoosp13_102	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96290.1	000000	-	80	Xoosp13_103	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96291.1	000000	-	62	Xoosp13_104	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96292.1	000000	-	139	Xoosp13_105	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96295.1	000000	-	196	Xoosp13_108	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96198.1	000000	-	184	Xoosp13_11	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96298.1	000000	-	195	Xoosp13_111	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96306.1	000000	-	54	Xoosp13_119	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96307.1	000000	-	137	Xoosp13_120	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96311.1	000000	-	53	Xoosp13_124	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96313.1	000000	-	60	Xoosp13_126	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96315.1	000000	-	158	Xoosp13_128	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96200.1	000000	-	71	Xoosp13_13	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96319.1	000000	-	124	Xoosp13_132	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96321.1	000000	-	72	Xoosp13_134	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96322.1	000000	-	127	Xoosp13_135	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96323.1	000000	-	119	Xoosp13_136	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96324.1	000000	-	95	Xoosp13_137	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96201.1	000000	-	48	Xoosp13_14	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96332.1	000000	-	68	Xoosp13_145	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96336.1	000000	-	83	Xoosp13_149	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96202.1	000000	-	59	Xoosp13_15	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96337.1	000000	-	38	Xoosp13_150	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96338.1	000000	-	123	Xoosp13_151	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96339.1	000000	-	48	Xoosp13_152	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96340.1	000000	-	57	Xoosp13_153	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96341.1	000000	-	58	Xoosp13_154	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96343.1	000000	-	97	Xoosp13_156	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96352.1	000000	-	65	Xoosp13_165	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96355.1	000000	-	154	Xoosp13_168	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96358.1	000000	-	124	Xoosp13_171	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96205.1	000000	-	125	Xoosp13_18	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96369.1	000000	-	37	Xoosp13_182	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96206.1	000000	-	60	Xoosp13_19	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96376.1	000000	-	101	Xoosp13_190	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96207.1	000000	-	88	Xoosp13_20	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96390.1	000000	-	92	Xoosp13_204	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96391.1	000000	-	39	Xoosp13_205	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96208.1	000000	-	123	Xoosp13_21	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96210.1	000000	-	139	Xoosp13_23	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96212.1	000000	-	64	Xoosp13_25	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96213.1	000000	-	134	Xoosp13_26	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96450.1	000000	-	80	Xoosp13_264	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96214.1	000000	-	72	Xoosp13_27	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96456.1	000000	-	44	Xoosp13_270	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96215.1	000000	-	57	Xoosp13_28	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96483.1	000000	-	219	Xoosp13_297	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96217.1	000000	-	176	Xoosp13_30	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96498.1	000000	-	72	Xoosp13_312	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96512.1	000000	-	73	Xoosp13_326	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96220.1	000000	-	42	Xoosp13_33	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96526.1	000000	-	55	Xoosp13_340	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96542.1	000000	-	137	Xoosp13_356	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96545.1	000000	-	205	Xoosp13_359	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96547.1	000000	-	71	Xoosp13_361	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96555.1	000000	-	65	Xoosp13_369	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96224.1	000000	-	57	Xoosp13_37	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96556.1	000000	-	152	Xoosp13_370	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96558.1	000000	-	85	Xoosp13_372	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96559.1	000000	-	39	Xoosp13_373	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96560.1	000000	-	83	Xoosp13_374	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96562.1	000000	-	45	Xoosp13_376	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96564.1	000000	-	100	Xoosp13_378	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96565.1	000000	-	106	Xoosp13_379	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96225.1	000000	-	75	Xoosp13_38	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96566.1	000000	-	37	Xoosp13_380	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96567.1	000000	-	63	Xoosp13_381	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96568.1	000000	-	115	Xoosp13_382	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96569.1	000000	-	66	Xoosp13_383	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96570.1	000000	-	87	Xoosp13_384	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96572.1	000000	-	71	Xoosp13_386	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96576.1	000000	-	43	Xoosp13_390	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96577.1	000000	-	38	Xoosp13_391	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96580.1	000000	-	46	Xoosp13_394	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96582.1	000000	-	88	Xoosp13_396	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96191.1	000000	-	42	Xoosp13_4	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96228.1	000000	-	121	Xoosp13_41	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96229.1	000000	-	84	Xoosp13_42	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96230.1	000000	-	128	Xoosp13_43	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96235.1	000000	-	77	Xoosp13_48	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96239.1	000000	-	90	Xoosp13_52	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96241.1	000000	-	170	Xoosp13_54	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96243.1	000000	-	43	Xoosp13_56	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96244.1	000000	-	108	Xoosp13_57	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96193.1	000000	-	88	Xoosp13_6	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96249.1	000000	-	111	Xoosp13_62	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96257.1	000000	-	80	Xoosp13_70	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96258.1	000000	-	106	Xoosp13_71	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96259.1	000000	-	111	Xoosp13_72	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96260.1	000000	-	44	Xoosp13_73	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96264.1	000000	-	62	Xoosp13_77	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96265.1	000000	-	69	Xoosp13_78	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96266.1	000000	-	70	Xoosp13_79	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96195.1	000000	-	71	Xoosp13_8	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96267.1	000000	-	79	Xoosp13_80	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96268.1	000000	-	94	Xoosp13_81	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96269.1	000000	-	46	Xoosp13_82	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96271.1	000000	-	96	Xoosp13_84	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96272.1	000000	-	61	Xoosp13_85	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96273.1	000000	-	207	Xoosp13_86	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96274.1	000000	-	51	Xoosp13_87	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96275.1	000000	-	93	Xoosp13_88	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96276.1	000000	-	87	Xoosp13_89	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96277.1	000000	-	54	Xoosp13_90	Xanthomonas phage Xoo-sp13	GCA_013364725.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
QDJ96280.1	000000	-	222	Xoosp13_93	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96281.1	000000	-	84	Xoosp13_94	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96283.1	000000	-	123	Xoosp13_96	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96284.1	000000	-	54	Xoosp13_97	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96285.1	000000	-	60	Xoosp13_98	Xanthomonas phage Xoo-sp13	GCA_013364725.1
QDJ96286.1	000000	-	55	Xoosp13_99	Xanthomonas phage Xoo-sp13	GCA_013364725.1
SOK58814.1	000000	-	110	g006	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58830.1	000000	-	73	g022	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58831.1	000000	-	126	g023	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58912.1	000000	-	127	g104	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59082.1	000000	-	38	g274	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59172.1	000000	-	68	g364	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59185.1	000000	-	173	g377	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59186.1	000000	-	38	g378	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59187.1	000000	-	117	g379	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59245.1	000000	-	42	g437	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59274.1	000000	-	56	g466	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK59291.1	000000	-	64	g483	Yersinia phage fHe-Yen9-03	GCA_002990515.1
SOK58281.1	000000	-	71	g004	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58324.1	000000	-	43	g047	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58358.1	000000	-	144	g081	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58625.1	000000	-	23	g348	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58731.1	000000	-	53	g454	Yersinia phage fHe-Yen9-04	GCA_002990485.1
SOK58777.1	000000	-	53	g500	Yersinia phage fHe-Yen9-04	GCA_002990485.1
CCE26025.1	000000	-	90	g001	Yersinia phage phiR1-37	GCA_000895615.1
CCE26029.1	000000	-	62	g005	Yersinia phage phiR1-37	GCA_000895615.1
CCE26031.1	000000	-	72	g007	Yersinia phage phiR1-37	GCA_000895615.1
CCE26033.1	000000	-	82	g009	Yersinia phage phiR1-37	GCA_000895615.1
CCE26036.1	000000	-	69	g012	Yersinia phage phiR1-37	GCA_000895615.1
CCE26038.1	000000	-	78	g014	Yersinia phage phiR1-37	GCA_000895615.1
CCE26039.1	000000	-	83	g015	Yersinia phage phiR1-37	GCA_000895615.1
CCE26041.1	000000	-	110	g017	Yersinia phage phiR1-37	GCA_000895615.1
CCE26042.1	000000	-	105	g018	Yersinia phage phiR1-37	GCA_000895615.1
CCE26043.1	000000	-	92	g019	Yersinia phage phiR1-37	GCA_000895615.1
CCE26045.1	000000	-	63	g021	Yersinia phage phiR1-37	GCA_000895615.1
CCE26047.1	000000	-	75	g023	Yersinia phage phiR1-37	GCA_000895615.1
CCE26048.1	000000	-	67	g024	Yersinia phage phiR1-37	GCA_000895615.1
CCE26049.1	000000	-	64	g025	Yersinia phage phiR1-37	GCA_000895615.1
CCE26051.1	000000	-	83	g027	Yersinia phage phiR1-37	GCA_000895615.1
CCE26052.1	000000	-	81	g028	Yersinia phage phiR1-37	GCA_000895615.1
CCE26053.1	000000	-	85	g029	Yersinia phage phiR1-37	GCA_000895615.1
CCE26055.1	000000	-	180	g031	Yersinia phage phiR1-37	GCA_000895615.1
CCE26056.1	000000	-	93	g032	Yersinia phage phiR1-37	GCA_000895615.1
CCE26057.1	000000	-	121	g033	Yersinia phage phiR1-37	GCA_000895615.1
CCE26058.1	000000	-	136	g034	Yersinia phage phiR1-37	GCA_000895615.1
CCE26059.1	000000	-	80	g035	Yersinia phage phiR1-37	GCA_000895615.1
CCE26060.1	000000	-	95	g036	Yersinia phage phiR1-37	GCA_000895615.1
CCE26061.1	000000	-	81	g037	Yersinia phage phiR1-37	GCA_000895615.1
CCE26062.1	000000	-	100	g038	Yersinia phage phiR1-37	GCA_000895615.1
CCE26063.1	000000	-	85	g039	Yersinia phage phiR1-37	GCA_000895615.1
CCE26065.1	000000	-	69	g041	Yersinia phage phiR1-37	GCA_000895615.1
CCE26066.1	000000	-	128	g042	Yersinia phage phiR1-37	GCA_000895615.1
CCE26068.1	000000	-	89	g044	Yersinia phage phiR1-37	GCA_000895615.1
CCE26069.1	000000	-	368	g045	Yersinia phage phiR1-37	GCA_000895615.1
CCE26072.1	000000	-	212	g048	Yersinia phage phiR1-37	GCA_000895615.1
CCE26074.1	000000	-	113	g050	Yersinia phage phiR1-37	GCA_000895615.1
CCE26075.1	000000	-	117	g051	Yersinia phage phiR1-37	GCA_000895615.1
CCE26076.1	000000	-	147	g052	Yersinia phage phiR1-37	GCA_000895615.1
CCE26077.1	000000	-	130	g053	Yersinia phage phiR1-37	GCA_000895615.1
CCE26078.1	000000	-	101	g054	Yersinia phage phiR1-37	GCA_000895615.1
CCE26079.1	000000	-	296	g055	Yersinia phage phiR1-37	GCA_000895615.1
CCE26081.1	000000	-	223	g057	Yersinia phage phiR1-37	GCA_000895615.1
CCE26082.1	000000	-	252	g058	Yersinia phage phiR1-37	GCA_000895615.1
CCE26083.1	000000	-	440	g059	Yersinia phage phiR1-37	GCA_000895615.1
CCE26087.1	000000	-	183	g063	Yersinia phage phiR1-37	GCA_000895615.1
CCE26088.1	000000	-	146	g064	Yersinia phage phiR1-37	GCA_000895615.1
CCE26089.1	000000	-	54	g065	Yersinia phage phiR1-37	GCA_000895615.1
CCE26096.1	000000	-	169	g072	Yersinia phage phiR1-37	GCA_000895615.1
CCE26097.1	000000	-	119	g073	Yersinia phage phiR1-37	GCA_000895615.1
CCE26098.1	000000	-	164	g074	Yersinia phage phiR1-37	GCA_000895615.1
CCE26102.1	000000	-	180	g078	Yersinia phage phiR1-37	GCA_000895615.1
CCE26104.1	000000	-	251	g080	Yersinia phage phiR1-37	GCA_000895615.1
CCE26105.1	000000	-	463	g081	Yersinia phage phiR1-37	GCA_000895615.1
CCE26111.1	000000	-	476	g087	Yersinia phage phiR1-37	GCA_000895615.1
CCE26112.1	000000	-	86	g088	Yersinia phage phiR1-37	GCA_000895615.1
CCE26114.1	000000	-	200	g090	Yersinia phage phiR1-37	GCA_000895615.1
CCE26115.1	000000	-	204	g091	Yersinia phage phiR1-37	GCA_000895615.1
CCE26116.1	000000	-	231	g092	Yersinia phage phiR1-37	GCA_000895615.1
CCE26118.1	000000	-	121	g094	Yersinia phage phiR1-37	GCA_000895615.1
CCE26122.1	000000	-	132	g098	Yersinia phage phiR1-37	GCA_000895615.1
CCE26128.1	000000	-	75	g104	Yersinia phage phiR1-37	GCA_000895615.1
CCE26129.1	000000	-	86	g105	Yersinia phage phiR1-37	GCA_000895615.1
CCE26130.1	000000	-	30	g106	Yersinia phage phiR1-37	GCA_000895615.1
CCE26134.1	000000	-	79	g110	Yersinia phage phiR1-37	GCA_000895615.1
CCE26135.1	000000	-	144	g111	Yersinia phage phiR1-37	GCA_000895615.1
CCE26136.1	000000	-	95	g112	Yersinia phage phiR1-37	GCA_000895615.1
CCE26137.1	000000	-	68	g113	Yersinia phage phiR1-37	GCA_000895615.1
CCE26138.1	000000	-	69	g114	Yersinia phage phiR1-37	GCA_000895615.1
CCE26139.1	000000	-	88	g115	Yersinia phage phiR1-37	GCA_000895615.1
CCE26141.1	000000	-	51	g117	Yersinia phage phiR1-37	GCA_000895615.1
CCE26142.1	000000	-	142	g118	Yersinia phage phiR1-37	GCA_000895615.1
CCE26143.1	000000	-	109	g119	Yersinia phage phiR1-37	GCA_000895615.1
CCE26146.1	000000	-	199	g122	Yersinia phage phiR1-37	GCA_000895615.1
CCE26147.1	000000	-	196	g123	Yersinia phage phiR1-37	GCA_000895615.1
CCE26149.1	000000	-	332	g125	Yersinia phage phiR1-37	GCA_000895615.1
CCE26150.1	000000	-	173	g126	Yersinia phage phiR1-37	GCA_000895615.1
CCE26151.1	000000	-	56	g127	Yersinia phage phiR1-37	GCA_000895615.1
CCE26154.1	000000	-	201	g130	Yersinia phage phiR1-37	GCA_000895615.1
CCE26160.1	000000	-	174	g136	Yersinia phage phiR1-37	GCA_000895615.1
CCE26161.1	000000	-	140	g137	Yersinia phage phiR1-37	GCA_000895615.1
CCE26163.1	000000	-	132	g139	Yersinia phage phiR1-37	GCA_000895615.1
CCE26164.1	000000	-	126	g140	Yersinia phage phiR1-37	GCA_000895615.1
CCE26165.1	000000	-	161	g141	Yersinia phage phiR1-37	GCA_000895615.1
CCE26170.1	000000	-	243	g146	Yersinia phage phiR1-37	GCA_000895615.1
CCE26171.1	000000	-	268	g147	Yersinia phage phiR1-37	GCA_000895615.1
CCE26176.1	000000	-	361	g152	Yersinia phage phiR1-37	GCA_000895615.1
CCE26183.1	000000	-	115	g159	Yersinia phage phiR1-37	GCA_000895615.1
CCE26185.1	000000	-	344	g161	Yersinia phage phiR1-37	GCA_000895615.1
CCE26186.1	000000	-	340	g162	Yersinia phage phiR1-37	GCA_000895615.1
CCE26187.1	000000	-	174	g163	Yersinia phage phiR1-37	GCA_000895615.1
CCE26190.1	000000	-	21	g166	Yersinia phage phiR1-37	GCA_000895615.1
CCE26193.1	000000	-	301	g169	Yersinia phage phiR1-37	GCA_000895615.1
CCE26196.1	000000	-	61	g172	Yersinia phage phiR1-37	GCA_000895615.1
CCE26197.1	000000	-	277	g173	Yersinia phage phiR1-37	GCA_000895615.1
CCE26198.1	000000	-	259	g174	Yersinia phage phiR1-37	GCA_000895615.1
CCE26199.1	000000	-	247	g175	Yersinia phage phiR1-37	GCA_000895615.1
CCE26200.1	000000	-	301	g176	Yersinia phage phiR1-37	GCA_000895615.1
CCE26204.1	000000	-	42	g180	Yersinia phage phiR1-37	GCA_000895615.1
CCE26205.1	000000	-	32	g181	Yersinia phage phiR1-37	GCA_000895615.1
CCE26206.1	000000	-	122	g182	Yersinia phage phiR1-37	GCA_000895615.1
CCE26207.1	000000	-	129	g183	Yersinia phage phiR1-37	GCA_000895615.1
CCE26209.1	000000	-	120	g185	Yersinia phage phiR1-37	GCA_000895615.1
CCE26210.1	000000	-	123	g186	Yersinia phage phiR1-37	GCA_000895615.1
CCE26213.1	000000	-	59	g189	Yersinia phage phiR1-37	GCA_000895615.1
CCE26214.1	000000	-	394	g190	Yersinia phage phiR1-37	GCA_000895615.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
CCE26216.1	000000	-	417	g192	Yersinia phage phiR1-37	GCA_000895615.1
CCE26217.1	000000	-	325	g193	Yersinia phage phiR1-37	GCA_000895615.1
CCE26219.1	000000	-	347	g195	Yersinia phage phiR1-37	GCA_000895615.1
CCE26220.1	000000	-	850	g196	Yersinia phage phiR1-37	GCA_000895615.1
CCE26221.1	000000	-	282	g197	Yersinia phage phiR1-37	GCA_000895615.1
CCE26222.1	000000	-	263	g198	Yersinia phage phiR1-37	GCA_000895615.1
CAI99861.1	000000	-	259	g199	Yersinia phage phiR1-37	GCA_000895615.1
CCE26223.1	000000	-	37	g200	Yersinia phage phiR1-37	GCA_000895615.1
CCE26224.1	000000	-	61	g201	Yersinia phage phiR1-37	GCA_000895615.1
CCE26225.1	000000	-	190	g202	Yersinia phage phiR1-37	GCA_000895615.1
CCE26232.1	000000	-	374	g209	Yersinia phage phiR1-37	GCA_000895615.1
CCE26233.1	000000	-	363	g210	Yersinia phage phiR1-37	GCA_000895615.1
CCE26234.1	000000	-	214	g211	Yersinia phage phiR1-37	GCA_000895615.1
CCE26235.1	000000	-	93	g212	Yersinia phage phiR1-37	GCA_000895615.1
CCE26237.1	000000	-	106	g214	Yersinia phage phiR1-37	GCA_000895615.1
CCE26243.1	000000	-	82	g220	Yersinia phage phiR1-37	GCA_000895615.1
CCE26244.1	000000	-	89	g221	Yersinia phage phiR1-37	GCA_000895615.1
CCE26245.1	000000	-	70	g222	Yersinia phage phiR1-37	GCA_000895615.1
CCE26246.1	000000	-	68	g223	Yersinia phage phiR1-37	GCA_000895615.1
CCE26249.1	000000	-	201	g226	Yersinia phage phiR1-37	GCA_000895615.1
CCE26250.1	000000	-	89	g227	Yersinia phage phiR1-37	GCA_000895615.1
CCE26252.1	000000	-	132	g229	Yersinia phage phiR1-37	GCA_000895615.1
CCE26255.1	000000	-	31	g232	Yersinia phage phiR1-37	GCA_000895615.1
CCE26261.1	000000	-	223	g238	Yersinia phage phiR1-37	GCA_000895615.1
CCE26262.1	000000	-	131	g239	Yersinia phage phiR1-37	GCA_000895615.1
CCE26265.1	000000	-	55	g242	Yersinia phage phiR1-37	GCA_000895615.1
CCE26271.1	000000	-	185	g248	Yersinia phage phiR1-37	GCA_000895615.1
CCE26272.1	000000	-	151	g249	Yersinia phage phiR1-37	GCA_000895615.1
CCE26274.1	000000	-	107	g251	Yersinia phage phiR1-37	GCA_000895615.1
CCE26275.1	000000	-	81	g252	Yersinia phage phiR1-37	GCA_000895615.1
CCE26276.1	000000	-	191	g253	Yersinia phage phiR1-37	GCA_000895615.1
CCE26278.1	000000	-	88	g255	Yersinia phage phiR1-37	GCA_000895615.1
CCE26279.1	000000	-	106	g256	Yersinia phage phiR1-37	GCA_000895615.1
CCE26280.1	000000	-	131	g257	Yersinia phage phiR1-37	GCA_000895615.1
CCE26282.1	000000	-	159	g259	Yersinia phage phiR1-37	GCA_000895615.1
CCE26283.1	000000	-	180	g260	Yersinia phage phiR1-37	GCA_000895615.1
CCE26287.1	000000	-	94	g264	Yersinia phage phiR1-37	GCA_000895615.1
CCE26289.1	000000	-	119	g266	Yersinia phage phiR1-37	GCA_000895615.1
CCE26291.1	000000	-	69	g268	Yersinia phage phiR1-37	GCA_000895615.1
CCE26294.1	000000	-	591	g271	Yersinia phage phiR1-37	GCA_000895615.1
CCE26295.1	000000	-	435	g272	Yersinia phage phiR1-37	GCA_000895615.1
CCE26296.1	000000	-	135	g273	Yersinia phage phiR1-37	GCA_000895615.1
CCE26298.1	000000	-	225	g275	Yersinia phage phiR1-37	GCA_000895615.1
CCE26302.1	000000	-	172	g279	Yersinia phage phiR1-37	GCA_000895615.1
CCE26303.1	000000	-	118	g280	Yersinia phage phiR1-37	GCA_000895615.1
CCE26304.1	000000	-	129	g281	Yersinia phage phiR1-37	GCA_000895615.1
CCE26306.1	000000	-	329	g283	Yersinia phage phiR1-37	GCA_000895615.1
CCE26314.1	000000	-	90	g291	Yersinia phage phiR1-37	GCA_000895615.1
CCE26315.1	000000	-	193	g292	Yersinia phage phiR1-37	GCA_000895615.1
CCE26316.1	000000	-	179	g293	Yersinia phage phiR1-37	GCA_000895615.1
CCE26322.1	000000	-	173	g299	Yersinia phage phiR1-37	GCA_000895615.1
CCE26324.1	000000	-	210	g301	Yersinia phage phiR1-37	GCA_000895615.1
CCE26326.1	000000	-	180	g303	Yersinia phage phiR1-37	GCA_000895615.1
CCE26333.1	000000	-	87	g310	Yersinia phage phiR1-37	GCA_000895615.1
CCE26335.1	000000	-	30	g312	Yersinia phage phiR1-37	GCA_000895615.1
CCE26339.1	000000	-	54	g316	Yersinia phage phiR1-37	GCA_000895615.1
CCE26341.1	000000	-	88	g318	Yersinia phage phiR1-37	GCA_000895615.1
CCE26343.1	000000	-	116	g320	Yersinia phage phiR1-37	GCA_000895615.1
CCE26344.1	000000	-	119	g321	Yersinia phage phiR1-37	GCA_000895615.1
CCE26345.1	000000	-	106	g322	Yersinia phage phiR1-37	GCA_000895615.1
CCE26346.1	000000	-	106	g323	Yersinia phage phiR1-37	GCA_000895615.1
CCE26347.1	000000	-	88	g324	Yersinia phage phiR1-37	GCA_000895615.1
CCE26348.1	000000	-	616	g325	Yersinia phage phiR1-37	GCA_000895615.1
CCE26349.1	000000	-	445	g326	Yersinia phage phiR1-37	GCA_000895615.1
CCE26353.1	000000	-	94	g330	Yersinia phage phiR1-37	GCA_000895615.1
CCE26361.1	000000	-	81	g338	Yersinia phage phiR1-37	GCA_000895615.1
CCE26362.1	000000	-	84	g339	Yersinia phage phiR1-37	GCA_000895615.1
CCE26363.1	000000	-	94	g340	Yersinia phage phiR1-37	GCA_000895615.1
CCE26364.1	000000	-	87	g341	Yersinia phage phiR1-37	GCA_000895615.1
CCE26365.1	000000	-	93	g342	Yersinia phage phiR1-37	GCA_000895615.1
CCE26366.1	000000	-	107	g343	Yersinia phage phiR1-37	GCA_000895615.1
CCE26367.1	000000	-	90	g344	Yersinia phage phiR1-37	GCA_000895615.1
CCE26368.1	000000	-	93	g345	Yersinia phage phiR1-37	GCA_000895615.1
CCE26369.1	000000	-	88	g346	Yersinia phage phiR1-37	GCA_000895615.1
CCE26370.1	000000	-	103	g347	Yersinia phage phiR1-37	GCA_000895615.1
CCE26371.1	000000	-	63	g348	Yersinia phage phiR1-37	GCA_000895615.1
CCE26372.1	000000	-	90	g349	Yersinia phage phiR1-37	GCA_000895615.1
CCE26373.1	000000	-	127	g350	Yersinia phage phiR1-37	GCA_000895615.1
CCE26374.1	000000	-	139	g351	Yersinia phage phiR1-37	GCA_000895615.1
CCE26375.1	000000	-	97	g352	Yersinia phage phiR1-37	GCA_000895615.1
CCE26376.1	000000	-	90	g353	Yersinia phage phiR1-37	GCA_000895615.1
CCE26379.1	000000	-	76	g356	Yersinia phage phiR1-37	GCA_000895615.1
CCE26380.1	000000	-	70	g357	Yersinia phage phiR1-37	GCA_000895615.1
CCE26382.1	000000	-	67	g359	Yersinia phage phiR1-37	GCA_000895615.1
CCE26383.1	000000	-	82	g360	Yersinia phage phiR1-37	GCA_000895615.1
CCE26384.1	000000	-	91	g361	Yersinia phage phiR1-37	GCA_000895615.1
CCE26387.1	000000	-	97	g364	Yersinia phage phiR1-37	GCA_000895615.1
CCE26388.1	000000	-	75	g365	Yersinia phage phiR1-37	GCA_000895615.1
CCE26389.1	000000	-	74	g366	Yersinia phage phiR1-37	GCA_000895615.1
prevph1000000009	000000	-	131	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000010	000000	-	96	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000022	000000	-	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000025	000000	-	173	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000026	000000	-	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000027	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000028	000000	-	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000029	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000039	000000	-	33	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000047	000000	-	33	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000049	000000	-	90	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000051	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000056	000000	-	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000057	000000	-	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000058	000000	-	163	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000069	000000	-	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000070	000000	-	91	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000080	000000	-	170	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000082	000000	-	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000083	000000	-	47	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000084	000000	-	86	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000085	000000	-	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000086	000000	-	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000088	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000090	000000	-	148	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000091	000000	-	94	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000092	000000	-	96	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000093	000000	-	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000094	000000	-	95	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000095	000000	-	64	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000096	000000	-	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000098	000000	-	140	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000104	000000	-	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000109	000000	-	148	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000111	000000	-	72	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000118	000000	-	62	-	Prevotella_phage_Lak-B8	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000136	000000	-	44	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000140	000000	-	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000141	000000	-	41	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000146	000000	-	339	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000147	000000	-	278	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000148	000000	-	117	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000152	000000	-	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000153	000000	-	40	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000164	000000	-	38	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000198	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000201	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000202	000000	-	138	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000203	000000	-	54	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000204	000000	-	106	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000205	000000	-	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000206	000000	-	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000207	000000	-	161	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000211	000000	-	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000216	000000	-	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000218	000000	-	32	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000221	000000	-	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000223	000000	-	41	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000241	000000	-	91	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000245	000000	-	31	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000247	000000	-	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000253	000000	-	79	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000276	000000	-	62	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000277	000000	-	45	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000278	000000	-	31	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000280	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000281	000000	-	33	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000282	000000	-	54	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000284	000000	-	45	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000288	000000	-	126	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000290	000000	-	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000294	000000	-	124	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000295	000000	-	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000309	000000	-	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000312	000000	-	39	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000343	000000	-	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000345	000000	-	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000346	000000	-	192	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000347	000000	-	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000348	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000388	000000	-	39	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000390	000000	-	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000391	000000	-	58	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000392	000000	-	95	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000393	000000	-	47	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000394	000000	-	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000395	000000	-	34	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000399	000000	-	66	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000401	000000	-	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000405	000000	-	47	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000410	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000412	000000	-	34	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000414	000000	-	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000415	000000	-	135	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000428	000000	-	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000439	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000440	000000	-	153	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000441	000000	-	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000442	000000	-	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000443	000000	-	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000444	000000	-	36	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000445	000000	-	83	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000446	000000	-	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000447	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000448	000000	-	58	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000450	000000	-	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000451	000000	-	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000452	000000	-	55	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000453	000000	-	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000454	000000	-	32	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000455	000000	-	84	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000456	000000	-	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000457	000000	-	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000458	000000	-	145	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000459	000000	-	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000460	000000	-	115	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000461	000000	-	33	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000466	000000	-	122	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000467	000000	-	334	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000470	000000	-	57	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000473	000000	-	40	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000474	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000475	000000	-	64	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000482	000000	-	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000483	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000500	000000	-	67	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000501	000000	-	117	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000502	000000	-	55	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000503	000000	-	42	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000505	000000	-	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000513	000000	-	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000527	000000	-	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000528	000000	-	30	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000529	000000	-	44	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000530	000000	-	88	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000532	000000	-	85	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000533	000000	-	82	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000534	000000	-	72	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000535	000000	-	44	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000536	000000	-	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000537	000000	-	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000538	000000	-	40	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000539	000000	-	115	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000540	000000	-	105	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000541	000000	-	113	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000542	000000	-	42	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000543	000000	-	95	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000544	000000	-	68	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000545	000000	-	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000546	000000	-	37	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000547	000000	-	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000550	000000	-	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000551	000000	-	41	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000553	000000	-	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000554	000000	-	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000555	000000	-	56	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000556	000000	-	97	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000557	000000	-	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000558	000000	-	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000559	000000	-	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000561	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prevph1000000562	000000	-	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000566	000000	-	54	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000567	000000	-	120	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000568	000000	-	94	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000569	000000	-	99	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000570	000000	-	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000571	000000	-	131	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000572	000000	-	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000573	000000	-	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000574	000000	-	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000575	000000	-	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000576	000000	-	62	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000577	000000	-	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000578	000000	-	136	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000579	000000	-	262	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000580	000000	-	110	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000583	000000	-	198	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000585	000000	-	75	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000586	000000	-	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000587	000000	-	38	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000588	000000	-	45	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000589	000000	-	43	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000590	000000	-	108	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000591	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000595	000000	-	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000597	000000	-	75	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000598	000000	-	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000599	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000600	000000	-	35	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000601	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000602	000000	-	49	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000605	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000621	000000	-	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000622	000000	-	43	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000627	000000	-	31	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000632	000000	-	45	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000635	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000642	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000643	000000	-	36	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000651	000000	-	123	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000664	000000	-	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000665	000000	-	48	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000666	000000	-	61	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000667	000000	-	182	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000668	000000	-	32	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000669	000000	-	36	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000670	000000	-	64	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000671	000000	-	71	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000672	000000	-	96	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000673	000000	-	119	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000674	000000	-	155	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000676	000000	-	141	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000677	000000	-	66	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000678	000000	-	237	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000679	000000	-	191	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000680	000000	-	123	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000681	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000682	000000	-	120	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000683	000000	-	42	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000684	000000	-	76	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000685	000000	-	103	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000686	000000	-	220	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000687	000000	-	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000688	000000	-	125	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000689	000000	-	87	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000690	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000691	000000	-	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000692	000000	-	77	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000694	000000	-	34	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000696	000000	-	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000697	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000699	000000	-	100	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000701	000000	-	72	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000702	000000	-	97	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000704	000000	-	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000705	000000	-	67	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000706	000000	-	86	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000707	000000	-	80	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000710	000000	-	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000711	000000	-	37	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000712	000000	-	62	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000713	000000	-	87	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000714	000000	-	86	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000719	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000721	000000	-	78	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000722	000000	-	57	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000723	000000	-	52	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000725	000000	-	46	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000726	000000	-	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000727	000000	-	42	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000728	000000	-	51	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000729	000000	-	63	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000730	000000	-	151	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000731	000000	-	33	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000738	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000749	000000	-	75	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000780	000000	-	133	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000781	000000	-	70	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000784	000000	-	124	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000785	000000	-	69	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000787	000000	-	59	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000812	000000	-	79	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000814	000000	-	37	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000815	000000	-	60	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000828	000000	-	124	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000832	000000	-	53	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000847	000000	-	50	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000848	000000	-	65	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000849	000000	-	99	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000850	000000	-	30	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prevph1000000851	000000	-	118	-	Prevotella_phage_Lak-B8	GCA_004379655.1
prev15ph1000000005	000000	-	41	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000044	000000	-	542	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000055	000000	-	312	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000065	000000	-	457	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000067	000000	-	2067	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000068	000000	-	573	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000070	000000	-	151	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000087	000000	-	257	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000092	000000	-	41	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000104	000000	-	166	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000124	000000	-	83	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000163	000000	-	1030	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000273	000000	-	758	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000314	000000	-	600	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1

Accession	Cluster.id	Annotation	Length	Protein_name	Phage	GCA
prev15ph1000000316	000000	-	269	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000318	000000	-	236	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000322	000000	-	488	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000339	000000	-	78	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000351	000000	-	1366	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000352	000000	-	517	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000353	000000	-	566	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000359	000000	-	553	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000382	000000	-	348	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000392	000000	-	70	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000402	000000	-	1829	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000403	000000	-	85	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000409	000000	-	887	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000413	000000	-	1302	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000414	000000	-	385	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000417	000000	-	627	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000422	000000	-	494	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000442	000000	-	40	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000479	000000	-	2897	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000483	000000	-	41	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000488	000000	-	141	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000489	000000	-	613	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000572	000000	-	464	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1
prev15ph1000000589	000000	-	744	-	Prevotella_phage_Lak-B8-code15	GCA_004379655.1