Bacteriolytic Potential of *Enterococcus* Phage iF6 Isolated from "Sextaphag®" Therapeutic Phage Cocktail and Properties of its Endolysins, Gp82 and Gp84

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Supplementary Information:

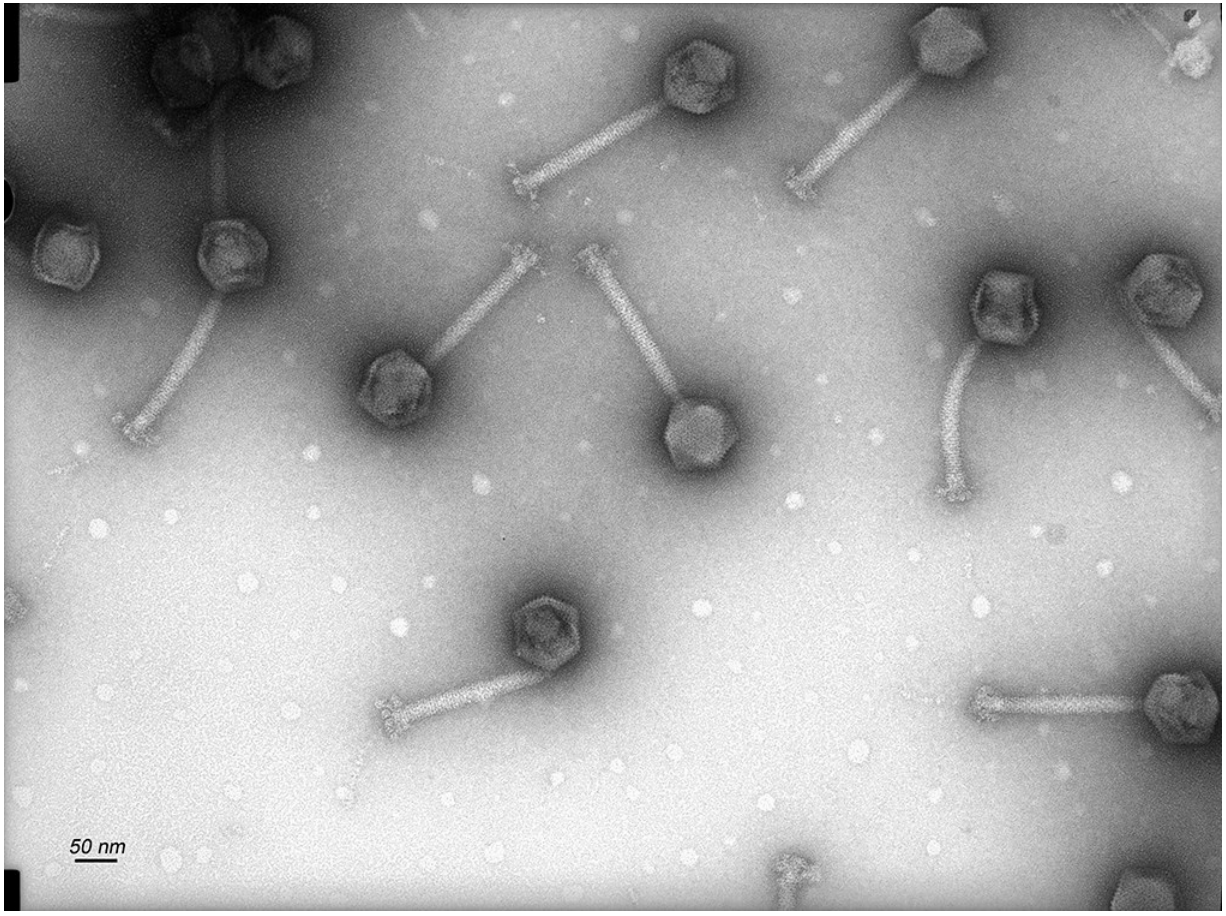


Figure S1. Transmission electron microscopy of *Enterococcus* phage iF6. This is the original TEM micrograph used to generate Figure 1 in the main text. The image was taken using a JEM-100 (JEOL, Japan) transmission electron microscope at 80 kV accelerating voltage on Kodak film SO-163 (Kodak, Cat. # 74144, Hatfield, PA, USA).

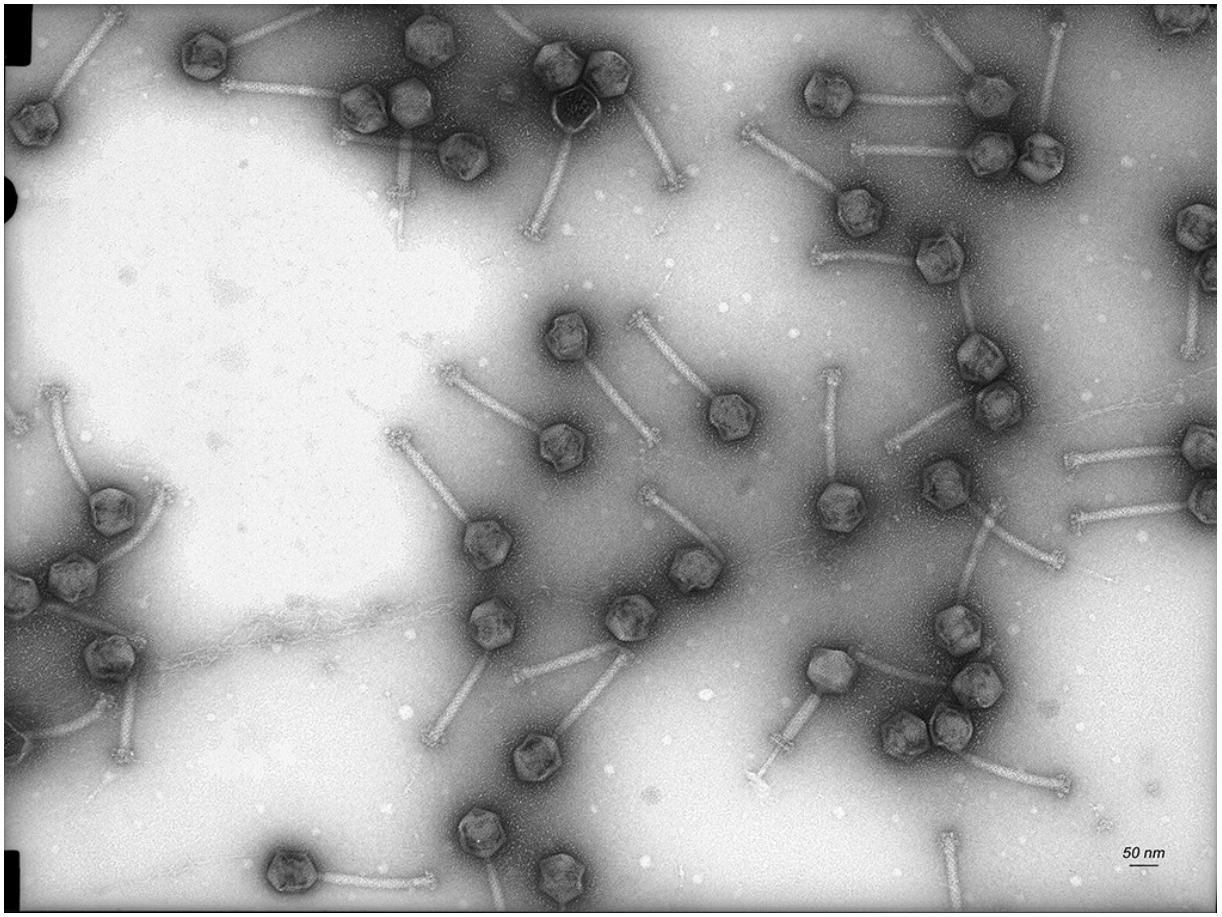


Figure S2. Transmission electron microscopy of *Enterococcus* phage iF6. This is the original TEM micrograph used to generate Figure 1 in the main text. The image was taken using a JEM-100 (JEOL, Japan) transmission electron microscope at 80 kV accelerating voltage on Kodak film SO-163 (Kodak, Cat. # 74144, Hatfield, PA, USA).

Table S1. The host range of the *Enterococcus* phage iF6 and the lytic spectrum of its endolysins determined for 26 *Enterococcus* strains and 3 strains from other genera of bacteria.

No.	Species	Strain	Source*	Cell lysis by:		
				iF6 Phage**	HU-Gp82 endolysin***	HU-Gp84 endolysins***
1	*E. avium*	B-1673	VKM	-	+	+
2	*E. durans*	B-603	VKM	-	++	++
3	*E. durans*	B-8257	VKPM	-	-	-
4	*E. durans*	B-11854	VKPM	-	-	++
5	*E. hirae*	B-12152	VKPM	-	-	+
6	*E. faecalis*	B-12629	VKPM	-	-	+
7	*E. faecalis*	B-4426	VKPM	-	-	+
8	*E. faecalis*	B-4053	VKPM	-	-	++
9	*E. faecium*	FS86	Laboratory collection	+	++	++
10	*E. faecium*	B-2579	VKPM	-	-	+
11	*E. faecium*	B-2990	VKPM	+	+	+
12	*E. faecium*	B-3490	VKPM	+	-	-
13	*E. faecium*	B-3491	VKPM	-	-	+
14	*E. faecium*	B-4054	VKPM	-	-	+
15	*E. faecium*	B-4489	VKPM	-	+	+
16	*E. faecium*	B-4991	VKPM	+	-	-
17	*E. faecium*	B-5000	VKPM	-	-	++
18	*E. faecium*	B-8551	VKPM	+	+	++
19	*E. faecium*	B-12648	VKPM	-	-	-
20	*E. thailandicus*	B-10684	VKPM	+	-	++
21	*E. sp*	B-1578	VKM	+	+	+
22	*E. sp*	B-1944	VKM	+	+	+
23	*E. sp*	B-3371	VKPM	-	-	-
24	*E. sp*	B-8711	VKPM	-	-	+
25	*E. sp*	B-8712	VKPM	-	+	++

26	*E. sp*	B-8713	VKPM	+	-	-
27	*E. coli*	XL1blue	Laboratory collection	-	-	-
28	*P. syringae*	B-268	BIM	-	-	-
29	*B. cereus*	B-370	VKM	-	-	-

* Source abbreviations: VKM: All-Russian Collection of Microorganisms; VKPM: National Bioresource Center – All-Russian collection of industrial microorganisms; BIM – the Belarusian collection of non-pathogenic microorganisms (BIM) of the Institute of Microbiology, National Academy of Sciences.

** Symbols for the host range of *Enterococcus* phage iF6: "+" – strains susceptible to the iF6 phage; "-" – strains resistant to the iF6 phage.

*** Symbols for the lytic spectrum of the HU-Gp82 and HU-Gp84 endolysins: "++" – strains inhibited by a low dose of endolysins (15 μg/mL and 11 μg/mL, respectively); "+" – strains inhibited by a higher dose of endolysins (30 μg/mL and 22 μg/mL, respectively); "-" – strains resistant to endolysins.

Table S2. Annotation of *Enterococcus* phage iF6.

ORF№	Start codon	Stop codon	Strand	Blast results		Conserved domains, Blast		Hhpred results	Annotation
				Name	E-val	Name, (region)	E-val	(Prob./E-val)	
1	497	652	+	hp	hp	-	-	('-', '-')	hp
2	703	969	+	hp	hp	-	-	d1vqqa2; d.175.1.1 (A:139-327) Penicillin binding protein 2a (PBP2A), middle domain {*Staphylococcus aureus* [TaxId: 1280]} (64.56/4.10e+00)	hp
3	986	1228	+	hp	hp	-	-	PF16112.6; DUF4830; Domain of unknown function (DUF4830) (95.11/1.30e-02)	hp
4	1245	1565	+	hp	hp	-	-	PF03871.15; RNA_pol_Rpb5_N; RNA polymerase Rpb5, N-terminal domain (88.98/2.60e+00)	hp
5	1639	1779	+	hp	hp	-	-	('-', '-')	hp
6	1869	2012	+	hp	hp	-	-	PF13035.7; DUF3896; Protein of unknown function (DUF3896) (87.29/2.50e+00)	hp
7	2417	2205	-	hp	hp	-	-	('-', '-')	hp
8	2745	2473	-	hp	hp	-	-	PF03886.14; ABC_trans_aux; ABC-type transport auxiliary	hp

								lipoprotein component (83.38/4.20e+00)	
9	3173	2763	-	hp	hp	-	-	('-', '-')	hp
10	3412	3197	-	hp	hp	-	-	PF06785.12; UPF0242; Uncharacterised protein family (UPF0242) N-terminus (87.68/2.70e+00)	hp
11	3640	3413	-	hp	hp	-	-	('-', '-')	hp
12	3875	3642	-	hp	hp	-	-	KOG2983; Uncharacterized conserved protein [Function unknown] (73.96/4.50e+00)	hp
13	4267	3962	-	hp	hp	-	-	PF07862.12; Nif11; Nif11 domain (86.96/1.90e+00)	hp
14	4476	4279	-	hp	hp	-	-	('-', '-')	hp
15	4640	4476	-	hp	hp	-	-	COG4416; Com; Mu-like prophage FluMu protein Com [Mobilome: prophages, transposons]. (83.46/4.70e-01)	hp
16	5052	4630	-	hp	hp	-	-	('-', '-')	hp
17	5137	5045	-	protein RtcB [*Enterococcus* phage vB_OCPT_Ben] RtcB protein [*Enterococcus* phage PEf771] protein RtcB [*Enterococcus* phage EFDG1]	5.0e-12 5.0e-12 5.0e-12	-	-	('-', '-')	hp

18	5318	5130	-	hp	hp	-	-	PF11460.9; DUF3007; Protein of unknown function (DUF3007) (79.24/2.40e+00)	hp
19	6150	5407	-	hp	hp	-	-	COG1996; RPC10; DNA-directed RNA polymerase, subunit RPC12/RpoP, contains C4-type Zn-finger [Transcription]. (86.18/7.60e-01)	hp
20	7082	6228	-	hp	hp	-	-	PF09954.10; DUF2188; Uncharacterized protein conserved in bacteria (DUF2188) (80.11/5.40e+00)	hp
21	7393	7079	-	NAD-dependent DNA ligase [*Streptococcus* phage Dp-1] gp102 [*Rhodococcus* phage ReqiPepy6] DNA ligase [*Clostridium* phage phi8074-B1]	7.0e-10 5.0e-09 3.0e-08	ligA (17-52)	1.24e-04	d1dgsa3; d.142.2.2 (A:1-314) Adenylation domain of NAD+-dependent DNA ligase {*Thermus filiformis* [TaxId: 276]} (99.79/5.90e-19) PF01653.19; DNA_ligase_aden; NAD-dependent DNA ligase adenylation domain (99.78/8.20e-19) d1ta8a_; d.142.2.2 (A:) Adenylation domain of NAD+-dependent DNA ligase {*Enterococcus faecalis* [TaxId: 1351]} (99.78/8.50e-19)	NAD-dependent DNA ligase adenylation domain containing protein
22	7878	7396	-	hp	hp	HTH_XRE (106-154)	4.68e-12	COG1395; COG1395; Predicted transcriptional regulator [Transcription]. (99.41/4.50e-13)	DNA-binding protein

								COG5606; COG5606; Predicted DNA-binding protein, XRE-type HTH domain [General function prediction only]. (98.67/1.20e-06) KOG3398; Transcription factor MBF1 [Transcription] (98.55/2.60e-06)	
23	8274	8044	-	hp	hp	-	-	PF14353.7; CpXC; CpXC protein(98.36/2.80e-06) PF11520.9; Cren7; Chromatin protein Cren7(98.29/5.60e-06) PF09538.11; FYDLN_acid; Protein of unknown function (FYDLN_acid) (97.98/1.40e-05)	Zn-binding domain containing protein
24	8582	8286	-	hp	hp	-	-	PF17399.3; DUF5405; Domain of unknown function (DUF5405) (99.57/4.20e-14)	DUF5405-containing protein
25	9028	8582	-	hp	hp	-	-	('-', '-')	hp
26	9614	9216	-	hp	hp	-	-	d1twfi1; g.41.3.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's yeast (*Saccharomyces cerevisiae*) [TaxId: 4932]} (91.09/1.80e-01)	hp
27	9870	9607	-	hp	hp	-	-	('-', '-')	hp
28	11580	9946	-	hp	hp	-	-	('-', '-')	hp
29	11916	11596	-	hp	hp	-	-	('-', '-')	hp

30	12730	11990	-	Serine/threonine protein phosphatase (EC [*Enterococcus* phage 163] serine/threonine protein phosphatase [*Enterococcus* phage EFDG1] serine/threonine protein phosphatase [*Enterococcus* phage EfV12-phi1]	1.0e-162 3.0e-159 5.0e-159	MPP_PPP_family (8-226) Metallophos (8-192) bacter_Pnkp (8-76)	1.24e-23 2.64e-09 1.82e-07	cd07413; MPP_PA3087; *Pseudomonas aeruginosa* PA3087 and related proteins, metallophosphatase domain.(99.9/8.00e-22) cd07421; MPP_Rhilphs; Rhilph phosphatases, metallophosphatase domain.(99.86/1.70e-20) d1g5ba_; d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda [TaxId: 10710]}(99.86/2.20e-20)	serine/threonine protein phosphatase
31	12987	12730	-	hp	hp	-	-	('-', '-')	hp
32	13592	12984	-	putative metallo-dependent phosphatase 1 [*Enterococcus* phage EFP01] Phosphoesterase [*Enterococcus* phage 163] phosphoesterase [*Enterococcus* phage vB_OCPT_Ben]	5.0e-135 1.0e-134 1.0e-133	MPP_AQ1575 (4-181) COG4186 (2-159) yfcE (1-145)	2.90e-34 3.73e-24 5.53e-05	COG4186; COG4186; Calcineurin-like phosphoesterase superfamily protein [General function prediction only]. (99.87/2.20e-20) d1xm7a1; d.159.1.8 (A:1-186) hp aq_1666 {*Aquifex aeolicus* [TaxId: 63363]} (99.81/5.20e-19) cd07390; MPP_AQ1575; *Aquifex aeolicus* AQ1575 and related proteins,	calcineurin-like phosphoesterase

								metallophosphatase domain. (99.8/1.40e-18)	
33	14164	13589	-	phosphoesterase [*Enterococcus* phage PEf771] phosphohydrolase [*Enterococcus* phage EFDG1] putative phosphoesterase or phosphohydrolase [*Enterococcus* phage EfsSzw-1]	9.0e-124 1.0e-123 2.0e-122	MPP_AQ1575 (4-166) COG4186 (1-165) Metallophos_2 (32-139)	9.62e-28 2.85e-25 3.26e-06	COG4186; COG4186; Calcineurin-like phosphoesterase superfamily protein [General function prediction only]. (99.84/9.20e-19) cd07390; MPP_AQ1575; *Aquifex aeolicus* AQ1575 and related proteins, metallophosphatase domain. (99.8/1.40e-18) d1xm7a1; d.159.1.8 (A:1-186) hp aq_1666 {*Aquifex aeolicus* [TaxId: 63363]} (99.76/2.40e-17)	calcineurin-like phosphoesterase
34	14695	14165	-	exonuclease [*Enterococcus* phage EFP01] exonuclease [*Enterococcus* phage PEf771] gp128 [*Bacillus* virus G]	7.0e-117 7.0e-117 3.0e-55	DUF5051 (1-164)	3.49e-09	COG2176; PolC; DNA polymerase III, alpha subunit (gram-positive type) [Replication, recombination and repair]. (99.85/6.20e-20) KOG0542; Predicted exonuclease [Replication, recombination and repair] (99.83/2.10e-18) KOG0304; mRNA deadenylase subunit [RNA processing and modification] (99.76/6.00e-17)	3' exoribonuclease family protein

								KOG3242 Oligoribonuclease (3'5' exoribonuclease) [RNA processing and modification] (99.71/1.1e-15)	
35	15076	14726	-	hp EFV12PHI1_12 Phage protein [*Enterococcus* phage 163] gp107 [*Lactococcus* virus KSY1]	8.0e-73 6.0e-70 8.0e-18	DUF3307 (8-116)	1.33e-04	PF11750.9; DUF3307; Protein of unknown function (DUF3307) (99.93/1.60e-24)	DUF3307-containing protein
36	15642	15073	-	hp	hp	-	-	('-', '-')	hp
37	15899	15639	-	hp	hp	-	-	('-', '-')	hp
38	16166	15900	-	Phage-related protein [*Clostridium* phage phiCD111] Phage protein [*Streptococcus* phage IC1]	6.0e-17 2.0e-15	-	-	PF14083.7; PGDYG; PGDYG protein (99.54/8.10e-14) PF14083.7; PGDYG; PGDYG protein (98.68/5.50e-08)	PGDYG motif containing protein
39	16436	16260	-	hp	hp	-	-	d1vk6a4; g.41.14.1 (A:97-125) NADH pyrophosphatase intervening domain {*Escherichia coli* [TaxId: 562]} (82.77/1.50e+00)	hp
40	17013	16450	-	hp	hp	-	-	('-', '-')	hp
41	17107	17015	-	hp	hp	-	-	d1dgsa1; a.60.2.2 (A:401-581) NAD+-dependent DNA ligase, domain 3 {*Thermus filiformis* [TaxId: 276]} (96.51/2.20e-03)	hp

								d1yuza2; g.41.5.1 (A:167-202) Nigerythrin, C-terminal domain {*Desulfovibrio vulgaris* [TaxId: 881]} (95.48/1.10e-02) COG1592; YotD; Rubrerythrin [Energy production and conversion]. (94.84/1.90e-02)	
42	17339	17181	-	hp	hp	-	-	('-', '-')	hp
43	18552	17428	-	transposase [*Geobacillus* virus E3] gp191 [*Brochothrix* phage A9] transposase [*Paenibacillus* phage Unity]	4.0e-153 7.0e-132 2.0e-113	InsQ (3-368) OrfB_IS605 (163-276) tspaseT_teng_C (242-316)	1.26e-61 1.22e-27 3.78e-10	COG0675; InsQ; Transposase [Mobilome: prophages, transposons]. (100.0/1.50e-35) PF18516.2; RuvC_1; RuvC nuclease domain (99.69/6.50e-16) PF01385.20; OrfB_IS605; Probable transposase (99.0/2.30e-08)	transposase
44	19384	18770	-	ribonucleotide reductase of class III (anaerobic), activating protein [*Enterococcus* phage EFDG1] ribonucleotide reductase of class III (anaerobic), activating protein [*Enterococcus* phage vB_OCPT_Ben]	2.0e-136 4.0e-136	Fer4_12 (27-169) NrdG (17-171)	2.00e-67 2.20e-61	cd17825; Radical_SAM_MoaA; Radical_SAM. (99.82/9.60e-20) cd17853; Radical_SAM; Radical_SAM (99.81/2.00e-19	ribonucleotide reductase of class III (anaerobic)

				ribonucleotide reductase of class III (anaerobic), activating protein [*Enterococcus* phage EfV12-phi1]	2.0e-135				
45	19670	19377	-	hp	hp	-	-	PF18450.2; zf_C2H2_6; Zinc Finger domain (95.73/3.50e-03) d1fu9a1; g.37.1.2 (A:3-36) (94.57/1.30e-02)	hp
46	20632	19670	-	thymidylate synthase [*Enterococcus* phage EFDG1] thymidylate synthase [*Enterococcus* phage vB_OCPT_Ben] thymidylate synthase [*Enterococcus* phage PEf771]	0.0e+00 0.0e+00 0.0e+00	Thymidylat_synt (53-320) TS_Pyrimidine_HMase (6-264) thym_sym (53-308)	8.19e-82 1.76e-52 1.80e-40	d1bkpa_; d.117.1.1 (A:) Thymidylate synthase {*Bacillus subtilis* [TaxId: 1423]} (100/3.20e-62) d1j3kc_; d.117.1.1 (C:) Bifunctional enzyme dihydrofolate reductase-thymidylate synthase, TS domain {Malaria parasite (*Plasmodium falciparum*) [TaxId: 5833]} (100/2.30e-60) d1tisa_; d.117.1.1 (A:) Thymidylate synthase {Bacteriophage T4 [TaxId: 10665]} (100/7.50e-60)	thymidylate synthase
47	21271	20648	-	hp	hp	-	-	PF10892.9; DUF2688; Protein of unknown function (DUF2688) (93.14/5.20e-02)	hp
48	22022	21273	-	hp	hp	-	-	('-', '-')	hp

49	22563	22096	-	hp	hp	-	-	d2fvva1 d.113.1.1 (A:8-142) Diphosphoinositol polyphosphate phosphohydrolase {Human (Homo sapiens) [TaxId: 9606]} (99.56/7.2e-13) cd18873 Nudix_ADPR_NadM_NrtR; Nudix hydrolase subfamily 7. (99.49/2e-12) Nucleoside triphosphate pyrophosphorylase (MutT) {*Escherichia coli* K-12 [TaxId: 83333]} (99.47/1e-11)	nucleoside triphosphate pyrophosphorylase
49	22563	22096	-	hp	hp	-	-	d2fvva1 d.113.1.1 (A:8-142) Diphosphoinositol polyphosphate phosphohydrolase {Human (Homo sapiens) [TaxId: 9606]} (99.56/7.2e-13) cd18873 Nudix_ADPR_NadM_NrtR; Nudix hydrolase subfamily 7. (99.49/2e-12) Nucleoside triphosphate pyrophosphorylase (MutT) {*Escherichia coli* K-12 [TaxId: 83333]} (99.47/1e-11)	nucleoside triphosphate pyrophosphorylase

50	23315	22578	-	hp	hp	NMN_transporter (44-232)	4.24e-10	COG3201; PnuC; Nicotinamide riboside transporter PnuC [Coenzyme transport and metabolism]. (100.0/2.40e-36) PF04973.13; NMN_transporter; Nicotinamide mononucleotide transporter (100.0/1.70e-32) PF04973.13; NMN_transporter; Nicotinamide mononucleotide transporter (98.69/1.50e-07)	nicotinamide mononucleotide transporter
51	23679	23317	-	hp	hp	-	-	PF03698.14; UPF0180; Uncharacterised protein family (UPF0180) (82.59/2.70e+00)	hp
52	24806	23679	-	nicotinamide-nucleotide adenylyltransferase, NadR family/ ribosylnicotinamide kinase [*Enterococcus* phage vB_OCPT_Ben] nicotinamide-nucleotide adenylyltransferase, NadR family / ribosylnicotinamide kinase [*Enterococcus* phage EfV12-phi1] nicotinamide-nucleotide adenylyltransferase, NadR family /	0.0e+00 0.0e+00 0.0e+00	PRK08099 (1-355) NadR3 (171-353) NMNAT_NadR (5-174)	1.14e-164 3.41e-65 9.06e-42	d1lw7a1; c.26.1.3 (A:57-219) Transcriptional regulator NadR, NMN-adenylyltransferase domain {*Haemophilus influenzae* [TaxId: 727]} (99.85/7.80e-20) cd02167; NMNAT_NadR; Nicotinamide/nicotinate mononucleotide adenylyltransferase of bifunctional NadR-like proteins. (99.78/2.70e-18) KOG2803; Choline phosphate cytidylyltransferase/Predicted CDP-ethanolamine synthase	NadR transcriptional regulator /nicotinamide-nucleotide adenylyltransferase, NadR family/ ribosylnicotinamide kinase

				ribosylnicotinamide kinase [*Enterococcus* phage EFDG1]				[Lipid transport and metabolism] (99.63/5.80e-16)	
53	25254	24892	-	HAD-like domain containing protein [*Enterococcus* phage EfsSzw-1] gp153 [*Listeria* virus P100] HAD-like domain containing protein [*Listeria* phage LMTA-94]	2.0e-57 3.0e-21 1.0e-20	Cof (8-78)	6.38e-03	d2obba1; c.108.1.25 (A:1-122) hp BT0820 {*Bacteroides thetaiotaomicron* [TaxId: 818]} (99.76/9.10e-17) PF06189.13; 5-nucleotidase; 5'-nucleotidase (99.3/9.30e-12) COG5663 YqfW; Uncharacterized protein, HAD superfamily [General function prediction only]. (99.11/2.9e-10) d1ltqa1; c.108.1.9 (A:153-301) Polynucleotide kinase, phosphatase domain {Bacteriophage T4 [TaxId: 10665]} (99.21/1.10e-10) PF12689.8; Acid_PPase; Acid Phosphatase (98.93/6.2e-9)	HAD-like family phosphatase
54	25588	25349	-	putative ribonucleotide reductase [*Enterococcus* phage EFP01] glutaredoxin-like protein [*Enterococcus* phage EfV12-phi1]	5.0e-48 4.0e-45	GlrX_NrdH (4-74) Glutaredoxin (4-48)	6.89e-18 9.46e-12 1.50e-09	d1r7ha_; c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {*Corynebacterium ammoniagenes* [TaxId: 1697]} (99.37/9.50e-11) d1h75a_; c.47.1.1 (A:) Glutaredoxin-like NRDH-	glutaredoxin-like NRDH-redoxin

				putative ribonucleotide reductase [*Enterococcus* phage EfsSzw-1]	6.0e-44	GrxC (3-76)		redoxin {*Escherichia coli* [TaxId: 562]} (99.36/1.10e-10) d1nhoa_; c.47.1.1 (A:) MTH807, thioredoxin/glutaredoxin-like protein {*Methanobacterium thermoautotrophicum* [TaxId: 145262]} (99.15/3.80e-09)	
55	26345	25581	-	Nicotinamide mononucleotide transporter [*Enterococcus* phage 163] membrane protein [*Enterococcus* phage EFP01] nicotinamide mononucleotide transporter [*Enterococcus* phage EfV12-phi1] NrdR-regulated deoxyribonucleotide transporter [*Enterococcus* phage EFDG1]	2.0e-171 1.0e-170 9.0e-170 1.0e-140	NMN_transporter (70-248) NMN_trans_PnuC (70-250)	1.59e-20 8.37e-14	COG3201; PnuC; Nicotinamide riboside transporter PnuC [Coenzyme transport and metabolism]. (100.0/1.20e-34) PF04973.13; NMN_transporter; Nicotinamide mononucleotide transporter (99.97/3.40e-30) PF04973.13; NMN_transporter; Nicotinamide mononucleotide transporter (98.33/3.00e-06)	PnuC-like nicotinamide mononucleotide transporter
56	27178	26363	-	deoxyguanosine kinase [*Enterococcus* phage PEf771] kinase [*Enterococcus* phage EF1]	0.0e+00 0.0e+00	Dck (1-207) dNK (2-193)	4.63e-61 2.86e-48	cd01673; dNK; Deoxyribonucleoside kinase (dNK) catalyzes the phosphorylation of deoxyribonucleosides to yield corresponding monophosphates (dNMPs). (99.83/1.60e-17)	deoxyribonucleoside kinase

				deoxynucleoside kinase family protein [*Enterococcus* phage EfsSzw-1]	0.0e+00			PF01712.20; dNK; Deoxynucleoside kinase (99.83/1.60e-17) COG1428; Dck; Deoxyadenosine/deoxycytidine kinase [Nucleotide transport and metabolism]. (99.83/4.20e-17)	
57	28119	27367	-	-	-	LAGLIDADG_2 (61-201)	3.42e-06	COG3780; COG3780; DNA endonuclease related to intein-encoded endonucleases [Replication, recombination and repair]. (99.87/1.80e-20) d1r7ma2; d.95.2.1 (A:121-225) DNA endonuclease I-SceI {Baker's yeast (*Saccharomyces cerevisiae*) [TaxId: 4932]} (99.74/1.90e-17) cd09958; LAGLIDADG_1_child_11_child_1 LAGLIDADG endonuclease. LAGLIDADG endonuclease (99.67/1.30e-15)	DNA endonuclease
58	30475	28370	-	ribonucleotide reductase of class III (anaerobic), large subunit [*Enterococcus* phage EfV12-phi1]	0.0e+00 0.0e+00	PRK09263 (14-698) NRDD	0e+00 0e+00	d1hk8a_; c.7.1.3 (A:) Class III anaerobic ribonucleotide reductase NRDD subunit {Bacteriophage T4 [TaxId: 10665]} (100.0/2.80e-91)	class III ribonucleotide reductase

				ribonucleotide reductase of class III (anaerobic), large subunit [*Enterococcus* phage EFDG1] Ribonucleotide reductase of class III (anaerobic), large subunit (EC [*Enterococcus* phage 163]	0.0e+00	(131-698)		PF13597.7; NRDD; Anaerobic ribonucleoside-triphosphate reductase (100.0/3.40e-83) COG1328; NrdD; Anaerobic ribonucleoside-triphosphate reductase [Nucleotide transport and metabolism]. (100.0/9.30e-82)	
59	30895	30626	-	hp	hp	-	-	PF13113.7; DUF3970; Protein of unknown function (DUF3970) (80.08/2.20e+00) PF10369.10; ALS_ss_C; Small subunit of acetolactate synthase (80.52/2.6)	hp
60	31737	30907	-	ParBc domain protein [*Streptococcus* phage phiARI0831b] ParB-like nuclease domain containing protein [uncultured *Mediterranean* phage uvMED] ParB-like nuclease domain containing protein [uncultured *Mediterranean* phage uvMED]	2.0e-14 1.0e-11 7.0e-09	pNOB8_ParB_N_like (25-83) ParB (29-90)	6.29e-14 1.78e-06	COG1475; Spo0J; Chromosome segregation protein Spo0J, contains ParB-like nuclease domain [Cell cycle control, cell division, chromosome partitioning]. (99.37/9.30e-12) d1vz0a2; d.268.1.1 (A:23-115) Putative partitioning protein ParB/Spo0J {*Thermus thermophilus* [TaxId: 274]} (99.19/2.10e-10) cd16402; ParB_N_like_MT; ParB N-terminal-like domain, some attached to C-terminal S-	ParB-like nuclease domain containing protein

								adenosylmethionine-dependent methyltransferase domain. (98.98/7.30e-09)	
61	32061	31756	-	putative scaffolding protein [*Enterococcus* phage EFDG1] hp [*Enterococcus* phage 163]	3.0e-60 1.0e-59	YnbB (11-85)	3.21e-03	COG5377; COG5377; Phage-related protein, predicted endonuclease [Mobilome: prophages, transposons]. (99.44/3.80e-12) PF05565.12; Sipho_Gp157; Siphovirus Gp157 (96.4/0.1)	putative endonuclease
62	32377	32162	-	putative transcriptional regulator [*Enterococcus* phage EfsSzw-1] repressor [*Enterococcus* phage vB_EfaM_Ef2.1] Phage protein [*Enterococcus* phage 156]	1.0e-40 5.0e-19 1.0e-18	HTH_XRE (10-64) HipB (10-71)	1.46e-11 8.85e-06	COG5606; COG5606; Predicted DNA-binding protein, XRE-type HTH domain [General function prediction only]. (98.76/3.10e-07) d1b0na2; a.35.1.3 (A:1-68) SinR repressor, DNA-binding domain {*Bacillus subtilis* [TaxId: 1423]} (98.7/3.70e-07) COG1395 COG1395; Predicted transcriptional regulator [Transcription]. (98.67/e-06)	putative transcriptional regulator

63	33968	32436	-	DUF2828 domain-containing protein [*Enterococcus* phage EfsSzw-1] Phage protein [*Enterococcus* phage 163] DUF2828 domain-containing protein [*Listeria* phage LP-048]	0.0e+00 0.0e+00 3.0e-121	DUF2828 (16-491)	6.55e-73	PF11443.9; DUF2828; Domain of unknown function (DUF2828) (100.0/1.40e-84) KOG4465; Uncharacterized conserved protein [Function unknown] (99.84/1.60e-19) d1yvra2; c.62.1.5 (A:364-537) 60-kda SS-A/Ro ribonucleoprotein, RoRNP {African clawed frog (*Xenopus laevis*) [TaxId: 8355]} (98.99/9.40e-08)	DUF2828 domain-containing protein
64	35020	34796	-	hp	hp	-	-	('-', '-')	hp
65	37328	36960	-	hp	hp	-	-	('-', '-')	hp
66	37902	37720	-	hp	hp	-	-	COG3112; YacL; Uncharacterized protein YacL, UPF0231 family [Function unknown]. (77.62/4.60e+00)	hp
67	39444	39223	-	hp	hp	-	-	PF18401.2; Thioredoxin_13; Thioredoxin-like domain (71.23/7.60e+00)	hp
68	39704	39453	-	hp	hp	-	-	('-', '-')	hp
69	44975	44637	-	hp [*Enterococcus* phage 163] structural protein [*Enterococcus* phage ECP3]	1.0e-70 3.0e-11	-	-	PF06289.12; FlbD; Flagellar and Swarming motility proteins (88.98/7.60e-01)	hp

				putative structural protein [*Enterococcus* phage phiM1EF22] structural protein [*Enterococcus* phage EF24C]	2.0e-10 2.0e-10				
70	45377	45030	-	hp EFP01_107 [*Enterococcus* phage EFP01] gp67 [*Listeria* virus A511] putative membrane bound protein [*Staphylococcus* phage f2b1] putative membrane protein [*Bacillus* phage Bcp1]	2.0e-72 1.0e-22 4.0e-16 5.0e-12	PHA02414 (1-114)	7.01e-50	PF10779.10; XhlA; Haemolysin XhlA (96.23/1.10e-01)	putative haemolysin XhlA
71	45674	45417	-	hp	hp	-	-	PF04678.14; MCU; Mitochondrial calcium uniporter (84.73/4.70e+00)	hp
72	45793	46062	+	hp	hp	-	-	COG3771; YciS; Uncharacterized membrane protein YciS, DUF1049 family [Function unknown]. (99.4/6.80e-12) COG5416; YrvD; Uncharacterized integral	putative membrane protein

								membrane protein [Function unknown]. (99.26/3.10e-11) PF06305.12; LapA_dom; Lipopolysaccharide assembly protein A domain (98.99/1.60e-09)	
73	46082	46360	+	gp71 [*Listeria* virus A511] membrane protein [*Staphylococcus* phage phiIPLA-C1C] Dmd [*Staphylococcus* phage JD007]	6.0e-16 2.0e-15 8.0e-10	-	-	PF10013.10; DUF2256; Uncharacterized protein conserved in bacteria (DUF2256) (90.96/1.30e-01)	hp
74	46365	46793	+	Phage protein [*Enterococcus* phage 156] gp72 [*Listeria* virus A511] ORF092 [*Staphylococcus* virus Twort]	4.0e-58 1.0e-19 40e-15	-	-	('-', '-')	hp
75	46793	47080	+	terminase large subunit [*Enterococcus* phage EFP01] terminase large subunit [*Enterococcus* phage EfV12-phi1]	6.0e-61 1.0e-54 1.0e-54	-	-	COG5525; YbcX; Phage terminase, large subunit GpA [Mobilome: prophages, transposons]. (67.42/2.30e+00) PF18305.2; DNA_pol_A_exoN; 3' to 5' exonuclease C-terminal domain (60.85/2.6)	putative terminase, large subunit

				terminase large subunit [*Enterococcus* phage EfsSzw-1]				PF03354.16; Terminase_1; Phage Terminase (63.85/5.3)	
76	47349	48269	+	hydrolase [*Lactobacillus* phage Iacchus] ORF031 [*Staphylococcus* virus Twort] hydrolase [*Staphylococcus* phage vB_SsapH-Golestan101-M] homing endonuclease [*Lactobacillus* phage 3-521] 3.0e-82	4.0e-90 4.0e-88 3.0e-80 2.0e-70	-	-	d1vsra_; c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {*Escherichia coli* [TaxId: 562]} (98.32/2.10e-05) PF14311.7; DUF4379; Probable Zinc-ribbon domain (97.68/1.90e-05) PF05265.14; DUF723; Protein of unknown function (DUF723) (98.12/1.80e-05)	VSR endonuclease
77	48715	49674	+	Phage protein [*Enterococcus* phage 156] VSR homing endonuclease [*Staphylococcus* phage phiIPLA-RODI] group I intron protein [*Staphylococcus* phage vB_SauM_Romulus]	0.0e+00 6.0e-47 1.0e-40	DUF559 (226-307) Vsr (195-290) YcjD(226-307)	6.33e-06 1.23e-04 3.30e-04	d1vsra_; c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {*Escherichia coli* [TaxId: 562]} (98.96/1.70e-08) COG3727; Vsr; G:T-mismatch repair DNA endonuclease, very short patch repair protein [Replication, recombination and repair]. (98.73/3.30e-07) PF14311.7; DUF4379; Probable Zinc-ribbon domain (98.25/8.50e-07)	VSR endonuclease

78	49705	51210	+	terminase large subunit [*Enterococcus* phage vB_OCPT_Ben] terminase large subunit [*Enterococcus* phage EFDG1] Phage terminase, large subunit [*Enterococcus* phage 163]	0.0e+00 0.0e+00 0.0e+00	Terminase_GpA(11-294) YbcX (11-283)	1.86e-17 4.23e-05	COG5525; YbcX; Phage terminase, large subunit GpA [Mobilome: prophages, transposons]. (100.0/2.20e-46) PF05876.13; Terminase_GpA; Phage terminase large subunit (GpA) (100.0/6.50e-41) PF03354.16; Terminase_1; Phage Terminase (99.84/1.00e-18)	terminase large subunit
79	51454	52299	+	Phage protein [*Enterococcus* phage 163] Phage protein [*Enterococcus* phage 156] unknown [*Listeria* phage 20422-1]	0.0e+00 1.0e-77 6.0e-28	-	-	cd10676; GNAT_1Y9W; GNAT. Acetyltransferase (GNAT) family. This family contains proteins with N-acetyltransferase functions. (97.01/4.60e-02) PF12568.9; PanZ; Acetyltransferase (GNAT) domain, PanZ(96.29/6.10e-02) d2g3aa1; d.108.1.1 (A:1-137) Probable acetyltransferase Atu2258 {*Agrobacterium tumefaciens* [TaxId: 358]} (96.7/7.30e-02)	putative N-acetyltransferase
80	52296	53123	+	Phage protein [*Enterococcus* phage 163]	0.0e+00 3.0e-66	-	-	('-', '-')	hp

				Phage protein [*Enterococcus* phage 156]					
81	53124	53480	+	hp	hp	-	-	('-', '-')	hp
82	53585	54853	+	Phage N-acetylmuramoyl-L-alanine amidase (EC [*Enterococcus* phage 163] putative N-acetylmuramoyl-L-alanine amidase [*Enterococcus* phage EFP01] N-acetylmuramoyl-L-alanine amidase [*Enterococcus* phage EFDG1]	0.0e+00 0.0e+00 0.0e+00	Amidase_2 (24-155) AmpD (1-254)	4.64e-24 7.28e-08	d1yb0a1; d.118.1.1 (A:1-157) N-acetylmuramoyl-L-alanine amidase PlyG {*Anthrax bacillus* (*Bacillus anthracis*) [TaxId: 1392]} (99.63/1.90e-14) d1lbaa_; d.118.1.1 (A:) Bacteriophage T7 lysozyme (Zn amidase) {Bacteriophage T7 [TaxId: 10760]} (99.55/1.80e-13) d2cb3a1; d.118.1.1 (A:174-344) Peptidoglycan-recognition protein-LE {Fruit fly (*Drosophila melanogaster*) [TaxId: 7227]} (99.53/3.10e-13)	N-acetylmuramoyl-L-alanine amidase
83	55011	55637	+	peptidoglycan-binding LysM [*Enterococcus* phage EFP01] Aggregation promoting factor [*Enterococcus* phage 163] aggregation promoting factor [*Enterococcus* phage EFDG1]	2.0e-119 8.0e-116 2.0e+115	LysM (35-81) spore_safA (39-82) PRK13914 (29-149)	1.62e-07 3.23e-07 6.91e-04	PF06737.15; Transglycosylas; Transglycosylase-like domain (98.4/6.60e-07) d1gd6a_; d.2.1.2 (A:) Lysozyme {Silkworm (*Bombyx mori*) [TaxId: 7091]} (97.04/3.90e-03) d1qqya_; d.2.1.2 (A:) Lysozyme {Dog (Canis familiaris), milk [TaxId: 9615]} (96.0/4.60e-02)	LysM domain containing peptidoglycan-binding protein

								KOG2850 Predicted peptidoglycan-binding protein, contains LysM domain [General function prediction only] (90.19/1.7)	
84	55741	56685	+	N-acetylmuramoyl-L-alanine amidase [*Enterococcus* phage EFDG1] N-acetylmuramoyl-L-alanine amidase [*Enterococcus* phage PEf771] n-acetylmuramoyl-L-alanine amidase [*Enterococcus* phage EfV12-phi1]	0.0e+00 0.0e+00 0.0e+00	Amidase_5(5-153) SH3_5(244-302)	6.92e-38 5.25e-06	COG0791; Spr; Cell wall-associated hydrolase, NlpC family [Cell wall/membrane/envelope biogenesis]. (98.58/2.40e-06) COG3234; *yfa*T; Uncharacterized conserved protein YfaT, DUF1175 family [Function unknown]. (98.24/2.80e-05) PF05382.14; Amidase_5; Bacteriophage peptidoglycan hydrolase (98.28/2.8e-04) PF08460.11; SH3_5; Bacterial SH3 domain (97.17/7.7e-03)	N-acetylmuramoyl-L-alanine amidase
85	56815	57159	+	hp	hp	-	-	PF06096.12; Baculo_8kDa; Baculoviridae 8.2 KDa protein (61.23/3.20e+00)	hp
86	57176	58864	+	Phage protein [*Enterococcus* phage 163]	0.0e+00 0.0e+00	Phage_portal (245-453) portal_HK97 (121-459)	1.10e-17 1.13e-07	COG4695; BeeE; Phage portal protein BeeE [Mobilome: prophages, transposons]. (100.0/1.10e-30)	portal protein

				portal protein [*Enterococcus* phage EFDG1] portal protein [*Enterococcus* phage PEf771]	0.0e+00	BeeE (245-467)	3.53e-06	PF04860.13; Phage_portal; Phage portal protein (99.97/5.90e-29) COG5518; COG5518; Bacteriophage capsid portal protein [Mobilome: prophages, transposons]. (99.97/2.90e-28)	
87	58964	59752	+	prohead protease [*Enterococcus* phage EFDG1] prohead protease [*Enterococcus* phage ECP3] Phage protein [*Enterococcus* phage 156]	0.0e+00 1.0e+140 5.0e+140	-	-	COG3740; COG3740; Phage head maturation protease [Mobilome: prophages, transposons]. (99.88/8.10e-21) PF04586.18; Peptidase_S78; Caudovirus prohead serine protease (99.79/3.30e-18) PF14550.7; Peptidase_S78_2; Putative phage serine protease XkdF(98.9/1.60e-08)	prohead protease
88	59752	60771	+	hp	hp	-	-	('-', '-')	hp

89	60894	62315	+	major capsid protein [*Enterococcus* phage EfV12-phi1] major capsid protein [*Enterococcus* phage vB_OCPT_Ben] major capsid protein [*Enterococcus* phage EFDG1]	0.0e+00 0.0e+00 0.0e+00	-	-	PF17236.3; DUF5309; Family of unknown function (DUF5309) (99.89/1.10e-21) d2fsya1; d.183.1.1 (A:104-383) Major capsid protein gp5 {Bacteriophage HK97 [TaxId: 37554]} (98.57/1.40e-06) COG4653; COG4653; Predicted phage phi-C31 gp36 major capsid-like protein [Mobilome: prophages, transposons]. (97.68/1.30e-03)	major capsid protein
90	62413	62664	+	putative lipoprotein [*Listeria* phage LMSP-25] putative lipoprotein [*Listeria* phage LMTA-34] gp87 [*Listeria* virus A511	5.0e-07 1.0e-06 2.0e-06	-	-	('-', '-')	hp

91	62676	63572	+	Phage protein [*Enterococcus* phage 163] structural protein [*Enterococcus* phage PBEF129] gp88 [*Listeria* virus A511]	0.0e+00 0.0e+00 4.0e-135	-	-	PF11436.9; DUF3199; Protein of unknown function (DUF3199) (97.67/6.80e-04) PF05135.14; Phage_connect_1; Phage gp6-like head-tail connector protein (97.23/9.50e-04) d1xn8a_; a.229.1.1 (A:)hp YqbG {*Bacillus subtilis* [TaxId: 1423]} (97.58/1.10e-03)	head completion protein
92	63586	64458	+	Phage protein [*Enterococcus* phage 163] capsid protein [*Enterococcus* phage PBEF129] gp89 [*Listeria* virus A511]	0.0e+00 6.0e-138 3.0e-75	-	-	PF17302.3; DUF5351; Family of unknown function (DUF5351) (85.4/7.10e-01)	hp
93	64451	65074	+	gp90 [*Listeria* virus A511] ORF5 [*Listeria* virus A511] ORF055 [*Staphylococcus* virus Twort]	5.0e-70 5.0e-59 2.0e-46	-	-	('-', '-')	hp

94	65078	65923	+	baseplate hub assembly protein [*Enterococcus* phage PEf771] Phage protein [*Enterococcus* phage 156] gp91 [*Listeria* virus A511]	0.0e+00 1.0e-146 8.0e-76	-	-	('-', '-')	hp
95	65923	66162	+	Phage protein [*Enterococcus* phage 163]	3.0e-46	-	-	('-', '-')	hp
96	66166	67875	+	major tail sheath protein [*Enterococcus* phage EFP01] Phage tail sheath [*Enterococcus* phage 163] Phage major tail sheath [*Enterococcus* phage 156]	0.0e+00 0.0e+00 0.0e+00	-	-	COG3497; COG3497; Phage tail sheath protein FI [Mobilome: prophages, transposons]. (99.95/5.80e-25) COG4386; COG4386; Mu-like prophage tail sheath protein gpL [Mobilome: prophages, transposons]. (99.96/5.90e-25) PF04984.15; Phage_sheath_1; Phage tail sheath protein subtilisin-like domain (99.05/9.5e-9)	tail sheath protein
97	67941	68363	+	tail tube protein [*Enterococcus* phage EFDG1] tail tube protein [*Enterococcus* phage EF24C]	1.0e-91 1.0e-89	-	-	PF10772.10; DUF2597; Protein of unknown function (DUF2597) (99.83/1.40e-19) d2guja1; b.106.1.3 (A:5-143) Phage-like element PBSX	tail tube protein

				tail tube protein [*Enterococcus* phage ECP3]	1.0e-89			protein XkdM {*Bacillus subtilis* [TaxId: 1423]} (99.65/2.40e-14) PF09393.11; DUF2001; Phage tail tube protein (99.45/1.40e-11) PF06199.12; Phage_tail_2; Phage tail tube protein (96.76/0.11)	
98	68454	69566	+	Phage protein [*Enterococcus* phage 156] ORF018 [*Staphylococcus* virus Twort] unknown [*Staphylococcus* virus Twort]	0.0e+00 1.0e-36 7.0e-34	-	-	d1vsra_; c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {*Escherichia coli* [TaxId: 562]} (98.51/1.40e-06) PF14311.7; DUF4379; Probable Zinc-ribbon domain (97.98/4.60e-06) COG3727; Vsr; G:T-mismatch repair DNA endonuclease, very short patch repair protein [Replication, recombination and repair]. (98.29/8.70e-06)	VSR endonuclease
99	69823	70296	+	hp EFP01_076 [*Enterococcus* phage EFP01] tail tape measure protein [*Enterococcus* phage EFDG1]	7.0e-105 2.0e-101 1.0e-31	-	-	PF10109.10; Phage_TAC_7; Phage tail assembly chaperone proteins, E, or 41 or 14 (39.22/130)	putative tail assembly chaperone protein

				tail assembly chaperone [*Bacillus* phage Chotacabras]					
100	70379	70945	+	Phage protein [*Enterococcus* phage 163] putative RNA polymerase [*Enterococcus* phage EFP01] tail assembly chaperone protein [*Bacillus* phage Bobb]	5.0e-121 3.0e-119 3.0e-14	-	-	('-', '-')	hp
101	70995	74642	+	tail length tape-measure protein [*Enterococcus* phage vB_OCPT_Ben] tail length tape-measure protein [*Enterococcus* phage EFDG1] tail length tape-measure protein [*Enterococcus* phage EfV12-phi1]	0.0e+00 0.0e+00 0.0e+00	LT_TF-like (988-1117) SLT (989-1179) Smc (18-281)	9.91e-30 2.36e-11 6.23e-09	COG5283; COG5283; Phage-related tail protein [Mobilome: prophages, transposons]. (99.65/2.40e-10) COG5280; YqbO; Phage-related minor tail protein [Mobilome: prophages, transposons]. (99.19/5.00e-06) COG3941 HI1514; Phage tail tape-measure protein, controls tail length [Mobilome: prophages, transposons]. (98.82/3e-04)	lytic transglycosylase-like domain containing tail tape measure protein
102	74692	77211	+	repressor protein C2 [*Enterococcus* phage EFP01]	0.0e+00	NLPC_P60 (706-835)	1.52e-13	COG0791; Spr; Cell wall-associated hydrolase, NlpC family [Cell	peptidoglycan hydrolase domain containing

				Secretory antigen SsaA-like protein [*Enterococcus* phage 163] putative tail lysin [*Enterococcus* phage EfsSzw-1]	0.0e+00 0.0e+00	PRK13914 (705-807)	3.15e-05	wall/membrane/envelope biogenesis]. (99.21/1.00e-10) COG4379 COG4379; Mu-like prophage tail protein gpP [Mobilome: prophages, transposons]. (98.35/4.3e-04) PF05382.14; Amidase_5; Bacteriophage peptidoglycan hydrolase (97.61/1e-03) PF14594.7; Sipho_Gp37; Siphovirus ReqiPepy6 Gp37-like protein (97.51/7.7e-02)	baseplate hub protein
103	77311	84240	+	Glycerophosphoryl diester phosphodiesterase (EC, phage variant [*Enterococcus* phage 163] glycerophosphoryl diester phosphodiesterase [*Enterococcus* phage EFDG1] structural component of the tail fiber [*Enterococcus* phage PEf771] putative tail fiber [*Enterococcus* phage EFP01]	0.0e+00 0.0e+00 0.0e+00 0.0e+00	-	-	d1k28a1 b.40.8.1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain {Bacteriophage T4 [TaxId: 10665]} (88.38/1.1) PF18352.2; Gp138_N; Phage protein Gp138 N-terminal domain (87.26/0.8) COG4384 gp45; Mu-like prophage protein gp45 [Mobilome: prophages, transposons]. (81.16/5.3) PF04717.13; Phage_base_V; Type VI secretion system/phage-	putative central tail fiber

								baseplate injector OB domain (58.03/50)	
104	84333	86744	+	Phage capsid and scaffold [*Enterococcus* phage 163] capsid and scaffold protein [*Enterococcus* phage vB_OCPT_Ben] capsid and scaffold protein [*Enterococcus* phage EFDG1] minor tail protein [*Bacillus* phage 035JT001] tail fiber protein [*Bacillus* phage Beyonphe]	0.0e+00 0.0e+00 0.0e+00 1.0e-86 1.0e-62	DUF859 (13-696)	1.45e-27	PF05895.13; DUF859; Siphovirus protein of unknown function (DUF859) (100.0/1.30e-67)	DUF859 containing protein
105	86741	87484	+	Phage protein [*Enterococcus* phage 156]	6.0e-33	-	-	PF14301.7; DUF4376; Domain of unknown function (DUF4376) (99.15/2.70e-09)	hp
106	87505	87651	+	Phage protein [*Enterococcus* phage 163]	5.0e-27	-	-	PF12512.9; DUF3717; Protein of unknown function (DUF3717) (92.66/5.30e-01)	hp
107	87806	88507	+	Phage protein [*Enterococcus* phage 163] gp100 [*Listeria* virus A511] ORF041 [*Staphylococcus* virus Twort]	7.0e-173 1.0e-79 3.0e-46	-	-	COG3499; COG3499; Phage protein U [Mobilome: prophages, transposons]. (97.11/4.20e-03) PF06995.12; Phage_P2_GpU; Phage P2 GpU (94.64/0.89)	tail tube terminator protein

108	88507	89043	+	Phage protein [*Enterococcus* phage 156] gp101 [*Listeria* virus A511] structural protein [*Staphylococcus* phage pSco-10]	4.0e-110 2.0e-52 5.0e-30	-	-	('-', '-')	hp
109	89030	89734	+	Phage baseplate assembly protein [*Enterococcus* phage 163] putative baseplate [*Enterococcus* phage EfsSzw-1] putative baseplate [*Enterococcus* phage EFP01] baseplate wedge subunit [*Staphylococcus* phage Stab23]	6.0e-174 1.0e-172 4.0e-172 3.0e-71	-	-	PF10934.9; DUF2634; Protein of unknown function (DUF2634) (99.61/2.20e-14) COG3628; COG3628; Phage baseplate assembly protein W [Mobilome: prophages, transposons]. (99.48/3.70e-12) d2ia7a1; d.373.1.1 (A:23-133) Uncharacterized protein GSU0986 {*Geobacter sulfurreducens* [TaxId: 35554]} (99.46/4.30e-12) PF11246.9; Phage_gp53; Base plate wedge protein 53 (26.31/190)	baseplate assembly protein
110	89749	90801	+	Phage baseplate [*Enterococcus* phage 163]	0.0e+00 0.0e+00	Baseplate_J (55-311) JayE(118-350)	2.41e-16 5.33e-05	COG3299; JayE; Uncharacterized phage protein gp47/JayE [Mobilome: prophages, transposons]. (100.0/4.70e-34)	baseplate assembly protein

				putative baseplate J protein [*Enterococcus* phage EFP01] baseplate protein [*Enterococcus* phage EfV12-phi1]	0.0e+00			COG3948; COG3948; Phage-related baseplate assembly protein [Mobilome: prophages, transposons]. (99.97/5.50e-30) PF04865.15; Baseplate_J; Baseplate J-like protein (99.97/1.00e-28)	
111	90813	95441	+	Phage protein [*Enterococcus* phage 163] Phage protein [*Enterococcus* phage 156] gp104 [*Listeria* virus A511] putative tail fiber protein complex [*Staphylococcus* phage KSAP7] tail morphogenetic protein [*Staphylococcus* phage pSco-10] minor tail protein [*Staphylococcus* phage Metroid]	0.0e+00 2.0e-154 2.0e-81 5.0e-71 9.0e-71 1.0e-70	Big_2 (1130-1202) YjdB (1130-1206)	2.42e-11 2.28e-09	PF11041.9; DUF2612; Protein of unknown function (DUF2612) (99.14/4.70e-10) PF10076.10; DUF2313; Uncharacterised protein conserved in bacteria (DUF2313) (98.99/5.90e-09) PF09684.11; Tail_P2_I; Phage tail protein (Tail_P2_I) (97.74/1.60e-04) COG4385 gpI; Bacteriophage P2-related tail formation protein [Mobilome: prophages, transposons]. (97.56/7.7e-04) COG3299 JayE; Uncharacterized phage protein gp47/JayE [Mobilome: prophages, transposons]. (96.76/8.6e-03)	baseplate assembly protein

								5IW9_B; Baseplate wedge protein gp25; contractile sheath, baseplate, wedge, sheath; HET: MSE; 2.47A {*Enterobacteria* phage T4}; (99.57/1.40e-13)	
112	95555	96100	+	Phage protein [*Enterococcus* phage 163] structural protein [*Enterococcus* phage PEf771] structural protein [*Enterococcus* phage EFP01]	7.0e-134 2.0e-132 4.0e-131	-	-	PF09215.11; Phage-Gp8; Bacteriophage T4, Gp8(99.86/7.10e-21) COG5301; COG5301; Phage-related tail fibre protein [Mobilome: prophages, transposons]. (98.27/3.50e-05) d1n7za_; b.127.1.1 (A:) Baseplate structural protein gp8 {Bacteriophage T4 [TaxId: 10665]} (97.86/1.20e-03) 6HHK_A; Gp105; bacteriophage baseplate protein, VIRAL PROTEIN; HET: MSE; 2.38A {*Listeria* phage A511}; (94.97/2.20e-02)	baseplate assembly protein
113	96117	97163	+	Phage protein [*Enterococcus* phage 156] group I intron protein [*Bacillus* phage Bobb]	1.0e-34 6.0e-17	-	-	PF01710.17; HTH_Tnp_IS630; Transposase (98.37/4.90e-06) d1vsra_; c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {*Escherichia coli* [TaxId: 562]} (98.39/5.60e-06)	VSR endonuclease

				DNA-binding protein [*Bacillus* phage Moonbeam] homing endonuclease [*Staphylococcus* phage pSco-10]	6.0e-14 9.0e-11			PF04936.13; DUF658; Protein of unknown function (DUF658) (97.82/1.90e-05) COG2852 YcjD; Very-short-patch-repair endonuclease [Replication, recombination and repair]. (97.73/4.9e-05)	
114	97166	100624	+	virulence-associated protein [*Enterococcus* phage vB_OCPT_Ben] virulence-associated protein [*Enterococcus* phage EfV12-phi1] putative adsorption associated tail protein [*Enterococcus* phage EFP01]	0.0e+00 0.0e+00 0.0e+00	DUF4815 (13-613)	0e+00	PF16075.6; DUF4815; Domain of unknown function (DUF4815) (100.0/4.80e-110)	putative adsorption associated tail protein
115	100705	101667	+	HNH endonuclease [*Staphylococcus* phage vB_SepS_SEP9] putative HNH endonuclease [Acinetobacter phage YMC-13-01-C62]	1.0e-49 2.0e-41 9.0e-40	-	-	PF07768.12; PVL_ORF50; PVL ORF-50-like family (98.15/6.70e-06) PF07768.12; PVL_ORF50; PVL ORF-50-like family (97.52/3.10e-04) PF04936.13; DUF658; Protein of unknown function (DUF658) (95.84/9.50e-02)	PVL ORF-50-like family protein

				putative HNH homing endonuclease [*Bacillus* phage Izhevsk]					
116	101745	101951	+	gp107 [*Listeria* virus A511] gp17.1 [*Bacillus* virus SPO1]	1.0e-06 5.0e-03	-	-	KOG4098; Molecular chaperone Prefoldin, subunit 2 [Posttranslational modification, protein turnover, chaperones] (94.07/6.50e-01)	hp
117	102144	105191	+	putative helicase [*Enterococcus* phage EFP01] DNA helicase [*Enterococcus* phage PBEF129] DNA helicase, phage-associated [*Enterococcus* phage 156]	0.0e+00 0.0e+00 0.0e+00	uvsW (745-1012) Intein_splicing (179-576) Hop (210-576) Helicase_C 872-967	6.66e-31 1.40e-22 3.25e-20 9.18e-13	KOG0339; ATP-dependent RNA helicase [RNA processing and modification] (99.93/8.40e-26) KOG0338; ATP-dependent RNA helicase [RNA processing and modification] (99.93/1.10e-25) KOG0346; RNA helicase [RNA processing and modification] (99.94/1.70e-25) 2OCA_A; ATP-dependent DNA helicase uvsW (E.C.3.6.1.8); ATP-dependent helicase, T4-bacteriophage, Recombination, HYDROLASE; 2.7A {*Enterobacteria* phage T4}(99.98/2.00e-30)	uvsW-like ATP-dependent DNA helicase

118	105207	106850	+	putative transcriptional regulator [*Enterococcus* phage EFP01] putative transcriptional regulator [*Enterococcus* phage EfsSzw-1] putative transcriptional regulator [*Enterococcus* phage phiEF17H]	0.0e+00 0.0e+00 0.0e+00	HTH_36 (27-71)	5.32e-04	d2gaua1; a.4.5.4 (A:152-232) Transcriptional regulator PG0396, C-terminal domain {*Porphyromonas gingivalis* [TaxId: 837]} (97.81/1.50e-04) d1ub9a_; a.4.5.28 (A:)hp PH1061 {*Pyrococcus horikoshii* [TaxId: 53953]} (97.56/1.90e-04) d3e5ua1; a.4.5.4 (A:148-227) Chlorophenol reduction protein CprK {*Desulfitobacterium hafniense* [TaxId: 49338]} (97.68/2.20e-04)	putative transcriptional regulator
119	106864	108336	+	DNA helicase [*Enterococcus* phage EfV12-phi1] DNA helicase [*Enterococcus* phage vB_OCPT_Ben] helicase/primase [*Enterococcus* phage PEf771] helicase DnaB-like [*Enterococcus* phage EFDG1]	0.0e+00 0.0e+00 0.0e+00 0.0e+00	41 (70-480) phage_DnaB (157-380) DnaB_C (190-380)	5.11e-16 5.46e-12 1.83e-10	COG0305; DnaB; Replicative DNA helicase [Replication, recombination and repair]. (100.0/9.30e-32) d1cr1a_; c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7 [TaxId: 10760]} (99.92/3.00e-22) PF03796.16; DnaB_C; DnaB-like helicase C terminal domain (99.89/2.80e-20)	DnaB-like replicative helicase

120	108336	109376	+	putative exonuclease [*Enterococcus* phage EFP01] recombination exonuclease [*Enterococcus* phage EfV12-phi1] Phage recombination exonuclease [*Enterococcus* phage 163]	0.0e+00 0.0e+00 0.0e+00	MPP_Mre11_N (8-223) SbcD (1-313) sbcd (1-231)	7.93e-24 5.65e-21 3.30e-14	COG0420; SbcD; DNA repair exonuclease SbcCD nuclease subunit [Replication, recombination and repair]. (99.95/9.20e-25) d3dsda_; d.159.1.4 (A:) Mre11 {*Pyrococcus furiosus* [TaxId: 2261]} (99.94/2.70e-24) KOG2310; DNA repair exonuclease MRE11 [Replication, recombination and repair] (99.9/1.10e-21)	DNA repair exonuclease SbcCD-like nuclease subunit
121	109495	111387	+	Phage recombination related exonuclease (EC [*Enterococcus* phage 163] putative exonuclease [*Enterococcus* phage EFP01] recombination endonuclease [*Enterococcus* phage EFDG1]	0.0e+00 0.0e+00 0.0e+00	46 (1-619) SbcC (3-424) sbcc (42-459)	2.92e-45 4.02e-25 7.53e-21	COG0419; SbcC; DNA repair exonuclease SbcCD ATPase subunit [Replication, recombination and repair]. (100.0/1.20e-29) COG5293; YydB; Uncharacterized protein YydD, contains DUF2326 domain [Function unknown]. (100.0/4.30e-28) KOG0962; DNA repair protein RAD50, ABC-type ATPase/SMC superfamily [Replication, recombination and repair] (100.0/4.40e-28)	DNA repair exonuclease SbcCD-like ATPase subunit

122	111401	112060	+	Phage protein [*Enterococcus* phage 163] putative repressor [*Enterococcus* phage EFP01] putative repressor [*Enterococcus* phage PBEF129]	1.0e-154 5.0e-151 4.0e-81	-	-	('-', '-')	hp
123	112064	113119	+	Phage DNA primase/helicase [*Enterococcus* phage 163] putative primase [*Enterococcus* phage EfsSzw-1] putative primase [*Enterococcus* phage EFP01]	0.0e+00 0.0e+00 0.0e+00	dnaG (50-325) dnaG (46-293) DnaG (50-328)	3.42e-17 4.39e-14 1.75e-12	COG0358; DnaG; DNA primase (bacterial type) [Replication, recombination and repair]. (100.0/8.90e-34) d1dd9a_; e.13.1.1 (A:) DNA primase DnaG catalytic core {*Escherichia coli* [TaxId: 562]} (99.93/3.00e-24) COG4643; COG4643; Uncharacterized domain associated with phage/plasmid primase [Mobilome: prophages, transposons]. (99.9/1.30e-22) 2AU3_A; DNA primase (E.C.2.7.7.-); Zinc Ribbon, TOPRIM, RNA POLYMERASE; 2.0A {*Aquifex aeolicus*}(99.97/3.10e-29)	DNA primase

124	113129	114010	+	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC [*Enterococcus* phage 163] deoxyuridine 5'-triphosphate nucleotidohydrolase [*Enterococcus* phage vB_OCPT_Ben] deoxyuridine 5'-triphosphate nucleotidohydrolase [*Enterococcus* phage EFDG1]	0.0e+00 0.0e+00 0.0e+00	Dut (83-292) trimeric_dUTPase (105-176)	2.68e-14 1.11e-06	COG0756; Dut; dUTPase [Nucleotide transport and metabolism, Defense mechanisms]. (99.93/1.10e-24) KOG3370; dUTPase [Nucleotide transport and metabolism] (99.93/1.50e-24) d1sixa1; b.85.4.1 (A:1-144) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {*Mycobacterium tuberculosis*, rv2697c [TaxId: 1773]} (99.93/3.70e-24)	dUTPase
125	114010	114246	+	putative dUTPase [*Enterococcus* phage vB_EfaH_EF1TV] putative dUTPase [*Enterococcus* phage EF24C] putative dUTPase [*Enterococcus* phage ECP3]	1.0e-07 5.0e-07 9.0e-07	-	-	('-', '-')	hp
126	114250	114561	+	Phage protein [*Enterococcus* phage 156]	6.0e-04	-	-	('-', '-')	hp
127	114548	114859	+	putative phosphotransferase/anion		-	-	d1nh2d1; a.32.1.1 (D:5-54) Small chain TOA2, N-terminal	hp

				transport protein [*Enterococcus* phage EFP01] putative phosphotransferase/anion transport protein [*Enterococcus* phage EF24C] putative phosphotransferase/anion transport protein [*Enterococcus* phage vB_EfaH_EF1TV]	4.0e-67 7.0e-12 1.0e-11			domain {Baker's yeast (*Saccharomyces cerevisiae*) [TaxId: 4932]} (84.88/3.00e+00)	
128	114852	115220	+	Phage protein (ACLAME 1549) [*Enterococcus* phage 163] gp121 [*Listeria* virus A511]	2.0e-82 2.0e-13	PHA02277 (11-117)	6.24e-05	d2elca1; a.46.2.1 (A:1-65) Anthranilate phosphoribosyltransferase (TrpD) {*Thermus thermophilus* [TaxId: 274]} (96.46/3.30e-02) d4eada1; a.46.2.1 (A:2-70) Thymidine phosphorylase {*Escherichia coli* [TaxId: 562]} (96.43/3.60e-02) d1k8ea1; a.46.2.1 (A:1-70) Anthranilate phosphoribosyltransferase (TrpD) {*Sulfolobus solfataricus* [TaxId: 2287]} (96.33/4.10e-02)	hp

129	115228	115800	+	hp	hp	-	-	('-', '-')	hp
130	115793	116770	+	VSR homing endonuclease [*Staphylococcus* phage Quidividi] homing endonuclease [*Bacillus* virus PBS1] group I intron-associated VSR homing endonuclease [*Staphylococcus* phage Terranova]	8.0e-47 2.0e-45 8.0e-44	DUF2726 (238-310)	1.13e-05	d1vsra_; c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {*Escherichia coli* [TaxId: 562]} (98.8/4.70e-08) COG3727; Vsr; G:T-mismatch repair DNA endonuclease, very short patch repair protein [Replication, recombination and repair]. (98.67/4.20e-07) COG2852; YcjD; Very-short-patch-repair endonuclease [Replication, recombination and repair]. (98.35/5.10e-06)	VSR endonuclease
131	116861	117445	+	putative resolvase [*Enterococcus* phage EFP01] Phage protein [*Enterococcus* phage 163] putative resolvase [*Enterococcus* phage ECP3]	5.0e-143 2.0e-138 3.0e-100	-	-	d1ob8a_; c.52.1.18 (A:) Holliday-junction resolvase SSO1176 {*Sulfolobus solfataricus* [TaxId: 2287]} (98.36/3.50e-06) COG1591; COG1591; Holliday junction resolvase, archaeal type [Replication, recombination and repair]. (97.81/1.80e-04) d1gefa_; c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {*Pyrococcus furiosus* [TaxId: 2261]} (97.62/8.10e-04)	Holliday-junction resolvase

132	117445	117810	+	hp	hp	-	-	('-', '-')	hp
133	117833	117970	+	hp	hp	-	-	('-', '-')	hp
134	117967	118389	+	Phage protein [*Enterococcus* phage 156] ORF050 [*Staphylococcus* virus 3a] ORF060 [*Staphylococcus* virus 96]	6.0e-32 4.0e-15 4.0e-15	DUF3310 (7-66)	2.83e-23	PF11753.9; DUF3310; Protein of unknwon function (DUF3310) (99.78/5.10e-19)	DUF3310 containing protein
135	118495	119289	+	Phage protein [*Enterococcus* phage 156] gp135 [*Listeria* virus A511] synaptonemal complex 1 (SCP-1) domain containing protein [*Listeria* phage LMTA-148]	4.0e-148 1.0e-89 2.0e-89	-	-	cd17835; Radical_SAM_spore_photoproduct_lyase; spore photoproduct lyase. Radical SAM superfamily. Enzymes of this family generate radicals by combining a 4Fe-4S cluster and S-adenosylmethionine (SAM) in close proximity. (91.55/6.10e+00)	hp
136	119282	119593	+	integration host factor [*Enterococcus* phage EFDG1] putative integration host factor [*Enterococcus* phage EfsSzw-1]	3.0e-71 1.0e-70 4.0e-59	Bac_DNA_binding(8-95) IHF (9-93)	9.00e-14 1.82e-06	d1mula_; a.55.1.1 (A:) HU protein {*Escherichia coli* [TaxId: 562]} (99.91/5.40e-23) d1p71a_; a.55.1.1 (A:) HU protein {Anabaena sp. [TaxId: 1167]} (99.91/1.20e-22)	integration host factor

				putative integration host factor [*Enterococcus* phage EF24C]				d1owfa_ a.55.1.1 (A:) Integration host factor alpha subunit (IHFA) {*Escherichia coli* [TaxId: 562]} (99.91/3.7e-22)	
137	119674	120516	+	DNA polymerase I [*Enterococcus* phage EfV12-phi1] putative DNA polymerase [*Enterococcus* phage EfsSzw-1] DNA polymerase I [*Enterococcus* phage PEf771]	0.0e+00 0.0e+00 0.0e+00	DNA_polA_I_Ecoli_like_exo (207-280) PRK05755 (167-280) UDG-F4_TTUDGA_SPO1dp_like (97-169)	1.31e-09 5.32e-08 2.61e-04	d1vk2a_; c.18.1.2 (A:) Thermophilic uracil-DNA glycosylase {*Thermotoga maritima* [TaxId: 2336]} (99.86/2.70e-20) d1ui0a_; c.18.1.2 (A:) Thermophilic uracil-DNA glycosylase {*Thermus thermophilus* [TaxId: 274]} (99.84/7.30e-20) COG1573; Udg4; Uracil-DNA glycosylase [Replication, recombination and repair]. (99.83/1.90e-19) COG0749 PolA; DNA polymerase I - 3'-5' exonuclease and polymerase domains [Replication, recombination and repair]. (97.07/0 8e-03)	3'-5' exonuclease and polymerase domains containing uracil DNA glycosylase family 4
138	120687	121163	+	gp86 [*Bacillus* phage W.Ph.]	5.0e-39	-	-	d1e7la2; d.4.1.5 (A:1-103) Recombination endonuclease VII, N-terminal domain	recombination endonuclease

				homing endonuclease [*Bacillus* phage Moonbeam] baseplate wedge protein gp25 [*Cronobacter* phage vB_CsaM_GAP31]	2.0e-28 2.0e-18			{Bacteriophage T4 [TaxId: 10665]} (98.26/1.70e-06) d4ogca2; d.4.1.8 (A:513-673) CRISPR-associated endonuclease Cas9/Csn1, HNH domain {*Actinomyces naeslundii* [TaxId: 1115803]} (98.05/4.30e-06) PF09665.11; RE_Alw26IDE; Type II restriction endonuclease (RE_Alw26IDE) (97.98/4.30e-06) PF05766.13; NinG; Bacteriophage Lambda NinG protein (97.84/1.4e-04)	
139	121242	123431	+	DNA polymerase I (EC, phage-associated [*Enterococcus* phage 163] DNA polymerase I [*Enterococcus* phage EfV12-phi1] DNA polymerase I [*Enterococcus* phage PEf771]	0.0e+00 0.0e+00 0.0e+00	DNA_pol_A (347-664) DNA_pol_A_pol_I_C (261-666) PRK05755 (137-670)	1.11e-104 2.49e-97 7.04e-83	COG0749; PolA; DNA polymerase I - 3'-5' exonuclease and polymerase domains [Replication, recombination and repair]. (100.0/2.50e-69) d1kfsa2; e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {*Escherichia coli* [TaxId: 562]} (100.0/4.90e-64) d3py8a2; e.8.1.1 (A:423-832) DNA polymerase I (Klenow	3'-5' exonuclease and polymerase domains containing DNA polymerase I

								fragment) {*Thermus aquaticus* [TaxId: 271]} (100.0/3.20e-63)	
140	123555	124085	+	gp139 [*Listeria* virus A511] ssDNA binding protein [*Bacillus* phage Chotacabras] ORF077 [*Staphylococcus* virus Twort]	1.0e-42 3.0e-35 6.0e-26	-	-	PF11056.9; UvsY; Recombination, repair and ssDNA binding protein UvsY (99.78/2.10e-17)	UvsY-like protein
141	124157	125473	+	Phage protein [*Enterococcus* phage 163] Phage protein [*Enterococcus* phage 156] gp71 [*Listeria* virus P100]	0.0e+00 3.0e-140 1.0e-45	PRK14971 (299-425)	4.82e-05	PF08804.11; gp32; gp32 DNA binding protein like (99.95/1.40e-26)	Gp32-like ssDNA binding protein
142	125554	126801	+	Phage recombinase [*Enterococcus* phage 163] recombinase A [*Enterococcus* phage PEf771] recombinase [*Enterococcus* phage EfV12-phi1]	0.0e+00 0.0e+00 0.0e+00	recA (38-358) RecA (45-290) tigrfam_recA (38-323)	1.79e-41 2.18e-35 2.46e-33	cd00983; recA; RecA is a bacterial enzyme which has roles in homologous recombination, DNA repair, and the induction of the SOS response. (100.0/3.80e-34) PF00154.22; RecA; recA bacterial DNA recombination protein (99.96/2.40e-26) d1u94a1; c.37.1.11 (A:6-268) RecA protein, ATPase-domain	recA protein

								{*Escherichia coli* [TaxId: 562]} (99.95/3.60e-25)	
143	126844	127218	+	Phage protein [*Enterococcus* phage 163] Phage protein [*Enterococcus* phage 156] gp142 [*Listeria* virus A511]	7.0e-90 6.0e-54 6.0e-19	-	-	PF06257.12; VEG; Biofilm formation stimulator VEG (94.48/5.00e-01)	hp
144	127211	127828	+	putative RNA polymerase sigma factor [*Enterococcus* phage EFP01] putative sigma factor [*Enterococcus* phage EfsSzw-1] putative sigma factor [*Enterococcus* phage ECP3]	3.0e-145 1.0e-141 2.0e-116	-	-	COG1595; RpoE; DNA-directed RNA polymerase specialized sigma subunit, sigma24 family [Transcription]. (99.84/3.80e-19) COG1191; FliA; DNA-directed RNA polymerase specialized sigma subunit [Transcription]. (99.85/6.20e-19) PF07638.12; Sigma70_ECF; ECF sigma factor (99.84/6.40e-19)	RNA polymerase sigma factor
145	127896	128174	+	holin-like protein [*Enterococcus* phage PEf771] putative holin [*Enterococcus* phage EfsSzw-1]	3.0e-63 2.0e-62	Holin_SPP1 (13-81)	1.51e-23	PF04688.14; Holin_SPP1; SPP1 phage holin (99.9/6.70e-23) COG5546; COG5546; Uncharacterized membrane protein [Function unknown]. (96.46/4.50e-02)	holin

				putative holin [*Enterococcus* phage EF24C]	9.0e-58			PF04531.14; Phage_holin_1; Bacteriophage holin (95.44/0.19)	
146	128223	129170	+	putative Ig-like protein [*Enterococcus* phage EFP01] major tail protein [*Enterococcus* phage EFDG1] major tail protein [*Enterococcus* phage EfV12-phi1]	0.0e+00 0.0e+00 0.0e+00	YjdB (195-315) PHA02283 (13-146) Big_2 (233-308)	3.16e-19 1.94e-18 6.30e-14	COG5492; YjdB; Uncharacterized conserved protein YjdB, contains Ig-like domain [General function prediction only]. (98.22/1.10e-03) COG5492; YjdB; Uncharacterized conserved protein YjdB, contains Ig-like domain [General function prediction only]. (97.36/9.00e-02)	Ig-like domain containing YjdB-like protein
147	129197	129640	+	putative DNA polymerase [*Enterococcus* phage EFP01] Phage protein [*Enterococcus* phage 163] structural protein [*Enterococcus* phage EfsSzw-1]	4.0e-96 5.0e-96 4.0e-95	PHA02283 (1-135)	2.23e-22	('-', '-')	hp
148	129748	129984	+	Phage protein [*Enterococcus* phage 156]	5.0e-07	-	-	PF10115.10; HlyU; Transcriptional activator HlyU (86.69/6.20e+00)	putative transcriptional activator HlyU

149	129977	130246	+	hp	hp	-	-	PF07852.12; DUF1642; Protein of unknown function (DUF1642) (98.15/8.50e-06)	hp
150	130221	131159	+	Phage protein [*Enterococcus* phage 156] gp147 [*Listeria* virus A511] phosphodiesterase [*Bacillus* phage Kioshi]	1.0e-114 9.0e-54 3.0e-22	-	-	COG2404; NrnB; Oligoribonuclease NrnB or cAMP/cGMP phosphodiesterase, DHH superfamily [Translation, ribosomal structure and biogenesis, Signal transduction mechanisms]. (99.92/1.70e-23) d1ir6a_; c.107.1.2 (A:) Exonuclease RecJ {*Thermus thermophilus* [TaxId: 274]} (99.92/8.50e-23) COG1107; COG1107; Archaea-specific RecJ-like exonuclease, contains DnaJ-type Zn finger domain [Replication, recombination and repair]. (99.91/4.10e-22)	DnaJ-type Zn-binding domain containing RecJ-like exonuclease
151	131217	132500	+	Phage protein [*Enterococcus* phage 163] metallophosphoesterase domain-containing protein [*Enterococcus* phage PEf771]	0.0e+00 0.0e+00	MPP_Mre11_N (168-391)	2.77e-05	d2a22a1; d.159.1.7 (A:4-196) MPP_DNA_pol_II_small_archeal_C; archeal DNA polymerase II, small subunit, C-terminal metallophosphatase domain. The small subunit of the archeal DNA polymerase II contains a C-terminal metallophosphatase domain. (99.57/7.90e-14)	metallophosphatase domain containing protein

				putative DNA repair exonuclease [*Enterococcus* phage EFP01]	0.0e+00			cd00144 MPP_PPP_family; phosphoprotein phosphatases of the metallophosphatase superfamily, metallophosphatase domain. (99.33/2.8e-11) cd00840 MPP_Mre11_N; Mre11 nuclease, N-terminal metallophosphatase domain. Mre11 (also known as SbcD in *Escherichia coli*) is a subunit of the MRX protein complex. (99.51/3.1e-13)	
152	132513	132881	+	gp149 [*Listeria* virus A511] gp81 [*Listeria* virus P100]	5.0e-07 5.0e-07	-	-	('-', '-')	hp
153	132926	133570	+	Phage protein [*Enterococcus* phage 163] gp150 [*Listeria* virus A511] gp118 [*Bacillus* phage W.Ph.]	1.0e-157 3.0e-23 1.0e-12	-	-	('-', '-')	hp
154	133567	134307	+	gp152 [*Listeria* virus A511] nuclease [*Bacillus* phage Chotacabras]	8.0e-100 3.0e-67	-	-	PF06319.13; MmcB-like; DNA repair protein MmcB-like (99.77/2.30e-17) d4qbna_; c.52.1.35 (A:) stNUC {*Salmonella* phage SETP3	MmcB-like protein

				gp124 [*Bacillus* phage W.Ph.]	3.0e-60			[TaxId: 424944]} (96.79/2.90e-02) COG1637 NucS; Endonuclease NucS, RecB family [Replication, recombination and repair]. (96.51/7.2e-02)	
155	134300	134803	+	Phage protein [*Enterococcus* phage 156] gp153 [*Listeria* virus A511] gp130 [*Bacillus* phage W.Ph.]	6.0e-61 4.0e-38 6.0e-16	-	-	('-', '-')	hp
156	134814	135680	+	DNA maturase A [*Enterococcus* phage EFP01] Phage protein [*Enterococcus* phage 156] phage protein [*Staphylococcus* phage MR003]	0.0e+00 2.0e-91 7.0e-04	-	-	('-', '-')	hp
157	135792	136340	+	hp	hp	-	-	('-', '-')	hp
158	136353	137201	+	Thioredoxin, phage-associated [*Enterococcus* phage 163]	0.0e+00	-	-	PF10127.10; RlaP; RNA repair pathway DNA polymerase beta family (99.88/6.10e-22)	nucleotidyltransferase

				thioredoxin [*Enterococcus* phage vB_OCPT_Ben] thioredoxin [*Enterococcus* phage EFDG1]	0.0e+00 0.0e+00			COG3541; YcgL; Predicted nucleotidyltransferase [General function prediction only]. (99.75/3.70e-17) d1knya2; d.218.1.1 (A:1-125) Kanamycin nucleotidyltransferase (KNTase), N-terminal domain {*Staphylococcus aureus* [TaxId: 1280]} (95.77/5.10e-02)	
159	137201	138928	+	PcfJ-like protein [*Enterococcus* phage PEf771] Phage protein [*Enterococcus* phage 156] putative PcfJ protein [*Bacillus* phage phiAGATE]	0.0e+00 2.0e-115 2.0e-33	PcfJ (412-558)	2.48e-27	PF14284.7; PcfJ; PcfJ-like protein (99.94/1.60e-25)	PcfJ-like protein
160	139203	139898	+	gp165 [*Listeria* virus A511] phage protein [*Staphylococcus* phage phiSA039] ORF048 [*Staphylococcus* virus Twort]	1.0e-76 2.0e-70 1.0e-68	-	-	PF11985.9; DUF3486; Protein of unknown function (DUF3486) (99.56/2.50e-13) PF17273.3; DUF5338; Family of unknown function (DUF5338) (97.33/1.20e-03) d1iufa1; a.4.1.7 (A:1-75) Ars-binding protein 1, ABP1 {Fission yeast	DUF3486 containing protein

								(*Schizosaccharomyces pombe*) [TaxId: 4896]} (96.74/8.90e-03)	
161	139912	140376	+	Phage protein [*Enterococcus* phage 163] gp166 [*Listeria* virus A511] structural protein [*Lactobacillus* phage 521B]	1.0e-110 2.0e-27 4.0e-17	-	-	PF09629.11; YorP; YorP protein (91.84/7.70e-01)	hp
162	140465	141145	+	hp	hp	-	-	('-', '-')	hp
163	141159	141893	+	hp	hp	-	-	('-', '-')	hp
164	141962	142255	+	hp	hp	-	-	COG5503; RpoEps; DNA-dependent RNA polymerase auxiliary subunit epsilon [Transcription, Defense mechanisms]. (69.09/2.30e+00)	hp
165	142328	144754	+	transposase domain containing protein [*Enterococcus* phage PEf771] Phage protein [*Enterococcus* phage 156] transposase domain-containing protein	0.0e+00 3.0e-23 1.0e-12	-	-	d1rr7a_; a.4.1.14 (A:) Middle operon regulator, Mor {Bacteriophage Mu [TaxId: 10677]} (92.84/5.70e-02)	hp

				[*Staphylococcus* phage Quidividi]					
166	144816	145259	+	minor coat protein [*Enterococcus* phage PEf771] minor coat protein [*Enterococcus* phage EFP01]	6.0e-97 3.0e-91	-	-	('-', '-')	hp
167	145277	145849	+	hp	hp	-	-	('-', '-')	hp
168	146057	146293	+	hp	hp	-	-	PF09925.10; DUF2157; Predicted membrane protein (DUF2157) (94.22/2.60e-01)	hp
169	146355	146603	+	repressor [*Enterococcus* phage EFDG1] putative transcriptional regulator [*Enterococcus* phage EF24C] putative XRE family transcriptional regulator 1 [*Bacillus* phage BSP10]	8.0e-52 6.0e-16 4.0e-07	HTH_XRE (23-77)	1.65e-10	COG5606; COG5606; Predicted DNA-binding protein, XRE-type HTH domain [General function prediction only]. (99.15/2.50e-09) d2icta_; a.35.1.3 (A:) Antitoxin HigA {*Escherichia coli* [TaxId: 562]} (99.13/2.80e-09) d1b0na2; a.35.1.3 (A:1-68) SinR repressor, DNA-binding domain {*Bacillus subtilis* [TaxId: 1423]} (99.06/1.70e-08)	transcriptional regulator
170	146636	147076	+	dnaJ domain protein [*Enterococcus* phage EFP01]	1.0e-91	-	-	d1q1ha_; a.4.5.41 (A:) Transcription factor E/IIe-alpha, N-terminal domain {*Sulfolobus*	transcriptional regulator

				DnaJ domain protein [*Enterococcus* phage PEf771] DnaJ domain protein [*Enterococcus* phage PEf771]	4.0e-49 6.0e-33			*solfataricus* [TaxId: 2287]} (95.09/1.60e-01)	
171	147228	147551	+	hp	hp	-	-	('-', '-')	hp
172	147568	148056	+	hp	hp	Sigma70_r4 (10-52)	5.23e-04	COG2826; Tra8; Transposase and inactivated derivatives, IS30 family [Mobilome: prophages, transposons]. (98.15/2.90e-05) d1tc3c_a.4.1.2 (C:) Transposase tc3a1-65 {Nematode (*Caenorhabditis elegans*) [TaxId: 6239]} (97.59/6.8e-04)	transposase
173	148641	148078	-	HNH endonuclease family protein [*Enterococcus* phage EFRM31] DNA endonuclease I-HmuI [*Lactobacillus* phage BH1] HNH endonuclease [*Lactobacillus* phage J-1]	5.0e-34 1.0e-33 2.0e-33	HNH_3 (65-108) NUMOD4 (3-53)	2.98e-10 9.88e-06	d1u3em1; d.4.1.3 (M:1-105) Intron-encoded homing endonuclease I-HmuI {Bacteriophage SPO1 [TaxId: 10685]} (99.94/2.00e-25) PF13392.7; HNH_3; HNH endonuclease (99.32/2.90e-12) PF05551.12; zf-His_Me_endon; Zinc-binding loop region of	HNH homing endonuclease

								homing endonuclease (99.29/3.90e-11)	
174	148843	149292	+	hp	hp	-	-	('-', '-')	hp
175	149719	149994	+	Phage protein [*Enterococcus* phage 156]	3.0e-11	-	-	PF06569.12; DUF1128; Protein of unknown function (DUF1128) (90.23/5.90e-01)	hp
176	150118	150246	+	hp	hp	-	-	('-', '-')	hp
177	150307	150495	+	hp	hp	-	-	PF13121.7; DUF3976; Domain of unknown function (DUF3976) (90.93/6.90e-01)	hp
178	150582	150875	+	hp	hp	-	-	('-', '-')	hp
179	151010	151249	+	hp	hp	-	-	('-', '-')	hp
180	151337	151591	+	hp	hp	-	-	('-', '-')	hp
181	151608	151985	+	gp24 [*Brochothrix* phage A9]	6.0e-05	-	-	('-', '-')	hp
182	152005	152178	+	Phage protein [*Enterococcus* phage 156]	7.0e-04	-	-	('-', '-')	hp
183	152358	152597	+	gp24 [*Brochothrix* phage A9]	1.0e-13	-	-	('-', '-')	hp
184	152685	153068	+	hp	hp	-	-	('-', '-')	hp
185	153185	153463	+	hp	hp	-	-	PF08954.12; Trimer_CC; Trimerisation motif (82.59/7.00e+00)	hp
186	153550	153963	+	TreP [*Staphylococcus* phage vB_Sau_Clo6]	2.0e-14	-	-	('-', '-')	hp

				TreP [*Staphylococcus* phage Stab22] TreP [*Staphylococcus* phage Stab21]	8.0e-14 8.0e-14				
187	154086	154355	+	hp	hp	-	-	('-', '-')	hp
188	154981	155136	+	Phage protein [*Enterococcus* phage VPE25] Phage protein [*Enterococcus* phage VFW] putative exonuclease [*Enterococcus* phage phiEF17H]	4.0e-05 2.0e-03 3.0e-03	-	-	('-', '-')	hp
189	155187	155453	+	hp	hp	-	-	d1vqqa2; d.175.1.1 (A:139-327) Penicillin binding protein 2a (PBP2A), middle domain {*Staphylococcus aureus* [TaxId: 1280]} (64.56/4.10e+00)	hp
190	155470	155712	+	hp	hp	-	-	PF16112.6; DUF4830; Domain of unknown function (DUF4830) (95.11/1.30e-02)	hp
191	155729	156049	+	hp	hp	-	-	PF03871.15; RNA_pol_Rpb5_N; RNA polymerase Rpb5, N-terminal domain (88.98/2.60e+00)	hp

192	156123	156263	+	hp	hp	-	-	('-', '-')	hp
193	156353	156496	+	gp16 [*Brochothrix* phage A9]	1.0e-10	-	-	PF13035.7; DUF3896; Protein of unknown function (DUF3896) (87.29/2.50e+00)	hp

Table S3. tRNA and tmRNA genes of the *Enterococcus* phage iF6.

ORF№	Start codon	Stop codon	Strand	Product	Anticodon
1	35400	35328	-	tRNA-Gly	tcc
2	36873	36801	-	tRNA-Ala	tgc
3	36952	36878	-	tRNA-Arg	tct
4	37442	37354	-	tRNA-Ser	tga
5	37624	37538	-	tRNA-Ser	gga
6	38416	38069	-	tmRNA	-
7	38733	38648	-	tRNA-Leu	tag
8	38902	38817	-	tRNA-Leu	taa
9	39150	39080	-	tRNA-His	gtg
10	39932	39859	-	tRNA-Ile	gat
11	40157	40086	-	tRNA-Val	tac
12	40461	40389	-	tRNA-Arg	acg
13	40638	40562	-	tRNA-Lys	ttt
14	40846	40771	-	tRNA-Lys	ctt
15	41111	41038	-	tRNA-Thr	tgt
16	41727	41654	-	tRNA-Phe	gaa
17	41922	41850	-	tRNA-Cys	gca
18	42235	42162	-	tRNA-Trp	cca
19	42518	42445	-	tRNA-Met	cat
20	42798	42725	-	tRNA-Glu	ttc
21	42878	42802	-	tRNA-Asp	gtc
22	44040	43967	-	tRNA-Arg	tcg
23	44202	44130	-	tRNA-Asn	gtt

Table S4. *Enterococcus* phage iF6 and the most closely related phages.

Name	Database accession number	Nucleic sequence length (GenBank)	GC-content, %	CDS (protein-coding)	Number of tRNAs/tmRNA *	BLASTn nucleotide identity to iF6, %**	Proteins shared with iF6 ***		Number of proteins shared with the phage by all of the previous phages of the table above
							number	%	
Enterococcus phage iF6	MT909815.1	156,592	37.1	193	23/1	-	-	-	-
Enterococcus phage 163	CAJDKA010000002.1	150,836	37.0	186	21/1	86	159	42.0	159
Enterococcus phage EFP01	NC_047796.1	155,053	37.0	193	7/0	82	146	37.8	140
Enterococcus phage EFDG1	NC_029009.1	147,589	37.2	192	23/1	80	142	36.7	123
Enterococcus phage PEf771	MN241318.1	151,052	37.0	197	22/1	81	147	37.6	117
Enterococcus phage vB_OCPT_Ben	MN027503.1	151,985	37.1	187	24/1	81	135	35.5	110
Enterococcus phage EfV12-phi1	NC_048087.1	152,770	37.0	191	23/1	82	135	35.2	108
Enterococcus phage 156	LR031359.1	141,133	35.8	209	7/0	40	86	21.4	73

* Determined using ARAGORN v1.2.41;
** Determined using BLASTn compared to iF6 phage (multiplying % coverage by % identity);
*** Determined using GET_HOMOLOGUES (COGtriangles algorithm, -t 0 -C 75).

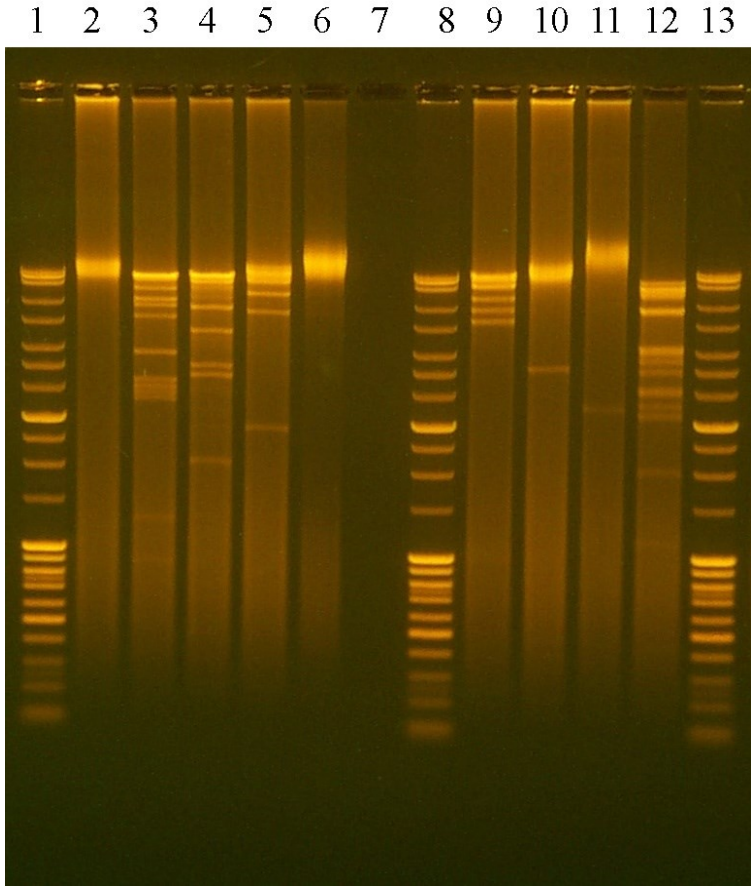


Figure S3. Restriction analysis of iF6 DNA. This is the original gel image used to generate Fig 8 in the main text. Kodak EDAS 290 Gel Documentation System ("Kodak") was used to capture the image. 1, 8 and 13 – molecular weight markers; 6 – intact phage DNA, 7 – the empty slot, 2 – EcoRI, 3 – NsbI, 4 – BlpI, 5 – XhoI, 9 – AfeI, 10 – SalI, 11 – SphI and 12 - KpnI.

Table S5. Primers used to locate the ends of the iF6 genome.

Purpose	Primer name	Primer sequence (5'-3')	№PCR	Template
Determination of the left genome end	RACE-L-iF6_rev1	CATCTAAGTCTTTCAAGTTGTCTAAGTTC	I PCR	Fragment contained the left genome end of iF6 after DNA tailing reaction
	AncherdT16V	GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTTTV		
	RACE-L-iF6_rev2	TTCTTTGTGTGGTCGTGCTC	II PCR	I PCR product
	Anch	GACCACGCGTATCGATGTCGAC		
Determination of the right genome end	RACE-R-iF6_fwd2	ACTACCAAGGGGGCAATACAG	I PCR	Fragment contained the right genome end of iF6 after DNA tailing reaction
	AncherdT16V	GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTTTV		
	RACE-R-iF6_fwd3	GGACAACGTACAGACAATTATACCG	II PCR	I PCR product
	Anch	GACCACGCGTATCGATGTCGAC		

Table S6. Primers used for cloning of the iF6 endolysins.

Target gene	GenBank protein number	Vector for cloning	Primer name	Primer sequence (5'-3')
iF6_82	QNL29441.1	pET33b(+)	if6_gp82_NcoI_for	TATATCCATGGCAGGAGAAGTATTTAGTAGT
			if6_gp82_NotI_rev	TATAGCGGCCGCCAATTTGTGAGTTCCACC
		pHUE	if6_gp82_EcoRI_for	TATAGAATTCATGGCAGGCGAAGT
			if6_gp82_KpnI_rev	TATTGGTACCTTACAATTTGTTAGTTCC
iF6_84	QNL29443.1	pET33b(+)	if6_gp84_NcoI_for	TATATCCATGGGTATGAGTAACATTAACATGGAAACC
			if6_gp84_NotI_rev	TATAGCGGCCGCCTTAAATGTACCCCATGCTTTC
		pHUE	if6_gp84_EcoRI_for	TATAGAATTCATGAGTAACATTAACATGGA
			if6_gp84_KpnI_rev	TATAGGTACCTTACTTAAATGTACCC

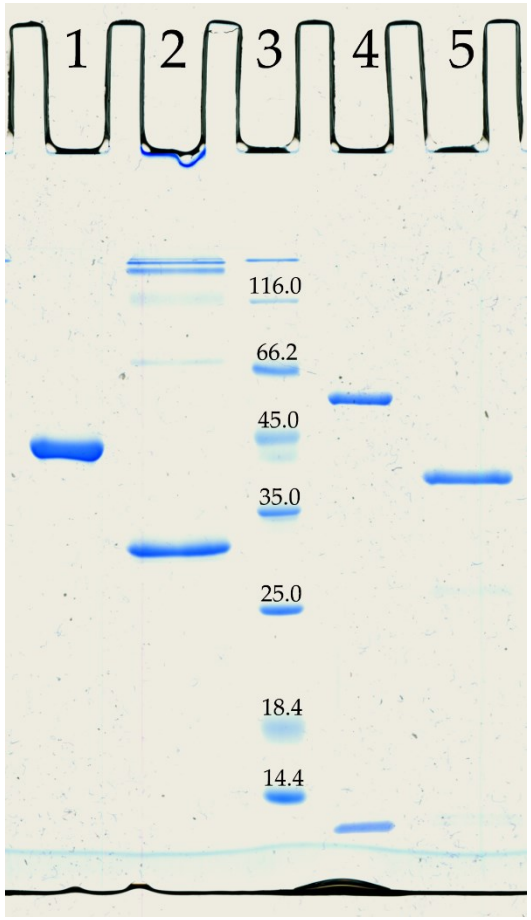


Figure S4. SDS-PAGE analysis of the iF6 phage endolysins. 1 and 2 – purified preparations of Gp82-H (47.6 kDa) and Gp84-H (35.5 kDa), respectively; 3 – Protein marker (Thermo scientific #26610); 4 and 5 – purified preparations of HU-Gp82 (57.4 kDa) and HU-Gp84 (45.5 kDa), respectively. The calculated molecular weights of endolysins shown in brackets. The polyacrylamide (12%) gel was stained with Coomassie Brilliant Blue G-250.