

Microorganisms

Supplementary Data

Identification and Full Genome Analysis of the First Putative Virus of Sea Buckthorn (*Hippophae rhamnoides* L.)

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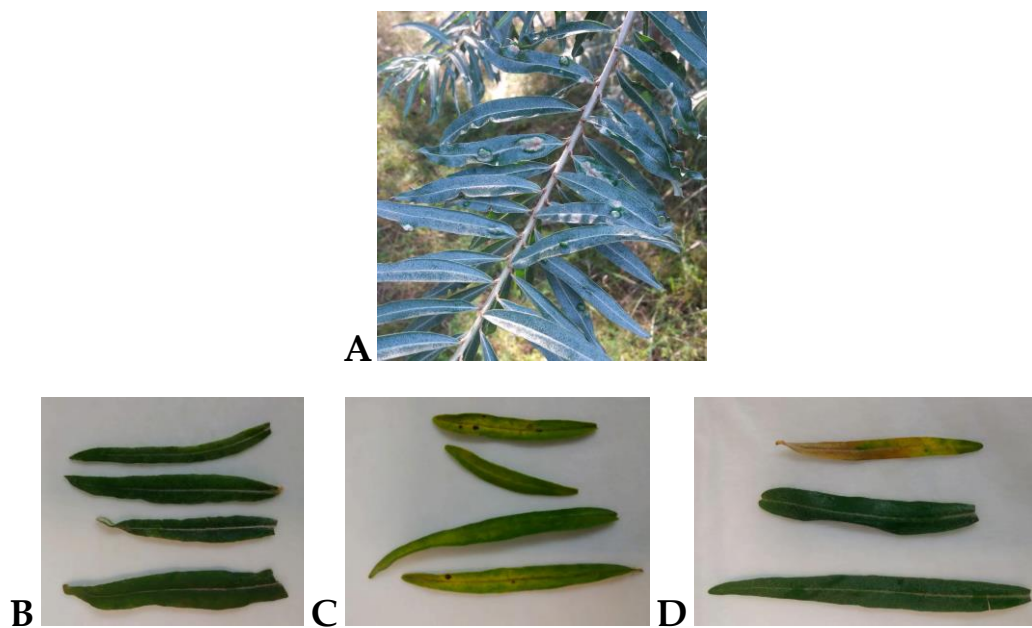
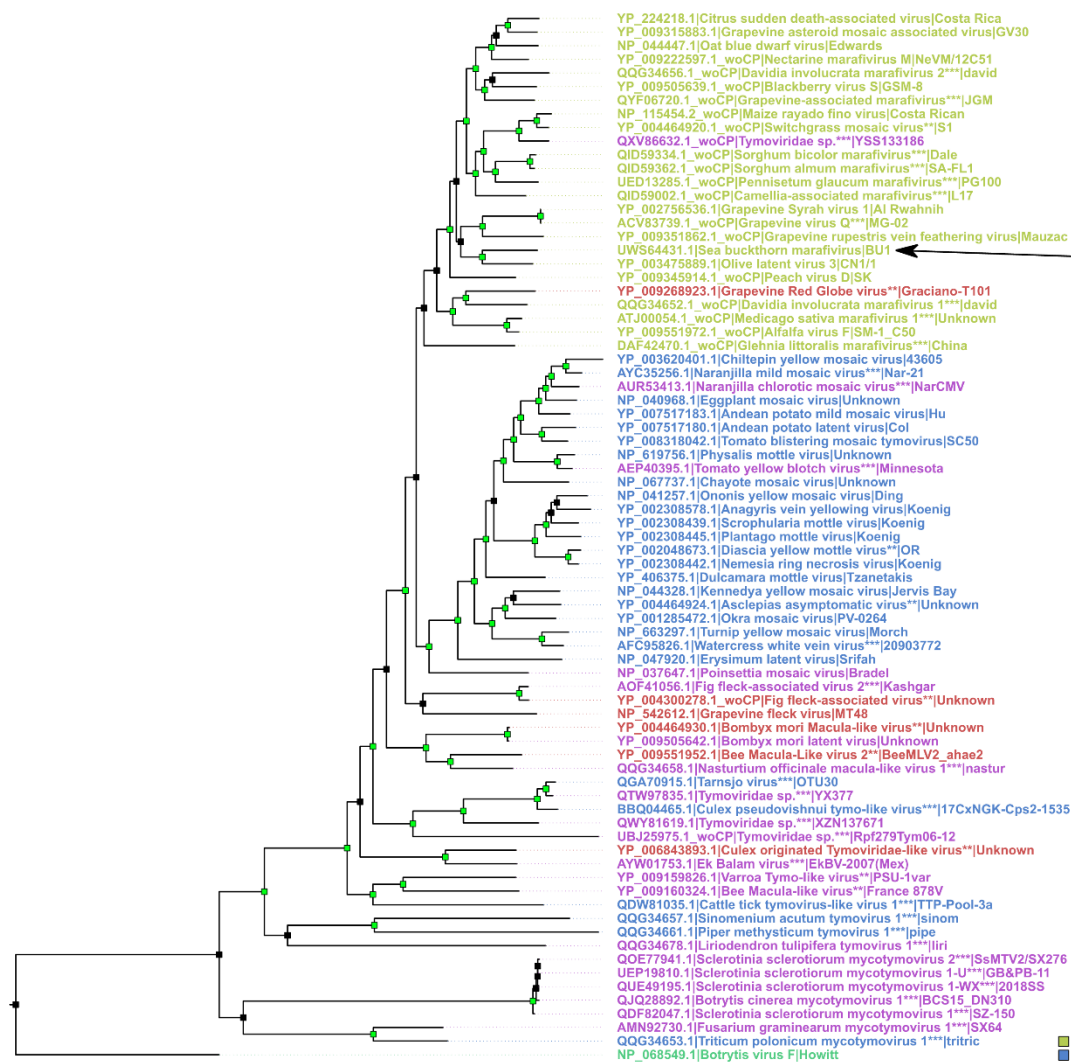


Figure S1. Sea buckthorn leaf samples collected in August 2017 and August 2021. A – representative leaf samples collected in August 2017; B-D – representative leaf samples collected in August 2021.



Maximum-likelihood

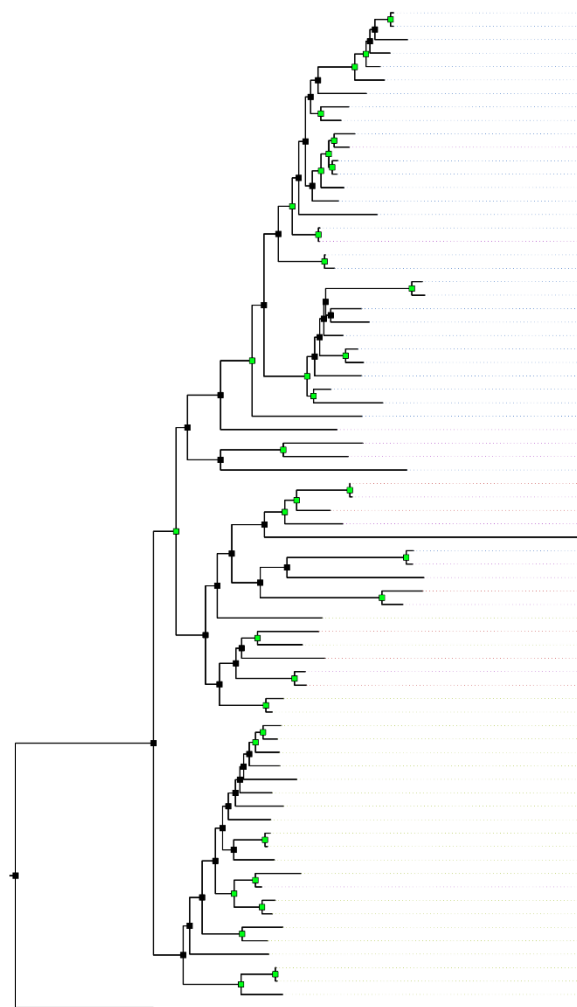
0.8



Neighbor-joining tree

0.04

Figure S2. Maximum-likelihood and neighbor-joining trees generated using *Tymoviridae* capsid protein sequence. Trees were drawn to scale with branch lengths in units of amino acid substitutions per site. In the case of capsid proteins that were encoded as part of the polyprotein, the last 300 aa of the polyprotein sequence containing presumed CP were used (indicated as “_300last” next to the accession number of a respective sequence). Tree tip labels are in the form of sequence accession number | virus name | strain and are colored based on the genera to which the virus belongs according to the legend. Two asterisks (**) after the virus name indicate that the virus originated from RefSeq and did not yet have a standing in the official virus taxonomy but was included in the analysis based on taxonomy associated with a RefSeq entry. Three asterisks (***) after the virus name indicate that the sequence originated from the Nuccore database and did not yet have a standing in the official virus taxonomy but was included in the analysis based on taxonomy associated with a complete or near-complete genome GenBank entry that was longer than 6000 bases in length. Botrytis virus F, which is a member of the *Gammaflexiviridae* family, genus *Mycoflexivirus*, serves as an outgroup at which the trees are rooted. The black arrow connects the sea buckthorn marafivirus (SBuMV) leaves in both trees.



Maximum-likelihood

YP_002048674.1|Diascia yellow mottle virus**|OR
 YP_002308443.1|Nemesia ring necrosis virus|Koenig
 NP_041258.1|Ononis yellow mosaic virus|Ding
 YP_002308446.1|Plantago mottle virus|Koenig
 YP_002308440.1|Scrophularia mottle virus|Koenig
 YP_002308579.1|Anagryis vein yellowing virus|Koenig
 NP_067738.1|Chayote mosaic virus|Unknown
 YP_007517181.1|Andean potato latent virus|Col
 YP_008318043.1|Tomato blistering mosaic tymovirus|SC50
 NP_040969.1|Eggplant mosaic virus|Unknown
 AUR53412.1|Naranjilla chlorotic mosaic virus**|NarCMV
 YP_003620402.1|Chiltepin yellow mosaic virus|43605
 AYC35257.1|Naranjilla mild mosaic virus**|Nar-21
 YP_007517184.1|Andean potato mild mosaic virus|Hu
 YP_009664769.1|Petunia vein banding virus|Koenig
 YP_009664771.1|Wild cucumber mosaic virus|Unknown
 NP_619757.1|Physalis mottle virus|Unknown
 AC196295.1|Tomato yellow blotch virus**|Minnesota
 YP_406376.1|Dulcamara mottle virus|Tzanetakis
 YP_009508097.1|Belladonna mottle virus|European
 NP_663298.1|Turnip yellow mosaic virus|Morch
 AFG95827.1|Watercress white vein virus**|20903772
 YP_001285473.1|Okra mosaic virus|PV-0264
 YP_009505641.1|Desmodium yellow mottle virus|Keese
 NP_044329.1|Kennedy yellow mosaic virus|Jervis Bay
 YP_009505640.1|Clitoria yellow vein virus|Mackenzie
 YP_009508099.1|Cacao yellow mosaic virus|Ding
 YP_004464925.1|Asclepias asymptomatic virus**|Unknown
 AAC58458.1|Calopogonium yellow vein virus**|Unknown
 YP_009664767.1|Passion fruit yellow mosaic virus|Unknown
 NP_047921.1|Erysimum latent virus|Srfah
 NP_037648.1|Poinsettia mosaic virus|Bradell
 YP_009159827.1|Varroa Tymo-like virus**|IPSU-1var
 YP_009160325.1|Bee Macula-like virus**|France 878V
 QDW81036.1|Cattle tick tymovirus-like virus 1**|ITTP-Pool-3a
 YP_004464931.1|Bombyx mori Macula-like virus**|Unknown
 YP_009505643.1|Bombyx mori latent virus|Unknown
 YP_009551953.1|Bee Macula-Like virus 2**|BeeMLV2_ahae2
 QQG34659.1|Nasturtium officinale macula-like virus 1**|Inastur
 QQG34679.1|Liriodendron tulipifera tymovirus 1**|Iliri
 BBQ04466.1|Culex pseudovishnui tymo-like virus**|17CxNGK-Cps2-1535
 QTW97836.1|Tymoviridae sp.**|YX377
 UBJ25975.1_300last|Tymoviridae sp.**|Rpf279Tym06-12
 YP_006843894.1|Culex originated Tymoviridae-like virus**|Unknown
 AYW01754.1|Ek Balam virus**|EkBV-2007(Mex)
 DAF42470.1_300last|Glehnia littoralis marafivirus**|China
 YP_009268924.1|Grapevine Red Globe virus**|Graciano-T101
 QQG34652.1_300last|Davidia involucreta marafivirus 1**|david
 NP_542613.1|Grapevine fleck virus|MT48
 AOF41058.1_300last|Fig fleck-associated virus 2**|Kashgar
 YP_004300278.1_300last|Fig fleck-associated virus**|Unknown
 ATJ00054.1_300last|Medicago sativa marafivirus 1**|Unknown
 YP_009551972.1_300last|Alfalfa virus FISM-1_C50
 YP_224219.1|Citrus sudden death-associated virus|Costa Rica
 YP_009222597.1_300last|Nectarine marafivirus M|NeVM/12C51
 YP_009315885.1|Grapevine asteroid mosaic associated virus|GV30
 NP_044448.1|Oat blue dwarf virus|Edwards
 QYF06720.1_300last|Grapevine-associated marafivirus**|JGM
 YP_009505639.1_300last|Blackberry virus S|GSM-8
 QQG34656.1_300last|Davidia involucreta marafivirus 2**|david
 QID59002.1_300last|Camellia-associated marafivirus**|L17
 QID59334.1_300last|Sorghum bicolor marafivirus**|Dale
 QID59362.1_300last|Sorghum alnum marafivirus**|SA-FL1
 UED13285.1_300last|Pennisetum glaucum marafivirus**|PG100
 AAK85135.1|Bermuda grass etched-line virus|Maccheroni
 QXV86632.1_300last|Tymoviridae sp.**|YSS133186
 NP_115454.2_300last|Maize rayado fino virus|Costa Rican
 YP_004464920.1_300last|Switchgrass mosaic virus**|S1
 UWS64432.1|Sea buckthorn marafivirus|BU1
 YP_003475891.1|Olive latent virus 3|CN1/1
 YP_009345914.1_300last|Peach virus D|SK
 YP_002775441.1|Grapevine Syrah virus 1|AI Rwahni
 ACV83739.1_300last|Grapevine virus Q**|MG-02
 YP_009351862.1_300last|Grapevine rupestris vein feathering virus|Mauzac
 NP_068550.1|Botrytis virus F|Howitt

■ Marafivirus
 ■ Tymovirus
 ■ Maculavirus
 ■ Unassigned
 ■ Mycoflexivirus*

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 NP_068550.1|Botrytis virus F|Howitt

Neighbor-joining tree

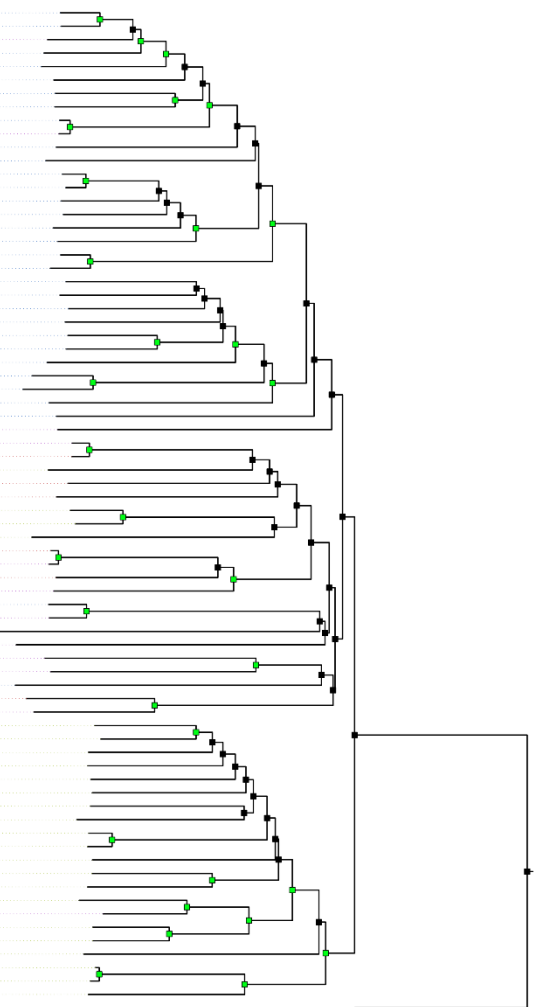
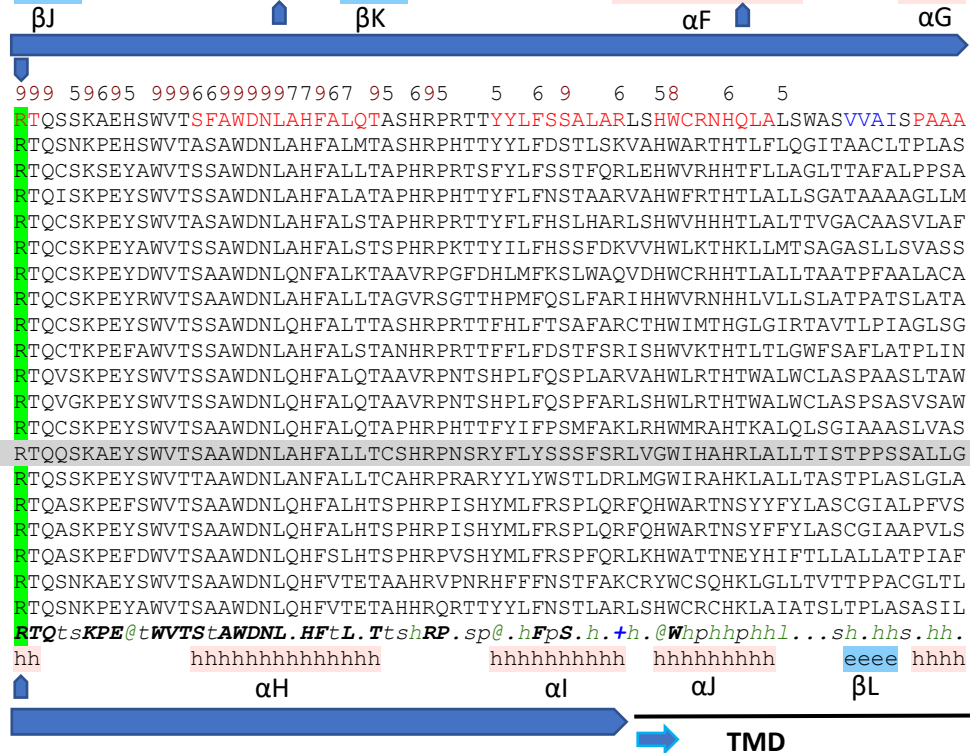


Figure S3. *Tymoviridae* polyprotein aa sequence with maximum-likelihood and neighbor-joining trees. Trees were drawn to scale with branch lengths in units of amino acid substitutions per site. In the case of polyproteins that encoded capsid proteins as well, the last 300 aa of the sequence were truncated (indicated as “_woCP” next to the accession number of a respective sequence). Tree tip labels are in the form of sequence accession number|virus name|strain and are colored based on the genera to which the virus belongs according to the legend. Two asterisks (**) after the virus name indicate that the virus originated from RefSeq and did not yet have a standing in the official virus taxonomy but was included in the analysis on the basis of taxonomy associated with a RefSeq entry. Three asterisks (***) after the virus name indicate that the sequence originated from the Nuccore database and does not yet have a standing in the official virus taxonomy but was included in the analysis on the basis of taxonomy associated with a complete or near-complete genome GenBank entry that was longer than 6000 bases in length. Botrytis virus F, which is a member of the *Gammaflexiviridae* family, genus *Mycoflexivirus*, serves as an outgroup at which the trees are rooted. The black arrow connects the Sea buckthorn marafivirus (SBuMV) leaves in both trees.

File S1. Alignment of marafivirus RP and CP with coded protein domain motifs using PROMALS3D.

Conservation:	9		
YP_009505639.1_BlVS	1	MER-----SNSNLFASSTAC CFSLAIP ISPLDFSPNAEESLLP-----	38
MZ422607.1_GaMV		-----	
ADD13602.1_OBDV	1	MT-----TYAFHPLLPTPTSFAT-----	18
AYC35261.1_CSDaV	1	MD-----RISARIPVAPATAGPTVYVPYPHTHPLLPRGVFTSGPIQPRHLFLPHHAQ	52
QLM05437.1_GAMaV	1	MD-----ASTPLPSFFHGPSPAVEVAPLPPSPECPLTPGFSLSPPSPSPLSPPPS-	50
YP_009222597.1_NeVM	1	MT-----PSNFPHLLARSSPKSSRTPAPTAPR-----	28
MZ305310.1_PGMV	1	ME-----	2
QID59334.1_SbMV	1	MA-----STSDQGPTGTPIWRRMP-----	19
QID59002.1_CaMaV	1	MEC-----SLFTSIIFSWTTSQNNITYSSTPATPVARAEGPYFDPEFAKPHLPGATG-	52
QQG34656.1_DiMV2	1	MS-----SPSTSSCDFVVSTSLIQDLRAQFLGSGNIKYAPLSASRPTFHDHLHPHF-	51
YP_004464920.1_SwMV	1	MS-----	2
NP_115454.2_MRfV	1	MS-----	2
QCC30252.1_PeDV	1	M-----	1
SBuMV-BU1	1	MA-----ALNPSFASFISTFPSPAPEEYHFTCPSPFLLEDVETSIPIL-	43
YP_003475889.1_OLV-3	1	MAA-----SWTSFSSLLSNPLSLAQRIILTPPHNPSIPSLPKSGFRSVTSLSDPSDAL-	52
YP_009551972.1_AVF	1	MS-----TNFQIIPLSFDDSSPSPSPNTAPAPSPKIKYITPHLSVRFHLVPKRF-	50
ATJ00054.1_MsMV1	1	MS-----TSYNIDLV-----DVSSPSLPETSQRISYLSPHLCVRFHLPVKAF-	42
QQG34652.1_DiMV1	1	MVLFYFGLGNELASRRFFSPSPNFHLNHLILQAAAASHLAFSTLKPSDIKPTTTTSSNIIP-LPRPTPI	69
YP_002756536.1_GSyV-1	1	MAAPAT-----AYASPSAAFFALFQEQLRCFR-----PLTLAHSRLYDAPVRPRQLP----	48
QUS93818.1_GRVfV	1	MAFPSNLSTM---LPAHLYQRPSHSLW--FNPSSQPFEVLPHMVPANFPHLFRNIPTFLERSMPVRS-	64
Consensus_aa:		Ms	
Consensus_ss:		eeeeeee	
Conservation:			
YP_009505639.1_BlVS		-----	
MZ422607.1_GaMV		-----	
ADD13602.1_OBDV		-----	
AYC35261.1_CSDaV	53	DAPIRCYRPLTYANHLRYDRSASSLKTSVPKLP-----	85
QLM05437.1_GAMaV	51	-----PSPISLTPEPSSLP-----QLPLSPAHLRCRVLNHV	80
YP_009222597.1_NeVM		-----	
MZ305310.1_PGMV		-----	
QID59334.1_SbMV		-----	
QID59002.1_CaMaV	53	-----PLTYRSYIRLVPAY-----GTPPKGLRPLLLKKSGL	82
QQG34656.1_DiMV2	52	-----YPASSALDAPLHHF-----RPLTLQRFHEQNWRTH	81
YP_004464920.1_SwMV		-----	
NP_115454.2_MRfV		-----	
QCC30252.1_PeDV		-----	
SBuMV-BU1		-----	
YP_003475889.1_OLV-3	53	-----TRAQMFSPTKAILSPAASPTPASQPDPPAEPCSDPPTETTVPSSKRALL	101
YP_009551972.1_AVF	51	-----PHSEPIF-----	57
ATJ00054.1_MsMV1	43	-----PRKPQPTF-----	50
QQG34652.1_DiMV1	70	RKPKPVFIPPPSTNVSRRRRVSHAAYAHQTPHSTSPYLNAPLTFPSLNTATPLPLSRHSPNTYHPHA	139
YP_002756536.1_GSyV-1	49	-----RLRSITV-----PITSLDEGFTPIILIA	70
QUS93818.1_GRVfV	65	-----LGDFKPSRLRPVTLFGGAPPPLGPIIHPAYVAPEPLSSIPITFAP--AA	111
Consensus_aa:		
Consensus_ss:			
		CS  MTase-GTase	
		6 96 5 9 79 97897 68759 5 659	
YP_009505639.1_BlVS	39	-----LQGA-----GFKDVIEALAP TSHRDTISSALLETTVDPF RS	74
MZ422607.1_GaMV	1	-----G-----GLKEVIEFLTPTIHRDTITSPLETTIATPFRS	33
ADD13602.1_OBDV	19	-----VTGG-----GLKDVIELSSTIHRDTIAAPLMEETLASPYRD	54
AYC35261.1_CSDaV	86	-----LTGG-----TLADAILSLAPTTHRDTIATPLMEALAEPYRQ	121
QLM05437.1_GAMaV	81	R-----LTGG-----GLMDVIQSLAPTTHRDTIASPLVEAIAEPYRR	117
YP_009222597.1_NeVM	29	-----LVGG-----GLREVLAALAPTTHRDTVAAPLLEAVATPFRD	64
MZ305310.1_PGMV	3	-----KAIISFLTPTNHRETITAPLLERIAAPFRG	31
QID59334.1_SbMV	20	-----FRGA-----GFADAVAALTPTIHRDTITAPLLES LAPSFRT	55
QID59002.1_CaMaV	83	GRSLP-----LRDLARQLHAASHPRPY LRGG -----GMRDAVDVLTPTTHRDTITAPLLES LAPTFRG	140
QQG34656.1_DiMV2	82	RIHLT-----GSSPNRVSFKSLPASPS LRGG -----CMKDAIDSLTPTTHRDTITAPLVENLATPFRS	139
YP_004464920.1_SwMV	3	-----VF LRGG -----HLLSGVESLTPTTHRDTITAPIVESLATPLRR	40
NP_115454.2_MRfV	3	-----SF LRGG -----HLLSGVESLTPTTHRDTITAPIVESLATPLRR	40
QCC30252.1_PeDV	2	-----FKTIIDSLSSTAHRDTVSSPLVEAVSQPLRE	32
SBuMV-BU1	44	-----PEQTPAQSQSTQELPL LSGG -----GMKDVLDFLTPTIHRDTVSSPIMEKIAAPLRS	96
YP_003475889.1_OLV-3	102	DSHSP-----SPVIPVDETAPISPPIR LTGS -----GLKDLVDFLNPTVHRDTIAAPLLETISQPLRD	159
YP_009551972.1_AVF	58	----- LSGG -----TLFQNAIDALSSTVHKDTITSPLESITKPF	94
ATJ00054.1_MsMV1	51	----- LSGG -----TLFQNAIDALSSTVHKDTITSPLESITKPF	87
QQG34652.1_DiMV1	140	KVHVPNLLFKPISTRKLIKQILRKSPPRIV LTGG APSTPFRSIFEALSSSTIHRDTVAAPLVEAVATPLRN	209
YP_002756536.1_GSyV-1	71	RPSLP----- LLGG -----GLKELVEMLAPTTHRDTVASPILEAVAGPLRT	111
QUS93818.1_GRVfV	112	EPKTP-----SPTAISRRFYRPS----- LSGG -----GLKELVEILNPTVHRDTVCSPLEAAAGPLRD	165
Consensus_aa:	 LpGG <i>h.phlp.LssThHRDTlhtPLLEsIt.Phrp</i>	
Consensus_ss:		hhhhhhhhh hhhhhhhhhhhhhhhhhhhhhhh	

Conservation:	7798677 56 5 7 9 9 96 79 7 67 9 979989 78 558 97969999958995877	
YP_009505639.1_BlVS	285	SLLIQRGEPLHSRHTAEFRTPPAILLPAPSSSLNQDVRHRLVPKVKYDAVFLLVVRTVRLTRVTDPAAGFI 354
MZ422607.1_GaMV	244	HLLIQRGLPPVHARHDELDFRVPAAILLPEASSLHQPIRDLRLAPKAVYEAIFIYVRAVRTLRRTDPAAGFV 313
ADD13602.1_OBDV	265	SLLIQRGIPPMHAHDSISFRGPRAVAIPEPSSSLHQDLRHLVPEDVYNALFLYVRAVRTLRVTDPAAGFV 334
AYC35261.1_CSDaV	332	SLLIQRGKPIIHLEEDSLFRAPKAVLLPEPSSSLQAVRDRLVPADVYQALFIFYVRAVRTLRVTDPAAGFV 401
QLM05437.1_GAMaV	328	SLLIQRGTTPPVHAERDTISFRAPKAVVLPNPSSLTQPLRDLRVPKDVYTAIFVYVRAVRTLRVTDPAAGFV 397
YP_009222597.1_NeVM	275	SLLIQRGVPVPHQEVDTVSFKAPRAVALPEPSSSLHQDLRHLVPKDVYDALFIYVRAVRTLRVTDPAAGFV 344
MZ305310.1_PGMV	242	SLLIQRGKPPIHVDDDTVEFTTPEAYALPQPASLHQDLRHLVPAKVYNELFVYVRAVRTLRRTDPAAGFV 311
QID59334.1_SbMV	265	SLLIQRGVPPHHAERDSVSFTGPDAILLPEPASLTQDPRHRLVPSKVYHELFIYVRAVRTLRVTDPAAGFV 334
QID59002.1_CaMaV	351	SMLIQRGEAPLHQYRSRASFRGPEAVCLPSPASLHQDLRHLVPKKVYDAIFMYVRAVRTLRVTDPAAGFV 420
QQG34656.1_DiMV2	350	HLLIQRGEPPVHSREDLLDFKVPQAILLPAPSSSLNQEIRHRLVPKKVYDSLFVYVRAVRTLRVTDPAAGFV 419
YP_004464920.1_SwMV	251	SLLIQRGRPPVFSAEDEVSRVDPDAIALPAPASLHQDLRHLVPRRVYDALFNYVRAVRTLRVTDPAAGFV 320
NP_115454.2_MRFV	251	SLLIQRGRPPVFAEDIASFRVDPDAVALPAPASLHQDLRHLVPRKVYDALFNYVRAVRTLRVTDPAAGFV 320
QCC30252.1_PeDV	243	SLLIQRGRPHMHEDEDTVYEFKVPKAVALLPEPASLRQDLRHLVPADVHDALFVYTRAVRTLRTDPAAGFV 312
SBuMV-BU1	307	SLLIQRGLPPVHSHDTHSFKVPDAIILLPEPAHLNQPIRHLRVPVAVYQAVLLYVRAVRTLRRTDPAAGFV 376
YP_003475889.1_OLV-3	370	SLLIQRGLPLPHQEHSQTAEKTPPEAILLPAPSHLQDLRHLRVPTRVYESIFVYVRAVRTLRVTDPSGYV 439
YP_009551972.1_AVF	305	SMLISKSNFPFDAETDTISFKVPSAILLPEPNSLSQDPRHRLVPTKIYHAIFAYVRAVRTLRVTDPAAGFI 374
ATJ00054.1_MsMV1	298	SMLITKSQLPFDASQDRIDEKVPSSAILLPEPNSLNQNPRLHRLVPTKIYHAIFAYVRAVRTLRVTDPAAGFI 367
QQG34652.1_DiMV1	420	SLLIQRGLAPITSSHDTITERTPSAILLPEANSIRQDIRHRLVPKDIYHNLFSTVRSVRTLRVTDPAAGYI 489
YP_002756536.1_GsYV-1	322	SLLIQRGKPSVHLEDEVSEFVGPDVALPEAAALRQDLRHLRVPRTVYDALFVYVRAVRTLRRTDPAAGFV 391
QUS93818.1_GRVFV	376	SLLITRGRPPV-LTDDSLFESSPDAVEIPAASSIQQSLRHLRVPKSAVYHSLFIYVRAVRTLRQTDPAAGYV 444
Consensus_aa:		SLLIQRG.sPhc.ppDphsFpsPpAlhLp.ssSLpQshRHRLVppVYptlFhYVRAVRTLRhTDPtGFV
Consensus_ss:	eeeeee	eeeeee hhhhhhhhhhhhhhh hhhhh



Conservation:	5 7 6	
YP_009505639.1_BlVS	425	LSSLVSKFLRSELNLSLAIFRRWI--KAPP-----HF-L-----FAPKAPFLSMSFRALRTGPLLFANTG 481
MZ422607.1_GaMV	384	LSALGLAHFSRCRISALSIFGHWL--VCPD-----FYL-----LKPAPFLRLAVAPASAPFRAFKGTF 440
ADD13602.1_OBDV	405	WLANLVARTSASHIQGLALARRWL--ITPP-----HLF-----RPPSPSFALLLQRNSTGPILLRGSR 461
AYC35261.1_CSDaV	472	TASWGFRAMISSHLVSLICKRWL--RAPP-----HLL-----WPEKAPWFQTLTRPKVTGPLIDLPIIL 528
QLM05437.1_GAMaV	468	VGCRVAAGLSNQQLRSLACLRRWI--VAPP-----HLPF-----FRPKAPLLELTLRPKVTGPLVNLPLV 525
YP_009222597.1_NeVM	415	SLFLAIGRVLNSHVHSFAVFRRWL--KPPP-----HLL-----WPPKAPLLELSLARSTGPTVLSGTP 471
MZ305310.1_PGMV	382	TIVKAGETLYHSHLDELTVARHRLVGSQPF-----RLSI-----WKERLPLFRIMHRECTGWTFFQGS 441
QID59334.1_SbMV	405	TGVSALGHLAHRHIDELTVAGRTLIGRAPR-----HFSI-----WKPATTFWRRLTHAPCTGWTLWPGTI 464
QID59002.1_CaMaV	491	ASCWLFHRLITGHVDQCAILGRWV--KVPF-----GMSKLPRI--ALPPAPWFSLQTHAGGAGIKLLRGTR 552
QQG34656.1_DiMV2	490	RLACSLSNFTCSKVTLSLLKFWI--IKPK-----YFF-----RLPPARLFSLTG-----LFKDTI 538
YP_004464920.1_SwMV	391	LAASRFGRLLTVLHTRDLRLFGCDL--IGRR-----FWPILPFQSPPEARFLWETHSACKPYTLFAGSA 450
NP_115454.2_MRFV	391	ATASALGRLLPLHTDRLRLFGFDI--IGRR-----FWPRLPFHGPEPRFLWETHPACRPPVLFADSA 450
QCC30252.1_PeDV	383	TAAYATARARCPIESLAVCGWWI--KSPP---TIKHALREAVGFPPQKAPQFSIALTPRPAAPFGWK--- 444
SBuMV-BU1	447	LTSFSLARFYWRQISTLVLFRRFPI--ISPPTSFLSRLSF-----RSALPPLFLKLTQVPRPVW----- 502
YP_003475889.1_OLV-3	510	SSALLACRPFWMRLDSLQLLNRWV--IKPS--FPRNLPFLLPKAFQPKASLFAEFLPRHAPS----- 568
YP_009551972.1_AVF	445	ALSLTSLHLSRCSVHHFSLFRHWF--VPPP-NPHFLFNFHSLFLLPKAPFSLQLHNPFPPTLSK--- 508
ATJ00054.1_MsMV1	438	LSSVLAHHYSRCSILHLALFKKWI--VAPP--SSNFLPFFLSSRFIPKAPFFSLALHNPVPRPTLRF--- 500
QQG34652.1_DiMV1	560	KLSSFLTTPAPRLYIKQLTVFSSHLL--VGRPSLAHRYLPPIIRH-FLTPTPRFSLHLGTRPAI----- 618
YP_002756536.1_GsYV-1	462	FTGAKLASAMSSRLTALAVFHHWV--VPPP-TLF-----FTPKAPLLAIQLTRLPQP--LFSSVP 516
QUS93818.1_GRVFV	515	LALGGVDLLWKHSIKHLVIAHRYLIGSAPL----HARLLPRFLVQQHYPRFSLALEPRVAAPVIHL--P 577
Consensus_aa:		h.t..h..h...plppshh..hl...sP.....h.h....h.s.hpl.h.s.....hl.....
Consensus_ss:	h	eeeeeeee hhhhhhhhhhh

Conservation:		6	65		8	8	6	896	99	759	9	
YP_009505639.1_BlVS	482	FQTRLFPTAAQNFCSAN	PLLASFF	-PVKPLHRG	-AFLASLLAASVPVALLLV	-RQFV	GPDS	PQSMH	DAYA			548
MZ422607.1_GaMV	441	LAFDVFPRLTQDLLHRVPLLRFF	-PRRPLPNA	-CWWACLA	ASIPAF	LWAC	-RWFV	GPDS	PQMH	DAYH		507
ADD13602.1_OBDV	462	LEFEAFPSLAPQLARRFFFLARLL	-PQKPINPW	-IVASLAVAVAI	PAASLAV	-RWF	FGPDT	PQAMH	DRYH			528
AYC35261.1_CSDaV	529	RPFRFLPSTCAKLGAKHPALATLL	-PAAPRPTW	-PLKVG	LALA	AVPCL	FLW	-RNF	IGPDS	PQMDH	SYH	595
QLM05437.1_GAMaV	526	RPFRFLPPTTCARLGARHPAVALFL	-PPKALTSS	-WLPYALG	AAAIPL	LALLGI	-RWFL	GPDS	PQAMH	DQYH		592
YP_009222597.1_NeVM	472	FAFKLLPKTFCRLGASYPSLAKFL	-PKCPIPRK	-YLWLS	IAAASL	PLIALGV	-RFFL	GPDS	PQSLH	DRYH		538
MZ305310.1_PGMV	442	FETRPFDNLCSRLG-KKPAFARFL	-PTRPIGGK	-WLWAMA	AAVA	AVPAALLAI	-RWVL	GPDS	PQALH	DRYQ		507
QID59334.1_SbMV	465	FETKILHRVAADLG-RSRWLARYL	-PNRPLHRY	-WTYAAL	GLSAVPA	IAIALAI	-RWFL	GPDS	PQALH	DRYQ		530
QID59002.1_CaMaV	553	FEFQLFNQLFRSWA-RNPWLAQFL	-PRRRMGKL	-GWSFLL	TSIMAP	ILSLAA	-RKFL	GPDS	PQSLH	DSYH		618
QQG34656.1_DiMV2	539	LQCQPFQNFQQLAIKFPAAHFL	-PQKPLPFI	-ALFMC	VASTL	APTVMGL	-RQFF	GPDS	PQAMH	DSYH		605
YP_004464920.1_SwMV	451	FECRVLGALAHRC	-PSPTLSRLF	-PEAQPARW	-VVGSL	LALAAVPLT	TALLV	-RWFL	GPDS	PQALH	DQYH	516
NP_115454.2_MRFV	451	FECQILAGLANRCS	-PSPFWSRLF	-PTASPPSW	-VAYSAL	LALAAVPLA	LAL	-RWFY	GPDS	PQALH	DQYH	516
QCC30252.1_PeDV	445	-----LLLKPLKQAPWLRPLY	-RDAPVPRF	-WIKATL	AAALAAAAA	AAAL	-RHFL	GPDT	PQMH	MHDKYV		503
SBuMV-BU1	503	---RLLPSLSMSLLSKFPVLRFF	-SDKPIPSW	-FYYVLC	SVSSIPL	LLLLSL	-RKFC	GPDS	PQALL	DNYT		566
YP_003475889.1_OLV-3	569	---RILPEFFDALLKKAPFLRPLF	-SDAPIPSW	-AWALCAT	GVAIP	IIALS	-RRFL	GPNS	PQALL	DEYQ		632
YP_009551972.1_AVF	509	---VLSFLLPTSFINQLKFL	-----QPRSLPKH	-TLHCTL	ALASLP	ILAALY	-RWFS	GPDT	PQALH	DQYE		568
ATJ00054.1_MsMV1	501	---ILSKFFPESFLSRFPSL	-----NPRNLPKS	-TVPVALL	LAAIP	PAFAALY	-RWFS	GPDT	PQALH	DQYE		560
QQG34652.1_DiMV1	619	---HPDFNLKPLLLHKIPWLISLL	-PKAPTPLA	-ATLFIA	SMASAI	PLAFWCH	-RRFF	GPDP	HDPQ	ALH	DQYQ	682
YP_002756536.1_GSyV-1	517	FLHKPLGKLSRLLLNRPFLRRFF	-PDAPIP	PTW-ARLLT	VAIASPA	VLWLA	-RHFI	GPDP	APQAL	NDHYV		583
QUS93818.1_GRVfV	578	FSQTVRLTFLTTLANHIPSLKRFL	-PRLSTPAL	-LKAAFC	LGLLTP	PLLLLLI	-RSFV	GPDS	PQMSD	DAYN		644
Consensus_aa:		...p...h...ph..p.	P.L.phh.s..shs...	hh.h.h.hh.h.hPhhhh.h.	R.Fh	GPDP	PQThhDpYp					
Consensus_ss:		hhhhhh	h	hhhhhhhhhhhhhhhhhh	hhh	hhhhhhhhhh						

Conservation:		896	9	9	7		8	5		8		
YP_009505639.1_BlVS	549	DLFHPADW	RLI	FN	RKPLF	ASPEP	---FLPIT	-----	TVPA	--PVD	-----	583
MZ422607.1_GaMV	508	ELFHPPELWRLTLRRSPLAVSAER	---FLPIET	FTTPE	-----	PTPPT	--PAQE	ATAET	PVL	-----		559
ADD13602.1_OBDV	529	TMFHPREWRLTLPRGPISGRSS	---FSPLPH	PPSP	-----	TPA	--PDS	RAGPLQ	PPSALPS	----		580
AYC35261.1_CSDaV	596	AMFHPQPWGLTLTRKAICCDRAP	---FLPIP	VVPSS	-----	DFKA	--PPT	PATPL	TSIPIK	GVEPQV		653
QLM05437.1_GAMaV	593	AMFHPPDWHLTLDRAPLLTHRQP	---FLSFEP	QPAP	-----	EELL	--PPT	AAVRLE	TTPAP	PPTSAQ	--	648
YP_009222597.1_NeVM	539	ALFHPEPWELVLKRGPVHVARAP	---FLPFT	P	-----	VDHV	--PLD	SD	-----			576
MZ305310.1_PGMV	508	ATFHADPWRLILHRGPITVGRRS	---FLPLQ	DL	-----	DTPK	--PQP	PDSP	-----			548
QID59334.1_SbMV	531	ATFHDPDWQLRLXRGPIFCGRRA	---FLPLE	HA	-----	PPAS	SP	-----				567
QID59002.1_CaMaV	619	AMFHPEPWTLTLDQGPVFCTSTP	---FLPVP	-----	TVPT	--PAA	ASF	PDN	-----			659
QQG34656.1_DiMV2	606	RMFHPELWHLTIERKSGRYSNPAQ	---FLPLD	FFPQ	PEPV	TSKAI	VSQA	--PSS	DVSR	PLSRL	LEVQTP	668
YP_004464920.1_SwMV	517	ATFHDPDSWLDLPRRLRSCVREP	---FLL	-----	TGAA	--PAST	PTS	AENF	SPD	-----		561
NP_115454.2_MRFV	517	ATFHDPDPWTLDLPRRLRRFERES	---FMR	-----	TGSA	--PLPL	SLP	-----				553
QCC30252.1_PeDV	504	ALFHPPQWQLKIKRGVIKTLPA	---FLPFE	-----	PT	--PPI	-----					536
SBuMV-BU1	567	DFHHSKPWTLTLDRAVHVRPSS	---FIPIES	LPPQ	APQPLY	GNSDHL	FHPAET	PTI	VPIS	NPDPSE	PF	631
YP_003475889.1_OLV-3	633	SYFHPKPWQLILEQGP	IFANPEP	---FSPH	-----	CQPI	--PSS	GPD	SAP	SSTL	GTTPM	681
YP_009551972.1_AVF	569	TYFHPKEWTL	SFPRKAITVTRIP	---FLP	-----	TDPI	--PIS	DA	-----			603
ATJ00054.1_MsMV1	561	EYFHPKEWSLFFQRKP	VHVT	TRSP	---FLP	-----	QDPI	--PVS	NA	-----		595
QQG34652.1_DiMV1	683	AYFHPKDWTLTLDRAPL	TTS	SPQ	---FLPF	-----						709
YP_002756536.1_GSyV-1	584	RFFHPDRWQLTFRQPRF	VALDR	---TFPW	LPQ	APE	-----	PTEPR	--DSD	VPLE	TVP	632
QUS93818.1_GRVfV	645	RYFHPSRWELSLERSPAS	VIPSPPA	FLPT	ASAAEP	-----	TEPR	--PSD	SPL	-----		690
Consensus_aa:		.hFHPp.WpL.hpR.sh.h...s..FLPh.....s..h..Ps.ss.....										
Consensus_ss:		hh	eeeeeeeeee									

Conservation:					9					5		
YP_009505639.1_BlVS	584	-----	LPQIE	---	SIAIP	-----	AP	----	SPAPP	S	602	
MZ422607.1_GaMV	560	-----	APAVP	---	ASTAP	-----	SPPS	PLP	ASE	PVQ	582	
ADD13602.1_OBDV	581	-----	THEPAPA	---	DLESP	-----	APQA	HAPQ	TE	PPS	605	
AYC35261.1_CSDaV	654	-----	SGEGVPPQSASSTGP	ASDSRRAPQPA	---	SSTGP	---	DPPT	QNTS	SAAPQP	697	
QLM05437.1_GAMaV	649	-----	VEPPT	PAEP	---	KSTRP	-----	APLK	PVL	VATPPP	675	
YP_009222597.1_NeVM	577	-----	SPAIP	---	APPVP	-----	QPQA	PLS	PV	TPAP	599	
MZ305310.1_PGMV	549	-----	GPPPP	---	SPAGE	-----	SES	ASF	TPE	KPAP	571	
QID59334.1_SbMV	568	-----	PSPA	---	DKPAT	-----	SPVH	VQT	PAT	PPP	589	
QID59002.1_CaMaV	660	-----	PPLPV	---	SEVSP	-----	QIPL	QAV	SP	SPSQ	683	
QQG34656.1_DiMV2	669	-----	SESQ	KEV	APSNLTQMP	-----	QSQ	KLS	PA	EAP	698	
YP_004464920.1_SwMV	562	-----	TPRPL	TS	LRAQA	-----	EPS	QPS	D	VQPPK	586	
NP_115454.2_MRFV	554	-----	PPEG	SLLP	VEPPL	-----	APS	D	PE	PALEP	579	
QCC30252.1_PeDV	537	-----	LPSD	---	SSDEE	-----	VEER	FQ	KL	API	558	
SBuMV-BU1	632	-----	PPPT	PIEL	PPFSPKKP	-----	VPS	VSK	P	PTSQEP	661	
YP_003475889.1_OLV-3	682	-----	YPSS	PAP	VE	---	EK	TIL	---	VPTVR	ALPAPPP	709
YP_009551972.1_AVF	604	-----	HPEPS	---	ESE	-----	IPL	F	N	STPNEHSP	624	
ATJ00054.1_MsMV1	596	-----	HPDPS	---	ESD	-----	IPL	E	P	SSSPLTTP	616	
QQG34652.1_DiMV1	710	-----	EPIPT	---	QESL	-----	NIPS	NAT	PAS	PAP	732	
YP_002756536.1_GSyV-1	633	-----	SPLPV	---	VAPLP	-----	APAT	S	V	PPVDTSA	655	
QUS93818.1_GRVfV	691	-----	VPL	---	---	-----	VP	S	R	LHPDTPPP	706	
Consensus_aa:	P.ss.....s.....ss.sss										
Consensus_ss:			eee									

Conservation: 6 5 8

YP_009505639.1_BlVS	603	TS-----LAPTPIPPVTSTLDPAPASASAPAA-----TPPAIAA	636
MZ422607.1_GaMV	583	ALQN----ASPAPAP---PAQLTSLSSSLTPAP-----RDTIFPLASTA	619
ADD13602.1_OBDV	606	PVIEQE--ARPDFFP--APA-----PRP-----APTP-SASA	632
AYC35261.1_CSDaV	698	PIESKVTFAQPIESV--APVVP--AGEP--PQSASSTGP-----ASVSRDPQVASSTTPDAPTLDVSVT	757
QLM05437.1_GAMaV	676	PVTAPT--SQPEPTQ--APAAPT-LAIPASPRALQAEADRIHSVQMAADRTPTETIAIVAAADALLPLAAST	740
YP_009222597.1_NeVM	600	VSRDSPT-SDPPGRDAEEKAVNAVLSLSPSPSQ-----PPVR	635
MZ305310.1_PGMV	572	AATQPQAQAPPVATPAPAEAEIEK-DHPPSVPA-----AAEA	607
QID59334.1_SbMV	590	P-----	590
QID59002.1_CaMaV	684	PDSSPT--PEPVPVPASTPPPPPELSEAPPPA-----VEAPQAPAP	723
QQG34656.1_DiMV2	699	KTSTE---PAPGPVPTIESAVQS-IARALNPDAVHNPD-----VNALKDINSTAEAVRDLLSPICPPS	758
YP_004464920.1_SwMV	587	SAVQPQVAPEPAPAP-ISPEPAASLPISAEPE-----VFEPPTSHSP	628
NP_115454.2_MRFV	580	PAA-----SVPAPAP--APA-----SEPPP-----SPESVAP	604
QCC30252.1_PeDV	559	PV-----PQPAP--STATPPQPAATAPPE-----AKPVAQQLIPAAPE	596
SBuMV-BU1	662	AVSNPPAPSSPQPPSTPSTPRYLPPHKASEPK-----LQVHPLPPPS	704
YP_003475889.1_OLV-3	710	SS-----VPPPSKP--SPAAPAPVTPPSLPT-----VIPPLSTPT	743
YP_009551972.1_AVF	625	S-----SSPEPSP--LPAVPPPSAIPVQLP-----TVASNNGPLDKRPSSSLL	667
ATJ00054.1_MsMV1	617	-----ESPESPPLAPTVPPPSAIPTVKLP-----STSSHNPLDKSKPAPSPL	660
QQG34652.1_DiMV1	733	TTQAQEHASTPLDTP--SKPPNPPTSSPTTTP-----CPTSDFVSSDRPHQSPL	780
YP_002756536.1_GSyV-1	656	TTVSAVEPSLSTESL--KTVEAPSGTTILQPRE-----LKDTIFPLPAAA	698
QUS93818.1_GRVFV	707	AE-----KQPEPTPC-VVASAPVLDASAPRA-----EETPAGLDM	741
Consensus_aa:		ss.....P.sss...s..s...s..P.s.....P.sss.	
Consensus_ss:			

Conservation: 6 6

YP_009505639.1_BlVS	637	PA-----PAPEPQAEALSL-----LIPSEHQPAAPPPIP	665
MZ422607.1_GaMV	620	PIAELTAPTA-----PVAEPSAPAPTDGR--PEDFAPPLDPSTVDAALLALGISIPSS	670
ADD13602.1_OBDV	633	PS-----PAPTSPAPEPPS-----PTASE-----QAASLIPA--	659
AYC35261.1_CSDaV	758	PPKTIYPIDHLQNDGFCRCSCVCEPLQAPVPSTPLTVS-----DHKEAQDAEALSSALQALGLAPT--	819
QLM05437.1_GAMaV	741	PAADSAPE-----PTVVPGPPEEVD-----PAGQA-----ALASLGLAPSLP	777
YP_009222597.1_NeVM	636	P-----PSPSVQAPASSD-----DLADRRDAENLAQALSSGLFTPD	673
MZ305310.1_PGMV	608	P-----PSARPVEPPSET-----QKQESQRPSPSEEAAMLCGERAP--	643
QID59334.1_SbMV	591	-----PSPEPASPEPD-----ADIPTP	609
QID59002.1_CaMaV	724	PAD-----PSDVPAQAPAVE-----FSFPDPPAETHVASMFGVPTPLD	761
QQG34656.1_DiMV2	759	LASHHQVA-----PASAPAIKTQPP-----TPSQSSDNLQATAMLSTAEVKLD	802
YP_004464920.1_SwMV	629	PAQPVADSE-----PTSQPSRRAPT-----VRQAALLGADLRFGLPPRSS	670
NP_115454.2_MRFV	605	PVAVVA-----PAVQPARAPSPS-----PALLGAELRFGDLPPVSA	640
QCC30252.1_PeDV	597	SQETVDAIKRQLADPM-----PALPAEGPSSPRPLSNALLCPPEGSEVLLEAPPADCAVTASPPPGF	658
SBuMV-BU1	705	PPVRIPQVGASGFV-----AQDLPAQELPLP-----TLSCELVDLDQQPSTPPSP	749
YP_003475889.1_OLV-3	744	PETRVPEVGKSGIV-----ASDLPPTEISFN-----PTLARCPRNFLGLCAPHPNPNPSHP	794
YP_009551972.1_AVF	668	TAIIDPSTNA-----PATSSSLPPATT-----NPTPVQSEFPDFPFSFSAQPTAPRI	713
ATJ00054.1_MsMV1	661	TSIIDPSTNEPLLKQP-----SLQPVSVPTDPDFDT-----TPSFP	696
QQG34652.1_DiMV1	781	DQFPVPPTD-----PQKGPAPPSTNEHL-FRHPLPKAPDALPENLFPDFFNQPAAPR	831
YP_002756536.1_GSyV-1	699	LAVTPPE-----PAPAPAEPVSAS-----TV	719
QUS93818.1_GRVFV	742	SATTV-----LEAKPPVQVSLV-----DEPPRP	764
Consensus_aa:		s.....P.s..Ps.....s..ss..	
Consensus_ss:		eee	

Conservation: 5 5

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YP_009505639.1_BlVS	666	-ELLPAAG-----QLQLE---SSGVVSNL-----TPAAPEPA-APEPSP	699
MZ422607.1_GaMV	671	DIVLPPSP-----AAAEPIPPPNLSLVQS-----SFGSVAAPVSS-LPAPT	711
ADD13602.1_OBDV	660	---PSS-----ALVVE---PSGVVSAS-----SWGATNQPAD--QVDDSP	691
AYC35261.1_CSDaV	820	-PTAPQSQ-----NLTV-----SSGAMHAS-----SWDQLSSPSS--DWDPSP	855
QLM05437.1_GAMaV	778	ASTGPSQ-----SANLE---PSGAVHAA-----TWDQSSAPSS--DWDTS	813
YP_009222597.1_NeVM	674	-HSEFPQP-----VVG-----SSGELHAR-----EWGQEDAPAS--DPESP	707
MZ305310.1_PGMV	644	---SPPNP-----LLTVE---PTGEVYSR-----EPAGPVTE-DPERVA	675
QID59334.1_SbMV	610	VPDAPART-----PVVDE--KTAIISDP-----EPPEPPKP-DPECSE	644
QID59002.1_CaMaV	762	GKPAAPNT-----PLTVE---ERGHVYTT-----APLPEPETPAASDP	796
QQG34656.1_DiMV2	803	QHLES-----NLHLE---PKGHVFS-----EPSWAE-VEGLSP	833
YP_004464920.1_SwMV	671	WAQDPELS-----PLGES---TQGTVFAG-----IPTPRE-ESALAR	704
NP_115454.2_MRFV	641	WSDDPEIS-----KLGES---TQGTVFAG-----TPGPRAP-EPDTAR	674
QCC30252.1_PeDV	659	TSSAAPSA-----PSQPE--APAQIEAFSSLLYGQDSISVQRDGSVVGAAHTTPEPL-SEEVSA	713
SBuMV-BU1	750	PPASPS-----PLVTD---DLGTVSAS-----RPKLDPT-ETTFSE	781
YP_003475889.1_OLV-3	795	EPSAPS-----PLITD---PSGSLTAI-----NPLEPPEF-EFNHAL	826
YP_009551972.1_AVF	714	VPACPPGF-----ENILSD--KFGALNSS-----TAPAEHPSEPSTP	749
ATJ00054.1_MsMV1	697	APRPPPGF-----ERVSD--KHGVITES-----NLPHEPESHVEVSP	732
QQG34652.1_DiMV1	832	SSSAPPASVNLRPQTFFVKPIQPQD-CETGNIIPP-----PEVLIPLAKPD-PPASP	882
YP_002756536.1_GSyV-1	720	LGTAPLSR-----DL-----HTGHVSTP-----ATEPGLV-EPEHSP	750
QUS93818.1_GRVFV	765	ESLLNPSAT-----QEELLIS--HTGTLTHT-----TPQPVTA-TPEVEP	801
Consensus_aa:		...s.....h..p....t..l.s.....s.s.....t.	
Consensus_ss:			

		PRO I																			
		★																			
Conservation:		9	9	77	865	6	6	8	7	56	9	9	9	6	69	6999	66	66	6	98	8
YP_009505639.1_BlVS	700	LQADSSARGPV	QLFSEL	FPGS	-YIGTTGA	FNSRY	RASGRAP	TPYP	AGTD	CLLV	TVSEATH	IPRED	LWSAL								768
MZ422607.1_GaMV	712	LESPTAAGPI	SMSFSE	LPAS	-YLGTS	GSFLCRR	RASGRCS	LPYP	MDCL	LVTVSEATH	IPRED	LWSAL									779
ADD13602.1_OBDV	692	LARDPSASGP	VRFYRDL	FPAN	-YAGDS	GTDFDR	FRASGRS	PTYP	MDCL	LVATEQ	ATRIS	REAL	WDCL								759
AYC35261.1_CSDaV	856	LARDSSASGP	PGMYSDL	FPAP	-YLPGT	GQFIFR	SRANRANI	PYPD	MDCL	LLSIEQ	ATRLP	KREAL	WDTL								923
QLM05437.1_GAMaV	814	LGRDGSANGP	IALYSEL	HPAN	-YLPST	GDGFLFR	DRANRAN	LPYPT	MDCL	LVAVEQ	ATRIP	KREAL	WDTL								881
YP_009222597.1_NeVM	708	LLRDPSACGP	VAMYSEL	HPGN	-YVPGT	GFLQFR	DRASGRAP	VPYPS	MDCL	LVAVEQ	ATRLP	KREAL	WDTL								775
MZ305310.1_PGMV	676	LQIDPTADGP	IGLYSEL	HPDC	-YEPRT	GDGFLARN	RNRSSR	SDLEY	PSGVD	CLLKAVA	QATNIS	VQAL	WTTL								744
QID59334.1_SbMV	645	LERDPSAAGP	ALPYDELY	PDC	-YTELS	AKFLSR	ARNALS	SAAPY	PAGVD	CLLTAV	SEATGL	QTQAL	WECL								713
QID59002.1_CaMaV	797	LGSDPSASGP	PIAFFRELY	PAS	-WLNQ	SGLFLCR	SRNSSR	SSHYP	PS	NDCL	LLAAV	SEATS	IPRETL	WETL							864
QQG34656.1_DiMV2	834	LQSDGSARGP	VAFFSQVH	PGS	-YIGTT	GQFNFR	ASRSPSS	KQSY	PVNTD	CLLRAVE	AGSGIS	RQAL	WECL								902
YP_004464920.1_SwMV	705	LEVDP	TASGP	IMEFRDL	QPG	L	YLGTT	GSFLTR	ARNVSS	STIQY	PARAAC	LLVAV	RNATSL	PLTAT	LWAAL						773
NP_115454.2_MRFV	675	LDADPSASGP	VMFREL	QKGA	-YIEPT	GAFLTR	ARNVSS	SSSI	PIYP	TRAA	CLLVAV	SQATGL	PLTRT	LWAAL							743
QCC30252.1_PeDV	714	LVRDPSAAGP	VLQFHD	LHPGA	-YLEATA	AAPFCRL	RNGQPS	NMPYP	Q	NDCL	LRTVHT	ATHI	PLAAL	RECL							781
SBuMV-BU1	782	LVDPSASGP	VSSFSELY	PNQ	-WCPGS	ATFPAR	VNRSSH	STSPY	PG	MDCL	LLKAIS	IPTGL	STKSL	WESL							849
YP_003475889.1_OLV-3	827	LGADPSGQGP	VQAQFNL	FPSTL	WLQGT	GFEFLTR	SRVQAP	SSAPY	P	MDCL	LHAIHT	ATRI	PKPTL	WAGL							895
YP_009551972.1_AVF	750	LLADQSAQGP	VVMFGL	YPAE	-YHSNC	DEFQTR	ARVNHSS	NLPR	VIND	CLLEAV	SSATN	ISKDAL	WNAL								818
ATJ00054.1_MsMV1	733	LMADSSAEGP	VPVLFGL	YPAE	-YHANC	DEFQTR	RRVDHSS	SLPR	PSVND	CLLEAV	SSATN	ITKDAL	WNAL								801
QQG34652.1_DiMV1	883	LLADPTATSD	VKLWSEHL	PRE	-YLSNC	GSFLFR	ERSTPAS	DL	PYPSTTD	CLLQAV	SKATG	IDPHAL	WRTL								951
YP_002756536.1_GSyV-1	751	LAADSSATGE	VSEFFNL	LHPAD	-WIAPT	ATFLARR	RGETI	SGAKY	P	MDCL	LLAAV	SAGANI	PKDAL	WKTI							818
QUS93818.1_GRVFV	802	LMVDASGAGP	VDSFSLVH	PGS	-YLPFS	GSFLSR	IRVSSL	SPAPY	P	LDCL	LVSVAG	ATGF	PKESL	WQSL							869
Consensus_aa:		L..DsoA.GP1..@.pL@Ps..@h.sot.F.hR.Rsss.SshPYPs..DCLL.tlp.AT.ls.psLWphL																			
Consensus_ss:		eehhhhh eeeee hh hhhhhhhhh hhhhhhhh																			

Conservation:		6996	8	6	9959	97	97	5	8	6	6	6	95	66	9	6	8																																															
YP_009505639.1_BlVS	769	VTNLPDCLLA	PC	E	I	S	K	H	G	L	S	T	D	H	F	A	V	L	A	F	F	Y	S	L	R	V	T	F	L	T	S	H	G	P	V	D	L	G	M	S	D	A	T	T	N	F	R	I	D	H	Q	P	E	S	K	D	L	----	834					
MZ422607.1_GaMV	780	CVNLPDSMLDAD	T	I	R	A	G	L	S	T	D	H	L	V	V	L	A	R	F	F	N	F	R	A	T	L	D	L	K	P	S	P	V	T	Y	G	L	S	D	S	P	V	H	F	H	I	T	Y	T	P	E	S	H	T	A	D	G	F	K	----	849			
ADD13602.1_OBDV	760	TATCPDSFLDPK	S	I	A	H	G	L	S	T	D	H	F	V	I	L	A	H	R	F	S	I	C	A	N	F	H	S	A	A	H	V	I	Q	L	G	M	A	D	A	T	S	T	F	M	I	N	H	T	A	G	S	A	G	L	----	825							
AYC35261.1_CSDaV	924	CAACPD	S	L	L	D	P	D	I	I	R	R	V	G	L	S	T	D	H	F	A	I	L	A	H	H	S	L	R	C	F	H	T	A	H	G	V	I	E	L	G	M	A	D	A	T	S	S	F	D	I	D	H	T	A	G	N	-----	986					
QLM05437.1_GAMaV	882	CATCPDSMLRP	E	D	I	R	R	E	G	L	S	T	D	H	F	A	V	L	A	H	H	S	L	A	A	D	F	H	S	A	S	G	I	I	P	I	G	M	A	D	A	S	A	K	F	A	I	T	H	T	A	G	S	G	S	A	----	947						
YP_009222597.1_NeVM	776	TSACPD	S	F	L	N	P	T	E	I	A	A	A	G	L	S	T	D	H	F	A	I	L	A	R	H	Y	S	L	R	A	T	F	H	S	G	P	S	T	F	T	I	G	M	E	D	A	T	S	T	F	A	I	N	H	T	P	G	Q	G	K	L	----	841
MZ305310.1_PGMV	745	TAELPD	S	M	L	N	P	I	E	V	Q	T	H	G	L	S	T	D	H	F	V	L	A	R	I	Y	R	L	R	A	F	L	T	K	F	G	D	I	T	L	G	V	E	N	A	T	S	S	F	T	I	R	H	T	G	E	Y	A	G	----	809			
QID59334.1_SbMV	714	CSQLPD	S	Q	L	G	D	D	I	S	K	G	L	T	D	H	F	V	L	A	R	I	Y	R	L	R	A	T	F	H	T	A	G	E	V	T	L	G	M	A	D	A	T	S	S	F	H	I	Q	H	T	A	G	N	-----	776								
QID59002.1_CaMaV	865	ITTLPD	S	L	L	D	S	S	E	I	R	V	H	G	L	S	T	D	H	F	C	V	L	A	M	H	S	L	R	A	R	F	I	S	E	G	I	D	A	E	L	G	L	E	N	A	V	H	T	F	T	I	N	H	F	P	G	K	D	G	S	----	930	
QQG34656.1_DiMV2	903	CNTCPD	S	L	I	D	P	K	E	I	E	V	H	G	L	S	T	D	H	F	A	I	L	A	R	A	F	S	L	K	C	T	F	I	T	K	D	L	R	V	D	L	G	M	H	D	A	T	T	S	F	S	I	D	H	T	P	G	S	-----	965			
YP_004464920.1_SwMV	774	AANLPD	S	I	L	D	G	S	L	V	R	L	G	T	T	D	H	F	A	V	L	A	R	I	F	S	L	R	C	F	R	V	S	D	H	I	D	V	E	L	G	V	A	D	A	T	S	R	F	T	I	R	H	T	-----	833								
NP_115454.2_MRFV	744	CANLPD	S	V	L	D	D	G	S	L	A	T	L	G	L	T	D	H	F	A	V	L	A	R	I	F	S	L	R	C	F	V	S	E	H	D	G	V	E	L	G	M	A	D	A	T	S	R	F	T	I	R	H	T	-----	803								
QCC30252.1_PeDV	782	CVQLPD	S	V	L	D	Y	E	L	I	Q	R	R	G	L	S	T	D	H	F	S	V	L	A	R	F	F	S	L	R	A	K	F	L	T	P	G	W	E	Q	P	L	G	M	A	D	T	A	T	H	T	F	V	L	H	T	P	T	A	T	----	847		
SBuMV-BU1	850	CATLPD	S	F	L	S	P	S	V	I	A	S	H	G	L	N	T	D	H	F	C	A	L	A	H	N	F	S	L	Q	C	H	F	H	S	G	S	N	I	Q	T	M	G	L	T	N	A	S	H	V	F	H	I	T	H	D	P	P	T	P	L	Q	----	915
YP_003475889.1_OLV-3	896	CSNLPD	S	F	L	D	P	Q	L	I	A	H	K	G	L	S	T	D	H	F	A	V	L	A	R	L	F	S	L	R	C	T	F	Q	S	R	S	G	T	Q	T	M	G	V	A	D	A	T	H	F	R	I	R	T	P	P	T	E	D	A	----	961		
YP_009551972.1_AVF	819	CTHLPD	H	F	L	D	H	N	D	I	V	R	R	G	L	N	T	K	H	L	T	L	C	F	V	Y	K	L	S	T	I	N	T	E	G	R	S	H	L	F	G	L	K	N	S	T	H	F	N	L	D	H	N	P	E	G	-----	881						
ATJ00054.1_MsMV1	802	CTHLPD	S	F	L	Q	H	E	D	V	L	R	A	G	L	N	T	K	H	L	V	L	C	V	Y	K	L	S	T	I	N	T	E	G	R	S	H	L	F	G	V	K	N	S	T	H	F	N	L	D	H	D	P	R	-----	864								
QQG34652.1_DiMV1	952	TSHLPD	S	L	L	D	T	A	E	I	T	Q	H	L	N	T	D	H	F	T	V	L	A	S	I	Y	D	L	K	C	T	F	L	T	N	H	G	P	I	E	F	G	V	A	N	A	P	T	S	F	T	I	R	H	T	P	P	T	S	N	A	----	1017	
YP_002756536.1_GSyV-1	819	CSYFPD	S	M	L	R	E	E	D	I	A	K	H	G	L	S	T	H	H	F	A	L	A	R	E	H	R	L	Q	A	T	F	H	S	A	G	N	Q	F	V	L	G	V	E	H	P	S	V	S	F	H	I	D	H	T	P	E	S	A	T	A	----	884	
QUS93818.1_GRVFV	870	CGILPD	S	Q	L	D	N	E	Q	V	R	T	Q	G	L	S	T	D	H	F	C	A	L	A	L	H	S	L	R	C	T	F	L	T	D	A	G	Q	Q	E	M	G	M	E	D	A	T	S	V	F	T	I	R	H	T	S	G	N	-----	932				
Consensus_aa:		hs.hPDSHlp..pl.p.GLSTcHFhhLA.h@pLptpFho.....hGh.sAsppFpIpHhs.s.....																																																														
Consensus_ss:		hhh hhh hhhh hhhhhhhhhhh eeeeeee eeeee eeeee eeeee hhh																																																														

		PRO II		CS		HEL ^[1]																
		★				→																
Conservation:		5999	5	6	75	6	78	5	8	996	59	5	7	6	99999	699899						
YP_009505639.1_BlVS	835	MGH	FSLH	----	QDSKPVPT	LNGGT	--	GSEL	ATAAT	RFNL	-DGCLLP	FNTVHT	FVT	AP	SRA	KNLISNMKN	896					
MZ422607.1_GaMV	850	PGH	FALS	----	TARPAN	LNGGL	--	APDL	ATAALRFNT	-GGALLPFHT	VHTYTT	Q	PAR	AKNLISNMKN		909						
ADD13602.1_OBDV	826	PGH	FSLR	----	LGDQPRAL	LNGGL	--	AQDL	AVAALRFNI	-SGDLLPTR	SVHTYRSW	PKRA	KNLVSNMKN		886							
AYC35261.1_CSDaV	987	PGH	FSLR	----	QSATPR	LNGGI	--	AQDL	AVAALRFNI	-DGTLLPIRS	VHVYSTW	PKRA	KNLSSNMKN		1046							
QLM05437.1_GAMaV	948	PGH	FALR	----	LPDSPK	LNGGL	--	AQDL	AVAALRFNH	-SGALLPFR	TAHPYTTW	PRRA	KNLSSNMKN		1007							
YP_009222597.1_NeVM	842	PGH	FSLR	----	LDHNSPK	LNGGL	--	AQDL	AVAALRFNV	-DGQLLP	IRS	VHSYRTW	PAR	AKNLISNMKN		902						
MZ305310.1_PGMV	810	MGH	FELV	---	ADTETSLPPP	INGGG	--	AEDL	AAAIMRYHAP	DGTVLP	I	FQVH	TRVTKP	PRRA	KNLVSNMKN	874						
QID59334.1_SbMV	777	PGH	FALIRP	PPTD	LASTLIPK	VNNGG	--	ARDLESS	IKAFRAKDGSL	PLFLK	VHQYTTD	PS	RA	KNLISNMKN		843						
QID59002.1_CaMaV	931	IGH	FALK	----	TPAHASK	LNGGL	--	ADDL	AAAALRFRTK	GGHFLP	FR	EAHYKSS	P	RA	KNLISNMKN	992						
QQG34656.1_DiMV2	966	PGH	FEFC	----	PNPALT	LTGSL	--	ADDL	AHAALRFNI	-KGVLLPFNT	VHHYHSKPS	RA	KNLISNMKN		1025							
YP_004464920.1_SwMV	834	PGH	FELV	----	ADDYSLPAL	V	GAS	TIPGAD	LAESCKRFV	ASDR	TVLP	FRD	VHIHRT	S	V	KRA	KNLISNMKN	899				
NP_115454.2_MRFV	804	PGH	FELV	----	ADNFSLPAL	V	GAS	TIPGAD	LAEACKRFV	APDR	TVLP	FRD	VHIHRT	D	V	RA	KNLISNMKN	869				
QCC30252.1_PeDV	848	IGH	FELV	----	ADGTSAPPPAL	LSGAG	--	AKDL	AI	I	ALSFR	T	-GGHLLP	IAHVNHY	TAPS	RA	KNLISNMKN	911				
SBuMV-BU1	916	PGH	FTYL	----	PTGNSV	LTGAF	--	AEDL	AQIALMFRV	-HDHLLP	FR	T	VHTYR	THP	IR	AKNLVSNMKN	975					
YP_003475889.1_OLV-3	962	PGH	FEYM	----	EEIPES	LTGAF	--	AQDL	AHFALSFRF	-NGYLLP	F	KHVHTY	T	S	N	V	S	RA	KNLISNMKN	1021		
YP_009551972.1_AVF	882	IGH	FSHS	----	TRPSHI	QLNGAR	--	AQDL	SHTILG	FRCS	SDSTLLP	F	KNIH	S	Y	T	H	V	S	RA	KNLISNMKN	943
ATJ00054.1_MsMV1	865	IGH	FTHS	----	TKVQ	PVTLNGAR	--	AQDL	KHTILG	FRCS	SDSTILP	F	KNIH	S	Y	T	H	V	RA	KNLISNMKN	926	
QQG34652.1_DiMV1	1018	PGH	FELV	----	SDAQPK	LNGSR	--	ADTL	QHIMK	SFRS	-DNALLP	FQKFHTY	MSN	TR	AKNLISNLK		1078					
YP_002756536.1_GSYV-1	885	PGH	FSLR	----	ADERQHS	PRLLGGR	--	AADLV	HAALKFKV	-GSAVLP	FQQAHDY	T	N	V	RA	KNLISNMKN	947					
QUS93818.1_GRVFV	933	PGH	FELV	----	RSSARPL	LNGAR	--	PAAD	I	VEHMK	R	FKV	-DGKILP	F	CEAHSY	T	SHV	RA	KNLISNMKN	994		
Consensus_aa:		.GHFph.....s.s..LsGt...t.DLs.hhb.Fph.sshlLPphppH.Ypo.s.RAKNLISNMKN																				
Consensus_ss:		ee hhhhhhhhhh eee hhhhhhhhhhhh																				

		MarBox-like	HEL I	HEL Ia	
Conservation:		9999779 559 6 69 55 89 5866 67 6 9697899799997 97 99 8 75789			
YP_009505639.1_BlVS	897	GFDGVLANIDPHHTSTARDRLCLDGIIDVAKPRVRLFHIAAGFAGCGKSYPIARLLKTPLFREFKVAVP			966
MZ422607.1_GaMV	910	GFDGILASIDPAHPSEARARLLTLDGVMVASPRSVRLIHLAGFAGCGKSYPIVSRLLKTATFKDFKLSVP			979
ADD13602.1_OBDV	887	GFDGVMASINPIRPSDAREKIVALDGLLDIAQPRSVRLIHIAGFPGCGKSTPIAKLLHTAAFRDFKLAVP			956
AYC35261.1_CSDaV	1047	GFDGIMANIHTPTKTNESREKILALDSQLDIAVRRSVRLIHIAGFPGCGKSFPISRLLRTPTFRNFKVAVP			1116
QLM05437.1_GAMaV	1008	GFDGVMATINPAKPSDAREKIIALDSSLDIAAPRSVRLIHIAGFPGCGKSYPIARLLSTPAFRNFKVAVP			1077
YP_009222597.1_NeVM	903	GFDGVMANIHTPTKTTEARERILALDQGLDIAQPRTVRLIHIAGFPGCGKSYPIISRLLKTAAFKDHKVAVP			972
MZ305310.1_PGMV	875	GFDGIMANVDPAPHPNFAREQILKLDGVLDISVPRKVRVLVHIAGFAGCGKSWPIAKLLTTPSFRNHKIAVP			944
QID59334.1_SbMV	844	GFDGVLANIDPTHNTARDRILALDGVMDIAQPRSLKLVIHIAGFAGCGKSWPIAGLLNSPAFHNEKVAVP			913
QID59002.1_CaMaV	993	GFDGVMANVDPGHAQEARTRILSLDGVMDISCPNRVRLVHLAGFAGCGKSWPIAQLLKTPTNFRNFKVAVP			1062
QQG34656.1_DiMV2	1026	GFDGILANADPLHTNEARDRLSLDGIIDISMPKHVRLVHIAGFAGCGKSYVPVKLLKSPSFKNFKLSVP			1095
YP_004464920.1_SwMV	900	GFDGVMAQANPLDPKSAERERFLMLDSCLDIAAPRVRLIHIAGFAGCGKSWPVAQLLKTPTAFRTFKLAVP			969
NP_115454.2_MRFV	870	GFDGVMAQANPLDPKSAERERFLMLDSCLDIAAPRVRLIHIAGFAGCGKSWPISHLLRTPTAFRVFKLAVP			939
QCC30252.1_PeDV	912	GFDGVLANIDPHRTHEARDRLLALDGIIMDLAPPRQVALIHIAGFAGCGKSYPIQKLLSHPAFHQHKVALP			981
SBuMV-BU1	976	GFDGVMASADPQNPKLARERILSLDGVLDIATPRSVRLIHIAGFPGCGKTYPIITRLLSHPSFRNFRVAVP			1045
YP_003475889.1_OLV-3	1022	GFDGVMASADPLHPGQTRERFLSMDNQLDIAVPRETRLIHISGFAGCGKTYPIITQLLKKPVFRQFRVAVP			1091
YP_009551972.1_AVF	944	GFDGVMANVDPPLHPSKARDSFLMLDQLLDVAASKSVSLVHLAGFAGCGKSYVPVQQLLKTPTAFQNFVKVSV			1013
ATJ00054.1_MsMV1	927	GFDGVMANVDPPLHPNKAARDSFLMLDQLLDVAAPKNVHLVHLAGFAGCGKSYVPVQQLLRTPTSFQNFVKVSV			996
QQG34652.1_DiMV1	1079	GFDGIMATVNPQDPNKAARHFFMALDHQMDIAAPRQVHLVHLAGFAGCGKSYPIQQLLQHSFRSSRVAVP			1148
YP_002756536.1_GSyV-1	948	GFDGVLANIDPAHTNESRDRLSLDGMAMIAAPRDVKLIHIAGFPGCGKSYPIAQLLKSRAFKHFKIAVP			1017
QUS93818.1_GRVfV	995	GFDGVLANIDPQHTNEARDRLSLDGSLDIAKPTVSLIHIAGFAGCGKSYPIQQLLTKPCRNKYIAVP			1064
Consensus_aa:		GFDG ^h l ^h ashsP. +sppAR-phL. LDs. h ^h Lt. PR ^h VpL ^h l ^h AGFsGCGK ^h oP ^h l. pLLppssF+p ^h K ^h LAVP			
Consensus_ss:		eeee hhhhhhhhhh eeeeeee hhhhhhhhhhhh eeeee			

		HEL Ia	HEL II	HEL III	
Conservation:		77999 999 5 99 799998999 786898997997999969966785 668			
YP_009505639.1_BlVS	967	TVELRAEWKDLLKIRPGAQWRSLSTWESSLLKSARILVIDEVYKMPRGYDLAVHADPT-----IELVIL-			1030
MZ422607.1_GaMV	980	TTELNRNEWKIGILNLPAGSQWRSLSTWESSLLKSARILVIDEVYKMPRGYDLDCIHADPT-----VEFVIA-			1043
ADD13602.1_OBDV	957	TTELNRSEWKELMKLSPSQAWRFGTWESSLLKSARILVIDEVYKMPRGYDLAIHSDS-----IEFVIA-			1020
AYC35261.1_CSDaV	1117	TVELRAEWKTITGLPASEAWRIGTWESSLLKSARVLVIDEVYKMPRGYDLAIHSDPT-----IEMVIA-			1180
QLM05437.1_GAMaV	1078	TVELRAEWKDLLKLPNAAWRIGTWESSLLKMARVLVIDEVYKMPRGYDLAIHADPT-----IEMVIA-			1141
YP_009222597.1_NeVM	973	TTELRAEWKDMKLKPSPAHVWRIGTWESSLLKAARVLVIDEVYKMPRGYDLAIHADPT-----IEFVIA-			1036
MZ305310.1_PGMV	945	TVELRAEWKALMDPRQDKWRFGTWESSLLKSARVLVIDEVYKMPRGYDLAIHADAA-----VEFVIL-			1008
QID59334.1_SbMV	914	TVELRTEWKDLLQSKPMDRWRVGTWESSLLKSARVLVIDEVYKMPRGYDLALHADSN-----VDFVIL-			977
QID59002.1_CaMaV	1063	TVELRTEWKELLSSPSEWRVGTWESSLLKSARVLVIDEVYKMPRGYDLAIHSDS-----VEFVFA-			1126
QQG34656.1_DiMV2	1096	TVELRSEWKELNLKKGQEWVGTWESCLLSARVLVIDEVYKMPRGYDLDSIHADPA-----LEFVLIV-			1159
YP_004464920.1_SwMV	970	TTELRDEWKGLMEPRDQDKWRFGTWESSLLKSARTVLVIDEVYKMPRGYDLAIHADAS-----IQFVIL-			1033
NP_115454.2_MRFV	940	TTELRDEWKALMDPRQDKWRFGTWESSLLKSARVLVIDEVYKMPRGYDLAIHADAA-----IQFVIL-			1003
QCC30252.1_PeDV	982	TVELRNEWKAAMKPKPANVWRISTWESSLLKSARVLVIDEVYKMPRGYDLAIHADPS-----VEFVIL-			1045
SBuMV-BU1	1046	TVELRSEWKDMLKLPKPAERWRIGTWESSLLKSARVLVIDEVYKMPRGYDLAIHSDS-----IQFVIV-			1109
YP_003475889.1_OLV-3	1092	TTELRSEWKDLLTLEPADRWRTWESSLLKSSRVLVIDEVYKMPRGYDLI----RTPPLIRPTQFVIIP			1157
YP_009551972.1_AVF	1014	STELRSEWKEAIKTKNSDNWRISTWESSLLKTARVLVIDEVYKMPRGYDLAIHADPT-----IEFVII-			1077
ATJ00054.1_MsMV1	997	STELRSEWKDAIKTKNSDNWRISTWESSLLKSARVLVIDEVYKMPRGYDLAIHADPT-----VEFVII-			1060
QQG34652.1_DiMV1	1149	TTELRTEWKEGMHLKSTTAWRVSTWESSLLKRSRVLVIDEVYKMPRGYDLDSILADPT-----LELVIL-			1212
YP_002756536.1_GSyV-1	1018	TVELRNEWKGVLVKVPQDNWRISTWESSLLKSARILVIDEVYKMPRGYDLAIHADPT-----IDLVIA-			1081
QUS93818.1_GRVfV	1065	TVELRNEWKDSLKSAPADRWRTWESSLLKSARIVVIDEVYKMPRGYDLAIHADST-----AQLFIV-			1128
Consensus_aa:		ThELR ^s EWK. hhp. .ssp. WRltTWESSLLK ^h oARlLVIDE ^h YKMPRGYDLAIHtDso. . . . lphVih.			
Consensus_ss:		hhhhhhhhhhh eeeeehhh eeeee hhhhhhhhhh eeeee			

		HEL III	HEL IV	
Conservation:		88896997988666 969 77 69 59 57 9 99 985959 66 7 6 7 7 95 6		
YP_009505639.1_BlVS	1031	LGDPLOQGVYHSTHPSSSTNSRLSPETHYLSKYIDFYCLWSHRIPQDVAKFFGVHSTNLAPGFSKWVPNLSP		1100
MZ422607.1_GaMV	1044	LGDPLOQGEYHSTSPSSSNSRLSSEVRHLAPFIDYYCWSRRIPKLVADFFQLPTLSSEPGFTRLIRHLPS		1113
ADD13602.1_OBDV	1021	LGDPLOQGEYHSTHPSSSNSRLIPEVSHLAPYLDYYCLWSYRVPQDVATFFQVQSHNPALGFARLSKQFPT		1090
AYC35261.1_CSDaV	1181	LGDPLOQGEYHSTHPSSSTNSRLSEPQHLMSMYLDFYCLWSHRVPQNVAAFFHVKTTSKQPGFCRYQRELP		1249
QLM05437.1_GAMaV	1142	LGDPLOQGEYHSTHASSTNARLLPEPRHLAPYLDYYCLWSHRIPRNVAFFQVPTSSTEEGFVRHVRELPG		1211
YP_009222597.1_NeVM	1037	LGDPLOQGEYHSTHPSSNSRLVGTETRLHAPYLDYYCLWSRRVPKLIADFFHVPTSNENPGFARYSRQFPT		1106
MZ305310.1_PGMV	1009	LGDPLOQGEYHSHAPQSTNARLHSEIIELSPYIDAYCWSRRIPKRIAKCLGVPTLSSKQGFVSFRRELPS		1078
QID59334.1_SbMV	978	LGDPLOQGEYHSTHASSNHRLSSEVHRLRPYIDVYCAWTRRLPRRIARIFNIPTTSEHGFVITYSKGFPH		1047
QID59002.1_CaMaV	1127	LGDPLOQGEYHSTHPSSSNRPLPSEISHLRRYIDFYCFWSHRIPRNVAQCLGVPTTSKLEGFATYTHQFPT		1196
QQG34656.1_DiMV2	1160	LGDPLOQGEYHSHHPSSSTNARLSSEILHLPYIDFYCMWSHRIPQDLARFFQIKSSNTSPGFRHHHLNLS		1229
YP_004464920.1_SwMV	1034	LGDPLOQGEYHSTHPSSSNARLSPEHRYLRPYIDFYCFWSRRIPQYVATILGVPTTSKVSFYARHSSQFPL		1103
NP_115454.2_MRFV	1004	LGDPLOQGEYHSTHPSSSNARLSPEHRYLRPYVDFYCFWSRRIPQNVARVLDVPTTSTEMGFARYSQFPP		1073
QCC30252.1_PeDV	1046	LGDPLOQGEYHSTHPSSSNARLSSELKHLRPYLDYCYLWSRRIPQQIARFFQVPTLSDAPGYVRYMRSEST		1115
SBuMV-BU1	1110	LGDPLOQGEYHSTSPDSSNSRLSPETSHLSRYIDFYCLWSHRVPHLISGVFQVPTSSSNPGFVSHHRSLLP		1179
YP_003475889.1_OLV-3	1158	WRSPSQGEYNSTHPSSNLRTITSEIIHLQPYIDFYCFWSYRIPKNVAACLKVPTTSNKTGFIRRLNSIPN		1227
YP_009551972.1_AVF	1078	LGDPLOQGEYHSHSNPSSSNHKLSPETSHLRKYIDFYCFWSRRIPQSVAAFFQVPTLNSPTSKFSKFPVSPV		1147
ATJ00054.1_MsMV1	1061	LGDPLOQGEYHSHSNPSSSNHRLSPETLHLKPYIDFYCFWSRRIPQSIAAFFQVPTLNSNPGFSKFVPSVPS		1130
QQG34652.1_DiMV1	1213	LGDPLOQGEYHSTHPSSSNHKISSEIPLKPYIDYYCLWSRRVPQVAKFFNIPLNPNLGSFSYTPHLPE		1282
YP_002756536.1_GSyV-1	1082	LGDPLOQGVYHSTHSDSSNHRLSSEVKHLQPYMDYYCLWSHRVPQDIGTFFGIKSTSTVPGFKSQYQANIPS		1151
QUS93818.1_GRVfV	1129	LGDPLOQGEYHSTNPSSNSRLASEIKHLQPYMDMYCMWSHRIPRNVARFVRVKTSSVEGVSSTSLVLAP		1198
Consensus_aa:		LGDPLOQGEYHsopP ^h SoN. RLssEh. +L. . YlDhYChWS+RlPp. lA. hh. l. o. sp. . G@. p@. . phss		
Consensus_ss:		e hhhhhh hhhhhh eeeee hhhhhhhh eeeee		

		HEL V										HEL VI																																																												
		8	67	56	55	96	7	877	999	979	6	56	99	676	99	68	699	9995	66	86	99																																																			
Conservation:																																																																								
YP_009505639.1_BlVS	1101	SS	K	I	L	T	N	S	Q	N	S	M	K	T	L	V	D	C	G	F	A	S	V	T	I	A	S	S	Q	G	S	T	Y	P	G	A	T	N	I	L	D	R	N	S	A	L	L	S	H	S	N	S	L	V	A	L	T	R	S	K	K	G	V	V	F	T	G	D	R			
MZ422607.1_GaMV	1114	Q	A	K	I	L	T	N	S	Q	N	S	S	R	V	L	N	D	C	G	R	A	S	T	T	I	A	S	S	Q	G	S	T	Y	D	G	P	S	I	L	L	D	R	H	T	A	L	L	S	P	A	H	S	L	V	A	L	T	R	S	K	V	G	I	I	F	V	G	D	V		
ADD13602.1_OBDV	1091	T	G	R	V	L	T	N	S	Q	N	S	M	L	T	M	T	Q	C	G	Y	S	A	V	T	I	A	S	S	Q	G	S	T	Y	S	G	A	T	H	I	H	L	D	R	N	S	S	L	S	P	S	H	S	L	V	A	L	T	R	S	R	T	G	V	F	F	S	G	D	P		
AYC35261.1_CSDaV	1250	N	S	R	I	L	N	S	Q	N	A	G	H	T	L	Q	Q	C	G	Y	A	A	V	T	I	A	S	S	Q	G	S	T	Y	E	N	A	C	I	H	L	D	R	N	S	S	L	S	P	A	H	S	M	V	A	L	T	R	S	K	V	G	V	F	T	G	D	P					
QLM05437.1_GAMaV	1212	D	S	R	I	L	T	N	S	Q	N	A	G	H	T	P	Q	Q	C	G	Y	A	A	V	T	I	A	S	S	Q	G	S	T	Y	P	G	A	C	I	H	L	D	R	N	S	S	L	S	H	A	H	P	L	V	A	L	T	R	S	R	K	G	V	L	F	T	G	D	L			
YP_009222597.1_NeVM	1107	D	A	R	V	L	T	N	S	Q	N	A	M	H	T	M	N	Q	C	G	Y	Q	S	V	T	I	A	S	S	Q	G	S	T	Y	S	G	A	C	I	H	L	D	K	N	S	A	L	L	S	H	G	H	S	L	V	A	L	T	R	S	R	T	G	V	I	F	T	G	D	P		
MZ305310.1_PGMV	1079	K	L	R	I	L	V	N	S	Q	S	A	M	K	T	L	N	Q	L	G	Y	Q	A	I	T	I	A	S	S	Q	G	S	T	Y	R	S	P	A	C	I	H	L	D	R	N	S	R	L	L	S	H	Q	N	S	L	V	A	V	T	R	S	T	E	G	I	I	F	T	G	D	F	
QID59334.1_SbMV	1048	A	R	K	V	L	A	N	A	R	T	A	T	T	L	Q	Q	L	G	Y	D	S	V	T	I	A	S	S	Q	G	S	T	Y	D	R	P	T	V	V	H	L	D	K	N	S	R	L	L	S	H	Q	H	S	L	V	A	M	T	R	S	R	R	G	I	I	F	T	G	D	A		
QID59002.1_CaMaV	1197	N	T	K	I	L	C	N	S	M	S	A	C	K	T	L	Q	Q	C	G	Y	D	S	V	T	I	A	S	S	Q	G	S	T	Y	S	G	P	A	C	I	H	L	D	R	N	S	R	L	L	S	A	S	H	S	L	V	A	I	T	R	S	K	A	G	V	I	F	T	G	D	R	
QQG34656.1_DiMV2	1230	T	C	K	I	M	A	N	S	Q	N	A	A	R	T	L	Q	D	C	G	Y	S	S	V	T	I	A	S	S	Q	G	S	T	Y	S	S	A	C	I	H	L	D	R	N	S	A	V	L	S	H	S	H	S	L	V	A	L	T	R	S	K	S	G	I	I	F	T	G	D	K		
YP_004464920.1_SwMV	1104	N	G	K	I	L	I	S	A	M	T	S	A	K	S	L	V	D	C	G	Y	Q	A	I	T	I	A	S	S	Q	G	S	T	Y	V	N	G	P	V	H	I	H	L	D	N	H	A	R	R	L	S	H	Q	H	S	L	V	A	I	T	R	S	R	A	G	L	V	F	T	G	D	P
NP_115454.2_MRFV	1074	F	G	K	I	L	I	S	A	R	D	S	A	K	S	L	A	D	C	G	Y	H	A	V	T	I	A	S	S	Q	G	S	T	I	A	G	P	A	V	H	L	D	N	H	S	R	R	L	S	H	Q	H	S	L	V	A	I	T	R	S	K	S	G	I	V	F	T	G	D	K		
QCC30252.1_PeDV	1116	S	A	K	L	L	A	N	S	I	P	T	A	K	T	L	Q	Q	V	G	Y	N	A	I	T	I	S	S	S	Q	G	S	T	L	D	G	P	A	F	I	H	L	D	R	H	S	T	L	S	H	H	S	L	V	A	L	T	R	S	R	A	G	V	V	F	T	G	D	K			
SBuMV-BU1	1180	N	S	K	I	L	T	C	S	Q	S	S	A	K	T	L	L	Q	C	G	Y	S	A	V	T	I	A	S	S	Q	G	S	T	Y	E	G	P	A	C	I	H	L	D	R	N	S	R	S	L	S	D	S	H	S	F	V	A	V	T	R	S	K	K	G	I	I	F	T	G	D	L	
YP_003475889.1_OLV-3	1228	A	N	K	V	L	T	C	S	Q	S	S	M	K	T	L	N	Q	C	G	F	S	S	V	T	I	A	S	S	Q	G	S	T	L	Q	E	A	C	I	H	L	D	R	N	S	R	N	L	S	N	S	H	S	L	V	A	L	T	R	S	K	S	G	I	I	F	T	G	D	F		
YP_009551972.1_AVF	1148	N	T	P	L	L	V	N	S	Q	S	A	S	Q	I	L	S	A	G	F	R	A	L	T	I	A	S	S	Q	G	A	T	F	S	A	P	T	A	I	H	L	D	K	N	T	K	S	L	S	P	Q	H	S	L	V	A	L	T	R	S	K	S	G	I	L	F	T	G	D	Q		
ATJ00054.1_MsMV1	1131	N	T	P	L	L	V	N	S	Q	S	A	S	Q	V	L	Q	A	A	G	F	R	A	L	T	I	A	S	S	Q	G	A	T	F	S	A	P	T	A	V	H	L	D	K	N	T	K	S	L	S	P	Q	H	S	L	V	A	L	T	R	S	K	V	G	I	L	F	T	G	D	Q	
QQG34652.1_DiMV1	1283	G	Y	P	V	L	A	C	S	N	N	Q	V	T	L	T	Q	C	G	F	R	S	V	S	V	A	S	S	Q	G	S	T	Y	T	K	G	V	V	L	H	L	D	R	N	S	K	L	L	S	L	A	H	S	L	V	A	L	T	R	S	K	D	L	I	I	F	S	G	D	K		
YP_002756536.1_GSyV-1	1152	N	L	R	Q	L	A	N	S	Q	S	A	A	K	V	L	N	Q	C	G	F	S	S	V	T	I	A	S	S	Q	G	S	T	Y	S	A	P	A	C	I	H	L	D	R	H	S	M	S	L	S	H	A	H	S	L	V	A	L	T	R	S	K	S	G	V	I	F	T	G	D	K	
QUS93818.1_GRVfV	1199	G	W	K	Q	L	T	N	S	M	N	A	A	R	T	L	N	D	C	G	F	A	A	T	I	A	S	S	Q	G	S	T	Y	N	H	P	A	C	I	N	L	D	K	N	S	S	Q	L	S	H	A	H	S	L	V	A	L	T	R	S	K	V	G	I	M	F	T	G	D	L		
Consensus_aa:		...lLhsSpst.poLpptG@.tlTtIASSOGST@p.shhhlbLD+pS..LS..hSLVALTRS+.GllFTGD.																																																																						
Consensus_ss:		eeeeehhhhhhhhhh hhh eeeee hhhheeeee eeeee h																																																																						

												CS										RdRp																																																
		6	9	65	5	57	5	85	9	6	95																																																											
Conservation:																																																																						
YP_009505639.1_BlVS	1171	K	M	L	E	E	G	P	T	S	N	L	L	F	S	R	Y	F	T	G	K	V	S	L	A	G	L	F	P	S	E	L	P	K	C	P	H	L	T	V	P	L	T	S	R	S	V	K	L	S	G	A	-----																	
MZ422607.1_GaMV	1184	A	Q	L	H	G	G	P	T	C	N	R	L	L	S	D	F	W	A	G	R	K	V	S	I	P	G	L	F	A	D	V	L	P	P	S	I	F	L	S	A	P	L	T	S	R	Q	R	S	V	S	G	A	G	A	S	A	P	A	W	T	P	C	S	L	R	N	G	P	E
ADD13602.1_OBDV	1161	A	L	L	N	G	G	P	N	S	N	L	M	F	S	A	F	F	Q	G	K	S	R	H	I	R	D	W	F	P	T	L	F	P	T	A	T	L	L	S	P	L	R	Q	R	H	N	R	L	T	G	A	L	--	A	P	E	V	P	S	H	L	L	P	D	L	P	S		
AYC35261.1_CSDaV	1320	A	Q	L	S	N	A	P	S	S	N	R	M	F	S	E	F	F	S	G	R	T	R	P	L	H	D	W	F	H	N	E	F	P	K	A	T	I	L	T	E	P	L	K	T	R	G	P	R	L	T	G	A	-----																
QLM05437.1_GAMaV	1282	G	I	L	T	G	H	T	T	S	N	R	M	F	A	E	F	Y	S	G	K	S	R	P	L	H	D	W	F	H	A	E	F	P	T	A	T	I	I	H	E	P	I	T	K	R	H	N	N	L	K	G	A	-----																
YP_009222597.1_NeVM	1177	S	I	L	L	K	G	A	S	T	S	N	T	M	F	S	L	L	M	S	G	K	T	R	P	I	Q	D	W	F	H	R	E	F	T	C	P	V	L	K	E	P	L	K	Q	R	H	N	R	L	T	G	A	H	--	G	E	T	-----											
MZ305310.1_PGMV	1149	A	L	L	D	G	T	P	S	A	N	I	L	S	H	V	A	Q	E	K	E	V	D	L	R	A	L	L	S	L	I	A	P	K	V	P	Y	L	V	A	P	I	K	S	R	K	L	T	L	R	G	G	-----																	
QID59334.1_SbMV	1118	S	I	L	D	G	T	S	Q	A	N	F	I	F	S	A	M	A	R	N	T	P	I	D	L	K	G	V	F	G	D	L	L	P	N	C	V	S	L	S	A	P	M	K	S	R	K	V	I	L	S	G	A	-----																
QID59002.1_CaMaV	1267	Q	L	L	D	G	T	P	S	S	N	A	M	F	S	A	L	F	A	G	K	P	Y	S	A	A	Q	L	S	E	L	F	P	P	C	P	R	I	S	E	P	I	T	S	R	R	T	L	L	K	G	A	A	S	H	A	S	L	P	Q	P	S	R	P	A	S	H	R	I	P
QQG34656.1_DiMV2	1300	M	L	L	S	G	T	S	T	S	N	Y	L	S	K	Y	W	N	G	D	K	V	H	L	S	S	L	F	P	S	E	L	P	K	C	P	H	I	T	E	P	I	T	S	R	K	L	K	L	Q	G	S	-----																	
YP_004464920.1_SwMV	1174	S	V	A	D	G	T	S	S	N	L	L	F	S	A	V	L	M	N	H	P	I	S	V	R	S	L	F	S	A	L	P	R	C	P	F	V	E	S	P	P	T	S	R	S	V	L	L	R	G	A	-----																		
NP_115454.2_MRFV	1144	A	A	A	D	G	T	S	S	A	N	L	L	F	S	A	V	L	L	D	R	L	S	V	R	S	L	F	S	A	L	L	P	C	C	P	F	V	T	E	P	P	T	S	R	A	V	L	L	R	G	A	-----																	
QCC30252.1_PeDV	1186	S	Q	L	S	G	L	S	A	S	N	L	M	F	S	A	L	A	S	N																																																		

Conservation:	5	95	6	6	6677669998597999	8	795	6	78
YP_009505639.1_BlVS	1236	APMIKSSSVSDV	LD	PVRPFLGDGDLNAPQISTHFLPETRRPLHFDIPSGKPSS-DSPASAEPTVPV	HEP	1304			
MZ422607.1_GaMV	1271	DPSVKSTEQRDV-ISHAPIVLGDGSLNAPQVSTHFLPETRRPLHFDLP	SAVCSS-VLSSPAAPTATAIEP			1338			
ADD13602.1_OBDV	1249	AAAVKPFDRSDV-LSWAPIAVGDGETNAPRIDTSFLPETRRPLHFDLP	SFRPQAPPPSDPAPSGTAFEP			1317			
AYC35261.1_CSDaV	1386	TPALKPDFQGDV-IIISAPIVLGSGELNAPQVSTHFLPETRRPLHWDIP	SAIPESATRPDSTEPTTCHPEP			1454			
QLM05437.1_GAMaV	1348	QPALKPSSSTADV-VLSAEIAGVGDSYNQPVSTHFLPETRRPLHFDLP	SARAEPADLPQSTEPSTTAFEP			1416			
YP_009222597.1_NeVM	1248	SPCIKPTEVSDI-ISADTVVLGDGALNRPQVSTHFLPEARRPLHSDLP	SAVPSSSELPSSADFTTPVHEP			1316			
MZ305310.1_PGMV	1206	-EKISPDYRGDVIIDCAAFGLGLGDECMRPVSTHFLPETRRPLHIDIA	SALPSSADRPQAPDHSATAYEP			1274			
QID59334.1_SbMV	1177	APPLKPDYQGDVILDLSAPFLGLGEANTPQVSTHFLPETRRPLHLDIP	SAKPENADRPTGPDHSDTAIEP			1246			
QID59002.1_CaMaV	1357	SSAITPDFRGDDVIDHSHPVSGDGSANSQISTHFLPETRRPLHLDIA	SAIPSSADRPSTDPDTTAFEP			1426			
QQG34656.1_DiMV2	1365	DPSVNSSFTADVINCINQSSIISGTGELNAPQISTHFLPETRRPLHFD	IPSAVPTA-CSLSDTDITTAYIEP			1433			
YP_004464920.1_SwMV	1238	SPPMRPDQGDVADIADLSAPFLGDGSSNAPQVSTHFLPESRRPLHFD	VPSARHQVADHPLKPDHSACAIEP			1307			
NP_115454.2_MRfV	1208	APPLGPDYVGDVILDSSAPILGDGSANAPQVSTHFLPETRRPLHFDIP	SARHQVADHPLAPDHSACAIEP			1277			
QCC30252.1_PeDV	1251	DHGFSPTTRDDVFLTQEDIVSGDELALQRVDTTFLPETRRPLHQDLPS	AINEP-APPTSVKFSDSAYEP			1319			
SBuMV-BU1	1385	ACVTDASSVADV-VAFAPLLHDFQPPVLPQVSTHFLPETRRPLHQDVPS	ALPEP-VSVSPVTHSDTAHEP			1452			
YP_003475889.1_OLV-3	1429	ARTTNPEATGDI-ITQSEIVLGDGELNMPQVSTHFLPETRRPLHFDNP	SALPSS-TVPSVDLSRTAFEP			1496			
YP_009551972.1_AVF	1278	SNPINSSFFIGDA-FSTASIFSGDGLNLPVSPHFLPETRLPLHFDLP	SAQISSAQPSDEVACSATPFTF			1346			
ATJ00054.1_MsMV1	1261	KPPINSSFFVGDA-YSTATIFSGDGLIAPRVSPHFLPETRLPLHFDIP	SAQVSSANPSNETNPSATPFTF			1329			
QQG34652.1_DiMV1	1454	YTSIDSNYTADIYLNQSNTYHTPTE-DTNQISTHFLPETRRPLHFDLP	STQSDPNPSSAFLPSSSAPEP			1522			
YP_002756536.1_GSyV-1	1282	-RVFNPERDDV-FVEAAVCGDGSNAPQVSTHFLPETRRPLHFDLP	SAKPEFAAHAPAPLDTFTFIEP			1349			
QUS93818.1_GRVfV	1334	---LGPTDLPDLLLPEAPIIRNGESNAPQVSTHFLPETRRPLHFDV	ASAIPEPAKPSGVDPLDLASITP			1400			
Consensus_aa:		s.shpss..sDl.ls.s..h.GsG..shPpISTHFLPETRRPLHbDlsSA..ps.s.s.s..oshhhpP							
Consensus_ss:		ee							

Conservation:	79989	97	66559	8	5875	698	95999	7	56	65576558	97	9	55	999995999
YP_009505639.1_BlVS	1305	VYPGETFENLAAHFLPCHDPEDREIHFRGQLSNQFP-HINRPFELACQSSSLLAAVH	SERDDPTLLPASI			1373								
MZ422607.1_GaMV	1339	VYPGETFENLAAHFLPPHSPEDREITYRSQLSNQFP-HINRPFELAAQPSSLLAAIHNEKNDPTLLAASI				1407								
ADD13602.1_OBDV	1318	VYPGETFENLVAHFLPAHDPTDREIHWRGQLSNQFP-HIDKEYHLAAQPMTLAPIHDSKHDPTLLAASI				1386								
AYC35261.1_CSDaV	1455	VYPGETFENLAAHFLPAHDPTDREIYWQQLSNQFP-HMDKEFHLLAAQPMSSLLAAVHGEKQDPTLLPASI				1523								
QLM05437.1_GAMaV	1417	VYPGETFENLAAHFLPAHDPTDREIHWAGQLSNQFP-HINKEYHLAAQPLSLLAAIHSEKDDPTLLPASI				1485								
YP_009222597.1_NeVM	1317	VYPGETFENLAAHFLPAHDPTREIVFRNTMSNQFP-HLNKDFHLSAQPSSLLAAIHSEKDDPTLLPASI				1385								
MZ305310.1_PGMV	1275	IYPGETFENVAHFLPAHDPAKKEINFRGMLSNQFP-HINMPFELSQAQPSNLLAAIHSSKHDPPTLLPASI				1343								
QID59334.1_SbMV	1247	IYPGESFEALAAHFLPAHDPTREIYYRGEMSSQFP-HLNRPFELSQAQPSNLLAAIHAPKQDPTLLAASI				1315								
QID59002.1_CaMaV	1427	VYPGETFENLAAHFLPAHDPEKDIYFKGQLSSQFP-HLNRDWSLSCQPSSLLAAIHSSKQDPTLLPASI				1495								
QQG34656.1_DiMV2	1434	VYPGETFENLAGHFLPCHDPAQREIHYMGQLSNQFP-HIDRPFHLSAQPSLLAAIHDSKQDPTLLPASI				1502								
YP_004464920.1_SwMV	1308	VYPGESFEQLAALFLPPTDAESKEIRFRGELSNQFP-HLDKPFELISAQPSLLAPVHNSKHDPPTLLPASI				1376								
NP_115454.2_MRfV	1278	VYPGESFESLASLFLPPTDAESKETIFRGEEMSNQFP-HLDKPFELGAQTSSLLAPLHNSKHDPPTLLPASI				1346								
QCC30252.1_PeDV	1320	VYPGEDFFALAAHFLQANDPTREILFRDITLSCQFP-FLDEPFEISCQPMALLAAHREKKDPTLLPASI				1388								
SBuMV-BU1	1453	VYPSENFENLVAHFLPRDPALEIYVQDQTSNQFP-LLDQPFHLSTLPSSLLAAIHSSKQDPTLLPASI				1521								
YP_003475889.1_OLV-3	1497	VYPGETFENIAGHFMGPRDPEVLEIIHNDQMSNQFP-LLDQPFSLAAQPSLLMAAIHNSQNDPTLLPASI				1565								
YP_009551972.1_AVF	1347	VYPGEDFFSLAAHFNPNHDPELKEILYRDACSNQFP-WVNLFPFEISCQPSLLAAIHSSKNDPTLLPASI				1415								
ATJ00054.1_MsMV1	1330	IYPGEDFFSLAAHFNPNCHDPELKEILYRDACSNQFP-WVNQPFFEISCQPSLLAAIHSSKNDPTLLPASI				1398								
QQG34652.1_DiMV1	1523	VYPGENFESVASSFIPPTDPETREIRFHGELSNQFP-YVNMPFKLSSLPSTLAAIHSSKHDPPTLLPASI				1591								
YP_002756536.1_GSyV-1	1350	VYPGETFENIAAHFLPAHDPEKDIYFKDQRSNQFP-FIDQPFHVGAPASLCAAVHSSKQDPTLLAASI				1418								
QUS93818.1_GRVfV	1401	VYPGESFENLARCFLPAHDPEKDIWYRNQLSNQFP-HMDKEFHLSAQPSLLAPVHSTARDPTLLKASI				1469								
Consensus_aa:		VYPGEsFEsIaThfLp+DPp.+EIH@psphSsQFP.@lspSfclttQPtOLAAIHspKpDPTLLsASI												
Consensus_ss:		hhhhhhhhh eeee hhhhhhhh												

Conservation:	99999965	69	76	697	99	97	5	8587	9	6	5977	875999	6997799789885697
YP_009505639.1_BlVS	1374	PKRLRFRPSSAPYRLTAKDEVLGSLLYEGLCRAYHRNSFTVLPFNETLYLECIALNEFAQLSSKTSQSVIM				1443							
MZ422607.1_GaMV	1408	QKRLRFRPSDAPYQLTSKDEILGSLLYEAWCEAYHRSPSDTVPFDPVLFACIALNEFAQLSSKTSQSVII				1477							
ADD13602.1_OBDV	1387	QKRLRFRPSAPYRITPRDELGLLFEGLCRAYHRSPSTHFPDEALFIECINLNEFAQLTSKQAVIM				1456							
AYC35261.1_CSDaV	1524	QKRLRFRPSDRPYQITPKDEILGQLLFEGLCRAYHRSPFHTEAFDPVLFACINLNEFAQLSSKTSQATIM				1593							
QLM05437.1_GAMaV	1486	QKRLRFRPTAPYFISPRDEILGQLLFEGLCRGYHRSPLSSEPFDPVLYAECICLNEFAQLTSKTSQAVIM				1555							
YP_009222597.1_NeVM	1386	GKRLRFRPSDAPYQITSKDEILGQLLYEGWCRAYSRNPNAEPPFDEALFACINLNEFAQLTSKTSQAVIM				1455							
MZ305310.1_PGMV	1344	SKRLRFRPSTRPYQITAKDELLGGLLFEGLCRAYHRSPELTHPFNEQLFIECIGLNEFAQLSSKTSQAVIM				1413							
QID59334.1_SbMV	1316	TKRLRFRPTSPYEITSKDELLGSLLFESLCRAYRRHPHSTVPFNETLFIECINLNEFAQLTSKTSQAVIM				1385							
QID59002.1_CaMaV	1496	AKRLRFRPSSKPYQITAKDQVLGQLLFEGLCRAYRRNPSTSTETFTFIECINLNEFAQLTSKTSQSVIM				1565							
QQG34656.1_DiMV2	1503	AKRLRFRPTSRPYTITARDELLGQLLFDLSCTAYHRSSSHLEDNEQLFIECIALNEFAQLSSKTSQNVIM				1572							
YP_004464920.1_SwMV	1377	AKRLRFRHNDASAYTISARDEILGGLLYEAWCRAYRRSPLDIEPFDPVLYAECINLNEFAQLSSKTSQATIM				1446							
NP_115454.2_MRfV	1347	GKRLRFRHSEAPYVIAPRDEILGSLLYAACRAYHRSPRDVEPFDPDLYAECINLNEFAQLSSKTSQATIM				1416							
QCC30252.1_PeDV	1389	PKRLRFRPSEAPYSITPKDEILGGLLFNSLCRAYRRNPNDTVPFDEVLFAECIALNEFAQLTSKTSQATIM				1458							
SBuMV-BU1	1522	GKRLRFRPSNNPYHLTAKDEFLGGQLFEGLCRAYHRNPNDSHPFDPILFAECINLNEFAQLTSKTSQSTII				1591							
YP_003475889.1_OLV-3	1566	GKRLRFRPSNAPYPIAEDQILGSLLFELCRAYRRHPEAVVPFNPIAFACINLNEFAQLTSKTSQAVII				1635							
YP_009551972.1_AVF	1416	QKRLRFRPNSSPYQISTKDEVGLILFNSLCRAYHRNPSDVVPFDELLFIECINANEFSQLSSKTSQAVIM				1485							
ATJ00054.1_MsMV1	1399	QKRLRFRPNSSPYISTKDEVGLILYNALCRAYNRNPSTVVPFDELLFIECINANEFAQLSSKTSQAVIM				1468							
QQG34652.1_DiMV1	1592	PKRLRFRHNDSPYQISPKDELLGTFLYTSLLKAYRRPLYSTEPFDEALFIECINANEFSQLTSKTSQNVIM				1661							
YP_002756536.1_GSyV-1	1419	EKRLRFRASDAPYQITAKDEILGSLMFEAHCRAMRRDPNVRVPFDEALFACIALNEFAQLTSKTSQAVIM				1488							
QUS93818.1_GRVfV	1470	GKRLRFRPSDSPYRLTSKDEILGSLLFDAHTAMLRSPCASVPFDENLFAECIALNEFAQLSSKTSQAIIM				1539							
Consensus_aa:		.KRLRFRsOs.PYpLos+DELG.hL@pthC+AYpRsP.ss.PFs.hLfheCISlNEFAQLoSKTQtHh											
Consensus_ss:		hhh hhhhhhhhhh hhhhhhhhhhhh hhhhhhhh hhhhhhhh hhhhh											

		RdRp I	RdRp II
Conservation:		695 9999999678979979599969659698	99999999999987795899999998 69 769 56
YP_009505639.1_BlVS	1444	ANSKRSDPDWRYS SAVRIFSKAQ HKVNENSIFG W KACQ TLALM HDA VLL LG PVKKYQ RM FDAQ DRPA L	1513
MZ422607.1_GaMV	1478	ANASRSDPDWRWSVVRI F SK TQ HKVNENSIFG S W K ACQ TLALM HDA VLL LG PVKKYQ RI FDAQ DRP STL	1547
ADD13602.1_OBDV	1457	GNARRSDPDWRWSAVRI F SK TQ HKVN EGS IFG A W K ACQ TLALM HDA VLL LG PVKKYQ RV FDA DRP AHL	1526
AYC35261.1_CSDaV	1594	GNARRSDPDWRWSAVRI F SK TQ HKVN EGS IFG S W K ACQ TLALM HDA VLL LG PVKKYQ RV FD QDRD RPHL	1663
QLM05437.1_GAMaV	1556	GNARRSDPDWRWSAVRI F SK AQ HKVN EGS IFG P W K ACQ TLALM HDA VLL LG PVKKYQ RV FD TRDRP STL	1625
YP_009222597.1_NeVM	1456	GNARRSDPDWRWSAVRI F SK AQ HKVN EGS IFG S W K ACQ TLALM HDA VLL LG PVKKYQ RM F DQDRP SHL	1525
MZ305310.1_PGMV	1414	ANACRSDPDWRWTAVRI F AK AQ HKVN EGS IFG P W K ACQ TLALM HDA VLL LG PVKKYQ RV FD EAER PSHL	1483
QID59334.1_SbMV	1386	ANASRSDPDWRWTAVRI F SK AQ HKVN EGS IFG S W K ACQ TLALM HDA VLL LG PVKKYQ RI F DEIDR PDHL	1455
QID59002.1_CaMaV	1566	ANASRSDPDWRWSAVRI F SK SQ HKVN EGS IFG P W K ACQ TLALM HDA I ILLG PVKKYQ RV LD QDRD PAHL	1635
QQG34656.1_DiMV2	1573	SNASRSDPDWRWSAVRI F SK TQ HKVNENSIFG D W K ACQ TLALM HDA I ILLG PVKKYQ RI FD QDR CPHL	1642
YP_004464920.1_SwMV	1447	ANANRSDPDWRWSAVRI F AK TQ HKVN EGS LF G S W KACQ TLALM HDA VLL LG PVKKYQ RV FD QDRD PSHL	1516
NP_115454.2_MRFV	1417	ANANRSDPDWRWSAVRI F AK TQ HKVN EGS LF G S W KACQ TLALM HDA VLL LG PVKKYQ RV FD QDRD PSHL	1486
QCC30252.1_PedV	1459	ANANRSDPDWRWTAVRI F AK TQ HKVN DGS IFG S W K ACQ TLALM HDA VLL LG PVKKYQ RV FD QADR PSHI	1528
SBuMV-BU1	1592	ANARRSDPDWRWTAVRI F SK TQ HKVN EGS LF D W K ACQ TLALM HDA VI ILLG PVKKYQ R H FDAR DPATI	1661
YP_003475889.1_OLV-3	1636	SNARRSDPDWRYSAVRI F SK TQ HKVN DGS FF G S W KACQ TLALM HDA VI ILLG PVKKYQ RL FD SEDR PSHI	1705
YP_009551972.1_AVF	1486	ANSDRSDPDWRWSAVKI F SK AQ HKVN EGS LF G D W KACQ TLALM HDA VI ALG PVKKYQ RL FD KDQ PSNI	1555
ATJ00054.1_MsMV1	1469	ANADRSDDPDWRWSAVRI F SK AQ HKVN EGS LF G D W KACQ TLALM HDA VI ALG PVKKYQ RI FD KTR PDNI	1538
QQG34652.1_DiMV1	1662	ANAYRSDPDWRWSAVRI F AK TQ HK TND ASIFG N W K ACQ TLALM HDA VI ILLG PVKKYQ RI FD KRDR PSNI	1731
YP_002756536.1_GSyV-1	1489	ANHERSDPDWRWTAVRI F AK NQ HKVN SGS LF G P W KACQ TLALM HDA VI LLF G P V KKY Q LI H DERDR PEHI	1558
QUS93818.1_GRVfV	1540	ANRDRSDPDWRWSAVRI F AK TQ HKVN DHS IFG G W K ACQ TLALM HDA VLL LG PVKKYQ RI FD AADR PSNI	1609
Consensus_aa:		tNtpRSDPDWR@oAVRI F t K o HKVN -t S LF G S W KACQ TLALM HDA VI LL LG P V KKY Q RI FD .pDRPsp1	
Consensus_ss:		h hhhhhhhhh h eeeee hhhhhhhhhhhhhhhhhhhhh e	

[illegible]

Conservation:

			6	5	5	5	5	75	585	Minor CP	
YP_009505639.1_B1VS	1773	SSAQRALLTSS	RQGRSLPDNPEVSKL	QGELL	QSFQ	-----	-----	-----	-----	FV	1810
MZ422607.1_GaMV	1807	PAAIRYRLHSHKFLTRSLPESPDVTAL	QEGELL	HMSQ	-----	-----	-----	-----	-----	L	1843
ADD13602.1_OBDV	1785	PSRLRLAILHSSRQHRSLPEDPAVSSL	QEGELL	HTFHA	-----	-----	-----	-----	-----	PM	1823
AYC35261.1_CSDaV	1923	SSAARVAILRSSRNSRSMPPDDPTLL	QEGELL	QHfq	-----	-----	-----	-----	-----		1958
QLM05437.1_GAMaV	1885	SSAARWAILHSSRSTRSQPEDPDVTRY	QEGELL	QHLQ	-----	-----	-----	-----	-----	SV	1922
YP_009222597.1_NeVM	1784	NSAARQILLHSSRNPRSLPEDPDTTKY	QEGELL	QTLQL	-----	-----	-----	-----	-----	SA	1822
MZ305310.1_PGMV	1743	NFKHRRQLHSSRQGRSLPDDPEVSKL	QEGELL	QTFQS	-----	-----	-----	-----	-----	NIKLPLSGGL	1789
QID59334.1_SbMV	1715	SVNHRRQILHSGRLGRSMPEDPQVSQ	QEGELL	QSFQS	-----	-----	-----	-----	-----	SIHLPLRGGC	1764
QID59002.1_CaMaV	1895	SAQDRRQILNSSRQSRMPEDPEVAQL	QAE	LG	YFHL	SGGSDG	SPNPAPHRT	PCGPGQ	QVIFPS	SAGSPSGS	1963
QQG34656.1_DiMV2	1902	NSSQRKAILHAHRPSKTSYQNP	EVSKL	QSELL	HSLQ	-----	-----	-----	-----	LA	1939
YP_004464920.1_SwMV	1776	NSSHRRQLHSSRRRPRSLPEDPEVSKL	QEGELL	HQFQ	-----	-----	-----	-----	-----	SLHLPLRGA	1822
NP_115454.2_MRFV	1746	NSSHRRQLHSSRRRPRSLPEDPEVSKL	QEGELL	HQFQ	-----	-----	-----	-----	-----	SLHLPLRGG	1792
QCC30252.1_PeDV	1788	RGASKSKIIAA-RKTRPMPEASDVSQ	HQ	QGL	PKPYTFQ	-----	-----	-----	-----	GL	1824
SBuMV-BU1	1921	SSAARFAVVKF-RQSRSPEDPEVSKL	QGH	LR	DF	FMSYFQ	RNSHRARNSQ	PPPPPPRP	IPPPPTPT	PPP	1988
YP_003475889.1_OLV-3	1965	SATARHLLIKS-RLTRPPPESEVSKL	QGQL	L	AS	FQHMFS	RASK	-----	-----	KS	2009
YP_009551972.1_AVF	1815	SSAQRI	SFLKLSKLYRQ-NRLPIH	SQHL	EGELL	PFMSNSSSS	LDFAPLADSNNFY	SNSDQVYH	PHSRSLP	-----	1882
ATJ00054.1_MsMV1	1798	SSAQRI	SFLKLTKNYRQ-NHLPVSTLH	EGELL	PMSN	-LSSTF	DSPI	SNIDNFFS	NTDQIYH	PHSRSLP	1864
QQG34652.1_DiMV1	1990	SSP	-----	-----	EGELL	PS	-----	FD	SLTHSPDLLT	QQTI	2025
YP_002756536.1_GSyV-1	1826	NSAQRK	VLLTRSPQLHFP	PGDAPEVSKL	QEGELL	QSF	-----	-----	-----	M	1862
QUS93818.1_GRFV	1869	SSLQRR	ALRGKAVRQHFP	GD	SK	EVTE	LQEGELL	HTFS	-----	MS	1906
Consensus_aa:		sts.R..llp.pp..+.scsP-lophQGL..hp.....									
Consensus ss:		hhhhhhhhhhhh									

Conservation:		CS		Major CP	
		6	55 5	5	
YP_009505639.1_BlVS	1811	PQPSM-----NNSLLL-----	PLFGG-----	LSPSLA	AHPMGP
MZ422607.1_GaMV	1844	NQSSM-----HPDTLL-----	PLHGG-----	SSNILPTPAIPSLPITPA-S	MANASL---
ADD13602.1_OBDV	1824	PSPPS-----L-----	PLFGG-----	LSPDNILTPHEFRTALYE--	SSAYPTPPNS
AYC35261.1_CSDaV	1959	-VPFM-----QSDTLL-----	PLTGG--SAP--	ILTPEAFSTSLAFS	MASD-----
QLM05437.1_GAMaV	1923	PSSRM-----NPD TLL-----	PLKGG--SAP--	QLTPEAFSLALAQS	MATPN-----
YP_009222597.1_NeVM	1823	PLHSM-----NHSTLL-----	PLTGGSSASAP--	SLTPLQFSEAVTQS	MASN-----
MZ305310.1_PGMV	1790	MENAL-----NCSTLTPD-----	VPLPLSGA-LNSGY--	DPAPLYQSA	MTTLA-----
QID59334.1_SbMV	1765	AEAHQ-----LLT-----	PLSGA-----	ISTPPGQTF	MALDA-----
QID59002.1_CaMaV	1964	PHHTL-----DCSTFSNCHMSDSLPELY	LSGGALNTPP--	ALSPSPSLLF	MASTP-----
QQG34656.1_DiMV2	1940	DQPSM-----QPETLL-----	PLTGS--NHPSQHFNIPQFSLP	MSDAS-----	
YP_004464920.1_SwMV	1823	PNPLA-----APFRLL-----	PLGSAS--LGPSYSVAPLQPPPA	SPASEPDS	MAENA---
NP_115454.2_MRFV	1793	PNPLA-----ALFRL-----	LQSSS--LGPTYAVAPIARAP	VLPSP	SMADNA---
QCC30252.1_FeDV	1825	TTHPL-----M-----	TLSGAA-----	SPANLAFLGSSAVPDLEF	M--S
SBuMV-BU1	1989	QPPSTSQSKPALHSSPSTFL-----	PLLPEPVLLDP---	VPVESALAS	PITPLDSSSVFDLP
YP_003475889.1_OLV-3	2010	KSPSQSYQPRQPATPTSVL-----	SPPSSPPLSPSTFAPPEPPPPPPPPPPPPPPSV	QGIGIP	
YP_009551972.1_AVF	1883	SNPLF-----	LSGGMALSAIEALAQLLPLIQGGRDLLASTSDVSSP		
ATJ00054.1_MsMV1	1865	QPPIF-----	LSGGSMALTALEALTQLLPLIQGKNLLTSTQDVPEQ		
QQG34652.1_DiMV1	2026	SHPPH-----L-----	PMEE	LALLPALRELLSKNSSDAH	PSPQTVA--
YP_002756536.1_GSyV-1	1863	MQPT-----L-----	PLTGG-----	LLLPPAVDAP	MSDD-SLA-----
QUS93818.1_GRVFV	1907	SPPSK-----	LTGG-----	LLLPTSPS	MSNEAT-----
Consensus_aa:		..S.....L.....	PL.tts...ss...hss...s.....s.....		
Consensus ss:		eee	hhh	hh	

Conservation:		55	5	6	8	6	59	88	75	CPI	6	
										9996		
YP_009055639.1_BlVS	1843	-----SQVGPAPP-NDD	RVDR	QPSLP----	LAPRVAEVSPLHA--	HIDY	PFQW	EVGT	YS	GD	KA	AFV
M2422607.1_GaMV	1886	-----TQVGPA	PA-ADSR	IDAQPSLP----	RAPRL	LESSVPV--	YIDY	PFQW	QI	AS	YTS	GS
ADD13602.1_OBDV	1863	PTSM	SGIHASQVGP	PPA-SDDRT	RQPSLP----	LAPRL	VESSLAVP--	YVDV	PFQW	AV	AS	YAG
AYC35261.1_CSDaV	1996	-----AQAGPAPS	-RDDR	VDRQ	PRLP----	AAPRVAE	VGLNAP--	SVDY	PFQW	VV	AS	YDG
QLM05437.1_GAMaV	1962	-----VQAGPPP	-SDDRT	DRQ	PPLP----	RAPRL	VEDASAIP--	FVDY	PFQW	VV	AS	YDGL
YP_009222597.1_NeVM	1863	-----GQVGPPP	-RDDR	VDRQ	PRLP----	VAPRVAE	VDLQAP--	TVDY	PFQW	VI	SS	YDG
M2305310.1_PGMV	1831	-----TNAGPAQ	-TDDR	VDRQ	PPLP----	PAPRV	ETAAP--	HIDL	PFQW	LL	GN	APG
QID59334.1_SbMV	1792	-----TKVGAPD	-RDDR	IDRQ	PPLP----	APPRV	LETQAPV--	HVDV	PFQW	VV	SS	YAGE
QID59002.1_CaMaV	2013	-----SDVGPPP	-SDDRR	DHQ	PRLP----	APSRV	VEALAPI--	YIDY	PFQW	KV	GT	YTGA
QQG34656.1_DiMV2	1977	-----TQVGRPSD	-RDDR	SDP	QPSLP----	LAPRL	RETKAQ---	EILY	PFQW	VV	GE	YDG
YP_004464920.1_SwMV	1866	-----TQVGPA	PA-RDDR	LDRQ	PAIP----	APPRV	LETAPH--	YIDL	PFQW	KI	TD	FTGA
NP_115454.2_MRFV	1834	-----TNQVGVP	PP-RDDR	VDRQ	PPLP----	DP	RVLETAPSH--	FLDL	PFQW	KV	TD	FTGA
QCC30252.1_PeDV	1857	NAQT----	PNVG	PRPD-SDVR	VDRQ	PLLPAPN	PGPPAPLPSKNP----	DVTV	PFQW	VI	SD	FDG
SBuMV-BU1	2043	LHLM	ANVQTGQDSS	APP	HRDR	FD	PQ	PGLP----	LAPSL	SQTS	SNQAP--	FVDV
YP_003475889.1_OLV-3	2066	LHF	MANTTPPPSG	PAPP-RDDR	VDRQ	PPLP----	LAPQI	QETSSVP--	HVDI	PFQW	LS	ASLT
YP_009551972.1_AVF	1925	SSAQ----	AEKSPAG	SSPDAR	VL	RAPPLP----	SPARQ	LS	TPVSTSS	ISLD	PFQW	NFFDL
ATJ00054.1_MsMV1	1907	TAAQ----	TPSSPAG	SSPDAR	VL	RAPPLP----	SPARQ	L	PTEVS	ASSLS	IEL	PFQW
QQG34652.1_DiMV1	2064	-----PAILPGSS	-SGM	RLVSP	PRLP----	APVRS	L	TPPAS	LAQDS	ISL	PFQW	FTY
YP_002756536.1_GsYV-1	1890	-----GRARSQRD	-PDHR	VDP	QPSLP----	LAPSV	QETPGGP--	AITV	PFQW	VA	L	VVK
QUS93818.1_GRV	1930	-----VPVSGRPS	RDDHRS	SDP	QVLP----	LAPKV	QESQAL----	ALS	IP	PFQW	VA	L
Consensus_aa:	s.stssss.pDsRhD.p.LP.....ssp..ps.s.h...lshPFQW.h.shsG.s...										
Consensus ss:	euee.....euee.....euee										

		CP II															CP III																																																						
Conservation:		7	6	5	7	5	7858	7	58	8	75	955	796	65	7	6966	5	9																																																					
YP_009050639.1_BlVS	1897	SDDL	S	A	S	K	T	L	K	T	L	T	A	G	Y	R	H	A	E	I	L	S	A	E	V	D	V	F	L	P	L	A	S	F	S	K	P	I	S	V	G	A	V	W	T	I	A	S	I	S	P	A	S	A	H	E	Q	S	Y	Y	G	G	R	L	L	T	L	G	1966		
MZ422607.1_ObMV	1939	TDDL	S	A	S	P	T	L	K	K	V	M	A	G	Y	R	H	A	E	L	L	H	V	E	L	F	S	P	L	P	Q	S	F	S	K	P	V	S	L	S	A	V	T	I	S	S	L	C	P	A	T	T	E	G	T	E	T	S	F	Y	G	G	R	V	F	T	I	G	2008		
ADD13602.1_ObDV	1926	TDDL	S	G	S	H	L	S	R	L	T	I	G	Y	R	H	A	E	L	S	A	E	L	F	A	P	L	A	A	F	S	K	P	I	S	V	T	A	V	T	I	A	S	I	A	P	A	T	T	E	L	Q	Y	Y	G	G	R	L	L	T	L	G	1995								
AYC35261.1_CSDaV	2050	SDDL	S	G	S	A	T	L	T	K	V	M	A	N	Y	R	H	A	E	L	T	S	V	E	L	V	C	P	L	A	A	F	S	K	P	I	S	V	S	A	V	W	T	I	A	S	I	S	P	A	S	A	S	E	T	S	Y	Y	G	G	R	L	F	T	V	G	2119				
QLM05437.1_GAMaV	2016	TDVL	S	G	S	K	T	L	S	T	I	T	A	N	Y	R	H	A	E	L	L	S	V	E	L	F	A	P	L	A	G	S	F	S	K	P	I	T	L	S	A	V	W	T	V	G	S	I	P	A	T	T	T	E	T	S	Y	Y	G	G	R	V	I	T	I	G	2085				
YP_009222597.1_NeVM	1917	TEDL	A	G	S	A	T	L	S	K	L	T	A	N	Y	R	H	A	E	L	S	V	E	L	V	A	P	L	A	A	F	S	K	P	I	S	I	S	V	W	T	I	A	S	I	T	P	A	T	T	T	E	S	Y	Y	G	G	R	L	I	T	V	G	1986							
MD305310.1_PGMV	1883	TDAM	A	T	S	V	N	I	S	K	L	M	A	G	Y	R	H	A	E	L	T	L	T	K	L	E	V	V	P	L	A	A	F	A	K	P	I	T	T	L	V	W	T	I	S	L	P	T	S	T	N	E	L	A	Y	G	G	R	Q	L	T	L	G	1952							
QID59334.1_SbMV	1845	SHTL	A	A	A	G	R	L	V	N	L	T	S	L	Y	R	H	A	E	L	L	H	A	E	V	F	A	P	T	W	N	A	F	S	K	P	V	S	A	V	W	T	V	A	D	I	P	A	T	T	K	E	Q	E	Y	Y	G	G	R	Y	L	T	L	G	1914						
QID59002.1_CaMaV	2066	TDDL	S	G	S	A	T	L	K	T	I	T	N	G	Y	R	H	A	E	L	S	V	E	A	E	F	S	P	L	A	A	S	F	G	K	P	I	T	F	S	V	W	T	V	A	D	V	A	P	A	T	L	T	E	T	A	Y	Y	G	G	R	I	T	I	G	2135					
QOG34656.1_DiMV2	2029	TEDL	S	A	S	S	S	L	N	K	V	T	A	G	Y	R	H	A	E	L	V	S	L	E	L	E	F	S	P	L	A	P	S	F	S	K	P	V	T	F	T	V	W	T	I	A	S	I	T	P	A	Q	T	K	E	T	T	Y	F	G	G	R	V	L	T	I	G	2098			
YP_004464920.1_SwMV	1919	TGDL	S	A	S	P	V	L	T	T	L	C	A	P	Y	R	H	A	E	L	S	V	E	L	S	L	A	P	C	P	P	S	F	T	K	P	I	M	F	T	V	W	T	P	A	T	L	S	P	T	D	G	K	E	T	D	Y	F	G	G	R	Q	I	S	I	G	1988				
NP_115454.2_MRFV	1887	TDDL	S	A	S	A	V	L	T	T	C	A	P	Y	R	H	A	E	L	L	V	E	I	S	V	A	P	C	P	S	F	S	K	P	I	M	F	T	V	W	T	P	A	T	L	S	P	A	D	G	K	E	T	D	Y	Y	G	G	R	Q	I	T	V	G	1956						
QCC30252.1_PeDV	1917	TLDL	S	A	S	S	T	L	K	K	V	T	A	Y	F	R	Y	A	E	I	Q	S	V	E	A	L	I	I	A	D	A	A	I	S	K	P	I	P	V	S	L	V	W	T	I	N	T	L	P	D	S	G	K	E	L	D	Y	F	G	G	R	I	V	A	G	1986					
SBuMV-BU1	2107	TTTL	A	S	A	S	P	V	L	T	T	L	C	A	P	Y	R	H	A	E	L	S	V	E	L	F	V	P	T	S	L	S	F	S	K	P	I	S	V	S	A	A	W	T	I	A	S	I	T	P	A	A	A	E	M	D	Y	Y	G	G	R	F	L	T	V	G	2176				
YP_003475889.1_OLV-3	2129	TVSL	S	A	S	Q	S	T	L	S	K	L	W	A	L	Y	R	H	A	E	L	S	V	E	A	E	F	V	P	T	A	S	S	F	K	P	I	S	I	S	C	A	W	T	I	A	S	I	T	P	A	S	D	G	K	E	T	D	Y	F	G	G	R	F	L	T	I	G	2198		
YP_009551972.1_AVF	1986	S	I	S	I	A	G	S	S	H	I	T	L	P	Q	Y	R	Y	A	R	L	I	N	L	E	V	V	F	P	M	A	I	S	M	K	P	Q	T	V	D	V	W	C	T	A	D	Q	T	I	D	G	K	I	M	A	T	Y	G	S	Q	R	I	S	I	G	2055					
ATJ00054.1_MsMV1	1968	S	L	S	I	A	G	S	T	H	I	T	S	L	P	Q	Y	R	Y	A	R	L	L	Q	E	L	V	V	F	P	M	S	I	M	K	P	Q	T	V	D	V	W	S	T	A	D	Q	T	I	D	E	K	I	M	A	T	Y	G	S	Q	R	I	S	I	G	2037					
QOG34652.1_DiMV1	2120	S	L	D	V	S	G	K	D	V	I	L	N	L	I	K	P	F	S	H	A	R	L	S	I	S	E	A	V	V	F	P	Y	S	A	S	L	T	Y	P	Q	T	F	D	A	V	W	S	T	A	D	S	V	I	A	G	A	D	I	N	V	Y	G	A	Q	R	V	T	F	G	2189
YP_002756536.1_GsYV-1	1942	T	V	D	P	P	R	A	K	S	L	T	Q	L	I	G	P	Y	R	H	A	R	L	S	L	E	A	I	L	M	P	T	L	N	A	F	Q	N	P	V	T	V	H	M	V	W	T	V	N	T	V	Q	P	A	S	G	E	E	L	F	Y	P	G	G	Q	A	L	T	V	G	2011
QUS93818.1_GRVfV	1982	T	V	D	L	A	A	S	T	L	K	K	L	T	D	P	F	R	S	C	E	I	T	H	L	E	V	V	L	M	P	T	L	N	A	F	N	N	P	V	T	L	H	C	V	W	T	V	N	S	I	Q	P	A	S	G	D	E	L	L	Y	G	G	Q	A	I	T	A	G	2051	
Consensus_aa:		o.sittstssllp ^h hs.yr@AcLhpl ^{Eh} .hhPh.sthppPlohshVwohssh..hsspbh.h@GGp.lolG																																																																					
Consensus ss:		eeeeee					hhhh					eeeeeeeeee					eeeeeeee					eeeeee					eee																																												

CP II

Conservation: CP III
 YP_009505639.1_BlVS 1967 **GPV**LMSSST**TRIP**LDVSRINP**VIK**SSVSYSSTP**RI**SYTVYS-AA----GTANTAL**ISVIIRGIVRL**SG--- 2028
 MZ422607.1_GaMV 2009 **GPV**LMSSSTVLPADLNRLNPVILSPVAFTDCPRYSYTIYKCD-----SSNTSNLVSVLIRGVVRLSG--- 2070
 ADD13602.1_OBDV 1996 **GPV**LMGSGVTRIPADLTRLNPVIKTAVGFTDCPRFTYSVYANS-----GSANTPLITVMVRGVIRLSG--- 2057
 AYC35261.1_CSDaV 2120 **GPV**LMSSSTTHLPADLTRLNPVLKGPVKYTDPCRFYSYSVYNSG-----GKTGTNLCTIILRGVVRLSG--- 2181
 QLM05437.1_GAMaV 2086 **GPV**LMNSTTAVPADLRLNPVIKQISYTDPCRFYSVYANG-----GTAGTNLVTVLIRGVVRLRS--- 2147
 YP_009222597.1_NeVM 1987 **GPV**LLSSTTRIPADLSRLNPILKSSVGKDTPRLSYTVYANS-----GTAGTNLCSVIIRGILRLSA--- 2048
 MZ305310.1_PGMV 1953 **GPV**LMGSTTTVPICDLTRINPHLKSSVTYNDTPRLTYTTYANS-----GAANAPLINFIVRGIIRLSG--- 2014
 QID59334.1_SbMV 1915 **GPV**AMGSGTTIVPADLARINPVIKSAVYIDGPRLSYTIYANG-----GTANTNLVNVITIRGSIRLSS--- 1976
 QID59002.1_CaMaV 2136 **GPV**LMSSSTSVPADLSRLNAVIKASVSYRDTPRLSYTACSCG-----GSANTNLAQVTLRGVVRLSG--- 2197
 QQG34656.1_DiMV2 2099 **GPV**LMSSSTSIADLSRLNPVIKSSVPFSDTPRFTFTSPGVSS-----ATKGSNLVSIILRGITIRLSG--- 2161
 YP_004464920.1_SwMV 1989 **GPV**LMSSSTTAIPADLTRMNPVIKSSVAYRDTPRWTMSVPAVSG---GDTKVNLATGFIRGVIRVSA--- 2051
 NP_115454.2_MRfV 1957 **GPV**MLSSTTAVPADLARMNPFIKSSVSYNTPRWTMSVPAVTG---GDTKIPLATAFVRGIVRVSA--- 2019
 QCC30252.1_PeDV 1987 **GPV**SLATRNVIPADLTRLTPIIKDRVSYSSTPRLTWTQAQKVAG---GAKGTTLCSLVIVGTILLSA--- 2049
 SBuMV-BU1 2177 **GPV**LLSSTTHIPCLNSINPTIKTSVSYSDTPRFTFTARAVSG---GSANAALALVIIRGVVRLSG--- 2239
 YP_003475889.1_OLV-3 2199 **GPV**LLSSTTHIPCDLRSINPTLRSSVEFRDTPRVTFARAVAG---ATANTPLAHFIIIRGVLRSLSG--- 2261
 YP_009551972.1_AVF 2056 **GPL**NMSSSHSILPANLSSLNPVVKDSVTYNDTPKLCVRFYENSCKALGITAPICASLFIRGNIQLSS--- 2122
 ATJ00054.1_MsMV1 2038 **GPL**NMSSSHSILPANLSQLNPVVKDSVTYNDTPRINVRFFENADCKALGISAPVCASLFIRGKIRLSS--- 2104
 QQG34652.1_DiMV1 2190 **GPV**SSSVLITIPADLTKMNPILRDSVTYKDCPKLNLAIFYTNHDNLALGKTTPNCGAVIIRGVIQGS--- 2256
 YP_002756536.1_GSyV-1 2012 **GPV**SMSALATVPADVSRLNPVIKGAFAFLDTPRLTGTTMKCA-----KSETSPMAYVIRGTLALSG--- 2073
 QUS93818.1_GRVFV 2052 **GPV**SMNALATVPADLSRLNPRIKSSVGYLTPRLTGTTMKCA-----TAQTLPLAYVMIRGMVSVSG--- 2113
 Consensus_aa: **GPV**.*h*tt*h*.*l*PADL*spl*N*ph*l*Kst*Vs@.*DhPRhohsh*..ss.....ts.sss*hh*.*lh***l****RG**.*lpl***St**...
 Consensus_ss: **eeee** **eee** **eeee** **eeeeeeeeeeee**

Conservation: 8 5
 YP_009505639.1_BlVS 2029 ---PSGNTVA----- 2035
 MZ422607.1_GaMV 2071 ---PSGAKLT----- 2077
 ADD13602.1_OBDV 2058 ---PSGNTVTATT-- 2067
 AYC35261.1_CSDaV 2182 ---PSGNLLA----- 2188
 QLM05437.1_GAMaV 2148 ---PSGNLLA----- 2154
 YP_009222597.1_NeVM 2049 ---PAGNILA----- 2055
 MZ305310.1_PGMV 2015 ---PSGNAF----- 2020
 QID59334.1_SbMV 1977 ---PSGGLLTSD--- 1985
 QID59002.1_CaMaV 2198 ---PTGNKLA----- 2204
 QQG34656.1_DiMV2 2162 ---PSGNHLA----- 2168
 YP_004464920.1_SwMV 2052 ---PSGAAIKAAS-- 2061
 NP_115454.2_MRfV 2020 ---PSGAATPSA--- 2028
 QCC30252.1_PeDV 2050 ---PTGTISI----- 2055
 SBuMV-BU1 2240 ---PSGGKFT----- 2246
 YP_003475889.1_OLV-3 2262 ---PSGAKFA----- 2268
 YP_009551972.1_AVF 2123 ---PTATPSK----- 2129
 ATJ00054.1_MsMV1 2105 ---PSATPTK----- 2111
 QQG34652.1_DiMV1 2257 ---VRPTPTK----- 2263
 YP_002756536.1_GSyV-1 2074 ---PVGTRLSE----- 2081
 QUS93818.1_GRVFV 2114 ---PMGIKL----- 2119
 Consensus_aa: ...**P**sts.*h*.....
 Consensus_ss: ...**P**sts.*h*.....

h - alpha-helix; **e** - beta-strand; **bold and uppercase letters** - conserved aa; **l** - aliphatic (I, V, L); **@** - aromatic (Y, H, W, F); **h** - hydrophobic (W, F, Y, M, L, I, V, A, C, T, H); **o** - alcohol (S, T); **p** - polar residues (D, E, H, K, N, Q, R, S, T); **t** - tiny (A, G, C, S); **s** - small (A, G, C, S, V, N, D, T, P); **b** - bulky residues (E, F, I, K, L, M, Q, R, W, Y); **+** - positively charged (K, R, H); **-** - negatively charged (D, E); charged (D, E, K, R, H); **bold** letters - conserved aa motifs; CS - protease cleavage site; highlighted in teal - protease catalytic diad aa, C and H; highlighted in yellow - start of PRO domain expressed in *E. coli*; highlighted in turquoise - tested cleavage site in *E. coli* [1]; MTase-Gtase - methyltransferase-guanylyltransferase; highlighted in bright green - marked conservative aa for MTase-Gtase domain; PRO - protease; TMD - transmembrane domain; Hel - helicase, RdRp - RNA dependent RNA polymerase; CP - coat protein; bold and light blue - putative M for major coat protein; highlighted in grey - sea buckthorn marafivirus (SBuMV) isolate BU1; sea buckthorn marafivirus (SBuMV) isolate BU1.

References

1. Patel, A.; McBride, J.A.M.; Mark, B.L. The endopeptidase of the maize-affecting marafivirus type member maize rayado fino virus doubles as a deubiquitinase. *The Journal of biological chemistry* **2021**, 297, 100957.

Table S1. Primers used for SBuMV CPs and genome fragment amplification and sequencing.

Primer name	Primer sequence	Application	Producer
M13seq-F	5' GCC AGG GTT TTC CCA GTC ACG A 3'	Forward Sequencing Primer	metabion
M13seq-R	5' GAG CGG ATA ACA ATT TCA CAC AGG 3'	Reverse Sequencing Primer	metabion
pJET1.2-F	5' CGA CTC ACT ATA GGG AGA GCG GC 3'	Forward Sequencing Primer	Thermo Fisher Scientific
pJET1.2-R	5' AAG AAC ATC GAT TTT CCA TGG CAG 3'	Reverse Sequencing Primer	Thermo Fisher Scientific
MetPro-seq2-R	5' AGG GTT CAG AAT CTG GGT TAG AAA TGG GAA C 3'	Sequencing and 5' RACE	metabion
MarRdRp-seq2-F	5' ACC TCT CAC GTG CAT GAG ACT AAC TGG CGA 3'	Sequencing and 3' RACE	metabion
MarCP-2F	5' GGT GGT CGT TTC CTC ACG GT 3'	3' RACE	metabion
MarHel-seq3F	5' TTG TCA TTG TCC TCG GAG ACC CTC TTC AAG GA 3'	Sequencing	metabion
MarRdRp-seq2-R	5' TCG CCA GTT AGT CTC ATG CAC GTG AGA GGT 3'	Reverse Sequencing Primer	metabion
MarRdRp-seq3R	5' GGA GGG TCG ATC GCG AGC ATC AAA GTG ACG T 3'	Sequencing	metabion
Mar-RdRp-R	5' TAA AAG AAG TCA CGC AAA TGA CCC TGT AAT TTT GAC A 3'	HEL-RdRp fragment amplification and sequencing of PCR product	metabion
Mar-Hel-F	5' GTT CTT GAC ATC GCC ACC CCC CGT 3'	HEL-RdRp fragment amplification and sequencing of PCR product	metabion
Mar-Met1-F	5' GCA GCT CTA AAT CCA TCC TTT GCA TCA TTC ATC TCC A 3'	MET fragment amplification and sequencing of PCR product	metabion
Mar-Met-R	5' CCA CCC CAC AAG GCG GGA 3'	MET fragment amplification and sequencing of PCR product	metabion
Mar-Pro2-F	5' TCC CGC CTT GTG GGG TGG ATC CAT GCT 3'	PRO fragment amplification and sequencing of PCR product	metabion
Mar-Pro2-R	5' ACG GAA CGG GGG GTG GCG ATG TCA AGA 3'	PRO fragment amplification and sequencing of PCR product	metabion
MetPro-seq2-R	5' AGG GTT CAG AAT CTG GGT TAG AAA TGG GAA C 3'	sequencing	metabion
MetPro-seq1-F	5' TCC GCT CTC ACT TGG CTG CAA ATC ACA ACC AT 3'	sequencing	metabion
MetPro-seq1-R	5' ATG GTT GTG ATT TGC AGC CAA GTG AGA GCG GA 3'	sequencing	metabion
Mar-CPL-F	5'TCT TAC TTC CAA CGA AAC TCC CGT 3'	Minor CP amplification	metabion
MarCP1F	5' CCA ATG TCC AGA CCG GG CA 3'	Major CP amplification	metabion
MarCP2R	5' TTA AGT GAA CTT TCC TCC AGA CGG T 3'	Minor and major CP amplification	metabion
MarBox1F	5' GAG AGC GAA TTC TTT CCC TGG A 3'	"Marafibox" amplification	metabion
MarBox1R	5' TGT GAG GTT TCT GGG GAG AGT CT 3'	"Marafibox" amplification	metabion
MARCP-short-Nde-F	5' TAC ATA TGG CCA ATG TCC AGA CCG GGC AGG A 3'	Major CP amplification for co-expression	metabion
MARCP-short-Xho-R	5' GAC TCG AGT TAA GTG AAC TTT CCT CCA GAC GGT 3'	Major CP amplification for co-expression	metabion
Mar-3UTR-RACE-R	5' GTA AGG TCT TGC TGG ACG ACC TTA TAC ACT 3'	CP-3'UTR fragment amplification and sequencing of PCR product	metabion
Mar-5UTR-RACE-F	5' GGT ATC TGT TTT TAC CCT CTT TCT AGC TTA ATC GCT 3'	5'UTR-PRO fragment amplification and sequencing of PCR product	metabion
SB-RdRp-CP-seq-F	5' TGG CGA GAT CCC GCT CTC TGT TCT CGA AGT CAT CTT 3'	RdRp-C-terminal part and CP fragment amplification	metabion

Table S2. The dataset used for evolutionary relationship analysis. Accessions of the selected publicly available *Tymoviridae* entries and the related sequence metadata are listed. Origin column: “E” indicates that the isolate was listed as an exemplar isolate for the species in ICTV virus metadata resource; “ICTV” indicates that the species is recognized in the official taxonomy of *Tymoviridae*, but no accession was present in virus metadata resource; "RefSeq" indicates that the virus does not yet have standing in the official virus taxonomy but was included in the analysis based on taxonomy associated with a RefSeq entry; "Nucore>6k" indicates that the virus does not yet have a standing in the official virus taxonomy but was included in the analysis based on taxonomy associated with a complete or near-complete genome GenBank entry that was longer than 6000 bases in length.

(Please see separate excel file.)

Table S3. Descriptions of the generated MSA and features of the resulting trees.

(Please see separate excel file.)