

A New Double-Stranded RNA Mycovirus in *Cryphonectria naterciae* Is Able to Cross the Species

Barrier and Is Deleterious to a New Host

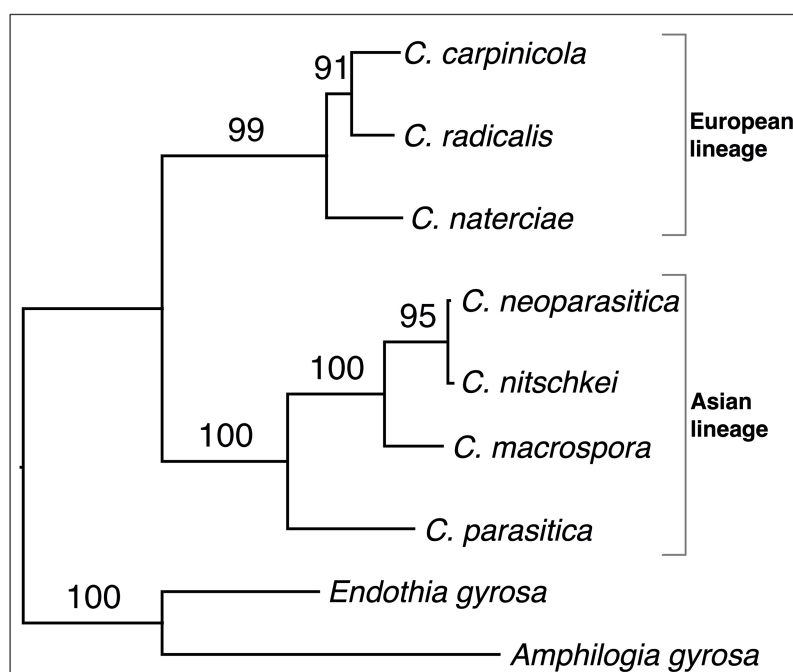
Journal of Fungi, 2021

C. Cornejo, S. Hisano, H. Bragança, N. Suzuki, D. Rigling

Content:

1	Phylogeny of the genus <i>Cryphonectria</i>	p. 1
3	Genetic markers and PCR protocols	p. 2
4	Specificity of newly designed primer for dsRNA	p. 3
5	Gel electrophoresis of dsRNA extracts	p. 4
6	RNA-seq report	p. 4
7	Alignment of RNA-seq <i>de novo</i> contigs	p. 4
8	BLASTp report	p. 5
9	Maximum likelihood phylogeny of ORF1 amino acid sequences	p. 5
10	Genotyping <i>Cryphonectria naterciae</i> DNA	p. 6
11	Phenotypic comparison of field-collected and experimentally infected <i>C. naterciae</i>	p. 6
12	Growth rates of field-collected and experimentally infected strains	p. 7
13	Fisher's exact test for inoculation experiments	p. 8
	References	p. 9
	Supplementary genome data	p. 10

1. Phylogeny of the genus *Cryphonectria*



Supplementary Figure S1. Phylogeny of the genus *Cryphonectria*, modified according to Cornejo et al. (2020). *Endothia gyrosa* and *Amphilogia gyrosa* act as out-group species.

2. Genetic markers and PCR protocols

RT-PCR and RLM-RACE primer were designed using the software CLC Main Workbench v7 (CLC bio, Qiagen Digital Insights, Hilden, Germany) based on RNA-seq contigs of *Cryphonectria naterciae* M10535, M10544, and M10545. While the Cn-Vir-ORF1 amplicon is located from position 2,680 to 3,184 completely within the ORF1 region, the amplicon of Cn-Vir-ORF2 starts at the 3'-end of ORF1 expanding into the ORF2 region from 6,039 to 6,517 in relation to the complete genome GenBank accession MZ736512.

SSR primer were developed in Msatcommander 1.0.8-beta (Faircloth 2008) using unassembled reads of genomic sequencing data of *C. naterciae*, developed previously in our lab for a parallel study (Stauber et al. 2020, 2021). Settings in Msatcommander accepted trinucleotide repeats ≥ 10 . A total of 6,880 trinucleotide loci were found including 21 primer pairs, of which eleven were discarded from further study due to primer dimer formation, monorepeats, compound-interrupted repeats, or duplicates. Of the 10 remaining primer pairs, the loci Cn-Msat6 and Cn-Msat10 were selected, which contained the trinucleotide motifs (AGG)_n and (ACC)_n, respectively. PCR reaction was designed using a fluorochrome-labelled M13-tail according to Schuelke (2000). PCR products were run with LIZ500 as an internal size standard on a 3130xl Genetic Analyzer and alleles were sized with GeneMapper v3.7 (Thermo Fisher Scientific, Waltham, Massachusetts, U.S.A.).

Supplementary Table S1. List of all primer pairs designed for this study.

Reaction	Locus	Primer label	Primer sequence	Amplicon size (nt)
RT-PCR ^a	ORF1	Cn-Vir_ORF1-F	5'-WTRGAGTGGGTRAGGGATG-3'	505
		Cn-Vir_ORF1-R1	3'-GTATTCKGGAACGTTGGA-5'	
	ORF2	Cn-Vir_ORF2-F1	5'-CTGAGCGGGTTGATATGAAY-3'	479
		Cn-Vir_ORF2-R2	3'-GRTCWGCCTCRAGATTATG-5'	
RLM-RACE ^b	5'-end	Cn_Vir_5end-R1	3'-GGAAGAGAGGCATAAGTTGGATA-5'	Variable
		Cn_Vir_5end-R2	3'-CCAGAGGGAAGAGAGGCATAA-5'	Variable
		Cn_Vir_5end-R3	3'-CCAGAGGGAAGAGAGGCATA-5'	Variable
	3'-end	Cn_Vir_3end-F1	5'-GGGTCTTATACATGGTGAGTTT-3'	Variable
		Cn_Vir_3end-F2	5'-AATCAAGCACAGAAGCTCAG-3'	Variable
		Cn_Vir_3end-F3	5'-AGGCGCCGAGGTTTAAACGTA-3'	Variable
SSR-PCR ^c	Cn-Msat6	Cn-Msat6-F ^d	5'-*GCAGAGACCTAATGTGCCAG-3'	See Table S5
		Cn-Msat6-R	5'-ATGTCCATTCTTGCTTGCC-3'	
	Cn-Msat10	Cn-Msat10-F ^d	5'-*AGGTCTGGAGGTAGGCTAGAG-3'	See Table S5
		Cn-Msat10-R	5'-TCAAGCGACTACAGCTAACAC-3'	

^a Protocol for RT-PCR using JumpStart REDTaq Ready Mix Reaction Mix (Merck KGaA, Darmstadt, Germany): 2 min 94°C initial denaturation; 30 cycles of 30 sec 94°C, 30 sec 55°C, 1 min 72°C; 10 min 72°C final extension.

^b Protocol using QuickTaq HS DyeMix DTM-101 (Toyobo, Osaka, Japan): 2 min 94°C initial denaturation; 30 cycles of 15 sec 95°C, 30 sec 53°C, 1 min 68°C; 5 min 68°C final extension.

^c Protocol using Type-it Multiplex PCR Master Mix (Qiagen, Hilden, Germany): 5 min 95°C initial denaturation; 30 cycles of 30 sec 95°C, 90 sec 60°C, 1 min 72°C; 45 min 72°C final extension.

^d Asterisk: M13-tail TGTAACACGACGGCCAGT fluorochrome-labelled at the 5'-end.

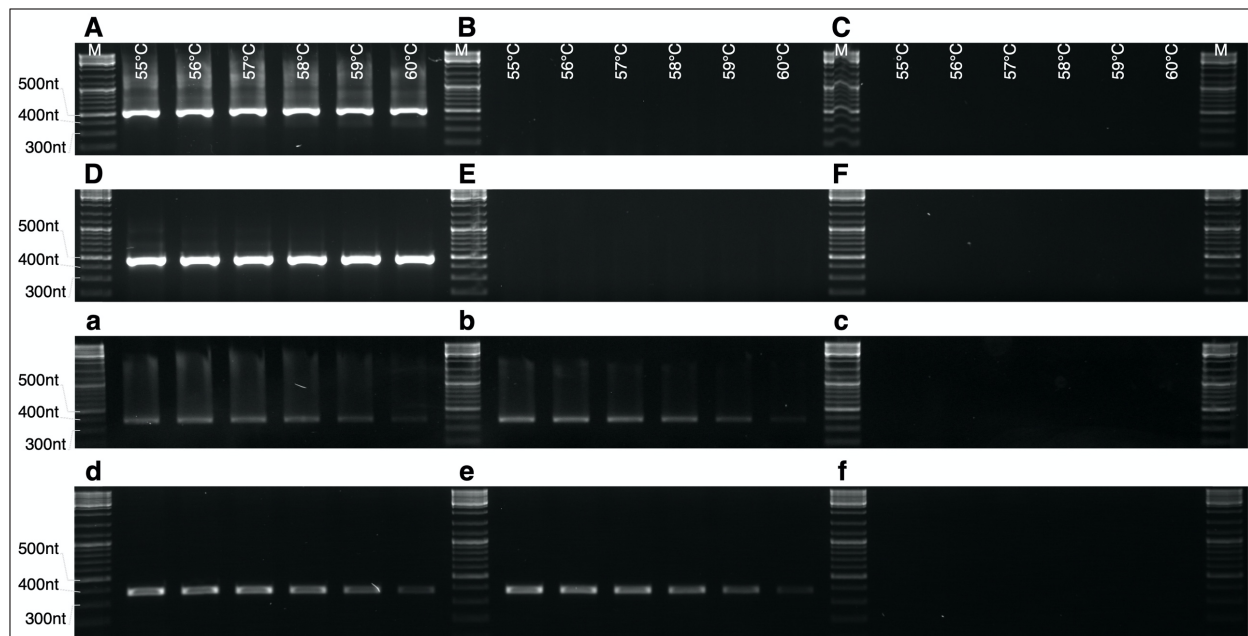
4. Specificity of newly designed primers for dsRNA detection

To exclude unspecific binding on fungal DNA, the primer specificity was first evaluated *in silico* using the Primer-BLAST option 'fungi (taxid:4751)' in the NCBI-suite (<https://www.ncbi.nlm.nih.gov>), refusing primer sequences that mismatched at <10 sites with any fungal DNA region.

In vitro tests used in TEST1: cDNA of dsRNA-positive and dsRNA-negative *C. naterciae* obtained from dsRNA-extraction using the Double-RNA Viral dsRNA Extraction Mini Kit (iNtRON Biotechnologies), treated with DNase and S1 nuclease (Thermo Fisher Scientific), and electrophoresed on a 1.5 % (w/v) agarose gel (Figure S2 A–F).

TEST2 used fungal DNA extracts of dsRNA-positive and dsRNA-negative *C. naterciae* obtained using the DNeasy Mini Kit (Qiagen). TEST2 was conceived as a duplex-PCR containing the Cn-Vir-ORF1 or Cn-Vir-ORF2 primer as well as the fungal primer for the *tef* gene (Carbone and Kohn 1999) to monitor the presence of fungal DNA (Figure S2 a–b, and d–e).

TEST3 used cDNA of the CHV1-positive *Cryphonectria parasitica* strain M3625 to check the specificity against another RNA virus, whose host may grow sympatrically with *C. naterciae* in the same trees (Figure S2 c, and f).



Supplementary Figure S2. PCR temperature gradients for testing the optimal annealing temperature as well as the specificity of newly designed primer pairs for dsRNA of *Cryphonectria naterciae*.

(A)–(F) TEST1 used cDNA of dsRNA-extraction. (A) dsRNA-positive strain M10535. Expected size of Cn-Vir-ORF1: 505 nt. (B) dsRNA-negative strain M10547. (D) dsRNA-positive strain M10535. Expected size of Cn-Vir-ORF2: 479 nt. (E) dsRNA-negative strain M10547. (C) & (F) Negative control of PCRs.

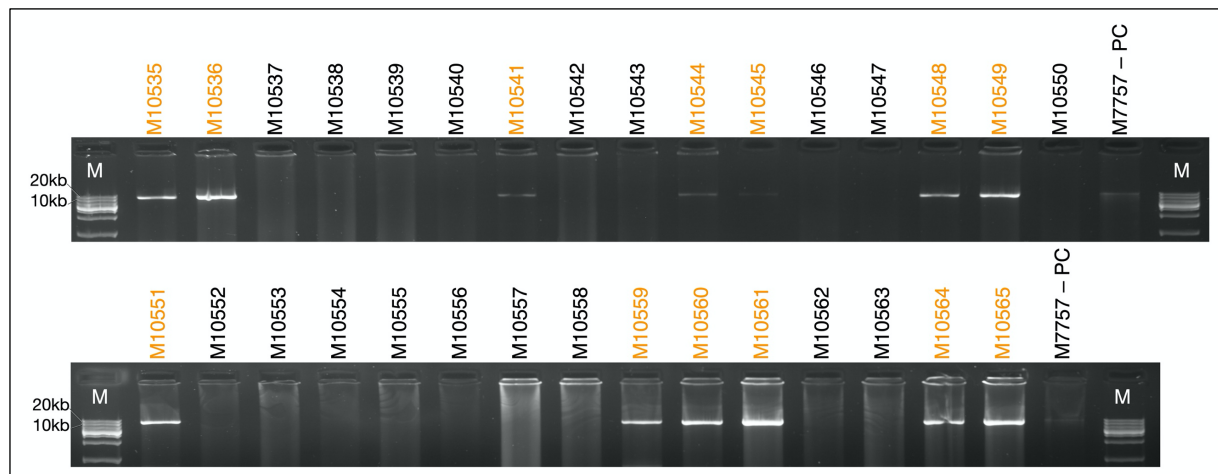
(a)–(b) and (d)–(e) TEST2 used fungal DNA of *Cryphonectria naterciae* and a duplex-PCR with Cn-Vir-ORF primer as well as *tef*-primer of amplicon size 375 nt. (a)–(c) Primer for Cn-Vir-ORF1 and *tef*. (a) DNA of the dsRNA-positive strain M10535. (b) DNA of the dsRNA-negative strain M10540. (d)–(f) Primer for Cn-Vir-ORF2 and *tef*. (d) DNA of the dsRNA-positive strain M10535. (e) DNA of the dsRNA-negative strain M10540.

(c) & (f) TEST3 used cDNA of the *Cryphonectria parasitica* CHV1-positive strain M3625.

M: Thermo Scientific GeneRuler 1 kb Plus DNA Ladder (SM1334).

5. Gel electrophoresis of dsRNA extracts

Of 31 *Cryphonectria naterciae* strains, screened by dsRNA extraction, 10 strains isolated from *Quercus suber* and 3 from *Castanea sativa* exhibited one segment at c. 10 kb by agarose gel electrophoresis.



Supplementary Figure S3. Gel electrophoresis of dsRNA extracts of all 31 studied *Cryphonectria naterciae* isolates. Orange letters highlight strains found to be dsRNA-positive. M7757-PC: The positive control for the dsRNA-extraction used a *Cryphonectria parasitica* strain infected with CHV1 (12.7 kb RNA virus). M: Thermo Scientific GeneRuler 1 kb Plus DNA Ladder (SM1334).

6. RNA-seq report

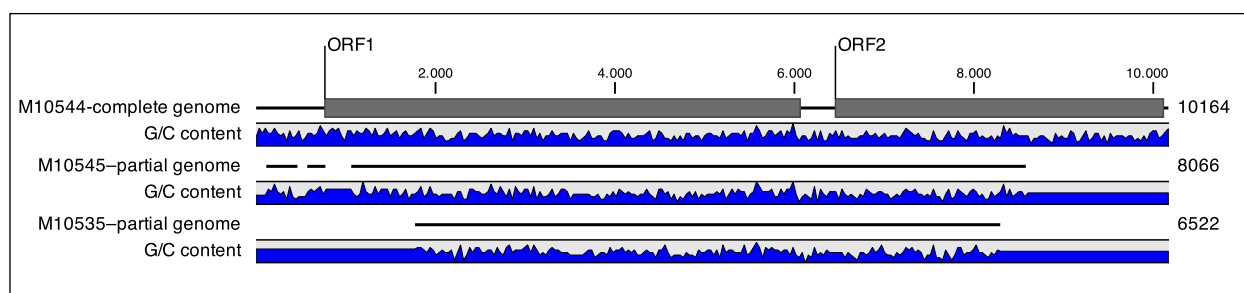
A subset of three dsRNA extracts (M10535, M10544, and M10545) was subjected to RNA-seq. Sequencing cDNA library was constructed using the TruSeq RNA Sample Prep Kit (Illumina, San Diego, California, U.S.A.) and sequenced on an Illumina MiSeq v2. *De novo* assembly of reads was carried out using Trinity v2.6.5 (Grabherr et al. 2011). Demultiplexing and trimming the adaptor residuals of raw data resulted in 1,034,424 reads with a mean read length of 159 nt and a mean Q20% of 95%.

Supplementary Table S2. Results of the *de novo* assembly of RNA-seq raw data.

<i>Cryphonectria naterciae</i> collection-ID	M10535	M10544	M10545
Contig length (nt)	6,522	5,346	8,066
Coverage of contigs	22,7427	27,6685	52,4069

7. Alignment of RNA-seq *de novo* contigs

The alignment was performed using CLC Main Workbench. ORF sequences found in the ORFfinder suite of NCBI were annotated directly on the alignment. The RNA-seq contig of M10545 contains deletions close to the 5'-end compared to the complete M10544-genome.



Supplementary Figure S4. Alignment of the complete M10544-genome and the partial genomes of M10535 and M10545 (black line). Grey boxes represent both ORFs. The blue graph outlines the G/C-content for each contig.

8. BLASTp report

Two open reading frames were detected on the genomic plus strand in all three contigs of M10535, M10544 and M10545. The amino acid sequences based on the complete genome of M10544, or partial sequences of M10535 and M10545 were used for BLASTp searches on UniProt (Altschul et al. 1997).

Supplementary Table S3. Results of BLASTp searches in the UniProt protein database. Last search on 22th of July 2021.

	M10535		M10544		M10545	
	ORF1	ORF2	ORF1	ORF2	ORF1	ORF2
Best match	FvV1 ^a	FvV2 ^b	FvV1	FvV1	FvV1	FvV2
Entry-ID	H6UNN1	H6UNN0	H6UNN1	H6UNN2	H6UNN1	H6UNN0
Protein	Putative protein ^c	RdRp ^d	Putative protein	RdRp	Putative protein	RdRp
Identity	45.8%	37.0%	47.7%	36.8%	46.4	45.6
Query length	1313	458	1770	1223	1595	719
E-value	0.0	2.1e-78	0.0	0.0	0.0	0.0

^a FvV1: *Fusarium virguliforme* dsRNA mycovirus 1 (Marvelli et al. 2014)

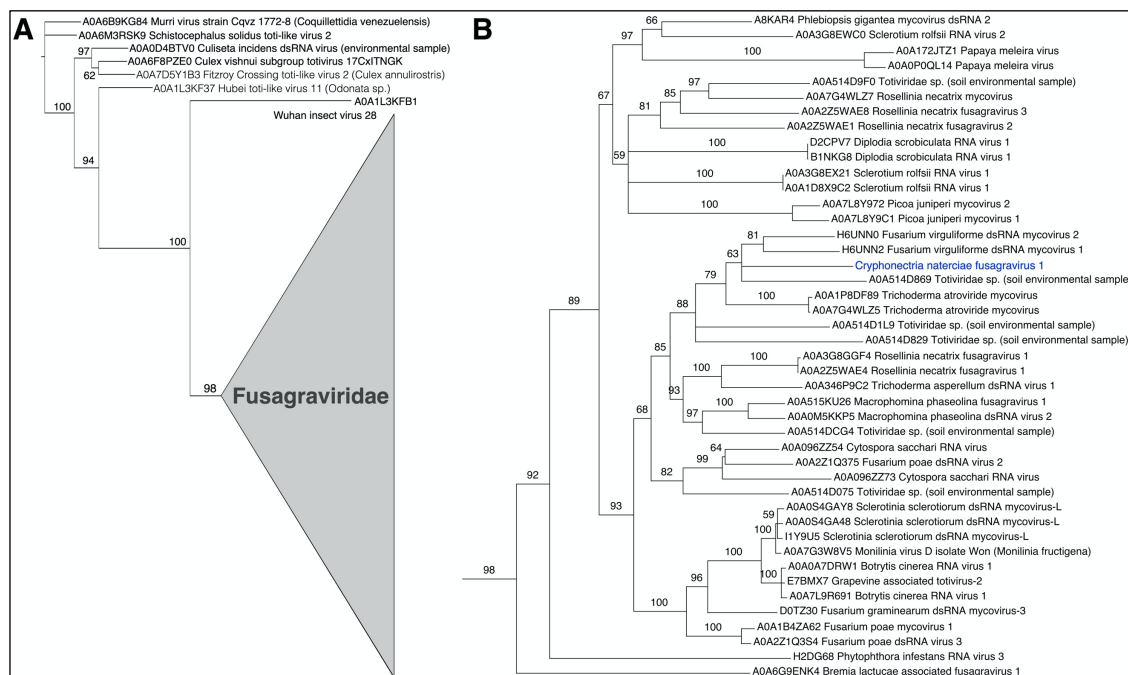
^b FvV2: *Fusarium virguliforme* dsRNA mycovirus 2 (Marvelli et al. 2014)

^c Putative protein: Putative structural/gag protein

^d RdRp: RNA-directed RNA polymerase

9. Maximum likelihood phylogeny of ORF1 amino acid sequences

Amino acid matrices of the full genome contig of M10544 together with the most closely related viral species recognized by BLASTp (Supplementary Data) were analysed by maximum likelihood as implemented in the software PhyML v3.0 (Guindon & Gascuel 2003; Guindon et al. 2010) and run on the ATGC bioinformatics platform (<http://www.atgc-montpellier.fr>), which first calculates the best fitting substitution model prior to tree reconstruction. Support for each internal branch of the phylogeny was calculated using the nonparametric bootstrap option with 100 bootstrap replicates. The output tree contains the best tree found among two starting trees. Unrooted trees, including branch support, were graphically represented with FigTree v1.4.4 (Raubaut 2018).



Supplementary Figure S5. (A) Most likely tree of amino acid ORF1-sequences, showing the phylogenetic relationship between the previously proposed family Fusagraviridae (collapsed) and close related insect viruses (1,945 polymorphic out of 2,006 amino acid sites; LG +G+I+F substitution model; 100 bootstrap replicates). (B) Details of collapsed most likely phylogeny in (A). Blue letters highlight the phylogenetic position of the novel virus candidate CnFGV1. Names and database accession numbers of related fusagraviruses included in the analysis are indicated in the tree. The numbers at nodes are values of > 50% of 1,000 bootstrap replicates.

10. Genotyping *Cryphonectria naterciae* DNA

To recognize genetically each isolate of *C. naterciae* individually prior and subsequent to pairing experiments, simple sequence repeats (SSR) markers were developed, which enable us to distinguish each strain individually combining two alleles.

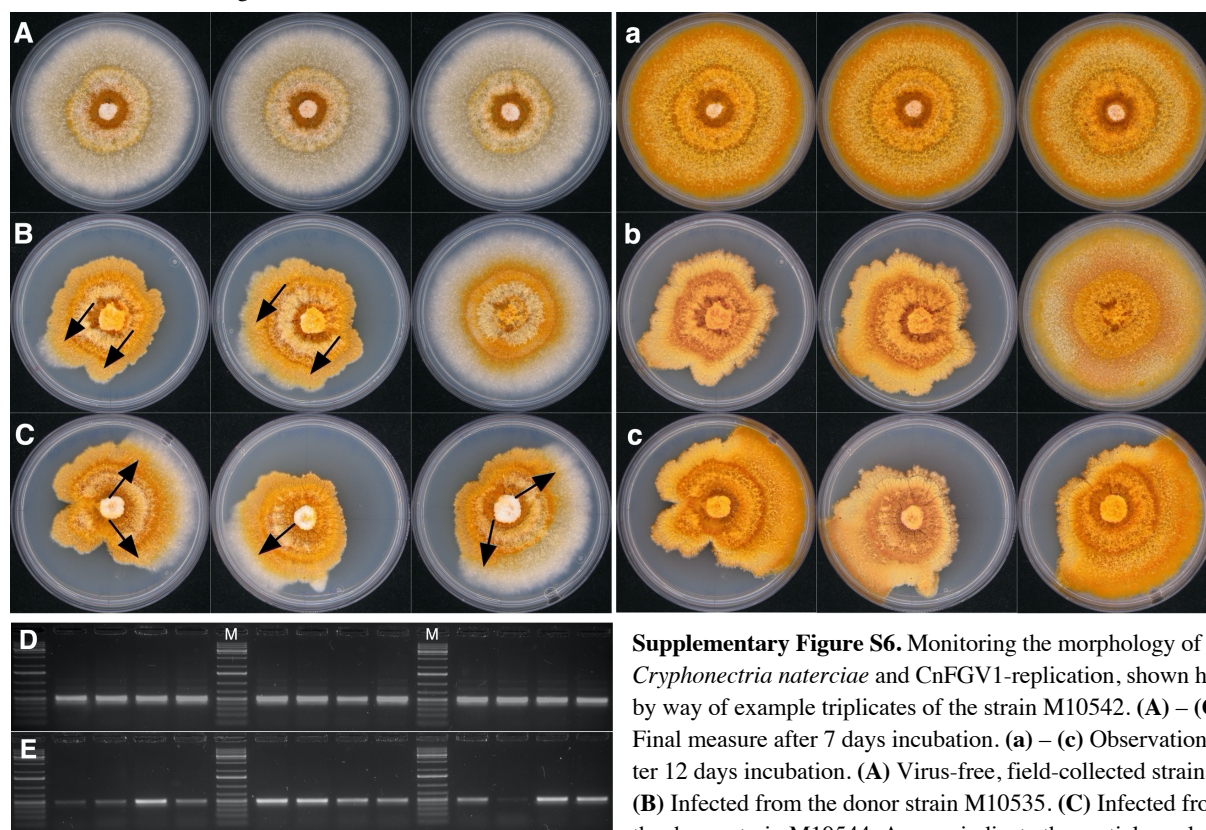
Supplementary Table S4. Genotyping two SSR-loci of *Cryphonectria naterciae* strains, which were used for the horizontal virus transmission. Each unique allele size was additionally symbolized by coloured circles or rectangles.

	Sample-ID	Collection-ID	Allele sizes Cn-Msat6 ^a	Allele sizes Cn-Msat10 ^a	Genotype
Donor strains	C0084	M10535	174 ●	160 ■	●■
	C0613	M10544	168 ●	172 ■	●■
	C0614	M10545	171 ●	150 ■	●■
Recipient strains	C0611	M10542	171 ●	172 ■	●■
	C0754	M10562	171 ●	172 ■	●■
	C0682	M10547	171 ●	172 ■	●■
	C0685	M10550	162 ●	163 ■	●■

^a Length (bp) in relation to the internal size standard.

11. Phenotype of the field-collected and the experimentally infected *Cryphonectria naterciae*

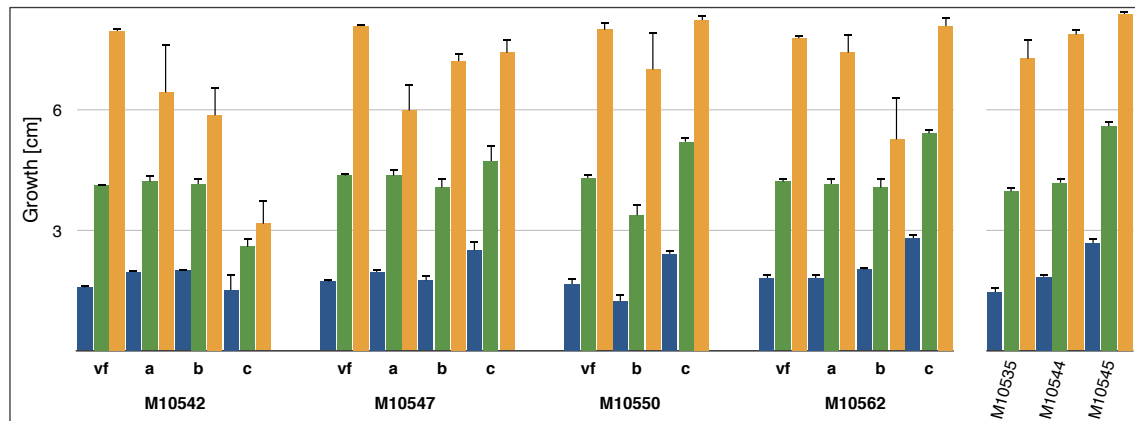
Isogenic virus-infected and virus-free isolates of *C. naterciae* were grown at 25 °C on PDA agar plates and their growth rates were measured regularly. A round agar plug (diam. 5 mm) was inoculated on the centre of each plate, and three replicate plates were made for each fungal isolate.



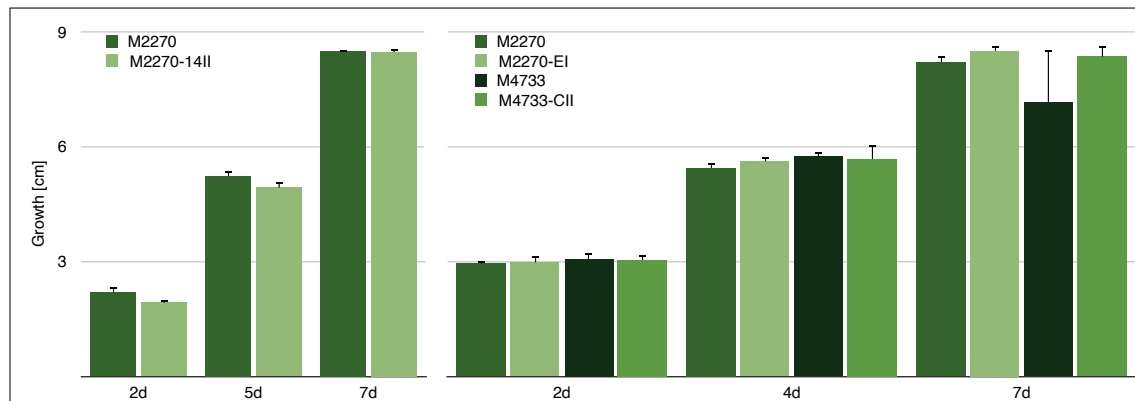
Supplementary Figure S6. Monitoring the morphology of *Cryphonectria naterciae* and CnFGV1-replication, shown here by way of example triplicates of the strain M10542. (A) – (C) Final measure after 7 days incubation. (a) – (c) Observations after 12 days incubation. (A) Virus-free, field-collected strains. (B) Infected from the donor strain M10535. (C) Infected from the donor strain M10544. Arrows indicate the partial regular growth of the mycelium. (D) – (E) Together with the last growth measure of (B) and (C), the presence of CnFGV1 was assessed by RT-PCR for each fungal replicate at the four coordinate points. M: Thermo Scientific GeneRuler 1 kb Plus DNA Ladder (SM1334).

Together with the last growth measure of (B) and (C), the presence of CnFGV1 was assessed by RT-PCR for each fungal replicate at the four coordinate points. M: Thermo Scientific GeneRuler 1 kb Plus DNA Ladder (SM1334).

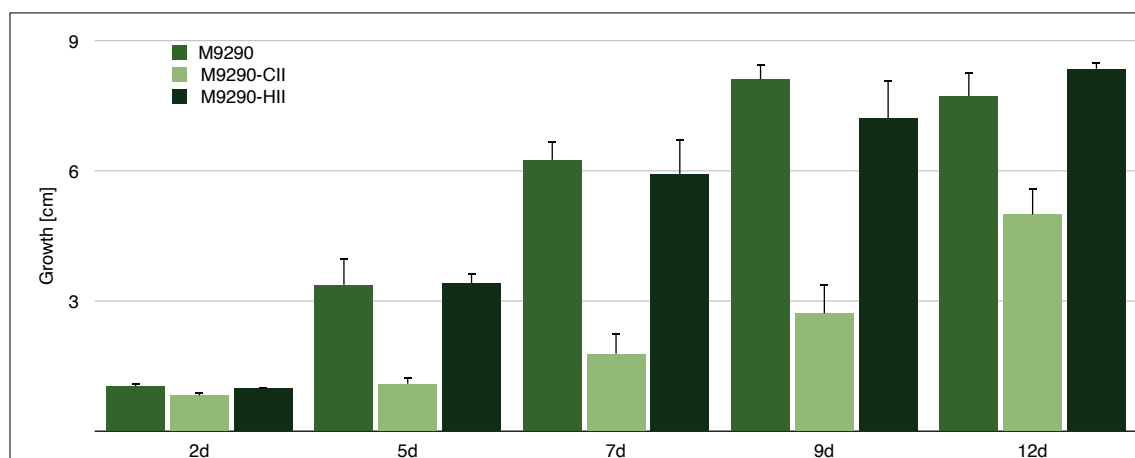
12. Growth rates of field-collected and experimentally infected strains



Supplementary Figure S7. Growth rate of CnFGV1-infected strains of *Cryphonectria naterciae*. Column height represents the growth after 2d, 4d, and 7d incubation of isogenic virus-free strains (= vf) or experimentally infected recipients M10452, M10547, M10550, and M10562. Donor strains are a = M10535, b = M10544, c = M10545. There was no CnFGV1 transmission from M10535 to M10550 (a missing). Vertical black lines indicate the standard deviation of 3 culture replicates. Columns at right show the growth rate of donor strains.



Supplementary Figure S8. Growth rate measure of cross-species infected strains. The columns represent the growth rate of isogenic virus-free and experimentally infected strains. **(Left)** The *C. radicalis* strain M2270-14II received CnFGV1 from donor strain M10544. **(Right)** Both *C. radicalis* strains M2270-EI and M4733-CII received CnFGV1 from donor strain M10545. Black lines indicate the standard deviation of triplicate cultures. All growth rate differences were non-significant according to a *t*-test.



Supplementary Figure S9. Growth rate measure of isogenic virus-free and experimentally infected strains of *C. carpinicola*. Both infected replicates M9290-CII and M9290-HII received CnFGV1 from donor strain M10545. Black lines indicate the standard deviation of triplicate cultures. The growth rate of M9290-CII was statistically significant ($P = 0.039$) slower; all other growth rate differences were non-significant according to a *t*-test.

Supplementary Table S5. Effect of the CnFGV1-infection on the fungus-plant interaction. (a) – (f) Listed are 2x2 contingency tables used to analyse differences in conidiation and formation of necrosis between CnFGV1-positive and CnFGV1-negative strains of *Cryphonectria naterciae*. The *p*-value of the two paired Fisher's exact test is given at each table end. All tests were not statistically significant. Fisher's tests were performed on the freely accessible platform www.graphpad.com (GraphPad Software, San Diego, CA, U.S.A.).

a) Differences in conidiation between CnFGV1-positive and CnFGV1-negative strains, applied to two tree species

	Pycnidia formed	No pycnidia formed	Total
<i>CnFGV1-positive</i>	2	34	36
<i>CnFGV1-negative</i>	7	29	36
Total	9	63	72

$p = 0.1514$

b) Differences in formation of necrosis between CnFGV1-positive and CnFGV1-negative strains

	Necrosis formed	No necrosis formed	Total
<i>CnFGV1-positive</i>	1	35	36
<i>CnFGV1-negative</i>	4	32	36
Total	5	67	72

$p = 0.3570$

c) Differences in conidiation between tree species, inoculated with CnFGV1-positive strains

	Pycnidia formed	No pycnidia formed	Total
<i>Quercus suber</i>	1	17	18
<i>Castanea sativa</i>	1	17	18
Total	2	34	36

$p = 1.0$

d) Differences in conidiation between tree species, inoculated with CnFGV1-negative strains

	Pycnidia formed	No pycnidia formed	Total
<i>Quercus suber</i>	3	15	18
<i>Castanea sativa</i>	4	14	18
Total	7	29	36

$p = 1.0$

e) Differences in formation of necrosis between tree species, inoculated with CnFGV1-positive strains

	Necrosis formed	No necrosis formed	Total
<i>Quercus suber</i>	0	18	18
<i>Castanea sativa</i>	1	17	18
Total	1	35	36

$p = 1.0$

f) Differences in formation of necrosis between tree species, inoculated with CnFGV1-negative strains

	Necrosis formed	No necrosis formed	Total
<i>Quercus suber</i>	2	16	18
<i>Castanea sativa</i>	2	16	18
Total	4	32	36

$p = 1.0$

References

- Cornejo, C., Hauser, A., Beenken, L., Cech, T. & Rigling, D. *Cryphonectria carpinicola* sp. nov. associated with hornbeam decline in Europe. *Fungal Biol.* **125**, 347-356, (2021).
- Faircloth, B. C. msatcommander: detection of microsatellite repeat arrays and automated, locus-specific primer design. *Mol. Ecol. Res.* **8**, 92-94, (2008).
- Stauber, L., Prospero, S., Croll, D. & Mitchell Aaron, P. Comparative genomics analyses of lifestyle transitions at the origin of an invasive fungal pathogen in the genus *Cryphonectria*. *mSphere* **5**, e00737-00720, 10.1128/mSphere.00737-20 (2020).
- Stauber, L., Badet, T., Feurtey, A., Prospero, S. & Croll, D. Emergence and diversification of a highly invasive chestnut pathogen lineage across southeastern Europe. *eLife* **10**, e56279, 10.7554/eLife.56279, (2021).
- Schuelke, M. An economic method for the fluorescent labeling of PCR fragments. *Nat. Biotechnol.* **18**, 233-234, (2000).
- Carbone, I. & Kohn, L. M. A method for designing primer sets for speciation studies in filamentous ascomycetes. *Mycologia* **91**, 553-556, (1999).
- Grabherr, M. G. *et al.* Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nat. biotechnol.* **29**, 644-652, (2011).
- Altschul, S. F. *et al.* Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* **25**, 3389-3402, (1997).
- Marvelli, R. A. *et al.* Identification of novel double-stranded RNA mycoviruses of *Fusarium virguliforme* and evidence of their effects on virulence. *Arch. Virol.* **159**, 349-352, (2014).
- Guindon, S. & Gascuel, O. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst. Biol.* **52**, 696-704, (2003).
- Guindon, S. *et al.* New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst. Biol.* **59**, 307-321, (2010).
- Rambaut A. 2018. FigTree v1.4.4. <https://github.com/rambaut/figtree>.

Supplementary Genome Data

A New Double-Stranded RNA Mycovirus in *Cryphonectria naterciae* Is Able to Cross the Species Barrier and Is Deleterious to a New Host

C. Cornejo, S. Hisano, H. Braganca, N. Suzuki, D. Rigling

Journal of Fungi 2021

Supplementary Data: Complete genome of collection-ID M10544 – GenBank accession MZ736512

Content:

1. ORFfinder search 22 July 2021 (last search)
2. NCBI Conserved Domain search of ORF1 Jul 16 2021 (last search)
3. UniProt BLASTp 22 July 2021 (last search)

1. ORFfinder BLASTp search of the complete genome M10544

Label	Strand	Frame	Start	Stop	Length (nt aa)
ORF2		+		2	758 6070 5313 1770
ORF1		+		1	6448 10119 3672 1223

>Sequence

758 6070 CDS

protein_id lcl|ORF2
product unnamed protein

6448 10119 CDS

protein_id lcl|ORF1
product unnamed protein

>lcl|ORF2

MVDRLTGHVFLDRKPKQSVRHRPMDSQQTLALNEAGSSASRSABAQQT
IGRGCNLSYFPASIRTHNFALAHGVKLSKSIQWLSSTSGGRVPALP
GVEHSCCAELECSANVCCGCTSTVERAERWSLPHPEGADGWVKSQAEEAP
IRWNDPCPFRRSMVRADQSTGHPPVMDSYGYSALTEAGSSASRSABAQQN
TIGRDGNLDSHNIAVSSTSGCPCGYKHGKDFECYALLANGVVPALTNYS
SPAIAARTFQFKRAISFETDLTALVAAERSINLASQVKYEFNPACSCRINE
VGSLVQGCQSVPHLYQIPSLNRWCDGTSAIAGGCYALWSGWARPAVM
RLGRAPTAEAILHLLGNTHKCMRHDSWRFCVRGGTEFVHILPDRFGVS
GKTLRLAMPASSRVGFSECVVNTTHSASFTRYQLSDSPFFSLIRSLLI
SFVFSFVYGALDFGERILCKQIPKHFPTRSLRKNGYCYLELPHIWHPF
VASLLGPKPPIRILRFLYVTLPLFLDFRVNFIVAKDMLDCDGRPVYHFA
TTGGSEVGRRTARGVLWALDADARLGQFTSPEDQDTSSQLLAKSSAVNA
IAPLGVRQVPTSLPIPIQISPGFTRRWAPNIFPTSLTSQPLEWVRDAQGH
LALSRESEFTYHYPEDSSLSRLPTRFSATLLSKWFFRREVDEAGCVTTAY
NRRFEPDTPSRTLDEFSAIGQVLDGNMSLDVLKADAGGSFSRALGSRN
QRLVPGWEAGVIPRWLQFRDFAIKAAARRAYKEFCFRVASRYTLATVASD
VCSNVPEYERHVIDTTTDDVQIIHINAEPPIAPPQNPQPPPIQWGEAALW
TPAMLQAVLDGRAQFIDGESYTREELAEIIACLAPSTHDNVPHLRPVDP
NDPDKETMLPSCARYSYPNGVTHIIVHHGNAPLPSIQDQNWIAQHAFSF
PSAMTLSTIIRSYSVRHSLEDLFVWAFEAVAYRSVGYTFADALGTNEPTA
TDDIIHAGSVPLDPLPRNCTGFAYFDCFFVPVSTTPELESYLSAPTEVFV
SSISLAHFRAVSIAGWAKAGSLGRVFNLAANQGNQFLRNHRKWLRF
YGELNVWSALHANTMGFYGFAPSPTRRTESNMLPNWWRDYCTPTLVNH
YLELWAMQVIPVFQVLPYYSREAKNSHVEWAPGTPDQTASLVSFNHRKV
RLAREVDVLEGHSWLGDAEYNSQFYAQQGNNGRFAYEGAQPKARFSFW
QGSYARSPVTPQAATPISLSNGRLNDPFADFILPGSFQSYRMLDDKIIN
WGVNEVSEHQLTNSEARRWWLASKGTAHVSLMVNVSPISQHYELDDLAD
YSVTIWEKDGRAALTFSNLNELLTKDNFNPTNIEESQKPFQTRFDSAPH
RFEQLRPTRVTNNRSSHAKARPALSSATDINRRIAEALRRPQAGNITYET
KYPHADDLPKMNSYDVNVTKDGFEPQNMAMPNDLSFTPADRLKKIQEAQ
AHLDDQFQEQYFAEQQQQAINRTRLQANRVASPATTRPIAPVPRRKARLP
SVINYPAPEPASYHKGRQSYVANKPLPPQPKPLVPNDAPAAGAQQAAIDL
ATLNARRGSLRPVHTVQGRRSLSPRANYLQRRADTSVPDEPARLHHVR

ERPQSQPIVSDPSDRGAALKSLEWSNPKPFLPPHDKQWLSQSIEDFPPL
PEQRPPPLDSSDHLDTADTSRIRNQPGNSSSQVDLSQIDWNGGPDVAKAS
ILDAFTTKASERVDMNNPKN

>lc1|ORF1
MSSEPCQVNDTIYRLYHNLEADQYSCATRVLTILGLRDIPHERFKDVSKL
GMHRPTLKFQLIRCFDPSFLLTEIDTSVDSLDTNIVNSIMLAHLEELPAR
ATHDMEVVLFLFNDHISLALAESFIRRHSSQVIEGALDRPHNFRSVSQFP
PVSGRAGAKVFLRPINLMSLGRPTILQCALMNVTIRIGPNRDWQAIPIA
LLLLQYLQIGGNDLMFFFCVNPCHILDLDLAKLAKRLKELHAYIRVNLRLP
RFAFLNLNSIGQREWARHLYGLETLVGRSELLELDITEEFKMRVADPALR
GVPELVDRDSGNFSYIRFDTSEYTRLLPQIANQMVESLLKEKVVNDMHE
FFQSRFLWAGSGGAPGAQVEWEDGTRLRLNKRGAALLGLKERQIRIDILDSV
NNPQFSDPVQWSVNAKFESGKLSILNTVLEHYVIQGYISHVDANVNQ
NTWYSVGQHNSARISNHLRLDDLSKNVGMWDYSDFNINHTFILMAQHT
LAMVEGLIRRGKTSGITPERMRVISRDLHKAAYTVIARFNTYLHDHDSQ
LTIKTARGLQSGERQTSRINSDCNYIDTLFVRLVSKRFFGYDVLNPVADH
SGDDAFETTKNYSOGMFAAALYNLTGAAGQAHKILMSYPSRGGGLGEYLR
LAYDAANKKVCYPIRAMMGLIHGEFFSNPIQPNERAAFLNQAQKLRR
RGFNVPDKLLKSIINANCFVLTSDSGVKFTYRPNLTTLVLPVILGGVGV
QEDDKSLVTAQLPISFKYGRDGLSCVAISPLLCDLRYESLSHTIDFVTL
DDVIYKVANITGLTEQCIKTGNWDQYYALGRVYTRYITGLKSSSVNSSR
VIIASNHLAMLKNNGFVLAITSNTRTGDRFKQHAQNYLERLGSVIRVTN
XRLKLVSHLLEISSVAPHPIGVIYPYNTNPKPLPLYQAPRIQAKETIKSSK
AQIPDIGVLYRNVTRIGPLYDDIAKSTLTGGWPKAAMNESLAEYGRALV
EWEKQTAIEYRFELLRLPSITRVKRYIENCLPEYLGSLGASSHGLPIFL
RTVQGYPCNQKVKHNYAANSALMRPLGLSVEKALNLLIEHAPGNTMLQKT
ISVLKHPSLGSKAQNMILTKLTFLKYSNSTPEAQRALFQYFTGDWSLVP
PAASQWSSDFTTLIRDLTLAGLEGDHFTPFMSQHALTLQPVTRALHIHYI
EKIVFNATISTLHRYFPGIILQD

2. NCBI Conserved Domain search of ORF1 Jul 16 2021

CDD - this is a superset including NCBI-curated domains and data imported from Pfam, SMART, COG, PRK, and TIGRFAM.

Pfam - a mirror of a recent Pfam-A database of curated seed alignments. Pfam version numbers do change with incremental updates. As with SMART, families describing very short motifs or peptides may be missing from the mirror. An HMM-based search engine is offered on the Pfam site.

Name	Accession	Description
RdRP_4	pfam02123	Viral RNA-directed RNA-polymerase; This family includes RNA-dependent RNA polymerase proteins ...
	Interval	E-value
	257-674	3.51e-24

Viral RNA-directed RNA-polymerase; This family includes RNA-dependent RNA polymerase proteins (RdRPs) from Luteovirus, Totivirus and Rotavirus.

Pssm-ID: 280316 Cd Length: 465 Bit Score: 107.55 E-value: 3.51e-24

	10	20	30	40	50	60	70
80							
lc1 ORF1						
	257 LNSIGQR--						
	EWARHLYGLETLVGRSELLELDITEEFKMRVADPalrgvpelvrdrsgnfsYIRFDTSEYTRLLPQIANQM	334					
Cdd:pfam02123	99 LKSLGLNasSPGPKLVEGNPLLGRGVT-NVDWEEEAKNRVDLA-----						
	VVCRLVLLPMEELRAHIDAV	160					
		90	100	110	120	130	140
160							
lc1 ORF1						
	335 VESLLKEKVVNDMHEFFQSRFLWAGSGGAPGAQVEWEDGTRLRLNKRGAALLGLK-						
	ERQIRdildsvnNPQFSDPVQWSVN	414					
Cdd:pfam02123	161 LDELVVRRLGLCDPIRLFVKNEPLWCVNGH-PDHKLR--EGRLRLSSVSLVDQLVRRMLF-----						
	EPQNNNEIAWWGS	230					
		170	180	190	200	210	220
240							

```

.....|.....|.....|.....|.....|.....|.....|.....|
lcl|ORF1      415 -----ALKFESGKLSILNTVLEHYVIQGYISHHV-
      DANVNQNTWYSVGQHNSARISNHLRLDDlSKNVGFMWDYSDFN 488
Cdd:pfam02123 231 vpskpSMKLEHGKSRAIYACDTRSYLAFEYLLAPVeKAWANKSVILNPGEGLDISGFDWSVQDWKR--
      GGVSLMLDYDDFN 308

      250      260      270      280      290      300      310
320

.....|.....|.....|.....|.....|.....|.....|.....|
lcl|ORF1      489 INHTFILMAqhtlAMVEGLIRRGktsgitpermrvISRDLHKAAYTVIARFN-
      TYLHDHDSQLTIKTARGLQSGERQTS 567
Cdd:pfam02123 309 SQHSTESMR-----AVFERLRRR-----LPDEPAEAAD-
      WLVCsMDsMYQLSDGTLAQRVPGTLKSGHRATT 370

      330      340      350      360      370      380      390
400

.....|.....|.....|.....|.....|.....|.....|.....|
lcl|ORF1      568 RINSDCNyIdtLFVRLVSKRFFGYdvlNpVADHSGDDAFETTKNYSDGMFAAALYNLTGAA-
      GQAHKilmsyPSRGGGLGE 647
Cdd:pfam02123 371 FINSVLNC---AYAELAGAPWADV----PTSIHMGDDVLEGLRTPADATSLLDKYARLGFKVNPSK-----
      QSVGHTIAE 438

      410      420
.....|.....|.....
lcl|ORF1      648 YLRLAYdaANRKVCGYPIRAMMGLIHG 674
Cdd:pfam02123 439 FLRVAF--CSHEVRGYLARAIAASLVSG 463

```

Blast search parameters

Data Source: Live blast search RID = F32HN992016
 User Options: Database: CDSEARCH/cdd Low complexity filter: no Composition Based Adjustment:
 yes E-value threshold: 0.01 Maximum number of hits: 500

References:

- Marchler-Bauer A et al. (2017), "CDD/SPARCLE: functional classification of proteins via sub-family domain architectures.", *Nucleic Acids Res.*45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", *Nucleic Acids Res.*43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", *Nucleic Acids Res.*39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", *Nucleic Acids Res.*32(W)327-331.

 3. UniProt BLASTp alignment of the complete genome M10544

BLASTP 2.9.0+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference for composition-based statistics: Alejandro A. Schaffer, L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", *Nucleic Acids Res.* 29:2994-3005.

Database: uniprotkb_viruses
 5,056,524 sequences; 1,856,704,045 total letters

Query= EMBOSS_001

++++++
Query ORF2: 25 best matches
++++++

Length=1770

	Score (Bits)	E Value
Sequences producing significant alignments:		
TR:H6UNN1 H6UNN1_9VIRU Putative structural/gag protein OS=Fusarium...	1003	0.0
TR:H6UNM9 H6UNM9_9VIRU Putative structural/gag protein OS=Fusarium...	950	0.0
TR:A0A7G4WLZ4 A0A7G4WLZ4_9VIRU Structural/gag protein OS=Trichoder...	835	0.0
TR:A0A1P8DF80 A0A1P8DF80_9VIRU Putative structural/gag protein OS=...	829	0.0
TR:A0A514DCE7 A0A514DCE7_9VIRU Uncharacterized protein OS=Totiviri...	531	1e-159
TR:A0A514D1M0 A0A514D1M0_9VIRU Uncharacterized protein (Fragment) ...	503	4e-154
TR:A0A7S5WLX3 A0A7S5WLX3_9VIRU Uncharacterized protein OS=Macropho...	468	2e-137
TR:A0A515KU39 A0A515KU39_9VIRU Uncharacterized protein OS=Macropho...	463	6e-135
TR:A0A7S5WLX7 A0A7S5WLX7_9VIRU Uncharacterized protein OS=Macropho...	434	1e-125
TR:A0A7S5WLX4 A0A7S5WLX4_9VIRU Uncharacterized protein OS=Macropho...	432	5e-125
TR:A0A0M4L069 A0A0M4L069_9VIRU Uncharacterized protein OS=Macropho...	430	2e-124
TR:A0A7S5WLW1 A0A7S5WLW1_9VIRU Uncharacterized protein OS=Macropho...	430	3e-124
TR:A0A0A7DSJ8 A0A0A7DSJ8_9VIRU Uncharacterized protein OS=Botrytis...	415	6e-119
TR:E7BMX6 E7BMX6_9VIRU Uncharacterized protein OS=Grapevine associ...	412	4e-118
TR:A0A2Z1Q370 A0A2Z1Q370_9VIRU Uncharacterized protein OS=Fusarium...	413	2e-117
TR:A0A7L9R666 A0A7L9R666_9VIRU Uncharacterized protein OS=Botrytis...	409	4e-117
TR:A0A346P9C1 A0A346P9C1_9VIRU Uncharacterized protein OS=Trichode...	409	6e-116
TR:A0A2Z5WAE5 A0A2Z5WAE5_9VIRU Uncharacterized protein OS=Rosellin...	393	7e-111
TR:I1Y9U4 I1Y9U4_9VIRU Uncharacterized protein OS=Sclerotinia scle...	387	2e-109
TR:A0A2L1GG75 A0A2L1GG75_9VIRU Uncharacterized protein OS=Rosellin...	388	4e-109
TR:A0A1B4ZA68 A0A1B4ZA68_9VIRU Uncharacterized protein OS=Fusarium...	370	1e-103
TR:A0A2Z1Q3B3 A0A2Z1Q3B3_9VIRU Uncharacterized protein OS=Fusarium...	364	1e-101
TR:D0TZ29 D0TZ29_9VIRU Uncharacterized protein OS=Fusarium gramine...	363	5e-101
TR:A0A7G3W8V4 A0A7G3W8V4_9VIRU Uncharacterized protein OS=Monilini...	254	4e-69
TR:A0A2Z5WAD8 A0A2Z5WAD8_9VIRU Putative structural protein OS=Rose...	166	5e-39
TR:A0A3G8EWB1 A0A3G8EWB1_9VIRU Uncharacterized protein OS=Scleroti...	164	6e-39

++++++
Query ORF1: 25 best matches
++++++

Length=1223

	Score (Bits)	E Value
Sequences producing significant alignments:		
TR:H6UNN2 H6UNN2_9VIRU RNA-directed RNA polymerase OS=Fusarium vir...	740	0.0
TR:H6UNN0 H6UNN0_9VIRU RNA-directed RNA polymerase OS=Fusarium vir...	736	0.0
TR:A0A7G4WLZ5 A0A7G4WLZ5_9VIRU RNA-directed RNA polymerase OS=Tric...	717	0.0
TR:A0A1P8DF89 A0A1P8DF89_9VIRU RNA-directed RNA polymerase OS=Tric...	710	0.0
TR:A0A514DCG4 A0A514DCG4_9VIRU RNA-directed RNA polymerase OS=Toti...	555	7e-175
TR:A0A346P9C2 A0A346P9C2_9VIRU RNA-directed RNA polymerase OS=Tric...	549	1e-171
TR:A0A0A7DRW1 A0A0A7DRW1_9VIRU RNA-directed RNA polymerase OS=Botr...	540	3e-168
TR:A0A7L9R691 A0A7L9R691_9VIRU RNA-directed RNA polymerase OS=Botr...	531	7e-165
TR:A0A0S4GAY8 A0A0S4GAY8_9VIRU RNA-directed RNA polymerase OS=Scle...	528	9e-164
TR:I1Y9U5 I1Y9U5_9VIRU RNA-directed RNA polymerase OS=Sclerotinia ...	521	5e-161
TR:A0A7G3W8V5 A0A7G3W8V5_9VIRU RNA-directed RNA polymerase OS=Moni...	520	1e-160
TR:A0A0S4GA48 A0A0S4GA48_9VIRU RNA-directed RNA polymerase OS=Scle...	520	2e-160
TR:A0A7S5WLX9 A0A7S5WLX9_9VIRU RNA-dependent RNA polymerase OS=Mac...	512	2e-158
TR:A0A7S5WLW9 A0A7S5WLW9_9VIRU RNA-dependent RNA polymerase OS=Mac...	507	6e-157
TR:A0A2Z5WAE4 A0A2Z5WAE4_9VIRU RNA-directed RNA polymerase OS=Rose...	505	2e-155
TR:A0A7S5WLX4 A0A7S5WLX4_9VIRU RNA-dependent RNA polymerase OS=Mac...	500	3e-153
TR:A0A3G8GGF4 A0A3G8GGF4_9VIRU RNA-directed RNA polymerase OS=Rose...	499	3e-153
TR:A0A7S5WLW5 A0A7S5WLW5_9VIRU RNA-dependent RNA polymerase OS=Mac...	490	5e-152
TR:A0A515KU26 A0A515KU26_9VIRU RNA-directed RNA polymerase OS=Macr...	491	3e-150
TR:A0A0M5KKP5 A0A0M5KKP5_9VIRU RNA-directed RNA polymerase OS=Macr...	485	4e-150
TR:A0A514D1L9 A0A514D1L9_9VIRU RNA-directed RNA polymerase (Fragme...	479	3e-149
TR:A0A2Z1Q3S4 A0A2Z1Q3S4_9VIRU RNA-directed RNA polymerase OS=Fusa...	480	1e-145
TR:A0A2Z1Q375 A0A2Z1Q375_9VIRU RNA-directed RNA polymerase OS=Fusa...	472	1e-142
TR:D0TZ30 D0TZ30_9VIRU RNA-directed RNA polymerase OS=Fusarium gra...	469	9e-142
TR:A0A1B4ZA62 A0A1B4ZA62_9VIRU RNA-directed RNA polymerase OS=Fusa...	452	3e-135
TR:A0A3G8EX21 A0A3G8EX21_9VIRU RNA-directed RNA polymerase OS=Scle...	381	4e-110

+++++
Query ORF2: query sequence and 24 best matches aligned
+++++

CLUSTAL O(1.2.4) multiple sequence alignment

```

lc1|ORF2                                MVDRLTGHVFLDRKPKQSVRHPRMDSQQTALNEAGSSASRSAVAQQTIGRCNLDSY 60
TR|H6UNN1|H6UNN1_9VIRU                  -----
TR|H6UNM9|H6UNM9_9VIRU                  -----
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU          -----
TR|A0A1P8DF80|A0A1P8DF80_9VIRU          -----
TR|A0A514DCE7|A0A514DCE7_9VIRU          -----
TR|A0A514D1M0|A0A514D1M0_9VIRU          -----
TR|A0A7S5WLV3|A0A7S5WLV3_9VIRU          -----
TR|A0A515KU39|A0A515KU39_9VIRU          -----
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU          -----
TR|A0A7S5WLV4|A0A7S5WLV4_9VIRU          -----
TR|A0A0M4L069|A0A0M4L069_9VIRU          -----
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU          -----
TR|A0A0A7DSJ8|A0A0A7DSJ8_9VIRU          -----
TR|A0A2Z1Q370|A0A2Z1Q370_9VIRU          -----
TR|E7BMX6|E7BMX6_9VIRU                  -----
TR|A0A7L9R666|A0A7L9R666_9VIRU          -----
TR|A0A346P9C1|A0A346P9C1_9VIRU          -----MAFSGNTERQTRLESSASQP----- 20
TR|A0A2Z5WAE5|A0A2Z5WAE5_9VIRU          -----
TR|A0A2L1GG75|A0A2L1GG75_9VIRU          -----MTMH-----AD----- 6
TR|I1Y9U4|I1Y9U4_9VIRU                  -----
TR|A0A1B4ZA68|A0A1B4ZA68_9VIRU          -----
TR|A0A2Z1Q3B3|A0A2Z1Q3B3_9VIRU          -----
TR|D0TZ29|D0TZ29_9VIRU                  -----
TR|A0A7G3W8V4|A0A7G3W8V4_9VIRU          -----
TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU          -----

```

```

lc1|ORF2                                FPASIRTHNFALAHGVKLSKSIAQWSLTSSSTSGGRVPALPGVEHSCCAELECSANVCCGC 120
TR|H6UNN1|H6UNN1_9VIRU                  -----
TR|H6UNM9|H6UNM9_9VIRU                  -----
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU          -----
TR|A0A1P8DF80|A0A1P8DF80_9VIRU          -----
TR|A0A514DCE7|A0A514DCE7_9VIRU          -----
TR|A0A514D1M0|A0A514D1M0_9VIRU          -----
TR|A0A7S5WLV3|A0A7S5WLV3_9VIRU          -----
TR|A0A515KU39|A0A515KU39_9VIRU          -----
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU          -----
TR|A0A7S5WLV4|A0A7S5WLV4_9VIRU          -----
TR|A0A0M4L069|A0A0M4L069_9VIRU          -----
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU          -----
TR|A0A0A7DSJ8|A0A0A7DSJ8_9VIRU          -----
TR|A0A2Z1Q370|A0A2Z1Q370_9VIRU          -----
TR|E7BMX6|E7BMX6_9VIRU                  -----
TR|A0A7L9R666|A0A7L9R666_9VIRU          -----
TR|A0A346P9C1|A0A346P9C1_9VIRU          -----
TR|A0A2Z5WAE5|A0A2Z5WAE5_9VIRU          -----
TR|A0A2L1GG75|A0A2L1GG75_9VIRU          -----
TR|I1Y9U4|I1Y9U4_9VIRU                  -----
TR|A0A1B4ZA68|A0A1B4ZA68_9VIRU          -----
TR|A0A2Z1Q3B3|A0A2Z1Q3B3_9VIRU          -----
TR|D0TZ29|D0TZ29_9VIRU                  -----
TR|A0A7G3W8V4|A0A7G3W8V4_9VIRU          -----
TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU          -----

```

```

lc1|ORF2                                TSTVERAERWSLPHPEGADGWVKSQAEEAPIRWNDCPPFRSMVMRADQSTGHPPVMDSYG 180
TR|H6UNN1|H6UNN1_9VIRU                  -----
TR|H6UNM9|H6UNM9_9VIRU                  -----
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU          -----MASFN 5
TR|A0A1P8DF80|A0A1P8DF80_9VIRU          -----MASFN 5
TR|A0A514DCE7|A0A514DCE7_9VIRU          -----
TR|A0A514D1M0|A0A514D1M0_9VIRU          -----
TR|A0A7S5WLV3|A0A7S5WLV3_9VIRU          -----
TR|A0A515KU39|A0A515KU39_9VIRU          -----MVC DGWSSPFME-----QTNVLLGSAREWRDNT 27

```

TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----	
TR	A0A7S5WLV4	A0A7S5WLV4_9VIRU	-----	
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----	
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----	
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----	MMSS 4
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	-----	MDYPR 5
TR	E7BMX6	E7BMX6_9VIRU	-----	MMSS 4
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----	MMSS 4
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----	VVAQQATIRRGSNLDS 38
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----	MDSYE 5
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----	QSIGHYPMDSYE 19
TR	I1Y9U4	I1Y9U4_9VIRU	-----	MSS 3
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----	MLNT 4
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----	MLNT 4
TR	D0TZ29	D0TZ29_9VIRU	-----	MAYSK 5
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----	

lc1	ORF2	YSALT--EAGSSAS----	RS-----	AVAQQNTIG-RDGNLDSHNIASVSTSG	220
TR	H6UNN1	H6UNN1_9VIRU	-----	MS-----S-SLSNLVSNF-----	12
TR	H6UNM9	H6UNM9_9VIRU	-----	MS-----SSN-----	5
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	NTTTT-----	ITNTTSAT-----	18
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	NTTTT-----	TTSTPTT-----	18
TR	A0A514DCE7	A0A514DCE7_9VIRU	-----		
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----		
TR	A0A7S5WLV3	A0A7S5WLV3_9VIRU	-----		
TR	A0A515KU39	A0A515KU39_9VIRU	YRGVSR-VTDD---	L-----K-----CKLGGGPLGMKLAHRKSPPSGMACPAG	66
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----		
TR	A0A7S5WLV4	A0A7S5WLV4_9VIRU	-----		
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----		
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----		
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	YGIKT--VNQTATVAVD----	A-----SAENGAQIN-RGGNLDSFSAGVNYSG	46
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	NTGRQS-SEEFSSARS-----	VMAQLNTIG-KDGNLDSQTINDSATGN	46
TR	E7BMX6	E7BMX6_9VIRU	YGIKT--VNQTATVAVD----	A-----SAENGAQIN-RGNLDSSTAGVNYSG	46
TR	A0A7L9R666	A0A7L9R666_9VIRU	YGIKT--VNQTATVAVD----	A-----SAENGAQIN-RGNLDSSTAGVNYSG	46
TR	A0A346P9C1	A0A346P9C1_9VIRU	VSAGPESTAAFTXGALRQLGITDMTGKLTIVILEKLG-DGSRLAASDSGERAL---	AS	94
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	Y-TTP-SSQSFAST--T-----	TGLT-NGSNKRDGNLDSQNTQFDGTST	45
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	C-TTP-SSQSFAST--T-----	TGLT-NGSNKRDGNLDSQNTQFDGTST	59
TR	I1Y9U4	I1Y9U4_9VIRU	YGITK--VNKTATVAVD----	A-----SALNGAQIN-RGNLDSYTTTSFA----	41
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	YASARA-VNSTAYASTCASGAA-----	SNVTGGSMNEAVGHVDSHLSVNS----	49
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	YASVRA-VNSTAYASTCASGAA-----	SNVTGGTANEAVGHVDSHSHSYAE----	49
TR	D0TZ29	D0TZ29_9VIRU	YQGRHA-SEEFSSAPR-----	T-----APVQQSSIG-KDGNLDNQASHLND----	43
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----		
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----		

lc1	ORF2	CPCGYKHGKDFECYALLANGVVPALTNYSPPSPAIARTRQFKRAISFETD-----	LTA	272	
TR	H6UNN1	H6UNN1_9VIRU	-----	LFEA-SSITTGTLTA-----PSSFQELGVSRA-----E-----GAR	41
TR	H6UNM9	H6UNM9_9VIRU	-----	IFDNTTSISESVYIS-----QRRALVTQGLTKA-----Q-----VKQ	38
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	SNSTQDEANIYKN--SIQAAVQA-----	AVFVSKE--TAGEFDTL--DECVFRVRG	63
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	SNTKQDEANIYKN--SIQAAVQA-----	AVFVSKE--TAGEFDTL--NECVFRVRG	63
TR	A0A514DCE7	A0A514DCE7_9VIRU	MSFF-----	TTMKN-----LFYRKE-SRSAPTSLS-----	25
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----		
TR	A0A7S5WLV3	A0A7S5WLV3_9VIRU	-----	M-----A-----SY--FTS-----	7
TR	A0A515KU39	A0A515KU39_9VIRU	TMDYLMNTQQVS-----	ASACNTLEA-----R-----GY--MTG-----	93
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----	MFCNLQNA-----MAYEAG-LNCF-----TSV-----	21
TR	A0A7S5WLV4	A0A7S5WLV4_9VIRU	-----	MASF-----LPS-----	7
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----	MASF-----ILA-----	7
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----	MFCNLQNA-----MAYEAG-LNCF-----TSV-----	21
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	I-----	SS-----S-----ASKADL-----	56
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	DKCRPVVTPLTS-----	ARILNRADNAHD-RLSKNRAS-KRGFPFTATTVNQNGFNGV-	97
TR	E7BMX6	E7BMX6_9VIRU	N-----	LS-----S-----VSKADL-----	56
TR	A0A7L9R666	A0A7L9R666_9VIRU	T-----	FS-----S-----ASKADL-----	56
TR	A0A346P9C1	A0A346P9C1_9VIRU	---QVR-----	N-----GQCFINAVV	107
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	---HQN-----	N-----NVCSDEVKM-	57
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	---HQN-----	N-----NVCSDFKK-	71
TR	I1Y9U4	I1Y9U4_9VIRU	-----	SKADLSA-----	48
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----		
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----		
TR	D0TZ29	D0TZ29_9VIRU	-----	S-----	44
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----		

TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU-----MSFNTN-----Y 7

lc1|ORF2 LVAAERSINLASQV-----KYEFNPACSCRINEVGSLSVQGCQSVPHLYQIPSLN-RWC 325
TR|H6UNN1|H6UNN1_9VIRU LKNKPLVFSASPGVYPP-----TCGCNIDNQGHVVTFCVHEHPVGLPLPLCHAS 92
TR|H6UNM9|H6UNM9_9VIRU LYKSE---RLATPVFPYIDVPSQPDITLCSFL-CPCLEGQTCGAHPGGPLPAIPCDWN 94
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU AGQRHVDITYCQPFP-----NSHKCKCLF--NSKLKGNCQSPPEGFPFI-----LN 108
TR|A0A1P8DF80|A0A1P8DF80_9VIRU AGQRHVDITYCQPFP-----STHKCKCLF--NSKLGRGNCQSPPEGFPV-----LN 108
TR|A0A514DCE7|A0A514DCE7_9VIRU TVSPARTFT--S-----AGSAEVTST-QTTSSGG-----WY 53
TR|A0A514D1M0|A0A514D1M0_9VIRU -----
TR|A0A7S5WL3|A0A7S5WL3_9VIRU A--LAQSFK-----KS-----QRSLSD-----LA 24
TR|A0A515KU39|A0A515KU39_9VIRU P--ATTVIA-----YIAGVTS-DLGADLAH-----VL 117
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU A--LAQSLK-----KSYSH-----LI 35
TR|A0A7S5WL4|A0A7S5WL4_9VIRU A--LAQSFK-----KSQTA-----LA 21
TR|A0A0M4L069|A0A0M4L069_9VIRU A--LAQSFK-----KSQPT-----LA 21
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU A--LAQSLK-----KSHPH-----FI 35
TR|A0A0A7DSJ8|A0A0A7DSJ8_9VIRU LVHARHSKN--E-----RFSFVFLSSALQRVYTA-----ML 85
TR|A0A2Z1Q370|A0A2Z1Q370_9VIRU TAPLLARYRASD-----P-----HNSAPVM---EGQVLGG-----RD 126
TR|E7BMX6|E7BMX6_9VIRU LVHAQHASKN--E-----QFSFVFL-SRWQRFCTA-----II 84
TR|A0A7L9R666|A0A7L9R666_9VIRU LVHAQHSKI--E-----RFSFVFFSSGWCFCFTA-----IL 85
TR|A0A346P9C1|A0A346P9C1_9VIRU PEDRYKLSHISD--WP-----TRTAFINALIETGARLEMARCLSLQLGGK-----WA 152
TR|A0A2Z5WAE5|A0A2Z5WAE5_9VIRU -STAAGSVNLS--FK-----GTI--TQRTMERGRIFAHHFAVI-----WL 93
TR|A0A2L1GG75|A0A2L1GG75_9VIRU -SNAAESINLS--FK-----GTI--TQRTMERGRIFAHNLAFA-----WL 107
TR|I1Y9U4|I1Y9U4_9VIRU FEPALLDKN--E-----QFSFVISFLTYLQNTK-----74
TR|A0A1B4ZA68|A0A1B4ZA68_9VIRU VFSARGDDV--Q-----SCLFLRRFCK-----IS 71
TR|A0A2Z1Q3B3|A0A2Z1Q3B3_9VIRU LVPSARDFS--S-----P-----PSASSMKR--TP-----LS 72
TR|D0TZ29|D0TZ29_9VIRU AVPSRPAPS--D-----KLSASFWSWCSFPFS-----68
TR|A0A7G3W8V4|A0A7G3W8V4_9VIRU -----
TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU NVPTG---RL-----NPEPFGCIE---GDVRIGSLSFGDAPYIQPSLE---- 44

lc1|ORF2 DGT-T-SAIAGG-----CYLALWSGWARPAVMRLGRAPTAEAILHLLGNTHKCM 373
TR|H6UNN1|H6UNN1_9VIRU -SL-V-KYVDGG-----CYAIGWKATAHAFAVKLLSGLPTAAQIMRLWIATDPQ 139
TR|H6UNM9|H6UNM9_9VIRU DDV-V-ATLKDC-----CYLLGFPVSARPHAFEYLARRLVSDIKRYAALTDPOG 142
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU DAT-V-SASDGL-----CYLLAWTPEYRYCVLSLLGFARRVGMIRDLYQRSHKGA 156
TR|A0A1P8DF80|A0A1P8DF80_9VIRU DAT-V-SASDGL-----CYLLAWTPEYRYCVLSLLGFVRRVGMIRDLYQRSHKGA 156
TR|A0A514DCE7|A0A514DCE7_9VIRU NKLSPSFFSFL-----FFLFS--TLSFPFLV-----ARVLVFIFFL--QNTLV 94
TR|A0A514D1M0|A0A514D1M0_9VIRU -----
TR|A0A7S5WL3|A0A7S5WL3_9VIRU AGLRSAFL--C-----LSLFL--FLASPFVCLLISFIPPAFIFLFFSEHSPGG 69
TR|A0A515KU39|A0A515KU39_9VIRU KRSRLSFFPLYL-----FLFFC--FLNSPFIIVLFSFLPALVFYLFSEPVPGV 165
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU AVLARFKAAYF-----LCLFG--FLASPFIVLIFSLLPPALVFYFIFYMPSLGV 83
TR|A0A7S5WL4|A0A7S5WL4_9VIRU AMGSRFMVAFLC-----FLLF--VLISPLVVLVLECIPPALVALSFFLLTNPGV 69
TR|A0A0M4L069|A0A0M4L069_9VIRU AMRAKFMAFLC-----FVFFM--ALVTPFVVLFIISFVPLALLFFSFFY--LLPGV 68
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU AVLARFKAAYF-----LCLFG--FLASPLVVLVLSFLPPALVFYFIFYMPSLGV 83
TR|A0A0A7DSJ8|A0A0A7DSJ8_9VIRU AFF-TSFVALFE-----REIYS--VFLSPYLL---IL-----111
TR|A0A2Z1Q370|A0A2Z1Q370_9VIRU GTS-RSFFLLWS-----FFL--FVSPVLFPA--GIAASVVLVCWCWI--LLNL 166
TR|E7BMX6|E7BMX6_9VIRU AFF-TSFVALFE-----REIYS--VFLSPHLL---IL-----110
TR|A0A7L9R666|A0A7L9R666_9VIRU ALF-TSFVALFE-----REIYS--VFISPHLL---IL-----111
TR|A0A346P9C1|A0A346P9C1_9VIRU RKMSHPHLEYGHLVPGGELNGVXILC--LPLPGHFRLLGGELPPVSRN-----SI 200
TR|A0A2Z5WAE5|A0A2Z5WAE5_9VIRU QIILV-----A--LS-ATSL-----VLRT-----SI 111
TR|A0A2L1GG75|A0A2L1GG75_9VIRU QIILV-----A--LS-ATSL-----VLRA-----SI 125
TR|I1Y9U4|I1Y9U4_9VIRU NIL-SYFAARFE-----CYISS--IFLTPYIL---VS-----100
TR|A0A1B4ZA68|A0A1B4ZA68_9VIRU AL--LSFVSRWF-----CFLLS--F--PFSF--FAL--ALMRCF--DLPLG 105
TR|A0A2Z1Q3B3|A0A2Z1Q3B3_9VIRU ALF-RSFWRWFF-----LYISS--FFSALSSF--FAI--SLLRCF--DLPGF 110
TR|D0TZ29|D0TZ29_9VIRU -----FVVLRF-----LFFLS--FTVSSFFSFLRYFI--SFVTCA-----100
TR|A0A7G3W8V4|A0A7G3W8V4_9VIRU -----
TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU -----RTDYVLKIENQTIAGLYKYS--ETPRSEWVRFLTERAKASAAALR-----86

lc1|ORF2 RHDSWRF-----CAVRG-GTEF-----VHILPDR-FGVSGKTLRLAMPASS 412
TR|H6UNN1|H6UNN1_9VIRU -----R-----CNPRV-----KLS---RS- 150
TR|H6UNM9|H6UNM9_9VIRU -----L-----NRRNV-----PVL---LSN 154
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU KRPSAKIFF--TRVCATTPRGGHY-----HHI-----SAATPAQK 189
TR|A0A1P8DF80|A0A1P8DF80_9VIRU KRPSAKIFF--TRVCATTPRGGHY-----HHI-----SAATPAQK 189
TR|A0A514DCE7|A0A514DCE7_9VIRU SRGI-HLLI---AVCPLW--FI-----DPLVKFM-LRD---E-LAIG-FRR 129
TR|A0A514D1M0|A0A514D1M0_9VIRU -----
TR|A0A7S5WL3|A0A7S5WL3_9VIRU VNLK-NLVI-----PQTY---E-----SLRLEN-ERT---V-LSPG-RAR 99
TR|A0A515KU39|A0A515KU39_9VIRU PSLK-NLVI-----PLTY---E-----ELHQRN-IQE---E-LSPG-RAR 195
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU LNRK-NLVI-----PPTY---E-----SLRSS--TPL---E-LSSG-RQR 112
TR|A0A7S5WL4|A0A7S5WL4_9VIRU SNRK-NLVI-----PPTY---E-----SLRNN--RPL---E-LSAG-KQR 98
TR|A0A0M4L069|A0A0M4L069_9VIRU LGRK-NLVI-----PPTY---E-----SLRSS--TPL---H-QSSG-RQR 97
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU FNRK-NLVI-----PPTY---E-----SLRSS--TPL---N-QSSG-RQR 112

TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----RSNIAQ---QT-----V--SPAL-YNF-----PS--RH	131
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	FFDSNQLVEALFQFNTIKW---RF-----AYM----	190
TR	E7BMX6	E7BMX6_9VIRU	-----RSNIAQ---QT-----V--SPAL-YNF-----PS--RH	130
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----RSNIAQ---QT-----V--SPAL-YNF-----PS--RH	131
TR	A0A346P9C1	A0A346P9C1_9VIRU	TAAVWSLLLS-YLVTAITFVSTEFSSALQTDYAYGHTIRPRL--AYV-GQI----H-P--	250
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	KPA--ELLVR-MLLDHADWVEK-LGVERVREAIGEAVGEKVEI--AYV-GRV----H-LPS	160
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	KPA--ELLIR-MLLDHADWVEK-LGVERVREAIGEAVGEKVEI--AYV-GRV----H-LPS	174
TR	I1Y9U4	I1Y9U4_9VIRU	-----HSNLAQ---QT-----V--SPAL-YSF-----PQ--RM	120
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	FVMQ-D-----LSSSLKW---ER-----V--TPTL-LTR---N-FAYG--RP	134
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	FLMH-D-----LSCSLKW---ER-----V--TPTL-LTR---N-FAFG--SS	139
TR	D0TZ29	D0TZ29_9VIRU	-----SPLSS---RN-----S--RPRR--AS---A-LAFG-RSD	122
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-RQAN-----PLCRALFSALQTIRASARPTRGAGLLHNPANSPYAQSGGGIAFGQVRK	138

1c1	ORF2	----	RVGFS---ECVVNTH-SASFTRYEQLSDSPFFSLLIRSLISFVFSFVY-GALD	462
TR	H6UNN1	H6UNN1_9VIRU	-----NADP-----	154
TR	H6UNM9	H6UNM9_9VIRU	-----KVGLP-----	159
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	----RD--K-----	192
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	----RD--K-----	192
TR	A0A514DCE7	A0A514DCE7_9VIRU	----NVKIP---FCSP-----YGFETCLF-----	146
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	----LA-V-----TLKVIL-----	108
TR	A0A515KU39	A0A515KU39_9VIRU	----LA-L-----TLKLLF-----	204
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	----LA-L-----TIMCLF-----	121
TR	A0A7S5WLV4	A0A7S5WLV4_9VIRU	----LA-L-----TLNLLL-----	107
TR	A0A0M4L069	A0A0M4L069_9VIRU	----LA-L-----TLKCLF-----	106
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	----LA-L-----TLKCLF-----	121
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	AYSMSLYRW---SCIPLLLY-SYGFLSFSQ-----AEH	160
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	----QESHs---TCLWKSRL-SLGFTTERL-----LD	214
TR	E7BMX6	E7BMX6_9VIRU	TYHMLGYRW---SCIPLLLY-SYGFLSFSQ-----AEH	159
TR	A0A7L9R666	A0A7L9R666_9VIRU	AYSMSLYRW---SCIPLLLY-SYGFLSFSQ-----AEH	160
TR	A0A346P9C1	A0A346P9C1_9VIRU	---LAFKEQ---TCLWEYFL-GCGLDAFQLAM-----LGITPLTSRLSTAQASALS	294
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	TYKVTRSPA---TCLWLWLVCDLGFNPVVLAL-----HGVPWYSYSITPAFSALL-	207
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	TYKVTRSPA---TCLWLWLVCDLGFNPVVLAL-----HGVPWYSYSITPAFSALL-	221
TR	I1Y9U4	I1Y9U4_9VIRU	AYDLLGYRW---NCIPLLLY-SYGFISLAQ-----AER	149
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	HHDLLSEMT---TCIPLALY-DFNIIISFSQ-----ALR	163
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	HHDLLAERT---TCIPLALY-DFNIIISFSQ-----ALR	168
TR	D0TZ29	D0TZ29_9VIRU	SINFLAHYT---TCIPLLLT-SYGLISPSQ-----ALH	151
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	---RLVKYWRPRVNKYWKLL-VAAYFDLRIK-----	166

1c1	ORF2	FGERILCKQIPKHFPTRPSLRKNGCYCLELPHPIWHPFVA-----SLLGPKPPIRILR	515	
TR	H6UNN1	H6UNN1_9VIRU	-----SVHH---LEL-----LHLGAS--LEG--	170
TR	H6UNM9	H6UNM9_9VIRU	-----EYHVPHYIIPA-----PHSDPLPRGPA--	181
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	-----SCDT-----VQSIFTNLDT---THNTCLLGLAARVTA--	221
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	-----SCDT-----VQSIFTNLDT---SHNSCLLGLAARVTA--	221
TR	A0A514DCE7	A0A514DCE7_9VIRU	TA-----TVEQFGYLPVTFILGMKP---CDTRYNIRVVVKHYGLAKMRLPFFASRPG--	194
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	SN-----RKS-----LA---TDGVFHTYVAGTDVVQKEP-AIIPANCG--	142
TR	A0A515KU39	A0A515KU39_9VIRU	TG-----RET-----IP---SSEGKEHKIWCCAIVTVELP-PAIPNSNG--	238
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	SN-----RTP-----DP---NQKPSPCYVEG--IIPPQPIGISA-AAG--	153
TR	A0A7S5WLV4	A0A7S5WLV4_9VIRU	AD-----RLA-----EE---HLVPITHLDAN--LLPKQPLAIKASSSG--	140
TR	A0A0M4L069	A0A0M4L069_9VIRU	SN-----RAA-----DP---HPKSPPSYAEG--IIPPQPIGISA-VAG--	138
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	SN-----RVP-----DP---CQKPSLCHAEG--IIPPQPIGISA-VAG--	153
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	FR-----NVQKFSDLPLSLRMSILR---H-RRSAILVRVSFQHVENLLAAPTGT--	205
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	MG-----IAPWMTSLQRSTKLLKLP---S---LP---LYYT---LP-FNSRLG--	249
TR	E7BMX6	E7BMX6_9VIRU	FR-----NIQKFSDLPLSLRMSILR---H-RRSAILVRVSFQHVENVLAPSTTG--	204
TR	A0A7L9R666	A0A7L9R666_9VIRU	FR-----NIQKFSDLPLSLRMSILR---H-RRSAILVRVSHQHVENVLAPPTTG--	205
TR	A0A346P9C1	A0A346P9C1_9VIRU	TG-----TNGFFIAYLRVGKTGLT---NHI-----	316
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----KSLGITGLP---GKITWARKSH--IHHVQALT-----	234
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----KSLGIIGLP---GKITWARKSH--IHHVQALS-----	248
TR	I1Y9U4	I1Y9U4_9VIRU	FR-----NIRKFSDLPLSLRASILR---S-RRSAILVRVFPKHVESLLAPNTSNA--	195
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	LR-----YVTSFSELPRPIRNSLAR---S-RHSRLLFRLYPGHIESSLRPI-LAF--	208
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	LK-----HVTSAQLPRPIKESLAR---S-RHSRLLFRLYPGHIESSLRPI-LNF--	213
TR	D0TZ29	D0TZ29_9VIRU	LS-----YVTKFTDLPKSLRDGILR---D-SRSHLLVRVYNRHVQSLLAQ--LKG--	196
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----VQRIPRSLSKIRAR-----IEKKLLNASPDR----	192

1c1	ORF2	FLYVTLPLFLDFRVNFIIVAKDMLDCDGRPVYHVVFATTGGSEVGRRTARGVLWALDADARLG	575
-----	------	---	-----

TR	H6UNN1	H6UNN1_9VIRU	-----SVLFSEAVASVSMT	184
TR	H6UNM9	H6UNM9_9VIRU	-----EILFWHLLDILPVG	195
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	-----ARASDSDEV-	231
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	-----ARASDSDEV-	231
TR	A0A514DCE7	A0A514DCE7_9VIRU	-----LPSVPHVSLFEFTGSFP-----HPTFAYLATHD----	222
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	-----FSLFLQ-----RTNN----	152
TR	A0A515KU39	A0A515KU39_9VIRU	-----FSIVLQ-----ATAN----	248
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----YSLFLQ-----VNNN----	163
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	-----YSLFLQ-----VNNN----	150
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----YSLFLQ-----VNNN----	148
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----YSLFLQ-----VNNN----	163
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----PYEL-----ISLRILLNST----	219
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	-----HVS-----TKYFP-----NSKFGFPLRLA-MK	270
TR	E7BMX6	E7BMX6_9VIRU	-----SYEL-----LSLRILLNSE----	218
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----SYEL-----VSLRILLNST----	219
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----STSPFKCSKLT-----RLPIDFL-----	334
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----SGDPLKLIS-----LKTL-----	247
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----SRDPLKLIS-----LKML-----	261
TR	I1Y9U4	I1Y9U4_9VIRU	-----HCLS-----ISLRELLNSP----	209
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----NYKL-----VTLGQMLHST----	222
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----NYRL-----VTLRQMLTTT----	227
TR	D0TZ29	D0TZ29_9VIRU	-----KYEL-----APLRCLLTSA----	210
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----MISVIGGAVASLV-KAGHSQAAAEMHNRMMHMLNGN-IA	229

1c1	ORF2	QFTSPEDQDTSQLLAKSSVAVNAIAPLGGVRQVPTSLPIPQI-SPGFTRRWAPNIFPT	634	
TR	H6UNN1	H6UNN1_9VIRU	DRIG--SSSDSDGGVKAREVYSPQSVAALGGVRLVPTSLPVPQL-APGFNQPWAPTWTPT	241
TR	H6UNM9	H6UNM9_9VIRU	AQ---LGSDEGSLNAKSAYSAPIEALGGVRVPTNIPAMQL-APGYARHWSFDLWAP	250
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	-----AKRVKDSGLKPAFSGTTPPISALGGVREVPTSLIVPRL-GDGYNRKWSTELFAT	284
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	-----AKRVKDSGLKPAFSGTTPPISALGGVREVPTSLIVPRL-GDGYNRKWSTELFAT	284
TR	A0A514DCE7	A0A514DCE7_9VIRU	--HLDPRGDDTSDKRVIDTFLSPAVPALGGVRVTLQMPVTGV-SRSLTERWYPGKFPR	279
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	--KRAHSLTGNIDGPVPTDRDFLSASIPALGGVRHVLTEYMTGVL-SSDLKTRWDPLRFPR	209
TR	A0A515KU39	A0A515KU39_9VIRU	--RAHSLTGNIAAGPVPTKDFLSASIPALGGVRHVLTEYMTGVL-SSDLKTGWDPPLRFPR	305
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	--RLMHTLNGNIAASLRPVQDFLSAAIPGLGGVRHVLTEYTTGVM-SSNLKERWSPLRYPR	220
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	--RRMHALNGNIANLRPVQDFLSAAIPGLGGVRHVLTEYTTGVM-SSNLKERWSPLRYPR	207
TR	A0A0M4L069	A0A0M4L069_9VIRU	--RLMHTLNGNIAASLRPVQDFLSAAIPGLGGVRHVLTEYTTGVM-STN1KERWSPLRYPR	205
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	--RLMHTLNGNIAASLRPVQDFLSAAIPGLGGVRHVLTEYTTGVM-SSNLKERWSPLRYPR	220
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	--ADYLATPYSTAESKPTMEFSTPSVPALGGARAVLTQLPTSAR-AAGLSKKWSPHMYPT	276
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	--YQFGATPG--KENEIKTSFSLNPIPLGGVKITLSQLPTETK-APDFDTKWTPSFFSP	325
TR	E7BMX6	E7BMX6_9VIRU	--AAYFATPYSTAESKPTMEFSTPSVPALGGARAVLTQLPTSAR-AAGLSKKWSPQMYPT	275
TR	A0A7L9R666	A0A7L9R666_9VIRU	--TAYLATPYSTAESKPTMEFSTPSVPALGGARAVLTQLPTSAR-AAGLSKKWSPHMYPT	276
TR	A0A346P9C1	A0A346P9C1_9VIRU	--TK---VHVFGELQAGSVTAPAIQALGGVRQVITSLINGRL-SGEAGKGWDWSLWPT	388
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	--TA--FSFGAAEELTVTGSYTAKEALGGVHMAPTSLPAERIASGGISRIWDWSLWPT	303
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	--TA--FSFGAAEELTVTGSYTAKEALGGVHMAPTSLPAERIASGGISRIWDWSLWPT	317
TR	I1Y9U4	I1Y9U4_9VIRU	--TEYLSTPYSTAEPNPTMEFSTPSVPALGGARAVLTQLPTSAR-AAGLNKKWAPTLYPT	266
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	--TTILATPYSQKEATPSMELTSPTLPLGGVRSVLTQLATSYSR-APNLNDRWHPTLFP	279
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	--STILATPYTQKEATPSMELTSPTLPLGGVRSVLTQLATSYSR-APNLNDRWHPTLFP	284
TR	D0TZ29	D0TZ29_9VIRU	--QEFLTPPYTEAECLKVSSAYSSPAIPALGGIRGVLTLQVLTGSK-ATGISNRWHPGHYP	267
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	QFFNDVPLTQTGDMNVFGSVKTSDDPLLGAVTVLTYELFGDA--PHSDARVGPETFYR	287

1c1	ORF2	SLTSQPLEW-VRD-AQGHLLALSRESEFTYHYHPEDSSLSRLPTRFSATLLSKWFFRR---	E 689	
TR	H6UNN1	H6UNN1_9VIRU	QATDDLQW-RRVDAQGRVSHLRTSNYVRHYPAELNNPRLPQAFSDTLESHWFREL---	P 297
TR	H6UNM9	H6UNM9_9VIRU	QVLEDPIQW-TPYLRGNDNAVVRTSDFVYHYPELDNPLPKTFSAHLSQNWFAQS---	E 306
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	QMIIEDIDW-TLSQNDHDVYFVRESEFVYHFPDELQNPRLPRHFTDNATFKWVSA--	QD 341
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	QMIIEDVDW-TLSQNDHDVHFNRESEFVYHFPDELQNPRLSRHFTDNATFKWVSA--	QD 341
TR	A0A514DCE7	A0A514DCE7_9VIRU	QMHTTAVDW-HVQRDPGALRVHRSNEYTRMFPDSSTRARLPSLFTDTMPTLLFTPT-RE-	336
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	QMTNIASDF-KLPNKDEDLGINRDNQYVRHFPKLMTPQLPQFVSTLRALIAFKR-NDE	267
TR	A0A515KU39	A0A515KU39_9VIRU	QMTNIASDF-KLFNRDEDLGINRDNQYVRHFPKLMTPQLPQFVSTLRALIAFKR-NDQ	363
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	QMTNSAIAW-RQTGDREDIFIDNPNEYVRHFPEIMTNPQLPEYFVHHLKMLSFLR-SDH	278
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	QMTNSAIAW-RQTGDREDIFIDNPNEYVRHFPEIMTNPQLPEYFVHHLKMLSFLR-SDH	265
TR	A0A0M4L069	A0A0M4L069_9VIRU	QMTNSAIAW-RQAGDREDIFIDNPNEYVRHFPEIMTNPQLPEYFVHHLKMLSFLR-SDH	263
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	QMTNSAIAW-RQTGDREDIFIDNPNEYVRHFPEIMTNPQLPEYFVHHLKMLAFLR-SDH	278
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	QAVDQRVVF-DVTAR--GIKSLRENNFVRSFPENLPQPRQPTHFSELLTSILAGRLSTST	333
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	SIVDRPLKH-A-YSQEGELITERESEFYRHYPPQGRVERLPSRFTETLKSVRWAPW--TL	381
TR	E7BMX6	E7BMX6_9VIRU	QAVDQRVVF-DVTAR--GIKSLRENNFVRSFPENLPQPRQPTHFSELLTSILAGRLSTST	332
TR	A0A7L9R666	A0A7L9R666_9VIRU	QAVDQRVVF-DVTAR--GIKSLRENNFVRSFPENLPQPRQPTHFSELLTSILAGRLSTST	333

TR	A0A346P9C1	A0A346P9C1_9VIRU	DMLRQRPTW-ILTNNNDIVSTRDSEFMRYFPEDTERTHLSQRFSETLKSVFVAFRASEAA	447
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	SLLSERVVAKVFGGAGGDIGIERSSTFYRHFPDTEITQLPERFESFLQSAFCFRVLG--	361
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	SLLSERVVAKVFGGAGGDIGIERSSTFYRHFPDTEITQLPERFESFLQSAFCFRALG--	375
TR	I1Y9U4	I1Y9U4_9VIRU	QAVDQRVVF-ETTAR--TIKTLRESNYVRSYPENLPQPRQPEHSELLGSIVAARLTNSQ	323
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	QATDVHNVY-EFAHR--RVNVVRRHNYIRSFPANHPNARQPEHFEDKSYTAILARE-APY	335
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	QATDVHNVY-EFSHR--RINVVRRHNYIRSFPANHPNARQPEHFEDRSLTAILARE-APR	340
TR	D0T2Z29	D0T2Z29_9VIRU	KAISQRLNY-RQVGT--EITYTERPNDYIRSFPDHISPPRLPEHFSDSLKSVIAGRTRDGN	324
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	TTTDQPLLM---GSDTAGCISRPNAFTVHYPEGSNR--LDTRREDNLVSRVMSHS----	337

1c1	ORF2		VDEAGCVTTAYNRRFEPDTP-----SRTTLDEFSaIGQVLDGN-MSLDVLKADADAGG	740
TR	H6UNN1	H6UNN1_9VIRU	DDAFARLPATYSRSFSPDVV-----TRSVLDEFTaIGQVMTNN-NSLEVLKEADAVG	348
TR	H6UNM9	H6UNM9_9VIRU	PSPDPTVVQCQYNRRFKPDIV-----ARSVLEEFSSIGLVMEGA-NNFDTLKDADSVA	357
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	GTPDRWLPTNYTRYFEPSTQ-----DRIVLEPFSaIGKMLSGE-LSLDVLKEADSSA	392
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	GTPDRWLPTNYTRYFEPSTQ-----DRIVLEPFSaIGKMLSGE-LSLDVLKEADSSA	392
TR	A0A514DCE7	A0A514DCE7_9VIRU	-DRTHILSAQYDRRWNLQDP-----VRTLSGPYAALARVLDGD-TSRDALVAADQTV	386
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	KGYNHKVECKFDRIWEPNSP-----NVRPLQERFVGLSGVLGAGS-LDQVSLKAAEQVG	319
TR	A0A515KU39	A0A515KU39_9VIRU	KEYNHRVECKFDRIWEPNSP-----NVRPLQERFVGLSGVLGAGS-LDQVSLKAAEQVG	415
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	RDHHHVIPDTDFSRWEPKKP-----NERPLQERFVGFAGVLGAGS-LDHASLQAAERVG	330
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	RDHHHVIPDTDFSRWEPKKP-----NERPLQERFVGFAGVLGAGS-LDHASLQAAERVG	317
TR	A0A0M4L069	A0A0M4L069_9VIRU	RDYHHIIPDTDFSRWEPKKP-----NERPLQERFVGFAGVLGAGS-LDHASLQAAERVG	315
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	RDHHHVIPDTDFSRWEPKKP-----NERPLQERFVGFAGVLGAGS-LDHASLQAAERVG	330
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	ASAAANTVPTQFNRSWQRQPI-----VDRTLAPQHaGLASVLEGIDYSKQSLAAEQAV	386
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	GNYTLLNIPVSYNQKSWISPA-----SHRLPATDFLDLAGLFGSA-TDPATLKAQDRV	433
TR	E7BMX6	E7BMX6_9VIRU	APAANTVATQFNRSWQRQPI-----VDRTLAPQHaGLASVLEGIDYSKQSLAAEQAV	385
TR	A0A7L9R666	A0A7L9R666_9VIRU	AAAANTVPAQFNRSWQRQPI-----VDRTLAPHHaGLASVLEGIDYSKQSLAAEQAI	386
TR	A0A346P9C1	A0A346P9C1_9VIRU	PLGNTIKDVAYTRSFIPSTL-----NRVLRTRYMALAPIMEGK-TDKEAFTNAQQLL	498
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	--GDATPAAQFTRSFRTPI-----NPELRPFASDLAGYLSGE-VGAEPFKQAAGVL	410
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	--GDATPAAQFTRSFRTPI-----NPELRPFASDLAGYLSGE-VGAEPFKQAAGVL	424
TR	I1Y9U4	I1Y9U4_9VIRU	AAGAHSPASFNRSWQRHPI-----IDRTLSPQHaGLASVLEGVDYSKQALASAEQAI	376
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	SNYAHSVPTSFNRNWMRAPI-----TDRILEQTHAGLANILDGSDYTRASFQAAEQAV	388
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	AAHAHSVPTGFNRNWMRSPFI-----TDRILEQTHAGLANILDGSDYTRASFQAAEQAV	393
TR	D0T2Z29	D0T2Z29_9VIRU	SPAAQAVPVDFTRNWAPRPL-----NDRVLSARAEGLSGILQGIDYSKSSLRNADEAL	377
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----HVRNNYVGKYVDVAPDQRHPGLGGPSRLEAASDVTGFWADH-QDPDQLKRAEIAL	391

1c1	ORF2		SFSRALGSRNQRLVPGWEAGVIPRWLQFRDFAIKAAARRAYKEFCFRVASRYTLATVASD	800
TR	H6UNN1	H6UNN1_9VIRU	GFSRALGSRGQRLVPGWEANIINRWQRFRELATRSNNLSYKEFSYRIASRYVLSQATAD	408
TR	H6UNM9	H6UNM9_9VIRU	SFSRALGSRGQRLVPGWEAAIVPRWQRFRLATRSSTARSYQEFaFRAVSRYICAETVGD	417
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	AFGRAMGSRGQRLIPGWEAGLTTWRQFRDFGTRQKISQHFLEFCYRLITRYIISRVTAQ	452
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	AFGRAMGSRGQRLIPGWEAGLTTWRQFRDFGTRQKISQHFLEFCYRLITRYIISRVTAQ	452
TR	A0A514DCE7	A0A514DCE7_9VIRU	AIDRFLDTRGNRQVERWEADQWPRWMLATFCSWANTRQSYFEAAAYRLWTRYFFARIFED	446
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----SRYIGAMAHD	11
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	AINRFLDSRGNRQVTRWEADQWGRWLRVANFAAFSGENFSYTVAFRLWARFYACQAANA	379
TR	A0A515KU39	A0A515KU39_9VIRU	AINRFLDSRGNRQVTRWEADQWGRWLRVANFAAFSGENFSYTVAFRLWARFFACQAANA	475
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	AINRFLDSRGNRQVAQWEAEQWGRWLRVSQFAGTSGDDFCYMQAAYRLWARWFTLQSGSL	390
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	AINRFLDSRGNRQVAQWEAEQWGRWLRVSQFAGTSGDDFCYMQAAYRLWARWFTLQASL	377
TR	A0A0M4L069	A0A0M4L069_9VIRU	AINRFLDSRGNRQVAQWEAEQWGRWLRVSQFAGTSGDDFCYMQAAYRLWARWFTLQSGSL	375
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	AINRFLDSRGNRQVAQWEAEQWGRWLRVSQFAGTSGDDFCYMQAAYRLWARWFTLQSGSL	390
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	SINRFLDTRGNRIIPRWEADQWNRWSGITSLYSLGQSDRSYLQIAYRLLSRYFFSLLAEE	446
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	AHLRFLGSRGDRILINGWQADNIPRGLRFSaFVRQAMRNHDYREIAFRLWSRLFLVDEFSA	493
TR	E7BMX6	E7BMX6_9VIRU	SINRFLDTRGNRIIPRWEADQWNRWSGITSLYSLGQSDRSYLQIAYRLLSRYFFSLLAEE	445
TR	A0A7L9R666	A0A7L9R666_9VIRU	SINRFLDTRGNRIIPRWEADQWNRWSGITSLYSLGQADRSYLQIAYRLLSRYFFSLLAEE	446
TR	A0A346P9C1	A0A346P9C1_9VIRU	SQHRFFGSKGRMIGDWDALMSRNQEIYELAGRA-RVREYRELAYRLWSKYLLANQTES	557
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	GLNRFLYTRGNRIIVVGWEANDYNRGLDIQRAYMHA-RVTEFRATAIRLWARYFVAVQARD	469
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	GLNRFLYTRGNRIIVVGWEANDYNRGLDIQRAYMHA-RVTEFRATAIRLWARYFVAVQARD	483
TR	I1Y9U4	I1Y9U4_9VIRU	SVNRFLDTRGNRIIVPRWEADQWNRWSGITSLYTLGQSDRNYFQICYRLLSRYFFSLLSEK	436
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	GMNRFLDTRGNKTVPRWEADAWNRSGLTNLFQIGKADRSYYQIAYRLLSRYYAALVAQE	448
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	GMNRFLDTRGNKTVPRWEADAWNRSGLTNLFQIGKADRSYYQIAYRLLSRYYAALVAQE	453
TR	D0T2Z29	D0T2Z29_9VIRU	SINRYLDTRGAKIIVPRWEGDQWNRWSGITSLFTVAARDRNYLSIAYRLLSRYYAALVAQE	437
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	SSHRATGMRGQKLILGWEATSPTRQIELRRIALADAEGSCYKRFFYRLWMRYFLAALSEC	451

1c1	ORF2		VCS-----NVPEYERHVIDTTTQVQIIHINAEPPIAPPQ-PNQPPPIPP	842
TR	H6UNN1	H6UNN1_9VIRU	LLA-----HIPDYMPVEDTSTDITIIHINADSIVPPPPPGGGPPPLP	451
TR	H6UNM9	H6UNM9_9VIRU	FIT-----RVPGYRRHVANTATDIQIIHINADSIIPPPAPGAPPAP	460
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	ALN-----RIQRYAPNVGDTHVHADIVINAATIVPAPPAPGVPAPALP	495
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	ALN-----RIQRYAPNVGDTHVHADIVINAATIVPAPPAPGVPAPALP	495

TR	A0A514DCE7	A0A514DCE7_9VIRU	FHS-----SNPTATMGVDGTGTACVLTFINAV-----PVT---GPNA	480
TR	A0A514D1M0	A0A514D1M0_9VIRU	LNA-----SVPGTTVHVANSATLTQITYINAATPIPPPGAPGAPPV-I	53
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	-----GNTSVKAVTPLQGTGVPLTFINAR-----PVT---GPNA	410
TR	A0A515KU39	A0A515KU39_9VIRU	-----GNTSVRAVTPPLQGTGVTLTFINAR-----PVT---GPNA	506
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----GGAGYNVCPQPGTDIGLTFINAR-----AVL---GPNA	421
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	-----GGAGYEVVCPRPQTDIGLTFINAR-----AVL---GPNA	408
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----GGAGYNIVCPQPGTDIGLTFINAR-----AVL---GPNA	406
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----GGAGYNVCPQPGTDIGLTFINAR-----AVL---GPNA	421
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----LSELTPLVTTAGTATTLTGLTTLTLLAPPFPPIPGQPIPLP	485
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	LREWN-----GTLDLPLYADMRLNPNPGGTPIALTFINAEAPAA-----PP	534
TR	E7BMX6	E7BMX6_9VIRU	-----LPEMTPLVTTVGTNTTLTGLTTLTLLAPPAPPVPGQPIPLP	484
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----LPELTPLVTTVGSNTTLTGLTTLTLLAPPAPPVPGQPIPLP	485
TR	A0A346P9C1	A0A346P9C1_9VIRU	MMR-----TLQGGTPTVINTAARCVITHMNAHYIPANP-----TAVPPLPV	598
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	LLR-----DEPAYARNVDDPSTRVAITHINAQYIPPL-----AGNPA	506
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	LLR-----DEPAYARNVDDPSTRAAITHINAQYVPP-----AGNPA	520
TR	I1Y9U4	I1Y9U4_9VIRU	-----LPGMTPVNNRQGTQAALTGLTTLTLLAPPATPVPGQPIPLP	475
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----PFEFRLAPTAIGTNVLTPLSTQLPPV---PFGAPAPQV	484
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----FPDFQLAPVAIGTGVALTPLSTQLPPV---PFGAPAPQV	489
TR	D0TZ29	D0TZ29_9VIRU	-----NDWFTPTVMDESTPITLPLTAEIPPLQLPIPGQPQV	476
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	NDATGADAPSVLTQLRPLTAADIDYDPQGLNGANRIQLESVSAVAPLVAG-----PGGP	505

1c1	ORF2		QWGEAALW-----TPAMLQAVLDGRAQFIDGESYTREELAEIIAC LAPSTHDNVPHLRP	897
TR	H6UNN1	H6UNN1_9VIRU	IWGEQAFW-----DPNMQQAMIDGRAQFVDGEGFSPEEIAAIIIGCLAPSAANVPYIVAP	506
TR	H6UNM9	H6UNM9_9VIRU	IWGEQQLW-----DPNMTQAMLEGRAQLIDGEGFSREELAAVVGCLAPSTYENVPQLIFE	515
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	VNGEDAFW-----APGAQQALLEGRAQFLDCEGEMERSEIAQLLGCLDQSTDNLPVLSD	550
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	VNGEDAFW-----APGAQQALLEGRAQFLDCEGEMERSEIAQLLGCLDQSTDNLPVLSD	550
TR	A0A514DCE7	A0A514DCE7_9VIRU	PNPEGPMW-----TDDAQSGKNGTKQFIDAQGLSENELLELISALAPLDDKDYIPHFL	535
TR	A0A514D1M0	A0A514D1M0_9VIRU	VNGEDHYW-----DYAAQTALLQGTQAFLDVEGLSRAEIAQALAAIVPTTHENVPFVRNQ	108
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	LNPEGPMW-----TDDAQDGLRMGTQKQFIDAEGELSEPELIELLSCMLPFNDIDHATHLV	465
TR	A0A515KU39	A0A515KU39_9VIRU	LNPEGPMW-----TDDAQDGLRMGTQKQFIDAEGELSEPELIELLTCMLPFSDIDHAAHLY	561
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	PNPEGPMW-----TDDAQMGLQDGSKQFIDAEGELSEELIELISVLAPVRNGNQLQMES	476
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	PNPEGPMW-----TDDAQMGLQDGSKQFIDAEGELSEELIELISVLAPVRNGNQLQMN	463
TR	A0A0M4L069	A0A0M4L069_9VIRU	PNPEGPMW-----TDDAQMGLQDGSKQFIDAEGELSEELIELISVLAPVRNGNQLQMES	461
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	PNPEGPMW-----TDDAQMGLQDGSKQFIDAEGELSEELIELISVLAPVRSGNQLQMES	476
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	VNPEAALF-----TQAAFSGLKTGTQAQLVDAEGLSEDELIELISAIVPLESANIPLLST-	539
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	VNPEQPMW-----EDIAQAGLRAGSKQFVDASDLSEQEVIELLSAMVPTEPGQSVRLRAA	589
TR	E7BMX6	E7BMX6_9VIRU	VNPEAALF-----TQAAFSGLKTGTQAQLVDAEGLSEDELIELLSAIVPVESANIPLLST-	538
TR	A0A7L9R666	A0A7L9R666_9VIRU	VNPEAALF-----TQAAFSGLKTGTQAQLVDAEGLSEDELIELLSAIVPVESANIPLLST-	539
TR	A0A346P9C1	A0A346P9C1_9VIRU	LNPEAPFW-----DPAAQLELTGKYKQFFDVSGMSKEQIAALIGCLDSTDLDRVPRLHID	653
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	VNPEAPLW-----TQAAQDGLAVGTQKQFIDAQGMSIDQVAELVGVMSPITVDNLP SLRLV	561
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	VNPEAPLW-----TQAAQDGLAVGTQKQFIDAQGMSIDQVAELVGVMSPITVDNLP SLRLV	575
TR	I1Y9U4	I1Y9U4_9VIRU	VNPEAALF-----TQAAFSGLKTGTQFVDAEGLSEDELVELLSAIVPVEHANIPLLRT-	529
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	QNPEAPLF-----APGAFEGKNGTKQFIDAEGELSEVVELLSAIVPQSRPQRLQFSRI	539
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	QNPEAPLF-----APGAFEGKNGTKQFIDAEGELSEVVELLSAIVPQGRQRLQFSKV	544
TR	D0TZ29	D0TZ29_9VIRU	GNPEAPLF-----TAAAFNGLRNGTKQFIDAEGLSLEELRELLAAIVPCDEANIPHVRY	531
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	VDPEAILKSDQHGAADTWDEIQRGATHLIDVEGMTDEMIRETLAFAANEVRYASSAWGF	565

1c1	ORF2		VDPND-----PDTKETMLPS--CARYSYPNGVTHIIVHHGNAP	933
TR	H6UNN1	H6UNN1_9VIRU	HPDSTH-----PLVSRTDRLPN--VTRHYFPNGTTHIIVHHGNSP	545
TR	H6UNM9	H6UNM9_9VIRU	EDVIEE-----GQEEFAQHYPY--VTRQTFPNVTRHIIVHHGSAP	554
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	D-----MNVLQVPV--IGRHTFPNGVQTIFVHTGNQP	580
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	D-----MNVLQVPV--IGRHTFPNGVQTIFVHTGNQP	580
TR	A0A514DCE7	A0A514DCE7_9VIRU	NSGDG-----DVKYINP--FMRYLFLNGTDEIFIHGNSP	568
TR	A0A514D1M0	A0A514D1M0_9VIRU	NPAAQG-----VARNERLEWLLH--IWRNIYPNGVCNVFLHFGNEP	147
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	RKKDTSNSEGESSEKKGKRELTDLEKFKNTHHMLTG--PTRYVFPNGVDEIFIHGNSD	523
TR	A0A515KU39	A0A515KU39_9VIRU	RKKDTSNSEGESSEKKGKQELSNLQKFKNTHNFLTG--PTRYVFPNGVDEIFIHGNSD	619
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	R-----NGVGPQQLYLF--PNRYLYDNGVDEIFIHFGNSA	510
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	R-----NGTGP HQLYLF--PNRYTFNNDVNEIFIHFGNSQ	497
TR	A0A0M4L069	A0A0M4L069_9VIRU	R-----NGAGPHQLYLF--PNRYLYDNGVDEIFIHFGNSA	495
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	R-----NGVGP HQLYLF--PNRYLYDNGVDEIFIHFGNSA	510
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-A-----ADPAETFFAG--PTRYTYDNTVNEVFIHFGNSA	571
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	DPPRVN-----GA---LPQEGPCNELDFVHP--LQRYSFPPNGVDEVFIHTGANA	633
TR	E7BMX6	E7BMX6_9VIRU	-A-----ANPPETFFAG--PTRYTYDNKVNEVFIHFGNSA	570
TR	A0A7L9R666	A0A7L9R666_9VIRU	-T-----ANPPETFFAG--PTRYTYDNKVNEVFIHFGNSV	571
TR	A0A346P9C1	A0A346P9C1_9VIRU	NG-----AGGHRVYWF--NGKFKFNNGVNEVFLHYGMGN	686
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	NG-----D---SYHFG--QSRHSIPNQVDEIFVHWGTPE	590
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	NG-----D---SYHFG--QSRHSIPNQVDEIFVHWGTPE	604
TR	I1Y9U4	I1Y9U4_9VIRU	-A-----APHNEDYFVG--PTRYTYANGVDEVLIHFGNSA	561

TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	ND-----	QGREYFSG--PTRYTFGNSVNEVFIHYGNP	572
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	ND-----	QGREYFCG--PTRYTYDNRVNEVFIHYGNP	577
TR	D0TZ29	D0TZ29_9VIRU	RPAD-----	LVQEIKPGSSAYHRYFFG--PTRYKYLNGVDEVFIHFGNPP	574
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	-----	-----
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	A-----	RRG--A-----AADEPGYYSALLPDRLLDCPTRFILHYGSRP	603

lc1	ORF2		LPSIQD-----	Q-----	NWIAQHAFSFPSSAMTLSTIIRSV	965
TR	H6UNN1	H6UNN1_9VIRU	IPPLAV-----	Q-----	AQIAATAFSYPSSAVLGSIMRAYCA	577
TR	H6UNM9	H6UNM9_9VIRU	IPPLAD-----	Q-----	QFIAAHAFDFPSAGILSTVLSYAA	586
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	VPSLAD-----	Q-----	QWIRDNAHSPDHDTIIGLIRSLCM	612
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	VPSPAD-----	Q-----	QWIRDNAHSPDHDTIIGLIRSLCM	612
TR	A0A514DCE7	A0A514DCE7_9VIRU	IPDLAT-----	Q-----	GRITANVFSVPKPTAIASVLRLLAS	600
TR	A0A514D1M0	A0A514D1M0_9VIRU	LPDQAT-----	R-----	NWIAQHANDAPDASIIISTVMRHFGS	179
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	IPDAAT-----	Q-----	QRIAESVFCPSAATIGSVIRYLAT	555
TR	A0A515KU39	A0A515KU39_9VIRU	IPDANT-----	Q-----	QRISESVFCPSAATIGSVIRYLAT	651
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	IPDAAA-----	Q-----	QRIRERVHGVSSSATVGSVIRYLAT	542
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	IPDAAT-----	Q-----	QRIRERVHGVSSSATVGSVIRYLAT	529
TR	A0A0M4L069	A0A0M4L069_9VIRU	IPDAAA-----	Q-----	QRIRERVHGVSSSATVGSVIRYLAT	527
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	IPDAAT-----	Q-----	QRIRERVHGVSSSATVGSVIRYLAT	542
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	IP--D-----	Q-----	AQIATQVHRVPPQAQILSVLRYLAM	600
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	KFDLPA-----	L-----	QIRASVCGVPSASAIITLRLVLSV	665
TR	E7BMX6	E7BMX6_9VIRU	IP--D-----	L-----	AQLATEVHRIPHAAQILSVLRYLAM	599
TR	A0A7L9R666	A0A7L9R666_9VIRU	VP--D-----	L-----	AQIATQVHRVPPQAQILSVLRYLAM	600
TR	A0A346P9C1	A0A346P9C1_9VIRU	LSPSPAD-----	Q-----	AWIAAHAFDFPSAVLASIIRIVAG	718
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	IPNAND-----	I-----	TYIANSAHRFPEVDIVDSVIRIFAG	622
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	IPNAND-----	I-----	AYIENFAHRFPEVDVVDVIRIFAG	636
TR	I1Y9U4	I1Y9U4_9VIRU	VP--D-----	L-----	AQIGALIHRAHQAKILSVLRYLAM	590
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	IP--NN-----	M-----	AQIAAQVHGTPNPNQILSVLRYLLM	602
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	IP--LN-----	M-----	AQLAAQVHRTPPQPNQILSVLRYLLM	607
TR	D0TZ29	D0TZ29_9VIRU	APTPAE-----	M-----	ADLSAHVHAPPSAPAIMSVLRYLIM	606
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	-----	MSVLRYLAM	9
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	GLNARVLENTLLGRGFPAPADPAAGIPAGPAIPGNPARSPWNVRPNRQLIASVIRFMIG	-----	-----	663

::*

lc1	ORF2		RHSLEDLFVWAFEAVAYRSVGTYF--	ADALGTNEPTA----	TDDIIHASGVDPDLFLPRNCT	1020
TR	H6UNN1	H6UNN1_9VIRU	RHALEESLIDAFDNALYRCTGFSF--	AEARGSDPNSA----	TREIVDSSGSSALFLPRNNT	632
TR	H6UNM9	H6UNM9_9VIRU	RHALEDVILAADFASIYRCVGYPF--	AAALGADRHHK----	SNVHVDSSGSAALYMPNNT	641
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	RHDLSTQFADAIIDMAVYRCVGYSF--	EDCFGTSNDRR----	TDDIIDGSGNSELFIIPNNT	667
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	RHDLSTQFADAIIDMAVYRCVGYSF--	EDCFGTSNDRR----	TDDIIDGSGNSELFIIPNNT	667
TR	A0A514DCE7	A0A514DCE7_9VIRU	RHGAERDIIIDALETVMYRGVGYHS--	DDFINRRKNYT----	SGEVLHSDGNWEFHSRLRNYT	655
TR	A0A514D1M0	A0A514D1M0_9VIRU	RHDLSSHFDIAIQTALYRTVGYKS--	ADARGADPKI----	DNSILDADGHSRLYVPRNNT	234
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	KHNAIRDLEQGLEAMLYRGVVFYS--	DNITGKRENLG----	SKQYINADGNWQLHLPRDMT	610
TR	A0A515KU39	A0A515KU39_9VIRU	KHNAIRDLEQGLEAVLYRGVVFYS--	DNITAKRENLG----	SKQYINADGNWQLHLPRDLT	706
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	KHNAIKDLENGLEAVMLRGFVYKS--	NMIRNRRANLR----	SRQYINADGNWGLYLPDRKT	597
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	KHNAIKDLENGLEAVMLRGFVYKS--	NMIRNRRANLR----	ARQYIHADGNWGLYLPDRKT	584
TR	A0A0M4L069	A0A0M4L069_9VIRU	KHNAIKDLENGLEAVMLRGFVYKS--	NMIRNRRANLR----	SRQYINADGNWGLYLPDRKT	582
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	KHNAIKDLENGLEAVMLRGFVYKS--	NMIRNRRANLR----	SRQYINADGNWGLYLPDRKT	597
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	RHGAAQIDDALEILMARIVLYTNSTQLRGLRNNAP--	-----	VGEYINSDGHYEMHLPLAKT	656
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	RHNASDHVDFGLELAMARNSIFSM--	RDFLSRDNCN----	RHSYTHSDLNNEIHLPRMYT	720
TR	E7BMX6	E7BMX6_9VIRU	RHGAAQIDDALEILMARIVLYTNSTQLRGLRNNAP--	-----	VGEYINSDGHYEMHLPLAKT	655
TR	A0A7L9R666	A0A7L9R666_9VIRU	RHGAAQIDDALEILMARIVLYTNSTQLRGLRNNAP--	-----	VGEYINSDGHYEMHLPLAKT	656
TR	A0A346P9C1	A0A346P9C1_9VIRU	KLXIAEDYQTGLDLALHHGVVYRN--	AD---IYNRLPNAPNQHNLIYASGNDELFLPRNVS	774	
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	KYGARSAIDIGCEYAMHKGVVYPV--	AGPRGIRGRKPSSENSSTRYLSDGCDDEMHLPRDRT	681	
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	KYGARSAIDIGCEYAMHKGVVYPV--	AGPRGIRGRKPSSENSSTRYLSDGCDDEMHLPRDRT	695	
TR	I1Y9U4	I1Y9U4_9VIRU	RHGAAADDIDNALETISRIVMYTNSTQLRGLRNNAP--	-----	TGVYINSDGHYELHPLIAKT	646
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	RHGAGSDIEDAAELLISRIALYSTGSGRLRGLRNNAP--	-----	NQEYINADGHYELHPLHPSKT	658
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	RHGAGTDIDDAELLISRIALYSTGSGRLRGLRNNAP--	-----	NQEYINADGHYELHPLHPSKT	663
TR	D0TZ29	D0TZ29_9VIRU	RHGASEVDVTAMELLIARIYMYHPNVGLRGLRNNAP--	-----	QDRYINADGHYSFHLPRAKT	662
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	RHGAAEDIDNAMETLMSRIVMYTNSTQLRGLRNNAP--	-----	TGVYINADGHYELHPLPLAKT	65
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	TTGAVKDCWDALDLALHTQNFSPSLDLVGLRDLGVR--	GLNLRWTS CGGTQELSLPRDVT	720	

. :

. :

:

lc1	ORF2		GFAYFDCFFV--	PVSTTPELESYLSAP--	TEVFSVSSISLAHFRAVSIWAGKAGSLLGRV	1077
TR	H6UNN1	H6UNN1_9VIRU	ARAYFDVFFS--	PLATTSIAENLLSST--	AKQYVHYGSLLGHVSRATSLAWAGKSASLVDSV	689
TR	H6UNM9	H6UNM9_9VIRU	IRGYFDVFFS--	PAPNSSNLENLLAMS--	GKHLHTGTLVNHCRAVSLAWAGKSASILGVT	698
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	AGDYFDIFFT--	PAPIDRDVEVFLSLQ--	TKQLTHSASLAVHTRTVAYNWAAGKAGSMLGDI	724
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	AGDYFDIFFT--	PAPIDREVEVFLSLQ--	TKQLTHSASLAVHTRTVAYNWAAGKAGSMLGDI	724
TR	A0A514DCE7	A0A514DCE7_9VIRU	AGGYFDALRV--	PVPLDQKIQYSLALP--	SEELINNLIFVSHARATSLWAAAFALSMGTGT	712
TR	A0A514D1M0	A0A514D1M0_9VIRU	RWGYFDVIFYQ--	PVALSSVVERFLSYS--	PREIVNIGTILPFCIAIALNASKALTLTLLGE	291
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	ASAYFDALRV--	PLEPSQLQYVLAMH--	PREVVQNSVLINHARAVSLNWAAYALSMLGQQ	667
TR	A0A515KU39	A0A515KU39_9VIRU	ASAYFDALRV--	PLEPSPKIQYMLAMH--	PREVVQNSALVNHARAVSLNWAAYALSMLGQQ	763

TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	SSAYFDALRV--PLEPSPMIQYMLQMQ--PREVVKNALFLCHSRAVSLNWASYAISMLGQQ	654
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	SSAYFDALRV--PLEPSPMIQYMLQMQ--PREVVKNALFLCHSRAVSLNWASYAISMLGQQ	641
TR	A0A0M4L069	A0A0M4L069_9VIRU	SSAYFDALRV--PLEPSPMIQYMLQMQ--PREVVKNALFLCHSRAVSLNWASYAISMLGQQ	639
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	SSAYFDALRV--PLEPSPMIQYMLQMQ--PREVVKNALFLCHSRAVSLNWASYAISMLGQQ	654
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	GSAYFDSFMV--PHAMTGDLPAPASLP--ARSVINNGVLFAQARAAALNWAAAWSMSGRS	713
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	AGAYVDAFLT--PGTVSAQTDLALELK--PCEVVNNAALIGFFRTTAINWAAYSLSAYGRV	777
TR	E7BMX6	E7BMX6_9VIRU	GSAYFDSFMV--PHAMTGDLPAPASLP--ARSVINNGVLFAQARAAALNWAAAWSMSGRS	712
TR	A0A7L9R666	A0A7L9R666_9VIRU	ASAYFDSFMV--PHAMTGDLPAPASLP--ARSVINNGVLFAQARAAALNWAAAWSMSGRS	713
TR	A0A346P9C1	A0A346P9C1_9VIRU	VDGYFVPFFE--PGVLQDSQPEMLAPNRRDDIIHVQSLISHARAVSLNWAAKAVTLLGQH	832
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	FIGYFTPFLLT--SGTSLDLAATTLAPEVNVRLMSAQUALVAHTRATSLNWACKSITMLGDQ	739
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	FIGYFTPFLLT--SGTSLDLAATTLAPEVNVRLMSAQUALVAHTRATSLNWACKSITMLGDQ	753
TR	I1Y9U4	I1Y9U4_9VIRU	APAYFDSFMV--PHAQTGDLPAPASLP--ARSVINNGVLFAQARAAALNWAGAASWAGRS	703
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	ASAYFDCFFV--PCFDTGTLGFFSSSLN--PELINQGVLFGNARAVSLNWAAATAWSMVGRS	715
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	ASAYFDCFFV--PCLDSGTLGYFSSFS--APELINQGVLFGNARVVALNWAAATAWSMVGRS	720
TR	D0TZ29	D0TZ29_9VIRU	ASAYFDAQFL--PADDTTRLNEFLSFS--SRELVNSGVLFQAARATALNWATAAYSMYGRQ	719
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	ASAYFDSFMV--PHAQTGDLPAPASLP--ARSVINNGVLFAQARAAALNWAGAASWAGRS	122
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	PTAYFDCARTRVPMYAPDISALLALS--PRRLFHTATLTAHAHAASLNWASFALSLRGE	779

* . : . : * . : .

lc1	ORF2		FNLAAN---QGNQFLRNHRTKWLRFY--ELNVWSALHANTMGFYGFAPSPTRRTES	1132
TR	H6UNN1	H6UNN1_9VIRU	FSAPAA---GGNQFIRNHRDKWLRLQYYS--ELNVWSALHANAQAQHFSPTRLTRTES	744
TR	H6UNM9	H6UNM9_9VIRU	WQOMGA---PVNQFVRNHRDKWLRLHYG--ELNIWSALHANAMAYQYGFAPSPHTRRTES	753
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	WAAPLA---GAPNDYVRNHATKWLRLNYYS--DINIWSGLAANAHATQYGFACASPLTRRTEL	780
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	WAAPLA---GAPNDYVRNHATKWLRLNYYS--DINIWSGLAANAHATQYGFACASPLTRRTEL	780
TR	A0A514DCE7	A0A514DCE7_9VIRU	WANLPG---NEANQFVANHIDVWLRTYNNENLDLWATVSANAMAYQYGYAPSQRARSTE	769
TR	A0A514D1M0	A0A514D1M0_9VIRU	WGMPVA---GGNQYLNRHWDKLARHYQSTVTLWSTIHANALAHQYGFAPPPICRAMEQ	347
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	WGVAPG---TATNQFIRNHVDVWLRLQYGIENINIWSTLHANAMALQYGFAPSSFARSTEG	724
TR	A0A515KU39	A0A515KU39_9VIRU	WGVAPG---TATNQFIRNHVDVWLRLQYGIENINIWSTLHANAMALQYGFAPSTFARSTEG	820
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	WAARPG---QVANQFVRNHIDAWLRRFGIENINLWSTAHANAMAHQYGFAPSPATARATEE	711
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	WAARPG---QVANQFVRNHIDAWLRRFGIENINLWSTAHANAMAHQYGFAPSPATARATEE	698
TR	A0A0M4L069	A0A0M4L069_9VIRU	WAARPG---QVANQFVRNHIDAWLRRFGIENINLWSTAHANAMAHQYGFAPSPATARATED	696
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	WAARPG---QVANQFVRNHIDAWLRRFGIENINLWSTAHANAMAHQYGFAPSPATARATEE	711
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	WVNSPG---RENNSYVRNHIDVFLRKYSDDLNLWTSNHNALAFHVGWLSLSTARSTE	770
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	WNRRPS---NEPDRIISFMSVLTTRTFSDKITAUSTVHNALAYQYGFGLSPSVRSTE	834
TR	E7BMX6	E7BMX6_9VIRU	WVNSPG---RENNSYVRNHIDVFLRKYSDDLNLWTSNHNALAFHVGWLSLSTARSTE	769
TR	A0A7L9R666	A0A7L9R666_9VIRU	WVNSPG---RENNSYVRNHIDVFLRKYSDDLNLWTSNHNALAFHVGWLSLSTARSTE	770
TR	A0A346P9C1	A0A346P9C1_9VIRU	WSAAAATPAAGLNMWLRNRIDAWIRDYNSYSNPSWSEMHINACATQFGFSITQRAAIMEA	892
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	WDARNV---RTANQWVRNHIDAIVRDYNSYDNAWSNHFANTTATQYSYSPSRDMRILEG	796
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	WDARNA---RTANQWVRNHIDAIVRDYNSYDNAWSNHFANATATQYSYSPSRDMRVLEG	810
TR	I1Y9U4	I1Y9U4_9VIRU	WVNTPG---TENNYSVRNHIDVFLRKYSDDLNLWTSNHNALAFHVGWLSLSTARSTE	760
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	WTNLPG---MEGNPFIRNHIDVWLRLRYSSDDLNLWSSCHNNTLALQYGFVGDARVRATEA	772
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	WTNLPG---TENNPFIRNHIDVWLRLRYSSDDLNLWSSCHNNTLALQYGFVGDARVRATEA	777
TR	D0TZ29	D0TZ29_9VIRU	WTNSPG---TE'NTYVVMKHVDVTLRKYYAEPLNVWASAHNNALAFVLDVALSSKALATEA	776
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	WVNAPG---TENNYSVRNHIDVFLRKYSDDLNLWTSNHNALAFHVGWLSLSTARSTE	179
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	WHAFTN---RAGVTQYQAHLDMSVAQLRRSDVTVWALHRIATAHMYGFAPALSTSLALG	837

: * : . . :

lc1	ORF2		NMLPNWWRDYCTPTLVNHYLELWAMQVIPPVQVLPYYSREAKNSHVEWAPGTPDQTASLV	1192
TR	H6UNN1	H6UNN1_9VIRU	GFVPGWWRPYVPVLTNHYLELWSMHLMPYQVLPYWDPDQSSSHVQWAKGTPDQTASLQ	804
TR	H6UNM9	H6UNM9_9VIRU	GSVVDWWRAYTPPTLTNHYLELWAMQVIPPVQVLPYYPDREETSHVDWAAGTPDQTASLL	813
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	GRLPNNWRAYVAPYITNHYLELWCMQVMPFTFQVLPYFDQNAQTSHVWRWAEAGTPDQSESRI	840
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	GRLPNNWRAYVAPYITNHYLELWCMQVMPFTFQVLPYFDQNAQTSHVWRWAEAGTPDQSESRI	840
TR	A0A514DCE7	A0A514DCE7_9VIRU	LRIAHFWSNFQIPTLTNHYHELMWMEIMPTFQVLPYHDNEG--TSHPTWDSGSPAPVADFA	828
TR	A0A514D1M0	A0A514D1M0_9VIRU	GEVTDWLSFQAPYLANHYMELWAAKTMMPFQVLPYYPDGETSHVQWPGDTPRPVQVNL	407
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	LSVLNWWTDYQAPYLANAYHELMWMMEMIPSHQLLPFYDENT--PAHPTWVDGRPHPTTDFM	783
TR	A0A515KU39	A0A515KU39_9VIRU	LTVLNWWTDYQAPYLANPYHELMWMMEMIPSHQLLPFYDENT--PAHPTWVDGRPHPTTDFM	879
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	LWVRNWWVDTQAPYLANPYLELWLMELIPSHQLLPFYDKEN--TVAPGQEPGSPMPALDFA	770
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	LWVRNWWVDTQAPYLANPYLELWLMELIPSHQLLPFYDKEN--TVAPGQEPGSPMPALDFA	757
TR	A0A0M4L069	A0A0M4L069_9VIRU	LWVRNWWVDTQAPYLANPYLELWLMELIPSHQLLPFYDKEN--VAPGQEPGSPMPALDFA	755
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	LWVRNWWVDTQAPYLANPYLELWLMELIPSHQLLPFYDKEN--IVAPGQEPGSPMPALDFA	770
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	NVVVNWWNDYHSPTLTNAYLELWQVECLPSHQVLPWDDRET--PSTVSWPSNTPPFIHDAY	829
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	GWLLDAHRDWTVPYVHNHYLELWAMKFIPTFQVLPYFDPEGSSSHVWGPSSSLNPPIPAYE	894
TR	E7BMX6	E7BMX6_9VIRU	NVVVNWWNDYHSPTLTNAYLELWQVECLPSHQVLPWDDRET--PSTVSWPSNTPPFIHDAY	828
TR	A0A7L9R666	A0A7L9R666_9VIRU	NVVVNWWNDYHSPTLTNAYLELWQVECLPSHQVLPWDDRET--PSTVSWPSNTPPFIHDAY	829
TR	A0A346P9C1	A0A346P9C1_9VIRU	GTVQAQWPAWQAPYLANHYCELMWMMKIPSFQVLPYYPDREARTSKFIVNDDYGSAPVSLQ	952
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	QYVANVWQSFMVPTLTNHYHELMWAMDMIPEYQILPYFDRAAQTHHVTVDANQPSIVGDMV	856
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	QYVASVWQSFMVPTLTNHYHELMWAMDMIPEYQILPYFDRAAQTHHVTVDANQPSIVGDMV	870
TR	I1Y9U4	I1Y9U4_9VIRU	NVVVNWWADYHVPTLTNAYLELWQVENLPSHQVLPWEDKET--PSTVSWPSNTPPFIHDAY	819
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	GRVVNWWSDHQAPYMNPNYHELWLAELKPSHQVLPYDDANA--PSTVSWPAQTTPFISDMY	831
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	GRVVNWWSDHQAPYMNPNYHELWLAELKPSHQVLPYDDANA--PSTVSWPSQTTPFISDMY	836
TR	D0TZ29	D0TZ29_9VIRU	NVVVNWWSDHQAPYLTNPYHELMWQCNMLPSHQVLPYHVDN--PATITWPDNCPLPISDAH	835
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	NVVVNWWADYHVPTLTNAYLELWQVENLPSHQVLPWEDKET--PSTVSWPSNTPPFIHDAY	238

TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU RTVAPIWQDRLAPYIANPYEMWMLQMLPIHMKLPSK-----GTAMDWPDDAQKPLRSAY 892
: * : * * : * . : * . **

lc1|ORF2 SFNHDRKVLRLAREVDVLEGHSLWDGGGAEYNSQFYAAQG----NNGRFAYEG-A--QPKA 1245
TR|H6UNN1|H6UNN1_9VIRU SFSADKKIRLARETEAFPGHAWLGDGGADYNAQFYVAQG----NDGQFAFEG-G--RHKA 857
TR|H6UNM9|H6UNM9_9VIRU TFSREKKIRLAPEMENRPGYHVLWDGGGAEYNAQFYAAQG----SNGQFSYEG-A--HPKS 866
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU SFRNNLNVRLAREFEAYPGHTWIGDGGSEFNQFYAAQG----NDGQFAYEG-A--LTKV 893
TR|A0A1P8DF80|A0A1P8DF80_9VIRU SFRNNLNVRLAREFEAYPGHTWIGDGGSEFNQFYAAQG----NDGQFAYEG-A--LTKV 893
TR|A0A514DCE7|A0A514DCE7_9VIRU SFQG--DVQLGRDLAAFTGRTWLGDGGYTHNAQFFAAQG----VDDQFRFEG-H--TPAF 879
TR|A0A514D1M0|A0A514D1M0_9VIRU AFNTARTLKAAREYDPIPGFSWLGDGGPEYNLQFYTAQG----NDGQWAKEG-G--AHKE 460
TR|A0A7S5WL3|A0A7S5WL3_9VIRU SFQN--WVEVARDLSPFSGRTWMSDGGATRNAQFYVAQG----VKNQFRFQG-G--QPKF 834
TR|A0A515KU39|A0A515KU39_9VIRU SFQN--WVEVARDLSPFSGRTWMSDGGATRNAQFYVAQG----VKNQFRFQG-G--QPKF 930
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU SFED--WVPVSRDLSPFSGCTWMSDGGMTRNAQFYAAQG----RNNQFRYEG-G--NPHF 821
TR|A0A7S5WL4|A0A7S5WL4_9VIRU SFED--WVPVSRDLSPFSGCTWMSDGGMTRNAQFYAAQG----RNNQFRYEG-G--NPHF 808
TR|A0A0M4L069|A0A0M4L069_9VIRU SFED--WVPVSRDLSPFSGCTWMSDGGMTRNAQFYAAQG----RNNQFRYEG-G--NPHF 806
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU SFED--WVPVSRDLSPFSGCTWMSDGGMTRNAQFYAAQG----RNNQFRYEG-G--NPHF 821
TR|A0A0A7DSJ8|A0A0A7DSJ8_9VIRU SFSSHLHVQVARDTPAEVGRRTFMGDGGAIANAQHFAAVG----TIGGFYED--AANAPKI 884
TR|A0A2Z1Q370|A0A2Z1Q370_9VIRU SFND--QVRLGRDMPFPLKQAWKQDGGFNRNAQFFAATG----LNGRYRHEG-A--AINV 945
TR|E7BMX6|E7BMX6_9VIRU SFSSHLHVQVARDTPAEVGRRTFMGDGGAIANAQHFAAIG----SVNGFRFED--AANAPKI 883
TR|A0A7L9R666|A0A7L9R666_9VIRU SFSSHLHVQVARDTPAEVGRRTFMGDGGAIANAQHFAAVG----SVNGFRYED--ATNAPKI 884
TR|A0A346P9C1|A0A346P9C1_9VIRU TFNASRELKVSREINAIPGRNYFGDGGSEYNGQLAAQGGGIGAGHWRFEN--AANAFRV 1011
TR|A0A2Z5WAE5|A0A2Z5WAE5_9VIRU TYNSQREVKVGRDRTTIFPGRNHIG--GGHEYNMQVYMAQGDFFENQQRWRFQP--GVQNRPP 914
TR|A0A2L1GG75|A0A2L1GG75_9VIRU TYNSQREVKVGRDRTTIFPGRNHIG--GGHEYNMQVYMAQGDFFENQQRWRFQP--GVQNRPP 928
TR|I1Y9U4|I1Y9U4_9VIRU SFAAHLHVQVARDTPAEVGRRTFMGDGGSTANAQHFAAIG----TLNGYRFES--AANTPAI 874
TR|A0A1B4ZA68|A0A1B4ZA68_9VIRU SFTQNTRELARVDPVETARSWMVDGGPTVNAQHLYAVG----NCLGYRFEQ--AANTPSV 886
TR|A0A2Z1Q3B3|A0A2Z1Q3B3_9VIRU SFSQNTRELARVPIETARSWMVDGGPTVNAQHLYAVG----RPTGYRFEQ--AANTPNV 891
TR|D0T2Z9|D0T2Z9_9VIRU SFANHLDELAKDFPAEAGRYWMDGGSTANAQFFAATG----LSSGFRFQG--HHNA--AL 889
TR|A0A7G3W8V4|A0A7G3W8V4_9VIRU SFTAHLHVQVARDTPAEIGRTFMGDGGSTANAQHFAAIG----TLNGYRFES--AANTPAI 293
TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU ET--DMPSLRVARALPAFHRRFTLQDGKMMYNLQHAASVPG---QTHFRNDLVNPDTPAF 948
: . * * * : : :

lc1|ORF2 RFSFWQ--GSYARSFPVTPQAATP--ISLSNGRLNDPFADFILPGSFQSYRMLDDKIINWGV 1303
TR|H6UNN1|H6UNN1_9VIRU RLFFWD--GIYARSFPNAPVQGNL--LTMTNGALNQPFSDFLPGSLLSYRHQIDRILSWG 915
TR|H6UNM9|H6UNM9_9VIRU TVVFWG--QYARSFPNAPNAGNY--ISMTDNVLGLPFSDFILPGSLASYRLTDDRNLNWGI 924
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU GLCRWD--GIYARQLPAAPVAGRA--ITL--GAAGSPFSDFILPGSLASYQFGNDRIQNWAV 949
TR|A0A1P8DF80|A0A1P8DF80_9VIRU GLCRWD--GIYARQLPAAPVAGRA--ITL--GAAGSPFSDFILPGSLASYQFGNDRIQNWAV 949
TR|A0A514DCE7|A0A514DCE7_9VIRU QLAYWQ--HQMVHQFPQNPASFTP---VVMATQGSPPADFLPLPGSLAGINLERNRTYAWGV 935
TR|A0A514D1M0|A0A514D1M0_9VIRU QLMHGP--GETMDQPPVPTPTVPVQHQHQMGLPNPNWADFLPLPGSLRSYQTHNRRIRNWSI 519
TR|A0A7S5WL3|A0A7S5WL3_9VIRU KLSRWT--AQYQHQPQNADQDP---TWMEPLNSPFADFLPLPGSLPALNMATNRVYAWGV 890
TR|A0A515KU39|A0A515KU39_9VIRU KLSRWT--AQYQHQPQNADQDP---TWMEPLNSPFADFLPLPGSLPALNMSINRVYAWGV 986
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU QLSRWA--ARFRHQAPQNTANVDI---AWMGDLNEPFADFILPGSMPCLRMEANRVYAWGV 877
TR|A0A7S5WL4|A0A7S5WL4_9VIRU QLSRWA--ARFRHQAPQNTANVDI---AWMGDLNEPFADFILPGSMPCLRMEANRVYAWGV 864
TR|A0A0M4L069|A0A0M4L069_9VIRU QLSRWA--ARFRHQAPQNTANVDI---AWMGDLNEPFADFILPGSMPCIRMEVNRVYAWGV 862
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU QLSRWA--ARFRHQAPQNTANVDI---AWMGDLNEPFADFILPGSMPCLRMEANRVYAWGV 877
TR|A0A0A7DSJ8|A0A0A7DSJ8_9VIRU SIARWR--QRHAFQFPVAPASQAP---VWMAEPGSPFADFLSPGSMNSHNVEANVAYSIGL 940
TR|A0A2Z1Q370|A0A2Z1Q370_9VIRU SLMRWS--GDRIDQIPAPAGAPV---QWLAPAGSNFSDFILPGSVVNYNHSRNSYSFGF 1001
TR|E7BMX6|E7BMX6_9VIRU SIARWR--QRHAFQFPVAPASQAP---VWMAEPGSPFADFLSPGSMNSHNVEANVAYSIGL 939
TR|A0A7L9R666|A0A7L9R666_9VIRU SIARWR--QRHAFQFPVAPASQSP---VWMAEPGSPFADFLSPGSMNSHNVEANVAYSIGL 940
TR|A0A346P9C1|A0A346P9C1_9VIRU LDPCWSETPYAYQLGQAWNRV---QTVYMAAPGNFADFALPGTMRFTQEIDNVLSWGF 1068
TR|A0A2Z5WAE5|A0A2Z5WAE5_9VIRU MLPAYTQLEYSYQLANPVWTTTAQNVIMWEPGSPFADFIQPGSLRHYIQAGNRLLAWAA 974
TR|A0A2L1GG75|A0A2L1GG75_9VIRU MLPAYTQLEYSYQLANPVWTTTAQNVIMWEPGSPFADFIQPGSLRHYIQAGNRLLAWAA 988
TR|I1Y9U4|I1Y9U4_9VIRU SLARWR--QRHAYQFPVAPATQAP---VWLAEPGTPFADFLSPGSLNSHNVEANVAYSIGV 930
TR|A0A1B4ZA68|A0A1B4ZA68_9VIRU SLARWR--HRHPYQFPQAPANQNV---VWMDAGGSPFADFALPGSLPTVNLEQNVSYTHGL 942
TR|A0A2Z1Q3B3|A0A2Z1Q3B3_9VIRU SLARWR--QRHPYQFPQAPANQNV---VWMDAGGSPFADFALPGSIPTVNLEQNVSYTHGL 947
TR|D0T2Z9|D0T2Z9_9VIRU ALLRWR--NRSLSQLPQAPAAQEP---SWMGDLSTPFSDFLLPGSIATANISQNTAYSHAI 945
TR|A0A7G3W8V4|A0A7G3W8V4_9VIRU SLARWR--QRHAYQFPVTPATQAP---VWMAEPGTPFADFISPGSLNSHNVEANVSYSYGV 349
TR|A0A2Z5WAD8|A0A2Z5WAD8_9VIRU ELLSWE--YPTQYQLPAAPAGFQP---TWLAPAGSLFGAWLLPGSVQNYSSSRIRANGI 1004
. . : ** : .

lc1|ORF2 NEVSEHQL--T--NSEARRWWLASKGTAHVSLMVNYVSPISQHYELDDLADYSVTIWEKD--G 1360
TR|H6UNN1|H6UNN1_9VIRU SDGSNNQL--T--PLEIQRWWLASKGRAHTSLMVNYVSPFAQHYERDVLADYTVTWEKD--S 972
TR|H6UNM9|H6UNM9_9VIRU KERTGVEL--T--PSEVRRWWSASKGLPHQSLMVNYISPSEHYEVDALSNTYTVTWEKD--S 981
TR|A0A7G4WLZ4|A0A7G4WLZ4_9VIRU QPNPRRPL--T--NQEASRWAAASKGQSNVSLMVNYVSPIAEHIEDSLADYSVWIENQ--S 1006
TR|A0A1P8DF80|A0A1P8DF80_9VIRU QPNPRRPL--T--NQEASRWAAASKGQSNVSLMVNYVSPIAEHIEDSLADYSVWIENQ--S 1006
TR|A0A514DCE7|A0A514DCE7_9VIRU RLPTGAHRS--DPIWRRWHQLGLQAPRQSLMVNYVHPLRERREIESLEDYSVLIEWEQ--N 993
TR|A0A514D1M0|A0A514D1M0_9VIRU RQIRETPL--T--AREAHRWWSAANELPHQSLMVNYLHPPFRERRAIEALSDYSVVLWEQD--N 576
TR|A0A7S5WL3|A0A7S5WL3_9VIRU HMPG--E--VD--PLVSRRWHSLSIESNESLMINYIHPLEKRQIESLHDYSIFIWEKD--N 945
TR|A0A515KU39|A0A515KU39_9VIRU HMQADS--TD--PLVSRRWHSLSIESPNESLMINYIHPLEKRQIESLHDYSIFIWEKD--N 1042
TR|A0A7S5WLX7|A0A7S5WLX7_9VIRU TMTD--H--GD--RQASRRWHGLSIGQGNNSLMINYVHPLKERREIEALQDYSIFIWEKD--N 932
TR|A0A7S5WL4|A0A7S5WL4_9VIRU TMTD--H--GD--RQASRRWHGLSIGQGNNSLMINYVHPLKERREIEALQDYSIFIWEKD--N 919
TR|A0A0M4L069|A0A0M4L069_9VIRU TMTD--H--GD--RQASRRWHGLSIGQGNNSLMINYVHPLKERREIEALQDYSIFIWEKD--N 917
TR|A0A7S5WLW1|A0A7S5WLW1_9VIRU TMTD--H--GD--RQASRRWHGLSIGQGNNSLMINYVHPLKERREIEALQDYSIFIWEKD--N 932

TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	TTADDITALDRRYTAQLWFDAARQVPKRSLMVNYVSPFPDRREFSSLQDYSIIVWEKE-N	999
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	RNNAQV---D-GETHRRWFDAARQEPHVSLMVNYIHP TKDSRQLDNLLDYSTIILEQG-N	1056
TR	E7BMX6	E7BMX6_9VIRU	TTADDVTTLDRRYTAQLWFDAARQVPKRSLMVNYVSPFPDRREFSSLQDYSIIVWEKE-N	998
TR	A0A7L9R666	A0A7L9R666_9VIRU	TSADDITALDRRYTAQLWFDAARQVPRRSLMVNYVSPFPDRREFSSLQDYSIIVWEKE-N	999
TR	A0A346P9C1	A0A346P9C1_9VIRU	RESQTAHNRMTAEQISRVHKLGCGLPHQSLMVNYINPYAIRSQVDQLADYSIVILSSG-A	1127
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	RENTTPGNGMAPDHVRRTRYRASLGAPHQSLMVNYVAPDAVHQEVDPPADYSFLIVTRG-S	1033
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	RENTTPGNGMAPDHVRRTRYRASLGAPHQSLMVNYVAPDAVHQEVDPPADYSFLIVTRG-S	1047
TR	I1Y9U4	I1Y9U4_9VIRU	TVNPNVSALDRRFTSQLWFDAARQVPKRSLMINYVSPFPDRREFASLQDYSIIVWEKE-N	989
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	QLQNNCSQAERNYLSQLWFDARQTPRRSLMINYVSPFPDRREFSTLQDYSIVVWEKG-N	1001
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	QLANDCPQADRTYLSQLWFDARQTPRRSLMINYVSPFPDRREFSTLQDYSIVVWEKG-N	1006
TR	D0TZ29	D0TZ29_9VIRU	TAKAGTSQADQNHLARLWFNTARQLPRSSSLAISYVSPYPERRELRTLQEYSIVVWENGQN	1005
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	TVNPDISALDRRFTSQLWFDAARQVAKRSLMINYVSPFPDRREFASLQDYSIIVWEKE-N	408
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	RATAPST-----VLRDAWARQVLDKQTSVGISYIPPPGFKIDTSGDAELFNVIWFKN-N	1058

. . : . * : :

lc1	ORF2	RFAALTFSNLNE--LLTKDNFNPTNIEESQKPFQTRFDSAPHRFEQLRPRTRVT--NNRSSH	1417	
TR	H6UNN1	H6UNN1_9VIRU	KFAGLTFSNITK--DLQDSTFNPDYISQQGPLTLNFD SAPRPMQNQPTRVA--ARQTNR	1029
TR	H6UNM9	H6UNM9_9VIRU	HFAGITFSNITR--QLSDAKFDP RSFVRDQTPFQLHFD SAPKAFEQNRSSRVL--RRTSRV	1038
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	GFAGLTVMNNYE--SFSNPDLPLSRLLPDQSPFTVPFDSAPKPYMQNQPTRIT--SKPSTR	1063
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	GFAGLTVMNNYE--SFSNPDLPLSRLLPDQSPFTVPFDSAPKPYMQNQPTRVT--SKPGTR	1063
TR	A0A514DCE7	A0A514DCE7_9VIRU	RFAGMSLIRYDMPNGSADTRFDPTGTVPLSK--AFDLP--GASAGPATTLNPNRVT--ARRVMG	1050
TR	A0A514D1M0	A0A514D1M0_9VIRU	MFAGLTFSNLFQ--EINKGDARFDTIRPQQSMFQLSSYAKPRTSEFFFNTRIS--SSQRYG	633
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	RYVGMTSVRYDMPDVAAGARFDPKGIPAMP--NYDIP--TMAGDEYRSVQPGRIA--KNKRKT	1002
TR	A0A515KU39	A0A515KU39_9VIRU	RYVGMTSVRYDMPDVAAGARFDPAGIPAMP--NYDIP--TMAGDEYRSVQPGRVA--KNKRKN	1099
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	KYTGMTAVRYDLPDVAAGARFDPKGV PAMP--NYDIP--AATGDEYMSVQPARIT--KNRKD--	988
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	KYTGMTAVRYDLPDVAAGARFDPKGV PAMP--NYDIP--AATGDEYMSVQPARIT--KNRKE--	975
TR	A0A0M4L069	A0A0M4L069_9VIRU	KYTGMTAVRYDLPDVAAGARFDPKGV PAMP--NYDIP--AATGDEYMSVQPARIT--KNRKE--	973
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	KYTGMTAVRYDLPDVAAGARFDPKGV PAMP--NYDIP--AATGDEYMSVQPARIT--KNRKE--	988
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	AYAGMSLVPVDFSPVSI--ADYKPAANLTFP--SLTRP--SAVDTS DI--AKNPRVA--SSKRAP	1054
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	NYTGMVVVPHHLPDYEIDSELNPARLLDFG--GRGEA--PPSAEPVALDKPTNLRVA-----	1109
TR	E7BMX6	E7BMX6_9VIRU	AYAGMSLVPVDFSPVSI--ADYKPAANLTFP--SLTRP--SAVDTS DI--AKNPRVA--SSKRAP	1053
TR	A0A7L9R666	A0A7L9R666_9VIRU	AYAGMSLVPVDFSPVSI--ADYKPAASLTFP--SLTRP--SAVDTS DI--AKNPRVA--SSKRAP	1054
TR	A0A346P9C1	A0A346P9C1_9VIRU	KFAGMALQPGHFTAVTADDRNLRE--RPQQSTFTHA--AADPSRGRDLAPVRIA--ARVA--	1181
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	SYAGMILQQHNAEIIIPAGTRIQPD--RPTQTPFTQA--YDIGLNPVAHAPVRIT--NSVR--	1087
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	SYAGMILQQHNAEIIIPAGTRIQPD--RPTQTPFTQA--YDIGLNPVAHAPVRIT--NSVR--	1101
TR	I1Y9U4	I1Y9U4_9VIRU	AYAGMSLVPVDFSPVSM--ADYKPASNLTFP--SLTRP--SAVDVSDV--ARNPRVA--SSKRAP	1044
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	TYAGMSLVPVDFAPTSI--ADYHPNPQLPMP--NVTRP--SAADVSDV--TKGRVARVRNTRKP	1057
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	TYAGMSLIPVDFAPTSI--ADYHPNPQLPMP--NVTRP--SAADVSDV--TKGRVARVRNTHKP	1062
TR	D0TZ29	D0TZ29_9VIRU	AFSGMSLMPANF SVQHM--DAFLPSKDLKLP--AFSRP--VAADISDS--SKSARVT--RSTPQP	1060
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	AYAGMSLVPVDFSPVSM--ADYKPASNLTFP--SLTRP--SAVDTS DI--AKNPRVA--SSKRAP	463
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	SYAGMTLEQVEPGQPLIGSSSLPLPEGPHSLPLTHL--ANDNYDMPKGGKRVW--AGRSQP	1115

: . :

lc1	ORF2	A--KEA-R-PA-----LSSATDIN-----R-RIAE	1437	
TR	H6UNN1	H6UNN1_9VIRU	-----P-----PVDVTNIN-----R-----	1039
TR	H6UNM9	H6UNM9_9VIRU	V--NRGAD-LA-----ASINNRLA-----H-----	1055
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	T--TTDQH-VEPLSSGT-----PISVADAFN-----	1086
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	Q--TADQD-TKPLGSNT-----SVSVADAFN-----	1086
TR	A0A514DCE7	A0A514DCE7_9VIRU	R--D--PNLMG-----RVQA-----VMRPRG	1067
TR	A0A514D1M0	A0A514D1M0_9VIRU	R--INSRR-VNKQAGGAYETPATHLKFGSISDEVK-----ERVAAI	671
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	G--G--KSSEEK--S-----DEENPRVKV-----TRFLEH	1026
TR	A0A515KU39	A0A515KU39_9VIRU	A--K--QQNEDNVDK-----EETNPRVKV-----TRYLEH	1125
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----VDAPPRTKV-----TKYLEM	1003
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	-----VDAPPRTKV-----TKYLEQ	990
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----VDAPPRTKV-----TKYLET	988
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----VDAPPRTKV-----TKYLEM	1003
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	R--AAASDILARLKE-----FNSPPPPP-----PSPEPK	1081
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	A--ARTGAPVARFHS-----RPRPPPVN-----RSSDPD	1136
TR	E7BMX6	E7BMX6_9VIRU	R--AAASDILSRLKE-----FNSPAPTP-----PSPGLS	1080
TR	A0A7L9R666	A0A7L9R666_9VIRU	R--AAASDILARLKE-----FNSPPPPP-----PSPGLS	1081
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----P-----N-----TSL-----	1186
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----P-----R-----QSLTGE	1095
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----S-----R-----QSPTGE	1109
TR	I1Y9U4	I1Y9U4_9VIRU	R--AAASDILNRFKE-----FNTPPSPE-----PAPTQH	1071
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	R--VASNVVADRLRE-----FQSEREHT-----	1078
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	R--VRSNVVVDRLRE-----YHQELSEP-----	1083
TR	D0TZ29	D0TZ29_9VIRU	R--ARAANVLEKINA-----FRRADPVN-----RSPDPD	1087
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	R--AAASDILNRFKE-----FNAPPPST-----PAPSHH	490
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	SPADVADEPADNFPL-----RSALGDPFSRPRTEEDVLYYKAAASAPQSSARPHRPVPG	1170

lc1	ORF2	-----LRRPQAGNITYETKYPLHADDLPKMNSYDVNVT--KDG	1473
-----	------	---	------

TR	H6UNN1	H6UNN1_9VIRU	-----RIAETGKITYKSKYPHFDELPPMESTPVEVT-EEG	1074
TR	H6UNM9	H6UNM9_9VIRU	-----RVKQSGLIEYQSKNPSFEDELPPMRSKVATAN-SNG	1090
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	-----KRIAATGSISYETKYPLFEDELPSFKTAEVSSD-QSG	1122
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	-----KRIAATGSISYETKYPLFEDELPSFKTAEVSSD-QAG	1122
TR	A0A514DCE7	A0A514DCE7_9VIRU	-----AVVNSPPIIEYRAKHPLTTDDVPRMDTYNAEMD-ERG	1103
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----ARGDQAGAITYTTKYPHTTDELPTLEDGVVEYD-AHA	707
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	-----GDLDRDATLTYKAKYPVNIDEVPALPANQVHMT-DTN	1062
TR	A0A515KU39	A0A515KU39_9VIRU	-----GDLDRDATLTYKAKYPVNIDQVPTLPENQVHMT-DTN	1161
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----GELERTGELKYNPIYPTNSDQVPKLPDAHVVMD-DKN	1039
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	-----GELDRGTGELKYNPSYPTNLEQVPKIPDAHVVMD-DRN	1026
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----GELERTGELKYNPIYPTNSDQVPKIPDAHVIMD-DKN	1024
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----GELERTGELKYNPVYPTNSDQVPKLPDAHVVMD-DKN	1039
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----HREPAAEALSIEAKYPIEEAQVPSDFRFYQPVVEEDR	1117
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	-----LTQGGALDISYSPNPNELVSDLPITLGRYEAQVT-DDG	1172
TR	E7BMX6	E7BMX6_9VIRU	-----QREPAQALSIEAKYPVEESQVPADFRFYQPVVEEDR	1116
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----QREPAQALSIEAKYPVEEAQVPADFRFYQPVVEEDR	1117
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----KTGQPAGKVHFQSKYPVWRDDIPRIPRIDVEVT-PQD	1222
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----KRVQLQGNLRYEPKYPVWRDQVPDLQSYQVHAE-AGQ	1131
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----RRVQLQGNLRYEPKYPVWRDQVPDLQSYQVHAE-AGQ	1145
TR	I1Y9U4	I1Y9U4_9VIRU	-----VNDTPAAQALSIEAKYPVEEAQVPADFKYQPVVAEDR	1108
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----EPKVSAGALSIESKYPVEQSELPPMQNYTAHVN-GPE	1113
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----EQRISGALSIEPKYPVEQSEVPPMQNYTAHVN-GPE	1118
TR	D0TZ29	D0TZ29_9VIRU	-----GIEGVTASLSHEAKYPVEMSQLPNNMNFSTKVEDGR	1124
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----ADEPPAARLSIESKYPVEEAQVPDGFYQPVVEDDR	527
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	VDGDSTLRGPRKLSDFEPQPHTGSRDYAHGPGQYAQKNPLNLRVVKARVSGAAPRG----	1226

. * ::

1c1	ORF2	FEYPQNMAPNDL-SFTPAD-----RLKKIQ-----	1497	
TR	H6UNN1	H6UNN1_9VIRU	IVVDPRQRPM-E-GDTPSS-----RLAEIN-----	1097
TR	H6UNM9	H6UNM9_9VIRU	IMIEENDGQP-V---DNSA-----RLAYVN-----	1111
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	LHFTTTP---LG-GRTPKG-----RLERIR-----	1143
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	LHFTTTP---LG-GRTPKG-----RLERIR-----	1143
TR	A0A514DCE7	A0A514DCE7_9VIRU	ITVGQEFIRP---GDMPTK-----RYE---PPLADG-----VQD	1131
TR	A0A514D1M0	A0A514D1M0_9VIRU	ISALPAERPD-----ATLA-----KLARIQ-----	728
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	IIYDPVPLAE---ARTPLD-----RLA---L-IDAK-----LSE	1089
TR	A0A515KU39	A0A515KU39_9VIRU	IIYDPVPLAE---ARTPLD-----RLA---L-IDAK-----LNE	1188
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	IVFDPAPLAE---SRTPAE-----RLA---Y-LNEK-----LRE	1066
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	IVFDPTPLAE---SRTPAE-----RLA---Y-LNEK-----LRE	1053
TR	A0A0M4L069	A0A0M4L069_9VIRU	IIFDPAPLAE---SRTPAE-----RLA---Y-LNEK-----LRE	1051
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	IVFDPAPLAE---SRTPAE-----RLA---Y-LNEK-----LRE	1066
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	VHVEPADAPD---AYDRLS-----KQQLKLAIEENN-----MQL	1147
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	IQIPQRPSAK---CEPSEYMAGAN-----S-----GYDAQLEADRN-----REL	1208
TR	E7BMX6	E7BMX6_9VIRU	VHVEPADAPD---AYDRLS-----KQQLKLAIEENN-----MQL	1146
TR	A0A7L9R666	A0A7L9R666_9VIRU	VHVEPADAPD---AYDRLS-----KQQLKLAIEENN-----MQL	1147
TR	A0A346P9C1	A0A346P9C1_9VIRU	IEVTAVDLPPEEPPQTVDDEGG---DGLTGHYTTDADDTPTPVRSN---FMTDEEIALR	1276
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	VTVDEHPVKPRSPKRTLPAPAETVYPDSSTSSVYESADDEPAPRGQPHHGLSDIEVDQL	1191
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	VTVDEHPVKPRSPKRTLPAPAETVYPDSSTSSVYESADEEPIPRRQSHHGLSDVEVDQL	1205
TR	I1Y9U4	I1Y9U4_9VIRU	VYVEPADAPD---AYDRLS-----KQQLKLAIEENN-----MQL	1138
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	VTLRD-SDTG---AFTRLQ-----KREMLQALQSN-----MEL	1142
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	VSITD-ADTG---AFTRLQ-----KREMLQALQTN-----MAL	1147
TR	D0TZ29	D0TZ29_9VIRU	ISVETSPSHE---ASLAAL-----RDELKRSAAAN-----AAL	1154
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	VHVEPADAPD---AYDRLS-----KQQLKLAIEENN-----MQL	557
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----SRPPRAAA-----D-----ALTAPP-----	1241

1c1	ORF2	-----E-----A---QAHLDDQFQYFAEQQQQQAI-NRT---R---L---	1525	
TR	H6UNN1	H6UNN1_9VIRU	-----A-----A---QQMINRMIEQYMSSEERTKAABV-RAA---A---A---	1125
TR	H6UNM9	H6UNM9_9VIRU	-----E-----M-----QARLDQARDELGTGNWQQEAAAM-RAA---A---R---	1139
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	-----E-----L---ELARDAEYEEYVRESQLKEAS-ARA---E---A---	1171
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	-----E-----L---ELARDAEYEEYVRESQLKEAS-ARA---E---A---	1171
TR	A0A514DCE7	A0A514DCE7_9VIRU	TSHLHR-----QLQQKEYEMDQAHQAWLAAEQIKAAK-SRA---AYAD---	1170
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----N-----Y---EAEQDALFQQMLAERSARIAI-PRP-----	754
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	VDGFEE-----QLQNERAELHRIE-----E-ARQ---QQID---	1117
TR	A0A515KU39	A0A515KU39_9VIRU	ADDFEE-----QLHREAEELCRIRD-----E-ARQ---QQID---	1216
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	TDDFQL-----ELEAERSKLQQLRD-----E-ARQ---HQAD---	1094
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	TDDFQL-----ELEAERSKLQQLRD-----E-ARQ---HQAD---	1081
TR	A0A0M4L069	A0A0M4L069_9VIRU	TDDFQL-----ELEAERSKLQQLRD-----E-ARQ---HQAD---	1079
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	TDDFQL-----ELEAERSKLQQLRD-----E-ARQ---HQAD---	1094
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	LAKIQN-----SPILGELDLDAERKR-REDFQ-KVES---A---RNER---	1182
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	DEQFRE-----FLRQSTNQLNEFRQ-----	1228
TR	E7BMX6	E7BMX6_9VIRU	LAKIQN-----SPILGELDLDAERKR-REDFQ-KVES---A---RNER---	1181
TR	A0A7L9R666	A0A7L9R666_9VIRU	LAKIQN-----SPILGELDLDAERRR-REDFQ-KAES---M---RNER---	1182

TR	A0A346P9C1	A0A346P9C1_9VIRU	LKKADSQGMVNSRALDFYRTQAMEEVSGKIDAEFNELLAE-----LNARAALKQQELQS	1330
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	LERIERDYAGNGHNINA----AQDARDRAVDDDFDQYLKSSRDQRKLNARIAAARKAVQ-	1246
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	LERIESDYAGNGHNUNA---SQDARDRVVDYDFEYLFKFSRDQRKLNARIAAARKAVQ-	1260
TR	I1Y9U4	I1Y9U4_9VIRU	LAKIQN-----SPILGELDLDAERKR-QDEFR-QLEA---A---RNAR--	1173
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	MAKLQA-----SPLLASPDREDLVQD-SAARR-AAEY---A---QQVR--	1177
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	MAKLQA-----SPLLASPDSEELVQD-SAARR-ASYE---A---QQNR--	1182
TR	D0TZ29	D0TZ29_9VIRU	LERIER-----SQLVPDFSLEHMRTQ-RPVEAVASYP---N---R-----	1187
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	LAKIQN-----SPILGELDLDAERKR-QEEFR-QLEA---A---RNAR--	592
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----ARREIDRINAIEWSNLRAKYDIDAARDLPTEH-P--	1273

1c1	ORF2		---QANRVA-----SPA-----TTRPI-APVPR-RKARL---PSV--INYP	1557
TR	H6UNN1	H6UNN1_9VIRU	---RQPRTQ-----SPP-----LWLPS-PKKP--RVA-----PK	1148
TR	H6UNM9	H6UNM9_9VIRU	---RAPAHE-----HTKSS-----LYIPA-TGTA--RKARA-EKRRSVSEAVVPT	1177
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	---NARKAA-----TPA-----YHTIV-TKRPPKTKGGASAVANSLSHMNFQR	1210
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	---NARKAA-----TPA-----YHTIV-TKRPPKTKGGASAVANSLSHMNFQR	1210
TR	A0A514DCE7	A0A514DCE7_9VIRU	---LQARQAERV-----ARGRS-----LPP--RPKAPSVQRPQSKR-----	1201
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----VPQ-----SWRPG-PPRQRAQVR-----P---SSWPR	777
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	---IAKRVAANT---KRHSEQRR-----RFT-----	1137
TR	A0A515KU39	A0A515KU39_9VIRU	---IAKRVAASS---RKHSEGRR-----RFT-----	1236
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	---IIARVAQNT---RKHNEARR-----RFT-----	1114
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	---IIARVAKNA---RKHNEARR-----RFT-----	1101
TR	A0A0M4L069	A0A0M4L069_9VIRU	---IIARVAQNT---RKHNEARR-----RFT-----	1099
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	---IIARVAQNT---RKHNEARR-----RFT-----	1114
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	---IQRRAS-----FVPFGPTRPRP---VLTP-----	1203
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	---ARVARTT---PPQRQSS-----SWVPR-SPGPRPIRHHSTESQ-----	1262
TR	E7BMX6	E7BMX6_9VIRU	---IQRRSS-----FVPFGPTRPRP---VLTP-----	1202
TR	A0A7L9R666	A0A7L9R666_9VIRU	---IQRRSS-----FVPFGPTRPRP---VLTP-----	1203
TR	A0A346P9C1	A0A346P9C1_9VIRU	YQGLRKRVAHVQRTNTLPHRRSFSVNNVKSATAIRPPRQSPRQSKSVA-----	1378
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	--DEVKKL-----EQTRQT-KRGTS---TQRTPSPRRQPHAP-----	1278
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	--GEVKKL-----DQGRQT-KRGTS---TQSAPSPRRQPHAP-----	1292
TR	I1Y9U4	I1Y9U4_9VIRU	---IQRRSS-----YVPFGPTRPRP---VLSP-----	1194
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	---IADRVAKAK---VPTSPKPR-----VKLPPTAPTQP---PVRAL-----	1212
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	---IAQRLAQAK---ATTSPKPR-----VKLPPPPARPAH---SPPTS-----	1217
TR	D0TZ29	D0TZ29_9VIRU	-----GL---TRSPRPQ-----RHTPRSPRPEGNRNLRLPASP-----S	1220
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	---IQRRAS-----YVPFGPARPRP---VLSP-----	613
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	---ARNRMV-----YLEHRFKN---LTEMAT---PGTPKPQLEKA-----	1305

1c1	ORF2		---PE-----PASYPH-----KGRQSYV	1571
TR	H6UNN1	H6UNN1_9VIRU	---PR-----PTSMPII	1157
TR	H6UNM9	H6UNM9_9VIRU	---SR-----QVTGAFN	1186
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	DRAPLPSSISVNTKGYKPKVNLPPPPQGYQWTTTPTNTHPPVFSEKPNPLSSVKDARSVR	1270
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	DRAPLPSSISVSTKGYKPKINLPPPPQGYQWTTTPTNTHPPVFSEEPNPLSSVKSARSVR	1270
TR	A0A514DCE7	A0A514DCE7_9VIRU	--NSDPPKT-RV-----PGGDK--V-----TTAF---EAHIPGH	1227
TR	A0A514D1M0	A0A514D1M0_9VIRU	SQRAV-----VTAQSGTIDKLADGQ---	797
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	--NPNQATY-LN-----PGMKK--A-----APAF---SNIPEH-	1162
TR	A0A515KU39	A0A515KU39_9VIRU	--NPDQATY-LN-----PGMRK--A-----APAY---SNIPVQ-	1261
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	--NPNQATY-LN-----PGMKK--A-----APAA---STIDKH-	1139
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	--NPNQATY-LN-----PGMKK--A-----APAV---SSISER-	1126
TR	A0A0M4L069	A0A0M4L069_9VIRU	--NPNQATY-LN-----PGMKK--A-----APAL---STIDKH-	1124
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	--NPNQATY-LN-----PGMKK--A-----APAA---STIDKH-	1139
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----R-----APAV---KRPQVHG	1215
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	-----VVRN-----RRSKMPQ-----HRPVYG	1279
TR	E7BMX6	E7BMX6_9VIRU	-----R-----APAA---KRPQVHG	1214
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----R-----APTV---KRPQVHG	1215
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----FSAQASGLDVGTAKAEFND-----AAAAVTQN-NAQ-----IQAA	1411
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----FSSHSGGLAPPTRTDVPV-----EQPRAELPPAK-----HDVA	1312
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----FSTHSGGLAPPTRKDVVPV-----EQPRTTELPPAK-----HDVA	1326
TR	I1Y9U4	I1Y9U4_9VIRU	-----R-----STPN---KPPLVHG	1206
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----S-----PIPE---HTVQVVG	1224
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----P-----AQPV---KTVQVVG	1229
TR	D0TZ29	D0TZ29_9VIRU	--QPQAACHLLF-----PVAQVPTPD-----PNAH---FGVPLRA	1250
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----R-----SAPS---KPPLVHG	625
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----VGENAAR-----PTAA-----GEFV	1320

1c1	ORF2		ANKPLPPQPKPLV--PNDAPAAGA-QQAAIDLATLN-----ARRGSLRP-----AVHT	1616
TR	H6UNN1	H6UNN1_9VIRU	ATKRLAPSEEPPII--PNDAAAVEA-QQRAMQLRDAV-----LSQK-ARP-----ATPT	1201
TR	H6UNM9	H6UNM9_9VIRU	YSGPLQDTTEPVV--PNDAAAVET-QESARQNADHL-----FMGTG-ALP-----ARQT	1230
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	FSGDAKAFPENVE--PNDASAAVV-QERADFLSTAS-----PVGLNRRNP-----AAII	1315
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	FSGDAKAFPENVE--PNDASAAVV-QERADFLSTAS-----PVGLNRRNP-----ATII	1315

TR	A0A514DCE7	A0A514DCE7_9VIRU	----QRLPAGPVA--PNDAPAGEA-QASLQQQQENL----	QRFID---N-----	QSRL	1266
TR	A0A514D1M0	A0A514D1M0_9VIRU	-SSQSTSKRKVVQ--FNDEAASAA-QDEALALKEIM----	ESVSNRMPP-----	AAVI	842
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	-----VEAV--PNDNSNGQA-QAGVGRMEQAF----	AGQYD---M-----	ADEI	1196
TR	A0A515KU39	A0A515KU39_9VIRU	-----VEAV--PNDANSNGQA-QSGVGNMEKAF----	SGQYD---M-----	ADEI	1295
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----IVTV--PNDANSNGQM-QAGVGALDQAF----	TGQFT---M-----	ADEL	1173
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	-----VTTV--PNDANSNGQM-QAGVGSLDQAF----	TGQFS---M-----	ADEL	1160
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----VTTV--PNDANSNGQM-QAGVGALDQAF----	TGQFT---M-----	ADEL	1158
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----VVTV--PNDANSNGQM-QAGVGALDQAF----	TGQFT---M-----	ADEL	1173
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	KLPPTEL RHAPVE--INDAAAEQV-QRQISQLGRPA----	SPRS-----		1252
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	T-FPTPPPSEPVV--SNDVDARHT-QSMWLKHGDYN----	TPNPL---A-----	SDAI	1321
TR	E7BMX6	E7BMX6_9VIRU	KLPPSEVKHAPVE--INDAAAEQV-QRQIPQLGRPV----	SPRT-----		1251
TR	A0A7L9R666	A0A7L9R666_9VIRU	KLPPSTELKHAPVE--INDAAAEQV-QRQIPQLGRPV----	SPRS-----		1252
TR	A0A346P9C1	A0A346P9C1_9VIRU	A-IKTHFSRPPV--KLPPSPPTLE-EIKANARENGFGLSTPKTDPQAFM-----	SGAV		1460
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	KLSPRPIRRPEPVV--TNDSSAAHA-Q----	AELQSINRALFENPPDAFPRTVRFVDVKDQI		1365
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	KLSPRPIRRPEPVV--TNDSSAAHA-Q----	AELQSINKALFENPPDAFPRTVRFDTKDQI		1379
TR	I1Y9U4	I1Y9U4_9VIRU	KLSENMKHAPVE--VNDAAAEV-QREVRSGLGRPV----	PPLT-----		1243
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	KLNEEILNHSPVE--VNDAAAPQV-QIQAQKFSTPI----	NRAS-----		1261
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	QLNEDILRHKPVE--VNDAAAEV-QIQAQKFAKPL----	DRAS-----		1266
TR	D0TZ29	D0TZ29_9VIRU	HLQPEFLAQKPV--PNDSSAAEV-QRRVPKYGVPS----	FPAHD---P-----	FKEL	1293
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	KLSEKEVKHAPVE--VNDAAAEV-QREVRSGLGPV----	SRPT-----		662
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	A-NPQRDRVTPIVRESNDGKVTVPKQESWLK-GDFV-----			1354

;

1c1	ORF2	VQG-----	RRSLSPRAN-----	YLQRRAHDTSVDPDEPARLHHVRERPO	1654		
TR	H6UNN1	H6UNN1_9VIRU	VRG-----	RTSPSKRSR-----	SR-----	ENANAVDP-----	1223
TR	H6UNM9	H6UNM9_9VIRU	PLG-----	RTPTPKRQR-----	SP-----	SNTRNGGR-----	1252
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	AGS-----	RRP-----			1321
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	AGS-----	RRS-----			1321
TR	A0A514DCE7	A0A514DCE7_9VIRU	RPHSRQS-----	DRPA-----		QRQ-----	1280
TR	A0A514D1M0	A0A514D1M0_9VIRU	AGS-----	RRSIKRQPS-----		AAEDHVAGKSNFRK-----	A-- 869
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	KRSYTQVG--GRGKVEEIPAIDFSGRKAQPVAVTGSMPRPVYSQIAGRK-----				1243
TR	A0A515KU39	A0A515KU39_9VIRU	KRSYTQIG--GRGKVDQVPATDFLESEHQPVVVTGSLPRTVYQGQIAGRK-----				1342
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	RDYTSKAKQQYGSSEDNIPATDFATQHRPVAVAGSLPRTVYANLNPRK-----				1221
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	NETYNKAKQLYGSSEDNIPAVDFSATQRTVPVITGSLPRTVYANPNHRK-----				1208
TR	A0A0M4L069	A0A0M4L069_9VIRU	RNTYSKAKQQYGSSEDNIPAVDFATQHKPVAVTGSMLPRTVYANSNPRK-----				1206
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	HDTYSKAKQQYGSSEDNIPATDFATQHKPVAVIAGSLPRTVYANLNPRK-----				1221
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----	TTDPFGALKA-----		DKAVPGTYIQ-----	1272
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	AHGNHQPGSKPTPVVRLPPVRPE-----		SQARGGYHTTAQGRTNHDP-----		1363
TR	E7BMX6	E7BMX6_9VIRU	-----	ITDPFAALKA-----		DKANPGTYIQ-----	1271
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----	VPDPFAMLA-----		DKANPGTYIQ-----	1272
TR	A0A346P9C1	A0A346P9C1_9VIRU	PISYSEEDSRAASIS-----				1476
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	PIG--GEADPSGSSAA-----				1379
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	PIG--GEADPSGSSAA-----				1393
TR	I1Y9U4	I1Y9U4_9VIRU	-----	TTDPFATLAG-----		DKRRPGTYIQ-----	1263
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----	GYG--AFPS-----		GTHAKGKSPM-----	1278
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----	GLG--SLPS-----		GTAKGKVS-----	1283
TR	D0TZ29	D0TZ29_9VIRU	S-----	EYDPSAEHPQ-----		GLEVS-----	1309
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----	VTDPFATLAA-----		DKQRPPTYIQ-----	682
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----	QKKSVN-----			1360

1c1	ORF2	SQPIVSDPSDRGAALKSLEWSNPKPFLPHDKQWLSQSIEDFP--PLPEQRPPP--LDSS	1711				
TR	H6UNN1	H6UNN1_9VIRU	-SPHGDSP-----	DPEEWDVYPE-----	TTPHAPPT--QLTPD	1255	
TR	H6UNM9	H6UNM9_9VIRU	-PDILAQTS-----	DSEQEMDVYPE-----	RTSSDETP--KVQRG	1284	
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	-----	ERPPFFPHPGQNSPYMSAARSLADELSEHQHES--GEENG		1360	
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	-----	DRPPFFSPHPGQNSPYMSGARSLAEELSEHQADF--DEKDG		1360	
TR	A0A514DCE7	A0A514DCE7_9VIRU	-----	FDVP--ARPS--EDQPTR-----	PPY-----	1297	
TR	A0A514D1M0	A0A514D1M0_9VIRU	-----	TAEN-----	ATDLDSEYSSQNEGDSPDDPRQHMPPIRFQHA	905	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	-----	RKNPEERVNTTR--DEASKN-----	TNL-----	1264	
TR	A0A515KU39	A0A515KU39_9VIRU	-----	RKNPEEKIAASS--GHKPKN-----	PNL-----	1363	
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	-----	RKVPEPASPK-----	NQT-----	1234	
TR	A0A7S5WL4	A0A7S5WL4_9VIRU	-----	RKAPEVSPR-----	TQA-----	1221	
TR	A0A0M4L069	A0A0M4L069_9VIRU	-----	RKVPEPVSPK-----	VQT-----	1219	
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	-----	RKVPEPVSPK-----	RQT-----	1234	
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	-----	KST--E---H-----	VDY-----	1280	
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	-----	PTGMTVVVPKHERDLHYS GP-----	TPT-----	1386	
TR	E7BMX6	E7BMX6_9VIRU	-----	KSS--E---D-----	LAF-----	1279	
TR	A0A7L9R666	A0A7L9R666_9VIRU	-----	KSA--E---H-----	LDY-----	1280	
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----				
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----				
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----				
TR	I1Y9U4	I1Y9U4_9VIRU	-----	KNE--T---P-----	LNF-----		1271

TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	-----LER--YHNNQ-----AES-----	1290
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	-----MSP--EGSH-D-----QGP-----	1294
TR	D0TZ29	D0TZ29_9VIRU	-----R--GHTQG-----AST-----	1319
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	-----KND--V---E-----VSF-----	690
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----FADLPGLPEDSSVEQHNPPLTDDH	1384

lc1	ORF2	DHL----	D-TADTSRIRNQPG--NSS----	SQVDLSQIDWNGGPDVAVKASILDFTTKAS	1760	
TR	H6UNN1	H6UNN1_9VIRU	QEF-----	FAEKRVAS--K--LPA----	GAIDFSTLGDASTPMSSSAGAAAAMQOVQ	1300
TR	H6UNM9	H6UNM9_9VIRU	ERTVQQVTLSDQHTRVRN--T--LPD----	GAVDLSDVVPTGNAATDMDQYLDAFSQTLR	1336	
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	EESENTGEVSSDESRSRQNV--	NPKESFRNRVRFGLDFVNDPHGSEDAIQRLEAFA	1418	
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	DGSENTGEVSSDESRSRQNI--	NPKENFRNRVRFGLDFTNDPHGSEDAIQRLEAFA	1418	
TR	A0A514DCE7	A0A514DCE7_9VIRU	----KHVPEGGG-----	AFGPPQPFEELAARIKLDQVTDGPDVYADR--SNADA-----	1341	
TR	A0A514D1M0	A0A514D1M0_9VIRU	DTS-VEGELTNGT-----	AEAIARGMND--GVDLK	932	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	----HHIPKPGS-----	TQPGGD-----VSVEHGPTDN-A-PHASEG-GDQQAISTAAQ	1305	
TR	A0A515KU39	A0A515KU39_9VIRU	----HSVKGPGG-----	VQADGS-----VSEHGPTDG-S-PHANR-GDGLAVSTAAQ	1404	
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	----QRAIPGQ-----	TQEDGS-----VSLDYNTHPAGR-DHATG-AEAARYEQAER	1276	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	----QRISVPGQ-----	KQEDGS-----VSLDYSTHPAGR-DHATG-SEAARYEQAER	1263	
TR	A0A0M4L069	A0A0M4L069_9VIRU	----QRIAVPGQ-----	TQEDGS-----VSLDYGTHPAGR-DHATG-AEAARYEQAER	1261	
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	----QRVAVPGQ-----	AQEDGS-----VSLDYSTHPAGR-DHATG-AEAARYEQAER	1276	
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	----DSL-----	GKEQLP-----QENFGHTG---ADVSV-QDGIATDSLAK	1313	
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	----HQL-----	PP---IEEINETVNS-----SGVPP-QDGFSHESDLR	1417	
TR	E7BMX6	E7BMX6_9VIRU	----DAL-----	GKEQLP-----QANFGHTG---ADVSV-QDGIATDSLAK	1312	
TR	A0A7L9R666	A0A7L9R666_9VIRU	----DTL-----	GKEQLP-----QENFGHTG---ADVSV-QDGLATDSLAK	1313	
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----D-----	AKD-----FSEAFNLGTGDE	1492	
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----D-----	IARLAAGANQA-----TSSRTQHAFDVNT---	1404	
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----D-----	IARLAAGANQA-----TSSRTQHAFDVNT---	1418	
TR	I1Y9U4	I1Y9U4_9VIRU	----DDL-----	VKEQLP-----ATNFGHTG---ADVNV-QDGIATDSLAK	1304	
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	----DVV-----	RPITPP-----TQVFAPDD-RDTLNAAP-ADGQAVSSLA	1326	
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	----DVV-----	LPAPPP-----AQTFAPDD-RDSLNAAP-ADGLAVSSLA	1330	
TR	D0TZ29	D0TZ29_9VIRU	----SELRLTGSSSRTNDLPPGT----	GTRITTPYGNN---TTDQNAVA-QDGLALTELA	1368	
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	----DDL-----	VKEQLP-----TTNFGNAG---ADIGV-QDGIATDSLAK	723	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	GTI---VEMSGALSD----	PGEPPA---GS-----VWGGENPALK-G-----	1415	

lc1	ORF2	-----	ERVDMNPNPKN-----	1770	
TR	H6UNN1	H6UNN1_9VIRU	L-----	VDPEVTQPKN-----	1311
TR	H6UNM9	H6UNM9_9VIRU	N-----	ADAQVTSPPKN-----	1347
TR	A0A7G4WLZ4	A0A7G4WLZ4_9VIRU	Q-----	ADATTRTPKN-----	1429
TR	A0A1P8DF80	A0A1P8DF80_9VIRU	Q-----	ADATTRTPKN-----	1429
TR	A0A514DCE7	A0A514DCE7_9VIRU	-----	YIPSFEQVEGLKRPFENFSGAQSYW	1365
TR	A0A514D1M0	A0A514D1M0_9VIRU	P-----	REMLTTPKN-----	943
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	KMDE-AWQQY--	SKEHEAVKSAEN-----	1326
TR	A0A515KU39	A0A515KU39_9VIRU	EMEK-AWQQY--	SDEHSGVKSAN-----	1425
TR	A0A7S5WLX7	A0A7S5WLX7_9VIRU	ALAPPAGSDYPGGAEGQALRSAEN-----	1300	
TR	A0A7S5WL3	A0A7S5WL3_9VIRU	SLAPPVAEDFPQGGEGQALKSAEN-----	1287	
TR	A0A0M4L069	A0A0M4L069_9VIRU	TLAPPVGSDDYPQNAEGQAMRSAEN-----	1285	
TR	A0A7S5WLW1	A0A7S5WLW1_9VIRU	ALAPPAGSDYPQGAEGQALRSAEN-----	1300	
TR	A0A0A7DSJ8	A0A0A7DSJ8_9VIRU	N-----	1314	
TR	A0A2Z1Q370	A0A2Z1Q370_9VIRU	SR-----	VFETDGVNSDPNVVFQSEN-	1438
TR	E7BMX6	E7BMX6_9VIRU	N-----	1313	
TR	A0A7L9R666	A0A7L9R666_9VIRU	N-----	1314	
TR	A0A346P9C1	A0A346P9C1_9VIRU	-----	LSRERALLPKN-----	1503
TR	A0A2Z5WAE5	A0A2Z5WAE5_9VIRU	-----	SPKN-----	1408
TR	A0A2L1GG75	A0A2L1GG75_9VIRU	-----	SPKN-----	1422
TR	I1Y9U4	I1Y9U4_9VIRU	N-----	1305	
TR	A0A1B4ZA68	A0A1B4ZA68_9VIRU	N-----	1327	
TR	A0A2Z1Q3B3	A0A2Z1Q3B3_9VIRU	N-----	1331	
TR	D0TZ29	D0TZ29_9VIRU	N-----	1369	
TR	A0A7G3W8V4	A0A7G3W8V4_9VIRU	N-----	724	
TR	A0A2Z5WAD8	A0A2Z5WAD8_9VIRU	-----		

+++++

Query ORF1: query sequence and 24 best matches aligned

+++++

CLUSTAL O(1.2.4) multiple sequence alignment

lc1	ORF1	-----	
TR	H6UNN2	H6UNN2_9VIRU	-----
TR	H6UNN0	H6UNN0_9VIRU	-----

TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	-----	
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	-----	
TR	A0A514DCG4	A0A514DCG4_9VIRU	-----	
TR	A0A346P9C2	A0A346P9C2_9VIRU	-----MN-----LA--AVNSYKLS----	12
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	-----MLSAYELLSKH-----SQGAKRVV--AGLTDSMS----	27
TR	A0A7L9R691	A0A7L9R691_9VIRU	-----MLSAYELLSKH-----SQGAKRVV--AGLTDSMS----	27
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	-----MLPAYETLCRH-----SQGAQKVV--AGLTDSMS----	27
TR	I1Y9U5 I1Y9U5_9VIRU		-----MLPAYETLSKH-----SQGAKKVV--AGLTDSMS----	27
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	-----MLPAYEKLSLH-----SQGAKKVV--AGLTDSMS----	27
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	-----MLPAYEMLSKH-----SQGAKKVV--AGLTDSMS----	27
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	-----	
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	-----	
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	-----	
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	-----MHLFDEP----VK--AAVTDTLA----	17
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	-----	
TR	A0A515KU26	A0A515KU26_9VIRU	-----	
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	-----	
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	-----	
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	-----MTDDNF----	6
TR	A0A514D1L9	A0A514D1L9_9VIRU	MKFQFLCSFVPFYIGQ--NHTLCLRIASLLQKAADHIYKFSVNEKVTSVDKLSSIFDMSDY	59
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	-----MFQSFLNLVSTETR-----INAEWPWIIPDPLIGEIA--QVLTRIRD----	40
TR	D0TZ30 D0TZ30_9VIRU		-----	
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	-----MTDGNF----	6

lc1 ORF1		-----		
TR	H6UNN2 H6UNN2_9VIRU		-----MLQYIFITPAPE	12
TR	H6UNN0 H6UNN0_9VIRU		-----MFYDFESAVATYK-----LNQE--ASDITHALMQYIFFTPAPP	36
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	-----	
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	-----	
TR	A0A514DCG4	A0A514DCG4_9VIRU	-----	
TR	A0A346P9C2	A0A346P9C2_9VIRU	----PGQSEEDSAI--IFDFVKIAEACD-----FNSP--PKNAFDAILCYIFLHPTPK	57
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	----ASTYKMSGTTYPGWDFSRLYSKYN-----LSTP--PNSYEEAAVASVLLNPRPD	74
TR	A0A7L9R691	A0A7L9R691_9VIRU	----ASTYKMSGTTYPGWDFSRLYSKYN-----LSTP--PSSYEEAAVASVLLNPRPD	74
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	----ASTYKMSGIAYEGWNFHYLYNKYN-----LDSP--PNSYEEAAVASVLLNPRPD	74
TR	I1Y9U5 I1Y9U5_9VIRU		----ASTYKMSGIAYEGWNHYLYNKYK-----LDSP--PSSYEEAAVASILLNPRPD	74
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	----ASTYKMSGVTYEGWNFHYLYNKYN-----LDSP--PTS YEEAAVATVLLNPRPD	74
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	----ASTYKMSGIAYEGWNFHYLYNKYK-----LDSP--PNSYEEAAVASILLNPRPD	74
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	-----MDDP--PENLVGAALRYIILHPVPI	23
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	-----	
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	-----MSDGSV--FYDAEGLFEAYS-----LNEM--PKDAFTATVGYIILNPVPR	41
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	----RRSPFKLRGKI--FYAFAEICAWEELATAPRLAINE--EERAIKAILIYIFIHPTPI	69
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	-----MSDGSV--FYDAEGLFEAYS-----LNEM--PKDAFTATVGYIMILNPVPR	41
TR	A0A515KU26	A0A515KU26_9VIRU	-----MGEF--PKDTAGAAALRYIILHPVPI	23
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	-----	
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	-----	
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	----TGSYKLSGKEYLGYDFS KIHSLYK-----LDRP--PTTLASA AAVARVMLHPQPD	53
TR	A0A514D1L9	A0A514D1L9_9VIRU	SCLASIKRCNLGESKIFFDIEGLYGYG-----LTDEIDCPNFDAIVYWLTLHPMP	112
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	----GRHKMRDGSY--FYDFSRLYDLFE-----LSKP--PDSTAKACAASILLHPTPS	85
TR	D0TZ30 D0TZ30_9VIRU		-----MSSKTYLGFNFNVLYRDYS-----LHRV--PENLQEAIVASVVLNPRPD	42
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	----TGSYKLSGNEYPGYDFS KIHSLYK-----LDRP--PTTLASA AAVARVMLHPQPD	53

lc1 ORF1		-----			
TR	H6UNN2 H6UNN2_9VIRU	SVWDFLPYNLIE-LAQSDPI-----LTSSAMKIL-----DQL----	V	44	
TR	H6UNN0 H6UNN0_9VIRU	SVC DHLPGFLLTAWDPREPV-----ISKAGFTLA-----SKT----	L	69	
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	-----MV-----SVA----	V	6
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	-----		
TR	A0A514DCG4	A0A514DCG4_9VIRU	-----		
TR	A0A346P9C2	A0A346P9C2_9VIRU	TVFDLVPTFEAHENWQTKTF-----QPVLSQKSIDLINDLP-----		93
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	ALNMTISP VYA---T-NELYATGSDV KPGIGSSWLTAFTTTTHL-HELRYERFEQS----	N	125
TR	A0A7L9R691	A0A7L9R691_9VIRU	ALNLSISPIYA---T-NELYAAPSPVKPGIGSAWLTDFSNTRL-PDLDRERFHQS----	N	125
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	ALNLTVAPIAA---T-SALYESSKPYKFGIGSSWLRAFNETPL-HLLEQERFAQS----	K	125
TR	I1Y9U5 I1Y9U5_9VIRU		APNLTVAPIAA---T-NALYESSKPYKFGIGSSWLRAFNEVPL-HLQEQERFAQK----	A	125
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	ALNLTVAPIAA---T-NLYESSKPYKFGIGSSWLRAFNETPI-HLLEQERFSQA----	P	125
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	ALNLTVAPIAA---T-NALYESSKPYKFGIGSSWLRAFNEAPL-HLQEQERFMQK----	A	125
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	QVFNFLPRLAVNAKA-LKGY-----KLSLGE GAINEILSQE-----		58
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	-----		
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	SIYQQIPTLG SNDKGISLHY-----KMSLTYSALDILNGY-----		76
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	QVY EYIPRLAVNNSGLLSNF-----KLSYTRKAIDQVRADN-----		105
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	SIYQQIPTLG SNDKGISLDY-----KMSLTYSALDILNGY-----		76
TR	A0A515KU26	A0A515KU26_9VIRU	QVYNFLPRLAVNSDS-LKAY-----KMSLT EGAISEIVTQN-----		58

TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	-----	
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	-----	
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	ALNLAIPPIHQLSNP---LALSPPNVVALGHAWLRNLTATRITRRKKERLLSSITFGE	109
TR	A0A514D1L9	A0A514D1L9_9VIRU	EVFNFLPNFESF-FDLTIPIN-QQLKIPLNDSRLLIRNLI-----SHK-----S	156
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	VVYNYIPSIMPDAPI-PEGLQLLASGGLVLNSQARQLRLLP-----	126
TR	D0TZ30	D0TZ30_9VIRU	ALNLRVSPLDQLCGQ-NAPLQLGKTVLPGLGHAWLDAFHTAKKSRELELQRFSTHT---	97
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	ALNLAIPPIHQLCNP----PLLSPPNKIALGSRWLQSLTSLRTRRRRKERLLSSISFGE	109

1c1	ORF1		MSSEPCQVNDTIYRLYHNLEADQ-YSCATRVLTILGLRDI--P-----HERFK	45
TR	H6UNN2	H6UNN2_9VIRU	PDSATSAGKVYYDIYANNYNDE-FSCATRLLTILGFNEF--D-----GERFE	89
TR	H6UNN0	H6UNN0_9VIRU	HDSETIGPGGQKYMCPNMDRDE-YSCATRLLTILGLRDI--P-----MERKE	114
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	Q--RRSSVFIGEWNFYHNMHTDD-KSCATRLLSLLGVRSI--P-----RERFA	49
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	-----MHTDD-KSCATRLLSLLGVRSV--P-----RERFA	27
TR	A0A514DCG4	A0A514DCG4_9VIRU	-----MFGYRYLYNYGTS-ASCAIRLLDILGVEWRSV-----ADDSV	38
TR	A0A346P9C2	A0A346P9C2_9VIRU	--RSQINLGGQHNYFLYRNDHVDL-GCCATRLATVLGYRY--TF-----SEHYN	137
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	----FTFPSLKDFVLFNTYGESKTASCATRVLQLLGCAYPLVDSHHLALAKQ---ALRLG	178
TR	A0A7L9R691	A0A7L9R691_9VIRU	----FSHTSLKDFCLFTNYGDSKNASCATRVLQLLGCAYPLVDSHHLALAKQ---ALRLG	178
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	----FQHPALADFTLFENYGLAPQASCATRVLELLGCVPVTDTHHLALAKQ---PMRLA	178
TR	I1Y9U5	I1Y9U5_9VIRU	----FQHPALTEFTLFENYGSTPQASCATRVLELLGCVPVTDHHLALAKQ---PMRLA	178
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	----FKHPDLNFTLFENYGTAPQASCATRVLELLGCVPVTDTHHLALAKQ---PMRLA	178
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	----FQHPALTEFTLFENYGSTPQASCATRVLELLGCVPVTDTHHLALAKQ---PMRLA	178
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	--WEEHTVWSTRYVYPNDVGDF-DSCATRVFKILGIQWEQYI-----E-DKL	102
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	-----MGKYSYNTDSGTL-SSCATRVFTLLGIQWEHSI-----Y-DAV	37
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	----NVPILKNYTWYPNDHVDL-NCCATRAAELLGYTH--TF-----TERAA	116
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	--S---SLVGNYSYYPNDSGTL-SSCATRVFNLLGIQWEHSI-----Y-DAV	145
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	----NVPILKNYAWYPNDHVDL-NCCATRAAELLGYTH--TF-----TERAA	116
TR	A0A515KU26	A0A515KU26_9VIRU	--STCGTIGSTLYWMPNDMGDF-DSCATRVFRLGLINWERYI-----E-DPV	102
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	-----	
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	-----	
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	FKSYEVNSRIGQYTYFPNYSGNLETSCATTLMSLLGNFYPIITDNDLLIKHTPSSTERPQ	169
TR	A0A514D1L9	A0A514D1L9_9VIRU	DDGQYQHTKDNTHIFFNYQADF-YSCATRALKILGLETL--V-----TEWGV	201
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	-QPLQVRVSLLSYNYENHGVIS-GVCIHRALHVLGLDNRYDH-----NELSAVG	174
TR	D0TZ30	D0TZ30_9VIRU	---HRFG-SATYAYFSNFGDPEKASCATRLQLGLVYPFTDENHLSGPRP---SGRPE	149
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	FRSYPADSTVGAFYTFPNYSGNLETSCATTLMSLLGVMPYITDRSDLLRLGPDSTEKPR	169

1c1	ORF1		DVSKLGMHRPTLKFQILRCFDPFSLLTEIDTSVDSLDTN-----IVNSIMLAHLEEL	97
TR	H6UNN2	H6UNN2_9VIRU	DVNKVGMRFPQLLRLLTMSLQLGIVLRTEHENTETLGERDLTC-SLI-KDSIFYMSANEG	147
TR	H6UNN0	H6UNN0_9VIRU	DIHALGPIPIVFRKLLMACWHSSTFHLDDASHQFESATMR-----EAI-ENDIQL-SATPT	167
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	DVDKVGWTVLNLQRLLLLSWHVGMVVDNTFEHIDSDGHPSKCL-ELMIQRSREFAS---S	105
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	DVDKVGWTVLNLQRLILLSWHVGMVIDSTFEHVNSDGHPSKCL-EIMIQRSREFAY---S	83
TR	A0A514DCG4	A0A514DCG4_9VIRU	DVTKFGVLPEDFRTLISISSISDSVACLTLTDSVYNYENAIIDFLAAII-----PVYTR	91
TR	A0A346P9C2	A0A346P9C2_9VIRU	DPYKLGVLQNETERMLSSSTWRRGKIVICYDE-PYDKPTDLLKHIAIT-----DSNLN	189
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	DPNKLGMQEPALANYLIAAWSPHSMVFDDSNABIEGFNE---EAYARLH-----A----	224
TR	A0A7L9R691	A0A7L9R691_9VIRU	DPNKLGMQEPALANYLIAAWSPHSMVFDDSNABIEGVNE---EVAQLH-----A----	224
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	DPNKLGMELPALVNYLISAWSPHGMVFNDLAMTESIDE---NCYDDL-----K----	224
TR	I1Y9U5	I1Y9U5_9VIRU	DPNKLGMELPALVNYLISAWSPYGMVFNDLVLTDEVDE---STYLKLL-----E----	224
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	DPNKLGMELPALVNYLISAWSPYGMVFNDLILSEGVKE---LTYRLRL-----E----	224
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	DPNKLGMELPALVNYLISAWSPYGMVFNDLVLTGVDGVE---NTYCKLL-----E----	224
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	DPNKVGQVATVFTDLIHKAAAGPDVGISY---DGDTYGVSSD-----	141
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	DPAKFGVIADTFNKYVRSSWHPKLIITY---PCYDGKMPFPN-----	78
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	DPYKLGVLQEVEKMLLLTWTKDGIIRLSE-SYGEHTKYSDV-AEII-----SSWLH	167
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	DPAKFGVIAQTFISKYIRSSWHPKIQVIVY---SYDYDQNLPAHI-----	186
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	DPYKLGVLQEVEKMLLLTWTKDGIIRLSE-SYGEHTKYSDV-AKTI-----SSWLL	167
TR	A0A515KU26	A0A515KU26_9VIRU	DPNKVGVMADVFDAMVHKAINDDVGVHRQ---RIKYDGLDYK-----	141
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	-----	
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	-----	
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	DPYKLGVPYPSFMAYICATVRPGIRVILEADAFEGPLERD--HFDAVI-----	215
TR	A0A514D1L9	A0A514D1L9_9VIRU	DVHKYGLGSDVFIERLQVAWSPGVVLVHSDTFCEGDLQLRDLH-----RFKWHQMGNL	254
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	DHMKLGIHFQVLRLLAPLPPTHKRFFISCTSMDEHHSQ---ALSII-----S----	220
TR	D0TZ30	D0TZ30_9VIRU	DPYKLGVAFHQLVHACFTAFDPGFFTFMEMPFPSTEDKTLATMDSLS-----S----	198
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	DPYKLGVPYPDFMAFICATVRPGIRAFVTDADFEGPFSRD--FFESLV-----	215

1c1	ORF1		PA-RATHDMEVVLFLFNDHISLALAESFIR---RHSQVIE-----GALDRPHPNF	143
TR	H6UNN2	H6UNN2_9VIRU	WEAY-PNKPAMVIVLFDHIAFALRRDYLV---RIQEAYLYRYLDDN--GRTTT---FK	197
TR	H6UNN0	H6UNN0_9VIRU	PQYYGIAPPVLIVILYADHVAFALRKDWLA---SQAYGFVASDVLDS--GSTTTLLSIR	221
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	AERSGLCEYYIHFNFDRHVSFAIKTAHLK---KYTQTL-----LEY--DSTT---PVH	151
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	AERSGLCGYYIHFNFDRHVSFAIKTAHLK---KYTQTL-----LAC--DTTT---PIH	129
TR	A0A514DCG4	A0A514DCG4_9VIRU	--GRVVKPPEIIILFSDHVMFCIHGKTAD---RFDELN--SRLSSE---PLTKKEIN	139
TR	A0A346P9C2	A0A346P9C2_9VIRU	NKQQPELTPQVIFWFYHNHVAFAINDDLTQ---DLTQHY--AKLWDDLKVKSGMPQVKR	243

TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	---TFPSAPIL-VCLHDGHVITYAIRRNFLFAELANYRAAY---QNASPHLSAQD----	KE	273
TR	A0A7L9R691	A0A7L9R691_9VIRU	---TFPLAPIL-VCLHDGHVITYAIRRDFLYVELTNYRSAY---QNASPYLSGRD----	KE	273
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	---DFPKAQIL-VCVHYGHISYAIRSALLQNELNIYRSAY---KNNTPQLTSSD----	KT	273
TR	I1Y9U5	I1Y9U5_9VIRU	---DFPKAQVL-VCVHYGHISYAVRGTFQLAEALNTYRSAY---HNQTPHLTSLD----	RD	273
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	---SFPHAQIL-VCVHHGHVSYAIRSLLQAEALNTYRSAY---QNQTPHLTSLE----	RS	273
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	---DFPKAQVL-VCVHYGHVSYAVRGTFQLTELNYSRAF---HNQTPHLTSLD----	KN	273
TR	A0A7S5WL9	A0A7S5WL9_9VIRU	--TIRGASKRLEIFVFRDHVCFALRNDLYE---QIAELE--LLHQES--AGMKIVDVRK		191
TR	A0A7S5WL9	A0A7S5WL9_9VIRU	--GWEQSDKELLFVYNDHVAYALRMDICS---RLRNLD--SDLRTYK-SRLAIKEMRD		129
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	ALATDVARPKIIFIWYANHIAFAVDNKFLE---KQTNLF--ARLSIK--HQPSLRNTFN		219
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	--DWGRSDKELLFVYNDHVSYAMRKDVFY---QLCRLG--EDLQNR-SRLAIKEVRD		237
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	GLEADVAPRKIIFIWYANHIAFAVENKFLE---VQMDLF--ARLSIK--YQPSLRNTFN		219
TR	A0A515KU26	A0A515KU26_9VIRU	--LFAHAEEKIEIVILNDHVLFAIRCIDLYN---QVTQLD--NDLKRS--KNMKISTVRD		191
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	-----	MRD	3
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	-----	MRD	3
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	---D-PSVKVLIVIHGSSHVSYVNSTLLNDELELYRDYAYFNASSFPATGFSIKQLLP		271
TR	A0A514D1L9	A0A514D1L9_9VIRU	INQVSAAPAWCVVIVQNDHVSFSIKDSILS---EQCIIPVKFKTNSN--SDFSPDYIS		308
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	---TYSGDHSCLVFVSHTHISFALNLSMISIRTYDELLEFLY--SHLP-----KGWLA		266
TR	D0TZ30	D0TZ30_9VIRU	---SFRPNCIL-AVVYPDHVQCVRRMSLETGLGYEENMLTYGHSRGQPLVTKAT----	AP	250
TR	A0A1B4ZAE6	A0A1B4ZAE6_9VIRU	---D-SGVRILIVHGVSHVSYVKTTFLODELDLYHDYAFNLNASSLPSLTGKSIKOLLP		271

1c1	ORF1	PIALLLLQYLIQ-IGGNDLMFFFCVN-----	PHILDDLTAKLAKRLKE	238	
TR	H6UNN2	H6UNN2_9VIRU	PINLILLKFLD-IVGEDLLWALCDT-----	HELWVSRQPEAAKLLKQ	293
TR	H6UNN0	H6UNN0_9VIRU	PINFLLLLPLD-EVGEDLVHYLIND-----	KQLFNLETDPDVVKRLKE	315
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	VTGMILLQYLN-IGAGDVLWFLITY-----	EQLWNSKFLLDAVKILKN	246
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	VTGMILLQYLN-VGAGDVLWYLITY-----	EKLWDSKFLLDAVKILKD	224
TR	A0A514DCG4	A0A514DCG4_9VIRU	SLSLPMLTWIS-PAGQDLCLFFLLN-----	SH-VLNLQFCDFYVKAKE	232
TR	A0A346P9C2	A0A346P9C2_9VIRU	ACALLLLPNLE-LTGTDLTRFICGN-----	PWIFMQDFKTYVKFCKY	336
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	VTTIALIPFLEGPAGRDLTLLFFLRN-----	MPVICSLSTNQVAKWLKA	370
TR	A0A7L9R691	A0A7L9R691_9VIRU	ITTVALLPFLEGPAGRDLTLLFFLRN-----	MPVICTLTTDQVAKWLKA	370
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	VTTVTLLPFLEGAAGIDLTLLFFLRN-----	MAVITTLSTNDAAKWLKA	370
TR	I1Y9U5	I1Y9U5_9VIRU	ITTVSLLPFLEGAAGIDLTLLFFLRN-----	MSTIVTLSTNDVAKWLKA	370
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	VTTVALLPFLEGAAGVDLTLLFFLRN-----	MPTIVTQTNDIAKWLKA	370
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	ITTVALVPFLEGPAGIDLTLLFFLRN-----	MSTIVTLSTNDVAKWLKA	370
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	GCAILLPPTN-ISGVDISLFFLQN-----	YKYILNKNFTEYITICKE	285
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	GLAVILLPVVS-LAGEDIGLFLFLLQN-----	SGYLFNQGGFDYIKSCKA	223
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	ATAVMLLPYLE-QAGRDIAIFLLNN-----	TSIFNLKFSIDYVKTCKE	312
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	GLAILLIPVVS-LAGEDIGLFLFLLN-----	YRIFKQGFSDYIKICKA	331
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	ATAVMLLPYLE-QAGRDIAIFLLNN-----	TSIFNLKFSIDYVKTCKE	312
TR	A0A515KU26	A0A515KU26_9VIRU	ACALLLLPYTN-HTGTDLSLFLFLLQN-----	FKWISRLDFVDYIKVCKE	285
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	GLAILLLPVVS-LAGEDIGLFLFLLQN-----	SGYLFNQGGFDYIKSCKA	97
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	GLAILLLPYVS-LAGEDIGLFLFLLN-----	SDYLFNQKFVDYIKTCKA	97
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	VTTLLLIPLYLESAGVELTLLFFLRS-----	ASVFFTLPEAEIAVKALKE	368
TR	A0A514DL19	A0A514DL19_9VIRU	IHGLLLSILVD-EAGSDLLIYYAFT-----	POLCTPLIADAAKLLKM	406

TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	AFNLTLLPFID-DLSEDIVLWLLHCNISSDALNALVFPKSLRVLTALFNAEFTTVAKAFKE	377
TR	D0T230	D0T230_9VIRU	ATTTLLPTLESKATPDILIFFLRN-----AEYLLATEFTTIVKRLKA	346
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	LTTLTLLIPYLESHAGVELTLFFLR-----APVFFKLPFVEAVKSLKE	368
			: : . :: . *	

1c1	ORF1		LHAYIRVNLRLPRFAFLNLSIGQREWARHLYGLETLVGRSELLELDITEEFKMRVADPA	298
TR	H6UNN2	H6UNN2_9VIRU	MHAQIKTAHRIPRLSAYFGRNYMARDWARRLYGLEVLVGRTEQFELDFSKEAIMRTIDPV	353
TR	H6UNN0	H6UNN0_9VIRU	YHTYSRLWHKPLCLMINYARSTHARDFARRLYGLDTLPGRSQQYTLDFTESEQVMRSIDPV	375
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	AHIETRIKHKLPNVSIHYARSTFARPWARSLYGLDTLPGRSEKFNLFQSEQLMRMIDTS	306
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	AHVETRIKHKLPNVSIHYARSTFARPWARSLYGLDTLPGRSEKFNLMNFQSEQLMRMIDTS	284
TR	A0A514DCG4	A0A514DCG4_9VIRU	VHQFARMHGTLPSPFAKKFKNVREQRAWSDSIYGVDIIGGRSEKLEFSAEEMVMRIADPT	292
TR	A0A346P9C2	A0A346P9C2_9VIRU	VHSMSTRHAQLPNYWLKYGRADEGRAWANAIYGFDIIGGRSELLSFDTKGEMLMRLADPV	396
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	AHAHARIFQCLPLALPAITIQEIRMYGDLIYGLDSLVRSELMLKLDFTAELFMRTADPI	430
TR	A0A7L9R691	A0A7L9R691_9VIRU	AHAHARIFQSLPLALPAITIQEIRMYGDLIYGLDSLVRSELMLKLDFTAELFMRTADPI	430
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	AHAYTRIYQCMPLALPGLLIPQIRAYGDLVYGLDSLVRSELMLKLDFTGELLMRTADPI	430
TR	I1Y9U5	I1Y9U5_9VIRU	AHAYTRIYQCMPLALPGLLIPQIRAYGDLVYGLDSLVRSELMLKLDFTGELLMRTADPI	430
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	AHAYTRIYQCMPLALPGLLIPQIRAYGDLVYGLDSLVRSELMLKLDFTSELLMRTADPI	430
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	AHAYTRIYQCMPLALPGLLIPQIRAYGDLVYGLDSLVRSELMLKLDFTGELLMRTADPI	430
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	IHHYVRMVGALPLFLRISIDVQDDRAWANHIYGDIIGGRSELMLHLDFTKETVMRLIDPA	345
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	IQQYTRMNGALPNYFRTPQTACDRAWANQLYGLDVIGGRSELMLHLDFTETVMRLIDPA	283
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	IHTNVRLTQQLPGYHKKWPEAHKGRAWANNIYGDIIGGRSELIKFDTGEFVMRTIDPA	372
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	IQQYTRMNGALPSYLRTPQTECDRAWANQLYGLDVIGGRSELMLHLDFTETVMRLIDPA	391
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	IHANVRLTQQLPGYHKKWPEAHKGRAWANNIYGDIIGGRSELKLFDTGEFVMRTIDPA	372
TR	A0A515KU26	A0A515KU26_9VIRU	VHHHVRMVGALPKYLRSIDVQDDRAWANNIYGDIIGGRSELMLHLDFTKETVMRLMDPA	345
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	IQQYTRMNGALPNYFRTPQTACDRAWANQLYGLDVIGGRSELMLHLDFTETVMRLIDPA	157
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	IQQYTRMNGALPNYFRTPQTACDRAWANQLYGLDVIGGRSELMLHLDFTETVMRLIDPA	157
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	VHNFIRQFSTIPGCGIPSLRITDARAYSDLLYGLDTIPGRSELNLDFDGLIMRAADPT	428
TR	A0A514D1L9	A0A514D1L9_9VIRU	VHTTGRLYYTLSTMLRKYPVYTGSRYSARIYGLDTLVGRSEKPLDSAGEMLMRTVDPF	466
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	VHTQGRFLSHLLGFGRIRPIHLARGYGLVYGFDTLAGRSEKYEKASFVDECLMRSVDPH	437
TR	D0T230	D0T230_9VIRU	INQFIRIYQRIPLGLPAYNINQLREFSDSLCGLDVLPGRSELLSLDFNAELLMRMADPA	406
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	AHSYIRQFSTLPGSGIPSLRITDARAYSDLLYGLDTIPGRSELLTLDFTSELIMRAADPT	428
			: : : * . : * . : * : : . * * *	

1c1	ORF1		LRGVPPELVDRDRSGNFSYIRFDT--SEYTRLLPQIANQMVESLLK--EKVVNLNDMHEFFQ	353
TR	H6UNN2	H6UNN2_9VIRU	NRALPEIRTHLNG-FKYISFSH--TALQDMLPVATRKFVNQLLK--DTAALTTLDEFYD	407
TR	H6UNN0	H6UNN0_9VIRU	ERALPEIRELPSG-IKYLFSNH--EAYYTLMPKIVRDSLRLVLT--DHVTLQGLTEFFS	429
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	KRAWPAIVEDKYG-NKYIKFFP--DRYTEQVKKIARKTAEDLIQ--SQTNLETFTEFFS	360
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	KRAWPAIVEDKYG-NNYIKFFP--DKYTEQVKKIARKTAEDLIQ--SQTNLETFTEFFS	338
TR	A0A514DCG4	A0A514DCG4_9VIRU	IRALPVIDRE--TG--LIALDR--HLYVAKRKEVTRAVVADLIR--PDVRLTLHHWFG	343
TR	A0A346P9C2	A0A346P9C2_9VIRU	KRGKLVITDFGL-----DITQ--HGVDYLDIDVKTAEENLIT--DDVSAETLEHWYA	445
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	RRAVPTLVQTSKGF--ELNLSE--ELYETYEDRAINTTFREVLP--EKLNLSEFEAWYA	483
TR	A0A7L9R691	A0A7L9R691_9VIRU	RRAVPTLTRATSGF--ELTLSE--ELYETYEDRAINTTFREVLP--DKLNLSEFEAWYA	483
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	KRAVPILQSTNAGY--ELHLNT--ALYDEYENRAINSTFNDLLP--ERINLESEFEAWYA	483
TR	I1Y9U5	I1Y9U5_9VIRU	QRAVPILQNTTAGY--ELHLST--ALYEEYEDRATNSTFNDLLP--EQINLESEFEAWYA	483
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	QRAVPILQNTNAGY--ELQLST--SMYEEYEDRATNSTFNDLLP--DHINLETFESWYA	483
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	QRAVPILQNTTAGY--ELHLST--ALYEEYEDRATNSTFNDLLP--EQINLESEFEAWYA	483
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	LRAVPYTYST--ER--RLYMSS--DLYERYEDESTQEAAREVIAKAAEDGVTLEGFDSWFD	399
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	LRAVPVYDIG--EG--RLYMSS--SLYEYEDATEEAAREVIAKAAEDGVTLEAFDNWFD	337
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	IRGILITTESKPNQ--LKYITG--PQYDSYLLSVIFRVTRKLR--PMVKLETMERWFN	425
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	LRAVPYTYDIG--ER--RLYMSS--SLYEYEDATEEAAREVIAKAAEDGVTLEAFDSWFD	445
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	IRGILITTESKPNQ--LKYITG--PQYDSYLLSVIFRVTRKLR--PMVKLETMERWFN	425
TR	A0A515KU26	A0A515KU26_9VIRU	LRAVPYTYST--ER--RLYMSS--DLYERYEDESTQEAAREVIAKAAEDGVTLEGFDSWFD	399
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	LRAVPVYDIG--EG--RLYMSS--SLYEYEDATEEAAREVIAKAAEDGVTLEAFDTWFD	211
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	LRAVPVYDIG--EG--RLYMSS--SLYEYEDATEEAAREVIAKAAEDGVTLEAFDNWFD	211
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	IRAVPTIDRSG-----NLFFDY--EKYSSYETAARETFDSILP--NRISVESFSSWYD	478
TR	A0A514D1L9	A0A514D1L9_9VIRU	RRGKLEIGTLANG-MRYLHYDTDGQYTRYMSVLTKQSFEALIK--EKTHAESFRHWFS	522
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	IRGIPKFDST--TK--QIYFDE--DAWTTMIKEVSREVVSELLE--RKVALTPFHKWYD	488
TR	D0T230	D0T230_9VIRU	IRGVPVLEG-----H--SLTFSS--SLYNQYEDVAIKQSFDDLLP--PVVQLEPFQWYN	455
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	IRAVPAIDATG-----KLVDY--EKYSLYETAARETFDSILP--SKISVESFASWYD	478
			*. : : :	

1c1	ORF1		SRLFWGASGGAPGAQVEWED-----GTRLRNLKRGALLGLKERQIRIDILD	398
TR	H6UNN2	H6UNN2_9VIRU	TRNYWASGGAPGAKITWEN-----SKEKYRVNKRKALLPKSRIRELLN	453
TR	H6UNN0	H6UNN0_9VIRU	ARAYWASGGAPGAKVTWDE-----SKEKLRNLKRGALLALREQIRIDLVF	475
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	NRMFWASGGAPGASVHWDD-----TKEKLRVNKRKALLSLKEQKVRNILE	406
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	NRMFWASGGAPGASVHWDD-----TKEKLRVNKRKALLSLKEQKARNILE	384
TR	A0A514DCG4	A0A514DCG4_9VIRU	NRMWWSASGGAPGATITWQD-----TKEKLRNLKRGALLAISEGDIRRVLA	389
TR	A0A346P9C2	A0A346P9C2_9VIRU	RRFFWGPPSGGAPGAKVSWTYASG-----ASDNFRLNKRKALLAIPFSQVQEILR	494
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	RRMFWSASGGAPGAKITWSDREG-----GDKLRNLKRGALLAIPAMHFTKILE	531
TR	A0A7L9R691	A0A7L9R691_9VIRU	RRMFWSASGGAPGAKITWSDREG-----GDKLRNLKRGALLAIPAMHFTKILE	531
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	RRMFWSASGGAPGAKIAWSDKNG-----GDAMRVNKRKALLAIPAAHFTNILE	531
TR	I1Y9U5	I1Y9U5_9VIRU	RRMFWSASGGAPGAKIAWSEKNG-----GDAMRVNKRKALLAIPAAHFTNILE	531

TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	RRMFWGASGGAPGAKIAWSEKNG-----GDAMRVNKRGALLAIPAAHFTNILE	531
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	RRMFWGASGGAPGAKIAWSEKNG-----GDAMRVNKRGALLAIPAAHFTNILE	531
TR	A0A7S5WL9	A0A7S5WL9_9VIRU	RRMFWGASGGAPGASIQWKK-----DNEKLRVNKRGALLNIPIDYIRKIMD	445
TR	A0A7S5WL9	A0A7S5WL9_9VIRU	RRMYWGASGGAPGATITWKK-----NDEKLRVNKRGALLSIPRDYIRKVMN	383
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	RRMFWAPSGGAPGAKLDWLTGDTERASLQQNRPDESRYLNKRGALLSLSLNDLKNTLS	485
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	RRMYWGASGGAPGATITWRK-----NNEKLRVNKRGALLSIPKDYIKVMG	491
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	RRMFWAPSGGAPGAKLDWLTGDTERASLQQNRPDESRYLNKRGALLSLSLNDLKNTLS	485
TR	A0A515KU26	A0A515KU26_9VIRU	RRMFWGASGGAPGATIQWKE-----NNEKLRVNKRGALLSIPVEYMRKIIS	445
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	RRMYWGASGGAPGATITWKK-----NDEKLRVNKRGALLSIPKDYIRKVMN	257
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	RRMYWGASGGAPGATITWRK-----NDEKLRVNKRGALLSIPRDYIRKVMN	257
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	RRMFWAASGGAPGAKVTWTHSSDPQDSSDHEGNSREKLRINKRGALLAIPKHFMMKVL	538
TR	A0A514D1L9	A0A514D1L9_9VIRU	RRMFWGASGGAPGAKVTWKD-----DEKLRLNKRGALLAIPYRVEKLWK	567
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	RRMFWGASGGSPGTIANWST-----GERLRLNKRGALLVTPEKSIRGMWD	533
TR	D0TZ30	D0TZ30_9VIRU	RRMFWAASGGSPGSKITWNIQQA-----ESKMRLNKRGGALLAIPAAHFRSILE	503
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	RRMFWAASGGAPGAKVTWTHQTQSD--LERADLNSKEEKLRLNKRGALLAIPKHFMMKVL	537

1c1 ORF1	GQHNSARISNHLRRLDDLDSKNVGMWDYSDFNINHTFILMAQHTLAMVEGLIRRGKTSGI	516
TR H6UNN2 H6UNN2_9VIRU	GHSNSARIANQLRRIADLKENVGFMWDYADFNINHAYYLISDLLLARI EAVLSRAREP--	571
TR H6UNN0 H6UNN0_9VIRU	GHSNPARIANQLRRLADLSHSGVMWDYADFNINHNFI LMAEELIARIDVMLERCTSP--	593
TR A0A7G4WLZ5 A0A7G4WLZ5_9VIRU	THDNPSRIANAMRRILDLKQRPGLMWDYADFNLNHTFFLMSQEY LARVEVLLERCDSH--	522
TR A0A1P8DF89 A0A1P8DF89_9VIRU	THDNPSRIANAMRRILDLKQRPGLMWDYADFNLNHTFFLMSQEY LARVEVLLERCDSH--	500
TR A0A514DCG4 A0A514DCG4_9VIRU	AHDNTARVANMLRRILEDLRS SHALMWDFADFNINHTFSDAQELYSVADVAERLSNE--	500
TR A0A346P9C2 A0A346P9C2_9VIRU	SHGNTARIANALRRISDLK RTPALMWDYADFNINHTLRMMLYTHTVRVMLLRLKYD--	606
TR A0A0A7DRW1 A0A0A7DRW1_9VIRU	ANAGAARLAAHARRLEALRHSVGMWDFADFNINHTFVGMEKLF SALSRELLARQYS--	642
TR A0A7L9R691 A0A7L9R691_9VIRU	ANAGAARLAAHARRLES LRHSVGMWDFADFNINHTFVGMEKLF SALSRELLTRAQYA--	642
TR A0A0S4GAY8 A0A0S4GAY8_9VIRU	ANAGAARLAAHANRLQMLRTQVGMWDFADFNINHTFTGMEKLF SALSARELLQRAKYS--	642
TR I1Y9U5 I1Y9U5_9VIRU	ANAGAARLAAHANRLQALRTQVGMWDFADFNINHTFSGMEKLF STLARELLRRARYS--	642
TR A0A7G3W8V5 A0A7G3W8V5_9VIRU	ANAGAARLAAHASRLHALRTQVGMWDFADFNINHTFSGMEKLF SALSARELLRRARYS--	642
TR A0A0S4GA48 A0A0S4GA48_9VIRU	ANAGAARLAAHANRLQALRTQVGMWDFADFNINHTFTGMEKLF ATLARELLRRARYS--	642
TR A0A7S5WL9 A0A7S5WL9_9VIRU	AHGLTARIANMLRRSEELRQHALMWDFSDFNINHTFRGMIKLYHVVSQVLLERGABA--	556
TR A0A7S5WL9 A0A7S5WL9_9VIRU	AHDMTARIANAYRRIGE LEHNLGLMWDFADFNINHTFSGMIKLFNVTVKVLQERGEHA--	494
TR A0A2Z5WAE4 A0A2Z5WAE4_9VIRU	AHGNTTRLANSLRRLSDLT-RTSLMWDYADFNINHTIKQMQLLYYASVS VLLERSETL--	596
TR A0A7S5WLX4 A0A7S5WLX4_9VIRU	AHDMTARIANTYRRIGELERYHGLMWDFADFNINHTFRGMIKLFNVTVKVLQERGEHA--	602
TR A0A3G8GGF4 A0A3G8GGF4_9VIRU	AHGNTTRLANSLRRLSDLT-RTALMWDYADFNINHTIKQMQLLYYASVS VLLERSETL--	596
TR A0A515KU26 A0A515KU26_9VIRU	AHGLTARVANMLRRTEELKTAHALMWDFSDFNINHTFRGMMLKLFNVVCDVLVERGABA--	556
TR A0A7S5WLW5 A0A7S5WLW5_9VIRU	AHDMTARIANAYRRIGE LEHNLGLMWDFADFNINHTFTSGMIKLFNVTVKVLQERGEHA--	368
TR A0A0M5KKP5 A0A0M5KKP5_9VIRU	AHDMTARIANAYRRIGE LERNHGLMWDFADFNINHTFSGMIKLFNVTVKVLQERGEHA--	368
TR A0A2Z1Q3S4 A0A2Z1Q3S4_9VIRU	SNSGLPKIMGHVRR LKALKNQVGCMDYADFNINHTFEGMRLLYETLTAALLKRIDWK--	649
TR A0A514D1L9 A0A514D1L9_9VIRU	GHSTSGRIANAIRRLSDVKLRTPLMWDYSDFNINHTYVNMALGYLYTGKVIINRMVIP--	683
TR A0A2Z1Q375 A0A2Z1Q375_9VIRU	KHHSAARVANHIRRLEDLQSGVATMDFSDYLNLEHTFPQMLA IMKSAL EEMVARGRDD--	644
TR D0TZ30 D0TZ30_9VIRU	ANAGFTKLTAHVERLQKLKCEVGLMWDFADFNINHTFDGMIKLF SALSARDNLLKRSRST--	614
TR A0A1B4ZA62 A0A1B4ZA62_9VIRU	SNSGLPKIMGHVRR LKALKTQVGCMDYADFNINHTFEGMRLLYETLTAALLKRIDWK--	648

1c1 ORF1	TPERMR--VISRDLHKAAAYTVIARFNTYLHDHD-SQLTIKTARGLQSGERQTSRINSDC	573
TR H6UNN2 H6UNN2_9VIRU	SPARLQ--TVGADLNACAAFLVILARYNTYLYDHD-TDVAIRSMRGLQSGERDTSRVNSDA	628
TR H6UNN0 H6UNN0_9VIRU	SGKELE--TLKKELYNCAFTVTARFNTYLSND-TGIVTQAKRGLQSGERDTSRVNSDS	650
TR A0A7G4WLZ5 A0A7G4WLZ5_9VIRU	LPMDVQN-TIRADMRAATAYAILARYNTYLHDPE-TMITTQAVRSLQSGERGTSINSDS	580
TR A0A1P8DF89 A0A1P8DF89_9VIRU	LPMDVQN-TIRADMRAATAYAILARYNTYLHDPE-TMITTQAVRSLQSGERGTSINSDS	558
TR A0A514DCG4 A0A514DCG4_9VIRU	NTSDLSRNIVRQDLSRVALHIVNARHNTYLSSTGGADPIIRAVRSLQSGERGTSFTNSMS	560
TR A0A346P9C2 A0A346P9C2_9VIRU	IPSRTLA-QIRQDFTDTRLXRTLNARNNTYLIDND-SDVIVRAQRSLQSGERGTSSTNSFF	664
TR A0A0A7DRW1 A0A0A7DRW1_9VIRU	NNPASTQ-KAARDIKQITSWVNAARHKTYLSND-SHAVLEIKRSLQSGERATMWNTLR	700
TR A0A7L9R691 A0A7L9R691_9VIRU	NNPAATQ-KAARDIKQITSWVNAARHKTYLSND-TQAILEIKRSLQSGERATMWNTLR	700
TR A0A0S4GAY8 A0A0S4GAY8_9VIRU	NGPQHTQ-QAAQDIKQITAWVNAARHKTYLSND-TKAVLEIKRSLQSGERATMWNTLR	700
TR I1Y9U5 I1Y9U5_9VIRU	NGPQHTQ-QAAQDIKQITAWVNAARHKTYLSND-TKAVLEIKRSLQSGERATMWNTLR	700
TR A0A7G3W8V5 A0A7G3W8V5_9VIRU	NGPQHTQ-QAARDIKQITAWVNAARHKTYLSND-TKAVLEIKRSLQSGERATMWNTLR	700
TR A0A0S4GA48 A0A0S4GA48_9VIRU	NGPHHTQ-QAAQDIKQITAWVNAARHKTYLSND-TKAVLEIKRSLQSGERATMWNTLR	700
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	TPPHIYE-AAKNNDINTATAWIKQARERTYVQDND-TGFVSKLVRSLSQSGERGTSFTNSMR	614
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	TPPHIYV-SAKEDLESALKWVRVARDNTYVKDND-TGFVSKLVRSLSQSGERATSFVNAMR	552
TR A0A2Z5WAE4 A0A2Z5WAE4_9VIRU	TSQGLVK-QIWNMDLDALKFSMDAKGAAYLHSAL-AKLTVLAARSLQSGERATSYVNSMS	654
TR A0A7S5WLX4 A0A7S5WLX4_9VIRU	TPPHIYT-NAVEDLGSALKWIRVARENTYVKDND-TGFISKLVRSLSQSGERATSFVNAMR	660
TR A0A3G8GGF4 A0A3G8GGF4_9VIRU	TSQGLVK-QIWNMDLDALKFSMDAKGAAYLHSAL-AKLTVLAARSLQSGERATSYVNSMS	654
TR A0A515KU26 A0A515KU26_9VIRU	TPKHIYE-AARKDIKAATAWILKARERTYVQDND-TGYISKLVRSLSQSGERGTSFTNSMR	614
TR A0A7S5WLW5 A0A7S5WLW5_9VIRU	TPPHIYV-SAKEDLESALKWVRVARDNTYVKDND-TGFVSKLVRSLSQSGERATSFVNAMR	426
TR A0A0M5KKP5 A0A0M5KKP5_9VIRU	TPPHIYV-SAKEDLESALKWVRVARDNTYVKDND-TGFVSKLVRSLSQSGERATSFVNAMR	426
TR A0A2Z1Q3S4 A0A2Z1Q3S4_9VIRU	NTPGDTQ-EAYNDIKRISSWVVRARLSTYVQDND-TGNIMKLARSLQSGERGTSFTNTLR	707
TR A0A514D1L9 A0A514D1L9_9VIRU	RNSKLYE-EIVDNISDDIRYIIQARFNTYLADDE-LGIMVKAVRSLQSGERATSDINTTQ	741
TR A0A2Z1Q375 A0A2Z1Q375_9VIRU	TMPTDYA-DAVGDLAAGDYVMTARARTFLNDKL-SGLVVRIVRGLQSGERSTSFNTLC	702
TR D0TZ30 D0TZ30_9VIRU	GTP-MYE-EAVNDITTTIKWVEAARSNTFISDND-AGNIAQVVRSLQSGERATSWINTLR	671
TR A0A1B4ZA62 A0A1B4ZA62_9VIRU	NTPGDTQ-EAYRDIKRISSWVVRARLSTYVQDND-SGNIMKLARSLQSGERGTSFTNTLR	706

: : * : : : * . * * * * * * * :

1c1 ORF1	NYIDTLFVRLVSKRFFGYDVL-NPVADHSGDDAFETTKNYSOGMFAALYNLTGAAGQAH	632
TR H6UNN2 H6UNN2_9VIRU	NRVDTEIVQMLGKKILGYTLL-KPHIDASGDDAFELTNSVSDAMYASALYNLTGAAGQVH	687
TR H6UNN0 H6UNN0_9VIRU	NDIDTRIVRHISKRMGLGYDCI-HPIVDESDDAFETTASLSDAMLASSLYNLGSAAGQVY	709
TR A0A7G4WLZ5 A0A7G4WLZ5_9VIRU	NETDTTIVRRVCKEMLGIDPI-VSVTDHAGDDAFENVISMTYAPLVCVSYNLGSAAGQAY	639
TR A0A1P8DF89 A0A1P8DF89_9VIRU	NETDTTIVRRVCKEMLGIDPI-VPVTDHAGDDAFENVISMTYAPLVCVSYNLGSAAGQAY	617
TR A0A514DCG4 A0A514DCG4_9VIRU	SEIDYQLVVYVLNEMLGINLRSSSRGDKLGDDVFPVPNMFTAILVCIVYNLTGAAGQLY	620
TR A0A346P9C2 A0A346P9C2_9VIRU	NKVDASIVRETGRLLGYDLL-PFASDKLGDDDFETVGHLLDAIYACSLFNLGSAAGQIX	723
TR A0A0A7DRW1 A0A0A7DRW1_9VIRU	NNVDHRIVSLASEQLFGYDLA-PDAGDKTGDDVFLTTRTVGDAVLMSAMYNLCAAGQAH	759
TR A0A7L9R691 A0A7L9R691_9VIRU	NNVDHRIVSLASEQLFGYDLA-PDAGDKTGDDVFLTTRTVGDAVLMSALYNLCAAGQAH	759
TR A0A0S4GAY8 A0A0S4GAY8_9VIRU	NNVDHRIVSLAAEKLFGYDLA-PQPGHKTGDDVFLTKTVGDAVLMSALYNLCAAGQAH	759
TR I1Y9U5 I1Y9U5_9VIRU	NNVDHRIVSLAAEKLFGYDLA-PQSGHKTGDDVFLVTKTVGDAVLMSALYNLCAAGQAH	759
TR A0A7G3W8V5 A0A7G3W8V5_9VIRU	NNVDHRIVSLAAEKLFGYDLA-PQPGHKTGDDVFLTKTVGDAVLMSALYNLCAAGQAH	759
TR A0A0S4GA48 A0A0S4GA48_9VIRU	NNVDHRIVSLTAEKLFGYDLA-PQAGHKTGDDVFLTKTVGDAVLMSALYNLCAAGQAH	759
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	NHIDFLIVKKTGSELFNTNFL-SQKGDQKQDDVFLPTKNMKEAVLACALYNITGSAGQLS	673
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	NHIDYLIVRKTAHNLF SRPFL-QKKGDKQKQDDVFLPVKNAVEATLACAIYNITGAAGQLS	611
TR A0A2Z5WAE4 A0A2Z5WAE4_9VIRU	NEVDTEIVKDTARRVLGMEVF-TGANDKLGDLDLFGTCSTMWEAVLTSALYNLTGSAGQVY	713
TR A0A7S5WLX4 A0A7S5WLX4_9VIRU	NHIDYLIVRKTAHNLF SRPFL-QKKGDKQKQDDVFLPVNAVEATLACAIYNITGAAGQLS	719
TR A0A3G8GGF4 A0A3G8GGF4_9VIRU	NEVDTEIVKDTARRVLGMEVF-TGANDKLGDLDLFGTCSTMWEAVLTSALYNLTGSAGQVY	713
TR A0A515KU26 A0A515KU26_9VIRU	NHIDYLIVRKTGSELFNTNFL-TRKGDQKQDDVFLPTKMDKEAVLACALYNITGSAGQLS	673
TR A0A7S5WLW5 A0A7S5WLW5_9VIRU	NHIDYLIVRKTAHNLF SRPFL-QKKGDKQKQDDVFLPVKNAVEATLACAIYNITGAAGQLS	485
TR A0A0M5KKP5 A0A0M5KKP5_9VIRU	NHIDYLIVRKTAHNLF SRPFL-QKKGDKQKQDDVFLPVKNAVEATLACAIYNITGAAGQLS	485
TR A0A2Z1Q3S4 A0A2Z1Q3S4_9VIRU	SNIDHGINVRAAALFGRPLT-HTQGDKTGDDVFLTRTMRDALLCALFNLTGSAAGQVY	766
TR A0A514D1L9 A0A514D1L9_9VIRU	NDIAVRLMDDASKRLFGFSVI-HSVGDRAGDDAFLTAKSLLYGSLCALFNLTGSAAGQVY	800
TR A0A2Z1Q375 A0A2Z1Q375_9VIRU	NKVD SVMVDRVAEQLFGRRLI-THQGDRLGDDVFLPVKNADMKDSILMCALFNLLGSSGQLY	761
TR D0TZ30 D0TZ30_9VIRU	NHVDHVIQQASHNLF GYNVS-PTQGYKTGDDVFLTPVSMQDALLTCAMYNLCGAGQVS	730
TR A0A1B4ZA62 A0A1B4ZA62_9VIRU	SNIDHGINVRTAAALFGRPLT-YTQGDKTGDDVFLVTRTMRDAILLCSLFNLGSAAGQVY	765

. : : . . * * * . . : : : * : *

1c1 ORF1	KILMSYP-----SRG-GGLGEYLRLAYDAANRKCVCYPIRAMMGLIHGE	675
TR H6UNN2 H6UNN2_9VIRU	KVSICRP-----TAG-GAEGEFLRLHYDARTHSVSGYPPIRAMVGFSGHGE	730
TR H6UNN0 H6UNN0_9VIRU	KISVSLP-----SYG-GAAGEFLRLPPAANRNRGRDPNRAVGGFSGHGE	752
TR A0A7G4WLZ5 A0A7G4WLZ5_9VIRU	KIAVSYA-----TFN-GASGEFLRLSYDAASNHIAGYPIRGMGFIHGE	682
TR A0A1P8DF89 A0A1P8DF89_9VIRU	KIAVSYA-----TFN-GASGEFLRLSYDAASNHIAGYPIRGMGFIHGE	660
TR A0A514DCG4 A0A514DCG4_9VIRU	KITNDYS-----DQV-GARGEYLRAYDAATPRVTGYPIRAMMGVIHGE	663
TR A0A346P9C2 A0A346P9C2_9VIRU	KILVEWV-----GKR-GSQGEYLRQNYDAATPTICGYPLRAMMGLIHGE	766
TR A0A0A7DRW1 A0A0A7DRW1_9VIRU	KILLSYP-----QHG-GARGEYVRYAYDASANRVSGYPLRALAGVVHGE	802
TR A0A7L9R691 A0A7L9R691_9VIRU	KILLSYP-----QHG-GARGEYVRYAYDASANRVSGYPLRALAGVVHGE	802
TR A0A0S4GAY8 A0A0S4GAY8_9VIRU	KILLSYP-----QHG-GARGEYVRYAYDASANRVSGYPLRALAGVVHGE	802
TR I1Y9U5 I1Y9U5_9VIRU	KILLSYP-----QHG-GARGEYVRYAYDASANRVSGYPLRALAGVVHGE	802
TR A0A7G3W8V5 A0A7G3W8V5_9VIRU	KILLSYP-----QHG-GARGEYVRYAYDASANRVSGYPLRALAGVVHGE	802
TR A0A0S4GA48 A0A0S4GA48_9VIRU	KILLSYP-----QHG-GARGEYVRYAYDASANRVSGYPLRALAGVVHGE	802
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	KITNDYS-----KPK-GARGEYLRAYDASHARTVSGYPIRAMMGVIHGE	716
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	KITNDYH-----KPE-AARGEYLRAYDGRNRIVSGYPIRAMMGVIHGE	654

TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	KLTMEYG-----GDI-SSYGEYLRLSYDQNNVTVTGYAPRAMMGFIHGE	756
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	KITNDYH-----QPE-AARGEYLRYAYDGKSRIVSGYPIRAMMGVIHGE	762
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	KLTMEYG-----GDI-SSYGEYLRLSYDQNNVTVTGYAPRAMMGFIHGE	756
TR	A0A515KU26	A0A515KU26_9VIRU	KITNDYS-----KPK-GARGEYLRYAYDANANTVSGYPIRAMMGVIHGE	716
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	KITNDYH-----KPE-AARGEYLRYAYDGRSRIVSGYPIRAMMGVIHGE	528
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	KITNDYH-----KPE-AARGEYLRYAYDGRTRIVSGYPIRAMMGVIHGE	528
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	KVLVSYP-----QLG-GARGEVFRYGYDASSGAVRGYPIRALSGFVHGE	809
TR	A0A514D1L9	A0A514D1L9_9VIRU	KINMNAIRNNALGSISTINSDRLISS-AGSGEFLRLSYDGATNEICGYPLRAMMGFIHGE	859
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	KITSEYC-----SPKNPGRGEFLRHSYDGASGRVSGYPIRAIVGFVHGE	805
TR	D0TZ30	D0TZ30_9VIRU	KIFVSYP-----ELG-GSRGEFVRGYDAGSNSVRGYPLRALTGLVHGE	773
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	KVLVSYP-----QLG-GARGEVFRYGYDASSGAVRGYPIRALSGFVHGE	808

* : . * : : * . * * : * . ***

lc1	ORF1	FFSNPIQPNERAAAFNLQAQKLRRRGFNVPDKLLKSIINANCFLVYTSDSGVKFTYRPN	735	
TR	H6UNN2	H6UNN2_9VIRU	YFNEPVPQPAQRYAAFINQRAKLTRRGWSCPGPLFDAVVRKHTKLVTY-DSGIRHIYTPN	789
TR	H6UNN0	H6UNN0_9VIRU	VFSEPVQPAPERMAAFISQKQLSRRGWCHPCDALFQALVRVNCRLRRTLRSKGIIITFVPD	812
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	FFAEALPQPFDRLASFLNQRNKLQRRGWVAPESLFHAVCRYNTRLTYTLPDGTKRHFYPD	742
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	FFAEALPQPFDRLASFLNQRNKLQRRGWVAPDSLFNAVCRYNTRLTYTLPDGTKRHFYPD	720
TR	A0A514DCG4	A0A514DCG4_9VIRU	FFSEPIPKPVERAATFIEQFSKLARRGWHPPTLLDNI IKRNCHVTYTAN-GLKRRVVPN	722
TR	A0A346P9C2	A0A346P9C2_9VIRU	FFSDPIQPFPNRTATLMQVAKLSRRGFTTPTRLINIWLKDNAALVYTNRQGVKKRIVGD	826
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	FFTEPVTNPADRGATLIQQFAKVARRGVVLPDALLDMMLNASVSLAYTDS-KGKHRVTV	861
TR	A0A7L9R691	A0A7L9R691_9VIRU	FFTEPVTNPADRGATLIQQFAKVARRGVVLPDALLDIMLDASVSLAYTDS-KGKHRVTV	861
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	FFTEPVTNPADRGATLIQQFAKVARRGVVLPDALLDAMLAKSTSLTYTKQ-GSKCRVTIP	861
TR	I1Y9U5	I1Y9U5_9VIRU	FFTEPVTNPADRGATLIQQFAKVARRGVVLPDALLDAMLAKSTSLTYTQ-RKKCRVTIP	861
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	FFTEPVTNPADRGATLIQQFAKVARRGVVLPDALLDAMLVKSTSLTYTSD-GKKSHVTIP	861
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	FFTEPVTNPADRGATLIQQFAKVARRGVVLPDALLDAMLAKSTSLTYTQ-RKKCRVTIP	861
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	FFDEPIPKPLERAATFVEQFEKLRRRGWTPPKTLLDRAIKRNCHLVYTDG-GVKNRVVTP	775
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	FFDEPIPKPLERAATFMEQFAKLQRRGWIPPKTLLERI IKRNCHLVYTHE-GVKNRVVTP	713
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	YMLDSVVTPIERTATILEQLNKLKRRGWCPPDHLVDSIVARNTSLVYTDKDGKHHVIGD	816
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	FFDEPIPKPLERAATFMEQFAKLQRRGWIPPKTLLERI IKRNCHLVYTDN-GTKNRVVPK	821
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	YMLDSVVTPIERTATILEQLNKLKRRGWCPPDHLVDSI IARNTSLVYTDKDGKHHVIGD	816
TR	A0A515KU26	A0A515KU26_9VIRU	FFDEPIPKPLERAATFVEQFEKLRRRGWTPPDTLLEAIKRNCHLVYTTG-SGKKKVVD	775
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	FFDEPIPKPLERAATFMEQFAKLQRRGWIPPKTLLERI IKRNCHLVYTHE-GIKNRVVP	587
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	FFDEPIPKPLERAATFMEQFAKLQRRGWIPPKTLLERI IKRNCHLVYTHE-GIKNRVVP	587
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	FFHDIHSPAERGAAILEQYAKLTRRGIHLPRGILESYLARATQLVYTQ-GVKHRVNVP	868
TR	A0A514D1L9	A0A514D1L9_9VIRU	FFAEPIDPPSRAATLLEQVSKLHRRGWHTPDWLFVKFSTCTLVFTTDAGIKKRFTPD	919
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	FFSEPLPAIYDRAATILEQVAKIQRGCTLPMSLVNESIRFNCRITKTLDGSIKKTIVAD	865
TR	D0TZ30	D0TZ30_9VIRU	YFNDPIISPADRCATILEQSKKLARRGIVVPKPIVSRLISKNCITLYSEG-NRKIRTTVP	832
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	FFHDIHSPAERGAAILEQYAKLTRRGIHLPKQVLESYLAATQLVYTDK-GSKHRVNVP	867

: : : . * * : : * * : * * * : : : : :

lc1	ORF1	LTLTVLPSILGGVGVQEDDKSL-VTAQLPISFK--Y--GRDGLSCVAISPL---LCDL	786	
TR	H6UNN2	H6UNN2_9VIRU	PRLVTLPSAMGGFVGYDAKEL-VSGCSPPYEI--T--WRTRKYTALFIPSGEGKTTLAR	844
TR	H6UNN0	H6UNN0_9VIRU	PRLVQLPAAFGGIGIQYKDKNM-IVDSHKPYRV--H--SPARRVDCFYIPSGEGKTMLSM	867
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	IETVLTAAFGGVGVDTVDSQL-LSQLSDKQIV--TPLHANCYDTIIPSGEGKTTLAR	799
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	IETVLTAAFGGVGVDTVDSQL-LSQLSDKQIV--TPLHANCYDAIIVIPSGEGKTTLAR	777
TR	A0A514DCG4	A0A514DCG4_9VIRU	LELTVTAAALGGVGVTTETLEANIVTESFSGSRADSRSTAATDCTLALCIPSGEGKTSLSV	782
TR	A0A346P9C2	A0A346P9C2_9VIRU	IHLATLPAVLGGIGITEAKDAVMVSTSNLLNIK-PPIQVAANTPVAVCIPSGEGKSTIAR	885
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	RQLIALPAALGGVGVTTETNGILHSELSPVHR-----QANGSYAICIPSGEGKTTLAR	914
TR	A0A7L9R691	A0A7L9R691_9VIRU	RQLIALPAALGGVGVTTETANGILHSETSPVLR-----QVNGSYAVCIPSGEGKTTLAR	914
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	RALIALPAALGGVGVTTETSGMLDASVVNT-----IMQDAFAICIPSGEGKTTLAR	914
TR	I1Y9U5	I1Y9U5_9VIRU	RDLIALPAALGGVGVTTETNGMLSAEESTTRT-----VMRDAFAICIPSGEGKTTLAR	914
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	RDLIALPAALGGVGVTTETSGMLSSDDSTIRT-----VMRTAFAICIPSGEGKTTLAR	914
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	RDLIALPAALGGVGVTTETNGMLSSDDSTIRT-----VMQEAFAICIPSGEGKTTLAR	914
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	KELVTLPSVFGGIGVTNTIDGKNLVQAHWNVAG-TLVPEKRDGYFAIYIPSGEGKSTIAK	834
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	LELVTLPAIFGGIGVTETISGAEMVQSQIPPLL-KNTLQELSGYIAVYIPSGEGKTTLAK	772
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	KRLAITPAIFGGIGVTQTQDAEIVSAGAGGLIR-P---VNAKSVALIIPSGEGKTYTAM	871
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	LELVTLPAIFGGIGVTETISGAEMVQSQVPPQL-TNTLQELGYIAIYIPSGEGKTTLAK	880
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	KKLAITPAIFGGIGVTQTQDVEIVSAGAGGLIR-P---VNAKPVALIIPSGEGKTYTAM	871
TR	A0A515KU26	A0A515KU26_9VIRU	IELVTLPSAAGGIGVTNTIDGKNMTQTHWDVRG-AIVPPSRNGYIAVYIPSGEGKSTIAK	834
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	LELVTLPAIFGGIGVTETISGAEMVQSQIPPLL-TNTLQELSGYIAVYIPSGEGKTTLAK	646
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	PELVTLPAIFGGIGVTETISGAEMVQSHTPPLL-TNTLQELSGYIAVYIPSGEGKTTLAK	646
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	LDLILTPAALGGVGISYNPSGLLSSVSGSSISE-----LQPIKAAIIPSGEGKTTLAQ	921
TR	A0A514D1L9	A0A514D1L9_9VIRU	LQLVTMPRAFGG-----	931
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	PLLALTAAFGGIGVTRAQESQALITGGGSIIS--VANDTDDHRYAFLIPSGEGKSSLAR	923
TR	D0TZ30	D0TZ30_9VIRU	PELVELPAALGGVGVTDQLDARLVTASSSLD-----LGLPEQRWAICIPSGEGKSTLAA	887
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	LELILTPAALGGVGISYNPSGLLSSVEGSTRE-----LQPIQAAILIPSGEGKTSLSR	920

* : **

lc1	ORF1	RYESLSHTIDFVTLDDVIYKVANITGLTEQCICKGNWDQYYALGRVYYTRYITGLKSSSV	846	
TR	H6UNN2	H6UNN2_9VIRU	QYP-----DLFIDHDTFVNDLILHPLRSEAFKSGDWKPVNAYLRNVIRIMIGDSG-SIL	897
TR	H6UNN0	H6UNN0_9VIRU	RHP-----TLFADHDSIVSAERLEGLRALAMETGDWSPTNAYLASCADLWAQAADVAEL	921

TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	RYP-----DIFIDHDSLVSINLALRSKAVSSGNWEPLNAYLRAEGERYMS-----	846
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	KYP-----DIFVDHDSLVSINLIALRSRAVSSGNWEPLNAYLRGEGERYMS-----	824
TR	A0A514DCG4	A0A514DCG4_9VIRU	KFP-----DTFYDHESAVDGTVLNALKQDAANTGDWNKLNRYLRNAVSET-----	827
TR	A0A346P9C2	A0A346P9C2_9VIRU	NYS-----IFIDHDSLIDQEFLDGLKEQAALTGSWNLVNRYLRRAEECE-----	930
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	RYP-----SLFADHDDYATA-HIRHLVKEARETGQYDKLNLAWRNAPIP-----	957
TR	A0A7L9R691	A0A7L9R691_9VIRU	RYP-----SLFVDHDDYADL-HIKKLLTEAKETGQYDKLNSAWRDAPVP-----	957
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	RYP-----DLFIDHDDCSTP-LHELKRRQALYTGQYDELNAAWRNVTYD-----	957
TR	I1Y9U5	I1Y9U5_9VIRU	RYP-----ELFVDHDDYSTP-EHEIKRKQAVYTGQYDELNAAWRNITYD-----	957
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	RYP-----ELFADHDDYSTP-ELEAKRRKAMYTQYDELNAAWRNVDYD-----	957
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	RYP-----DLFVDHDDYSTL-EHEIKRKQAAVYTGQYDELNAAWRNIVYD-----	957
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	RIGH----PDLVDHDSL-VGPAFEGRLARANITGDWKPVNAYLRDLT--R-----	878
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	KLQK----Q-VAVDHDEL-VGPAFLALRDNASLTGDWKPVNRYLRDCA--R-----	815
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	RYSG-----FAIDHDSLVDETIARPLREHANLTGDWKPVNKYLRHVANEFL-----	916
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	KLKG----M-VALDHDEL-VGPAFLSLRERASSTGDWKPVNRYLRCA--R-----	923
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	RYSG-----FAIDHDSLVDETIARPLREHANLTGDWKPVNKYLRHVADFL-----	916
TR	A0A515KU26	A0A515KU26_9VIRU	RIGH----PSVVIDHDSL-VGPAFEVVIKAKATLTGDWKPVNAYLRSLT--V-----	878
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	KLGR----L-VAVDHDEL-VGPAFLALRENASLTGDWKPVNRYLRDCA--R-----	689
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	KLGH----Q-VAVDHDEL-VGPAFLALRECASTGDWKPVNKYLRDCA--R-----	689
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	SHP-----EYFVDHDLISLTDLAILKADAVATGHWQKVNAYLRSVSP-----	965
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	LYP-----NLFVDHDDLISVPYFQELRANAVLTGTWKPVNNTYLRSLVPSR-----	968
TR	D0TZ30	D0TZ30_9VIRU	KYP-----TLFIDHDSLGLP-QFHELLRVATMSGQWRALNSYLKSIVPE-----	930
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	MYP-----EYFVDHDLISACDLEILRADAVSTGHWEKVNYSYLRSVTP-----	964

lc1	ORF1	---	NSSRVIIASNHLAML-KNN--GFVLAYTSNTRTGDREFKQHAQNYLERLGSG----	V	895
TR	H6UNN2	H6UNN2_9VIRU	NGPFGPKVILTWGPDITPQNIT--GVALLLK--DLTGLRANVA--NRASILRSV----	P	946
TR	H6UNN0	H6UNN0_9VIRU	DGFSQRPILLTWGPDTPVKHFT--GYGLLLK--QLTGLRANKA--NRRSLMASG----	C	970
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	--VNRSKILLTWPSTAPKKSR--ICALLQ--QPVGRLANIA--NRSSIINDM----	N	893
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	--VNRGKILLTWPSTAPSRSR--ICALLQ--QPVGRLANIA--NRSSIMNDM----	N	871
TR	A0A514DCG4	A0A514DCG4_9VIRU	--DLNRNVLLTWAIDTVPAFIK--SKIGMLK--DGTALRANIA--NRKAIRAS-----		873
TR	A0A346P9C2	A0A346P9C2_9VIRU	DVMLGRRVLLTWSKDTAPVGSR--TYGFLT--RGTGLRANKA--NRATLTREF-----		978
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	----TDKVLTLWHPSTVPHGME-VLAACILS--KGTGLRANTA--NRAALRQAVRNHLLS		1008
TR	A0A7L9R691	A0A7L9R691_9VIRU	----KHKVLTLWHPNTVPHGTE-ILAACMLS--KGIGLRANAA--NRAALRQAVANNLLS		1008
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	----RTKILLTWHPTVPTGVK-VLAAAMLV--TGNGLRANKA--NRSALRQAVVNNLLG		1008
TR	I1Y9U5	I1Y9U5_9VIRU	----KSKILLTWHPTVPTGVK-VLAAAMLV--TGTGLRANKA--NRTALRQAVQHLLA		1008
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	----KSKILLTWHPTVPTGVK-VLTAAMLA--TGNGLRANKA--NRAALRQAVSQNLLS		1008
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	----KSKILLTWHPTVPAGVK-VLAAAMLV--TGNGLRANKA--NRTALRQAVQNLLA		1008
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	--GLKDVLLTWGPDTHSVGRIGELISILLR--KPTSLRANQA--NRRSIVKA-----		925
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	--GVTGRLLLTWGPDTAPAEGRIGEYTIMLR--KPTALRANKA--NRAALLKN-----		862
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	VNAHVPMKMLLTWSRDTAPIGIR--CFAAVLE--OPTGIRANIA--NRASVQREF-----		964
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	--GIKGRVLLTWGPDTPAENRLGEYTVMLR--KPTALRANRA--NRAALLKS-----		970
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	VHAHTPMKMLLTWSRDTAPIGIR--CFAAVLE--LPTGIRANIA--NRASVQREF-----		964
TR	A0A515KU26	A0A515KU26_9VIRU	--GLRDVLLTWGHETCDSDGRIGELISILLR--QPTSLRANKA--NRKAILKA-----		925
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	--GVTGRLLLTWGPDTAPAEGRIGEYTIMLR--KPTALRANRA--NRAALLKN-----		736
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	--GVTGRLLLTWGPDTAPAEGRIGEYTIMLR--KPTALRANRA--NRAALLKN-----		736
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	----PGKVLTLWSPETVPHDSL-VIGAFMLT--KPSGLRANAA--NRKSLMLAVQKGSLS		1016
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----		
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	----DRRILLTWSQQTVPHPNYR-VIAAFLLQ--QPSALRANIA--NRETILKTS-----		1013
TR	D0TZ30	D0TZ30_9VIRU	----DPRILLTWGPATIPSSRG--ILGAFLLA--RPSGIRANTA--NRKSIQDLATQGGLS		981
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	----VGKVLTLWAPETVPPGCE-VLGAFMLT--KPSGLRANAA--NRKSLVLAVNNGSIP		1015

lc1	ORF1	---	I-RVTNXXRKLVSLLHLEISSVAP-----	HPIGVIYP-YNTNPKPLPLYQAPRIQAKE	944
TR	H6UNN2	H6UNN2_9VIRU	KQSIHYKYNFAERNSAAVALCGPTG-----	EEVRVSYM-KFEAPSVPPRYAIFKGVDAAG	999
TR	H6UNN0	H6UNN0_9VIRU	P--YREFSTWYKRDAFALACVGGSA-----	TRATISYS-YESKIPLPVMQYPTHEAGQ	1021
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	KKYIHMFKNYSERDAYLMSITAGLT-----	G---LTYKVYQRTGDAIPKFNWPRVDSKD	944
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	KKYVHMFKNYSERDAYLMSITAGLT-----	G---LTYKVYQRTGDAIPKFNWPRVDSKD	922
TR	A0A514DCG4	A0A514DCG4_9VIRU	SMKVIEVDNHLQLQEQAFLAIEM-----	SNVADVLHLR-KYVADTAPPVYKWPTVPATQ	927
TR	A0A346P9C2	A0A346P9C2_9VIRU	GNKLSIQNFSELHANVIMLYCRL-----	LTANSWEVR-VFESSMPKPEYIKPKIDTVT	1031
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	KEKLKTFNSMAGLLAYATQATIERVDIVRSRTFAMVSND	-DHNKIGSLPMLNVPAGASS	1067
TR	A0A7L9R691	A0A7L9R691_9VIRU	KEKLKTFNTMGALLAYVTQTAIERIDVRSRTFAMVSND	-DHSKIGSLPMLNITPVGASS	1067
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	KKALRLYPNSRMFAELTQLAIEQVDIVRSRTFAMVSKQ	-NPNEVGTLPLMLRIEIPVGATS	1067
TR	I1Y9U5	I1Y9U5_9VIRU	KKALRVYPNSRMFAELTQLAIEQVDIVRSRTFAMVSKQ	-NHNDIGSLPMLRIEIPIGATS	1067
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	KKALKIYPNNRMFAEITQLAIEQVIDIIRSRTFAMVNKQ	-NFNEIGTLPLMKIEIPVGATS	1067
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	KKALRVYPNSRMFAEITQLAIEQVDIVRSRTFAMVSNQ	-NHNDIGSLPMLRIEIPIGATS	1067
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	GRNLEFSDSYSHTLAKVITVILKMRR-VIENGREKVTIR	-EFVSTRHPPQFTYPRVAASS	983
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	KRNLRLCDNWAQMFASVIDIVLTHGR-LEAATETQLKIQ	-VFESHKPKPKFMYPRIAATD	920
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	GKNVARFKSTQGISYAAKLYLQY-----	MSTNTYSVD-VFESTSQLPQYKLPKPATA	1017
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	KRNLRLCDNWAQMFACVVDIMLTHGR-LETPKETQLKVR	-IFESEYKPKPKFMYPRVAATD	1028
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	GKNAARFKSTQGISYAAKLYLQY-----	MSTNTYSVD-VFESTSQLPQYKLPKPATA	1017
TR	A0A515KU26	A0A515KU26_9VIRU	KRNIEFSDSYTHSLAKVMACVLKLN-RVTENGKELIKVR	-EFSSTKNTPTQFTYPRVAASA	983

TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	KRNLRLCDNWAQMFTSVIDIVLTHGR-LEAATETQMKIR-VFESEHKPKPFMYPRIAATD	794
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	KRNLRLCDNWAQMFASVIDIVLTHGR-LEAATETQMKIR-VFESEHKPKPFMYPRIAATD	794
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	RKVFKLCPNHGVLVKNALHCLSAY-AVQGGVVRTSF-VN-EDNVVKPLPRLQLPSLGAHK	1073
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	RRIVTFFPPTHQRLEIAAVNLANALTR----TSHTSTVIN-TRGALTTPPPTLTLRINDTRG	1068
TR	D0TZ30	D0TZ30_9VIRU	KDKLIIAQNHQORDRAILKLATQLLK-PGSKLRKRFDVK-DTGEVMRAPFFQFPRLPASE	1039
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	KKKFQMCATHGILTQKALHTLSAY-LIQGGIIRTSF-VD-ANDVVKPLPRLKPLTLGAHK	1072

1c1	ORF1		TIKSSKAQIPDIGVLYRFNVTR-IGPLYDDIAKSTLTGGWPKAAMNESLAEYGRALVEWE	1003
TR	H6UNN2	H6UNN2_9VIRU	ILRNTKTTLADYAVLNKYGVTE-TVALDREVVESSLGSAWPKQLMTDSLADYGRQLARWE	1058
TR	H6UNN0	H6UNN0_9VIRU	IIRRSKTVIPDFEKLTLSGVES-LTPVYADLLQSSFSGAWPKTELYDAIANYAGAMHEWQ	1080
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	LLRRSKTVIKDHATLYRHNLSM-DVSITDAIAQSALSAGAWPKDALYKSIADHARQLAEWA	1003
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	LLHRSKTVIKDHATLHRHNLM-DVSITDAIAQSALSAGAWPKDALYKSIADHARQLAEWA	981
TR	A0A514DCG4	A0A514DCG4_9VIRU	MLRMNKTTHINDYDLRKFAASKYSSVDNAAVESGLIGGYKVTENNSIAKYAERLDKWQ	987
TR	A0A346P9C2	A0A346P9C2_9VIRU	LAKNSKLSVGDFDTLRRFNVPI-NRAVYDEIGHLSALSGGYPKNQLNESLAQYASNIDKWW	1090
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	ILRAAKTHVVDYDLSRRFGVSDKTQVVDTALLKSALTAAYPSTVISNALATLGKDLHEYL	1127
TR	A0A7L9R691	A0A7L9R691_9VIRU	ILRAAKTHVVDYDLSRRFGVSDKTQVVDTALLKSALTAAYPSTVISNALATLGKDLHEYL	1127
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	ILRAAKTHVVDYESLRFGVSGKTHIVDTALLKSALTAAYPASTISNALAKLGEDLHDYL	1127
TR	I1Y9U5	I1Y9U5_9VIRU	ILRAAKTHVVDYESMRFGVSGKTHIVDTALLKSALTAAYPASTISNALAKLGEDLHNYL	1127
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	ILRAAKTHVVDYESLRFGVSGKTHIVDTALLKSALTAAYPASTISNALAKLGEDLHDYL	1127
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	ILRAAKTHVVDYESMRFGVSGKTHIVDTALLKSALTAAYPASTISNALAKLGEDLHHYL	1127
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	ILRRAKTHLCDYEAARHFVAD-TGFIDEAALESALTGAYPKNPLYDSIARYAKDLQEW	1042
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	ILRRAKTHLADYDAVRSFGIPE-TGFVDDAALESALTAAYPKDPLYQAIADYARRDLWQ	979
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	ILRKAKTHVIDYDTLNRVGIQV-VSSIDDALLESASVSGAVPKRLLSQALADYAKALDSWQ	1076
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	ILRRAKTHLADYDAVRSFGIAE-TSFIDEAALESALTAAYPKDPLYQAIADYAKKLDKWQ	1087
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	ILRKAKTHVIDYDTLNRVGIQV-VSSIDDALLESASVSGAVPKRLLSQALADYAKALDGWQ	1076
TR	A0A515KU26	A0A515KU26_9VIRU	ILRRARTHLSDYEAARKFVAD-TAFIDEAALESALTGAFFPKDPLYQAIADYARRDLWV	1042
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	ILRRAKTHLADYDAVRSFGIPE-TGFVDDAALESALTAAYPKDPLYQAIADYARRDLWQ	853
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	ILRRAKTHLADYDAVRSFGIPE-TDFVDDAALESALTAAYPKDPLYQAIADYARRDLWQ	853
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	ILRRSKTKVVDYQTMKAFGVESKIPDLDESLLSSGLTAALPARTVSDAARQAKALDVHL	1133
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	TLKRARVHLSDDNALNRLGLTS-QVDLSRDVLDGVMSSGGYKPKLLRKAVDAYANDLLKWT	1127
TR	D0TZ30	D0TZ30_9VIRU	VMRRAKVQVVDYQSLHLYGAGSKIDQLDQSLTSGLTGALPKSLLSNALAKQAKELQHYL	1099
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	ILRRARTKVVDYQTMKAFGVESKIPDLDESLLSSGLTAALPARTVSDAARQAKALDVHL	1132

1c1	ORF1		KQTAIEYRFELLRNLPISIT-RVKRY-IENCLPEYLGSLGA----SSHGLPIFLRTVQGY	1057
TR	H6UNN2	H6UNN2_9VIRU	KSCHFETSEMLITRVYVHY-KLEAY-VRHLVRFHLGIK---STSEGGGRPILENNKIGYP	1113
TR	H6UNN0	H6UNN0_9VIRU	TTGTWRAKTITIDGLPTLS-ALRPF-VTHQVVTSLGLA---AINSRATPLFNKNKVGYP	1135
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	RKSSFYEYKI IAPLKLCDN-KFISE-AVSTSMYVLGLSGSLDHSNTGGGLTFILNDLLRP	1061
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	RKSSFYEYKI IAPLKLCDN-EFVAE-AVSTSMYVLGLSGSLNHSNAGGGLTFVILNDLLRP	1039
TR	A0A514DCG4	A0A514DCG4_9VIRU	KTGRFEQIATVKIPLFASLSDPLQDLIDMRIRFHLGIVGSAKVHVVGPTGSLIRNQEY	1047
TR	A0A346P9C2	A0A346P9C2_9VIRU	NAGHWEVKYLYARPLFTLAQ-VKAQV-DEIISVNLAIYLVGRK--HRTEDAFELNKDGH	1146
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	RTHKIMPIRVAPLK-ISTT-GAFQQL-KLSYSRTITQL-----HTSTGG	1168
TR	A0A7L9R691	A0A7L9R691_9VIRU	RSHKIRPIRVAPLK-ISTV-NVLQQL-KLAYSRTIVHL-----HTSGGG	1168
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	ETHTRIPRIAPVD-PKAK-TAFPLL-RQAYLRTLENY-----TATTPG	1168
TR	I1Y9U5	I1Y9U5_9VIRU	ETHTIKPIRMAPVD-PRAK-TAFPLL-RQAYLRTLENY-----TALASG	1168
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	QTHTIKPIRVAPVD-PKAK-SAFPLL-RQAYLRTLENY-----TAANPG	1168
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	QAHSIKPIRMAPVD-PKAK-TAFPLL-RQAYLRTLENY-----TALAPG	1168
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	KGGKYLTKNILIPSGDVS---FSLHSVATFLNSLAIRPGGS---FNGRDLITNLGDYP	1095
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	KTGCFKQRAVSIKPDYDNE---IGRSIYQFLNALGIIPGGS---INYQSLSLNVEGY	1032
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	KAGHYTEKI IHVSGNLRLTQPIRTYV-ENVIHDNLALTDATGH---VQTSSKFRNLNSHNP	1133
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	RTGRFVERTVNVKPDNYDE---LGRVLVIYQFLNALGIVPGGS---INYSSLSLNVEGY	1140
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	KAGHYTEKI IHVSGNLRLTQPIRAYI-ECVIHDNLALTDATGY--VQTSSKFRNLNSHNP	1133
TR	A0A515KU26	A0A515KU26_9VIRU	QAGRYIEKVIPIQDDYQL---FARLSVATFLTALSIPGGS---FNGKDLIKNEDGY	1095
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	KAGCFRQRAVGIPKDNIDE---IGRSIYQLLHALGIIPGGS---INYQSLSLNVEGY	906
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	KTGCFRQKTVSIPKDDYDQ---IGRSIYQLLHALGIMPGRS---INYQSLSLNIEGY	906
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	AGLRKVYVKTTLPIELHST-ELVTLM-RKLLHSLIHGAP-----NSAGDSNLKPYA	1182
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	ATVRDVSFTVTLPHTYDQTV---TNAERIFFRSIGANVVK--PLSQTTIFRRNREGYP	1182
TR	D0TZ30	D0TZ30_9VIRU	NQGTFSYVPPTLDDFHPQ-ASIKAI-AQQVRDQLRDY-----FAGVTA	1141
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	ATLRKVYVKTTLPIEIKTQ-DIVMLM-RKTLNSLIHGTP-----NSERGSNLHPYE	1181

1c1	ORF1		NCQKVKNHYAANSALMRPLGLSVEKALNLLIEHAPGN-----TMLQKTISVLK-----	1105
TR	H6UNN2	H6UNN2_9VIRU	AAIPVKHHFNAIPSLVAFALT'NVVSFMLLLDHALKQLPNNHKSNAALRKLLVDFTT-P	1172
TR	H6UNN0	H6UNN0_9VIRU	AAVPVRHHYNGKPAALLRPLGLTVGVSLTLLFDPKLLRRRTPGSRSLRMYEIVIGDAVK--	1193
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	ATKRLKHHYNIPTLRLCLGCSVNASTQYLIKCSDG-----HNLEKILSLMA-RER-S	1113
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	ATKRLKHHYNIPTLRLCLGCSVNASTQYLIKCSNG-----DNLEKILSLMA-SER-S	1091
TR	A0A514DCG4	A0A514DCG4_9VIRU	DIKPLVHNYGCVIRIVPTLGLSLNQSFRCLLDAVT--PRGDMPGRIGRLLRVIDIAL---	1102
TR	A0A346P9C2	A0A346P9C2_9VIRU	AIHEVKHHYSSITRLMRPIGASTQVTIKTIIDGQL--PT-RYTGDLGRLYTTLFRTTR--S	1201

TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	FIPAPRHSYNSLVGLMRPAGFSNGAALALAIAPK--PS-KAPGKLGKLFSLFLDIATA-H	1224
TR	A0A7L9R691	A0A7L9R691_9VIRU	FVPAPRHSYNSLVGLMRPAGFSNGAALALAIAPK--PS-KAPGKLGKLFSLFLDIATA-H	1224
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	YVAAPRHSYNSIVGLMRPTGFSNGAALALAIAPK--PS-GAPGKLGKLFSLFLHIALA-Q	1224
TR	I1Y9U5	I1Y9U5_9VIRU	YVPAPRHSYNSIVGLMRPTGFSNGAALALAIAPK--PS-GAPGKLGKLFSLFLHIALA-R	1224
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	FVAAPRHSYNSIVGLMRPTGFSNGAALALAIAPK--PT-GAPGKLGKLFSLFLNIALA-R	1224
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	YVPAPRHSYNSIVGLMRPTGFSNGAALALAVSAPT--PS-GAPGKLGKLFSLFLHIALA-R	1224
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	QVTHMRHFYNCIDRVTAAGCSMGLVVRRLLISKQN--AT-KYSGSLGKMYTFLEILK--R	1150
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	ITSRLTHFYNCIDRITALSGCSLGLVVRRLLIDKQD--TT-KYSGNLGKLYSFLVILG--Q	1087
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	DTHEITHYGYFLTSLNTFNLTSTNAGLNLLDEMT--PL-RYSGRIGKLYRLYKLQR--P	1188
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	ITERLTHFYNCIDRITALSGCSLGLVVRRLLIDKQD--TT-KYSGNLGKLYSFLVILE--Q	1195
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	DTHEITHYGYFLTSLNTFNLTSTNAGLNLLDEMA--PL-RYSGRIGKLYRLYKLQR--P	1188
TR	A0A515KU26	A0A515KU26_9VIRU	VIGHMRHFYNCVDRLTPAGCSMGLVVRRLLISKQT--PI-KYAGALGKIYNFLENLK--R	1150
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	ITSRLTHFYNCIDRITALSGCSLGLVVRRLLIDKQD--TT-KYSGNLGKLYSFLVILG--Q	961
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	ITSRLTHFYNCIDRITALSGCSLGLVVRRLLIEKQD--TT-KYSGNLGKLYSFLVILG--Q	961
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	PVLHPTHYHGATPSLIRPLGFSNGKALALTIDGQRANLT-AVPGRLGKLLTLLKRASR-L	1240
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	-----
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	MTSRIVHYYSCLERLILPSGFSIGAGVRKSIQCMPT--SIGPYPLSTKIILFCQKLLSLVD	1240
TR	D0TZ30	D0TZ30_9VIRU	RVAAPGHNYNSMIALQLPLGSDGAGLQLAITSQK--PV-KYAGKLGQLWSVFHIAAMK-P	1197
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	PVLHPTHYHGSIPSLIRPLAFSNGKALALAIIDGQSVNLT-DVPGRMGNLLTLLKRANR-F	1239

1c1	ORF1	-----HPSLGSKAQNMLITKLTFLKESYN-----STPEAQRALFYQYFTGDWSLVP	1150	
TR	H6UNN2	H6UNN2_9VIRU	-----HQLTKRRASPVQDHLNWITRFD-----SNDDVQLFAYRWFKGDFFLLP	1217
TR	H6UNN0	H6UNN0_9VIRU	-----QARHQGSSKAILRDYQAWLSGYLG-----APEHEQEFVARWLTADLSLLP	1238
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	-----FARSKQRATKQFDEVIEFINRLGLLKQEPPLAFNKVSPSLAEAWFTGSLQLLP	1167
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	-----FSHSHQRATKQFDEVIEFIDRLGLLKQEPPLAFGKVVSPSLAEAWFTGGLQLLP	1145
TR	A0A514DCG4	A0A514DCG4_9VIRU	GSVSEASIDVTTQNRKTLRAVRDFILRAEPIYVRGSD----ANRVNNIFDYCDGNLSLFP	1157
TR	A0A346P9C2	A0A346P9C2_9VIRU	QFLRQETASIGVGVDSSTITEMRDFIDAV--MGSEDKTT-RSLGLPSNLFKYIQGDLQLIP	1258
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	GKTADASA-----SAALLKYAHEVHAFYVYSTK-----SEEAESLYQYLSGNVSFFP	1272
TR	A0A7L9R691	A0A7L9R691_9VIRU	GKTADAST-----SAALLKYSQEVHAFYALSSK-----SEGAADSLFYQYLSGNVSFFP	1272
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	GKVSDDAA-----SDSVGKYSQEVRRILYALAQ-----SPSADNLFYDLSGNVSFFP	1272
TR	I1Y9U5	I1Y9U5_9VIRU	GKVSDDAA-----SDSVGKYSQEVRRILYALAKN-----SPNADNLYDLSGNVSFFP	1272
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	GKVSDDAA-----SDSIGKYSQEVRRILYSLAQD-----SPNADNLYNLSGNVSFFP	1272
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	GKVSDDAA-----SDSVGKYSQEVRRILYALAKD-----SPNADNLYDLSGNVSFFP	1272
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	RRDSATSLQNSYKEVDTLSDIIDFIDRAMS-HSR-D-----EKNARQVYEYISGTLSPFI	1203
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	RKESLANLSLSYKETDTINDIRGFIIDSTMA-NQNSD-----SDIGNRVFEYIVGQSRLLP	1141
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	NAVETRHNRY-----QFNRLSEFFFEYAAQFSEKSQLL-AYATFSANFDKYIDSSLSLIP	1241
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	RKESLANLSLSYKETDTIKDIRLFIIDSTMA-NQNSD-----SDIGNRVFEYIVGQSRLLP	1249
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	NAVETRHNRY-----QFNRLSEFFFEYAAQFSEKNRLL-AYATFSANFDKYIDSSLSLIP	1241
TR	A0A515KU26	A0A515KU26_9VIRU	RRDSATSLQNSYKEVDTLSDIQFIDRAMA-TGG-D-----REAAHQVYISITGTLSPFI	1203
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	RKESLANLSLSYKETDTINDIRDFIIDSTMA-NQNSD-----SDIGNRVFEYIVGQSRLLP	1015
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	RKESLANLSLSYKETDTINDIRDFIIDSTMA-NQNSD-----SDIGNRVFEYIVGQSRLLP	1015
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	VRKGDGNA-----ASTVLRFEFGLRSTLAVIGT-----NSESISNLMAYVEGTFFNLYP	1288
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	-----
TR	A0A2Z1Q375	A0A2Z1Q375_9VIRU	EKDRQVQIMNKKGQLNPLFKVSHTQSMQA-----A-LPPSCDEFIMNYITGDLQFIP	1292
TR	D0TZ30	D0TZ30_9VIRU	RLVP-AQ-----ALRIDAYAAATLQRFQCNVNPA-----TNEVHALIYQYLSGDLNLYP	1244
TR	A0A1B4ZA62	A0A1B4ZA62_9VIRU	LRRGDGKA-----AGTIHRFEAFLRNLSLTGL-----DSTSTKNLADYVEGTFLNLYP	1287

1c1	ORF1	PAAS-QWSSDFTTLIRDLTLAGLEGDHFTPFMSQHALTLQPVTRALHIHYIEKIVFNATI	1209	
TR	H6UNN2	H6UNN2_9VIRU	PHAT-QYSSDFTTLARDITLVVVECAV-RGELFRHLAGMPSIKAFTIKVLELVDVTNLIQ	1275
TR	H6UNN0	H6UNN0_9VIRU	PSNT-DSADLVTFIRDITCYTEVKLD-DGLLLRTMSRYDAQHAACFFMLTERAINHLVL	1296
TR	A0A7G4WLZ5	A0A7G4WLZ5_9VIRU	PATC-HQSADLSTFVRDITLNVIEHIF-LAYLNS---TNDLQQIVVTIHHYERMAQYAIN	1222
TR	A0A1P8DF89	A0A1P8DF89_9VIRU	PAIC-HQSADLSTFVRDITLNVIEHIF-LARLNR---TNDLQQIVVTIHHYERMAQYAIN	1200
TR	A0A514DCG4	A0A514DCG4_9VIRU	PSNP-GLSIEVISFIRDVTLVLVLENSH---EFQELFDSDKVQIACYVRQLERIVLQRFV	1212
TR	A0A346P9C2	A0A346P9C2_9VIRU	PVNP-GVSAELISFIRASALMCLEANT---PQLRQWLSIDINVSCLIAFRTYEHTMLMLL	1314
TR	A0A0A7DRW1	A0A0A7DRW1_9VIRU	PAGG--FPAEMLALARDLALQHIETSH---TTLLS---GPAEHLRTACAAIESLAILAIV	1324
TR	A0A7L9R691	A0A7L9R691_9VIRU	PSGG--FPAEMLALARDLTLQHIETAH---PTLLS---GPAEHLRTACAAIESLAILAIV	1324
TR	A0A0S4GAY8	A0A0S4GAY8_9VIRU	PKGG--YPAEMLALARDLALQHIETAKQ---PALLT---GPAEQLRSVCSVLDSLAILAIV	1324
TR	I1Y9U5	I1Y9U5_9VIRU	PKGG--YPAEMLALARDLALQHIETNQ---PALLT---GPAEQLRSVCSVLDSLAILAIV	1324
TR	A0A7G3W8V5	A0A7G3W8V5_9VIRU	PKGG--YPAEMLALARDLALQHIETSTQ---PTLLT---GPAEQLRSVCSVLDSLAILAIV	1324
TR	A0A0S4GA48	A0A0S4GA48_9VIRU	PKGG--YPAEMLALARDLALQHIETHQ---PALLT---GPAEQLRSVCSVLDSLAILAIV	1324
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	PFNC-GISTDIISGLRAASLVLENHIF---LSRITLPA--QELAVWFSRCEYQTSIFFM	1256
TR	A0A7S5WLW9	A0A7S5WLW9_9VIRU	PYPN-GVNAEIIAISIRASVLVVIENHY---KYRITLEP--IVFALWQRFVEFALVFFF	1194
TR	A0A2Z5WAE4	A0A2Z5WAE4_9VIRU	PLND-DTSVEFVSFCRSATLRYFESNS---ERFFDLLTRQPNELTVTFWVVEQHLISQVIR	1297
TR	A0A7S5WLX4	A0A7S5WLX4_9VIRU	PYPN-GVNAEIIAISIRASVLVVIENHY---KYRITLEP--IVFALWQRFIEFAALIFFF	1302
TR	A0A3G8GGF4	A0A3G8GGF4_9VIRU	PLND-DTSVEFVSFCRSATLRYFESDS---ERFFDLLTRQPSSETVTFWVVEQHLISQVIR	1297
TR	A0A515KU26	A0A515KU26_9VIRU	PFNC-GISTDIISGLRAALVVFEDHF---LARVTLPA--QELAVWFSQGEYHTLSFFI	1256
TR	A0A7S5WLW5	A0A7S5WLW5_9VIRU	PYPN-GINAEIIAISIRASVLVVIENHY---KYRITLEP--IVFALWQRFVEFALVFFF	1068
TR	A0A0M5KKP5	A0A0M5KKP5_9VIRU	PYPN-GVNAEIIAISAVRASVLVVIENHY---KHRTITLEP--IVFALWQRFVEFALVFFF	1068
TR	A0A2Z1Q3S4	A0A2Z1Q3S4_9VIRU	PQNM-TVPAELVSLERDLALSIFEMHY---LNTLT---LDPPLIRELISVLDTAHHLAVV	1341
TR	A0A514D1L9	A0A514D1L9_9VIRU	-----	-----

TR A0A2Z1Q375 A0A2Z1Q375_9VIRU	PANRRNHSSDFISLLRDVTLAIESDP---ILMRKLALANNRDRVYTIYQLEDMVALNLE	1349
TR D0TZ30 D0TZ30_9VIRU	PSAS-HLSSELASVTRDLALMTFEARH---LDTFV---RGADYLRRELISALDTCAQLALC	1297
TR A0A1B4ZA62 A0A1B4ZA62_9VIRU	PQNM-TVPAELVSLERDLALAHFEEHY---IPVLK---FEAPLVRELISVLDAAAHLAGV	1340

lc1 ORF1	STLHRYFPGIILQD	1223
TR H6UNN2 H6UNN2_9VIRU	MMLHEIIPGITLKD	1289
TR H6UNN0 H6UNN0_9VIRU	ETIQTYYPGVSLKD	1310
TR A0A7G4WLZ5 A0A7G4WLZ5_9VIRU	KVLHGLIPGIIMQD	1236
TR A0A1P8DF89 A0A1P8DF89_9VIRU	KVLNGLIPGIIMQD	1214
TR A0A514DCG4 A0A514DCG4_9VIRU	KIIDTQFYGLILHD	1226
TR A0A346P9C2 A0A346P9C2_9VIRU	RALSVNYPGINFKD	1328
TR A0A0A7DRW1 A0A0A7DRW1_9VIRU	STLQERLPGFIIRD	1338
TR A0A7L9R691 A0A7L9R691_9VIRU	STLQERLPGFIIRD	1338
TR A0A0S4GAY8 A0A0S4GAY8_9VIRU	SALQEKLPGFIIRD	1338
TR I1Y9U5 I1Y9U5_9VIRU	SALQEKLPGFIIRD	1338
TR A0A7G3W8V5 A0A7G3W8V5_9VIRU	SALQEKLPGFIIRD	1338
TR A0A0S4GA48 A0A0S4GA48_9VIRU	SALQEKLPGFIIRD	1338
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	EKYMSSPEATLLMD	1270
TR A0A7S5WLW9 A0A7S5WLW9_9VIRU	RNYQQAEGSVLLLD	1208
TR A0A2Z5WAE4 A0A2Z5WAE4_9VIRU	QELGKRFPGIILKD	1311
TR A0A7S5WLX4 A0A7S5WLX4_9VIRU	ENYQQAEGSVLLLD	1316
TR A0A3G8GGF4 A0A3G8GGF4_9VIRU	QELGKRFPGIILKD	1311
TR A0A515KU26 A0A515KU26_9VIRU	DNYLSSQEAILLMD	1270
TR A0A7S5WLW5 A0A7S5WLW5_9VIRU	RNYQQAEGSVLLLD	1082
TR A0A0M5KKP5 A0A0M5KKP5_9VIRU	RNYQQTEGSVLLLD	1082
TR A0A2Z1Q3S4 A0A2Z1Q3S4_9VIRU	QTLQEEFPGFLIRD	1355
TR A0A514D1L9 A0A514D1L9_9VIRU	-----	
TR A0A2Z1Q375 A0A2Z1Q375_9VIRU	RRFLDA-LHVILSD	1362
TR D0TZ30 D0TZ30_9VIRU	QVLDEFAPNFIIRD	1311
TR A0A1B4ZA62 A0A1B4ZA62_9VIRU	QILQEEFPGFVIRD	1354