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Zostera virus T – a novel virus of the genus *Tepovirus* identified in the eelgrass, *Zostera muelleri*

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Summary. – Analysis of a transcriptome dataset obtained from tissue samples of the eelgrass *Zostera muelleri*, an aquatic flowering plant species of the family *Zosteraceae*, yielded three genome sequence contigs of a novel RNA virus. Sequence comparison and phylogenetic analysis revealed that the novel RNA virus, named Zostera virus T (ZoVT), belongs to the genus *Tepovirus* of the family *Betaflexiviridae*. The three genome contigs of ZoVT showed 88.2–97.2% nucleotide sequence identity to each other, indicating that they descended from a common ancestor. The ZoVT genome contains three open reading frames (ORFs): ORF1 encodes a 1816 amino acid (aa) replicase (REP) with RNA-dependent RNA polymerase (RdRp) activity; ORF2, a 398 aa movement protein (MP); and ORF3, a 240 aa coat protein (CP). The phylogenetic analysis using REP sequences of ZoVT and other *Betaflexiviridae* viruses showed that Prunus virus T is the closest known virus to ZoVT, whereas potato virus T, the type species of the genus *Tepovirus*, is the second closest virus. Genome sequences of ZoVT, which is the third tepovirus species identified to date, may be useful for investigating the evolution and molecular biology of tepoviruses.

Keywords: Zostera virus T; Tepovirus; Betaflexiviridae; eelgrass; Zostera muelleri

Introduction

Eelgrass (the genus *Zostera*) is an aquatic monocotyledonous flowering plant of the family *Zosteraceae* that has adapted to live a fully submerged lifecycle in the marine environment (Les *et al.*, 1997; Lee *et al.*, 2016; Olsen *et al.*, 2016). Eelgrass plays an important role in coastal and estuarine ecosystems around the world. These plants act as carbon sinks and form habitats promoting the diversity of marine organisms (Dahl *et al.*, 2016; Reynolds *et al.*, 2016). Several genomic and transcriptomic analyses of two representative eelgrass species *Zostera muelleri* and *Zostera marina* have been performed to investigate the genetic basis of adaptation from a terrestrial to a marine habitat (Wissler *et al.*, 2011; Schliep *et al.*, 2015; Lee *et al.*, 2016; Olsen *et al.*, 2016; Pernice *et al.*, 2016; Davey *et al.*, 2018; Kim *et al.*, 2018b; Sablok *et al.*, 2018).

RNA samples isolated from plant tissues often carry exogenous RNA molecules derived from infectious viruses. Therefore, plant transcriptome datasets provide a suitable resource for the identification of novel RNA virus genome sequences (Nibert *et al.*, 2016; Kim *et al.*, 2018a; Park *et al.*, 2018). Previously, a partial sequence of the RNA-dependent RNA polymerase (RdRp) region of an RNA virus of the genus *Endornavirus* was detected in the eelgrass species *Z. marina* (Fukuhara *et al.*, 2006). Genome sequences of two RNA virus species of the genus *Amalgavirus* were identified from a *Z. marina* transcriptome dataset (Park *et al.*, 2018).

In this study, we analyzed a transcriptome dataset obtained from nine samples of *Z. muelleri* and identified three genome sequence contigs of a novel virus that belongs to the genus *Tepovirus* of the family *Betaflexiviridae*. *Betaflexi-*

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Abbreviations: CP = coat protein; MP = movement protein; PrVT = prunus virus T; PVT = potato virus T; RdRp = RNA-dependent RNA polymerase; SRA = Sequence Read Archive; ZoVT = Zostera virus T *viridae* is a family of plant-infecting viruses with a flexuous particle and positive-sense single-stranded RNA genome of 6–9 kb (Adams *et al.*, 2012, 2016).

The *Betaflexiviridae* family is composed of 11 recognized genera divided into two subfamilies: *Trivirinae* and *Quinvirinae* (Adams *et al.*, 2016). The subfamily *Trivirinae* has eight genera, namely, *Capillovirus*, *Chordovirus*, *Citrivirus*, *Divavirus*, *Prunevirus*, *Tepovirus*, *Trichovirus*, and *Vitivirus* (Adams *et al.*, 2016). *Trivirinae* viruses have three common open reading frames (ORFs) for a replicase (REP), a movement protein (MP), and a coat protein (CP) (Adams *et al.*, 2012; Rubino *et al.*, 2012; Chavan *et al.*, 2013; Marais *et al.*, 2015b). Viruses of the genus *Prunevirus* have an additional ORF for a nucleic acid-binding protein (NBP) (Veerakone *et al.*, 2018). Viruses of the genus *Vitivirus* have two additional ORFs for an NBP and a 20 kDa protein (Martelli *et al.*, 1997).

The subfamily *Quinvirinae* has three genera, namely, *Carlavirus*, *Foveavirus*, and *Robigovirus* (Adams *et al.*, 2016). *Quinvirinae* viruses have five common ORFs that encode a REP, three triple gene block proteins (TGB1, TGB2, and TGB3), and a CP (Morozov and Solovyev, 2003; Prosser *et al.*, 2015; Jo *et al.*, 2017). Viruses of the genus *Carlavirus* have an additional ORF for an NBP (Adams *et al.*, 2012; Li *et al.*, 2013).

Materials and Methods

Transcriptome dataset. A *Z. muelleri* transcriptome dataset (41 Gbp; nine paired-end), which was used to investigate plant responses to varying light intensities, was obtained from the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI). SRA Acc. Nos. were as follows: ERR884047, ERR884048, ERR884049, ERR884050, ERR884051, ERR884052, ERR884053, ERR884054, and ERR884055.

Raw RNA-seq reads were filtered to remove low-quality reads using the Sickle program (version 1.33; https://github.com/najoshi/sickle) with the parameters: -q 30 -l 50. High-quality reads were used to produce a *de novo* assembly using the SPAdes Genome Assembler (version 3.12.0; http://cab.spbu.ru/software/spades) with the parameter "--rna" (Bankevich *et al.*, 2012). Sequence assembly was performed separately for each of the nine RNA-seq runs. Contigs equal to or longer than 1000 bp were selected for further analysis.

Known viral RdRp motif sequences. A representative set of viral RdRp motif sequences was prepared from the Pfam database (release 32.0; http://pfam.xfam.org). Pfam families containing the keyword "RNA-dependent RNA polymerase" were reviewed, and 22 viral RdRp families were selected (PF00602, PF00603, PF00604, PF00680, PF00946, PF00972, PF00978, PF00998, PF02123, PF03035, PF03431, PF04196, PF04197, PF05788, PF05919, PF06317, PF07925, PF08467, PF08716, PF08717, PF12426, and PF17501). A total of 2539 RdRp motif sequences were initially collected from these 22 Pfam families. The sequences were clustered to reduce redundancy by using the USEARCH program (version 11.0.667, https://drive5.com/usearch) (Edgar, 2010) with the following parameters: -cluster_fast *input* -id 0.9 -centroids *output* -sort length. As the result, 2195 representative RdRp motif sequences were selected and converted to a BLAST-searchable database.

Identification and annotation of viral genome contig. BLASTX searches were performed against the known RdRp motif database by using the eelgrass transcriptome contigs as queries to identify putative viral genome contigs. Sequencing depth of a putative viral contig was examined by mapping the RNA-seq reads to the contigs with the BWA program (version 0.7.17-r1194-dirty; https://github.com/lh3/bwa) (Li and Durbin, 2009). High-quality contig sequences were obtained by extracting segments supported by two or more RNA-seq reads. The mapped RNA-seq reads were analyzed using the SAMtools and BCFtools programs (version 1.9; http://www.htslib.org) (Li, 2011) to identify single nucleotide polymorphisms (SNPs). Sequence similarity searches of viral contigs against all known nucleotide and protein sequences were conducted using BLAST at the NCBI website (https://blast.ncbi.nlm.nih.gov/Blast.cgi). ORFs of a virus genome and the protein sequences were deduced using the BLASTX results and ORFfinder analysis with default settings (https://www.ncbi.nlm.nih.gov/orffinder). Functional domains in the viral proteins were predicted using Pfam.

Sequence comparison and phylogenetic analysis. Pairwise identities of the protein sequences were calculated using the FASTA program (version 36.3.6; https://github.com/wrpearson/fasta36) (Pearson and Lipman, 1988). Multiple sequence alignments were generated using the MUSCLE program (version 3.8.31; https://www.drive5.com/muscle) (Edgar, 2004). The phylogenetic relationships among the viruses were inferred using the neighbor-joining method implemented in the ClustalW2 program (version 2.1; http://www.clustal.org/clustal2) (Saitou and Nei, 1987; Larkin *et al.*, 2007). Positions with gaps were excluded. Bootstrap values were calculated from 1000 replicates.

Results and Discussion

In this study, nine *Z. muelleri* RNA-seq samples were assembled into *de novo* contig assemblies. Comparison of sequence similarities between the contigs and the viral RdRp motif database (as described within Materials and Methods) identified three viral contigs. These viral contigs were from three different samples (SRA Acc. Nos. ERR884049, ERR884050, and ERR884051). They had a strong protein sequence identity (73.7% identity and alignment length of 353 aa residues) with an RdRp motif sequence present in a Prunus virus T (PrVT) replicase (UniProt Acc. No. A0A075DMT8) (Marais *et al.*, 2015a). PrVT is an RNA virus that belongs to the genus *Tepovirus* of the family *Betaflexiviridae*, implying that these three contigs are genome sequences from a novel virus of the genus *Tepovirus*.

Table 1. ORFs of ZoVT genome sequences

Contig	SRA Acc. No.	Reads[a]	NCBI Acc. No.	Genome size (nt)	ORF	Position (nt)	Protein size (aa)
Z1	ERR884049	74,842	MK514426	6992	replicase	57–5507	1816
					movement protein	5419–6615	398
					coat protein	6218–6940	240
Z2	ERR884050	1886	MK514427	6971	replicase	52–5502	1816
					movement protein	5414–6610	398
					coat protein	6213–6935	240
Z3	ERR884051	18,207	MK514428	6927	replicase	53–5503	1816
					movement protein	5415–6611	240
					coat protein	6214–6927[b]	>238

[a]Number of raw reads. [b]Partial.

The three genome contigs were named Z1 (ERR884049), Z2 (ERR884050), and Z3 (ERR884051) (Table 1). Their lengths were 6992 bp (Z1), 6971 bp (Z2), and 6927 bp (Z3). The number of assembled reads were 74,842 (Z1), 1886 (Z2), and 18,207 (Z3). The contigs Z1 and Z2 have one SNP each (C/T polymorphism at position 5961 in Z1 and G/T at 1753 in Z2). Z3 has no variant nucleotides. Such results indicate that these contigs were derived from highly homogeneous viral populations. Sequence comparisons revealed very strong nucleotide (nt) sequence identities among the contigs: Z1 vs. Z2 97.2%; Z1 vs. Z3 88.2%; and Z2 vs. Z3 88.2%. This suggests that all three sequences were derived from the same or closely related virus species. Sequence similarities also suggest that Z1 and Z2 share a more recent common ancestor, while Z3 diverged earlier.

Results from the BLASTX searches using Z1, Z2, and Z3 as queries revealed that they had highest protein sequence similarity to proteins of two recognized *Tepovirus* species, PrVT and potato virus T (PVT) (Russo *et al.*, 2009; Marais *et al.*, 2015a). They also showed significant sequence similarities to viruses of other genera of the family *Betaflexiviridae*, such as Actinidia virus B (AcVB), grapevine virus A (GVA), grapevine virus E (GVE), apple stem grooving virus (ASGV), cherry virus A (CVA), Diuris virus A (DiVA), and Ocimum basilicum RNA virus 1 (ObRV1) (Yoshikawa *et al.*, 1992; Minafra *et al.*, 1994; Jelkmann, 1995; Nakaune *et al.*, 2008; Blouin *et al.*, 2012; Wylie *et al.*, 2013; Goh *et al.*, 2018). Therefore, the contigs Z1, Z2, and Z3 were considered genome sequences of a novel virus, named Zostera virus T (ZoVT), of the genus *Tepovirus* within the family *Betaflexiviridae*. The

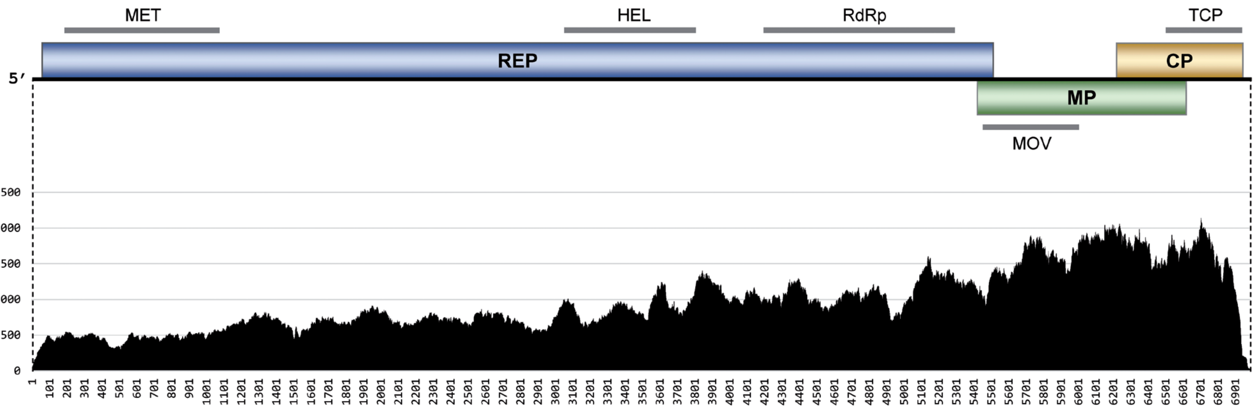


Fig. 1

Schematic representation of the ZoVT genome organization

Schematic of the ZoVT Z1 genome contig (6992 bp) is presented at the top. Three ORFs for a replicase (REP), a movement protein (MP), and a coat protein (CP) are depicted as boxes (see Table 1 for coordinates and lengths of ORFs). Functional domains predicted using Pfam are marked by lines above or below ORFs: viral methyltransferase domain (MET), viral RNA helicase domain (HEL), RNA-dependent RNA polymerase domain (RdRp), viral movement protein domain (MOV), and trichovirus coat protein domain (TCP). Sequencing depth of the ZoVT genome contig is depicted by the histogram represented at the bottom of the figure. The X-axis represents genomic position, and Y-axis sequencing depth.

Table 2. Sequence comparison of the REP of ZoVT and representative *Betaflexiviridae* viruses

No.	Genus	Full name	Acronym	NCBI	Identity	Alignment
1	*Tepovirus*	Prunus virus T	PrVT	AHM92766.1	49.2%	1832
2		Prunus virus T	PrVT	YP_009051684.1	48.1%	1839
3		Potato virus T	PVT	ADX41471.1	32.1%	1857
4		Potato virus T	PVT	YP_002019748.1	32.1%	1850
5		Potato virus T	PVT	AFV39891.1	32.3%	1853
6		Potato virus T	PVT	AFU55321.1	32.4%	1853
7		Potato virus T	PVT	AXK90539.1	32.5%	1841
8	*Vitivirus*	Actinidia virus B	AcVB	YP_004935358.1	29.9%	1861
9		Grapevine virus A	GVA	NP_619662.1	29.0%	1813
10		Grapevine virus E	GVE	YP_002117775.1	27.4%	1834
11	*Capillovirus*	Apple stem grooving virus	ASGV	NP_044335.1	26.7%	1855
12		Cherry virus A	CVA	NP_620106.1	26.7%	1880
13	*Divavirus*	Diuris virus A	DiVA	YP_006905850.1	31.4%	1847
14		Ocimum basilicum RNA virus 1	ObRV1	YP_009408144.1	29.7%	1892
15	*Trichovirus*	Apple chlorotic leaf spot virus	ACLSV	NP_040551.1	29.4%	1925
16		Grapevine Pinot gris virus	GPGV	YP_004732978.2	29.8%	1951
17	*Chordovirus*	Carrot Ch virus 1	CtChV-1	YP_009103999.1	29.2%	1911
18		Carrot Ch virus 2	CtChV-2	YP_009103996.1	30.5%	1908
19	*Prunevirus*	Apricot vein clearing associated virus	AVCaV	YP_008997790.1	28.4%	1865
20		Caucasus prunus virus	CPrV	AKN08994.1	27.7%	2023
21	*Citrivirus*	Citrus leaf blotch virus	CLBV	NP_624333.1	28.8%	2015
22		Citrus leaf blotch virus	CLBV	AFA43536.1	28.7%	2034
23	*Carlavirus*	Garlic common latent virus	GCLV	YP_004936159.1	27.0%	1986
24		Coleus vein necrosis virus	CVNV	YP_001430021.1	26.3%	2023
25		Phlox virus B	PhlVB	YP_001552317.1	27.0%	2095
26	*Foveavirus*	Apple stem pitting virus	ASPV	NP_604464.1	26.6%	2213
27		Asian prunus virus 1	APV1	YP_009094347.1	27.3%	2063
28	*Robigovirus*	Cherry twisted leaf associated virus	CTLaV	YP_009046478.1	25.9%	2081
29		Cherry rusty mottle associated virus	CRMaV	YP_007761581.1	27.2%	2054

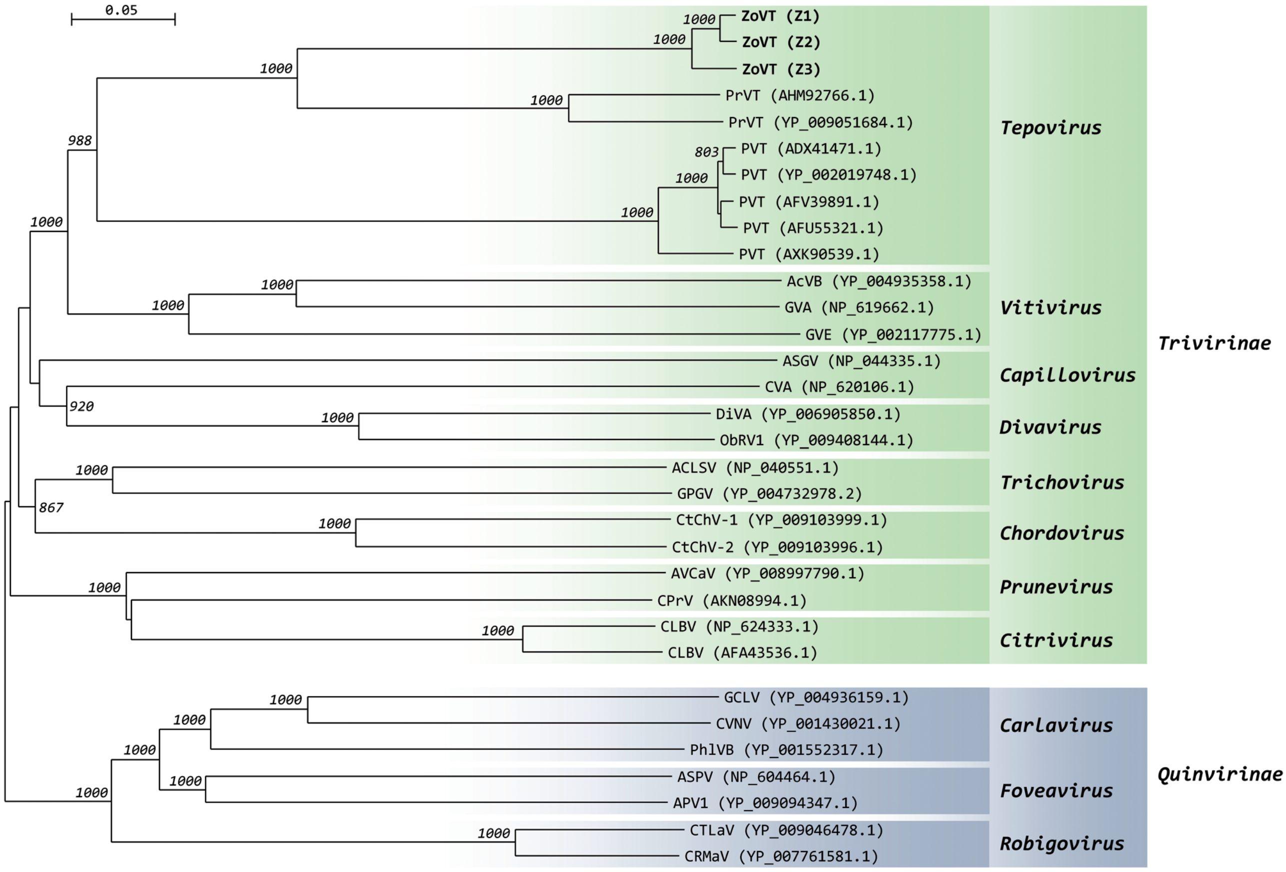
ZoVT genome contig sequences were deposited at NCBI under MK514426 (Z1), MK514427 (Z2), and MK514428 (Z3).

The ZoVT genome Z1 contig was predicted to have three ORFs, a characteristic of the tepoviruses (Fig. 1 and Table 1): ORF1 encodes a 1816-amino acid (aa)-long REP; ORF2, a 398-aa-long MP; and ORF3, a 240-aa-long CP. The MP ORF starts within the REP ORF and ends within the CP ORF. Z2 and Z3 contain the same set of ORFs with the same lengths. Z3, however, is partial and the CP is truncated at aa 238 out of 240. The REP sequences of the three contigs shared 91.4–98.1% identity; MP sequences 95.7–99.2%; and CP sequences 97.5–100%. Z1 was chosen to represent the three genome sequences for further analyses, because it was the longest and covered the entirety of the other two contig sequences.

The ZoVT REP was annotated as having three known functional protein domains (Fig. 1): a viral methyltransferase domain (Pfam Acc. No. PF01660) at position 43–338 aa; a viral (superfamily 1) RNA helicase domain (PF01443) at 998–1248 aa; and an RdRp domain (PF00978) at 1379–1743 aa. The MP has a viral movement protein domain (PF01107) at 10–193 aa. The CP has a trichovirus coat protein domain (PF05892) at 94–239 aa.

BLASTP was performed using the ZoVT REP sequence as a query to collect homologous sequences. As expected, the highest sequence identity was with the PrVT REP, and the second highest with the PVT REP. PrVT and PVT are members of the genus *Tepovirus*, in which PVT is the type species. REP sequences of members of other *Betaflexiviridae* genera including *Vitivirus* (AcVB, GVA, and GVE), *Capillovirus* (ASGV and CVA), and *Divavirus* (DiVA and ObRV1), also showed significant sequence identities (Table 2).

For the phylogenetic analysis, REP sequences of the genus *Tepovirus* (PrVT and PVT) and representative members of the other *Betaflexiviridae* genera were collected (Table 2). Pairwise comparison revealed that the ZoVT REP had 25.9–49.2% identities with REP protein sequences of known *Betaflexiviridae* viruses. PrVT REP sequences showed the



Phylogenetic relationship of ZoVT and other *Betaflexiviridae* viruses

A phylogenetic tree was inferred from multiple alignments of REP sequences of ZoVT and other *Betaflexiviridae* viruses. ZoVT formed a subclade with PrVT within the genus *Tepovirus* of the subfamily *Trivirinae*. The subfamily *Quinvirinae* was used as an outgroup. Bootstrap values of 70% or higher, calculated from 1000 replicates, are shown at the tree nodes. Full names of the viruses are provided in Table 2.

highest identity with the ZoVT REP (48.1–49.2%) and alignment lengths of 1832–1839 aa. The second closest were PVT REP sequences with 32.1–32.5% identities and alignment lengths of 1841–1857 aa. REP sequences of viruses that belong to other *Betaflexiviridae* genera showed 25.9–31.4% identities and alignment lengths of 1813–2095 aa. The alignment lengths were generally longer than the ZoVT REP sequence (1816 aa) because lengths of some REP sequences were longer and gaps were introduced to maximize the sequence alignment.

A multiple alignment of REP sequences from the three ZoVT genome contigs and 29 other *Betaflexiviridae* viruses was performed (Supplementary Data S1). The phylogenetic position of ZoVT within the family *Betaflexiviridae* was inferred using the neighbor-joining method (Fig. 2). ZoVT and PrVT formed a strong subclade with bootstrap value of 1000 out of 1000 replicates within the genus *Tepovirus*, which is consistent with the protein sequence comparison. PVT, the type species of the genus *Tepovirus*, formed the sister taxon to the ZoVT/PrVT subclade. Among the genera of the subfamily *Trivirinae*, the genus *Vitivirus* was inferred to be the sister taxon to the genus *Tepovirus* with strong bootstrap support (1000 out of 1000 replicates).

In conclusion, eelgrass *Z. muelleri* transcriptome data were analyzed, allowing identification of three viral genome sequences derived from ZoVT, a novel member of the genus *Tepovirus* of the family *Betaflexiviridae*. Sequence comparison and phylogenetic analysis indicated that ZoVT is most closely related to PrVT. To the best of our knowledge, ZoVT is the third species of the genus *Tepovirus*. The ZoVT genome sequences identified in this study may be useful for investigating the evolution and molecular biology of aquatic plant-infecting tepoviruses.

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Supplementary information is available in the online version of the paper.

References

Adams MJ, Candresse T, Hammond J, Kreuze JF, Martelli GP, Namba S, Pearson MN, Ryu KH, Saldarelli P, Yoshikawa N (2012): Family – Betaflexiviridae. In King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (Eds): Virus Taxonomy: Classification and Nomenclature of Viruses Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, San Diego, pp. 920–941. https://doi.org/10.1016/B978-0-12-384684-6.00078-1

Adams MJ, Lefkowitz EJ, King AMQ, Harrach B, Harrison RL, Knowles NJ, Kropinski AM, Krupovic M, Kuhn JH, Mushegian AR, Nibert M, Sabanadzovic S, Sanfaçon H, Siddell SG, Simmonds P, Varsani A, Zerbini FM, Gorbalenya AE, Davison AJ (2016): Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Arch. Virol. 161, 2921–2949. https://doi.org/10.1007/s00705-016-2977-6

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA (2012): SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J. Comput. Biol. 19, 455–477. https://doi.org/10.1089/cmb.2012.0021

Blouin AG, Chavan RR, Pearson MN, MacDiarmid RM, Cohen D (2012): Detection and characterisation of two novel vitiviruses infecting Actinidia. Arch. Virol. 157, 713–722. https://doi.org/10.1007/s00705-011-1219-1

Chavan RR, Blouin AG, Cohen D, Pearson MN (2013): Characterization of the complete genome of a novel citrivirus infecting Actinidia chinensis. Arch. Virol. 158, 1679–1686. https://doi.org/10.1007/s00705-013-1654-2

Dahl M, Deyanova D, Gutschow S, Asplund ME, Lyimo LD, Karamfilov V, Santos R, Bjork M, Gullstrom M (2016): Sediment properties as important predictors of carbon storage in Zostera marina meadows: A comparison of four European areas. PLOS ONE 11, e0167493. https://doi.org/10.1371/journal.pone.0167493

Davey PA, Pernice M, Ashworth J, Kuzhiumparambil U, Szabo M, Dolferus R, Ralph PJ (2018): A new mechanistic understanding of light-limitation in the seagrass Zostera muelleri. Mar. Environ. Res. 134, 55–67. https://doi.org/10.1016/j.marenvres.2017.12.012

Edgar RC (2004): MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32, 1792–1797. https://doi.org/10.1093/nar/gkh340

Edgar RC (2010): Search and clustering orders of magnitude faster than BLAST. Bioinformatics 26, 2460–2461. https://doi.org/10.1093/bioinformatics/btq461

Fukuhara T, Koga R, Aoki N, Yuki C, Yamamoto N, Oyama N, Udagawa T, Horiuchi H, Miyazaki S, Higashi Y, Takeshita M, Ikeda K, Arakawa M, Matsumoto N, Moriyama H (2006): The wide distribution of endornaviruses, large double-stranded RNA replicons with plasmid-like properties. Arch. Virol. 151, 995–1002. https://doi.org/10.1007/s00705-005-0688-5

Goh CJ, Park D, Kim H, Sebastiani F, Hahn Y (2018): Novel Divavirus (the family Betaflexiviridae) and Mitovirus (the family Narnaviridae) species identified in basil (Ocimum basilicum). Acta Virol. 62, 304–309. https://doi.org/10.4149/av_2018_224

Jelkmann W (1995): Cherry virus A: cDNA cloning of dsRNA, nucleotide sequence analysis and serology reveal a new plant capillovirus in sweet cherry. J. Gen. Virol. 76 (Pt 8), 2015–2024. https://doi.org/10.1099/0022-1317-76-8-2015

Jo Y, Song M-K, Choi H, Park J-S, Lee J-W, Lian S, Lee BC, Cho WK (2017): Genome sequence of grapevine virus T, a novel foveavirus infecting grapevine. Genome Announc. 5. https://doi.org/10.1128/genomeA.00995-17

Kim H, Park D, Hahn Y (2018a): Identification of novel RNA viruses in alfalfa (Medicago sativa): an Alphapartitivirus, a Deltapartitivirus, and a Marafivirus. Gene 638, 7–12. https://doi.org/10.1016/j.gene.2017.09.069

Kim M, Brodersen KE, Szabo M, Larkum AWD, Raven JA, Ralph PJ, Pernice M (2018b): Low oxygen affects photophysiology and the level of expression of two-carbon metabolism genes in the seagrass Zostera muelleri. Photosynth. Res. 136, 147–160. https://doi.org/10.1007/s11120-017-0452-1

Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, Valentin F, Wallace IM, Wilm A, Lopez R, Thompson JD, Gibson TJ, Higgins DG (2007): Clustal W and Clustal X version 2.0. Bioinformatics 23, 2947–2948. https://doi.org/10.1093/bioinformatics/btm404

Lee H, Golicz AA, Bayer PE, Jiao Y, Tang H, Paterson AH, Sablok G, Krishnaraj RR, Chan CK, Batley J, Kendrick GA, Larkum AW, Ralph PJ, Edwards D (2016): The genome of a southern hemisphere seagrass species (Zostera muelleri). Plant Physiol. 172, 272–283. https://doi.org/10.1104/pp.16.00868

Les DH, Cleland MA, Waycott M (1997): Phylogenetic studies in Alismatidae, II: Evolution of marine angiosperms (seagrasses) and hydrophily. Syst. Bot. 22, 443–463. https://doi.org/10.2307/2419820

Li H (2011): A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. Bioinformatics 27, 2987–2993. https://doi.org/10.1093/bioinformatics/btr509

Li H, Durbin R (2009): Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics 25, 1754–1760. https://doi.org/10.1093/bioinformatics/btp324

Li YY, Zhang RN, Xiang HY, Abouelnasr H, Li DW, Yu JL, McBeath JH, Han CG (2013): Discovery and characterization of a novel carlavirus infecting potatoes in China. PLOS ONE 8, e69255. https://doi.org/10.1371/journal.pone.0069255

Marais A, Faure C, Mustafayev E, Barone M, Alioto D, Candresse T (2015a): Characterization by deep sequencing of Prunus virus T, a novel Tepovirus infecting Prunus species. Phytopathology 105, 135–140. https://doi.org/10.1094/PHYTO-04-14-0125-R

Marais A, Faure C, Mustafayev E, Candresse T (2015b): Characterization of new isolates of apricot vein clearing-associated virus and of a new Prunus-infecting virus: Evidence for recombination as a driving force in Betaflexiviridae evolution. PLOS ONE 10, e0129469. https://doi.org/10.1371/journal.pone.0129469

Martelli GP, Minafra A, Saldarelli P (1997): Vitivirus, a new genus of plant viruses. Arch. Virol. 142, 1929–1932. https://doi.org/10.1007/s007050050088

Minafra A, Saldarelli P, Grieco F, Martelli GP (1994): Nucleotide sequence of the 3‘ terminal region of the RNA of two filamentous grapevine viruses. Arch. Virol. 137, 249–261. https://doi.org/10.1007/BF01309473

Morozov SY, Solovyev AG (2003): Triple gene block: modular design of a multifunctional machine for plant virus movement. J. Gen. Virol. 84, 1351–1366. https://doi.org/10.1099/vir.0.18922-0

Nakaune R, Toda S, Mochizuki M, Nakano M (2008): Identification and characterization of a new vitivirus from grapevine. Arch. Virol. 153, 1827–1832. https://doi.org/10.1007/s00705-008-0188-5

Nibert ML, Pyle JD, Firth AE (2016): A +1 ribosomal frameshifting motif prevalent among plant amalgaviruses. Virology 498, 201–208. https://doi.org/10.1016/j.virol.2016.07.002

Olsen JL, Rouze P, Verhelst B, Lin YC, Bayer T, Collen J, Dattolo E, De Paoli E, Dittami S, Maumus F, Michel G, Kersting A, Lauritano C, Lohaus R, Topel M, Tonon T, Vanneste K, Amirebrahimi M, Brakel J, Bostrom C, Chovatia M, Grimwood J, Jenkins JW, Jueterbock A, Mraz A, Stam WT, Tice H, Bornberg-Bauer E, Green PJ, Pearson GA, Procaccini G, Duarte CM, Schmutz J, Reusch TB, Van de Peer Y (2016): The genome of the seagrass Zostera marina reveals angiosperm adaptation to the sea. Nature 530, 331–335. https://doi.org/10.1038/nature16548

Park D, Goh CJ, Kim H, Hahn Y (2018): Identification of two novel amalgaviruses in the common eelgrass (Zostera marina) and in silico analysis of the amalgavirus +1 programmed ribosomal frameshifting sites. Plant Pathol. J. 34, 150-156.

Pearson WR, Lipman DJ (1988): Improved tools for biological sequence comparison. Proc. Natl. Acad. Sci. USA 85, 2444–2448. https://doi.org/10.1073/pnas.85.8.2444

Pernice M, Sinutok S, Sablok G, Commault AS, Schliep M, Macreadie PI, Rasheed MA, Ralph PJ (2016): Molecular physiology reveals ammonium uptake and related gene expression in the seagrass Zostera muelleri. Mar. Environ. Res. 122, 126–134. https://doi.org/10.1016/j.marenvres.2016.10.003

Prosser SW, Xiao H, Li C, Nelson RS, Meng B (2015): Subcellular localization and membrane association of the replicase protein of grapevine rupestris stem pitting-associated virus, family Betaflexiviridae. J. Gen. Virol. 96, 921–932. https://doi.org/10.1099/jgv.0.000019

Reynolds LK, DuBois K, Abbott JM, Williams SL, Stachowicz JJ (2016): Response of a habitat-forming marine plant to a simulated warming event is delayed, genotype specific, and varies with phenology. PLOS ONE 11, e0154532. https://doi.org/10.1371/journal.pone.0154532

Rubino L, Russo M, De Stradis A, Martelli GP (2012): Tepovirus, a novel genus in the family Betaflexiviridae. Arch. Virol. 157, 1629–1633. https://doi.org/10.1007/s00705-012-1342-7

Russo M, Rubino L, De Stradis A, Martelli GP (2009): The complete nucleotide sequence of potato virus T. Arch. Virol. 154, 321–325. https://doi.org/10.1007/s00705-008-0300-x

Sablok G, Hayward RJ, Davey PA, Santos RP, Schliep M, Larkum A, Pernice M, Dolferus R, Ralph PJ (2018): SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. Sci. Rep. 8, 2749. https://doi.org/10.1038/s41598-017-18782-0

Saitou N, Nei M (1987): The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4, 406–425.

Schliep M, Pernice M, Sinutok S, Bryant CV, York PH, Rasheed MA, Ralph PJ (2015): Evaluation of reference genes for RT-qPCR studies in the seagrass Zostera muelleri exposed to light limitation. Sci. Rep. 5, 17051. https://doi.org/10.1038/srep17051

Veerakone S, Liefting LW, Tang J, Ward LI (2018): The complete nucleotide sequence and genome organisation of a novel member of the family Betaflexiviridae from Actinidia chinensis. Arch. Virol. 163, 1367–1370. https://doi.org/10.1007/s00705-017-3701-x

Wissler L, Codoner FM, Gu J, Reusch TB, Olsen JL, Procaccini G, Bornberg-Bauer E (2011): Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. BMC Evol. Biol. 11, 8. https://doi.org/10.1186/1471-2148-11-8

Wylie SJ, Li H, Dixon KW, Richards H, Jones MG (2013): Exotic and indigenous viruses infect wild populations and captive collections of temperate terrestrial orchids (Diuris species) in Australia. Virus Res. 171, 22–32. https://doi.org/10.1016/j.virusres.2012.10.003

Yoshikawa N, Sasaki E, Kato M, Takahashi T (1992): The nucleotide sequence of apple stem grooving capillovirus genome. Virology 191, 98–105. https://doi.org/10.1016/0042-6822(92)90170-T

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Supplementary information

Zostera virus T – a novel virus of the genus *Tepovirus* identified in the eelgrass, *Zostera muelleri*

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Supplementary Data S1. Multiple sequence alignment of the replicase protein sequences of ZoVT and other *Betaflexiviridae* viruses

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ZoVT:Z1                ---MAFSYRTPAQELLSCLPSEDQTRVNDPSVTSLCFQEKNS-SSYYSYNLSDCQKMFCSK--VGVPLSVQLFRVHPHPY    74
ZoVT:Z2                ---MAFSYRTPAQELLSCLPSEDQTRVNDPSVTSLCFQEKNS-SSYYSYNLSDCQKMFCSK--VGVPLSVQLFRVHPHPY    74
ZoVT:Z3                ---MAFSYRTPAQELLSCLPSEDQTRVNDPSVTSLCFQEKNS-SSYYSYNLSDCQKMFCSK--VGVPLSVQLFKVHPHPY    74
PrVT:YP_009051684.1    ---MAFSYRTPAEEFLSKLPSASQETVDEYALRSLRDQEKAS-SRNYSYHLTDTQKSFCSK--VGVPLSVNNFMVHPHPY    74
PrVT:AHM92766.1        ---MAFSYRTPAEEFLSTLPSTSQELVSKYAVKSLENQEKAS-SHNYSYHLTDTQKNFCSS--VGVPLSVHNFMVHPHPY    74
PVT:ADX41471.1         ---MSFSFRTPAELFVQSLPKEYAEAXFKSHATNFQIRSDKG-IGLFDFACSSVVKERLTK--AGIPVSAFCNREHSHPA    74
PVT:YP_002019748.1     ---MSFSFRTPAELFVQSLPKEYAEACFKSHAANFQIRSDKG-VGLFDFACSSVVKERLTK--AGIPVSAFCNQEHSHPA    74
PVT:AFV39891.1         ---MSFSFRTPAELFVQSLPKEYAEACFKSHAANFQIRSDKG-IGLFDFACSSVVKERLTK--AGIPVSAFCNQEHSHPA    74
PVT:AFU55321.1         ---MSFSFRTPAELFVQSLPKEYAEACFKSHAANFQIRSDKG-IGLFDFACSSVVKERLTK--AGIPVSAFCNQEHSHPA    74
PVT:AXK90539.1         ---MSFSFRTPAELFVQSLPKEYAEACFKSHATNFQIRSDKG-IGLFDFACSSVVKERLTK--AGIPVSAFCNQEHSHPA    74
AcVB:YP_004935358.1    MSISVSSQRMAAASLMQNGSTVEIESIKTLKTERLKKCETRS-DGLFDYYVSDFLRDYLAK--KGVHTSVHSFQAHAHPF    77
GVA:NP_619662.1        MSISVSSQRVAVSNLYTNGSEESVKAIKELKSKRLLETETRL-DGLFDYYIPDTLREILTG--YGMEFSVHSFQGHAHPV    77
GVE:YP_002117775.1     MSLGASSQRVAYANLYANIGSDKLSEVRDRKASTVNSIEAYA-SGLFDYYVSDDVYDFLAS--KGLPLSINCFRTHSHPI    77
ASGV:NP_044335.1       ---MAFTYRNPLEIAINKLPSKQSDQLLSLTTDEIEKTLEVT-NRFFSFSITPEDQELLTK--HGLTLAPIGFKSHSHPI    74
CVA:NP_620106.1        ---MAFVAKFAEENYFNSLPSNVTDAFLRDGFNAEHNRFEIL-SRHFAFALKPSQRTYLND--CGIQLAPIASKTHPHPV    74
DiVA:YP_006905850.1    ---MALSYRTPTEYLINQLPARLTDNIAVKQVDLIQSDEDCY-GSYLNYNLSKEQKKFLVD--KGLYLSPYSWRHHSHPA    74
ObRV1:YP_009408144.1   ---MSLIYRTPVENLINQLPSRLTENVAVKQVDILQNMEESI-GKYFNFNLSKEQKKFLVD--KGVYLSPFSWKHHSHPG    74
ACLSV:NP_040551.1      ---MAFSYRTPQEELLSRLPQSQQEVISGFQYERIQKEEEKK-VENFSFYLPEKTREWFTK--SGVYLSPFAYVNHSHPG    74
GPGV:YP_004732978.2    ---MTFFYRTPTEELISKFTSEEQARIYAPSQRYIENTEIGSNSLFFSYNLKEIQKKFFIS--NGIELSPFSFKAHSHPA    75
CtChV-1:YP_009103999.1 ---MSYGFRTPQEKILSTFSPSFIDNVQSTSGRTFEDEENRI-GKFFNFNLDDRKKEFASN--SGIYLSPYSYKSHSHPL    74
CtChV-2:YP_009103996.1 ---MSYSYRTPQEKILSTLNPTLIDGVASFSGRIFEENESRL-GKYFNYHLSDKKKEFAAQ--AGIYLSPYSFQSHSHPL    74
AVCaV:YP_008997790.1   ---MALLYRTPQVNLLGSFPQKHVEIIYNLQFERFKKICICRFCIFLTHSEKNQKKVASIRGWLGVPLHPTPYLAHSHPF    77
CPrV:AKN08994.1        --MASVTVRTPMEKFFAANDKNDQRSILTSGVNFVKKFCDDK-GIHFAYYVNDRKKEALTN--LGVTLHPIPFLTHSHPF    75
CLBV:NP_624333.1       --MALMSNKTAIESILGNFEKKHVDAIYNAAAQTILSHSEFR-NKHFAYSLNSYQKKIASK--VGIELYPNGYLPHSHPL    75
CLBV:AFA43536.1        --MALMSNKTAIESILGNFEKKHVDAVYNAAAQTIISHSEFR-NKHFAYALTSYQKKIASK--VGIELYPNGYMPHSHPL    75
GCLV:YP_004936159.1    ---MALTYRSPLEEVLTSFSASEQSLIAEPAITSYRGLERDL-FHFFNYNVGPYAKEKLIG--AGVYLSPFSGVPHSHPV    74
CVNV:YP_001430021.1    ---MALTFRSPLEEVLTNFSSTEQSLISKTAINHYSNLESSL-FNFFNLNVDAYSKEKLIN--SGIYLSPFSGVPHSHPV    74
PhlVB:YP_001552317.1   ---MALTYRSPLEENVAAYDASVQSTIASTSACYYKDTEADK-FRFFNYFVNPTAKKKLIE--AGLYLSPYSAMPHSHPV    74
ASPV:NP_604464.1       ---MALLSRTAAEEVIASFTSEEQSRISTQAVLALTNVEKDK-HDLFNYALPELAKMRLFN--SGIYLSPHSYRPHSHPV    74
APV1:YP_009094347.1    ---MALTYRSPIGEVLNRFTSEEQSRVSSTSVSRLTQFEVNN-HKLFSFAMSEKAKEKLIK--VGIYLSPFSFEPHSHPV    74
CTLaV:YP_009046478.1   ---MALHTITPAENVLAQFSSEEASRIGASAISNFSKLEADY-HNLFHFHLPAYAKKKLSE--RGFYLSPFSYETHSHPV    74
CRMaV:YP_007761581.1   ---MALHTITPAEGVLAQFSSEEASRIGASAISNFSKLESEY-HSLFHFHLPAYAKSKLSN--RGFYLSPFSYETHSHPV    74
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ZoVT:Z1                 CKTMENFLLYDNLYHYRSMID-----NYVSIKVDKVNLLKR----------GG---H--RNG-FVKIINRVIADRDVLRY   133
ZoVT:Z2                 CKTMENFLLYDNLYHYRSMID-----NYVSIKVDKVNLLKR----------GG---H--RNG-FVKIINRVIADRDVLRY   133
ZoVT:Z3                 CKTMENFLLYDNLYHYRSIID-----NYVSIKVDKVNLLKR----------GG---H--RNG-FVKIINRVIADRDVLRY   133
PrVT:YP_009051684.1     CKTMENFLLHDNLFHYRNLID-----TYVSIKEEKVGLLNR----------SR------GLN-FHRVINRCVADRDNIRY   132
PrVT:AHM92766.1         CKTMENFILHDNLFHYRHLVS-----IYVSIKEEKVSLLNR----------SQ------GLN-FHRVINRCVADMDKLRY   132
PVT:ADX41471.1          SKMIENHXLYNILPNYLNLKN----YTAISIKDSKVRKLLK----------NG---VD-----SLETFNRLFSCKDALRY   132
PVT:YP_002019748.1      SKMIENHLLYNILPNYLNLKN----YTAISIKDSKVRKLLK----------NG---VD-----SLETFNRLFSCKDALRY   132
PVT:AFV39891.1          SKMIENHFLYNILPNYLNLKN----YTAISIKDSKVRKLLK----------NG---VD-----SLETFNRLVSCKDALRY   132
PVT:AFU55321.1          SKMIENHFLYNILPNYLNLKN----YTAISIKDSKVRKLLK----------NG---VD-----SLETFNRLFSCKDALRY   132
PVT:AXK90539.1          SKMIENHFLYNILPNYLNLKN----YTAISIKDSKVRKLLK----------NG---VD-----SLETFNRLFSCKDALRY   132
AcVB:YP_004935358.1     SKMIENHLLYNIMSQYIEKTT-----LFMSFKGSKIKKLLL----------NH---KSGADLKNLKCYNRLVHIKDHLRY   139
GVA:NP_619662.1         SKMIENHMLYRVAPNYFSS-N----TLVVSCKESKIKRLRL----------KN---ANNRNL-NFTQYNRLVHANHHHRY   138
GVE:YP_002117775.1      SKMIENHFIFNLIGNNLAKDS-----TFISFKEDKLVLLEN---------------KKSRIDGNTCIINRLVHAKDALRY   137
ASGV:NP_044335.1        SKMIENHLLYICVPSLLSSFKS---VAFFSLRENKVDSFLK----------MHSVFSHGKIK-SLGMYNAIIDGKDKYRY   140
CVA:NP_620106.1         SKIIENHLLYCVVSNMISNFKF---LVFLSIKEVKAEYIWN----------KN------TADTVREISNRILDIKDAFRY   135
DiVA:YP_006905850.1     CKTIENWLLYKEIGSYAKHVSKQQTIAFISLREGKLNAIKK------IHFEKK---NNKVACEKICSFNRYYHTKDRLRY   145
ObRV1:YP_009408144.1    CKTIENWLLYNEIGFHIRHICRDSSVAFLSLREGKLKNLEK------IHFRQG---NHDQTNDKIRSFNKIHSPKDCLRY   145
ACLSV:NP_040551.1       CKTLENHLLFNVVASYISKYSY---VACLSIKSNKMSKMER---------------LGPNSVKTYDILNRLVTAKDKARY   136
GPGV:YP_004732978.2     CKTLENYFLFSFLPSFISH-SGIRELFLFSIKKAKVTRLKN---------------LVDNV--QLNHLNRLVEVKDKMRY   137
CtChV-1:YP_009103999.1  CKTIENHLLYVVIPPLIQNFNN---LNVVSMKESKLKILHE----------SS---DAPKKM-SINLINRLMDVKDSFRY   137
CtChV-2:YP_009103996.1  CKTIENYLLYVVMPPMIANFNN---LYVVSMKESKLRILHS---------------NSQLTGISLNLINRLVDVKDSFRY   136
AVCaV:YP_008997790.1    SKMLENHILLNVLPGHITG-S----WVFSSIKPSKVESLAT----------KG------KKS-VLKTINRLLCAKDFGRY   135
CPrV:AKN08994.1         CKTLENHLLINVLPNLLGNGH----WVFTSVKKAKVNSVIK---------------LAGGVSNNVDIVNRCICAKDFGRY   136
CLBV:NP_624333.1        SKIFENHLLFDVLPGVVNTSR----LVMCSIKESKVLVFKG-IRDKSRRQVSDLNALNSLNNSHTSFINRLVASKDVSRY   150
CLBV:AFA43536.1         SKIFENHILFDVLPDVVSTSK----LIMCSIKESKVLIFKNIRDRKKDNGALGFCGKDTSASDHTSFVNRLVAPKDIRRY   151
GCLV:YP_004936159.1     CKTLENHLLYRVLPSILDNS-----FLFVGIKESKLNFLRA---------------RHQNLS-MVELVNRYVTSADRTRY   133
CVNV:YP_001430021.1     CKTLENHILYRVLPSLIDST-----FTFVGIKEAKLQFLRQ---------------RHSHLN-LVQLINRYVTSADRLRY   133
PhlVB:YP_001552317.1    CKTLENYFLFEVIPSKIDNR-----FFFVGIKNEKLSMLKA---------------RNTHLS-TVEKVNRYVTSADKVRY   133
ASPV:NP_604464.1        CKTLENNILFNILPSYLDNS-----FYLVSIKKNKVDFLKR---------------RHPDLQ-MVETINRYISSIDKTRY   133
APV1:YP_009094347.1     CKTLENHILYNILVNKLDNS-----FYAIGIKGSKVNFLKS---------------RSKNLS-MLEYMNRIVTSADKYRY   133
CTLaV:YP_009046478.1    SKTIESHLINIKLPNYINE-D----FLIVGIKDNKLSVLRK----------EK------KLR-FLEAVNRCVTSHDIQRY   132
CRMaV:YP_007761581.1    SKTIESHLINVKLPNYITE-D----FLIVGIKENKLSVLRK----------DK------KMR-FLEALNRCVTSHDIQRY   132
                        .* :*.  :                    . .  *   .                             *         **


ZoVT:Z1                 GP----------CGYNKEFMSE-DFLSGEKG--------------KSWFFHDELHHWNLEDLTKFIKRANP-ERMLATLV   187
ZoVT:Z2                 GP----------CGYNKEFMSE-DFLSGEKG--------------KSWFFHDELHHWNLEDLTRFIRRANP-ERMLATLV   187
ZoVT:Z3                 GP----------CGYNKEFMCE-DFLSGEKG--------------KSWFFHDELHHWNLEDLKKFIRRANP-ERMLATLV   187
PrVT:YP_009051684.1     KN----------CVSKSFFEDT-RNHAPNQS--------------KSWFFHDELHHWDVNEFADFLGNFKP-KKVIASCV   186
PrVT:AHM92766.1         RN----------YVNRSFFENK-NNFIPNQS--------------KSWFFHDELHHWTVNEMSDFLHNFKP-ERVLASCV   186
PVT:ADX41471.1          -------VDPETCDMDKFIARV-HHS-------------------TRIFLFDELHYWSMNSLSDFLDRSNV-KELLATIV   184
PVT:YP_002019748.1      -------VDPETCDMDKFIARV-HHS-------------------TRIFLFDELHYWSMNSLSDFLDRSNV-KELLATIV   184
PVT:AFV39891.1          -------VDPETCDMDKFIARV-HHS-------------------TRIFLFDELHYWSMNSLSDFLDRSNV-KELLATIV   184
PVT:AFU55321.1          -------VDPETCDMDKFIARV-HHS-------------------TRIFLFDELHYWSMNSLSDFLDRSNV-RELLATIV   184
PVT:AXK90539.1          -------VDPETCDMDKFIARV-HHS-------------------TRIFLFDELHYWSMNSLSDFLDRSNV-KELLATIV   184
AcVB:YP_004935358.1     -------TDPHKELDMAHLPEL-ARLSETC---------------ETAVIHDEVQYWSLQDFQLVLGQMNKVKRLMYSII   196
GVA:NP_619662.1         ENA----FRELDVGNLTNLINK-EDQS------------------ECIFIHDEVQYWSLDEMQRFLGSLSKVDRVVYSII   195
GVE:YP_002117775.1      -------KDPLRNLWFDEDQKT-MKGLAEP---------------DRVIIHDEVHYWNLKDFQRFLSYINC--PLIYTVI   192
ASGV:NP_044335.1        GDVEFSSFRDRVIGLRDQCLTR-NKFP------------------KVLFLHDELHFLSPFDMAFLFETIPEIDRVVATTV   201
CVA:NP_620106.1         GPTNT--VNGGINNFSFFCANL-NRRFNNRAIKP-----------DCFFIHDEVHFWSPAELCEFLFTVEP-KNVLATVV   200
DiVA:YP_006905850.1     SD-----SSGREIIYKSFDKIG-DQIGPR----------------ASFYIHDECHYWSPNDLSNFLSRTKA-ESILATVI   202
ObRV1:YP_009408144.1    SS-----FSDRETLYQSFRDIG-MKMEKR----------------SCYFIHDECHYWNPADLDRFIRYTDA-ESIMFTVI   202
ACLSV:NP_040551.1       GPL---------AKPERSPCPK-K---------------------TNIFIHDEIHYWSRDQLETFLQVHRP-KNLWATLV   184
GPGV:YP_004732978.2     GMD----VSPERIEKRKTG--------------------------LDIFIHDEIHHWSKAQLISFLEVHRP-RNIMATVV   186
CtChV-1:YP_009103999.1  KSGDGLSIKYPTQLLESNTRDY-DPLMDVRIEKG-----------SNFLFHDELHYWTFSMMLDFLEKFEP-SHVICTAV   204
CtChV-2:YP_009103996.1  KDGGDYSVKYPTDLLKWNSDKKYDPLLDCSIEKG-----------RNFLFHDEMHYWSFDMMLDFLRKFEP-DNVLCTVI   204
AVCaV:YP_008997790.1    D------VDTDSSVIRSISREA-PDILPEPFVRAVKG--------RNVMIHDEVHHWTLDDMLGFLDRARP-NRFVFSVV   199
CPrV:AKN08994.1         D------FEPGSVDQKINILSK-DHLFPKNFIRSVRK--------KKIFIHDEVHHWSHLNMIQFLEETAT-PLLLCSVV   200
CLBV:NP_624333.1        TEEADAFFQSKKGSPELFSRNF-IKSLENK---------------EAVFFHDEVHHWTKAQMFSFLKSTKV-KRFIFTVV   213
CLBV:AFA43536.1         TEEADAFFSSKKKNDPELFSNNFIRCISNK---------------EAVFFHDEVHHWTKAQMFSFLKRTKV-RRFIFTIV   215
GCLV:YP_004936159.1     PNDFHLSITAEQCFNR--YDGF-KHLGP--GLRKLLPHC-ITVKPRRLFLHDELHYWCERDLVTFLSAVKP-EKVLGTVV   206
CVNV:YP_001430021.1     PSEFH--ITPSKAIEV--CEKW-GRFGKSDSLRELLPAC-ITHKPRALFLHDELHYWNLKELKVFLLAVKP-EKLLGTLV   206
PhlVB:YP_001552317.1    GSDFV--VRPTEKIPG--LIRQ-RPCLDGVTLKDLVPEL-MRKSAKHLFMHDEIHYWSARDLITFLEVIQP-EVMYATMV   206
ASPV:NP_604464.1        GGFFH--VSPSKISAKFKCDRR-TGFEDDASLIDLIPGC-MEGARKRFFFHDELHYWTKEALITFLDHVKP-EVMLASIV   208
APV1:YP_009094347.1     GSD----FTTLSTQQIDNLCSK-QSLEKCGTLRELVPLVKMSKKKRNFFLHDELHYWSSHDLMLFLDSINP-DHLLATIV   207
CTLaV:YP_009046478.1    GPSFH--FEKAKSNWKTDFSEV-NLSAGVQSLLPRVLFDKGRIQDAQIFLYDELHYWSMRDIVDFLEITRA-KTLIGSFV   208
CRMaV:YP_007761581.1    GPSFH--FEKARSNWRSDFSGV-NLSAGVQSLLPRILFDKGKMFDSQIFLYDELHYWSMKDIVDFLEISKA-KTIIGSFV   208
                                                                         :.** :.     :  .:        .  : :
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ZoVT:Z1                 IPPEIFQ-LKNSMNPSFYDYE-II--KRNDQDQSVSFNFYPDGSRESAYFQK--TYDFWFKMKHL--NID---GQF--YT   254
ZoVT:Z2                 IPPEIFQ-LKNSMNPSFYDYE-II--KRNDQDQSVSFNFYPDGSRESAYFQK--TYDFWFKMKHL--NID---GQF--YT   254
ZoVT:Z3                 IPPEIFQ-LKNSMNPSFYDYE-II--KRNDQDQSVSFNFYPDGSRESAYFQK--TYDFWFKMKHL--NID---GQF--YT   254
PrVT:YP_009051684.1     FPVEVFS-SDESCNPSFYRYL-IH--EKKKGE--VRFTFFPDGSKESSYFQR--SSDWIFRFKYF--EIG---SEI--YT   251
PrVT:AHM92766.1         LPVEVFS-SDESCNPSFYKYQ-IH--GRCRGV--VEFTFYPDGSRESSYYQK--SSDWIFKYKHF--EIG---GEI--YT   251
PVT:ADX41471.1          FPIEILLGSKRSLNPELYEFE-IS--R-------GKLHFFPDGCTSESYSQPK-DCD-ILKVNRI-VTKT---GKI--FS   246
PVT:YP_002019748.1      FPIEILLGSKRSLNPELYEFE-IS--R-------GKLHFFPDGCTSESYSQPK-DCD-ILKVNRI-VTKT---GKI--FS   246
PVT:AFV39891.1          FPVEVLLGSKRSLNPELYEFE-IS--R-------GKLHFFPDGCTSESYSQPK-DCD-ILKVNRI-VTKT---GKI--FS   246
PVT:AFU55321.1          FPVEILLGSKRSLNPELYEFE-IS--R-------GKLHFFPDGCTSESYSQPK-DCG-ILKVNRI-VTKT---GKI--FS   246
PVT:AXK90539.1          FPVEILLGSKRSLNPELYEFE-IS--R-------GKLHFFPDGCTSESYSQPK-DCD-ILKVNRI-VTKT---GKV--FS   246
AcVB:YP_004935358.1     YPAEIDQGYEHSLFPEAYHFE-RR--G-------GYFIWLPDGQSDGAYKQPI-N-PWLLSTSKT-IDSR---GRT--WT   258
GVA:NP_619662.1         YPSEVEAGYSQSLFPEAYTFD-LK--D-------RRLVWYPDGKAEGAYTQPV-N-PWLLRCSKT-EDSK---GRS--WT   257
GVE:YP_002117775.1      YPAELHAGYPFSLYPELYDFR-VSEDG-------KTFTWMPDGKCCGSYKQPV-N-PWLLSTNKT-MDLK---GRT--WT   256
ASGV:NP_044335.1        FPIELLFGDKVSKEPRVYTYK-VH--G-------SSFSFYPDGVASECYEQNLANSKWPFTCSGI-QWAN---RKI---R   264
CVA:NP_620106.1         IPPELLEGLDYSFNSVAYDFKKVD----------GNLYYFPDKSKGKPYQQPM--DPWLLKCNKISMIKN---GEIFSYS   265
DiVA:YP_006905850.1     HPTEIDVGKDCSHLPFLYEFE-VS--D-------NNIFFFPDGNRSEGYEQPK-TAGWWLKMRRF--YSD---GEV--YS   264
ObRV1:YP_009408144.1    HPVEVDVGKTSSHLPFLYEFC-ID--G-------ETLHFFPDGNKSEGYEQPL-SAGWWLKMSRF--ISR---GEV--YN   264
ACLSV:NP_040551.1       FPPEILAGYKSSVLPFLYQFE-IH--G-------KDLVYMPDGVRSESYTQPL-ENGFLLSSSSI-IIKNRVTGVEIRYQ   252
GPGV:YP_004732978.2     FPIEILGGFKSSVLKFLYEFE-CR--N-------GKLFYYPDGVMSEAYVQTL-ESSYLFKTNLI-KTSK---G-H--YS   248
CtChV-1:YP_009103999.1  FPVEILEGIKQSLYPEVYSFEILQ--T-------GNFVFAPDGVYSESYEQSV-NMKWLFSASSF--KVR---DQI--YS   267
CtChV-2:YP_009103996.1  FPVEIFSGVKQSLFPDVYSFQIIK--N-------KRFVFAPDGCYSESYEQSV-DMKWLFSAASF--VVD---DLL--YS   267
AVCaV:YP_008997790.1    YPVELLAGILESQNPKMYKFQDSK--S-------DKIVFFPDGRASEGYEQRA-NLRWLFCASHF--RTS---GSI--WT   262
CPrV:AKN08994.1         FPPELLGGIKTPQNSALYGFQ-VD--G-------DKLFFFPDGSRSEMYEQPS-NLNWLFEASYI-HTSA---G-T--YT   262
CLBV:NP_624333.1        YPPEILKKFANSQNPKVYDFK-VD--K-------GRLFFFPDGVKTEAYEQKL-NMEWLFSASHL--RSG---DCV--WT   275
CLBV:AFA43536.1         YPPELLKKFANSQNPKVYDFK-VD--K-------GRLFFFPDGVKTEAYEQKL-NMEWLFSASHF--KSG---DQT--WT   277
GCLV:YP_004936159.1     YPPELLKGVKFSLNKWCYDFD-VE--G-------DDLIFYPDGVRTESYTQPL-SGCFYLKVGTL-KLLD---GSV--YH   269
CVNV:YP_001430021.1     FPPELLQGVHESLNPWCYTFE-VD--D-------KWLHYYPDGVKTEGYTQPR-NSGYLLRLSKI-HLSD---GST--YC   269
PhlVB:YP_001552317.1    YPPELLVGSKFSLFKWCYEFD-VI--G-------NDFFFYPDGVRTEGYLQPL-KNGYLLKAKRI-LLPD---GGV--YH   269
ASPV:NP_604464.1        FPPEILAGAKESLNPWCYTFR-IV--G-------KDLVFFPDGEQSEAYIQPV-AGSYLLRTGKI-TTPS---GDI--FQ   271
APV1:YP_009094347.1     FPPEILAGAQESLNPWCYSFQ-RH--G-------SKLTFFPDGVQSESYTQPL-SAGYILQASKI-VCPS---GQV--YS   270
CTLaV:YP_009046478.1    FPTEILAGSDRSLNPWAYDFK-IQ--G-------DKLIYAPDGVWAESYEQPL-AAGQILKYNKI-ITQQ---G-V--YS   270
CRMaV:YP_007761581.1    FPSEILAGARTSLNPWAYEFK-IK--G-------DKLIYAPDGVWSESYEQPL-SAGQLLKFNKI-MTRN---G-S--YS   270
                         * *:      .     * :                : : **      * *        :


ZoVT:Z1                 ISFMRSIKCHHMILIEK-GKLKTNPFYVSDFAECINAKMIGFSR--ISH-ESIP-IRELVFKREIIYLMSLKKPDMHSAT   329
ZoVT:Z2                 ISFMRSIKCHHMILIEK-GKLKTNPFYVSDFAECINAKMIGFSR--ISH-ESIP-IRELVFKKEIIYLMSLKKPDMHSAT   329
ZoVT:Z3                 ISFMRSIKCHHMILIEK-GKLKTNPYYVSDFAECINAKMIGFSR--ISH-ESIP-IRELVFKREIIYLMSLKKPDMHSAT   329
PrVT:YP_009051684.1     LSFLRSIKCHHLILIEK-GKLETNDYYISDEAECASLRMFGTAV--AGK-ITAP-IRVEVLKREMIYLLSLKKSDMNSAA   326
PrVT:AHM92766.1         LSFLRSIKCHHLILIER-GRLETNRFFISDSAECASLKMFGTAV--AGK-ICAP-IRVEVLKREMIYLLSLKKSDMNSAA   326
PVT:ADX41471.1          VELIHTIGANHMVMIKE-GSFDVDSERFFDRSSALTTSLLIPTR--AG--KALR-IRRKFLLRLIIYLFSLKKPDHHSAI   320
PVT:YP_002019748.1      VELIHTIGANHMVMIKE-GSFDVDSERFFDRSSALTTSLLMPTR--AG--KALR-IRRKFLLRLIIYLFSLKKPDHHSAI   320
PVT:AFV39891.1          VELIHTIGANHMVMIKE-GSFDVDSERFFDRSSALTTSLLMPTR--AG--KALR-IRRKFLLRLIIYLFSLKKPDHHSAI   320
PVT:AFU55321.1          VELIHTIGANHMVMIKE-GSFDVDSERFFDRSSALTTSLLMPTR--AG--KALR-IRRKFLLRLIIYLFSLKKPDHHSAI   320
PVT:AXK90539.1          VELVHTIGANHMIMIKE-GSFDVDSERFFDRSSALTTSLLMPTR--AG--KALR-IRRKFLLRLIIYLFSLKKPDHHSAI   320
AcVB:YP_004935358.1     IGKVTSFASHHLFVASL-GSTITEDEYTYDDYTVIPRGALSSGR--RDY-SGMY-LRSRYVQAVLLYLMALKKPDSSSAV   333
GVA:NP_619662.1         ITKLQTIGAHHLFSAIK-GSYLTEESYKYDNFTIINPNDVLKGK--RGG-KPLY-LRARMIKPTLLYLLALKKSDSNSAV   332
GVE:YP_002117775.1      LTKLESVGSHHLFLCTP-GDLVTEDEAVYNDFTLVDPKLFSSLT------QRMPKLRAGYMHKVIHYLMALRKPDAASAV   329
ASGV:NP_044335.1        VTKLQSLFAHHVFSFDR-GR-ACNEFNHFDKPSCLLAEEMRLLT--KRF-DKAV-INRSTVSSLSTYMACLKTANAASAV   338
CVA:NP_620106.1         IGLLESVGANHLFSFQR-NK-VVESTRFFNDFDCLDMRKLLPINVENGKIKGYN-IRTWVFKKILSYIVCLKKGDSESSL   342
DiVA:YP_006905850.1     VTLLRTIGPFHLIYISR-GSLASESRRFFDDFNILDLPVKYAKNNLIKK-MKLL-LRNNFMIKIVSYIKSLKKPDKESAI   341
ObRV1:YP_009408144.1    VTLLRSIGPFHLMFLSR-GGRVVESKRFFTDFNILDIPSRFNHQHFTRD-VNMI-LRANFIKKIISYIKSLKKPDRESAI   341
ACLSV:NP_040551.1       VSLVYSLGSHHLFHIYPAEDLMKEEVRRFGPYDLFDVGSLFVKP--VRV-PIQD-FPLSVFKKIFIYMSSLKKPDVQSAV   328
GPGV:YP_004732978.2     VSLHRSVGSHHFFQISKYESEILQSHRAFGPYDVLDVGSLFRGK--VRV-SIEG-VSLTHFKKILIYLMSLKKPDVNSAV   324
CtChV-1:YP_009103999.1  VDLIKTIGAHHLFTIVK-GRRISRSIRLFKGFDTLDMSAFLGTK--YKM-PIAD-VHFSFFKKIVIYLKSLKKPDTQSAV   342
CtChV-2:YP_009103996.1  VDLIKTVGAHHLFAITK-GKRIVKEIRFFREFDILDLSAFSGTE--YKL-PVVD-VHFSFFKKIVIYLKSLKKPDSQSAV   342
AVCaV:YP_008997790.1    VKRIYSAYSHHLFEVVP-GNYFTDEIRFFNDFETIDLQCIFKSR-FLCR-DFVP-ISKDLVERVYSYLICLKKPDMQSAM   338
CPrV:AKN08994.1         VKMVGSFYAHHLFQISK-GEKITDSVRFFADFNTIDMSVIHKER-FKYY-DLIP-IKKSHIEKIYTYLLCLKKPDVESAI   338
CLBV:NP_624333.1        VTRHKSIYAHHLFEISI-GELVTDSKLFFSDYNSIDMSKIFLDR-FRSY-EVFP-ISIEHLYKVYSYLLCLKKPDLESGL   351
CLBV:AFA43536.1         VTRHKSIYSHHLFEVSM-GELISDSKIFFSDYGSIDMSKIFLDR-FRSY-EVFP-IAIEHLYKVYSYLLCLKKPDLESGL   353
GCLV:YP_004936159.1     IDVVHSTFCHHLISITA-GEAVRAPTNSFSNFDATTCRGLPNIA-FRSLGPCIA-VPYPVISRVYRYLRTLQKPDLQSAM   346
CVNV:YP_001430021.1     VDLVYSCYSHHIIALTL-GDAVRKPFNAFSGFDATTFQGLKKLD-LRGIGPCLP-ISFSVVNRIYRYLRTLQKPDLASAM   346
PhlVB:YP_001552317.1    VDVVQSKFAHHLIAITR-GESMGPNVRAFGPFDATTCQGLEPLT-SDVS-HCFP-VSFEVVSRVYRYLRTLKKPDVQSAM   345
ASPV:NP_604464.1        LDLLKSSFSHHLISITK-GEAIGQKMRFFNGFEAVAMKGLNPLR-RKVE-SCLP-ISKNTILKIYRYLRTLKKPDLQSAM   347
APV1:YP_009094347.1     VDLVYSAFAHHIVSITK-GDLPGLERRFFSNFEATGVKHLSGLS-YSVR-DCIP-VSSELISKLYRYIRTLKKPDLQSCM   346
CTLaV:YP_009046478.1    VQVRDSIYSHCLVIINR-DNLLNEEFRVYSEFDAVSIRRLNYLG-GNSD-DIIP-VRYEVILSVFKYIRTLKKPDLQSGM   346
CRMaV:YP_007761581.1    VQVRDSIYSHCLVIINR-DELLCEEFRVFSDFDAISIRKIGYLG-GNAD-DIIP-VRHEVVLSIFKYIRTLKKPDLQSGM   346
                        :    :     ..                                          .    .     *:  *.. :  *
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ZoVT:Z1                   AKLRMLSSEDYTTGELLFFNALACEIDSVKG-----LHADISLLKHVQMAMLRSFP-KRVRNHF--CKGYKESDFEQMLI   401
ZoVT:Z2                   AKLRMLSSEDYTTGELLFFNALACEIDSVKG-----LHADISLLKHVQMAILRSFP-KRVRNHF--CKGYKESDFEQMLI   401
ZoVT:Z3                   AKLRMLSSEDYTTGELLFFNALACEIDSVKG-----LHTDVSLLKHVQMAMLRSFP-KRVRNHF--CKGYKESDFEQMLM   401
PrVT:YP_009051684.1       AKLRQLSQEDYHPQELCFFLNLAGRIESVKG-----IFKDRGLVSTVIDCFAQTFP-DRIARWI--SKTTDENSFLRLIS   398
PrVT:AHM92766.1           AKLRQLSQEDYHPQELCFFLNLAGRIESVKG-----IFKDRGLVSTIMDCFAKAFP-NRLARWM--SNTIDENSFLQLIS   398
PVT:ADX41471.1            AKIRQSSDDSIFCDEIMLADHVGKIFEKLDP---ASPFGVKGVFDLLTSIFKDIFL---LDGLFNWSDRRKSEKFVEFMR   394
PVT:YP_002019748.1        AKIRQSSDDSIFCDEIMLADHVGKIFEKLDP---ASPFGVKGVFDLLTSIFKDIFL---LDGLFNWSDRRKSEKFVEFMR   394
PVT:AFV39891.1            AKIRQSSDDSIFCDEIMLADHVGKIFEKLDP---ASPFGVKGVFDLLTGIFKDIFL---LDGLFNWSDRRKSEKFVEFMR   394
PVT:AFU55321.1            AKIRQSSDDSIFCDEIMLADHVGKIFEKLDP---ASPFGVKGVLDLLTGIFKDIFL---LDGLFNWSDRRKSEKFVEFMR   394
PVT:AXK90539.1            AKIRQSSDDSIFCDEIMLADHIGKIFEKLDP---ASPFGVKGVFDLLSGIFKDIFL---MDGLFNWSDRRKSEKFVEFMR   394
AcVB:YP_004935358.1       AKMRQLTNGDENPAESLFMAQIARQLQDAKL---YDSMGTFNLKEAVWNGFCGALG-DSITYLI-DKEQYKVSSMEKFIL   408
GVA:NP_619662.1           AKLRMLSSREENMDEALFVAQLAKQIKDTAL---YDKMGNPNLRSILSESFYDIAG-SLFTRLF-NRPEYDARCLEKFIR   407
GVE:YP_002117775.1        SKLRQLSKGDETTDEMIFSGTIATQIAELKY--FTEVGGLIDLTRALKVGFARLFG--QSIEYFSNKKWYHLDCFTNTVQ   405
ASGV:NP_044335.1          AKLRQLEKRDLYPDELNFVYSFGEHFKNFGM---RDDFDV-SVLQWVKDKFCQVMP-HFIAASFFEPTEFHLN-MRKLLN   412
CVA:NP_620106.1           AKLRQLSDSSPSSDELLLIGDFFDLMTRVKIFNKRSPWSFLSDAKNYVDSWIIQSP--FLRRIFPVGSRAITELIRDWIA   420
DiVA:YP_006905850.1       AKLRMLSEDEFSLEEMIFVDGLVDTLLKNGY---KSIWEN-GWVEWFICGLKDCLPDALHSAMF--RSHFKAKQNLDLLM   415
ObRV1:YP_009408144.1      AKLRMMSEDDFSIEEMLFVEGLIESMLKDGI---RSIWEK-GWMDGFMATLRDLLPPSIHSALF--RKDFKARENLMVLI   415
ACLSV:NP_040551.1         AKLRQLSDADISIESVFMIQEFASRIEKNGV----ESWSC-SFWGCMKDWFFDKLP---YREVL--EKIGLADDFTRRLM   398
GPGV:YP_004732978.2       AKLRQLSNEDVDTNEMWVIRDLAERITHGVS-----KWSNVGIRTILRDWMVDLCP---FKKNF--ERYHLIDDFDRYLM   394
CtChV-1:YP_009103999.1    AKLRQLVGDSISLTEVLFIEDFASRFQEHGA----AKLSNDGIFDQFIHSLKSILP-EFVRRLM---GSFQRDNLLKQIS   414
CtChV-2:YP_009103996.1    AKLRQLVGDNISLTEMLFIEDFAERFQQLGS----AKFSIDGIFDQMAESLKSLLP-LFFRKML---GSFGRDNIMKQIA   414
AVCaV:YP_008997790.1      AKLKQLMGDDLDVRVQVFFRSLVHRILNESE--CFSLFDV-SIVNKWKKKFLDFAPDWLLNGFM----TWKSGNFIKKLG   411
CPrV:AKN08994.1           AKLRQLMEDEQDCRVVEFFCTFAKKLITDTK-GAINLFGD-SFLQKAKDSFIMALP-NSIASCF--DRWHGLNIF-HFLF   412
CLBV:NP_624333.1          AKLRQIIGDDVEIKEFLFFEQFCKRLIERQT--SWGLFGH-SFFEKLTDMALSSLP-NSIARIF--PQWKKKNTF-EFLF   424
CLBV:AFA43536.1           AKLRQIIGDDVEIKEFLFFEQFCKRLIERQT--SWGLFGY-SFFDKLTDLALSKMP-NVVARMF--PQWKKKNTF-EFLF   426
GCLV:YP_004936159.1       AKLSQIMPEPTGY-QIKFMTEFSKMVIDTPV---GASFFQVAIFEKFKGFLTTFFP-KYVAARF---DVARIRSLDEFVE   418
CVNV:YP_001430021.1       AKLSQILPEPTSF-QIKFIREFSELVIKTET--CSNLFQN-NVLLDIKNFFASQLP-KRLAATV---DAYKISSLDEFLE   418
PhlVB:YP_001552317.1      AKLSQLIPEPSGV-EIKFLQDFASLIISTNT--IKSILCP-SRLPLFLGGWLRKLP-KPLAQRF---KTVAEVSLDDFIS   417
ASPV:NP_604464.1          AKLSQVCKDPNGY-EIKFFEEFSKLCLKCDT---LNTNMIPDMKRIVQGFFLKLFP-NPISRNF---KVVQQLHLDNFIE   419
APV1:YP_009094347.1       AKLSQIVPNPTGT-EIKFTEDFARLTMDVQP--MRSMLMP-ETAKLIGSLFSSFLP-FKMARFF---DCYKACSLDKFIH   418
CTLaV:YP_009046478.1      AKHRQLVDEPTGF-EVRFIEDFVQFILENHE--KFNLIGQ-KFSNFLSSACIEVLP-RYMQRFF---KSFKGYSLGKFIE   418
CRMaV:YP_007761581.1      AKHRQLVDNPTGF-EIRFIEDFVQFILEHHE--KFNLIEQ-KFSNFFSSACINLLP-RYMQRFF---NSFKGYSLGKFIE   418
                          :*               .   .                                         .              :


ZoVT:Z1                   NSNGFQVKFKRCEYPKNHL---------------VETLESF---LSGDELESESEDDASIKEDGRKEQLRIDNRREEQYL   463
ZoVT:Z2                   NSNGFQVKFKRCEYPKNHL---------------VEALESF---LSSDELESESEDDVSIKEDGRKEQLRIDNRREEQYL   463
ZoVT:Z3                   NSSGFQVKIKRCEYPRNYL---------------VKTLESF---LSSDELESESEDEISTKEDGRKEQLRIDSRGEGQYL   463
PrVT:YP_009051684.1       SMEGMKLTIKRESFPVEN---FLE----------FDVKDGI---SEQFILDLMEEKMSGGTDAKMDTSYSVATSRNKNFV   462
PrVT:AHM92766.1           SMEGMKLSVERVTFPVEN---FFE----------FNVKDGI---DEQYILDLMDEKFSGVGDPQPDTSYSVKVSRNKNYI   462
PVT:ADX41471.1            ALDYQTNKVVTCTFSG------------------GVMRSGF---LAEFFLDNDCEASEGLDEVISRFDTFFDPKKEYSA-   452
PVT:YP_002019748.1        ALDYQTNKVVTCTFSG------------------GVMRSGF---LAEFFLDNDCEASEGLDEVISRFDTFFDPKKEYSA-   452
PVT:AFV39891.1            ALDYQTNKVVTCTFSG------------------GIMRSGF---LAEFFLDNDCEASEGLDEVISRFDTFFDPKKEYSA-   452
PVT:AFU55321.1            ALDYQTNKVVTCTFSG------------------GIMRSGF---LAEFFLDNDCEASEGLDEVISRFDTFFDPKKEYSA-   452
PVT:AXK90539.1            ALDYQTNKVVTCTFSG------------------GIMRSGF---LAEFFLDNDCEASEGLDEVISRFDTFFDPKKEFSA-   452
AcVB:YP_004935358.1       RCSSARITITRTFRDYQ---------------------------PRRTKLGPELGTSWTGEEDEEL--------------   447
GVA:NP_619662.1           SCETTEIHVERRYMEG------------------IRRGASF---KVQNVMDWVEDDSANALSEVNFLDISWNDRVSE---   463
GVE:YP_002117775.1        FMVKAEVRIKMGYRPM----------------------------VDGLGPEHEVVEPAGLEK------------------   439
ASGV:NP_044335.1          DLATKGIEVPLSVI--------------------ILDKVNF---IETRFHARMFDIAQAIGVNLDLLGKRFDYEAESEEY   469
CVA:NP_620106.1           NAESLKIQTTCSSLTF----------------------------SDSFEMIKTDSISEFGEHILGNISGGLSSAIEAC--   470
DiVA:YP_006905850.1       NMKTLSIVVETEDFYPYSK---------------VDCIKE----IKEYFLNSCDYLQRDNIDKIIRSSFRGEYIYDYD--   474
ObRV1:YP_009408144.1      DLKPLTITLPTADYHMRSI---------------IHRSVG----IDIQYLNDEQMEFKGVQEDLMNSKSRGAFLFGSN--   474
ACLSV:NP_040551.1         KIKPLAFDIHTTDRPLTVRMI-------------IDQIWE----ERLSSFDNISNIVFYGRREWLNNGVLPKVKKKGLAK   461
GPGV:YP_004732978.2       SIKPLSFSFNCS----------------------DDVDYAF---EPEEDLPDFIDDFWFGSEKKMIRDPLVKMIEMGRE-   448
CtChV-1:YP_009103999.1    EAKAFEVRIETCSINRNYD---------------NNALWRY---IKDLAFHDVNELQSDKLLFKEREKGEDEESRDRRNI   476
CtChV-2:YP_009103996.1    MAEPFSVSIETCRVDKNYDNNSV-----------FRFLNGF---FSCSIDPLPCDALLYKGDDFDCSKGKYASQNIENSD   480
AVCaV:YP_008997790.1      EHEAAR-QVQEGAYPEGW------------------MINLF---LANYGIRMCCHQHS----------------------   447
CPrV:AKN08994.1           TLDTIRVKVETKVVDRGYRTQMFDDLEVKDDVMSTKLPEAI---DTLFFGGQLVKGGDRRTVVIKSLDGLIKFSRSKNLY   489
CLBV:NP_624333.1          SLGTLVVDVERKVCFEH-----------------VLEEWGFEVVITDENAYLDPLSIFAINENFNEDRVDDGYLERIRLP   487
CLBV:AFA43536.1           SLGTLVVEIERRVCFEH-----------------ILEEWGFEVVITDENAYLDPLSVFALNENFNEERVDDGYLDRVKLP   489
GCLV:YP_004936159.1       HMCPYTFKIKAVVHDMRLHQLL------------FPRDEEMPR-DEDFDTIRALEMQWGGGANGERIGAAYTVGPFCDYP   485
CVNV:YP_001430021.1       KMEPYSFTIKLVEATALMDIIFNF----------DRDIEGF---EHEVDIVAELEAFANPKNPHAHNAKTTPYFCEPYCD   485
PhlVB:YP_001552317.1      IMEPFSFRQELCDVDWNY----------------FHTFBFFE--FTEADFGIEMAALMDHKFXYGKVASLLERQSQPYSG   479
ASPV:NP_604464.1          TLEEFNFSINTESLSLNWKDDLEF----------VNLTFG----DTDFNVEDSFAEAWGTKKDVVNITTVHHSP----YL   481
APV1:YP_009094347.1       DLEPFSFSVETKVINSRSNPMFEA----------VTLGETM---SSEEVLKILAKLDMGAPTSLEGLTGKFKYSSEAY--   483
CTLaV:YP_009046478.1      EIEPFSFTVKCRTYSR------------------FSFKNSF---IEEEEARERDGDPIY--KQFSKSQSFNSTAYPDCLF   475
CRMaV:YP_007761581.1      EIEPFSFTLRCSTYSR------------------FGFKTSF---IEEEEAAVADKDPLCLTLKLANNKPSCFESYPDLIF   477
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ZoVT:Z1                 YNKEALFN-------KNELPNKRIRDDMIKKKIKE--DEYIIKKNNRIRELIDR-RRCSF-------------SILEEKS   520
ZoVT:Z2                 YSKEALFN-------ENELPNKKIREDIIREKIKE--DEHIIKKNRRIRELTDR-RRCSF-------------SILEEKS   520
ZoVT:Z3                 YNKKTLFC-------EKELPNKRIRDIRIKERIKE--KENIVKKNNRIRELIDR-RECSL-------------SILEERS   520
PrVT:YP_009051684.1     LLDFKQRK-------WARLAEKEEKEPEQRIEIPGEIQELSFEEARFYHGIPGM-KRAFD-------------SRVEHDS   521
PrVT:AHM92766.1         LTDFKAKK-------WERLADKESKEITTRVDIPGEMYEISLEEARFFSGLVGK-RNTMF-------------HEIKEGE   521
PVT:ADX41471.1          ---------------HALRVNIKDRTPSPYGPMKARTPSVVLHREYITKVELSS-KAKKV-------------NVLKERL   503
PVT:YP_002019748.1      ---------------HALRVNIKDRTPNPYGPMKARTPSVVLHREYITKVEFSS-KAKKV-------------NVLKERL   503
PVT:AFV39891.1          ---------------HALRVNIKDRASSPYGPMKARTPSVVLHREYITKVELSS-KAKKV-------------NVLEERL   503
PVT:AFU55321.1          ---------------HALRVNIKDRVPSPYGPMKARTPSVVLHREYITKIELSS-KAKKV-------------NVLKERL   503
PVT:AXK90539.1          ---------------HALRVSIRDRVPAPYGPMRAKTNSVVLHREYITKVELSS-KEKKV-------------NILREKL   503
AcVB:YP_004935358.1     ---------------QEIYHVVVKEGDRERTPYSLKGDEILDNKERRSDLMIQCARMDLL------------ENTKELPS   500
GVA:NP_619662.1         ---------------PYGIECIHGEGSRIRVPLSRILRAHELIAGVQTDVEINF--------------------------   502
GVE:YP_002117775.1      ---------------RREYQGLRGVEAIADGGVPERKRQPYSMVFSDCERM-----------------------------   475
ASGV:NP_044335.1        FS-------------ENGYIFMPSKSNPERNWILNSGS------------------------------------------   494
CVA:NP_620106.1         ------------------------RNWLTSKRFSGGSYSMVSRNGLLVDSMR----------------------------   498
DiVA:YP_006905850.1     ---------------TSGYYSI--RTTSGKMELHGPDSRHLMRSAHDCISYEANIKLFGN-------------NHMEKMR   524
ObRV1:YP_009408144.1    ---------------RGNYHIENGITSSHIVKFSNGSSDYFDTMDLVEGINPLVNRSFDF--------------------   519
ACLSV:NP_040551.1       LIPGREVD-------SHNYPREIYSDLLSSTSIWRSYDDDFRHRSASPLVILRSNRAYS--------------EAAKFSS   520
GPGV:YP_004732978.2     ---------------SQGYSVVPTSYQQAAVCIFSMDENCIGWRNRGVKVLLRA-SRSSY-------------TVLRDEF   499
CtChV-1:YP_009103999.1  VNGF-----------TPSFYSYPGGDNTKFKKIKIGLLKEEPGVLRDITMIELK-SNKGY-------------SLIDEKL   531
CtChV-2:YP_009103996.1  RANLVHKF-------TPRFFSSKSDDKMSKSDFYRIKIYDERTDITKGASFILK-SNRSY-------------SSLEEQI   539
AVCaV:YP_008997790.1    ---------------ADGVTIETGSGPISFCSLKMENHFDYLRCLSSGVSKEHT-------------------GLL----   489
CPrV:AKN08994.1         KMHIIFLLNPSLIRGNIRNFCSNGRSLCANDQLESGPLKTSHYKFKLPTFFSKW-SEMPFSRSLSYHEIPFLKSFVHFRE   568
CLBV:NP_624333.1        FWNLNDYDLKRKRVNAYNILSYRFEEERKIESAQKGPNKMLQIEWYGIKEFKVD-PFISNSITEFTLLEALLGKRIDPKK   566
CLBV:AFA43536.1         FWNLKDYDPKRGRANKYDLLCYKFEEERKNDLRERGPHKMLQIEWYGIREFDDPFIANGI--SEFTILEALIGKRIHKER   567
GCLV:YP_004936159.1     VIDAQKV--------FQLLRVISREWSFSFSMVQYCERGDYTEFMQASKLIWFSSKLAGW-------------DVCLATY   544
CVNV:YP_001430021.1     AVEFCVQK-------MAKLVLVKAAGLLYHGMPVMGGHQAHDIFLDVARRIPLVDYCCGF-------------GLEEEIR   545
PhlVB:YP_001552317.1    LVNGVKQPLLE----CPTECILKGFTTAIYKDLIDVYAKDVISCWVAVDVEHRLRNNTNY-------------CVDIGAF   542
ASPV:NP_604464.1        VSKFESYD-------HQFHSILSVKSISALTRIAKIVLSLYDPCVVEAFSESRV-TNLAV-------------NVIIAAN   540
APV1:YP_009094347.1     ---------------HGLHHVLDGCGPHVFRRLVRKIADSFCNEFGIYRKSSYV-SSVAI-------------TVLQRKT   534
CTLaV:YP_009046478.1    HASQSVFSN------PHPNLIRRLVTLFISTWVGKTEADYYTSLLSLKKSLSQK-GLKLF-------------RLHDDRY   535
CRMaV:YP_007761581.1    NAHTLVFAS------SHPSITLMLVKSFINMWVGKTNDRYYQSLVALRQALNQK-GAKLF-------------MLHNESY   537


ZoVT:Z1                 IEEMMLILPLI-----------------------------------FRSKNKKFK--------------------IYFCK   545
ZoVT:Z2                 IEEMMLMLPLI-----------------------------------FRSKNKKFR--------------------IYFCK   545
ZoVT:Z3                 VEEMMYILPLI-----------------------------------FRSKNKKFK--------------------INFCN   545
PrVT:YP_009051684.1     I-------------------------------------------------------------------------------   522
PrVT:AHM92766.1         M-------------------------------------------------------------------------------   522
PVT:ADX41471.1          T-------------------------------------------------------------------------------   504
PVT:YP_002019748.1      T-------------------------------------------------------------------------------   504
PVT:AFV39891.1          T-------------------------------------------------------------------------------   504
PVT:AFU55321.1          T-------------------------------------------------------------------------------   504
PVT:AXK90539.1          T-------------------------------------------------------------------------------   504
AcVB:YP_004935358.1     INEPMVFSPID---------------------------------------------------------------------   511
GVA:NP_619662.1         --------------------------------------------------------------------------------   502
GVE:YP_002117775.1      --------------------------------------------------------------------------------   475
ASGV:NP_044335.1        --------------------------------------------------------------------------------   494
CVA:NP_620106.1         --------------------------------------------------------------------------------   498
DiVA:YP_006905850.1     IENRFWFLNDE---------------------------------------------------------------------   535
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------   519
ACLSV:NP_040551.1       NCLSLCAAPCD----------------------------EVIARTPFELNHRREK--------------------KELSL   552
GPGV:YP_004732978.2     FSAPLLLECSE----------------------------------PEKLKFTYDD--------------------LPFYQ   525
CtChV-1:YP_009103999.1  IEYNNKKLMAA--------------------------------MKEFGQNCQRDR--------------------RSFRP   559
CtChV-2:YP_009103996.1  NELFRKLSLAA--------------------------------DIKYPGSFQRDR--------------------KNFIP   567
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------   489
CPrV:AKN08994.1         NNIKRFVDPIFDMIIDEMNQLDLDIMNDGEEAAVEILDVNSNLDGKQSEHHDEEF--------------------VTPTG   628
CLBV:NP_624333.1        YSYSKQACTLSNYLTFLCAEGLDGFNLEEHLERRLKAAGHDVSDDEEEELTSAEQ--------------------AGPIK   626
CLBV:AFA43536.1         YSYSKQADVLAKCLSFVCEIGGGGEGLEFVLERRLQSAGRDPIESELEGLGKKTAESSGEADAANTLLETQISGLVAFIP   647
GCLV:YP_004936159.1     NKYVHMRHSDW------------------------------------KRRLKSFR--------------------SIGCA   568
CVNV:YP_001430021.1     LVFIEKFIGLV------------------------------------RKHSRSNV--------------------LEIPT   569
PhlVB:YP_001552317.1    KKLLLEPNHVN--------------------------------STIRSLVNKALR--------------------SRLSS   570
ASPV:NP_604464.1        LRACFAVTDLW-----------------------------RIFEGILLKECKRAQ--------------------GKMRK   571
APV1:YP_009094347.1     NSNLSFIFGTD---------------------------LNPMIIGFVRNYFASRR--------------------SSLLI   567
CTLaV:YP_009046478.1    FSLTRLANLMDSFSFKATLKNEVMKRLRLGGSLRGLLRYDPISENPSDKKDQRAR--------------------SNFSS   595
CRMaV:YP_007761581.1    NSLVILANLMDSHLFKNLLRNEIRKRLRLRNSVRGLLRNDLPPSCPDAKREVRFI--------------------SCYKS   597
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ZoVT:Z1                 LYLG--------------PNEI-----LVYSRGTMSYHHRV---------------------------------------   567
ZoVT:Z2                 LYLG--------------PNEI-----LVYSRRTMSYHHRV---------------------------------------   567
ZoVT:Z3                 LYLG--------------PNEI-----LVFSRKTMSYHYRE---------------------------------------   567
PrVT:YP_009051684.1     --------------------------------------------------------------------------------   522
PrVT:AHM92766.1         --------------------------------------------------------------------------------   522
PVT:ADX41471.1          --------------------------------------------------------------------------------   504
PVT:YP_002019748.1      --------------------------------------------------------------------------------   504
PVT:AFV39891.1          --------------------------------------------------------------------------------   504
PVT:AFU55321.1          --------------------------------------------------------------------------------   504
PVT:AXK90539.1          --------------------------------------------------------------------------------   504
AcVB:YP_004935358.1     --------------------------------------------------------------------------------   511
GVA:NP_619662.1         --------------------------------------------------------------------------------   502
GVE:YP_002117775.1      --------------------------------------------------------------------------------   475
ASGV:NP_044335.1        --------------------------------------------------------------------------------   494
CVA:NP_620106.1         --------------------------------------------------------------------------------   498
DiVA:YP_006905850.1     --------------------------------------------------------------------------------   535
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------   519
ACLSV:NP_040551.1       KCLD-----------------------FHIKKMKVKNVLEL---------------------------------------   570
GPGV:YP_004732978.2     FLSEDQE-----------IDGY-----FLRESVLDSIKDKAFHYSEGFFDP-----------------------------   560
CtChV-1:YP_009103999.1  FYIEIMLSGS-----------------FLPLRQICGDFTASC--------------------------------------   584
CtChV-2:YP_009103996.1  FFLTK---------------------------------------------------------------------------   572
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------   489
CPrV:AKN08994.1         LKGGDGLVTIESIEVD--PSEF-----RTPASELCGLATEPVSFPGDSCSVLMGNEPIAVADEYNICDVEGDGNCFMRAL   701
CLBV:NP_624333.1        ILADPLGFMKECLEEIPIETEP-----SLEERGQFSTDYHSEKFEINYNDIFNPHNCMNTHGDEIPTPSDGNCFFSAFTE   701
CLBV:AFA43536.1         TFSDEGESQHRADLEVESEGEIGKEESFEEGTLSCAEGHEAIKFEIDFSDIFRPHNCMNTHGYEIPTPMDGNCFFSAFAA   727
GCLV:YP_004936159.1     WFCMRV---------------------RSYERYICAYPDQAKSYKA----------------------------------   593
CVNV:YP_001430021.1     ------------------GLDW-----FMFPRRR----------------------------------------------   580
PhlVB:YP_001552317.1    WFEI--------------GPAW-----FLKAGRAHTRFLTSYPHD-----------------------------------   596
ASPV:NP_604464.1        RFHFEL------------GIRW-----FLFVDVSNQWFLPPCR-------------------------------------   597
APV1:YP_009094347.1     WFHDR-------------PESW-----FQFSRLRANQKFLRSPIWPNDLGLVEFRMRKNLALEISNFDRNSNLRKLGSFQ   629
CTLaV:YP_009046478.1    VVSE-----------------------LLSISSECPPSSTLTKTSGLQ--------------------------------   620
CRMaV:YP_007761581.1    LLAD-----------------------FKKMSEECS--------------------------------------------   610


ZoVT:Z1                 -----------------GDKLLNCKSFKDIEAEEKEKKGKENFFKKMFEQDEIEDVEMDEEDIENEITD--SRSFSIGEC   628
ZoVT:Z2                 -----------------GDKLLNCKSFKDIEAEEKEKKGKENFFKKMFEQDEIEDVEMDEEDIENEITD--SRSFSIGEC   628
ZoVT:Z3                 -----------------GDKLLNSKSFKDIETEEKERKNRENFLKKMFKQNEIEDVEMEEENFEEENVD--LRCFSIGEC   628
PrVT:YP_009051684.1     -----------------TGSFTKRRDPVLLTNYAHWGLPKREGIREVVMWDAEEEISQKEGGLKVMEGV--IHPNTLSSD   583
PrVT:AHM92766.1         -----------------DGIFFKRRDPIFLTNFEHWKLPVKKGIREVTMKDAFQAEEQAEDMPPEEQFK--PKEEERADS   583
PVT:ADX41471.1          --------------------------------------------------------------------------------   504
PVT:YP_002019748.1      --------------------------------------------------------------------------------   504
PVT:AFV39891.1          --------------------------------------------------------------------------------   504
PVT:AFU55321.1          --------------------------------------------------------------------------------   504
PVT:AXK90539.1          --------------------------------------------------------------------------------   504
AcVB:YP_004935358.1     -------------------------GFRSMRRFMIREGPIRGFSGLAIGWENDPNIRLKEGRITHEQYENIISGTKQATK   566
GVA:NP_619662.1         -----------------PRYVCSSRALIHFRQYLIKLGRFSFMESRAIKDIEDIQAGLEEGVITEEEAELRLLPTTKPKI   565
GVE:YP_002117775.1      --------------------------------------------------------------------------------   475
ASGV:NP_044335.1        --------------------------------------------------------------------------------   494
CVA:NP_620106.1         --------------------------------------------------------------------------------   498
DiVA:YP_006905850.1     ---------------------------------------------KRFENAKRESISRC---------------------   549
ObRV1:YP_009408144.1    -------------------------------------------------------IKNCYPDSFDIIRN--NKEFQSNAI   542
ACLSV:NP_040551.1       -----------------EVKLRERNTRISLSKKGVKKAGRSRMIPVHLLKPTCGEGNGKPEERNKEEAKIPMNEGTSKEE   633
GPGV:YP_004732978.2     -----------------ILFASSRGTFLGHSEMTDLSTSLNTLDKVIAENGEKSDVPILSADESSESVN--VKLLNESLT   621
CtChV-1:YP_009103999.1  -----------------VHETLDDMLDVLSEIKMAYPLTTDVIQLEKDVETKLEEISANANENEDSVTMVSVSSSSSSST   647
CtChV-2:YP_009103996.1  -----------------NFRMMPQLCYRDFVQSNQKEAIEEVIDMLDMIISPMPQIVTVEEIKDCLSVA--EVESSIDPQ   633
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------   489
CPrV:AKN08994.1         LTSIKGDDRTYPGSRSRLLNLSRQIGVNLTDSEEAQILREGEQFDEWMIMFTVNVMNLSLKIFQGDVSI--PRTLSPKLV   779
CLBV:NP_624333.1        TFEVERPDTLRSDFS--DWLMEFNGGSYASLAEMIRPNGVFMEAELIYLFCVFRGVTLIIHDRTHEKEN--VYAVHRGFE   777
CLBV:AFA43536.1         TFDCPDSKDLRSNFA--DWLDTFDGGSYADMGVKIRPNGVFMEAELIYLFCIYREVTLIMHDRTNDRES--VFAIHLGFE   803
GCLV:YP_004936159.1     -----------------LDEAYSTVVADLLGSLARNKLIISAAAPKFDKTSKVPREGVAEEIPAHCART--SAAFASAPC   654
CVNV:YP_001430021.1     -----------------NVFYLTCTPEAIVATKLMRGMWDNVVNELAASSALIKRIGITLSDRNTPVAP--LEVVLPPAP   641
PhlVB:YP_001552317.1    -----------------AIVYKEAKQGWSHVLKELAGGSRSLKHREMDYWFEKDRSSKDSGGTVENDED--DKGEPEGVV   657
ASPV:NP_604464.1        -----------------DGLIARSVSFDQFIKGCQRDNSLHNGRMSLRQVLKGPKLQALFDVSELSIIH--NVEMENAPE   658
APV1:YP_009094347.1     TAPTNSKSNTSSSEGASNHQREQRDQCDEATLQVNFQREIEFCMGSLPEANSFKSFTPCVEAVAETSYE--VQPLEPEPE   707
CTLaV:YP_009046478.1    -----------------QELWKMKKEVVTKQAPVLNEEQKPYKIPSEREKCSTQAIEKNEEPKSEVVST--KGETPPETS   681
CRMaV:YP_007761581.1    -----------------PILTLIATGGPFEQLNAMKKDFVLINQPSVGKFEKVKKCISKSTDASPDGGK--EHKLEPQHS   671
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ZoVT:Z1                  SNSRQIEREP-------------------NDIFDCSTDESIDEIDAEI----ENSKFK-------CSSNFNDGL----KV   674
ZoVT:Z2                  SNSRQIEREP-------------------NDIFDCSTDESIDEIDAEI----ENSRFK-------CSSNFNDGL----KV   674
ZoVT:Z3                  SGSRQIEKGL-------------------NDIFDCSTDESIDEIEAEI----ENNRFK-------CSDNFNDGL----RG   674
PrVT:YP_009051684.1      CAEDSESCGS--------------------VSGNDESMSSEEKEECEY----INGRFS-------PNGSFVESL----SM   628
PrVT:AHM92766.1          CGSEEEEEEL--------------------ERHNEMDLSSDDEEECTF----ISGKFS-------PNESFLDSL----RM   628
PVT:ADX41471.1           -----------------------------------------------------------------GEVSFEEAR------   513
PVT:YP_002019748.1       -----------------------------------------------------------------GEVSFEEAR------   513
PVT:AFV39891.1           -----------------------------------------------------------------GEVSFEEAR------   513
PVT:AFU55321.1           -----------------------------------------------------------------GEVSFEEAR------   513
PVT:AXK90539.1           -----------------------------------------------------------------GEVSFEEAR------   513
AcVB:YP_004935358.1      KQMGQITKCP-------------------------------------------------------CGAELKRTK----VE   587
GVA:NP_619662.1          TEIHMDDDTP-----------------GTSGESDVEKFKSVRSL---------------------CREEIYSEK------   601
GVE:YP_002117775.1       -----------------------------------------------------------------CDAGDPVGE------   484
ASGV:NP_044335.1         -----------------------------------------------------------------LKIDYSRLV------   503
CVA:NP_620106.1          -----------------------------------------------------------------QNTSFSCEV------   507
DiVA:YP_006905850.1      -----------------------------KTIFDEYDAILEEELPDDS-----------------IFKGFNKGV------   577
ObRV1:YP_009408144.1     NRSLKKSEPI----------------------HKNYGVVIINELSSPT-----------------VFEGFNKGY----IM   579
ACLSV:NP_040551.1        KGSEPPHSEV-----------------KREGVRLDEQHISEPLLSFKLDDFVGREKL--------CSAGLIKTVGNDYLL   688
GPGV:YP_004732978.2      YDAEPSECEV----------------PSVESKHEPEQIESSGEIIPESWTFVDNNNKEFY-----CDGAFSLEL----DF   676
CtChV-1:YP_009103999.1   SGREIEIDTS----------------DLSDHLNDIRGIKPDDRWSDLVVEIKDSSFLQ-------CGIDLDNLL------   698
CtChV-2:YP_009103996.1   EGNFQEKAEG-------------------SEENLFFSNSDDSEMLDNIKRVKIEDENL-------LSYGYSHRIDSLCEG   687
AVCaV:YP_008997790.1     -----------------------------------------------------------------GKTTYPSGP----II   500
CPrV:AKN08994.1          NTHGNDAKEIAILHRGNHFLGLLKKCTSESGAHDFDGNQPVEASSDNH----FDETFE-------TGFNDFEEL----RK   844
CLBV:NP_624333.1         EGHMVHRGNH----------------FVGIETYNISTLTSDPLLGD-------------------IPCGFSEEI----TK   818
CLBV:AFA43536.1          EGHMVQRGDH----------------FLGIETYRIDGFASDPNLSE-------------------LPCGYSEEL----RN   844
GCLV:YP_004936159.1      GSTASSECCV----------------------FELNPPAQIADLSCS------------------CDRTLAVLN----VL   690
CVNV:YP_001430021.1      EPIKQEGSNG----------------SVGVSNELAEDAIANFTPPAFI----RNFSCS-------CGLEMPISS----VV   690
PhlVB:YP_001552317.1     SSSSDDGSDD-----------------KSSQEYIEVDTKVVRRMTCS------------------CGVSMEIKT----LL   698
ASPV:NP_604464.1         AGSTLDAGIK--------------------PTSSPLEVVPIENARCNL----APCKCDLNCFIQPADVNSLHGN----LV   710
APV1:YP_009094347.1      ANGLVLGCIP----------------DASTPAFTFNSANQKDRLFSSV----VEENI--------TDIGILSPM----EL   755
CTLaV:YP_009046478.1     KTTSKFGELL----------------ATPEATAVSEPTDNVLASSDLF----ISSIIK-------TGPFGDHGV----IE   730
CRMaV:YP_007761581.1     EGVNAKTDEV-------------------IPKRVDQPEPKTEEGKTGSSDQFISSIIK-------VGPFKEPST----IS   721


ZoVT:Z1                  ---LFKSKET--LIHESFNVIYISKIELASINVRGKKIFNN-ELLIEPEKIL-------NRETNSLLVLK-IKQKGEFES   740
ZoVT:Z2                  ---LFKSKET--LIHESFNVIYISKIELASINVRGKKITNN-ELLIEPEKIL-------NRETNSLLVLK-IKQKGEFES   740
ZoVT:Z3                  ---LFKSKET--LVQENLNAIYISKIESASISIKEKKFVSN-ELLMEPEKIL-------NRETNSSLVLK-LNKEGKFES   740
PrVT:YP_009051684.1      ---LLNSKAA--YLHGGRKTILFSTVTGLDYGFGPHKYKQI-PCDFMEDLLK-------KVGFNSCLAQM-YGEGGSIGA   694
PrVT:AHM92766.1          ---MLNSKAA--YPHGGRRTMLFSTVTGLDYGFGPHRYEQV-KCDFMEELLK-------KTGFNSCLAQK-YEEGGSIGP   694
PVT:ADX41471.1           -----------------LQRMWYSDSQFVAGLAPKLRYVKMLTWKKDQELFS--------------------------EF   550
PVT:YP_002019748.1       -----------------LQRMRYSDSQFVAGLAPKLRYVKMLTWKKDQKLFS--------------------------EF   550
PVT:AFV39891.1           -----------------LQRMWYSDSQFVTGLVPKLRYVKMLTWKEDQKLFS--------------------------EF   550
PVT:AFU55321.1           -----------------LQRMWYSDSQFVAGLVPKLRYVKMLTWKEDQKLFS--------------------------EL   550
PVT:AXK90539.1           -----------------MQRMWYSDSQLVIGLVPKLRYVKMLTWTENQKLFD--------------------------GF   550
AcVB:YP_004935358.1      GGYIRSLIPGWTDQLQGRKAAFYSRHS-EEYSYPGGSHKTR-GWPAEIERMR--NELGLGEDFDHCLCQI-YEKGAGIPY   662
GVA:NP_619662.1          --------------LKGREVAFYSRHS-KEYKYNGGSHRSL-GWDEALNELT--QELGLDDSYDHCLIQR-YTAGGSIGF   662
GVE:YP_002117775.1       ------------------------LNEFKRMLGHPNNCENQ-KWMY-------------------------FEATPTPGQ   514
ASGV:NP_044335.1         -----------------RARRFRLRRDFLDPISKGKSPRKQ-LF---------------------------LESTGNIKS   538
CVA:NP_620106.1          ---FVDLFPS------TIRPAFYSDPN-----FTKVESFEP-EWDFLLGSWI----------FNHKQVRLCYEPSNSHAD   562
DiVA:YP_006905850.1      --------------------SFFKKKT---------------------------------MRMNECLIML---RTGVYNK   601
ObRV1:YP_009408144.1     V-------LK--GSMSGTRLIVYIVCA-AYLMHKQLEYNET-KANEVSSKHM-------NKKEKEMMILD-FMKTGDTDD   640
ACLSV:NP_040551.1        LARQIECMPL--SQLRGKKAAYFCLDFPMVYFHDKVSYPTF-EATGEIRHVMMKARSKWGIDFNSALIQV-YNDGCRLPL   764
GPGV:YP_004732978.2      AS-ILEGLKP--LNLRGRKAFFFHSNG-LPYFHDSVLYRTL-EVPGWLEEIFFKANEHFDVNFNSCLMQV-YEQDGSVGW   750
CtChV-1:YP_009103999.1   -----KGIKS--QKLKTRKAFYFCKDANFDYGHDKVKYQNM-GWPNFISELNKIACDVTGFKFNSVLINE-YTRGGRIHW   769
CtChV-2:YP_009103996.1   LQEKIEGMKG--KKINVRKAFYFCKNSRFDYGHDKYKYENL-GWPKFISDICDEGEKMTGKKFNSALINS-YCRGGKIYF   763
AVCaV:YP_008997790.1     N--ALQGLKP--KSFRGRSSFFFARSNEIDYGHNGFKYRTE-NWFAELDDFI-----PSDLIFNACLVQV-YDKGSKIGF   569
CPrV:AKN08994.1          VVGSISMFKK--TPLKNRDAFFFSESKSIDYGHNRIKYAHN-HWNGVDQLLP----SSLRNDYNAMLIQV-YKEGGSIGM   916
CLBV:NP_624333.1         FHFRPDHFNC--AQFRGRKAAFITKVD-ADYGHNGMVYPHN-SWVPSLEEII--QICGQGDDFNCALINF-YEANSSLGF   891
CLBV:AFA43536.1          FHFKPEHFNC--AQFRGRKGAFLTKVD-ADYGHNGMVYPHN-AWVPSLDEII--RICDHGDDFNCALINF-YGPNSSLGF   917
GCLV:YP_004936159.1      AYEALELEFP--DQLPGCRAGWYVKGPQVADVGGFLGCQQL-RWLDFFDSFL-ELHGAQPGSYNSCFAQV-FDLDSTFEY   765
CVNV:YP_001430021.1      GGDFVYFDLP--DVLPGRRAAWFTKDGSTAYTYKGGKHASM-GWDERLDLLL-EIHGFEGSLFDSALVQE-YEQGARIGF   765
PhlVB:YP_001552317.1     GSDMHAFKAK--DRLKGRVGGWYSKDG-TPYLYTGGSHISQ-GWPDWLELWM--QINKVPDKYNSCLYQI-YEEGASVGY   771
ASPV:NP_604464.1         FLDFIGGS-------KGRGASFYSRDL-KGYSYTGFSHVSR-GWPAFLDKFL-SDNKIPLNFYNQCLVQE-YSTGHGLSM   779
APV1:YP_009094347.1      V--LPSSAEA--TPLNGRQCYFFTRCGCIDYGHNKIRYKPN-KWFSGLDSIL----KDESTYYNACPLQI-YEAGAGIGF   825
CTLaV:YP_009046478.1     FIRSLSFNDG--HSHNGRKALFFSRGG-FAYGFNSVTYQSS-GWPSAFEEIY-------GDRFNSCLVQK-YEKSAKLGL   798
CRMaV:YP_007761581.1     FVEGLDFSKG--HNHKGRKSLFFSEGG-FSYGFGSIVYPSQ-GWPNAFKELY-------GDRFNSCLVQK-YNADATLGF   789
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ZoVT:Z1                 SFLNKEEIN--LDYIELLKLKGYAILSIEENGTCV----------NRDLKLEEIERVSLNE---ETSFKFRNLEEEDVIM   805
ZoVT:Z2                 SFLNREEIN--LDYIELLKLKGYATLSVEENGTCV----------NRDLKLEEIERVNLNE---ETSFKFRNLEEEDVIM   805
ZoVT:Z3                 SFLKKKEID--SDCIEVLQLKGHVVLSVNESGTYV----------NRSFKSEEIEKIKLNE---KTSFEFRNFEEEDAII   805
PrVT:YP_009051684.1     HYDDEKVYD--DDEILTWNLEGEADFTMFKKTGTE----------SVHLTRNQVLVMPKGCSRGEEKFKHAVENCTEGRI   762
PrVT:AHM92766.1         HFDDERVYD--DDEILTWNVEGEADFVMLKREGTE----------IVHLTPGSVVLMPKGSSRGPEKFKHSVHGCTKGRV   762
PVT:ADX41471.1          PSEESNEVE-MEDAFELRKRRTLXXX-XKERDENG-----------------------------ANSEECEQLDSEDDVG   599
PVT:YP_002019748.1      PSEESNEVE--MEDAFELRKGRTLKRGTKERDEDG-----------------------------ANSEECEQLDSEDDVG   599
PVT:AFV39891.1          PSEESDEVE-MEDAFECEEKENSEEEGPKERNENG-----------------------------ANSEEYEQLDSEDDVG   600
PVT:AFU55321.1          PSEESNEVE-MEDAFECEEKENSEEEGSKERDENG-----------------------------ANSEECEQLDSEDDVG   600
PVT:AXK90539.1          TSEESDEVE-MEDAFEYEQIEDAEKEGSEKEDEGE-----------------------------ADLKEDERSSSEDDVG   600
AcVB:YP_004935358.1     HADDETCYK--EPSVVTVNLFGEADFKTKCTNEL-----------SFRLTDGDVLTMGKGF---QSNHKHSVQNTGPGRV   726
GVA:NP_619662.1         HADDEPCYL-PGGSVVTVNLHGDATFEVKENQSGKIE--------KKELHDGDVYVMGPGM---QQTHKHRVTSHTDGRC   730
GVE:YP_002117775.1      NFVYQEVAK--DIYIKVYLITNPPLHELLLEGLIT-----------------------------LEEYKSMRGQLPGTET   563
ASGV:NP_044335.1        NPNAEKNSE-------------SGEIKIEGSAENDQ----------------------------PHEVSHTSMETEDGQG   577
CVA:NP_620106.1         SEEDVNRTS-------------------------------------------------------ETSSPEKTIADSSSVS   587
DiVA:YP_006905850.1     SKLISNIKH-VDDPFSTMEKHKRDRLNKVIKYYIG------------------------GV---EYEMPSSQVSELEEIT   653
ObRV1:YP_009408144.1    HVSKSRSTD-------------------------------------------------------EQKTKEQT--------   657
ACLSV:NP_040551.1       HSDNEECYD--DDGILTINVVGDAKFHTTCHDE------------VIDLKQGNEILMPAGY---QKKNRHAVEVASEGRT   827
GPGV:YP_004732978.2     HFDDEDCYD--DDPILTMNFNGTALFEIKNVVSSK-------------LDHKDFILMKSGL---QKREKHRVQYTSEGRI   812
CtChV-1:YP_009103999.1  HADDENVYDLDRNPVLTVNMIGEGMFSVKMGKYEH----------SFPMSPGDMILMKNGA---QKRMKHSVIA-KDRRV   835
CtChV-2:YP_009103996.1  HADDEHVYDSSDNPVLTINARGRGIFKYKVNKTGAVT--------ECLLDEGEAILMKEGA---QLRGKHSVHAISQ-RI   831
AVCaV:YP_008997790.1    HKDNEQCYA--GYPILTVNF-GLALFEFDSGE-------------AFNLTDGDTILLSGDY---LRKKRHRVTSLSDSRI   630
CPrV:AKN08994.1         HRDNEKVYD--NDSILSINLNGDALFQIEAKSSKRY---------SFRMKDGDYFLMKRDF---QAKFRHGVQGATEGRI   982
CLBV:NP_624333.1        HRDNERVYN--DDPILTVCTFGEGRFTIEFKDQVT----------SFLMTAGSFFLMPKGF---QKKARHSVSN-EMSRV   955
CLBV:AFA43536.1         HRDNERVYN--DDPILTVCTEGEGFFSIEFKEQTA----------SFLMTAGSFFLMPRGF---QRKARHSVRN-ELPRV   981
GCLV:YP_004936159.1     HSGDGGVFE-EGAPAYLFQTRGTSRVHVQGLGCCG----------ERALLGPMCFEMPASL---LLEHRWKISKSSTGCT   831
CVNV:YP_001430021.1     HSDDESIFK-VGSEILTMQLKGTSRFAIQGSRCYG----------SSALLGGCHFTMPAGF---QETHKHSVAECSSGRT   831
PhlVB:YP_001552317.1    HADDEPIFK-KGEEIHTCNLSGKAVFEIKCRNGAG----------GEYLEGPMQFTMPMDF---QGTHKHSVSGTTKGRE   837
ASPV:NP_604464.1        HKDDESIYD-INHQVLTVNYSGDAIFCIECLGSGF----------EIPLSGPQMLLMPFGF---QKEHRHGIKSPSKGRI   845
APV1:YP_009094347.1     HSDNEKVYH--RSPIKTINFCGEADFVVKAKGKRDVGVNA-----TCHMKTGQFFTMDSNF---QSYYQHSVQNCSEGRV   895
CTLaV:YP_009046478.1    HKDDEDCYD-DEHEVMTVNLFGTATLIFTADGAKGLERADPSKFLEITLSHGEYLLMPNGF---QKKFKHGVSCTSAGRI   874
CRMaV:YP_007761581.1    HADDEQCYD-QDHEVLTINLFGSATICFTKGDFSALNTSNPKLYLEVGLDHCDWLLMPRGF---QRNYKHSIKGTSEGRI   865


ZoVT:Z1                 MVMFKQTHRA----------------------------------------------------------------------   815
ZoVT:Z2                 MVMFKQTHRA----------------------------------------------------------------------   815
ZoVT:Z3                 MVMFKQTHRA----------------------------------------------------------------------   815
PrVT:YP_009051684.1     SITFRHQKRFMNG-------------------------------------------------------------------   775
PrVT:AHM92766.1         SITFRHQKRFMNG-------------------------------------------------------------------   775
PVT:ADX41471.1          SFEY----------------------------------------------------------------------------   603
PVT:YP_002019748.1      SFDY----------------------------------------------------------------------------   603
PVT:AFV39891.1          SFEY----------------------------------------------------------------------------   604
PVT:AFU55321.1          SFEY----------------------------------------------------------------------------   604
PVT:AXK90539.1          SFEY----------------------------------------------------------------------------   604
AcVB:YP_004935358.1     SLTFRNSIISNQA-------------------------------------------------------------------   739
GVA:NP_619662.1         SITLRNKTVDYEAR------------------------------------------------------------------   744
GVE:YP_002117775.1      SIVVRKDEVQ----------------------------------------------------------------------   573
ASGV:NP_044335.1        ---FEGSI------------------------------------------------------------------------   582
CVA:NP_620106.1         PFVSSNHEEGT---------------------------------------------------------------------   598
DiVA:YP_006905850.1     EITP----------------------------------------------------------------------------   657
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------   657
ACLSV:NP_040551.1       SVTLRVHKRD----------------------------------------------------------------------   837
GPGV:YP_004732978.2     SLTLRVQKR-----------------------------------------------------------------------   821
CtChV-1:YP_009103999.1  SLTFREQIRS----------------------------------------------------------------------   845
CtChV-2:YP_009103996.1  SITLRDQKRS----------------------------------------------------------------------   841
AVCaV:YP_008997790.1    SLTFRRHVCR----------------------------------------------------------------------   640
CPrV:AKN08994.1         NVTFRKHV------------------------------------------------------------------------   990
CLBV:NP_624333.1        SITFRKHV------------------------------------------------------------------------   963
CLBV:AFA43536.1         SITFRKHI------------------------------------------------------------------------   989
GCLV:YP_004936159.1     IMTFRKLRQGEPPVVET---------------------------------------------------------------   848
CVNV:YP_001430021.1     SITFRVLKGTEQPSAPLHPTNEKVEPGGG---------------------------------------------------   860
PhlVB:YP_001552317.1    SVTFRVLRACETAQEKEVDAEQEPESPPDTDEENELDKEKLSEDEAGGSEEKEVEAEPCGSSDQ----------------   901
ASPV:NP_604464.1        SLTFRLTKEGDSQVPIQEVVTICDHGDSDDRAALKALERRSHQSGGRPAVELEGHEREKVNSDSSDSAPVQEFLIQIDSS   925
APV1:YP_009094347.1     SLTFRYHVNNIAGLPIKH--------------------------------------------------------------   913
CTLaV:YP_009046478.1    SLTLRKQARSMSGATLHAGAD-----------------------------------------------------------   895
CRMaV:YP_007761581.1    SLTFRKQRRTLEGSLIQSRA------------------------------------------------------------   885
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ZoVT:Z1                 --------------------------------------------------------------------------------   815
ZoVT:Z2                 --------------------------------------------------------------------------------   815
ZoVT:Z3                 --------------------------------------------------------------------------------   815
PrVT:YP_009051684.1     --------------------------------------------------------------------------------   775
PrVT:AHM92766.1         --------------------------------------------------------------------------------   775
PVT:ADX41471.1          --------------------------------------------------------------------------------   603
PVT:YP_002019748.1      --------------------------------------------------------------------------------   603
PVT:AFV39891.1          --------------------------------------------------------------------------------   604
PVT:AFU55321.1          --------------------------------------------------------------------------------   604
PVT:AXK90539.1          --------------------------------------------------------------------------------   604
AcVB:YP_004935358.1     --------------------------------------------------------------------------------   739
GVA:NP_619662.1         --------------------------------------------------------------------------------   744
GVE:YP_002117775.1      --------------------------------------------------------------------------------   573
ASGV:NP_044335.1        --------------------------------------------------------------------------------   582
CVA:NP_620106.1         --------------------------------------------------------------------------------   598
DiVA:YP_006905850.1     --------------------------------------------------------------------------------   657
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------   657
ACLSV:NP_040551.1       --------------------------------------------------------------------------------   837
GPGV:YP_004732978.2     --------------------------------------------------------------------------------   821
CtChV-1:YP_009103999.1  --------------------------------------------------------------------------------   845
CtChV-2:YP_009103996.1  --------------------------------------------------------------------------------   841
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------   640
CPrV:AKN08994.1         --------------------------------------------------------------------------------   990
CLBV:NP_624333.1        --------------------------------------------------------------------------------   963
CLBV:AFA43536.1         --------------------------------------------------------------------------------   989
GCLV:YP_004936159.1     --------------------------------------------------------------------------------   848
CVNV:YP_001430021.1     --------------------------------------------------------------------------------   860
PhlVB:YP_001552317.1    --------------------------------------------------------------------------------   901
ASPV:NP_604464.1        LLEYALKSLSGLSKNVVNCDMCLCNSPWLKNEELRFSEALRDLAFAQGLIQLIDFLCLKVLRCAEVNRIISELPTHVFPL  1005
APV1:YP_009094347.1     --------------------------------------------------------------------------------   913
CTLaV:YP_009046478.1    --------------------------------------------------------------------------------   895
CRMaV:YP_007761581.1    --------------------------------------------------------------------------------   885


ZoVT:Z1                 --------------------------------------------------------------------------------   815
ZoVT:Z2                 --------------------------------------------------------------------------------   815
ZoVT:Z3                 --------------------------------------------------------------------------------   815
PrVT:YP_009051684.1     --------------------------------------------------------------------------------   775
PrVT:AHM92766.1         --------------------------------------------------------------------------------   775
PVT:ADX41471.1          --------------------------------------------------------------------------------   603
PVT:YP_002019748.1      --------------------------------------------------------------------------------   603
PVT:AFV39891.1          --------------------------------------------------------------------------------   604
PVT:AFU55321.1          --------------------------------------------------------------------------------   604
PVT:AXK90539.1          --------------------------------------------------------------------------------   604
AcVB:YP_004935358.1     --------------------------------------------------------------------------------   739
GVA:NP_619662.1         --------------------------------------------------------------------------------   744
GVE:YP_002117775.1      --------------------------------------------------------------------------------   573
ASGV:NP_044335.1        --------------------------------------------------------------------------------   582
CVA:NP_620106.1         --------------------------------------------------------------------------------   598
DiVA:YP_006905850.1     --------------------------------------------------------------------------------   657
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------   657
ACLSV:NP_040551.1       --------------------------------------------------------------------------------   837
GPGV:YP_004732978.2     --------------------------------------------------------------------------------   821
CtChV-1:YP_009103999.1  --------------------------------------------------------------------------------   845
CtChV-2:YP_009103996.1  --------------------------------------------------------------------------------   841
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------   640
CPrV:AKN08994.1         --------------------------------------------------------------------------------   990
CLBV:NP_624333.1        --------------------------------------------------------------------------------   963
CLBV:AFA43536.1         --------------------------------------------------------------------------------   989
GCLV:YP_004936159.1     ---------------------------------------------------TAPTVQKGVGVDSSFTWEQYGVTILSSHM   877
CVNV:YP_001430021.1     ---------------------------------------------------AVSSRLGAPEELSAFDYQIGPVRVENVGG   889
PhlVB:YP_001552317.1    ---------------------------------------------------SGECGGSEASRDETLAVDMECCTIEYKEM   930
ASPV:NP_604464.1        RGTMHIVDLDDESIRGDVKEGSFSGFRRWKVMSCSTDLIMLAFLKPKMTLGGELRSHEDECELSDLTEKLHGCSVILSRK  1085
APV1:YP_009094347.1     -----------------------------------------------------------TCGEFGDTESLFDVLIRRSFS   934
CTLaV:YP_009046478.1    ---------------------------------------------------GGNNNGSGNEEDDSYYEEMNKCSISSAPD   924
CRMaV:YP_007761581.1    ---------------------------------------------------ESGDSNSDDGEGGFYFEEINKCSITSAPD   914
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ZoVT:Z1                  --------------------------------------------------------------------------------   815
ZoVT:Z2                  --------------------------------------------------------------------------------   815
ZoVT:Z3                  --------------------------------------------------------------------------------   815
PrVT:YP_009051684.1      --------------------------------------------------------------------------------   775
PrVT:AHM92766.1          --------------------------------------------------------------------------------   775
PVT:ADX41471.1           --------------------------------------------------------------------------------   603
PVT:YP_002019748.1       --------------------------------------------------------------------------------   603
PVT:AFV39891.1           --------------------------------------------------------------------------------   604
PVT:AFU55321.1           --------------------------------------------------------------------------------   604
PVT:AXK90539.1           --------------------------------------------------------------------------------   604
AcVB:YP_004935358.1      --------------------------------------------------------------------------------   739
GVA:NP_619662.1          --------------------------------------------------------------------------------   744
GVE:YP_002117775.1       --------------------------------------------------------------------------------   573
ASGV:NP_044335.1         --------------------------------------------------------------------------------   582
CVA:NP_620106.1          --------------------------------------------------------------------------------   598
DiVA:YP_006905850.1      --------------------------------------------------------------------------------   657
ObRV1:YP_009408144.1     --------------------------------------------------------------------------------   657
ACLSV:NP_040551.1        --------------------------------------------------------------------------------   837
GPGV:YP_004732978.2      --------------------------------------------------------------------------------   821
CtChV-1:YP_009103999.1   --------------------------------------------------------------------------------   845
CtChV-2:YP_009103996.1   --------------------------------------------------------------------------------   841
AVCaV:YP_008997790.1     --------------------------------------------------------------------------------   640
CPrV:AKN08994.1          --------------------------------------------------------------------------------   990
CLBV:NP_624333.1         --------------------------------------------------------------------------------   963
CLBV:AFA43536.1          --------------------------------------------------------------------------------   989
GCLV:YP_004936159.1      SKAPDGRIEPQRGDGSCFFHCMEPFTNLEASLLRRTIAKEMARDSKVLESDLVECQGNGPVSDGVIAYTIRFLGLKVRFF   957
CVNV:YP_001430021.1      PRAGSYTLTDVPGDGSCFFHAVGLSFNLTGLALRRALLDAAPEIGGMFPAEAFAELRGGGAVSDVCVCYVAHALKSSIAV   969
PhlVB:YP_001552317.1     PKGIKYNKVDVRGDGNCFWYALECALGLDPMEMKRLCKQVKYKDPTKQRKLNDQLQTGAYAEDEIISAATHIFNFQLICL  1010
ASPV:NP_604464.1         FEPDLFHSFDVEADGNCFWHSVGPLIGVDGEYLKRILHDQAKKDGVKCPRLSKQLEGNTWAEREAVAYFCSHYGIRLNVL  1165
APV1:YP_009094347.1      YSSKNFHTFPVPGDGSCFWHSLGALLGVDGEELKKISAREILKNEVLSRNLSLSAQMENKQYAERESIAAFCRIQSIHLV  1014
CTLaV:YP_009046478.1     SAKCSLSVFPVKADGDCFWHAVSSIFGLDALELKNLVKERAIEEGCVDQKHMKDFLHEMEAKVYASNASITATCFLMNIK  1004
CRMaV:YP_007761581.1     SVKCSLSVFPVKADGDCFWHAVSSIFGLEAKELKQLVHDRAIAEGCIDKCHMKDFLHEMEPKVYASNASLAATCYLMNLK   994


ZoVT:Z1                  -------------DGSSVDSLKVRHRELPN-------NLYEITQNLVNGCFIDCLCDFLKMSRCQTISIMYSY--DDAV-   872
ZoVT:Z2                  -------------DGSSVDSLKVRHRELPN-------NLYEITQNLVNGCFVDCLCDFLKMSRCQTISVMYSY--DDAV-   872
ZoVT:Z3                  -------------DGSSVDSLKVRHRELPS-------NLYEITQNLVNGCFIDCLCDFLKMSRCQTISVMYSY--DDAI-   872
PrVT:YP_009051684.1      -------------EPVEIENFKRSFIQLPD-------NLCDLISKMSNACFLDCLADHLCMNRSAVFNLLFDQ--DKSV-   832
PrVT:AHM92766.1          -------------DPVEIENYKRTQMEIPE-------NLDEMIKKMSNACFLDCLADHLAMNRNGVFNLLFDQ--DRSV-   832
PVT:ADX41471.1           -------------EETKADSXEIDFEAILN-------RVNSG--GLRGVCLLDALAKITGTKREITLXXLLGR--DGTW-   658
PVT:YP_002019748.1       -------------EETKADSYEIDFEAILN---------RVNSGGLRGVCLLDALAKITGTKREITLSILLGR--DGTW-   658
PVT:AFV39891.1           -------------EETKADSYEIDFEAILN---------RVNSGGLRGVCLLDALAKITGTKREITLSILLGR--DGTW-   659
PVT:AFU55321.1           -------------EETKADSYEIDFEAILN---------RVNSGGLRGVCLLDALAKITGTKREITLSILLGR--DGTW-   659
PVT:AXK90539.1           -------------EETKADSYEIDFEAILS-------KVNSG--GLKGVCLLDALSKITGTKREITLSILLGR--DGTW-   659
AcVB:YP_004935358.1      -------------DEDDLSEYEETEAGFDE-------TLVVLEKNVKNLCCLDRIAEHMGVKREVCASIIHSK--MPRA-   796
GVA:NP_619662.1          -------------KGDEDSEYEEDKAELDE-------GIDYLQKNQGNMCSLKAFADHMQLSTPSVIAIVNGA--SPQT-   801
GVE:YP_002117775.1       -------------ETEADDSFDNDMVKLKE--------------IKKNLCLIQPIAEHFALKAPVLISKATVEI-PN---   622
ASGV:NP_044335.1         -------------PVDLINCFEPEEIKLPK-------------RRRKNDCVFKAISAHLGIDSQDLLNFLVNEDISDEL-   635
CVA:NP_620106.1          -------------SSQQSEEKPISEQEKKE--------------TRKNDCFFKAVGETIGIPANSLIERILCSD-SEDLK   650
DiVA:YP_006905850.1      -------------INRLSSSNPMDEKTFRN---------------LANKCCFDCIMEIKKIDHVALVNYIT----ETKF-   704
ObRV1:YP_009408144.1     -------------NLSICESKPIDERTFCN---------------LKNKCCFDSVLKCLNIDLFELVDRLK----GSVF-   704
ACLSV:NP_040551.1        -------------FSFESKLRFIKGKFD---------------------CLFVSVAEIIHKKPEEIMMFI------PHI-   876
GPGV:YP_004732978.2      -----------------PPNFHHGLRFLP-----------------KVGCFLQAVSEQVFTKVEDLAIKLGTLY-GDIL-   865
CtChV-1:YP_009103999.1   -------------KSLISLASSIEEEEIND---------------LKESCLIDSLAEEIRISRSKLINLLVKE--DSTF-   894
CtChV-2:YP_009103996.1   -------------FSKLNESCNLKEEDLLD---------------LKESCLIKALAKEIKISELKLSNLIINE--DPTY-   890
AVCaV:YP_008997790.1     -------------MNKSPLEFFSNNGKLG-----------------KNKCIIHAVAMALGQTSNTVANKIVAQ--RPDL-   687
CPrV:AKN08994.1          -------------RNSRNEPIYLGISKF------------------KNICLMRSLSILEKRPLYDILLALIKKN-KNYW-  1037
CLBV:NP_624333.1         -------------RRLNGSPIAIREENY------------------KNTCLINAFSKAMKRSKQAIIAKLKTVN-SPFW-  1010
CLBV:AFA43536.1          -------------RRLDGSPIAIRQDNY------------------RNVCLIRALSKALNRGMQAIIAKLKTVN-NPFW-  1036
GCLV:YP_004936159.1      SPELNEVR-----KFSTCTATNFWVDVLHH-------GNHFDLLYPTNDCVLIALEQGLGRKRGDILKVLSRPQ-HSDI-  1023
CVNV:YP_001430021.1      ISHHEGCM-----RVFCPDNWENKIDLLHK-------DGHYNVVNYKNDCALLAVAETLGRTKREVTEVVCKAK-HGGL-  1035
PhlVB:YP_001552317.1     S------------AGDTGLVVYSPKREFSQVVYMHIENQHFNWVEPKNNCLVRAIAVSLNRKTSEVLKVLEEGS-CVGS-  1076
ASPV:NP_604464.1         Y------------TREECTWIFKPHEVLKA-ATLICQDNHFKPCMPVNGCVIRAISSALNRREVDVLAVLGKPA-HEDL-  1230
APV1:YP_009094347.1      VLLPD--------QNFSYEFLPMQNAEVTQ-LFVKLSGEHFEPALPINGCVVKSIAETLNQTEAKILSVIGRPN-NRLI-  1083
CTLaV:YP_009046478.1     LIIKLVESKHSGWVVVEPLNSSNEKISLGY-LVLNQRVQHFDLAVPKEGCVIRAISEFLKQNPTKVLSVLSANC-SKEL-  1081
CRMaV:YP_007761581.1     LIIKLTGLEDDSWVVVEPLALSNERASIGY-LVLNQKCHHFDLAVPKEGCVVRAVSEFLKQNPTKILSVLSANC-SKDL-  1071
                                                                          *  .  .
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ZoVT:Z1                --LDLIVNDKGFTVAEMINILIKMDIPGVIFDGKK--NIRYLEHGSYTDIFLR-VREDHVSME---S-------LMYDGT   937
ZoVT:Z2                --LDLIVNDKGFTVAEMINILIKMDIPGVIFDGKK--NIRYLEHGSYTDIFLR-VREDHVSME---S-------LMCDET   937
ZoVT:Z3                --LDLIVNDKGFTVAEMINILIKMDIPGVIFDGSK--NIRYLEHGSYTDIFLR-VREDHVSME---S-------LMCDET   937
PrVT:YP_009051684.1    --ITNVLEDKGFTLSEVIDHLMNLDIPGRIVSNGE--VINYLEKGSFKPIDLL-MRDGHIGLNVQHD-------VLYDTK   900
PrVT:AHM92766.1        --LTNVVEDKGFTLAEVIDHLTNLDIPGRIVSSGE--VINYLEKGSFKPIDLM-MRDGHIGLNVQHQ-------VLYNSK   900
PVT:ADX41471.1         --ADWFLKDKGATFDDVFKAVSDLDLNCTICTKEG--SFNAHVNRNYKHNFLY-LFDEHVSLERPKV-------MLFEQV   726
PVT:YP_002019748.1     --ADWFLKDKGATFDDVFKAVSDLDLNCTICTKEG--SFNAHVNRNYKHNFLY-LFDEHVSLERPKV-------MLFEQV   726
PVT:AFV39891.1         --ADWFLKDKGATFDDVFKAVSDLDLNCTICTKEG--SFNAHVNRNYKHNFLY-LFDEHVSLERPKV-------MLFEQV   727
PVT:AFU55321.1         --ADWFLKDKGATFDDVFKAVSDLDLNCTICTKEG--SFNAHVNRNYKHNFLY-LFDEHVSLERPKI-------MLFEQV   727
PVT:AXK90539.1         --ADWFLKDKGATFDDVFKAVSDLDINCTICTKEG--SFNAHVNKNYKHSFLY-LFDEHVSLERPKL-------MMFEKK   727
AcVB:YP_004935358.1    --IEEFKEG-GMSISTFIHVVKQLDLACYIQNERG----NIQVPGKFRELKVS-ATGEHMSAYLGPT-------ATSTLA   861
GVA:NP_619662.1        --LREIEDG-GYSLATLVNLSKALDFPIAIHGERG----YAETPGSYRRLHLK-ITSGHVEPFEGVT-------SKGGFR   866
GVE:YP_002117775.1     --FARYLSDKGLSMPGLYMLCKNMGLTLSILSDEG----YLHLQGSYKPLGLV-IKDDHATPGRYIQ-------RQNRPA   688
ASGV:NP_044335.1       --LDCIEEDKGLSHEMIEEVLITKGLSMVYTSDFKEMAVLNRKYGVNGKMYCT-IKGNHCELSSKEC-------FIRLLK   705
CVA:NP_620106.1        PVIEQLNLDHPISSKLLEVCCKFLGYRVHIYYGDS--IIKLNDDINMHAIHIGGKPGHLFCINQERS-------KIPKDS   721
DiVA:YP_006905850.1    --MDLLLKDNGLLQKELIELCNFLNIKVNIINQSG--TRLIYENDNDNTLI---LTERHCKLVKTES-------ISDWLL   770
ObRV1:YP_009408144.1   --IELLIKDQGLLESEFLDLLDLLGLNENVMNAAG---FLVKECTESSGIFI--LSSNHCRFISKEE-------CGDWFN   770
ACLSV:NP_040551.1      --MDRCVSNRGCSLDDAKAICEKYEIKIECEGDCG--LVECGTSGLSIGRML--LRGNHFSVASVRR-------SSMDSL   943
GPGV:YP_004732978.2    --ANW-----GVSLADVDKFAEKLGIRLVLTNGFE--VIRAGVEGPEVSMSF--SNGHFRSNSNSRM-------NKGKGV   927
CtChV-1:YP_009103999.1 --LIKIKDDKGLTIDDLSIIANLLNLSVRVLIDGQ-WSYFGVKESNYRLISLK-LIKRHFSVYNGEV-------LKLALG   963
CtChV-2:YP_009103996.1 --LDKIKKDRGMTIDDLEKISNLLCLKVRVLIDGQ-WQYFGVKESNFRGVSLR-LSGSHFDAYEKES-------IKIALG   959
AVCaV:YP_008997790.1   --LQCLVDDEMLDKQTTETICVIMNLHATIVNEDEGETMELNPEG---------LIKSSFSVLDEHM-------MVLSDI   749
CPrV:AKN08994.1        --TSFLEFGVGGTLADLNQAAEDLSFRFELYMNEK--WIAGGNRGPIYRLN---LSDDHFSVHRELSGNVEDTQLNFSKA  1110
CLBV:NP_624333.1       --SRYLSEGNGGSIEDCQSACEALDVTVDLNVNGK---CVVLGKGALRISMA--LRNNHFSVINAAQ-------LMERTF  1076
CLBV:AFA43536.1        --SRFLSDGNGGSVEDCLAACEALGITVDLFVDGK---CLVLGEGAVRVSLA--LKDNHFSVVEEHR-------SIQRTF  1102
GCLV:YP_004936159.1    --FQIATGGVGLTLELLEPIFQCFQIDARVLCGSE--VFTYPTSGTFALDFE--LADGHLSFKSARR-------KETVSS  1090
CVNV:YP_001430021.1    --LRSMRTGEGLKVELLGELFKIFSIKALVKCNGQ--LHRLNPEGKILGHYR--LEDGHIQVDKGLI-------KQLGSA  1102
PhlVB:YP_001552317.1   --VGTLWRGEGVALEDLDFYFDRFGINAMVEFEGK--AYNFNETGHLPAAFT--LKDGHIEFIGRNS--PSTVPMMRGRV  1148
ASPV:NP_604464.1       --FEEVAEGRGFSIFDLTRLFEIFSICGSVDTGGE--LIMVNENGRIPAEFS--LEKEHLAHIPTLS-------RRKFSP  1297
APV1:YP_009094347.1    --LEGLVEGEGLNIEDLEAAFSVFGICARVSTERG--VFTLNKEGNLHANYE--LKSGHIMYLKKAS-------SSQFAP  1150
CTLaV:YP_009046478.1   --LHELMSGLGIQEFFLEEIFKVFDICAEVSDGEK--SRILNANGSRSAKFT--VEQDHFSFSPGVK-------ASTNLG  1148
CRMaV:YP_007761581.1   --LHELMSGLGIQEFHLEEIFSIFDICAEVSDGAS--SRVLNKKGSRSAKFI--VDKDHFSFCPGTK-------ASTNLG  1138


ZoVT:Z1                GTLNID----------------------ESLEMS-----GANRVHPSYS-VERARVCMKSLQEGATG-------IVLTKF   982
ZoVT:Z2                GTLNID----------------------ESLEMS-----GANRVHPSYS-VERARVCMKSLQEGATG-------IVLTKF   982
ZoVT:Z3                GTLNID----------------------ESLEMS-----GANRVHPSYS-VERARICMKSLQEGATG-------IVLTKF   982
PrVT:YP_009051684.1    EVKVEELI-------------------------------GADIIRPHFS-VERARVLVKSMMEGMTG-------VILNRF   941
PrVT:AHM92766.1        DIRVEDLI-------------------------------GADVIKPNFS-VERARKLVKSMMEGLTG-------VVLNRF   941
PVT:ADX41471.1         RHQKIDFL-------------------GAFEKCP-----GAGKFRYEAL-AERGSLLASALKDNLTG-------VISSKF   774
PVT:YP_002019748.1     RHQKIDFL-------------------GAFEKCP-----GAGKFRYEAL-AERGSLLASALKDNLTG-------VISSKF   774
PVT:AFV39891.1         RHQKIDFL-------------------GAFEKCP-----GAGKFRYEAL-AERGSLLASALKDNLTG-------VISSKF   775
PVT:AFU55321.1         RHQKINFL-------------------GAFEKCP-----GAGKFRYEAL-AERGSLLASALKDNLTG-------VISSKF   775
PVT:AXK90539.1         KHQVVNYL-------------------GAFENCP-----GAGRFEYEAT-AERAELLASALKDNLTG-------VISSKF   775
AcVB:YP_004935358.1    TA---------------------------LDFNP-----DVSRLSIEVT-QSRAIHLLESFREGFTG-------VNLNKY   901
GVA:NP_619662.1        EA---------------------------MLLGD-----GVGVGHFRVD-KAKADRLAQSFYNGNTG-------VLLGKY   906
GVE:YP_002117775.1     EALAVNP--------------------------------GVGQMEIEVV-SENARALQASFEKGFTG-------LILNDH   728
ASGV:NP_044335.1       EGGEAQMS------------------NENLNADS-----LFDLGRFVHN-RDRAVKLAKSMARGTTG--------LLNEF   753
CVA:NP_620106.1        QIKVPEVG---------PQSFIGSIFSKTYGSGS-----SAPIHLGQID-ITKALVLVSAFESMNLGVRVDRKAILEGQL   786
DiVA:YP_006905850.1    DDN------------------------KDFLDVT-----GVSSIIKNVFDYKRSKKLYDSLSKGTSG-------VFFNMI   814
ObRV1:YP_009408144.1   KVK------------------------GGLISLP-----GVNYLLKDINCIKRAGRLFKSLSRGNTG-------ILFNSI   814
ACLSV:NP_040551.1      ANSSKEIK-----SDGVLDHVTFNFHKRLKLVEP-----DLTNADIKVD-SSRAGKLLKSLMDGMTG-------IVSHNS  1005
GPGV:YP_004732978.2    ESFPKEFA------RKVSDEMSNDANPQIIQNLNEVYGVFLNQTIFKLD-PKRAQRLLKSLLDGSTG-------VHCNSS   993
CtChV-1:YP_009103999.1 DESSDKLI-KLSDSG-----FYNSFLNKIDPRNK-----FVNKFDRMIN-FERAALLIHSFLRGSTG-------VVTSSG  1024
CtChV-2:YP_009103996.1 DEVSEKKVQKSADGA-----FFEGFLQRIDPKNE-----FVNRFERVID-LDRAAKLIDSFQKGTTG-------VICSEN  1021
AVCaV:YP_008997790.1   PNCRSKKG---IDICMSPDLANSNCAANYEVTCQ-----NLQVIQYQAD-HERAIKLMNSFLAGTTG-------AVLNEL   813
CPrV:AKN08994.1        KSKQSNFS------------SSDDDNSFDLDSIE-----HVNKSLFEPL-NDAAELLRQSFLNRTTG-------KILSDA  1165
CLBV:NP_624333.1       VSHLLEKG------------NVNVLEGFDAMLSGDVGAAGVNKIQFAAN-FEFARILANSFLNMTTG-------ICLGKA  1136
CLBV:AFA43536.1        VSHLAKKS------------NLRVMDGLDEMLQSEMST-GVNCVQFIAD-FEHARVLANSFLNMTTG-------ICLSRA  1161
GCLV:YP_004936159.1    CLKVVEAS----------------PHGRLVLNCA-----GTGVL-FEIC-SNTAHKLAESLFDGRTG-------IVSSKL  1140
CVNV:YP_001430021.1    PVKVIEHP---------------VHGSGMVLIAA-----VATQLSFEIN-AEIGDKLAECLVSGRTG-------VISSQL  1154
PhlVB:YP_001552317.1   NTLTVSPN-------------------SLLIIKA-----AGSTIEFRPD-YSRAKCLADCFHTGCTG-------VMNSKI  1196
ASPV:NP_604464.1       IVSDLNRV----------------SNSAMRFLAI-----NGAEVDYRPS-IDRASTLLDSFEIGATG-------VLCQGI  1348
APV1:YP_009094347.1    TNPIQNFN----------------GQGPEIFLRG-----IVSEVDYKPS-WGRARNLEESLLNGTTG-------ILCDRT  1201
CTLaV:YP_009046478.1   SFKAPSGG------------QTIPIEQYETFLRG-----NANVIPFTPS-LIAAKKLANSFLSGQTG-------VINSKI  1203
CRMaV:YP_007761581.1   VFKAPSGC------------PMIAIEKYDEFLRS-----SANVVPFTPS-LPLAKKLADSFLSGQTG-------VINSKI  1193
                                                                            .     .:     *
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ZoVT:Z1                 KFEFNKILPNHSNKTFC----------------------------------ISGFAGSGKSRGIQDLCCGIL--------  1020
ZoVT:Z2                 KFEFNKILPNHSNKTFC----------------------------------ISGFAGSGKSRGIQDLCCGIL--------  1020
ZoVT:Z3                 KFEFNKILPNHSNKTFC----------------------------------ISGFAGSGKSRGIQDLCCGIL--------  1020
PrVT:YP_009051684.1     KHAFNELLPRHENRVMC----------------------------------IAGFAGSGKSRALQGVCASVL--------   979
PrVT:AHM92766.1         KYAFNELLPHHGNKVMC----------------------------------IAGFAGSGKSRALQGVCSSVL--------   979
PVT:ADX41471.1          NWDPKCEFVDIEKEILV----------------------------------VAGFAGSGKTRGICQIVKSMF--------   812
PVT:YP_002019748.1      NWDPKCEFVDIEKEILV----------------------------------VAGFAGSGKTRGICQIVKSMF--------   812
PVT:AFV39891.1          NWDPKCEFVDIEKEILV----------------------------------VAGFAGSGKTRGICQIVKSMF--------   813
PVT:AFU55321.1          NWDPKCEFVNIEKEILV----------------------------------VAGFAGSGKTRGICQIVKSMF--------   813
PVT:AXK90539.1          NWDPKCSFDNVKKEILV----------------------------------VSGFAGSGKTRGICQVVRAMF--------   813
AcVB:YP_004935358.1     QKRP--LGTDIDNTLID-------------------------------VYGLFGFAGSGKSYYPQTLLRCCN--------   940
GVA:NP_619662.1         NKGKMHTGEIEEPKEVLT---------------------------------AFGFAGSGKSHWCQTILKHCS--------   945
GVE:YP_002117775.1      RGKWAAKIPQGARAQLT-------------------------------VSMCLGFAGSGKTSSITQMLKLGH--------   769
ASGV:NP_044335.1        DLEFCKNMVTLSELFPENFS------SVVG--------------------LRLGFAGSGKTHKVLQWINYTP--------   799
CVA:NP_620106.1         ISNGFLAFLKRKNNEGHKVI------KIQS----------------LPVYPFIGFAGSGKSFGLTEKLINGD--------   836
DiVA:YP_006905850.1     KKKNDESEKKKDKNRVIEMM--------NFFFEDEINEKRKLTGRSEPIYGFFGFAGSGKSREIQNYINTNY--------   878
ObRV1:YP_009408144.1    KKKSDESEKRKDKNRVIEFL------NLIF-DNDDDHEVEIVK-RDEPIYGFFGFAGSGKSRAIQGFINSEF--------   878
ACLSV:NP_040551.1       THEGWRMIKGINSTSEMRSFMNMVRGQIEEPKSDLFDKVQELNFMKVKIYGIFGFAGSGKSHAIQNLIQTEF--------  1077
GPGV:YP_004732978.2     LKEGWKMIPNAKSSEFVTKN---------YINSSDIWKGSALWNAKINISGIFGFAGSGKSHGIQRLLNEKF--------  1056
CtChV-1:YP_009103999.1  FNNGVDYFSGRKRNIDPESF------RDPK----FLKEMTKGD-AVVKGAVILGFAGCGKSRPVQMALDSMD--------  1085
CtChV-2:YP_009103996.1  FGLGVKPFSGREKNLDSSKF------DDPS----FLKKLIGEE-FLIKGAAIIGFAGCGKSRPVQMALSNMD--------  1082
AVCaV:YP_008997790.1    VFKGSRFFTFMDSVNERKSD------------------------FVEELSFVPGFAGSGKSLGLLNEVKRISREIHLAKE   869
CPrV:AKN08994.1         FGENGAHLRRIRIVKSDDPF-------------------------PEEVYFSCGFAGSGKSLSLQSKLKSNF--------  1212
CLBV:NP_624333.1        LDNGEKYFLHILKDRVKQIG--------------------------IDVTMVCGFAGSGKSRKLQSWLHSRK--------  1182
CLBV:AFA43536.1         LDNGEKYFLHMSEERPKQIG--------------------------FDVTAICGFAGSGKSRQLQSWLHARK--------  1207
GCLV:YP_004936159.1     FNNRERFEVSSTSLLPRTLN------------------------------VICGVFGCGKSTLLCKALEKGL--------  1182
CVNV:YP_001430021.1     FNGRQKLTIPAGSDGKSRAV-----------------------------NLITGVFGCGKSTLMKRSFESGL--------  1197
PhlVB:YP_001552317.1    FNNSEHLLAHVNINDRPNTV---------------------------QINSVLGTFGSGKSSLFRRFFDANP--------  1241
ASPV:NP_604464.1        KEAQKDLASKLIPELVHERK----------------------------LIMILGTFGCGKSSLFKKFIEKSP--------  1392
APV1:YP_009094347.1     INLQKNWLTVDRKLNDNSRN----------------------------LGVVLGTFGSGKSSLFKRFIVKNP--------  1245
CTLaV:YP_009046478.1    ISGQYDWLADTNKLCFDERK----------------------------IGAIVGTFGSGKSHNVIELLRHNL--------  1247
CRMaV:YP_007761581.1    VAGQYDWLANTNKLCFEERR----------------------------VGAIVGTFGSGKSHNVIELIRHNL--------  1237
                                                                             *  *.**:


ZoVT:Z1                 -------------------NSEN-VILISPRSNLRSDWEKKIRNGLNNQN----------------------------FK  1052
ZoVT:Z2                 -------------------NSEN-VILISPRSNLRSDWEKKIRNGLNNQN----------------------------FK  1052
ZoVT:Z3                 -------------------NSEN-VILISPRSNLRNDWENKIKNGLNNQN----------------------------FK  1052
PrVT:YP_009051684.1     -------------------NKKN-VILSSPRKNLLRDWESKIDEKLKGKE----------------------------RL  1011
PrVT:AHM92766.1         -------------------NKKN-VILSSPRKNLLRDWESKIGDKLKGKE----------------------------MH  1011
PVT:ADX41471.1          -------------------NNKK-TLVLSPRKNLADDWVKNLANLHRP------------------------------SH   842
PVT:YP_002019748.1      -------------------NNKK-TLVLSPRKNLADDWVKNLANLHRP------------------------------SH   842
PVT:AFV39891.1          -------------------NNKK-TLVLSPRKNLADDWVKNLANLHRP------------------------------SH   843
PVT:AFU55321.1          -------------------NNKK-TLVLSPRKNLADDWVKNLANLHRP------------------------------SH   843
PVT:AXK90539.1          -------------------NKKT-TLVLSPRKNLADDWVKNLANLHRP------------------------------SN   843
AcVB:YP_004935358.1     -------------------MKDT--LVIVPRKALKADWSEKVK-----------------------------------DG   964
GVA:NP_619662.1         -------------------VEKV--LVISPRKVLRDDWVAKIS-----------------------------------KK   969
GVE:YP_002117775.1      -------------------QMAV--AVVSPRKNLCEEWKKELLD----------------------------------TD   794
ASGV:NP_044335.1        -------------------SVKR--MFISPRRMLADEVEPQLKG----------------------------------TA   824
CVA:NP_620106.1         -------------------CSQN-FMFTAPRKKIIGQIHERIDSRQYDDKLKIS------------------------RK   872
DiVA:YP_006905850.1     -------------------NMDGCVTVVSPRVELLKDWEKKISVAN--------------------------------KK   907
ObRV1:YP_009408144.1    -------------------NKKGFVTIISPRSELLKDWQSKVKTQN--------------------------------KH   907
ACLSV:NP_040551.1       -------------------KGSQGIMVICPRRFLAKDWSEKGV-----------------------------------DE  1103
GPGV:YP_004732978.2     -------------------SGSNEILLISPRVLLAEDWRDKV------------------------------------KH  1081
CtChV-1:YP_009103999.1  -------------------SPMK-ILLISPRVNLLADWKLKVSN----------------------------------KN  1111
CtChV-2:YP_009103996.1  -------------------SPLK-VLLISPRVNLLDDWKKKVNN----------------------------------GN  1108
AVCaV:YP_008997790.1    KKGMGKGSGKGHEKKERNRGNLKSMCIISPRRNLADDWETKLGPSAL-------------------------------EH   918
CPrV:AKN08994.1         -------------------KLKF--LVICPRVELKEDWERKVKC----------------------------------SS  1237
CLBV:NP_624333.1        -------------------KGNF--CVVSPRTNLAADWAFKLELEPN-------------------------------EQ  1210
CLBV:AFA43536.1         -------------------RGNF--CVVSPRNNLAADWSFKLELEPN-------------------------------EK  1235
GCLV:YP_004936159.1     -------------------GV---CIFVTPRRSLAEQMTQLVQSVETS------------------------------TS  1210
CVNV:YP_001430021.1     -------------------GSKC--YFVTPRRSLADIFSDELTSGRIKTK----------------------------TT  1228
PhlVB:YP_001552317.1    -------------------GKGV--FYVSPRRALADEFRQKLENAVVRTKRKKGASSKNGAGASTGPDPNSQAERMKRKN  1300
ASPV:NP_604464.1        -------------------GKAI--TFVSPRRSLAESINHDLGLARVGGKKTGKSK--------------------DLKN  1431
APV1:YP_009094347.1     -------------------SRSI--VFVSPRRSLADQIKDDLGLNTKRGKS---------------------------LR  1277
CTLaV:YP_009046478.1    -------------------GYQN--LIISPRRSLKEQFINMLDLVQARSKGKK-------------------------AS  1281
CRMaV:YP_007761581.1    -------------------GYQN--LIISPRRNLKDQFINMLDLVNARSKGKK-------------------------TS  1271
                                                     **  :
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ZoVT:Z1                IKLRTYETGIIEINKR-RDYTNDKPIIIIDEVSLLPGGYIDLIN--------------------SIIPEG----------  1101
ZoVT:Z2                IKLRTYETGIIEINKR-RDYTNDKPIIIIDEVSLLPGGYIDLIN--------------------SIIPEG----------  1101
ZoVT:Z3                IKLRTYETGIIEINKR-RDYTNDKPIIIIDEVSLLPGGYIDLIN--------------------SLIPEG----------  1101
PrVT:YP_009051684.1    IKLKTFELAISAITRMVKKEQDGKLTVIIDEATLLPGGYLDLVN--------------------SLVPEG----------  1061
PrVT:AHM92766.1        IKLRTFELAVSAITRMVLKEGDVKLTVIIDEVTLLPGGYIDLIN--------------------SLIPEG----------  1061
PVT:ADX41471.1         VKVMTFEAGLRRVQKS--------SLIVIDELSLMPNGYLDMLI---------------------NMNEE----------   883
PVT:YP_002019748.1     VKVMTFEAGLRRVQKS--------SLIVIDELSLMPNGYLDMLI---------------------NMNEE----------   883
PVT:AFV39891.1         VKVMTFEAGLRRVQKS--------SLIVIDELSLMPNGYLDMLI---------------------NMNEE----------   884
PVT:AFU55321.1         VKAMTFEAGLRRVQKS--------SLIVIDELSLMPNGYLDMLI---------------------NMNEE----------   884
PVT:AXK90539.1         VKVMTFESGLRRVQKS--------DLVIIDELSLMPNGYLDMLI---------------------NMNRE----------   884
AcVB:YP_004935358.1    AIVRTFESAFNGRKGY--------ENIIIDEVGLLPPGYIDLVH--------------------ANFQYD----------  1006
GVA:NP_619662.1        HRVVTFEVAFM--DDY------GCKDIVIDEIGLLPPGYIDLVI--------------------AAHQPR----------  1011
GVE:YP_002117775.1     VCVYTYESFLL--NHK-----HKLDLLILDEIPLFPPGYIDLVH--------------------FIKSVE----------   837
ASGV:NP_044335.1       CQVHTWETALKKIDGT-------FMEVFVDEIGLYPPGYLTLLQMCAFRKIVKGQSENFLKGKLLELSKTC---------   888
CVA:NP_620106.1        KNFSTFENTLLSLVNK--------PLVIMDECSLNPPGFIDLVLIKSLDSIIRKSNKDFDHFFSSSVLSEGIIANVASPI   944
DiVA:YP_006905850.1    IRFSTYEKALT--LSY-----YEDELVVVDEIGLLPPGYISLLSLVTAFRVNKISHN-------IRLSKRNYSKYVENQS   973
ObRV1:YP_009408144.1   IRFLTFERALT--VTY-----QESELIVIDEIGLMPPGYMSLLNIITSIKFEEVSNN-------FRLSRRNFRNFIGSPR   973
ACLSV:NP_040551.1      KDIKTFESALK--SDV-----KGKRLFILDEISLLPKGFTDLLM--------------------LKMHMEGIL-----KK  1151
GPGV:YP_004732978.2    LKTMTFESAIKGCLAG-------YKWIILDEVTLFPNGYLDLLV--------------------LKLAHYNEI-----NL  1129
CtChV-1:YP_009103999.1 VTFKTYESALK--ENL-----SKFSLIIIDEFPLTPRGYTDVIA--------------------YKSKVDNLTCRLEKKV  1164
CtChV-2:YP_009103996.1 LILKTYESALK--ENF-----AEFSMIVIDEFLLVPRGYLDVAA--------------------FKSKMDCKVCKSKPRI  1161
AVCaV:YP_008997790.1   CSVTTFEVLFKASISK-------IKLIVVDELTLFPNGYIDLLI--------------------FRIRTE-------SPD   964
CPrV:AKN08994.1        HKVCTFEVALL--QNL-----SRVELIVIDELGLFPRGYLDLMI--------------------FKLRTE------KNFK  1284
CLBV:NP_624333.1       RKVSTFEKFIK--TDK-----SKLDLIVIDELTLFPNGYLDLLV--------------------YELADV-------NRH  1256
CLBV:AFA43536.1        RKVATFESFIK--MDK-----SKLDMIVLDELTLFPNGYLDLLI--------------------YELDKF-------NSH  1281
GCLV:YP_004936159.1    VTILTFEKFLHQMVNV-----KEGSTIIFDEFQLYPPGYFDLVC--------------------SQLTDG----------  1255
CVNV:YP_001430021.1    VVVQTYEKFLRMLESV-----EPRDVVIFDEMQLFPHGYFDLTF--------------------SIMSQE----------  1273
PhlVB:YP_001552317.1   WLVCTFEIILKKIHLV-----KPGMALILDEIQLYPPGYLDLIC--------------------ALCAEG----------  1345
ASPV:NP_604464.1       VRVKTFELFILHLDSI-----KEGHTVVIDEIQLFPPGYIDLII--------------------LGLKPN----------  1476
APV1:YP_009094347.1    VRVLTLESFIKAVFTF------KAASVVLDEVQLYPPGYLDLVM--------------------LCLSLN----------  1321
CTLaV:YP_009046478.1   TEVATFEVALKKTGML------KKVRIFIDETQLLPPGYLDLVC--------------------LIAGPD----------  1325
CRMaV:YP_007761581.1   TDVVTFEVALKKNGLL------KKARIFIDEAQLLPPGYLDLIC--------------------LIAGSD----------  1315
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ZoVT:Z1                STMVLIFDPLQSSYYSPKAVH---HSLPDIFEPLY-------------------------------------------GQ  1135
ZoVT:Z2                STMVLIFDPLQSSYYSPKAAH---HSLPDIFEPLY-------------------------------------------GQ  1135
ZoVT:Z3                STMVLIFDPLQSSYYSPKAAH---HSLPDIFEPLY-------------------------------------------GQ  1135
PrVT:YP_009051684.1    STIILLFDPLQSHYYSKSDVR---VNLGPVLTPIF-------------------------------------------GQ  1095
PrVT:AHM92766.1        STIILLFDPLQSHYYSKMDVS---ANLGPVLTPIF-------------------------------------------GQ  1095
PVT:ADX41471.1         ATFITLFDPLQARYHAKSDVLRV-SPENDVDRIKV---------------------------------------------   917
PVT:YP_002019748.1     ATFITLFDPLQARYHAKSDVLRV-SPENDVDRIKV---------------------------------------------   917
PVT:AFV39891.1         ATFITLFDPLQARYHAKSDVLRV-SPENDVDRIKV---------------------------------------------   918
PVT:AFU55321.1         ATFITLFDPLQARYHAKSDVLRV-SPENDVDRIKV---------------------------------------------   918
PVT:AXK90539.1         ATFITLFDPLQARYHSKSDILRV-SPENDVDRIKV---------------------------------------------   918
AcVB:YP_004935358.1    -TMLLLGDPLQSEYYNKGDSLFLEPISESVFDRLM-------------------------------------------GK  1042
GVA:NP_619662.1        -TLVLLGDPLQSTYHSKRDNVVLEASQEDVFNRVR-------------------------------------------GK  1047
GVE:YP_002117775.1     -HILLLGDPLQTSYHADGDALTLSGVEGDIFRRLQAKKSGICPCGMHFKPSRYMGPNVEFDFDEADKLKGREAIFFSRGG   916
ASGV:NP_044335.1       LNIRCFGDPLQLRYYSAEDTNLL-DKTHDIDLMIK-------------------------------------------TI   924
CVA:NP_620106.1        ACIAVTGDTLQSSFYSESCGKLM-QYKNDIKTLCAL------------------------------------------SH   981
DiVA:YP_006905850.1    SRLVLLGDHLQGRYYNESDFRSL-SQPDEIDFIMM-------------------------------------------NE  1009
ObRV1:YP_009408144.1   SRLVVLGDHLQCRYYNDSDVRSL-DPKDEIVFLME-------------------------------------------NE  1009
ACLSV:NP_040551.1      STIVCIGDPLQAGYFCPKDDNYL-SREGEIKRLFK-------------------------------------------GG  1187
GPGV:YP_004732978.2    KHITLVGDPLQANYFNERDCNLL-GSVKMVDSVFK-------------------------------------------DV  1165
CtChV-1:YP_009103999.1 TKLLLIGDPLQASYYSESDDDLL-AQGGELSS-LE-------------------------------------------ID  1199
CtChV-2:YP_009103996.1 PKFLLLGDPLQAGYYNALDDHLI-PEKSEMET-LE-------------------------------------------IR  1196
AVCaV:YP_008997790.1   CKLILIFDPLQARYDSAQDRAIL-GSEHDVDLILG-------------------------------------------DS  1000
CPrV:AKN08994.1        GKVMLLFDPLQARYHSDSDERFL-HEIHECDRITS-------------------------------------------GA  1320
CLBV:NP_624333.1       CQIILLFDPLQARYHNKMDESIL-TFEHDVDRLIG-------------------------------------------GQ  1292
CLBV:AFA43536.1        CHLILLFDPLQARYHNKMDEAVL-NFEHDVDRLIG-------------------------------------------GQ  1317
GCLV:YP_004936159.1    ISLHLLGDPCQSDYDNAKDRGVFEGLLPDHQRILQ-------------------------------------------GI  1292
CVNV:YP_001430021.1    VPTVCLGDLCQSDYDCATDRSELGCYQSDMQRLLQ-------------------------------------------SA  1310
PhlVB:YP_001552317.1   VHIVIGGDPIQSDYDNEKDRNWLSNLPPCIDSVLE-------------------------------------------GA  1382
ASPV:NP_604464.1       VNIIIAGDPCQSDYDCSSDRHIFAGSESDIMRILS-------------------------------------------GR  1513
APV1:YP_009094347.1    CQIYLAGDPCQSDYDSAKDRALFDGLKGDIFEVLS-------------------------------------------GK  1358
CTLaV:YP_009046478.1   ASILVMGDPAQSSYDSADDRMAFIGDRGCLDVLLD-------------------------------------------NK  1362
CRMaV:YP_007761581.1   SSILVMGDPAQSSYDSAEDRMMFAGDKGCLDRLLE-------------------------------------------GK  1352
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ZoVT:Z1                 S-FD----------------------------------------------------------------------------  1138
ZoVT:Z2                 S-FD----------------------------------------------------------------------------  1138
ZoVT:Z3                 S-FD----------------------------------------------------------------------------  1138
PrVT:YP_009051684.1     E-FR----------------------------------------------------------------------------  1098
PrVT:AHM92766.1         E-YR----------------------------------------------------------------------------  1098
PVT:ADX41471.1          --PK----------------------------------------------------------------------------   919
PVT:YP_002019748.1      --PK----------------------------------------------------------------------------   919
PVT:AFV39891.1          --PK----------------------------------------------------------------------------   920
PVT:AFU55321.1          --PK----------------------------------------------------------------------------   920
PVT:AXK90539.1          --PK----------------------------------------------------------------------------   920
AcVB:YP_004935358.1     K--N----------------------------------------------------------------------------  1044
GVA:NP_619662.1         --LP----------------------------------------------------------------------------  1049
GVE:YP_002117775.1      EGYKYNGGDHKSSGWVGELDQIIDACNINADSFDHCLVQRYIPGGSIKPHADNEPIYPVNNPILTVQLTGSCTFTLSCRK   996
ASGV:NP_044335.1        K-HK----------------------------------------------------------------------------   927
CVA:NP_620106.1         TRLP----------------------------------------------------------------------------   985
DiVA:YP_006905850.1     E-IL----------------------------------------------------------------------------  1012
ObRV1:YP_009408144.1    E-II----------------------------------------------------------------------------  1012
ACLSV:NP_040551.1       --VN----------------------------------------------------------------------------  1189
GPGV:YP_004732978.2     K-------------------------------------------------------------------------------  1166
CtChV-1:YP_009103999.1  Y-PR----------------------------------------------------------------------------  1202
CtChV-2:YP_009103996.1  K-PK----------------------------------------------------------------------------  1199
AVCaV:YP_008997790.1    E-VD----------------------------------------------------------------------------  1003
CPrV:AKN08994.1         K-IN----------------------------------------------------------------------------  1323
CLBV:NP_624333.1        N-IE----------------------------------------------------------------------------  1295
CLBV:AFA43536.1         D-LR----------------------------------------------------------------------------  1320
GCLV:YP_004936159.1     Q-FR----------------------------------------------------------------------------  1295
CVNV:YP_001430021.1     K-YT----------------------------------------------------------------------------  1313
PhlVB:YP_001552317.1    E-YK----------------------------------------------------------------------------  1385
ASPV:NP_604464.1        S-YK----------------------------------------------------------------------------  1516
APV1:YP_009094347.1     K-YK----------------------------------------------------------------------------  1361
CTLaV:YP_009046478.1    R-YV----------------------------------------------------------------------------  1365
CRMaV:YP_007761581.1    K-YV----------------------------------------------------------------------------  1355


ZoVT:Z1                 -------------------------------------------------------YKYYSYRF--GDLFKIE--------  1153
ZoVT:Z2                 -------------------------------------------------------YKYYSYRF--GDLFKIE--------  1153
ZoVT:Z3                 -------------------------------------------------------YKYYSYRF--GDLFKVE--------  1153
PrVT:YP_009051684.1     -------------------------------------------------------YRGYSYRF--PKLFDLE--------  1113
PrVT:AHM92766.1         -------------------------------------------------------YRGYTYRF--PELFKVE--------  1113
PVT:ADX41471.1          -------------------------------------------------------YLFFSKRM--SSELDFF--------   934
PVT:YP_002019748.1      -------------------------------------------------------YLFFSKRM--SSELDFF--------   934
PVT:AFV39891.1          -------------------------------------------------------YLFFSKRM--SSELDFF--------   935
PVT:AFU55321.1          -------------------------------------------------------YLFFSKRM--SSELDFF--------   935
PVT:AXK90539.1          -------------------------------------------------------YLFFSKRL--SSELDFF--------   935
AcVB:YP_004935358.1     -------------------------------------------------------YLYKTHRL--PSNQKLF--------  1059
GVA:NP_619662.1         -------------------------------------------------------YLCYSHRL--PRNCKLF--------  1064
GVE:YP_002117775.1      GDTSLHLEGAQFFLMPNGRQKGHKHSVVAHDHRVSLTFRSTRPLELMSGKIQAVPYLFLTNRL--SSKQKIM--------  1066
ASGV:NP_044335.1        -------------------------------------------------------YLFQGYRF--GQWFQEL--------   942
CVA:NP_620106.1         -------------------------------------------------------YLFGSKRF--GYFTGFL--------  1000
DiVA:YP_006905850.1     -------------------------------------------------------YLNYSHRLNKMHFYKP---------  1028
ObRV1:YP_009408144.1    -------------------------------------------------------YLNYSHRMSRSHHYKP---------  1028
ACLSV:NP_040551.1       -------------------------------------------------------YKWYSYRIN-KFIAKKL--------  1205
GPGV:YP_004732978.2     -------------------------------------------------------YQYQSYRIP-ANVAGRF--------  1182
CtChV-1:YP_009103999.1  -------------------------------------------------------YLLYSHRLP-KGMKSMM--------  1218
CtChV-2:YP_009103996.1  -------------------------------------------------------YLYYSHRLS-SSLGGIL--------  1215
AVCaV:YP_008997790.1    -------------------------------------------------------YMYQSKRFESEELFNLFEDLKKNEV  1028
CPrV:AKN08994.1         -------------------------------------------------------YLFESWRLSKKFFGNFF-------V  1341
CLBV:NP_624333.1        -------------------------------------------------------YIYSTHRMS-RYFNRFF--------  1311
CLBV:AFA43536.1         -------------------------------------------------------YIYSSHRMS-KYFNRFF--------  1336
GCLV:YP_004936159.1     -------------------------------------------------------YATRSYRFSNPNFVGRL--------  1312
CVNV:YP_001430021.1     -------------------------------------------------------YYTRSHRFQNSNFAGRL--------  1330
PhlVB:YP_001552317.1    -------------------------------------------------------YVIKSRRFKNGNFQGRL--------  1402
ASPV:NP_604464.1        -------------------------------------------------------FNILSQRFRNPVFYGRL--------  1533
APV1:YP_009094347.1     -------------------------------------------------------FNVSSRRFQSEMFVGRL--------  1378
CTLaV:YP_009046478.1    -------------------------------------------------------YLSESKRFRNPMFLGRL--------  1382
CRMaV:YP_007761581.1    -------------------------------------------------------YLSESKRFRNPMFVGRL--------  1372
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ZoVT:Z1                 GLSMMGGME-ISEHHMKIFKQPEAVKKVF-----SDPIFISPSEAKAN-----ELRRYGD------SYTFGTSQGLTF-D  1215
ZoVT:Z2                 GLNMMGGME-ISEHHMKIFKQPEAVKKVF-----SDPIFISPSEAKAN-----ELRRYGD------SYTFGTSQGLTF-D  1215
ZoVT:Z3                 GLSMMGGME-ISEHHMKVFKQPEAVKKIL-----NDPIFISPSEAKAN-----ELRRYGD------SYTFGTSQGLTF-D  1215
PrVT:YP_009051684.1     DFEYGHGD--VDPNHMRVFAQPQAVREAI-----KRPVFLCPSDDKRS-----ELSNFGE------AYTFGTSQGLTF-D  1174
PrVT:AHM92766.1         GFEFGKGE--IDKNHMRIFAQPQAVREAV-----KKPVFLCPSEDKRN-----ELSNFGE------AYTFGTSQGLTF-D  1174
PVT:ADX41471.1          DVRCSSDQK-KWELHGKQYREPAALFRDI---KGQEFTILSPSFETAR-----EMSKYADIKDGCKSMTFGESQGLTV-N  1004
PVT:YP_002019748.1      DVRCSSDQK-KWELHGKQYREPAALFRDI---KGQEFTILSPSFETAR-----EMSKYADIKDGCKSMTFGESQGLTV-N  1004
PVT:AFV39891.1          DIRCSSDQK-KWELHGKQYREPAALFRDI---KGQEFTILSPSFETAR-----EMSKYADIKDGCKSMTFGESQGLTV-N  1005
PVT:AFU55321.1          DIKCSSDQK-KWELHGKQYREPAALFRDI---KGQEFTILSPSFETAR-----EMSKYADIKDGCKSMTFGESQGLTV-N  1005
PVT:AXK90539.1          DIGCSSDQK-KWELHGKQYREPAALFRDI---KGQEYTILSPSFETAR-----EMSKYADERNGCKSMTFGESQGLTV-N  1005
AcVB:YP_004935358.1     DVPSKGE---RSENYLKGAEGDA-----------NYDLIITASRAAKE-----KRGQKGS--------TIGESQGLSV-R  1111
GVA:NP_619662.1         EIECMG----AESEKRVVYRSNRL----------KDEPTICATRAMKE-----EKGSG--------WYTVSETQGLSF-K  1116
GVE:YP_002117775.1      EVPSYG----VSDFEVKEIKKLN-----------KETLTICFSRATVE-----EERDNLT------ICTVGQAQGLSR-D  1119
ASGV:NP_044335.1        -VNMPTRVD-ESKFSRKFFADISSVKTE------DYGLILVAKREDKG-----VFAGRVP------VATVSESQGMTISK  1003
CVA:NP_620106.1         KLGYYNQME----SKAFTIDNMETLQKAIGTSMDKFGVLVTSRADKSD-----FELDFPN------VCTINEAQGSTF-N  1064
DiVA:YP_006905850.1     GVEMLGE---DENIISRRFSNVFSAKKTI-----PEAQLLVASRDEQV-----RFKELD-------AKTFGESQGLTF-D  1087
ObRV1:YP_009408144.1    GVVFLND---ADSVPTKRFLNTLVAKKSI-----PNAQVLVASHDEQI-----RFRDLG-------AKTFGESQGLTF-D  1087
ACLSV:NP_040551.1       AIETMNDFI-GIDEQSSIYKDMPSAHHFMEKKGNHIEVILVASMVEKE-----LYSNYGN------VMTFGESQGLTF-N  1272
GPGV:YP_004732978.2     DVWDKNRHE-PIDCHGTFYSDLSSAKLHAKRCNQKIDVVLVASELEKK-----YFSNQCK------CITYGESQGLTF-D  1249
CtChV-1:YP_009103999.1  DINMLGSF--EGETKWKLYNSAAAAFSEK-----AFDVILVAGRQEKT-----FFGNFT-------VMTFGESQGLTF-N  1278
CtChV-2:YP_009103996.1  DVPMLGPI--NELNQLNLYNSAAAAFSER-----AFDVILVAGRQEKS-----FFSNYT-------VMTFGESQGLTF-D  1275
AVCaV:YP_008997790.1    DAESRETGK-GAKFRPRMYTNLLTMKVEEENQGNPIDVLLVGSFDEAG-----LFASSIK------TMTFGESQGLTV-D  1095
CPrV:AKN08994.1         DIELRNSG--SVNYELDFFDNHIVAANEAKKRGFPIDLILVASRDEKN-----SFAGKVN------VLTFGEAQGLTV-K  1407
CLBV:NP_624333.1        DVPCFNQADRTEEQRLWIFDDVYSIPSICSDRQEPCDVLLVESDLEKK-----AFSPIIN------VMTFGESQGLTF-N  1379
CLBV:AFA43536.1         DVPCFNQAETTKEQRLWILDDVYSITSVCIDQGEPCDVLLVESDLEKK-----AFSPVIN------VMTFGESQGLTF-N  1404
GCLV:YP_004936159.1     PCAISNTNE-DDFEDFEILEGIEQVQEI------DVECYLVSSFIEKQ-----AVRALVGLDKV--VQTFGESTGLTY-D  1377
CVNV:YP_001430021.1     PCQFQPEYF-TNHEDFTILHGFESLNDIA-----GLDCILVSSFNEKTAVKALTFGRVS-------VQTFGESTGLTF-N  1396
PhlVB:YP_001552317.1    PCEFGTQMEGQATEEHLLYSGLEHLHVIP---QEFSKVFLVSSFEEKKIVEAHFPGSNPT------VLTFGESTGLNF-K  1472
ASPV:NP_604464.1        PCNLNKTRLTLDEEEYTLWDSIQEFSMMG---RKDCPVVLVSSFEEKKIVAA-HLGLKMK------CITYGESTGLNF-Q  1602
APV1:YP_009094347.1     PCRMDTKAM-TENENFHWLESIESAAEVS---NTEYDVVLVSSFEEKKIVWA-HLGRDLE------VLTFGESTGLTF-N  1446
CTLaV:YP_009046478.1    PCTFDQSRMTLEKEEYAVFSSFKDFKNDYL--SPKIKTFLVSSFTEKTVVKA-NMGRNVL------VYTFGKSTGMNF-D  1452
CRMaV:YP_007761581.1    PCTFDSSRLTLEKEEYAVFDSFKAFKADYL--SPKIKTFLVSSFTEKTVVKA-NMGRNVS------IFTFGESTGMNF-D  1442
                                                               :                            * . : * .


ZoVT:Z1                 FVVISVDMDGPLVSNAHWMVALTRARKG-FAFVVCSSITLNDFKAKVKTKIIGKVLNKAVVSKDFM-RASGGKIMDHANL  1293
ZoVT:Z2                 FVVISVDMDGPLVSNAHWMVALTRARKG-FAFVVCSSITLNDFKAKVKTKIIGKVLNKAVVSKDFM-RASGGKIMDHVNL  1293
ZoVT:Z3                 FVVISIDMDGPLVSNAHWMVALTRARKG-FAFVVCSSITLNDFKAKVKTKIIGKVLNRTIVSKDFM-RASGGKIMDHANL  1293
PrVT:YP_009051684.1     FVCISIDMDGSVTSDFHWMVALTRARRG-FCFLTCASTSMRTFMDNNRAKLIGKVLKKEQISKKFW-WNLGGRALEGARA  1252
PrVT:AHM92766.1         FVCISLDMDGSVTSDFHWMVALTRARKG-FCFLTCASTSLRNFKESNRAKLIGKVLNKEIISKKFW-WNLGGRALDNARC  1252
PVT:ADX41471.1          KAVIVVDQDLVATSVLHWIVALTRSRQG-FVILVHKVFDMKTLIQPVQNSIIGLVLRGVKVSREHL-INTAGKCLSEAEI  1082
PVT:YP_002019748.1      KAVIVVDQDLVATSVLHWIVALTRSRQG-FVILVHKVFDMKTLIQPVQNSIIGLVLRGVKVQENIF-INTAGKCLSEAEI  1082
PVT:AFV39891.1          KAVIVVDQDLVATSVLHWIVALTRSRQG-FVILVHKVFDMKTLIQPVQNSIIGLVLRGIKVSREHL-INTAGKCLSEAEI  1083
PVT:AFU55321.1          KAVIVVDQDLVATSVLHWIVALTRSRQG-FVILVHKVFDMKTLIQPVQNSIIGLVLRGIKVSREHL-INTAGKCLSEAEM  1083
PVT:AXK90539.1          KAVIVVDQDLIATSVLHWIVALTRSRQG-FVILIHKVFDMKTLIQPVQNSIIGLVLRGVKVSKEHL-INTAGKCLADAEI  1083
AcVB:YP_004935358.1     RVKLVIDRDWGLLNDKAVMVALTRARNT-LSVEVDKSMK-EHLKVHAKSSILKMFLRGQMIKRELI-MEMMGTDNGDVEL  1188
GVA:NP_619662.1         SCLIYLDEHWAKKEDEDVMVALTRSRGE-IGIHVTPALK-KKLITNAKSTLLKKVLKGETYRRSEI-VAMVRKHIPETTV  1193
GVE:YP_002117775.1      VVQIMFDHGSLKCADETIIIALTRARKAVHLFYKIGKTDLKNCSSP----ILRAFISNGKIPEKLLVDKVRGKLGDCRLL  1195
ASGV:NP_044335.1        RVLICLDQNLFAGGANAAIVAITRSKVG-FDFIL-KGNSLKEVQRMAQKTIWQFIIEGKSIPMERIVNMNPGASFYESPL  1081
CVA:NP_620106.1         SVILIVTRDFFSNPIESIIVAITRHQKNLLIYFPAAIQGEMDFLSRRFPIHSNVVLKNFSVLDNLIKDKLNPFQLIQEDP  1144
DiVA:YP_006905850.1     EIIIVLSPPAVNCSINMWNVAMTRARKG-VHFALNGFDTVDDFINRVKGTPVNAMILGSPFEIHRT----PGGKDKEIKI  1162
ObRV1:YP_009408144.1    ESIIVLSPPSTNCSLFMWNVAMSRSIKG-VHFALNGFDSIDDFLNRVKGTPVAAMILGMKFDIH---AQPMSTPEDCKII  1163
ACLSV:NP_040551.1       CGVIVLSEEAKLCSDAHIMVAITRFRRG-FCFALGSKGSKEDYMRSMKSGLLQRICSGVGASKEFI----LGSSSVNLIL  1347
GPGV:YP_004732978.2     YGLISLSEESRLCSDNHIYVALTRFKKG-FGFFQNFRGDLGTFKSNLGSKLLGRYINLRDNLKPFM----MQMLDINLDF  1324
CtChV-1:YP_009103999.1  KVCIALTEDSLLASDNHMMVGLTRAKET-INFIKGFGYPLNEYVKKAGNKLIGKVLQGKVIKRAEL-ENMSG--MEDVTF  1354
CtChV-2:YP_009103996.1  KVAIALSEDTLLCSDNHIVVALTRARKQ-ISLIKCFGYDEKEFFKRAGTKLIGKVLNKKKIKRVQL-ENMLA--LEDLKL  1351
AVCaV:YP_008997790.1    HAAILLSENSALSDDHRWLVALTRARKK-VTFLCLHLSGLNGFLSTMENRLVAAVINKGLVTKKRL-SSMVRAKLNYVKF  1173
CPrV:AKN08994.1         HSCIVLSEYAEKQDDYRWVVALTRAKEK-ISFITSHRSGLTGFMSSMIGRPIHAFLTGLPFTSNRM-NWMVNCELVECHR  1485
CLBV:NP_624333.1        HVCILLSESSAASNEFRWMVALTRARTR-FSLCSTFLGGIEEFKVKRKESLITSILQGEKITFNRL-NLMLKCNLIRREK  1457
CLBV:AFA43536.1         HVCILLSESSAASNEFRWMVALTRAKTR-LSFCSTFLGGMDEFKIKRGESLVTSILEGKQITFERS-NMMVKCNLIKQEK  1482
GCLV:YP_004936159.1     CVAVVVSEASKLASERRWITALTRARKR-VTFITNLGCSKHLIAEIFSNRALGRFLSCTASIDNLR-CLLPGEPNFVEEL  1455
CVNV:YP_001430021.1     SGAIFISEVSKLASEQRWLTALSRFRMN-LTFVSDLGCDSSMLAEVFSGRVLGRFLSGKANVCDLR-GLLAGSPDLQEDF  1474
PhlVB:YP_001552317.1    YGTIIITNVSAHTSEKRWVTALSRFSEN-ICFVNLVNLSWSELARMYATRVLGRFLGKRAKLSDLL-EHLPGVAVFTDSY  1550
ASPV:NP_604464.1        KGAILVTYESALTSDRRWWTALSRFSHD-IHFINGMGVTWDNAITHFVGKPLHKFFTKRACNDDII-DLLPGRPELIEGF  1680
APV1:YP_009094347.1     RGIILISHESTLTSERRWITALSRFRLN-IIFVNLVGNCLEDACQVFHDRTLDRFLTKRATIANIV-DQLPGLPELTNDF  1524
CTLaV:YP_009046478.1    YVCVLLTQDSMLVDERRWVVALSRAKIN-MSFVNLSGLSLPEFCTQMVGGVVHKFFTGTATFNDLR-SLLPGDPIFSKKF  1530
CRMaV:YP_007761581.1    YVCVLLTQDSMLVDERRWVVALSRAKIN-ISFINLSGLTLPEFCTQMMGGVVHKFFTSTATFNDLR-ELLPGDPIFSKRF  1520
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ZoVT:Z1                 IGD---SKKGRTREEFEDTLENDPWIKTQLIFLENPELQKEE-MNEMVFKSSP-PRTHLMISSEGNAFINGPHLNRAREF  1368
ZoVT:Z2                 IGD---SKKGRTREEFEDTLENDPWIKTQLIFLENPELQKEE-INEMVFKSSP-PRTHLMISSEGNAFINGPHLNRAREF  1368
ZoVT:Z3                 IGD---SKKGRTREEFEDTLENDPWIKTQLVFLESPELQKEE-TNEMVFKSSP-PRTHLMISNEGNAFINGPHLNKAREF  1368
PrVT:YP_009051684.1     VKKDEFSKLGKTREEFEESLEGDPWLKGMLNYLEGDDANDPE-PEEPIRKDSP-PRTHLMIAPVEHQFAEEMHLLRAREF  1330
PrVT:AHM92766.1         VDKDEFVKLGKTREEFEEALGGDPWLKGLLNYLEGDDAKDPE-PEEPVRKDSP-PRTHLMLAPVEHQFAEEMHLLKAREF  1330
PVT:ADX41471.1          VEE---LETFKRTEEDEDLLEGDPWLKGQLFLCQSVELDEVT-PEEPLRHESP-PRTHLPL-PVEGLTPLLMSNVKARED  1156
PVT:YP_002019748.1      VEE---LETFKRTEEDEDLLEGDPWLKGQLFLCQSVELDEVT-PEEPLRHESP-PRTHLPL-PVEGLTPLLMSNVKARED  1156
PVT:AFV39891.1          VEE---LETFKRTEDDEDLLEGDPWLKGQLFLCQSVELDEVT-PEEPLRHESP-PRTHLPL-PVEGLTPLLMSNVKARED  1157
PVT:AFU55321.1          VEE---LETFKRTEEDEDLLEGDLWLKGQLFLCQSVELDEVT-PEEPLRHESP-PRTHLPL-PVEGLTPLLMSNVKARED  1157
PVT:AXK90539.1          IED---LETFKRTEEDEDLLEGDPWLKGQLFLCEAVELDEAV-PEEPLRHESP-PRTHLPL-PVEGKVPLLMSDIKAREE  1157
AcVB:YP_004935358.1     IEK---ETRFADSDDMEDKLSGDPYLKGLLRLYDDVEMEEEE-VPDVSLPEPQ--KTHLPISTKENELA--PSLLRAREH  1260
GVA:NP_619662.1         LFE---ESRLAETVDYEARLAGDPYLKSLLALYDEIEMEDIE-IEEPVTLEPT--KTHLALSTKMNELA--PFDLKAKEH  1265
GVE:YP_002117775.1      TEN---VFIGADSATIGDHLAGDPGLKAMLLILEAEEMEPEI-FEEETVPETI--RTHLGVTTFANEQFAF--GLKAKEE  1267
ASGV:NP_044335.1        DVG---------NSSIQDKASNDLFIMPFINLAEEEVDPEEV-VGDVIQPVEW-FKCHVPVFDTDPTLAEIFDKVAAKEK  1150
CVA:NP_620106.1         FGH-----------DFEVKLEGDPFLKSELSLVNEIKLQQIE-ENSIESKENL--KTHLPI-SYSGLWNLEISEMRARED  1209
DiVA:YP_006905850.1     IKV---CRLGMSNEDVEMKLMGDPFLKSIIPSLDEGLSIEQE-YHDIICESPV-PKIHLPIESIQGHVSYVSSMLKERGE  1237
ObRV1:YP_009408144.1    CSD----RLCLSSSDVENKLEGDPFLKSIIPSMDEGLCVHHE-YQDVNFELPT-PKIHLPIESIQSHVAFVSSMIRNREF  1237
ACLSV:NP_040551.1       SEKDIAKGAGIDEMDREARLEGDVWLKSMIYLGKRYHMVEPL-GQVIKLTDDA-IKCHIPVCSSQTLGPEL-DNIQAREY  1424
GPGV:YP_004732978.2     MDD---RNQVGAGIEMENKMSGDPWLKGLLDLQAVEEVEDMF-FEDLNIIEPT-GKVHLPLASRNDEF----EKIRARES  1395
CtChV-1:YP_009103999.1  ITE------PPTFGGHEDKVQGDPWMKSLLTLTQREDSQEVE-LIEPDIVESK-MKVHINITDKSYALMIINDQLRAKEN  1426
CtChV-2:YP_009103996.1  ISS------EPKFGTQEERTEGDPWMKGLLTHIQEVIMEECE-PQMAKPDDVK-MKVHVPITDKSFALTIINDQIRAREY  1423
AVCaV:YP_008997790.1    KGL-----AGKDEVDREDRLEGDLFLKGVIFLGQRCEIMEPE-IVEPVMAKED-MKTHFFVCQENFAQCYNFDNIRAKEL  1246
CPrV:AKN08994.1         ATG------GRDEVDREDRLEGDPFLKPFVFLGQRINSEEYE-IIEPEVIEPK-GRVHLCISQENYALARNFDLIRAKEY  1557
CLBV:NP_624333.1        ENG------CRDEVDREERLEGDPFLKPFIFLGQRVEKDEDE-VEEVKIREPT-CQTHLYITEPNFGLCYNFDFIREKEQ  1529
CLBV:AFA43536.1         KNG------CSDEVDREERLEGDPFLKPFIFLGHRIQKSHDE-VGEIEVREPT-CQTHLYITEPNFGLCYNFDFIREKEQ  1554
GCLV:YP_004936159.1     VPT-----IGANLGVVEEKVSGDPWLKTMLFLGQVADVADEI-DVDEALQIEP-FKTHVARSNLEGVRALWHDKIRLKEH  1528
CVNV:YP_001430021.1     PTT-----VGKNQGLVEEKVVGDPWLKAMLFLGQETDEQEVA-PEVAEVALEV-FKTHAPRCELEGVRARWHEKIQAKEF  1547
PhlVB:YP_001552317.1    DEN-----IGKDEGVREEKVQGDPWLKGMVDLFQIEDVEEEE-EQLEEMQTEW-FKVHLPQAELESVRAKWVHKILAKEF  1623
ASPV:NP_604464.1        QSQ-----VGADEGVREAKLVGDPWLKTKIFLGQNPDFEIEI-ADEVEAAEDW-FKTHIPIMSLEAVRAQWVHKLISRED  1753
APV1:YP_009094347.1     GDK-----VGRSEGVMEAKLSGDPWLKTEIDLLQDEDQEMEE-LAEEVKHEPW-FKTHLPLFELESIRASWVHRIMNREY  1597
CTLaV:YP_009046478.1    QRL------GSDEVDREARLSGDPWLKTKVFLGQREVRPVEE-PISVENLKDIKIKVHCPVGSMGATFAEVQSKLKVKEA  1603
CRMaV:YP_007761581.1    QRL------GKDEVDREARLLGDPWLKAKVFLGQREEKIESIHVNDEGLKDIK-VKVHCPIGSIGSTLADIQAGVRVKEA  1593
                                             .*  :   :                         . *                   .


ZoVT:Z1                 REFKGRG-MWSEQFDDCR---KERKFKY----NRAETFETIYPNHNGTDSLTMWAAIKKRLKMSDPYTERRKLERLMSTG  1440
ZoVT:Z2                 REFKGRG-MWSEQFDDCR---KERKFKY----NRAETFETIYPNHNGTDSLTMWAAIKKRLKMSDPYTERRKLERLMSTG  1440
ZoVT:Z3                 REFKGRG-MWSEQFDDCR---KERKFRY----NRAETFETIYPNHNGTDSLTMWAAIKKRLKMSDPYTERRKLERLMSTG  1440
PrVT:YP_009051684.1     REFRNSN-LWSEQFDDCR---KTRKVIH----NRAETFEQIYPSHKNSDTLTFWAAIKKRMKMSDPYSERRKLERCMPVG  1402
PrVT:AHM92766.1         REFRNSN-MWSDQFDDSR---KTRKVIH----NRAETFEQIYPSHKNSDTLTFWAAIKKRIKMSDPFSERRKLERCMPIG  1402
PVT:ADX41471.1          REFITPS-GWSKQFRDDK---ENVDWRN---VSYADAFETIYPKHEASDDITLWAAIQKRIVMADPFRNAMKLXKVEPIS  1229
PVT:YP_002019748.1      REFITPS-GWSKQFRDDK---ENVDWRN---VSYADAFETIYPKHEASDDITLWAAIQKRIVMADPFRNAMKLQKVEPIS  1229
PVT:AFV39891.1          REFITPS-GWSKQFRDDK---ENVDWRN---VSYADAFETIYPKHEASDDITLWAAIQKRIVMADPFRNAMKLQKVEPIS  1230
PVT:AFU55321.1          REFITPS-GWSKQFRDDK---ENVDWRN---VSYADAFETIYPKHEASDDITLWAAIQKRIVMADPFRNAIKLQKVEPIS  1230
PVT:AXK90539.1          REFVTPC-GWSKQFRDDK---ENVDWRN---VSYADAFETIYPKHEASDDITLWAAIQKRIVLADPFRNAMKLQKVEAIS  1230
AcVB:YP_004935358.1     REARTPA-GTTEQIDEMG------YKME---PENPMTHKALYLHHRNSDVATFFLSVKKRLRFMDREKNHRRFNKVKGFG  1330
GVA:NP_619662.1         REQHTEA-GRTEQI-DEN-----GYQGE---VGDPMTHKALYLRHTSDDTATFMMSVKKRLRFRNYEANRRKYKTCHGIG  1335
GVE:YP_002117775.1      REHHIHGTGFSTQIRDNI------ASEF---HPGPSAPSSIYLHHTAEDDVLFILSIKKRLRFADFEKNCASFERKKKLG  1338
ASGV:NP_044335.1        REFQSVL-GLSNQFLDME----KNGCKI---DILPFARQNVFPHHQASDDVTFWAGVQKRIRKSNWRREKSKFEEFESQG  1222
CVA:NP_620106.1         REFKKFGVGWSKQFKDEP---NQKDQVE---DNCAMLPEAVFPRHFANDDLTFWSAVKKRLVFKNPLSNAHDFEKAKPFG  1283
DiVA:YP_006905850.1     REFKGDG-CMSEQFPDFW--KTGEPGHY---LSQSERFQSIFPKHQNSDSLTFLAAVKKRLKFSSPSVERERFEKVRHLG  1311
ObRV1:YP_009408144.1    REFIGDG-EMSEQFPDFF--KQSETGSF---LSQAERFQAIFPKHSNGDSLTFFAAVKKRLKFSSPQIEREKFEKVRHLG  1311
ACLSV:NP_040551.1       REFKGKN-GWSNQFREEA----GPNWKFPYKVNQAMSYEAVYPRHKMDDDLTFLAAIKKRLRFDNVANNYAKFKAAESRG  1499
GPGV:YP_004732978.2     RELKKLDFDWSMQFEDCG--VKIKRVLN---GNLCENFSAVYPVHQACDEMTFLAAVKKRLRFSNPAKNLTKFRGATAAG  1470
CtChV-1:YP_009103999.1  REFKSKD-SWSNQFKDND---QNLNLET---STGPVNFEAIFPRHQTFDDVTFWMAVKKRLSFSNPLVESEKLNKAWIKG  1499
CtChV-2:YP_009103996.1  REFKVGD-SWSTQFKDDN---KNLKLES---STGPVNFESIFPRHTSFDDVTFWAAVKKRLSFSNPITEGEKLKSAFVKG  1496
AVCaV:YP_008997790.1    REFRIGH-RVTNQFIDNYEIVQHVQKKH---TAGPLRFEAIYPRHCADDDVTFLMAVHKRLRFSNEMKEREKLERAHGTG  1322
CPrV:AKN08994.1         REAKLMG-LETNQFCHDYNRVGAQGSRH---VASPLRFESIFPRHRSDDDLTFWMAVKKRLRFSEEFLERAKLKDSYSVG  1633
CLBV:NP_624333.1        REYREDM-LVTNQFCDSYDKVHINGKRE---TPGPLRFKAIYPKHSADDDMTFWMAVRKRLVFREEEENYQRLSRAHLVG  1605
CLBV:AFA43536.1         REYREDM-LVTNQFCDSYDKVHINGKRE---TPGPLRFKAIYPKHSADDDMTFWMAVKKRLVFREEEENYQRLSRAHLVG  1630
GCLV:YP_004936159.1     REKRMGY-LVSEQFTDMH--SKNMGKKL---TNAAERFETIYPKHKGSDTVTFIMGARKRLRFSKPAVEARKLMDASNFS  1602
CVNV:YP_001430021.1     REKRMGY-LVSEQFTDEH--SKNNGKKL---TNAAERFETIYPKHKNSDTVTFIMGARKRLRFSKPLVEARKLQDAKVYG  1621
PhlVB:YP_001552317.1    REVRIGH-LVSEQFTDEH--PREQGKQL---TNAAERFEAIYPRHKANDTVTFMMAVKKRLKFSRPATEKAKLVEAMPYG  1697
ASPV:NP_604464.1        REFRIGD-ITTEQFTDDH--SKNRGQEL---TNAAERYEAIYPRHKGTDTATFLMAVKKRLSFSSPAAEHAKLRRAKPFG  1827
APV1:YP_009094347.1     REVRCGS-ETTTQFPDDH--PSGAKITL---ANAAERFEAIYPRHRGSDSVTFLMAVKKRLSFSQPSKESAKLNRAKPYG  1671
CTLaV:YP_009046478.1    REHRIDT-IVTEQFAEVH---KGRGKIL---TAAPDNFEAIYPRHKAGDTATFVMAARKRLKFSLPAKEKQKFMSAIPYG  1676
CRMaV:YP_007761581.1    REFRIDN-LVTEQFSEVH---KGKGKVL---TAAPDNFEAIYPRHKAGDTATFVMAARKRLKFSFPARERQKYMAAIPYG  1666
                        **        : *:                        . ::  *   *   :  . .**:       :          .
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ZoVT:Z1                KSLFEIFKKEYGLRRDVRVNT-DEI--YADFIDRRLNKSKALISAHSERSDPDWICNHFFLFMKTQLCTKYEKRFSDAKA  1517
ZoVT:Z2                KSLFEIFKKEYGLRRDVRVNT-DEI--YADFIDRRLNKSKALISAHSERSDPDWICNHFFLFMKTQLCTKYEKRFSDAKA  1517
ZoVT:Z3                KSLFEIFRKEYGLRRDVRINR-DEI--YADFIDRRLNKSKALISAHSERSDPDWVCNHFFLFMKTQLCTKYEKRFSDAKA  1517
PrVT:YP_009051684.1    ENLCRLFVEEYGLKRGWQVDI-EST--EREFLLKRVEKAKKMIEAHSERSDPDWMVNHFFLFMKTQLCTKFEKRFSDAKA  1479
PrVT:AHM92766.1        ENLCKIFIEEYGLKRGVIVDV-EST--EREFLLKRVEKAKKMIEAHSERSDPDWLVNHFFLFMKTQLCTKFEKRFSDAKA  1479
PVT:ADX41471.1         AEIFNEMNKILLLNPHVSVDR-DQV--YKEFLRKRLNKSKKLIESHSERSSDDWPIDHFFLFMKSQLCTKFEKRFVDAKA  1306
PVT:YP_002019748.1     AEIFNEMNKILLLNPHVSVDR-DQV--YKEFLRKRLNKSKKLIESHSERSSDDWPIDHFFLFMKSQLCTKFEKRFVDAKA  1306
PVT:AFV39891.1         AEIFNEMNKILLLNPHVSVDR-DQV--YKEFLRKRLNKSKKLIESHSERSSDDWPIDHFFLFMKSQLCTKFEKRFVDAKA  1307
PVT:AFU55321.1         AEIFNEMNKILLLNPHVNVDR-DQV--YKEFLRKRLNKSKKLIESHSERSSDDWPIDHFFLFMKSQLCTKFEKRFVDAKA  1307
PVT:AXK90539.1         AEIFNEMNKILCLNPHVSVDR-DQV--YKEFLKKRLNKSKKLIESHAERSSDDWPIDHFFLFMKSQLCTKFEKRFADAKA  1307
AcVB:YP_004935358.1    KQLFKVLKETYNLRQPDKLPDLDRI--EAEFARKRLNKSKNLIEKHSYRSDPDWPSHYLKIFLKQQVCTKMEKRGVDAKA  1408
GVA:NP_619662.1        HQMFSVFKDTYQLKEIDSLPELERC--EMEFMKKRIEKSTGLIEKHAGRSDPDWPSNYLKIFLKQQTCTKMEKRGVDAKA  1413
GVE:YP_002117775.1     ESIFTEFLKRADFMNFTYPPQVDETSMELDFTMKRIQKSARILEAHSYRSDADWPSNYLKIFIKNQDCTKMEKRGSDAKA  1418
ASGV:NP_044335.1       KELLQEFISMLPFEFKVNIKEIEDG--EKSFLEKRKLKSEKMWANHSERSDIDWKLDHAFLFMKSQYCTKEGKMFTEAKA  1300
CVA:NP_620106.1        KELLNIFLRKVPLMPNFDQRMYDES--VSEFEEKKISKNAAMIGAHHDRSTTDWPTNEIFLFIKSQLCTKKEKMFCDAKA  1361
DiVA:YP_006905850.1    NEMLDIFLDKIKIDNKLNSEMMARS--YNEYVLKKVSKTANTIASHSSRSEPDWKLNEIFLFMKTQLCTKFEKRFSDAKA  1389
ObRV1:YP_009408144.1   SEMFELLLEKIPLDNKNDDLMMQIC--VNEYIERKVSKPAGTIKSHSGRSDCDWKLNDVFLFIKTQLCTKYEKRFSDAKA  1389
ACLSV:NP_040551.1      KYLTKIFLKHVPIKCGRDQRLLDQC--RQEFEETKLSKSAATIGAHSQRSDSDWPLDKIFLFMKSQLCTKFEKRFTEAKA  1577
GPGV:YP_004732978.2    KILLKNFLKFIPIPSETFPELLSEA--KREFQEVKLKKSEGTIAGNSGRSDPDWSWDRVFLFMKSQQCTKFEKRFCEAKA  1548
CtChV-1:YP_009103999.1 SILHKEFTRLIRVNSHFRPDLFEKA--LNDFEDVRMRKSEKLIMAHAGRSDPDWDIRNFLLFMKSQLCKKAEKAFCDAKA  1577
CtChV-2:YP_009103996.1 SILYKEFRKIIRVQGDFRPDLFDKA--LSDFERVRVAKSKKLIEAHAGRSDPDWDVKKFLLFMKSQLCKKAEKAFSDAKA  1574
AVCaV:YP_008997790.1   SILFHNLIQKLGLNFTWDNQLFEEC--VNDFECKKLEKSKAVLANHSIRSDNDWSPNWVFLFMKSQLCTKYEKQYVDAKA  1400
CPrV:AKN08994.1        NLLYQNLKEKLSLSFSWDQGLLDEC--LNDFETKKLLKSKATLANHSIRSDIDWSMDKIFLFMKSQLCTKYEKQYVDAKA  1711
CLBV:NP_624333.1       GLLYTNFKKKMGLEFTFDQGLLEES--INAFEKKKLEKSCGTIKSHSIRSDIDWALNDVFLFMKSQLCTKYEKQFVDAKA  1683
CLBV:AFA43536.1        GLLYRNFKNKLGLEFTFDQGLFEES--VNAFEKKKLEKSCGTIKSHSIRSDVDWALNDVFLFMKSQLCTKYEKQFVDAKA  1708
GCLV:YP_004936159.1    EFMLQEFLKHVPLKKPHNQAFMDAS--LADFEEKKTSKSAATIANHAGRSCRDWLIDTGLVFMKSQHCTKFDNRFRDAKA  1680
CVNV:YP_001430021.1    EFMLQNFPKYVPLRKQHNKGFMDKA--LRDFESKKVSKSAAIIANHAGRSCRDWLADVGLVFMKSQHCTKFDNRFRDAKA  1699
PhlVB:YP_001552317.1   KFMLKEFLKKIPMNKSRDTKMMEQS--KLEFEEKKLSKSAATIENHSGRSCRDWLIDIGLIFSKSQLCTKFDNRFRVAKA  1775
ASPV:NP_604464.1       KFLLDTFLKRVPLNSSHDEKMMQEA--VHAFEEKKLSKSMATIENHSGRSCEDWPVDKALIFMKSQLCTKFDNRFRSAKA  1905
APV1:YP_009094347.1    KFLVSEFLKRIPLRGNLDPILFAKA--KRDFEEKKTSKSAAVIENHSGRSCRDWLADVGFIFMKSQFCSKWDNRFRDAKA  1749
CTLaV:YP_009046478.1   DTMLKVFLNKVRLKPNFDHRLFEEA--RNDFEEKKLQKSMATLENHSGRSDPDWEIEKALIFMKSQLCTKFDNRFRDAKA  1754
CRMaV:YP_007761581.1   VSMLQVFLKRIKLQSNFDHRLFEEA--RADFEEKKLQKSMATLENHSGRSDPDWSVEKALIFMKSQLCTKFDNRFRNAKA  1744
                         :   :     .                 :   .  *       :  **  **      :* * * *.*  :    ***


ZoVT:Z1                GQTLACFSHSVLTRFGVPIKEVEEKMRFCLKDNIYIHSGKKLDELNNWCIKYA---TGYGTDSDYESFDRSQDALILAFE  1594
ZoVT:Z2                GQTLACFSHSVLTRFGVPIKEVEEKMRFCLKDNIYIHSGKKLDELNDWCIKYA---TGYGTDSDYESFDRSQDALILAFE  1594
ZoVT:Z3                GQTLACFSHSVLTRFGVPIKEVEEKMRFCLKDNIYIHSGKKLDELNNWCIKYA---TGYGTDSDYESFDRSQDALILAFE  1594
PrVT:YP_009051684.1    GQTLACFSHQVLARFGVPIRVAEKKLRAQLGENIYIHSGKQLDELNEWCMGYA---KGYGTDSDYESFDRSQDALILAFE  1556
PrVT:AHM92766.1        GQTLACFSHQVLARFGVPIRIAEKRLRSQLNDNIYIHSGKQLDELNEWCIRYS---QGYGTDSDYESFDRSQDALVLAFE  1556
PVT:ADX41471.1         GQTLACFSHKLLTRFGPAFREFEKKFTANLPPSWYIHTMKNFDQLNNWVINYV--DQEEGTESDYEAFDRSQDAIILGLE  1384
PVT:YP_002019748.1     GQTLACFSHKLLTRFGPAFREFEKKFTANLPPSWYIHTMKNFDQLNNWVINYV--DQEEGTESDYEAFDRSQDAIILGLE  1384
PVT:AFV39891.1         GQTLACFSHKLLTRFGPAFREFEKKFTANLPPSWYIHTMKNFDQLNNWVINYV--DQEEGTESDYEAFDRSQDAIILGLE  1385
PVT:AFU55321.1         GQTLACFSHKLLTRFGPAFREFEKKFTANLPPSWYIHTMKNFDQLNNWVINYV--DQEEGTESDYEAFDRSQDAIILGLE  1385
PVT:AXK90539.1         GQTLACFSHKLLTRFGPAFREFEKKFTANLPPSWYIHTMKNFDQLNNWVINFV--DQEEGTESDYEAFDRSQDAIILGLE  1385
AcVB:YP_004935358.1    GQTIACFCHAVLCKFGPLLRRTEKALRAQLGDNVLIYSQLNYTDLDKWCKNFV--PSMLGTDSDYEAFDRSQDERILDFE  1486
GVA:NP_619662.1        GQTIACFAHSVLCRFGPILRQTEKALRELLPEKLMIYSQKKYMDLDKWAKTWV--ESMMGTDSDYEAFDRSQDEKVLDLE  1491
GVE:YP_002117775.1     GQTIACFSHAVLCKFGPILRKTEAQLRKILPPHVMIFSQKNYEDLDKWSKDYF--NDHSGTDSDYEAFDRSQDGAILAFE  1496
ASGV:NP_044335.1       GQTLACFQHIVLFRFGPMLRAIESAFLRSCGDSYYIHSGKNFFCLDSFVTKNASVFDGFSIESDYTAFDSSQDHVILAFE  1380
CVA:NP_620106.1        GQTLACFSHLILCKFAPLNRYIEKKVTQSLPGNFYIHQKKNFDELERWVKSYN--FSGVCTESDYKAYDASQDSCTLAFE  1439
DiVA:YP_006905850.1    GQTLACFSHIILNRFAAPTRYVEKKISEGLGKNFYIHQKKNFDVLNDWVVANN--FDSYCLESDYEAFDSSQDCLILAFE  1467
ObRV1:YP_009408144.1   GQTLACFSHVILNRFAAPARYIEKKLSLCLPDNYYIHQKKNFDMLNAWVVRND--FSDECLESDYEAFDSSQDCLILAFE  1467
ACLSV:NP_040551.1      GQTLACFPHKILVEFSPWCRYTEKVLTANLPDNYYIHQRKNFSELEDFARRFS--NGSICVESDYTAFDVSQDHTILAFE  1655
GPGV:YP_004732978.2    GQTLACFSHEILCHFSPWCRYMEKVFSKYCPENFYIHQRKDFDKLAEFSRKYC--KGGFCIESDYVAFDVSQDHNVLAFE  1626
CtChV-1:YP_009103999.1 GQTIACFAHGVLFKFSAWCRYAELKINEVMPEAFYVHSKKNFDELERWVKGNF--IGPICVESDYEAFDASQDSTILAFE  1655
CtChV-2:YP_009103996.1 GQTIACFAHGVLFKFSAWARYAELKMMEKMPDSFYIHSRKNFDELEKWVKMNF--IGPICVESDYEAFDASQDATILAFE  1652
AVCaV:YP_008997790.1   GQTLACFQHMILVTFAPYCRYMEKQLRAQLPGEIYIHSNKNFNDLNEWVKKHA--GDDLCVESDYEAFDASQDQYILSFE  1478
CPrV:AKN08994.1        GQTLACFSHLVLAKFAPYCRYMEKMLRRNLKEEIYIHSNKNFNDLNDWVVKFF--EEGEKVESDYEAFDASQDHYVLAFE  1789
CLBV:NP_624333.1       GQTLACFQHLILVQFAPWCRYLETQIRNQLPEEIYIHSNKNFDDLNAWVKKFF--QRDICVESDYEAFDASQDEYILSFE  1761
CLBV:AFA43536.1        GQTLACFQHLILVQFAPWCRYLEAQIRNQLPEEIYIHSNKNFDDLYRWVKNFF--QKDICVESDYEAFDVCQDEYILSFE  1786
GCLV:YP_004936159.1    AQAIVCFQHAVLCRLAPFVRYIERKIAEVLPEKFYIHSGKGLEELNAWVTRGR--FEGVCTESDYEAFDASQDQYILAFE  1758
CVNV:YP_001430021.1    AQSIVCFQHAVLCRFAPYMRYIEMKLQEVLPSNFYVHSGKGLDELSEWVKKGK--FEGICTESDYEAFDASQDQYIMAFE  1777
PhlVB:YP_001552317.1   AQSIVCFQHEVLCRFAPYMRYIEKKLHQALPGNFYIHSGKGLEELNEWVMRGR--FDGVCTESDYEAFDASQDQYIMAFE  1853
ASPV:NP_604464.1       GQTLACFQHSVLCRFAPYMRYIESKVTEVLPKNLYIHSGKNIDDLAAWVTTSK--FNGVCTESDYEAFDASQDHFILAFE  1983
APV1:YP_009094347.1    GQTLACFHHSILCRFAPYMRYIEYKLQAASPSNLYIHSGKNLEDLNEWVIRNK--FSGMSTESDYEAFDSSQDHFILSFE  1827
CTLaV:YP_009046478.1   GQTLACFHHNVLCRLAPYIRYIEKKVFDALPRNLYIHSGKNFDDLRDWVINSN--FSGMCTESDYEAFDSSQDANILAFE  1832
CRMaV:YP_007761581.1   GQTLACFHHDVLCRLAPYIRYIEKKVFKALPSNLYIHSARNFDDLRDWVIKNN--FTGVCTESDYEAFDSSQDVNILAFE  1822
                       .*::.** * :*  :.   .  *  .         :.       *  :             :*** ::* .**   : :*
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ZoVT:Z1                 IHLLEFFGWTKDLIYDYVSIKLRLGCRLGNLAIMRFTGEFGTFFLNTCCNMLFTCLRYRFD-SKTPFAFAGDDMFSPKRL  1673
ZoVT:Z2                 IHLLEFFGWTKDLIYDYVSIKLRLGCRLGNLAIMRFTGEFGTFFLNTCCNMLFTCLRYRFD-SKTPFAFAGDDMFSPKRL  1673
ZoVT:Z3                 IHLLEFFGWTKDLIYDYISIKLRLGCRLGNLAIMRFTGEFGTFFLNTCCNMLFTCLRYKFD-SKTPFAFAGDDMFSPKRL  1673
PrVT:YP_009051684.1     LHLLRFLGWSVDQVEDYVTLKLRLGCRLGYLAIMRFTGEFGTFFLNTCCNMLFTCLRYKIN-KNTPIAFAGDDMFSPGRL  1635
PrVT:AHM92766.1         IHLLRFLGWNTDLIDDYVAIKLRLGCRLGYLAIMRFTGEFGTFFLNTCCNMLFTCLRYKIN-RRTPIAFAGDDMFSPGRL  1635
PVT:ADX41471.1          IECLKLFGWDQDLIDDYRKLKLWMGCRLGAIAIMRFTGEFGTFFFNTIANIAFTCLRYNIT-RDTVIAFAGDDMYASGKL  1463
PVT:YP_002019748.1      IECLKLFGWDQDLIDDYRKLKLRMGCRWGAIAIMRFTGEFGTFFFNTIANIAFTCLRYNIT-RDTVIAFAGDDMYASGKL  1463
PVT:AFV39891.1          IECLKLFGWDQDLIDDYRKLKLWMGCRLGAIAIMRFTGEFGTFFFNTIANIAFTCLRYNIT-RDTVIAFAGDDMYASGKL  1464
PVT:AFU55321.1          IECLKLFGWDQDLIDDYRKLKLWMGCRLGAIAIMRFTGEFGTFFFNTIANIAFTCLRYNIT-RDTVIAFAGDDMYASGKL  1464
PVT:AXK90539.1          IKCLELFGWDQDLIDDYRKLKLWMGCRLGAIAIMRFTGEFGTFFFNTIANIAFTCLRYNIS-RDTVIAFAGDDMYASGRL  1464
AcVB:YP_004935358.1     MEVLKFFLWPEEVINEYKELKLMMGSSMGSLAVMRFSGEFGTFFFNTICNMAFTCLRYKIN-KDTPICYAGDDMYAPGHL  1565
GVA:NP_619662.1         VEVLRFFLWPEDLIREYEELKLMMGCALGDLAVMRFSGEFGTFFFNTVCNMVFSCMRYHID-RNTPMCFAGDDMYSPGIL  1570
GVE:YP_002117775.1      ICLLRHFLWPEELIEEYKTLKLMMGCQLGDLAVMRFSGEFGTFFFNTMCNMAFSYLRYQLG-PYQPIAFAGDDMVAPGRL  1575
ASGV:NP_044335.1        MALLQYLGVSKEFQLDYLRLKLTLGCRLGSLAIMRFTGEFCTFLFNTFANMLFTQLKYKIDPRRHRILFAGDDMCSLSSL  1460
CVA:NP_620106.1         YKLLRYLAFSNSLIEDYLYLKMHLNCKLGNLAIIRFTGEFCTFLFNTLTNMLFTFMKYDVR-KTHAICFAGDDMCANVRL  1518
DiVA:YP_006905850.1     YELLKYLGWDQSLLDDYLDLKFNLGCRLGNLAVMRFTGEFGTFLFNTLANMVFTFMTYDLN-GTESICFAGDDMCCNRGI  1546
ObRV1:YP_009408144.1    YELLKYMGWSQSLLDDYLDLKFNLGCRLGNLAVMRFTGEFGTFLFNTLANMVFTFMSYDLT-GKEAICFAGDDMCCNKGI  1546
ACLSV:NP_040551.1       VELLRHFGWDDRVLQSYIKMKCTLGCRLGGFAIMRFTGEFSTFLFNTLANMVFTFCRYEVP-DGTPICFAGDDMCALRNL  1734
GPGV:YP_004732978.2     VQLMEHIRIPECVISDYIRMKTELGCKLGNFAIMRFTGEFCTFLFNTFCNMAFTFMRYQMS-GHEPICFAGDDMCALADL  1705
CtChV-1:YP_009103999.1  CLILKDVGWPHDLIEDYKTLKLELGCKLGMLAIMRFTGEFGTFFFNTLANMAFTFCRYNVN-RTTPICFAGDDMCILTNA  1734
CtChV-2:YP_009103996.1  VQFLKEVGWPQDLIEDYIELKVNLGCKLGNLAIMRFTGEFGTFFLNTLANMAFTFCRYNVN-RTTPICFAGDDMCILTDA  1731
AVCaV:YP_008997790.1    LFMMRHMHIPEQIIQAYIDLKVNLGCKLGHFAIMRFTGEFSTFLFNTLANMAFTMCRYEWN-SGDPIAFAGDDMCALKNL  1557
CPrV:AKN08994.1         VCVMEDMGLPNWFINDYIDLKCTLGCKLGHFAIMRFTGEFSTFLFNTLANMAFTFARYECD-HKTPIAFAGDDMCMLKAC  1868
CLBV:NP_624333.1        IHLMKDAHFPQKIIDAYIDLKCKLGCKLGHFSIMRFTGEFCTFLFNTLANMAFTMCRYEWR-RGQPIAFAGDDMCALNNL  1840
CLBV:AFA43536.1         IHLMKDAHFPQRVIDAYIDLKCKLGCKLGHFSIMRFTGEFCTFLFNTLANIAFTLCRYEWR-RGQPIAFAGDDMCALNNL  1865
GCLV:YP_004936159.1     LHVMKYLGLPRDLIEDYKFIKMHLGSKLGNFAIMRFSGEASTFLFNTMANMLFTFLRYEIK-GHERICFAGDDMCANARL  1837
CVNV:YP_001430021.1     LKVMEYLGIPKDLIADYVYIKTHLGSKLGNFAIMRYSGEASTFLFNTMANMLFTFLRYDVK-GNEFICFAGDDMCANTKL  1856
PhlVB:YP_001552317.1    IEMIKYLGLPADLISDYEFIKTHLGSKLGNFAIMRFSGEASTFLFNTMANMLFTFLRYEIR-GNEFICFAGDDMCASKRL  1932
ASPV:NP_604464.1        LEVMKFLGLPSDLIADYTFIKTHLGSKLGSFAIMRFTGEASTFLFNTMANMLFTFLRYDLN-GREAICFAGDDMCANSRL  2062
APV1:YP_009094347.1     IEIMKHLQLPWDLIEDYVYIKTHLGSKLGNFAIMRFTGEASTFLFNTMANMLFTFLRYDLN-GSEAICFAGDDMCANRRL  1906
CTLaV:YP_009046478.1    VSLMNYLNLPRDLIEDYKHLKFNTHSKLGQFAVMRFTGEAGTFLFNTLANMVFTFMRYETN-GRESICFAGDDMCANKLL  1911
CRMaV:YP_007761581.1    VSLMEYLRLPRDLIEDYKYLKFHTHSKLGQFAVMRFTGEAGTFLFNTLANMVFTFMRYEIN-GREAICFAGDDMCANKLL  1901
                           :            *  :*    .  * ::::*::**  **::**  *: *:   *        : :*****


ZoVT:Z1                 DVRHD--REFLLKRFSLKAKVSFSRRPMFCGWRMSKYGIVKEPRLVLERFEIAKERGILKECLINYCLEVSFAYRLGDKL  1751
ZoVT:Z2                 DVRHD--REFLLKRFSLKAKVSFSRRPMFCGWRMSKYGIVKEPRLVLERFEIAKERGILKECLINYCLEVSFAYRLGDKL  1751
ZoVT:Z3                 DVRYD--REFLLKRFSLKAKVSFSRKPMFCGWRMSKYGIVKEPRLVLERFEIAKERGILKECLINYCLEVSFAYRLGDKL  1751
PrVT:YP_009051684.1     EVRRD--REFLLNRFSLKAKVNFSKEPMFCGWRMTPYGIVKEPKLVLERFKIAEERGCFKECLINYCLEVSFAYRLGERL  1713
PrVT:AHM92766.1         EVRRD--REFLLNRFSLKAKVNFSKEPMFCGWRMTQYGIVKEPKLVLERFKIAEERGCFKECLINYCLEVSFAYRLGERL  1713
PVT:ADX41471.1          EIRKD--REDLLAHLTLKAKVQFTEKPMFCGWYIKKMGIVKEPRLVLERWLIAERKKVIDQCFINYSIEVSYGYRLGEYL  1541
PVT:YP_002019748.1      EIRKD--REDLLAHLTLKAKVQFTEKPMFCGWYIKKMGIVKEPRLVLERWLIAERKKVIDQCFINYSIEVSYGYRLGEYL  1541
PVT:AFV39891.1          EIRKD--REDLLAHLTLKAKVQFTEKPMFCGWYIKKMGIVKEPRLVLERWLIAERKKVIDQCFINYSIEVSYGYRLGEYL  1542
PVT:AFU55321.1          EIRKD--REDLLAHLTLKAKVQFTEKPMFCGWYIKKMGIVKEPRLVLERWLIAERKKVIDQCFINYSIEVSYGYRLGEYL  1542
PVT:AXK90539.1          EIRKD--REDLLSHLTLKAKVQFTDKPMFCGWYIKKKGIVKEPRLVLERWLIAERKKVIDQCFINYSIEVSYGYRLGEYL  1542
AcVB:YP_004935358.1     IISKE--HEGTLDQLSLKAKVRVSTEPLFCGWRMSPYGIVKDPNLLLDRWKIAKRGGNLDQCMVNYSLEACYGYRLGEYL  1643
GVA:NP_619662.1         RVKKD--YEATLDQLTLKAKVHISEEPLFCGWRMSPFGIIKEPNLILDRWKIALRSGNLSLCLVNYAIEASFGYRLSEHL  1648
GVE:YP_002117775.1      VVNES--MNSVLNQLELKAKVNYSDSPLFCGWRMSPYGIVKDPNLLLDRLEMKRAEGKLDDCIANYALEASYGYRLSDHL  1653
ASGV:NP_044335.1        KRRRGERATRLMKSFSLTAVEEVRKFPMFCGWYLSPYGIIKSPKLLWARIKMMSERQLLKECVDNYLFEAIFAYRLGERL  1540
CVA:NP_620106.1         PENHE--YSSLLKKFSLKAKVDFTRSPTFCGWNLSRYGIVKKPELIAARLAVARQKGEVNLVLDSYFLEHLYAYNKGDHL  1596
DiVA:YP_006905850.1     KARVDGKYDHILKRLTLKAKAVITKEPTFCGWRLTKYGIFKKPELVLERFLIAIEKGRLLDVIDSYYIECSYAYNLGERL  1626
ObRV1:YP_009408144.1    RRRTDGRFDHILNRLSLKAKAVITTEPTFCGWRLTKYGIFKKPELVLERFLIAIEKNKLKDVIDSYYLECSYAYSLGERL  1626
ACLSV:NP_040551.1       REIDT--HEFILSKLSLKAKVNRTKVPMFCGWRLCCDGLIKEPCLIYERLQVAIENGRLMDVIDSYFLEFSFAYKLGERL  1812
GPGV:YP_004732978.2     KESDE--YNAFFKSFSLKAKVCRTVKPLFCGWRLTKFGLYKEPVLVYERLKIAIEKDKLDLVIDSYFLEFCYAYKLGSWL  1783
CtChV-1:YP_009103999.1  KIRNE--MNDFIGSLKLKAKVEWKINPIFCGWILSRRGILKLPSLVYYRLNIAKEKGNLKDCIDSYMIEAGYAYRKGAFI  1812
CtChV-2:YP_009103996.1  KVRHD--LDEFINSLKLKAKVEWKINPIFCGWILSRYGILKLPSLVYYRLCIALEKGNLKDCIDSYMIEAGYAYRKGAFI  1809
AVCaV:YP_008997790.1    KVTDQ--FNNVFEKISLKAKTQITEVPMFCGWRLSRFGIVKEPELVYNRFMVALERGNVKDCLENYAIEVSYAYSLGERL  1635
CPrV:AKN08994.1         KVSDK--FEDVLSKLSLKAKVIRTEMPMFCGWNLSRYGIVKEPELVFNRFMVAKKRGNIDECLENYAIEVSYAYSLGEKL  1946
CLBV:NP_624333.1        AVCHD--FDDLFELISLKAKVERTETPMFCGWRLTPYGIVKEPELVYNRFQVAIEEGKVLECLENYAIEVSYAYSLSERL  1918
CLBV:AFA43536.1         PICHD--FDDLFELISLKAKVERTESPMFCGWRLTPYGIVKEPELVYNRFQIAIEEGKVMECLENYAIEVSYAYSLSERL  1943
GCLV:YP_004936159.1     RHRLD--QEKFLGLLKLKAKVSFTQKPTFCGWNLCSDGIYKKPQLVLERLCIAKETNNLACCIDNYALEVAFAYKMGERA  1915
CVNV:YP_001430021.1     RKVDT--HESFLSKLKLKAKVGFVNKPTFCGWNLCSDGIYKKPQLVLERLCIAKETNNLTSCIDNYAIEVSYAYRMSEKA  1934
PhlVB:YP_001552317.1    PLSRA--YEGFLSKLKLKAKVFFVKSPTFCGWHLSPDGIYKKPQLVMERMCIAKEKGNLIDCIDNYAIELSYAYKMGELA  2010
ASPV:NP_604464.1        KVTNR--FSNFLDKIKLKAKVQFTATPTFCGWGLCEHGVFKKPDLVLERLQIARETRNLENCIDNYAIEVSCAYKMGENL  2140
APV1:YP_009094347.1     RVSKK--NENFLGKIKLKAKVQFTEKPTFCGWNLCMDGIFKRPQLVLERLCVAREKDNLANCLDSYAIEVGYAFALGEKI  1984
CTLaV:YP_009046478.1    RKKKE--YEHVLDRMTLKAKMQHTTEPTFCGWRLGPFGIIKRPQLVQERIPIALEKGNFNECIDNYAIEVSHAYNLGDRL  1989
CRMaV:YP_007761581.1    RKKSE--FEHILDRMTLKAKVQHTTEPTFCGWRLGNFGIVKRPQLVQERILIALEKGNFHECIDNYAIEVSYAYNLGERL  1979
                                   :  : *.*       * **** :   *: * * *:  *  :      .   . .* :*   .:  .
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ZoVT:Z1                 YEVID---NIEDQQELVRFVVKKKHLLPPKVR------------------------------------------------  1780
ZoVT:Z2                 YEVID---NIEDQQELVRFVVKKKHLLPPKVR------------------------------------------------  1780
ZoVT:Z3                 YEVID---NIEDQQELVRFVVKKKHLLPPKVR------------------------------------------------  1780
PrVT:YP_009051684.1     YDVIK---NIQDKQALVRIVVKNKKFLPKKIR------------------------------------------------  1742
PrVT:AHM92766.1         YEVIK---NVQDQQALVRIVVKNKKFLPRKIR------------------------------------------------  1742
PVT:ADX41471.1          WEYFD---NLEDFQAIVRLVIKKKKQLPPAIR------------------------------------------------  1570
PVT:YP_002019748.1      WEYFD---NLEDFQAIVRLVIKKKKQLPPAIR------------------------------------------------  1570
PVT:AFV39891.1          WEYFD---NLEDFQAIVRLVIKKKKQLPPAIR------------------------------------------------  1571
PVT:AFU55321.1          WEYFD---NLEDFQAIVRLVIKKKKQLPPAIR------------------------------------------------  1571
PVT:AXK90539.1          WEYFD---NLEDFQAIVRLVIKKKKQLPPAIR------------------------------------------------  1571
AcVB:YP_004935358.1     FDINI---DIDAQQELVREIIKIKHKLPKGIR------------------------------------------------  1672
GVA:NP_619662.1         YDVNI---DVDAQQELVREIVIKKHLLPKKIS------------------------------------------------  1677
GVE:YP_002117775.1      YDLNI---DLDAFQELIRKIVMLKHKLPPAIA------------------------------------------------  1682
ASGV:NP_044335.1        YTILK-EEDFEYHYLVIRFFVRNSKLLTGLSK------------------------------------------------  1571
CVA:NP_620106.1         FEILS-EKELEHHYNLTRFFVKNSKLLKGESKKKFMETKEIEGGLFGECDFGNDSIFKDYINRVKNKVEIDLLNERILRI  1675
DiVA:YP_006905850.1     FECFS-EKDFSAHYCCIRIVHKNKSLLKGLSLERYREN------------------------------------------  1663
ObRV1:YP_009408144.1    FECFS-EKDFVAHYCCIRLVHLHKDLLRGQSLDKYISN------------------------------------------  1663
ACLSV:NP_040551.1       YSHLE-IEQLNYHQVLTRFFIRNKHLLRGDSR------------------------------------------------  1843
GPGV:YP_004732978.2     DWVLD-EEQADYQQRLSRFFVKKRHLLKGKSL------------------------------------------------  1814
CtChV-1:YP_009103999.1  EELLD-EDQMSFHQLVIRSMIKSKHLMKGSSI------------------------------------------------  1843
CtChV-2:YP_009103996.1  DELLT-EEQMNFHQLVIRRMIKAKHLMKGSSV------------------------------------------------  1840
AVCaV:YP_008997790.1    FDILKREEQLEYHQAVVRFIVKHLGNLRTKVK------------------------------------------------  1667
CPrV:AKN08994.1         YEVLKREEQVEYHQAVVRFIVQRLDKLKTKVK------------------------------------------------  1978
CLBV:NP_624333.1        YEVLKSERQVQYHQAVVRFIVTHIDKLKTKVR------------------------------------------------  1950
CLBV:AFA43536.1         YEVLKSERQIQYHQAVVRFIVTHIDKLKTRVK------------------------------------------------  1975
GCLV:YP_004936159.1     VLRMD-EEELQSHYNCVRIILQNKNLIKSNVL------------------------------------------------  1946
CVNV:YP_001430021.1     TMRMS-EEELDSHYNCLRIIIKNKHLMKSEAA------------------------------------------------  1965
PhlVB:YP_001552317.1    LCRMD-EEETEAFYNCVRIVVKNKHLLKSDIK------------------------------------------------  2041
ASPV:NP_604464.1        NLYLT-PQEVDAHYNCVRFIVQHNHLLKSNIR------------------------------------------------  2171
APV1:YP_009094347.1     LQYMD-EEALQNHYNCVRFIIKHSHLLKSSVR------------------------------------------------  2015
CTLaV:YP_009046478.1    ISIMS-EKELDAHYFCVRTFLQHKSLFSSNAL------------------------------------------------  2020
CRMaV:YP_007761581.1    ISIMS-EKELDAHYFCVRTFLQNKKLFSSNAL------------------------------------------------  2010
                                         * .      :


ZoVT:Z1                 --------------------------------------------------------------------------------  1780
ZoVT:Z2                 --------------------------------------------------------------------------------  1780
ZoVT:Z3                 --------------------------------------------------------------------------------  1780
PrVT:YP_009051684.1     --------------------------------------------------------------------------------  1742
PrVT:AHM92766.1         --------------------------------------------------------------------------------  1742
PVT:ADX41471.1          --------------------------------------------------------------------------------  1570
PVT:YP_002019748.1      --------------------------------------------------------------------------------  1570
PVT:AFV39891.1          --------------------------------------------------------------------------------  1571
PVT:AFU55321.1          --------------------------------------------------------------------------------  1571
PVT:AXK90539.1          --------------------------------------------------------------------------------  1571
AcVB:YP_004935358.1     --------------------------------------------------------------------------------  1672
GVA:NP_619662.1         --------------------------------------------------------------------------------  1677
GVE:YP_002117775.1      --------------------------------------------------------------------------------  1682
ASGV:NP_044335.1        --------------------------------------------------------------------------------  1571
CVA:NP_620106.1         NTEMNQFDPRIYMMNKIGFVTSTSMFEAGHIASNESNQVKSLPPQTSWPYDEVKPYMPLSLRNSYESRTKGNRLLSILRN  1755
DiVA:YP_006905850.1     --------------------------------------------------------------------------------  1663
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------  1663
ACLSV:NP_040551.1       --------------------------------------------------------------------------------  1843
GPGV:YP_004732978.2     --------------------------------------------------------------------------------  1814
CtChV-1:YP_009103999.1  --------------------------------------------------------------------------------  1843
CtChV-2:YP_009103996.1  --------------------------------------------------------------------------------  1840
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------  1667
CPrV:AKN08994.1         --------------------------------------------------------------------------------  1978
CLBV:NP_624333.1        --------------------------------------------------------------------------------  1950
CLBV:AFA43536.1         --------------------------------------------------------------------------------  1975
GCLV:YP_004936159.1     --------------------------------------------------------------------------------  1946
CVNV:YP_001430021.1     --------------------------------------------------------------------------------  1965
PhlVB:YP_001552317.1    --------------------------------------------------------------------------------  2041
ASPV:NP_604464.1        --------------------------------------------------------------------------------  2171
APV1:YP_009094347.1     --------------------------------------------------------------------------------  2015
CTLaV:YP_009046478.1    --------------------------------------------------------------------------------  2020
CRMaV:YP_007761581.1    --------------------------------------------------------------------------------  2010
```

```
ZoVT:Z1                 ---------------------KEFESY-----------------------------------------------------  1786
ZoVT:Z2                 ---------------------KEFESY-----------------------------------------------------  1786
ZoVT:Z3                 ---------------------KEFESY-----------------------------------------------------  1786
PrVT:YP_009051684.1     ---------------------KEFESF-----------------------------------------------------  1748
PrVT:AHM92766.1         ---------------------KEFESF-----------------------------------------------------  1748
PVT:ADX41471.1          ---------------------RIFETS-----------------------------------------------------  1576
PVT:YP_002019748.1      ---------------------RIFETS-----------------------------------------------------  1576
PVT:AFV39891.1          ---------------------RIFETS-----------------------------------------------------  1577
PVT:AFU55321.1          ---------------------RIFETS-----------------------------------------------------  1577
PVT:AXK90539.1          ---------------------RLFETS-----------------------------------------------------  1577
AcVB:YP_004935358.1     ---------------------KLFSSD-----------------------------------------------------  1678
GVA:NP_619662.1         ---------------------DLFSED-----------------------------------------------------  1683
GVE:YP_002117775.1      ---------------------SLFKEE-----------------------------------------------------  1688
ASGV:NP_044335.1        ---------------------SLIFEIGEGIGSKWLSSTSTASSRRSNLQTSKLMLSRPQSFTRMQPFSNQTCLIASKGL  1630
CVA:NP_620106.1         QKHLCDLGSGSILGLRVLEGLKMFKEE-----CRSYQSRSFFKESQETNQEFSLMQFVPRTFTVMQMPSIPKCSQLLKDF  1830
DiVA:YP_006905850.1     ---------------------RRFKHSCKSWIQRPSYRSSTMEDETLIASGSVRCTQMGVSSKTRRLTQFREQKVQFQLN  1722
ObRV1:YP_009408144.1    ---------------------QRFGLGCKLLGQKHLSKSLMEVKRTSTASVLVVSTPMEVTHKIQRLMLHRNLRVPYLSE  1722
ACLSV:NP_040551.1       ---------------------HNISEL-----------------------------------------------------  1849
GPGV:YP_004732978.2     ---------------------DYITHC-----------------------------------------------------  1820
CtChV-1:YP_009103999.1  ---------------------HILEDL-----------------------------------------------------  1849
CtChV-2:YP_009103996.1  ---------------------EILKEI-----------------------------------------------------  1846
AVCaV:YP_008997790.1    ---------------------DLFAEQ-----------------------------------------------------  1673
CPrV:AKN08994.1         ---------------------DLFSDQ-----------------------------------------------------  1984
CLBV:NP_624333.1        ---------------------DLFLEQ-----------------------------------------------------  1956
CLBV:AFA43536.1         ---------------------DLFLEQ-----------------------------------------------------  1981
GCLV:YP_004936159.1     ---------------------TYFSA------------------------------------------------------  1951
CVNV:YP_001430021.1     ---------------------NIFKAS-----------------------------------------------------  1971
PhlVB:YP_001552317.1    ---------------------NLFTTR-----------------------------------------------------  2047
ASPV:NP_604464.1        ---------------------DLFKGE-----------------------------------------------------  2177
APV1:YP_009094347.1     ---------------------DLFLSG-----------------------------------------------------  2021
CTLaV:YP_009046478.1    ---------------------EFFSEG-----------------------------------------------------  2026
CRMaV:YP_007761581.1    ---------------------EFFSES-----------------------------------------------------  2016
                                               :


ZoVT:Z1                 --------------------------------------------------------------------------------  1786
ZoVT:Z2                 --------------------------------------------------------------------------------  1786
ZoVT:Z3                 --------------------------------------------------------------------------------  1786
PrVT:YP_009051684.1     --------------------------------------------------------------------------------  1748
PrVT:AHM92766.1         --------------------------------------------------------------------------------  1748
PVT:ADX41471.1          --------------------------------------------------------------------------------  1576
PVT:YP_002019748.1      --------------------------------------------------------------------------------  1576
PVT:AFV39891.1          --------------------------------------------------------------------------------  1577
PVT:AFU55321.1          --------------------------------------------------------------------------------  1577
PVT:AXK90539.1          --------------------------------------------------------------------------------  1577
AcVB:YP_004935358.1     --------------------------------------------------------------------------------  1678
GVA:NP_619662.1         --------------------------------------------------------------------------------  1683
GVE:YP_002117775.1      --------------------------------------------------------------------------------  1688
ASGV:NP_044335.1        NQTSRFPLDLVTASSCLISNCLMTPKLIQSGRKATSTNTYTMESSWLGSKQCCQTLEAWKGESLYMMEPAWIRKEATFAR  1710
CVA:NP_620106.1         SLQLLYLQAALAKAMLHSSIFLMKLSWRLSKKPLLSTQCFILGQSSYVLHAFSSLKSRSMAELYTLIPGFWTKMMHAKQV  1910
DiVA:YP_006905850.1     QLMGSPGLLKEYLLLTQMLLMRRETRRSIQKSILEQLSSVSTSLVIMNVRCQEEDVCWLTVEEVEEVELSKPLSLIYPKD  1802
ObRV1:YP_009408144.1    CQKGGLVLSREYQSLTQRLCVMREQRKSIKKLTLVQLLSVYTSMATMTKKPAKENACWLMEGEMMKMVSLTPSGLMFQKV  1802
ACLSV:NP_040551.1       --------------------------------------------------------------------------------  1849
GPGV:YP_004732978.2     --------------------------------------------------------------------------------  1820
CtChV-1:YP_009103999.1  --------------------------------------------------------------------------------  1849
CtChV-2:YP_009103996.1  --------------------------------------------------------------------------------  1846
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------  1673
CPrV:AKN08994.1         --------------------------------------------------------------------------------  1984
CLBV:NP_624333.1        --------------------------------------------------------------------------------  1956
CLBV:AFA43536.1         --------------------------------------------------------------------------------  1981
GCLV:YP_004936159.1     --------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1     --------------------------------------------------------------------------------  1971
PhlVB:YP_001552317.1    --------------------------------------------------------------------------------  2047
ASPV:NP_604464.1        --------------------------------------------------------------------------------  2177
APV1:YP_009094347.1     --------------------------------------------------------------------------------  2021
CTLaV:YP_009046478.1    --------------------------------------------------------------------------------  2026
CRMaV:YP_007761581.1    --------------------------------------------------------------------------------  2016
```

```
ZoVT:Z1                --------------------------------------------------------------------------------  1786
ZoVT:Z2                --------------------------------------------------------------------------------  1786
ZoVT:Z3                --------------------------------------------------------------------------------  1786
PrVT:YP_009051684.1    --------------------------------------------------------------------------------  1748
PrVT:AHM92766.1        --------------------------------------------------------------------------------  1748
PVT:ADX41471.1         --------------------------------------------------------------------------------  1576
PVT:YP_002019748.1     --------------------------------------------------------------------------------  1576
PVT:AFV39891.1         --------------------------------------------------------------------------------  1577
PVT:AFU55321.1         --------------------------------------------------------------------------------  1577
PVT:AXK90539.1         --------------------------------------------------------------------------------  1577
AcVB:YP_004935358.1    --------------------------------------------------------------------------------  1678
GVA:NP_619662.1        --------------------------------------------------------------------------------  1683
GVE:YP_002117775.1     --------------------------------------------------------------------------------  1688
ASGV:NP_044335.1       IFSSLSLTVATLVSGQSTVCLPQTQIWPKGLDFVWTLIVHNMNRTLSCLLLTLELHTDASTLQGFWKPKLAIQDGLHRQS  1790
CVA:NP_620106.1        LVSSCKLDQPITFIGQIIQCPHMIQTCIGLLESSLNSMQSMLLTIPTYSSLTLESCTSSVIRALQRRQLPQMLGHSFKHF  1990
DiVA:YP_006905850.1    QPTSCSYQMQSLTFMMSYLTGPVKCSSSLTMLITVVVPTHLLLRLGQYIACLMSSIAITEWEFQEERVPLEVSIRKYIAL  1882
ObRV1:YP_009408144.1   QLILSLHQMLFLISMMSCLTRPVSCTFHLKVLSTEKVQDRLLLRLELSTGCQMHSTVIISWEFQGGGEILVAPFRKFMAQ  1882
ACLSV:NP_040551.1      --------------------------------------------------------------------------------  1849
GPGV:YP_004732978.2    --------------------------------------------------------------------------------  1820
CtChV-1:YP_009103999.1 --------------------------------------------------------------------------------  1849
CtChV-2:YP_009103996.1 --------------------------------------------------------------------------------  1846
AVCaV:YP_008997790.1   --------------------------------------------------------------------------------  1673
CPrV:AKN08994.1        --------------------------------------------------------------------------------  1984
CLBV:NP_624333.1       --------------------------------------------------------------------------------  1956
CLBV:AFA43536.1        --------------------------------------------------------------------------------  1981
GCLV:YP_004936159.1    --------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1    --------------------------------------------------------------------------------  1971
PhlVB:YP_001552317.1   --------------------------------------------------------------------------------  2047
ASPV:NP_604464.1       --------------------------------------------------------------------------------  2177
APV1:YP_009094347.1    --------------------------------------------------------------------------------  2021
CTLaV:YP_009046478.1   --------------------------------------------------------------------------------  2026
CRMaV:YP_007761581.1   --------------------------------------------------------------------------------  2016


ZoVT:Z1                --------------------------------------------------------------------------------  1786
ZoVT:Z2                --------------------------------------------------------------------------------  1786
ZoVT:Z3                --------------------------------------------------------------------------------  1786
PrVT:YP_009051684.1    --------------------------------------------------------------------------------  1748
PrVT:AHM92766.1        --------------------------------------------------------------------------------  1748
PVT:ADX41471.1         --------------------------------------------------------------------------------  1576
PVT:YP_002019748.1     --------------------------------------------------------------------------------  1576
PVT:AFV39891.1         --------------------------------------------------------------------------------  1577
PVT:AFU55321.1         --------------------------------------------------------------------------------  1577
PVT:AXK90539.1         --------------------------------------------------------------------------------  1577
AcVB:YP_004935358.1    --------------------------------------------------------------------------------  1678
GVA:NP_619662.1        --------------------------------------------------------------------------------  1683
GVE:YP_002117775.1     --------------------------------------------------------------------------------  1688
ASGV:NP_044335.1       AAVKHLNSMRKSRWPSWIADPRCFWKKVHQTCTLKRDCSEVTRLEGHAQFPLKGGQTQGCKKREDLGPSRLELKDLEKMS  1870
CVA:NP_620106.1        LGLLDYQILNPFLRMKILSILQLWHSLTSVLTRVSGKVVSLKAHHVQQEPEGIMPEARDRVLSQSQKLLVKILNNKKEIC  2070
DiVA:YP_006905850.1    RPYQRKMRSQCCQRCVSQERLEEYLMLREALALNLKGVREVLS---------CLGEKEALL----SFEIIVSEKGLVKLR  1949
ObRV1:YP_009408144.1   ALYNQEM-------CIRQ--LKKWLKPKERVELVRLELNQVWNYHRGQGKKLCLGKKEDLAFIGNTLWIVTFLKSLMK--  1951
ACLSV:NP_040551.1      --------------------------------------------------------------------------------  1849
GPGV:YP_004732978.2    --------------------------------------------------------------------------------  1820
CtChV-1:YP_009103999.1 --------------------------------------------------------------------------------  1849
CtChV-2:YP_009103996.1 --------------------------------------------------------------------------------  1846
AVCaV:YP_008997790.1   --------------------------------------------------------------------------------  1673
CPrV:AKN08994.1        --------------------------------------------------------------------------------  1984
CLBV:NP_624333.1       --------------------------------------------------------------------------------  1956
CLBV:AFA43536.1        --------------------------------------------------------------------------------  1981
GCLV:YP_004936159.1    --------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1    --------------------------------------------------------------------------------  1971
PhlVB:YP_001552317.1   --------------------------------------------------------------------------------  2047
ASPV:NP_604464.1       --------------------------------------------------------------------------------  2177
APV1:YP_009094347.1    --------------------------------------------------------------------------------  2021
CTLaV:YP_009046478.1   --------------------------------------------------------------------------------  2026
CRMaV:YP_007761581.1   --------------------------------------------------------------------------------  2016
```

```
ZoVT:Z1                  --------------------------------------------------------------------------------  1786
ZoVT:Z2                  --------------------------------------------------------------------------------  1786
ZoVT:Z3                  --------------------------------------------------------------------------------  1786
PrVT:YP_009051684.1      --------------------------------------------------------------------------------  1748
PrVT:AHM92766.1          --------------------------------------------------------------------------------  1748
PVT:ADX41471.1           --------------------------------------------------------------------------------  1576
PVT:YP_002019748.1       --------------------------------------------------------------------------------  1576
PVT:AFV39891.1           --------------------------------------------------------------------------------  1577
PVT:AFU55321.1           --------------------------------------------------------------------------------  1577
PVT:AXK90539.1           --------------------------------------------------------------------------------  1577
AcVB:YP_004935358.1      --------------------------------------------------------------------------------  1678
GVA:NP_619662.1          --------------------------------------------------------------------------------  1683
GVE:YP_002117775.1       --------------------------------------------------------------------------------  1688
ASGV:NP_044335.1         LEDVLQQARRHRVGVYLWKTHIDPAKELLTVPPPEGFKEGESFEGKELYLLLCNHYCKYLFGNIAVFGSSDKTQFPAVGF  1950
CVA:NP_620106.1          LGQIHVGLKIFSSIQNRGFQLIKNSSTDLISAILKGGTQISSMALSIVEQNYNEIRRGLGNYIWENMIDPRDLLHLTAKP  2150
DiVA:YP_006905850.1      KIYAGLGQAQEVLMKETFLKRFWIINLGLPVNAENFKVTSGKQAMVDQAANLALSNWINETTGFQGEAYGVRLRKLRRRT  2029
ObRV1:YP_009408144.1     --GATLGQAQVTLMKEEFLKTYWAVRLALPYNHQTHRVTSGKMAGAEAQANQALRNWIDDATGFQGEAYGVRMRKLRRRT  2029
ACLSV:NP_040551.1        --------------------------------------------------------------------------------  1849
GPGV:YP_004732978.2      --------------------------------------------------------------------------------  1820
CtChV-1:YP_009103999.1   --------------------------------------------------------------------------------  1849
CtChV-2:YP_009103996.1   --------------------------------------------------------------------------------  1846
AVCaV:YP_008997790.1     --------------------------------------------------------------------------------  1673
CPrV:AKN08994.1          --------------------------------------------------------------------------------  1984
CLBV:NP_624333.1         --------------------------------------------------------------------------------  1956
CLBV:AFA43536.1          --------------------------------------------------------------------------------  1981
GCLV:YP_004936159.1      --------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1      --------------------------------------------------------------------------------  1971
PhlVB:YP_001552317.1     --------------------------------------------------------------------------------  2047
ASPV:NP_604464.1         --------------------------------------------------------------------------------  2177
APV1:YP_009094347.1      --------------------------------------------------------------------------------  2021
CTLaV:YP_009046478.1     --------------------------------------------------------------------------------  2026
CRMaV:YP_007761581.1     --------------------------------------------------------------------------------  2016


ZoVT:Z1                  --------------------------------------------------DH-EFGGCES-VQEEGECNRVHSFGCGLEC  1814
ZoVT:Z2                  --------------------------------------------------DH-EFGGCES-VQEEGECNRVHSFGCGLEC  1814
ZoVT:Z3                  --------------------------------------------------DH-EFGGCES-VQEEGECNRVHSFGCGLEC  1814
PrVT:YP_009051684.1      --------------------------------------------------DH-EFGGCGS-VQEEGECDRVHRFGCGLEC  1776
PrVT:AHM92766.1          --------------------------------------------------DH-EFGGSES-VQEEGECDRVHRFGCGLEC  1776
PVT:ADX41471.1           --------------------------------------------------NGVDFSGE---VQETMGGEGEHHGSCGLWC  1603
PVT:YP_002019748.1       --------------------------------------------------NGVDFSGE---VQETMGGEGEHHGSCGLWC  1603
PVT:AFV39891.1           --------------------------------------------------NGVDFSGE---VQETMGGEGEHHGSCGLWC  1604
PVT:AFU55321.1           --------------------------------------------------NGVDFSGE---VQETMGREGEHHGSCGLWC  1604
PVT:AXK90539.1           --------------------------------------------------NGVDFGGE---VQEAMGGEREHHGSCGLWC  1604
AcVB:YP_004935358.1      --------------------------------------------------PTECGSDGEELEFRVRNEGGIESPTETED-  1707
GVA:NP_619662.1          --------------------------------------------------ECERHSDGDE-DFLSNDVARLYRIE-----  1707
GVE:YP_002117775.1       --------------------------------------------------EDIVSSDEEA--------------------  1698
ASGV:NP_044335.1         DTPPVH--------------------------------------------YNLTTTPKEG-ETDEGRKARAGSSGEKTKI  1985
CVA:NP_620106.1          AVEASEGVAATPAITLSENQRAVKNTIRNYYLRIMFGNLAVMGTSEQTDYPGEHLAIPRP-VIENQEALTAHLPAGMSLL  2229
DiVA:YP_006905850.1      LLRQHWVSVFKEYVKNLGHANTPAEFTAAESEIYGRVMSDFAAYAFGIMAEE-GFSPATI-YNEVPASYTIEYPQPVGAL  2107
ObRV1:YP_009408144.1     LLRDYWVSHMKAEFQNLGHANEPQSFTAAESTLYGNIMSDFASHAFGVLAED-GFSPATV-YSSVNASYTVDYRAPVGNK  2107
ACLSV:NP_040551.1        --------------------------------------------------EWLSDEDGDNDKGSQIEDRRRGYSNCWGEK  1879
GPGV:YP_004732978.2      --------------------------------------------------DYLSDGSDEEDSKGFWEDCNRGYSNCGVAF  1850
CtChV-1:YP_009103999.1   --------------------------------------------------VD-SYSDGV---------------------  1857
CtChV-2:YP_009103996.1   --------------------------------------------------QD-CFSDGVD-D------------------  1856
AVCaV:YP_008997790.1     --------------------------------------------------SN-EDSC-----------------------  1679
CPrV:AKN08994.1          --------------------------------------------------NV----------------------------  1986
CLBV:NP_624333.1         --------------------------------------------------SS-DEDI-----------------------  1962
CLBV:AFA43536.1          --------------------------------------------------SS-DEDI-----------------------  1987
GCLV:YP_004936159.1      --------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1      --------------------------------------------------DV-GLGI-----------------------  1977
PhlVB:YP_001552317.1     --------------------------------------------------AL-EE-------------------------  2051
ASPV:NP_604464.1         --------------------------------------------------SL-PASS-----------------------  2183
APV1:YP_009094347.1      --------------------------------------------------M-----------------------------  2022
CTLaV:YP_009046478.1     --------------------------------------------------ES-CKSPDRN-FG-----------------  2037
CRMaV:YP_007761581.1     --------------------------------------------------EG-CLSPERN-FG-----------------  2027
```

```
ZoVT:Z1                 NL------------------------------------------------------------------------------  1816
ZoVT:Z2                 NL------------------------------------------------------------------------------  1816
ZoVT:Z3                 NL------------------------------------------------------------------------------  1816
PrVT:YP_009051684.1     NI------------------------------------------------------------------------------  1778
PrVT:AHM92766.1         NL------------------------------------------------------------------------------  1778
PVT:ADX41471.1          NLH-----------------------------------------------------------------------------  1606
PVT:YP_002019748.1      NLH-----------------------------------------------------------------------------  1606
PVT:AFV39891.1          NLH-----------------------------------------------------------------------------  1607
PVT:AFU55321.1          NLH-----------------------------------------------------------------------------  1607
PVT:AXK90539.1          NLH-----------------------------------------------------------------------------  1607
AcVB:YP_004935358.1     --------------------------------------------------------------------------------  1707
GVA:NP_619662.1         --------------------------------------------------------------------------------  1707
GVE:YP_002117775.1      --------------------------------------------------------------------------------  1698
ASGV:NP_044335.1        WRIDLSNVVPELKTFAATSRQNSLNECTFRKLCEPFADLAREFLHERWSKGLATNIYKKWPKAFEKSPWVAFDFATGLKM  2065
CVA:NP_620106.1         TF-------ATNVKAWGVVGAEGKFAGLTFRQLCEPFAEQAYNFFRENHGAVSFIYLKNPGAYFNCPAVVFDFNKGLPLT  2302
DiVA:YP_006905850.1     NVSFSPAEVSRQFKYYANSSGNSCFANITWRQIGESFAEDIVRYFKELQVDAQSWLVRSNPVLAGNAPWVALDVTDGLDV  2187
ObRV1:YP_009408144.1    TVEFSPAEVARVFKYLYQSSANPIFENMTWRQCGEAFAGDIVRYFKELQPDAQSWLVKSNPVLAGNAPWVALDVTDGLDI  2187
ACLSV:NP_040551.1       LQNLF---------------------------------------------------------------------------  1884
GPGV:YP_004732978.2     KFYIQ---------------------------------------------------------------------------  1855
CtChV-1:YP_009103999.1  --------------------------------------------------------------------------------  1857
CtChV-2:YP_009103996.1  --------------------------------------------------------------------------------  1856
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------  1679
CPrV:AKN08994.1         --------------------------------------------------------------------------------  1986
CLBV:NP_624333.1        --------------------------------------------------------------------------------  1962
CLBV:AFA43536.1         --------------------------------------------------------------------------------  1987
GCLV:YP_004936159.1     --------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1     --------------------------------------------------------------------------------  1977
PhlVB:YP_001552317.1    --------------------------------------------------------------------------------  2051
ASPV:NP_604464.1        --------------------------------------------------------------------------------  2183
APV1:YP_009094347.1     --------------------------------------------------------------------------------  2022
CTLaV:YP_009046478.1    --------------------------------------------------------------------------------  2037
CRMaV:YP_007761581.1    --------------------------------------------------------------------------------  2027


ZoVT:Z1                 ----------------------------------------                                          1816
ZoVT:Z2                 ----------------------------------------                                          1816
ZoVT:Z3                 ----------------------------------------                                          1816
PrVT:YP_009051684.1     ----------------------------------------                                          1778
PrVT:AHM92766.1         ----------------------------------------                                          1778
PVT:ADX41471.1          ----------------------------------------                                          1606
PVT:YP_002019748.1      ----------------------------------------                                          1606
PVT:AFV39891.1          ----------------------------------------                                          1607
PVT:AFU55321.1          ----------------------------------------                                          1607
PVT:AXK90539.1          ----------------------------------------                                          1607
AcVB:YP_004935358.1     ----------------------------------------                                          1707
GVA:NP_619662.1         ----------------------------------------                                          1707
GVE:YP_002117775.1      ----------------------------------------                                          1698
ASGV:NP_044335.1        NRLTPDEKQVIDRMTKRLFRTEGQKGVFEAGSESNLELEG                                          2105
CVA:NP_620106.1         IIKIGKNANAISACNQRLFNREGKKAVFAAQGEVNLSFDA                                          2342
DiVA:YP_006905850.1     RRLNPEEKKVIARAKNHLLKSMQLKGRESLSAEALLES--                                          2225
ObRV1:YP_009408144.1    RHLNPEEKKVIARAKNHLLRSMQLKGRESLSAEALLES--                                          2225
ACLSV:NP_040551.1       ----------------------------------------                                          1884
GPGV:YP_004732978.2     ----------------------------------------                                          1855
CtChV-1:YP_009103999.1  ----------------------------------------                                          1857
CtChV-2:YP_009103996.1  ----------------------------------------                                          1856
AVCaV:YP_008997790.1    ----------------------------------------                                          1679
CPrV:AKN08994.1         ----------------------------------------                                          1986
CLBV:NP_624333.1        ----------------------------------------                                          1962
CLBV:AFA43536.1         ----------------------------------------                                          1987
GCLV:YP_004936159.1     ----------------------------------------                                          1951
CVNV:YP_001430021.1     ----------------------------------------                                          1977
PhlVB:YP_001552317.1    ----------------------------------------                                          2051
ASPV:NP_604464.1        ----------------------------------------                                          2183
APV1:YP_009094347.1     ----------------------------------------                                          2022
CTLaV:YP_009046478.1    ----------------------------------------                                          2037
CRMaV:YP_007761581.1    ----------------------------------------                                          2027
```