

A novel tepovirus, Agave virus T, identified by the analysis of the transcriptome data of blue agave (*Agave tequilana*)

Chul Jun Goh, Dongbin Park, Yoonsoo Hahn*

Department of Life Science, Chung-Ang University, Seoul 06974, Republic of Korea

Received January 8, 2021; accepted January 19, 2021

Summary. – The genome sequence of a novel RNA virus was identified by analyzing transcriptome data obtained from the stem sample of a blue agave (*Agave tequilana*) plant. Sequence comparison and phylogenetic analysis showed that the RNA virus, Agave virus T (AgVT), was a new member of the genus *Tepovirus* in the family *Betaflexiviridae*. AgVT genome had three open reading frames: a 1605-amino acid (aa) replicase (REP), 355-aa movement protein (MP), and 220-aa coat protein (CP). Phylogenetic analyses based on the REP, MP, and CP sequences of AgVT, previously reported tepoviruses, and other *Betaflexiviridae* viruses revealed that tepoviruses could be classified into two subclades: “potato virus T (PVT)-clade” and “Prunus virus T (PrVT)-clade.” PVT, the type species and founding member of the genus *Tepovirus*, belong to “PVT-clade” along with AgVT, while the other five tepoviruses belong to “PrVT-clade.” The genome sequence of AgVT may be useful for studying the phylogenetic relationships between tepoviruses and other closely related viruses.

Keywords: Agave virus T; Tepovirus; Betaflexiviridae; blue agave; *Agave tequilana*

Introduction

Tepoviruses (the genus *Tepovirus*) are plant-infecting RNA viruses of the family *Betaflexiviridae*. The members of this family have a monopartite, positive-sense, single-stranded RNA genome of size 6–9 kb, and the virions exist as flexuous filamentous particles (Adams et al., 2012; Rubino et al., 2012). Thirteen genera in the family *Betaflexiviridae* have been reported and were classified into two subfamilies: *Trivirinae* and *Quinvirinae* (<https://talk.ictvonline.org>, last accessed on December 5, 2020).

The subfamily *Trivirinae* comprises 10 genera, including *Capillovirus*, *Chordovirus*, *Citrivirus*, *Divavirus*,

Prunevirus, *Ravavirus*, *Tepovirus*, *Trichovirus*, *Vitivirus*, and *Wamavirus*. Viruses of the subfamily *Trivirinae* have three common open reading frames (ORFs) that encode a replicase (REP), movement protein (MP), and coat protein (CP) (Adams et al., 2012; Rubino et al., 2012). Members of the genera *Capillovirus* and *Divavirus* have a fused REP-CP ORF, while those of the other genera have independent REP and CP ORFs (Yoshikawa et al., 1992; Goh et al., 2018). The subfamily *Quinvirinae* consists of three genera: *Carlavirus*, *Foveavirus*, and *Robigovirus*. Viruses of the subfamily *Quinvirinae* have five common ORFs encoding an REP, three triple gene block proteins (TGB1, TGB2, and TGB3), and a CP (Morozov and Solovyev, 2003; Prosser et al., 2015). Members of some genera have one or more additional ORFs (Martelli et al., 1997; Adams et al., 2012; Veerakone et al., 2018).

Blue agave (*Agave tequilana*), also known as tequila agave, belongs to the genus *Agave*, which are succulent monocotyledonous plants native to the arid regions of North America (Coleman-Derr et al., 2016). *Agave* species are highly tolerant to drought and heat stress, because

*Corresponding author. E-mail: hahny@cau.ac.kr; phone: +82-2-820-5812.

Abbreviations: AgVT = Agave virus T; CP = coat protein; GVA = grapevine virus A; MP = movement protein; ORF = open reading frame; PrVT = Prunus virus T; PVT = potato virus T; RdRp = RNA-dependent RNA polymerase; REP = replicase

they employ the crassulacean acid metabolism in photosynthesis, which enhances water-use efficiency (Borland et al., 2009). Blue agave is an economically important plant in Mexico used in the production of the popular distilled spirit tequila (Cedeno, 1995). Because of its economic importance, blue agave has been subjected to various molecular genetic studies, including transcriptome analyses (Gross et al., 2013; Coleman-Derr et al., 2016; Huang et al., 2018).

Transcriptome data obtained from samples of plant tissue infected with RNA viruses often contain virus-derived reads (Nibert et al., 2016). Contig assembly of plant transcriptome data and comprehensive sequence analysis have yielded numerous complete genome sequences of novel RNA viruses (Kim et al., 2018; Park et al., 2018, 2020; Goh et al., 2019, 2020). In this study, we identified the genome sequence of a novel virus belonging to the genus *Tepovirus* of the family *Betaflexiviridae* in the transcriptome dataset acquired from the stem sample of a blue agave plant (Gross et al., 2013).

Materials and Methods

The transcriptome data (a total of 71.8 gigabases) obtained using the samples from the stem of a blue agave plant (Gross et al., 2013) were downloaded from the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI). SRA Acc. Nos. are SRR789714, SRR789715, SRR789716, SRR789717, SRR789718, SRR789719, SRR789720, SRR789724, SRR789725, SRR789726, SRR789727, and SRR789728. Low-quality reads were filtered out using the sickle program (version 1.33; <https://github.com/najoshi/sickle>) with the parameter “-q 30 -l 55.” High-quality reads from all 12 sequencing runs were pooled and subjected to *de novo* transcriptome assembly using the SPAdes Genome Assembler (version 3.14.1; <http://cab.spbu.ru/software/spades>) with the parameter “--rna.”

The transcriptome contigs were compared with known viral RNA-dependent RNA polymerase (RdRp) domain sequences using the DIAMOND program (version 2.0.4; <http://www.diamondsearch.org/index.php>). A total of 2565 viral RdRp domain sequences were selected from 22 families (PF00602, PF00603, PF00604, PF00680, PF00946, PF00972, PF00978, PF00998, PF02123, PF03035, PF03431, PF04196, PF04197, PF05788, PF05919, PF06317, PF07925, PF08467, PF08716, PF08717, PF12426, and PF17501) available in the Pfam database (release 33.1; <https://pfam.xfam.org>).

Sequencing depth of a putative viral contig was assessed by mapping the RNA-seq reads to the contig sequence using the URMAP program (version 1.0.1480; <https://drive5.com/urmap>). Putative ORFs in the viral genome sequence were inferred based on BLASTX search results against all known viral protein sequences. Conserved domains in protein sequences were

predicted using the InterPro web server (version 82.0; <https://www.ebi.ac.uk/interpro>).

Pairwise identities of protein sequences were examined using the needle program of the EMBOSS package (version 6.6.0.0; <http://emboss.open-bio.org>) using default parameters. Multiple sequence alignments were generated using the MAFFT program (version 7.475; <https://mafft.cbrc.jp/alignment/software>) with the parameter “--auto.” Phylogenetic analysis was performed using the neighbor-joining method in the ClustalW2 program (version 2.1; <http://www.clustal.org/clustal2>), after removing gaps in the sequence alignment.

Results and Discussion

RNA-seq reads obtained from the blue agave stem sample were assembled into contigs (Gross et al., 2013). When these contig sequences were compared with known viral RdRp sequences, numerous contigs were identified to contain an RdRp domain. Among them, a 6408-bp contig showed strong sequence similarity to that of the RdRp domain of the potato virus T (PVT) REP sequence (UniProt Acc. No. B5ACE2) (Russo et al., 2009). PVT is the type species of the genus *Tepovirus* of the family *Betaflexiviridae*, suggesting that the contig was derived from a virus related to the genus *Tepovirus*.

A BLASTX search of the NCBI protein database using the 6408-bp contig as a query confirmed that it had ORFs with the highest sequence similarities to proteins encoded by the PVT genome sequence. Therefore, this contig was considered the genome sequence of a novel virus belonging to the genus *Tepovirus* of the family *Betaflexiviridae*, and it was tentatively named as Agave virus T (AgVT). The genome sequence of this virus was deposited in the NCBI database (Acc. No. MW323519).

AgVT genome was predicted to have three complete protein-coding ORFs (Fig. 1 and Table 1): ORF1, encoding a 1605-amino acid (aa) REP; ORF2, a 355-aa MP; and ORF3, a 220-aa CP. The MP ORF overlapped with the REP and CP ORFs. AgVT proteins were predicted to possess conserved domains that are typically present in other members of the family *Betaflexiviridae*. REP had a viral methyltransferase domain (InterPro Acc. No. IPR002588) at aa positions 43–329, a “viral RNA helicase core domain” (IPR027351) at aa positions 761–1077, and an “viral RNA-dependent RNA polymerase domain” (IPR001788) at aa positions 1252–1493. MP had a “viral movement protein domain” (IPR028919) at aa positions 11–194. CP had a “viral coat protein domain” (IPR008879) at aa positions 40–215.

For sequence comparison and phylogenetic analysis, genome and protein sequences of previously reported tepoviruses, including four PVT, two *Prunus* virus T (PrVT), two *Zostera* virus T (ZoVT), one cherry virus T

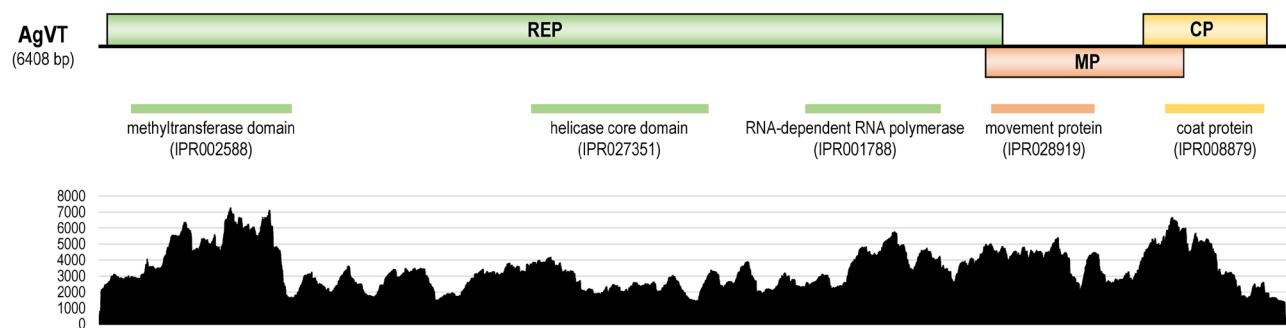


Fig. 1

Schematic representation of the AgVT genome organization

A schematic figure of the AgVT genome sequence is presented at the top. Three ORFs corresponding to the replicase (REP), the movement protein (MP), and the coat protein (CP) are depicted as boxes. Predicted InterPro domains are marked using lines below the ORFs with corresponding InterPro Acc. Nos. The sequencing depth is shown at the bottom. See Table 1 for the coordinates of the ORFs and InterPro domains.

(ChVT), one Ficus tepovirus A (FiTA), and one Trichosanthes tepovirus A (TrTA), were collected (Russo *et al.*, 2009; Marais *et al.*, 2015, 2020; Goh *et al.*, 2019). Sequences of representative members of the other 12 *Betaflexiviridae* genera were also retrieved, including grapevine virus A (GVA), Actinidia virus B (AcVB), apple stem grooving virus A, Ribes americanum virus A, grapevine Pinot gris virus (GPGV), carrot Ch virus 1, Ocimum basilicum RNA virus 1, citrus leaf blotch virus, apricot vein clearing associated virus, watermelon virus A, cherry rusty mottle associated virus, Phlox virus B, and apple stem pitting virus (Yoshikawa *et al.*, 1992; Nakaune *et al.*, 2008; Goh *et al.*, 2018). Thirty-four known *Betaflexiviridae* virus genome sequences were retrieved for sequence comparison and phylogenetic analyses (Table 2).

Pairwise comparisons of protein sequences revealed that AgVT REP had 25.7–43.8% aa identity with those of other *Betaflexiviridae* viruses. Four PVT REP sequences exhibited the highest similarity to AgVT REP sequence with 43.6–43.8% aa identity. Other tepovirus REP sequences showed 32.3–33.1% aa identity with AgVT REP sequence. REP sequences of viruses belonging to other

Betaflexiviridae genera showed 24.7–30.6% aa identity with AgVT REP sequence. Comparison between the REP protein sequences confirmed that PVT was the most closely related to AgVT, among the currently known tepoviruses.

Multiple alignments of 35 REP sequences from AgVT, 11 other tepovirus, and 23 other *Betaflexiviridae* virus genomes were generated (Supplementary Fig. S1). The phylogenetic position of AgVT within the family *Betaflexiviridae* was inferred using the neighbor-joining method (Fig. 2). The subfamily *Quinvirinae* was used as the out-group. AgVT was placed as a sister taxon of the four PVT sequences within the genus *Tepovirus* in accordance with the sequence comparison results. Among the genera of the subfamily *Trivirinae*, the genus *Vitivirus* was inferred to be the sister genus of *Tepovirus*.

PVT and PrVT are two currently approved species of the genus *Tepovirus* (<https://talk.ictvonline.org>, last accessed on December 5, 2020). According to the phylogenetic analysis, 12 REP sequences from seven tepoviruses were classified into two subclades: “PVT-clade” and “PrVT-clade.” AgVT belonged to “PVT-clade” as the second member after PVT, which is the type species and found-

Table 1. ORFs of AgVT genome sequence

ORF	ORF position (nt)	Protein length (aa)	Domain position (aa)	InterPro domain name	InterPro Acc. No.
Replicase (REP)	43–4860	1605	43–329	alphavirus-like methyltransferase (MT) domain	IPR002588
			761–1077	(+) RNA virus helicase core domain	IPR027351
			1252–1493	tymovirus, RNA-dependent RNA polymerase	IPR001788
Movement protein (MP)	4769–5836	355	11–194	viral movement protein	IPR028919
Coat protein (CP)	5616–6278	220	40–215	coat protein, trichovirus/vitivirus	IPR008879

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

No	Subfamily	Genus	Virus	Acronym	NCBI	Identity ^a
1	Trivirinae	Tepovirus	Potato virus T	PVT	YP_002019748.1	723/1657 (43.6%)
2			Potato virus T	PVT	ADX41471.1	724/1657 (43.7%)
3			Potato virus T	PVT	AFU55321.1	723/1649 (43.8%)
4			Potato virus T	PVT	AXK90539.1	723/1652 (43.8%)
5			Prunus virus T	PrVT	YP_009051684.1	620/1881 (33.0%)
6			Prunus virus T	PrVT	AHM92766.1	620/1875 (33.1%)
7			Zostera virus T	ZoVT	QBS17025.1	621/1905 (32.6%)
8			Zostera virus T	ZoVT	QBS17031.1	616/1904 (32.4%)
9			Cherry virus T	ChVT	QNG41875.1	618/1893 (32.6%)
10			Ficus tepovirus A	FiTA	QED42804.1	605/1874 (32.3%)
11			Trichosanthes tepovirus A	TrTA	QED42832.1	607/1865 (32.5%)
12	Vitivirus	Grapevine virus A	GVA	NP_619662.1	560/1830 (30.6%)	
13		Actinidia virus B	AcVB	YP_004935358.1	531/1813 (29.3%)	
14	Capillovirus	Apple stem grooving virus	ASGV	NP_044335.1	536/1785 (30.0%) ^b	
15		Yacon virus A	YaVA	YP_009268859.1	524/1784 (29.4%) ^b	
16	Ravavirus	Ribes americanum virus A	RAVA	YP_009553496.1	514/1971 (26.1%)	
17	Trichovirus	Apple chlorotic leaf spot virus	ACLSV	NP_040551.1	568/1976 (28.7%)	
18		Grapevine Pinot gris virus	GPGV	YP_004732978.2	551/1937 (28.4%)	
19	Chordovirus	Carrot Ch virus 1	CtChV-1	YP_009103999.1	572/1959 (29.2%)	
20		Carrot Ch virus 2	CtChV-2	YP_009103996.1	568/1946 (29.2%)	
21	Divavirus	Diuris virus A	DiVA	YP_006905850.1	552/1857 (29.7%) ^b	
22		Ocimum basilicum RNA virus 1	ObRV1	YP_009408144.1	547/1837 (29.8%) ^b	
23	Citrivirus	Citrus leaf blotch virus	CLBV	NP_624333.1	581/2042 (28.5%)	
24		Citrus leaf blotch virus	CLBV	AFA43536.1	565/2080 (27.2%)	
25	Prunevirus	Apricot vein clearing associated virus	AVCaV	YP_008997790.1	532/1825 (29.2%)	
26		Caucasus prunus virus	CPrV	YP_009505632.1	569/2121 (26.8%)	
27	Wamavirus	Watermelon virus A	WVA	YP_009357235.1	552/1907 (28.9%)	
28		Watermelon virus A	WVA	QEA69426.1	558/1922 (29.0%)	
29	Quinvirinae	Robigovirus	Cherry rusty mottle associated virus	CRMaV	YP_007761581.1	548/2121 (25.8%)
30			Cherry twisted leaf associated virus	CTLaV	YP_009046478.1	560/2163 (25.9%)
31		Carlavirus	Phlox virus B	PhlVB	YP_001552317.1	554/2155 (25.7%)
32			Garlic common latent virus	GCLV	YP_004936159.1	544/2060 (26.4%)
33		Foveavirus	Apple stem pitting virus	ASPV	NP_604464.1	564/2279 (24.7%)
34			Asian prunus virus 1	APV1	YP_009094347.1	572/2112 (27.1%)

^aProtein sequence identity in the form of “number of identical residues/aligned length (percent identity).” ^bCP regions were removed from the capillovirus and divavirus REP-CP protein sequences.

ing member of the genus *Tepovirus*. Bootstrap analysis strongly supported the placement of both subclades with 100% bootstrap values. However, the *Tepovirus* clade, and hence the monophyletic origin of “PVT-clade” and “PrVT-clade” viruses, was only marginally supported with a bootstrap value of 72.1%. This suggested the possibility

that “PrVT-clade” might be classified as a novel genus different from “PVT-clade.”

The monophyletic relationship between “PVT-clade” and “PrVT-clade” was further investigated using MP and CP sequences of all tepoviruses, two vitiviruses (GVA and AcVB), and a trichovirus (GPGV). Multiple alignments of

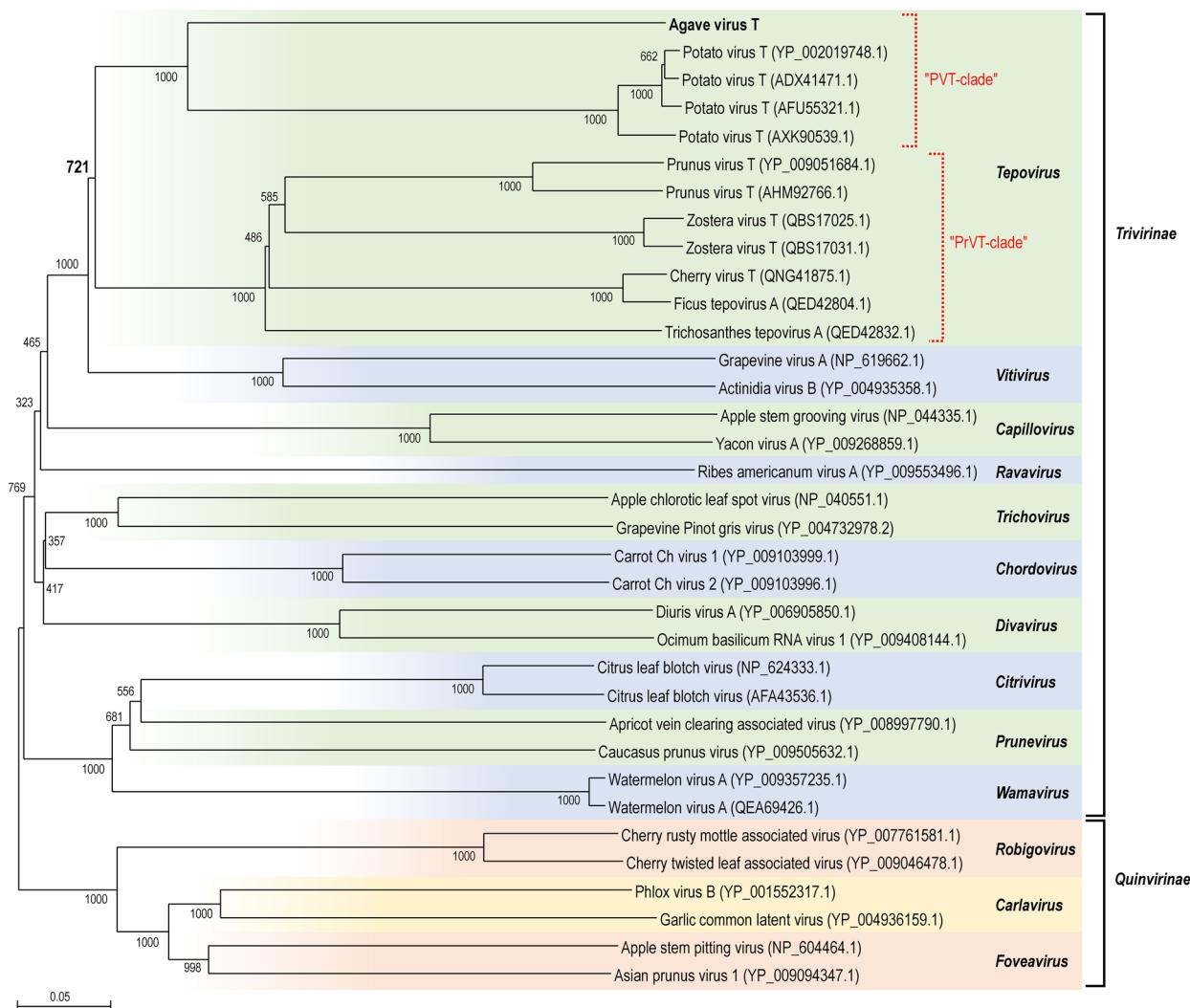


Fig. 2

Phylogenetic position of AgVT among *Betaflexiviridae* viruses

A phylogenetic tree was constructed based on REP sequences of AgVT, previously known tepoviruses, and representative members of the family *Betaflexiviridae* using the neighbor-joining method. Tepoviruses can be classified into two subclades: "PVT-clade" and "PrVT-clade." AgVT is the second member of "PVT-clade." The subfamily *Quinvirinae* was used as the outgroup. The NCBI protein sequence Acc. Nos. are in parentheses. Bootstrap supporting values calculated from 1000 replicates are shown at the nodes. The bootstrap value for the *Tepovirus* clade is highlighted in bold.

MP and CP sequences were generated (Supplementary Figs. S2 and S3, respectively). Phylogenetic trees of MP and CP sequences were constructed using the neighbor-joining method (Fig. 3). In each tree, the sequence of GPGV was used as the outgroup. In both trees, the monophyletic origin of all 12 tepovirus sequences was represented. The monophyletic relationship of "PVT-clade" and "PrVT-clade" was strongly supported in the MP tree with a bootstrap value of 94.4%. However, in the CP tree, the placement of the *Tepovirus* clade was very weakly supported with a bootstrap value of 57.2%. These results indicate the

need for performing more comprehensive phylogenetic analyses to clearly understand the relationship between "PVT-clade" and "PrVT-clade" within the genus *Tepovirus* as well as within the family *Betaflexiviridae*.

In conclusion, the genome sequence of AgVT, a putative novel member of the genus *Tepovirus* of the family *Betaflexiviridae*, was identified from transcriptome data obtained from the stem sample of a blue agave plant. Sequence comparison and phylogenetic analyses indicated that AgVT was the closest relative of PVT among all currently known tepoviruses, thereby forming a distinct

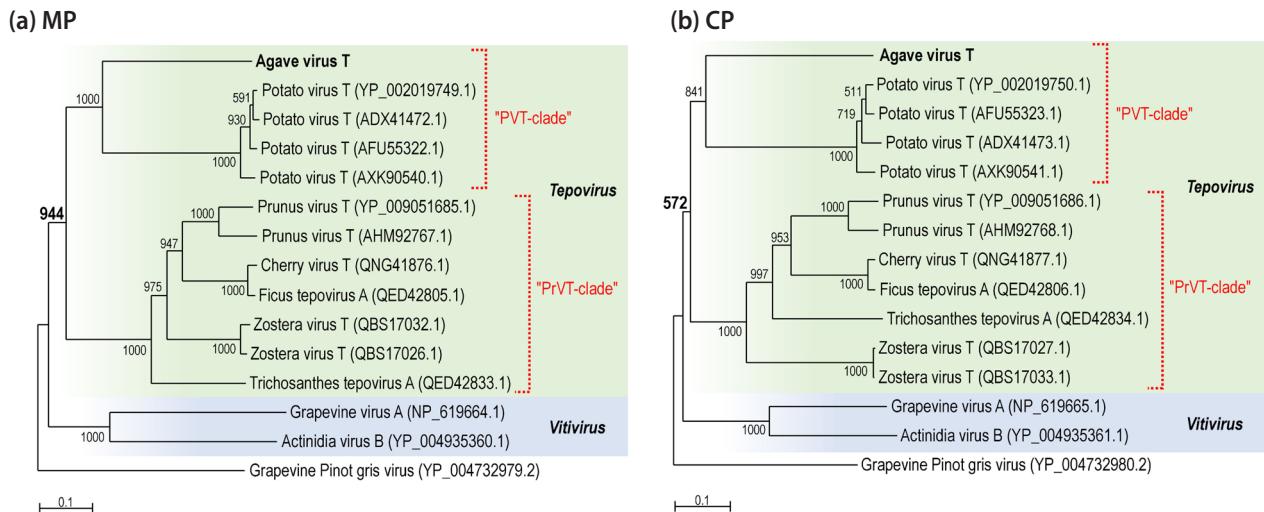


Fig. 3

Phylogenetic relationships of tepoviruses inferred from MP and CP sequences

Neighbor-joining phylogenetic trees were inferred from MP (a) and CP (b) sequences of tepoviruses, two vitiviruses, and a trichovirus. Two subclades ("PVT-clade" and "PrVT-clade") were reproduced within the genus *Tepovirus*. The sequence from the grapevine Pinot gris virus, a trichovirus, was used as the outgroup. The NCBI protein sequence Acc. Nos. are in parentheses. Bootstrap supporting values calculated from 1000 replicates are presented at the nodes. The bootstrap value for the *Tepovirus* clade is indicated in bold.

subclade. The AgVT genome sequence may be useful for studying the phylogenetic relationships of tepoviruses and other closely related *Betaflexiviridae* viruses.

Acknowledgments. This work was supported by the National Research Foundation of Korea (NRF) funded by the Government of Korea (grant Nos. 2018R1A5A1025077 and 2020R1A2C1013403).

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, N.Y (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>
- Borland AM, Griffiths H, Hartwell J, Smith JA (2009): Exploiting the potential of plants with crassulacean acid metabolism for bioenergy production on marginal lands. *J. Exp. Bot.* 60, 2879–2896. <https://doi.org/10.1093/jxb/erp118>
- Cedeno M (1995): Tequila production. *Crit. Rev. Biotechnol.* 15, 1–11. <https://doi.org/10.3109/07388559509150529>
- Coleman-Derr D, Desgarennes D, Fonseca-Garcia C, Gross S, Clingenpeel S, Woyke T, North G, Visel A, Partida-Martinez LP, Tringe SG (2016): Plant compartment and biogeography affect microbiome composition in cultivated and native *Agave* species. *New Phytol.* 209, 798–811. <https://doi.org/10.1111/nph.13697>
- Goh CJ, Park D, Hahn Y (2020): Identification of *Trichosanthes* associated rhabdovirus 1, a novel member of the genus *Cytorhabdovirus* of the family Rhabdoviridae, in the *Trichosanthes kirilowii* transcriptome. *Acta Virol.* 64, 36–43. https://doi.org/10.4149/av_2020_105
- Goh CJ, Park D, Kim H, Sebastiani F, Hahn Y (2018): Novel Diclavivirus (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
- Goh CJ, Park D, Lee JS, Davey PA, Pernice M, Ralph PJ, Hahn Y (2019): *Zostera* virus T - a novel virus of the genus *Tepovirus* identified in the eelgrass, *Zostera muelleri*. *Acta Virol.* 63, 366–372. https://doi.org/10.4149/av_2019_409
- Gross SM, Martin JA, Simpson J, Abraham-Juarez MJ, Wang Z, Visel A (2013): De novo transcriptome assembly of drought tolerant CAM plants, *Agave deserti* and *Agave tequilana*. *BMC Genomics* 14, 563. <https://doi.org/10.1186/1471-2164-14-563>
- Huang X, Wang B, Xi J, Zhang Y, He C, Zheng J, Gao J, Chen H, Zhang S, Wu W, Liang Y, Yi K (2018): Transcriptome comparison reveals distinct selection patterns in domesticated and wild *Agave* species, the important CAM plants. *Int. J. Genomics* 2018, 5716518. <https://doi.org/10.1155/2018/5716518>

- Kim H, Park D, Hahn Y (2018): 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>
- Marais A, Faure C, Mustafayev E, Barone M, Alioto D, Candresse T (2015): Characterization by deep sequencing of *Prunus* virus T, a novel telovirus infecting *Prunus* species. *Phytopathology* 105, 135-140. <https://doi.org/10.1094/PHYTO-04-14-0125-R>
- Marais A, Šafářová D, Navrátil M, Faure C, Cornaggia D, Brans Y, Suchá J, Candresse T (2020): Complete genome sequence of cherry virus T, a novel cherry-infecting telovirus. *Arch. Virol.* 165, 1711-1714. <https://doi.org/10.1007/s00705-020-04656-w>
- 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>
- 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>
- 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.
- Park D, Goh CJ, Lee JS, Sebastiani F, Hahn Y (2020): Identification of *Pistacia*-associated flexivirus 1, a putative mycovirus of the family Gammaflexiviridae, in the mastic tree (*Pistacia lentiscus*) transcriptome. *Acta Virol.* 64, 28-35. https://doi.org/10.4149/av_2020_104
- 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>
- 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>
- 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>
- 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](https://doi.org/10.1016/0042-6822(92)90170-T)

A novel tepovirus, Agave virus T, identified by the analysis of the transcriptome data of blue agave (*Agave tequilana*)

Chul Jun Goh, Dongbin Park, Yoonsoo Hahn*

Department of Life Science, Chung-Ang University, Seoul 06974, Republic of Korea

Received January 8, 2021; accepted January 19, 2021

Summary. – The genome sequence of a novel RNA virus was identified by analyzing transcriptome data obtained from the stem sample of a blue agave (*Agave tequilana*) plant. Sequence comparison and phylogenetic analysis showed that the RNA virus, Agave virus T (AgVT), was a new member of the genus *Tepovirus* in the family *Betaflexiviridae*. AgVT genome had three open reading frames: a 1605-amino acid (aa) replicase (REP), 355-aa movement protein (MP), and 220-aa coat protein (CP). Phylogenetic analyses based on the REP, MP, and CP sequences of AgVT, previously reported tepoviruses, and other *Betaflexiviridae* viruses revealed that tepoviruses could be classified into two subclades: “potato virus T (PVT)-clade” and “Prunus virus T (PrVT)-clade.” PVT, the type species and founding member of the genus *Tepovirus*, belong to “PVT-clade” along with AgVT, while the other five tepoviruses belong to “PrVT-clade.” The genome sequence of AgVT may be useful for studying the phylogenetic relationships between tepoviruses and other closely related viruses.

Keywords: Agave virus T; Tepovirus; Betaflexiviridae; blue agave; *Agave tequilana*

*Corresponding author. E-mail: hahny@cau.ac.kr; phone: +82-2-820-5812.

Fig. S1. Alignment of replicase sequences of AgVT and related viruses

AgVT	MAF---NFRPAEFLNLNSVPKAQSDKIHA-IDARRFKESHEADCS-LFDVVYHDEAKERLTD---AGMOLSPNAWGIHSHPASKMIEHNLLYKVIPEDIKGKS---LVIGFVKL	103
PVT:YP_002019748.1	MSF---SFRTPAEFLVQSLPKKEYAECFK---SHAANFQIRSDKGVG-LDFDFACSVVAKERLTK---AGIPVSACFNCQEHSHPASKMIEHNLLYPNLYNLKN---YTAISIKD	103
PVT:ADX41471.1	MSF---SFRTPAEFLVQSLPKKEYAECFK---SHATNFQIRSDKGIG-LDFDFACSVVAKERLTK---AGIPVSACFNCREHSHPASKMIEHNLLYPNLYNLKN---YTAISIKD	103
PVT:AFU55321.1	MSF---SFRTPAEFLVQSLPKKEYAECFK---SHAANFQIRSDKGIG-LDFDFACSVVAKERLTK---AGIPVSACFNCQEHSHPASKMIEHNLLYPNLYNLKN---YTAISIKD	103
PVT:AKX90539.1	MSF---SFRTPAEFLVQSLPKKEYAECFK---SHATNFQIRSDKGIG-LDFDFACSVVAKERLTK---AGIPVSACFNCQEHSHPASKMIEHNLLYPNLYNLKN---YTAISIKD	103
PrVT:YP_009051684.1	MAF---SFRTPAEFLVQSLPKKEYAECFK---SHATNFQIRSDKGIG-LDFDFACSVVAKERLTK---AGIPVSACFNCQEHSHPASKMIEHNLLYPNLYNLKN---YTAISIKD	103
PrVT:AHM92766.1	MAF---SYRTPAEFLSTLPLSTSQELVSK---YAVKSLSENEOKASSH-NYSVHLTDTQKNCFS---VGVLPSVNNFMVPHPHPYCKTMENFLHDNLFHYRHLV---SIYVSIKE	102
ZoVT:QBS17025.1	MAF---SYRTPAQEFLSCLPSEDOTRVND-PSVTSLCFQEKENSSS-YSSYNLSDCQKMFCSK---VGVLPSVOLFRVPHPHPYCKTMENFLHDNLFHYRHLV---DNVSVIK	102
ZoVT:QBS17031.1	MAF---SYRTPAQEFLSCLPSEDOTRVND-PSVTSLCFQEKENSSS-YSSYNLSDCQKMFCSK---VGVLPSVOLFRVPHPHPYCKTMENFLHDNLFHYRHLV---DNVSVIK	102
ChVT:QNG41875.1	MAY---QYRNPAQLFFSSLPSQESQITVE-SALKLNLNLKLEKSSAD-YSSVLTQDQASFCTK---VGVLPSVHCFVNPHPHPSKTIENFLFSNISNLYNTNI---KNFISIKE	102
FiTA:QED42804.1	MAY---QYRNPAQLFFSSLPSQESQITVE-SALKLNLNLKLEKSSAD-YSSVLTQDQASFCTK---VGVLPSVHCFVNPHPHPSKTIENFLFSNISNLYNTNI---KNFISIKE	102
TrTA:QED42832.1	MAY---TYRTPAQFLFQSSLSEDQEEHIS---HISIKRPAEFLVQSLPKKEYAECFK---NGIELSPLSPKAHSHPACKTLENFLFPLSPFISHSGIR-ELFLFSIKK	102
GVA:NP_619662.1	MSISVSSQRVAVSNLYTNGSEEVKAIKE-LKSKRLLETETRLDG-LFDVVYDPTLREILTG---YGMFESVHSFQGHAPHSVKMIEHNLLYVAPNPFYNSNN---TLVSCKE	105
AcVB:YP_004935358.1	MSISVSSQRVAVSNLYTNGSEEVKAIKE-LKSKRLLETETRLDG-LFDVVYDPTLREILTG---YGMFESVHSFQGHAPHSVKMIEHNLLYVAPNPFYNSNN---TLVSCKE	105
ASGV:NP_044335.1	MAF---TYRNPLLEIAINKLPSKOSQDLLS-TLTDTEKTELETVRN-FSFSVTPEDQELLK---HGLTLAPIGFKSHPSHKMIEHNLLYICVPSLSSFKS---VAFFSLRP	104
YaVA:YP_009268859.1	MAF---TYRNPLDIAISLPLSKQADQLLA-LTTEDEVIKTIDOSND-LFSYAIKPEEQLL---KGIPALAPIGFRVSHSPMCMKMVNLYLYICIPSLLKEFKS---VAFFSLRP	104
RAVA:YP_009553496.1	MAL---FETPVPUVRLRTMDRDRQIPIYDLEIESHEHERRFR---FSYNPVARSISFLLA---NGIYLSKRNWRSHSPHKTICKENHMLFVEAASIPLRDVD---YTVMMSRD	105
ACLSV:NP_040551.1	MAL---SYRTPQEEFLSRLPSQESQEVISG-FQYERIQQKEKEVKE-NFSYFLPEKTRWTFTK---SGVYLSPFAYVHNSHPGCKTLEHNLFNVASYISKSY---VACLSIKS	104
GPVG:YP_004732978.2	MTF---FYRTPQEEFLSRLPSQESQEVISG-FQYERIQQKEKEVKE-NFSYFLPEKTRWTFTK---SGVYLSPFAYVHNSHPGCKTLEHNLFNVASYISKSY---VACLSIKS	104
CtChV-1:YP_009103999.1	MSY---SFRTPQEIKLSTFSFPSFINDNVS-TSRTGFEDDENRIGK---FFNPNLDRRKFEFASN---SGYIPLSPSYKSQHSPHKLCTIENHLLYVPIPLQNFNN---LNVSVMKE	104
CtChV-2:YP_009103996.1	MSY---SFRTPQEIKLSTNLPTLDGVS-FGSRIFEENERSR---KGYVHNLSDQKFFKAQ---AGIYLSPSPYFSQHSHPSHKLCTIENHLLYVMPMPMIANFNN---LYVVSME	104
DiVA:YP_009050850.1	MAL---SYRTPTEYINLQPARLTION-AQVLDLQISDCECGY---LYNLYNLNLKSEQKFVLD---KGVLSPSPWKKHHSHPGCKTLEHNLWLYNEIGHFIRHICRDSVAFSLRE	107
ObrV1:YP_009408144.1	MSL---IYRTPENINLQPSLRTENVAW-KOVDIQLNMEESIGK-YFNFLNLSEKQKKFLD---KGVLSPSPWKKHHSHPGCKTLEHNLWLYNEIGHFIRHICRDSVAFSLRE	107
CLBV:NP_624333.1	MAL---MSNKTAIESILGNFNEKKHDAINY-AAAQTLNLSEHRSR---KGVLSPSPWKKHHSHPGCKTLEHNLWLYNEIGHFIRHICRDSVAFSLRE	104
CLBV:AF4A3536.1	MAL---MSNKTAIESILGNFNEKKHDAINY-AAAQTLNLSEHRSR---KGVLSPSPWKKHHSHPGCKTLEHNLWLYNEIGHFIRHICRDSVAFSLRE	104
ACVa:YP_008997790.1	MAL---LYRTPQVNLNQFSPQPKHVEIYNN---NGESEKQKVASINGRQWGLPQHPTVLAHSFQSKMLEHNLHILNLPGLHITGS---WVFSSIKP	105
CPvP:YP_009505632.1	MAS---VTRTPMKEFKAANDKNDQRSILT---SGVNFVFKKCFDDKG1-HFAYVNVDRKEALTN---LGLVTPILPHLTHSPFCCKTLEHNLHILNLPNLGNHG---WVFSTVK	104
WVA:YP_009357235.1	MAL---LSQTKLGELEKFMGSLDRAETKLHY---TAVEELRRNSVDLNK-FSVEYEMDSEKRLYL---RGVLEPFGGYKAHSHPVKTLEHNLWLYLPVIVGVR---INMVSIQR	104
WVA:QEA69426.1	MAL---LSQTKLGELEKFMGSLDRAETKLHY---TAVEELRRNSVDLNK-FSVEYEMDSEKRLYL---RGVLEPFGGYKAHSHPVKTLEHNLWLYLPVIVGVR---INMVSIQR	104
CRMav:YP_007761581.1	MAL---HTTPAEGVLQFSSSEASRIGA-SAINSNFSKLESEYHS-LHFHLPAYAKSKLSN---RGFVLPSPFSEYETHSPVKTLEHNLWLYLPVIVGVR---FLIVGIKE	102
CTLaV:YP_009046478.1	MAL---HTTPAENVLQFSSSEASRIGA-SAINSNFSKLEADYHN-LHFHLPAYAKSKLSN---RGFVLPSPFSEYETHSPVKTLEHNLWLYLPVIVGVR---FLIVGIKE	102
Ph1BV:YP_001552317.1	MAL---TYRSPLEENVAADYDASQVOSTIS-TSACYKDTADKFR---FFNYVNPVTTAKKLLIE---AGLYLSPSPYAMPHSPVCKTLEHNLWLYLPVIVGVR---FFFVGIK	102
GCLV:YP_004936159.1	MAL---TYRSPLEEVTLFSASEQSLIA---PAITSYRGLERLHH-FHNNVNGVPYAKEKLG---AGVYLSPSPVPHSPVCKTLEHNLWLYLPVIVGVR---FFFVGIK	102
ASPV:NP_604464.1	MAL---LRSRTEAEEVIASFESTEQSRIST-QAVALTNEVKEDKHDH-LFNLYPALELAKMRFLN---SGIYLSPSPYRSHPSVCKTLEHNLWLYLPVIVGVR---FLYVSIKK	102
APV1:YP_009094347.1	MAL---TYRSPIGEVLRNFTSEEQSRVSS-TSRSVRLTQFEVNNH-LFSFAMSEAKEKLK---VGYIYLSPSPFEPHSHPVCKTLEHNLWLYLPVIVGVR---FYAIGIKG	102

* :

AgVT	SKVRKLLKNGV---DSLETFNRLFSCKDALRVDPETC---DMDKFIARVHH---STRIFLFLDELHY	161
PVT:YP_002019748.1	SKVRKLLKNGV---DSLETFNRLFSCKDALRVDPETC---DMDKFIARVHH---STRIFLFLDELHY	161
PVT:AFU55321.1	SKVRKLLKNGV---DSLETFNRLFSCKDALRVDPETC---DMDKFIARVHH---STRIFLFLDELHY	161
PVT:AKX90539.1	SKVRKLLKNGV---DSLETFNRLFSCKDALRVDPETC---DMDKFIARVHH---STRIFLFLDELHY	161
PrVT:YP_009051684.1	EKVLGLNRSRG---LNFHRVIRNCVADRDRNIRYKNCVSKSF---FEDTRNHAPNO---SKSWFFHDELHH	163
PrVT:AHM92766.1	EKVLGLNRSRG---LNFHRVIRNCVADRDRNIRYKNCVSKSF---FENKNNFIPNO---SKSWFFHDELHH	163
ZoVT:QBS17025.1	EKVLNLRLKRGH---RNGFVKIIINRVIADRDVLRYGPGCYNKE---FMSDEFDSLGEK---GKSWFHDELHH	164
ZoVT:QBS17031.1	EKVLNLRLKRGH---RNGFVKIIINRVIADRDVLRYGPGCYNKE---FMCEDFLSGEK---GKSWFHDELHH	164
ChVT:QNG41875.1	SKYVNLTPNSR---NSFHRLLNRIIAADRDRKLYSTELKVNKN---SLAQGGI---DESWFHFDELHH	162
FiTA:QED42804.1	SKYVNLTPNSR---NSFHRLLNRIIAADRDRKLYSTELKVNKN---SLAQGGI---DESWFHFDELHH	162
TrTA:QED42832.1	EKEFKLTRGRH---SSPTKLINRAIADRDRKLYTRKNIKPSP---NQKQVNDGKR---NERWFHFDELHH	164
GVA:NP_619662.1	SKIKRLLKRNA---NNRNLNTQYQNLRVLHANHHRYNAFREDLVG---NLTNLINKEDO---SEC1FIHDEVQY	171
AcVB:YP_004935358.1	SKIKRLLKRNA---SGADLNLKCYNRNLVHKDHYRTPDHCKELMA---HPLCALRSET---CETAVIHDDEVQY	172
ASGV:NP_044335.1	SKIKRLLKRNA---SGHKLTSGLMGNMIAIDGKDKYRGDVFESSFDRVIG---LRDOCTRNF---PKVLFHDEVHF	177
YaVA:YP_009268859.1	SKIKRLLKRNA---SGHKLTSGLMGNMIAIDGKDKYRGDVFESSFDRVIG---RFDRCRANKF---PKVLFHDEVHF	177
RAVA:YP_009553496.1	SKFKLAIKARS---DHDMEVLRNRYIEAKDF-VFVYRSGSSGTVFDM---ASSSKNWSESV---GGNVFHDDEVQY	168
ACLSV:NP_040551.1	SKFKLAIKARS---DHDMEVLRNRYIEAKDF-VFVYRSGSSGTVFDM---CP-KKTNFIFHDEVYH	161
GPVG:YP_004732978.2	AKVTRKLNVLV---NQVLNHLRNLVEVKDMRKYGD---VSPIERERKRT---GLD1FIHDEIHH	163
CtChV-1:YP_009103999.1	AKVTRKLNVLV---NQVLNHLRNLVEVKDMRKYGD---ESNT-RDYPPLDMVRIEK---GSNFLFHDELHY	181
CtChV-2:YP_009103996.1	SKLRLHSNSQ---APKMSINSLNRLMDVKDOSFRYKSQGDLSIKYPTQLL---KWNSDKKYPPLDCSIEK---GRNFLFHDEMH	181
DiVA:YP_009050850.1	SKLRLHSNSQ---LTG1SINLNLINRVDKVSFVYRKYDGGDSYVVKYPTDLL---SFDKQDQIGP---RASFYIHDECHY	179
ObrV1:YP_009408144.1	GKLNAAKKIHFEEKKN---NVKACEKICFSNRYYHTKDRLYRSSEGREIYK---SDRIGMMEK---RSCYFIHDECHY	179
CLBV:NP_624333.1	GKLNAAKKIHFEEKKN---HQDTNDKRSNFKLHSPLDCKLRSYSSDFTSDRVL---KELFSSTFIMKFRTSKAYDCIFIHDECHY	174
CLBV:AF4A3536.1	GKLNAAKKIHFEEKKN---KSKVLFKGR1K---DNGALGFGKDTASDHTSVNRLVAPDKDIRRTEAADFSSK---KGGS-PELFSRNFISKLE---NKEAVFFHDEVVH	190
ACVa:YP_008997790.1	GKLNAAKKIHFEEKKN---KSKVLFKGR1K---DNGALGFGKDTASDHTSVNRLVAPDKDIRRTEAADFSSK---KKNND-PELFSNNFIRCIS---NKEAVFFHDEVVH	192
CPvP:YP_009505632.1	KVSKLIFNTRDRK---NGVNLNHLRNLVEVKDMRKYGD---SREA-DPLPEPVRVAKR---GRNVMIHDEVVH	176
WVA:YP_009357235.1	KVSKLIFNTRDRK---GVSNNVDIVNRCICAOKDFGRYDPEPGVQDK---INILSKDHLPFKNFIRS---KKK1FIHDEVVH	177
WVA:QEA69426.1	KVVLNLSLKMN---YTELNTNRIIDSKDISRYGADEDVFNDER---KELFSSTFIMKFRTSKAYDCIFIHDECHY	174
CRMav:YP_007761581.1	KVVLNLSLKMN---YTELNTNRIIDSKDISRYGADEDVFNDER---KELFSSTFIMKFRTSKAYDCIFIHDECHY	174
CTLaV:YP_009046478.1	NKLSVLRKEKK---LRFLEALNRCVTSHDIQRYGSPFHFKEKARSN---WRSDFSGVN-LSAGV-QSLLPRLIDFKGKMF---DSQFLYFDEVLY	185
Ph1BV:YP_001552317.1	NKLSVLRKEKK---LRFLEALNRCVTSHDIQRYGSPFHFKEKARSN---WKTDFSEVN-SAGV-QSLLPRLIDFKGKMF---DSQFLYFDEVLY	185
GCLV:YP_004936159.1	NKLSVLRKEKK---LRFLEALNRCVTSHDIQRYGSPFHFKEKARSN---SREA-DPLPEPVRVAKR---GRNVMIHDEVVH	183
ASPV:NP_604464.1	NKLSVLRKEKK---LRFLEALNRCVTSHDIQRYGSPFHFKEKARSN---WNLSPMREDFD-SRPLDF---IDLIPGCMEGA---RKRFFFFHDELHY	185
APV1:YP_009094347.1	NKLSVLRKEKK---LRFLEALNRCVTSHDIQRYGSPFHFKEKARSN---WNLSPMREDFD-SRPLDF---IDLIPGCMEGA---RKRFFFFHDELHY	184

* :

AgVT	WSDLQNLNELLEN-SSLDFLVATWVHPFEVEMGEKSLNPELYNFV-KDQD---LNFYNGPKVEEAVYQPKHLP---LHFIESEFJNKRGR---FAVERTYSLGAHHVF	260
PVT:YP_002019748.1	WSMNSLMSDFLDR-SNVKELLATIVPIEIIILGSKRSLNPELYFEF---SRGK---LHFPPDGTCTSESYSPQKDCD---ILKVNRLVITKTGK---FSVLELIHTIGANMV	259
PVT:ADX41471.1	WSMNSLMSDFLDR-SNVKELLATIVPIEIIILGSKRSLNPELYFEF---SRGK---LHFPPDGTCTSESYSPQKDCD---ILKVNRLVITKTGK---FSVLELIHTIGANMV	259
PVT:AFU55321.1	WSMNSLMSDFLDR-SNVKELLATIVPIEIIILGSKRSLNPELYFEF---SRGK---LHFPPDGTCTSESYSPQKDCD---ILKVNRLVITKTGK---FSVLELIHTIGANMV	259
PVT:AKX90539.1	WSMNSLMSDFLDR-SNVKELLATIVPIEIIILGSKRSLNPELYFEF---SRGK---LHFPPDGTCTSESYSPQKDCD---ILKVNRLVITKTGK---FSVLELIHTIGANMV	259
PrVT:YP_009051684.1	WVDFNEADFLGN-FPKPKVITASCVPVPEIILGSKRSLNPELYFEF---SDESCNPSFYKQI---HEKK---KEVGRFTFPDFGKSESSYFORSDS---WIFRFKPYFEI-GSEI---YTLSFLRSIKCHHLLI	264
PrVT:AHM92766.1	WVDFNEADFLGN-FPKPKVITASCVPVPEIILGSKRSLNPELYFEF---SDESCNPSFYKQI---HEKK---KEVGRFTFPDFGKSESSYFORSDS---WIFRFKPYFEI-GSEI---YTLSFLRSIKCHHLLI	264
ZoVT:QBS17025.1	WLNDLTK1KF1K---ANPERMLATLVP1PEI1F-LKNRNSMPSYF1DYL---IKRNNDQDSQVSFNFYDPSGRESAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	267
ZoVT:QBS17031.1	WLNDLTK1KF1K---ANPERMLATLVP1PEI1F-LKNRNSMPSYF1DYL---IKRNNDQDSQVSFNFYDPSGRESAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	267
ChVT:QNG41875.1	WSFEDMYDFLKE-SKPKRITIASIICPIEVFD---SENMSNPSFYTFEV---HXRHS---KRRVFSYDPSGRESAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	264
FiTA:QED42804.1	WSFEDMYDFLKE-SKPKRITIASIICPIEVFD---SENMSNPSFYTFEV---HXRHS---KRRVFSYDPSGRESAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	264
TrTA:QED42832.1	WSPDFVYGFGLD-NQPEMVLASVCPVPEF---CAESMNPFSFYTFEV---HXRHS---KRRVFSYDPSGRESAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	265
GVA:NP_619662.1	WSLDEMORFLGSLSKVDRVYNSIYLIPEAVGYSQSLF-PFEAYTDL---LWVYDPPGKAEAGYOPVNP---WLLRCSKTEDSKGRS---WTITKLQIGAHHHLF	270
AcVB:YP_004935358.1	WSLQDFQLVLGQMNKVKRLMYSIYPAEIDQGYEHSL-FPEAYHFER---RGY---FIWLPDQGSDQGAYKOPNP---WLLSTSKTIDSRGR---WTIGKVTFSASHHLLF	271
ASGV:NP_044335.1	WSLQDFQLVLGQMNKVKRLMYSIYPAEIDQGYEHSL-FPEAYHFER---RGY---FIWLPDQGSDQGAYKOPNP---WLLSTSKTIDSRGR---WTIGKVTFSASHHLLF	271
YaVA:YP_009268859.1	WSKRMQYMFYLDS-VPSENPFVYTAVVPTEVAGLDSYLPSPVFT---LKGDK---LMFSPDVHSEIMPQKPNM-WLFKANKFRT-STGV---W5LVLRLRSAVAHHHF	266
RAVA:YP_009553496.1	WSKRMQYMFYLDS-VPSENPFVYTAVVPTEVAGLDSYLPSPVFT---LKGDK---LMFSPDVHSEIMPQKPNM-WLFKANKFRT-STGV---W5LVLRLRSAVAHHHF	266
ACLSV:NP_040551.1	WSRDLQMFYLDS-VPSENPFVYTAVVPTEVAGLDSYLPSPVFT---LKGDK---LMFSPDVHSEIMPQKPNM-WLFKANKFRT-STGV---W5LVLRLRSAVAHHHF	265
GPVG:YP_004732978.2	WTSDLQMFYLDS-VPSENPFVYTAVVPTEVAGLDSYLPSPVFT---LKGDK---LMFSPDVHSEIMPQKPNM-WLFKANKFRT-STGV---W5LVLRLRSAVAHHHF	265
CtChV-1:YP_009103999.1	WTFSMMLDFLEK-FEPHSVITACPVPEI1LEGKFSLNLPELYFEF---LWVYDPPGVMSEAYQFTYD---LWVYDPPGVMSEAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	265
CtChV-2:YP_009103996.1	WTFSMMLDFLEK-FEPHSVITACPVPEI1LEGKFSLNLPELYFEF---LWVYDPPGVMSEAYQFTYD---LWVYDPPGVMSEAYQFTYD---WFKWFMKHLN1-DGQF---YTI5FMSRISIKCHHMLI	265
DIVa:YP_009050850.1	WSPNDSLNSLNSR---TKAESILATVPIE1FIDVGKDSHLPFLYEV-FDNN---IFFFPDGRNRESEGYQPKTAG-WLKMGRFYS-DGEV---Y5V1LRT1GPFHLI	277
ObRV1:YP_009408144.1	WSPNDSLNSLNSR---TKAESILATVPIE1FIDVGKDSHLPFLYEV-FDNN---IFFFPDGRNRESEGYQPKTAG-WLKMGRFYS-DGEV---Y5V1LRT1GPFHLI	277
CLBV:NP_624333.1	WTPKAQMFSFLKS-TKVKRFTFVVPPEI1LKKFANSQNPQVYDFKVK---DKGR---LHFPPDGTCTSESYSPQKDCD---ILKVNRLVITKTGK---FSVLELIHTIGANMV	288
CLBV:AF4A3536.1	WTPKAQMFSFLKS-TKVKRFTFVVPPEI1LKKFANSQNPQVYDFKVK---DKGR---LHFPPDGTCTSESYSPQKDCD---ILKVNRLVITKTGK---FSVLELIHTIGANMV	288
ACVa:YP_008997790.1	WTLDDMLDFLDR-ARPNRFVFSVPPVPEI1LKKFANSQNPQVYDFKVK---DKGR---IVFFPDGRASEGYQORANLR-WLFCASHFR-SGS---WTFTRHKSIAHHHF	275
CPvP:YP_009505632.1	WTLDDMLDFLDR-ARPNRFVFSVPPVPEI1LKKFANSQNPQVYDFKVK---DKGR---IVFFPDGRASEGYQORANLR-WLFCASHFR-SGS---WTFTRHKSIAHHHF	275
WVA:YP_009357235.1	WTLDDMLDFLDR-ARPNRFVFSVPPVPEI1LKKFANSQNPQVYDFKVK---DKGR---IVFFPDGRASEGYQORANLR-WLFCASHFR-SGS---WTFTRHKSIAHHHF	275
WVA:QEA69426.1	WSLNDITYTIEE-VKPKRMLVSVVPELLGLIYESSIONLNLKAYDF-EINDDT---FSFVLPDQGVKTEAYNQRLNLD-WLMKGSYLR-NNGV---YTIRLLKLAHHMF	273
CRMav:YP_007761581.1	WSLNDITYTIEE-VKPKRMLVSVVPELLGLIYESSIONLNLKAYDF-EINDDT---FSFVLPDQGVKTEAYNQRLNLD-WLMKGSYLR-NNGV---YTIRLLKLAHHMF	273
CTLaV:YP_009046478.1	WSPMDKIVDFLE1-SKAKT1IGSVPFVPEI1LAGARTSLNPLWAEYFKI-KGDK---LIYAPDPGVSESYEQLPAG-OILKYNKII---QOGV---Y5VQVRDSIYSHCLV	283
Ph1BV:YP_001552317.1	WSPMDKIVDFLE1-SKAKT1IGSVPFVPEI1LAGARTSLNPLWAEYFKI-KGDK---LIYAPDPGVSESYEQLPAG-OILKYNKII---QOGV---Y5VQVRDSIYSHCLV	283
GCLV:YP_004936159.1	WSPMDRIVDFLE1-TRAKTLGGSFVFTPEI1LAGDSRSLNPWAYDFK1-QGDK---LIYAPDPGVSESYEQLPAG-OILKYNKII---QOGV---Y5VQVRDSIYSHCLV	283
ASPV:NP_604464.1	WSPMDRIVDFLE1-TRAKTLGGSFVFTPEI1LAGDSRSLNPWAYDFK1-QGDK---LIYAPDPGVSESYEQLPAG-OILKYNKII---QOGV---Y5VQVRDSIYSHCLV	283
APV1:YP_009094347.1	WSPMDLMLFLDS-INPDHLLATIVPPEI1LAGQESLNPWCYFSQ---HGSK---LTFPPDGVQSESYTQPLSAG-YIQLQASKIVCPGSQV---Y5VLDVYSAFAHHF	283

* :

AgVT	VIQRCG-LLTQSQQVAPSTSAMSFWLGL--FGTPGAVRVRINIFKKLITYLMSLKKPDRESAVAKRQLCNSEIFTDELLFAVHLGLIAEMGM-DDNFGRQGVKFVLRGLA	370
PVT:YP_002019748.1	MIKEGS-FDVSERFDRSSALTTSLMPTR--AGKALIRRKFLLRLIYLFLSKKPDHSIAIKIRQSSDDSFICDEIMLADHVKGIFEKLP-ASPGFGVKGVFDLTSIFK	369
PVT:ADX41471.1	MIKEGS-FDVSERFDRSSALTTSLMPTR--AGKALIRRKFLLRLIYLFLSKKPDHSIAIKIRQSSDDSFICDEIMLADHVKGIFEKLP-ASPGFGVKGVFDLTSIFK	369
PVT:AFU55321.1	MIKEGS-FDVSERFDRSSALTTSLMPTR--AGKALIRRKFLLRLIYLFLSKKPDHSIAIKIRQSSDDSFICDEIMLADHVKGIFEKLP-ASPGFGVKGVFDLTSIFK	369
PVT:AKX90539.1	MIKEGS-FDVSERFDRSSALTTSLMPTR--AGKALIRRKFLLRLIYLFLSKKPDHSIAIKIRQSSDDSFICDEIMLADHVKGIFEKLP-ASPGFGVKGVFDLTSIFK	369
PrVT:YP_009051684.1	LIEGK-LETNDYISDEAECSLRMFTGAV-AGK-ITAPIRVEVLKREMIYLSLKKSDMSAALKRQLQSQEDYHPQELCFFLNLAGRIESV--KGIFKDGRGVSTIMDCFA	373
PrVT:AHM92766.1	LIEGK-LETNRFFLSDSAECASLKMFTGAV-AGK-ICAPIRVEVLKREMIYLSLKKSDMSAALKRQLQSQEDYHPQELCFFLNLAGRIESV--KGIFKDGRGVSTIMDCFA	373
ZoVT:QBS17025.1	LIEGK-LKTNPFYVVDFAECINAKMIGFSR-ISH-ESPIRELVFKREIYIYMLSLKKPDMSATAKLRLMSEDYTTGELLFFNALACEIDSV--KGLHTDVSLLKHVQAMAL	376
ZoVT:QBS17031.1	LIEGK-FETSPPYVVDYSECISARLFGTR-YN-SFMPIRFEVLKELIYLLSLKKCDPNSAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	371
ChVT:QNG41875.1	LIEGK-FETSPPYVVDYSECISARLFGTR-YN-SFMPIRFEVLKELIYLLSLKKCDPNSAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	371
Fita:QED42804.1	LVEKGK-FETSPPYVVDYSECISARLFGTR-YN-SFMPIRFEVLKELIYLLSLKKCDPNSAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	371
TrTA:QED42822.1	LIEGK-LKTSERTYISDNSELCCSVPDTSR-IKKGRLIPWIRWKEIYIYMLSLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	375
GVA:NP_619662.1	SAIKGS-YLTEESYKYDNFTIINPNDVLKGK-RGG-KPLYLARMIKPTTLYLALAKSDNSAVAKRLRMLSSRENEHMEALFVAQLAKQIKDTAL-YDKMGNPNLRSILSESFY	381
AcVb:YP_004935358.1	VASLGS-TITEDEYTYDDTVIPRGAVRVRINIFKKLITYLMSLKKPDHSATAKLRLMSEDYTTGELLFFNALACEIDSV--KGLHTDVSLLKHVQAMAL	382
ASGV:NP_044335.1	SFDRGR-ACNEFNH-FDKPCSCLLAEMLRLT-KRF-DKAVINRSTVSSLSTYMACLKTAANASAASAVAKRLRLEKDRDLPDELFVNFSFGEHKNFGM--RDFDVSVLQWKDFK	386
YaVa:YP_009268859.1	FLRKGD-FPTNDVFVNSNSELVDSMLNQRLG-RPSKGIRVEVLLKVLMYALSLLKCDPNSAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	376
RAVA:YP_009553496.1	HIYPAEDELMKVEERRFGPYDLFVGSFLGVF-PVR-PIQDFPLSVFQK-VRV-SIEGVSFTHFKKIIYIYMLSLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	375
ACLSV:NP_040551.1	QISKEYSEILOSHARFAGPYDVLWDVGSLFRK-RV-SIEGVSFTHFKKIIYIYMLSLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	371
GPGV:YP_004732978.2	TIVKGR-R1RSRSLRGKFGFTDLDMSAFLGKT-YKM-PIADVHFSFFKIVIYIYMLSLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	390
CtChv:1:YP_009103999.1	A1TKGK-R1VKRVEFRFDEFDILDSAFSGTE-YKL--PVVHDVFSFFKIVIYIYMLSLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	390
CtChv:2:YP_009103996.1	IVSRRG-LASERSRFDDDNFLDLPVYAKNNL1KMKKLLRNFMKIVKSYIYIYMLSLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	376
DiVa:YP_006905850.1	FLSRGK-RVVEKRNHF-FDKPCSCLLAEMLRLT-KRF-DKAVINRSTVSSLSTYMACLKTAANASAASAVAKRLRLEKDRDLPDELFVNFSFGEHKNFGM--RDFDVSVLQWKDFK	386
ObRV1:YP_009408144.1	E1S1GE-LVTDSLKLFPSDYNISDMKSIFLDR-FRSVEYPIEHELYIYVSYLCLLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	400
CLBV:NP_624333.1	EVSMSGE-L1SDSCKISIFDSDYGSIMSKIFLDR-FRSVEYPIEHELYIYVSYLCLLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	402
CLBV:YP_0044353.1	EVPGPN-YETDEIRFNFDTILOCIFKSR-LFCRDFVPSKDLVERVSYIYCLLKKPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	389
AVCa:YP_008997790.1	IT1RND-LLCECIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
CPrV:YP_009505632.1	IT1RND-LLNEEFRVYSEFADISIRNLNYLG-GNSDSDIPVRVHEVILSFKY1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
WVA:YP_009357235.1	IT1RNDR-E1LCCEIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
WVA:QEAG9426.1	IT1RNDR-E1LCCEIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
CRMa:YP_007761581.1	IT1RNDR-E1LCCEIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
CTLaV:YP_009046478.1	IT1RNDR-E1LCCEIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
Ph1VB:YP_001552317.1	IT1RNDR-E1LCCEIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
GCLV:YP_004936159.1	IT1RNDR-E1LCCEIRVPSDFDAISIRKIGYLG-GNADDIPVRVHEVLSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RVDFTDLFLSCLYSNFC	394
ASPV:NP_604464.1	SITKGE-AIGQKMRFFNGFEAVAMKGLNPLR-RKVESCLPISKNTILK1YR1RLTLLKPDQ50SAALKL50SQVKCDPONGY-EIKFFEEFSKCLKCDT-LNTNMIPDMKRIVQGFL	395
APV1:YP_009094347.1	SITKGE-LPGLERRFSNFEATGVKHLGSGS-YSVRDCIPVSELEISKLYR1RLLKPDQ50SAALKL50SQVKCDPONGY-EIKFFEEFSKCLKCDT-LNTNMIPDMKRIVQGFL	394

AgVT	SLFPARVAAILN-AKMANS-RKMGELHFLDEPSVVVNTY--KFQKGCRVY---SFIHEFIFDNDYVAEEE-----DVAQDFEERF-	445
PVT:YP_002019748.1	DIF--LLDGFNWSDRRKS-EKFVEFMRALDYQTNKVTC--TFSGGVMRS--GFLAEFFLNDNCEASEG-----LDEVISRFDTFF-	444
PVT:ADX41471.1	DIF--LLDGFNWSDRRKS-EKFVEFMRALDYQTNKVTC--TFSGGVMRS--GFLAEFFLNDNCEASEG-----LDEVISRFDTFF-	444
PVT:AFU55321.1	DIF--LLDGFNWSDRRKS-EKFVEFMRALDYQTNKVTC--TFSGGVMRS--GFLAEFFLNDNCEASEG-----LDEVISRFDTFF-	444
PVT:AKX90539.1	DIF--LLDGFNWSDRRKS-EKFVEFMRALDYQTNKVTC--TFSGGVMRS--GFLAEFFLNDNCEASEG-----LDEVISRFDTFF-	444
PrVT:YP_009051684.1	QTFPDRRIARWI--SKTDE-NSFLRLISMEGMLTIKE--SFP-----VENFELFDVWDKGIS-----EQFILDLMDEKFSFGVG-	443
PrVT:AHM92766.1	KAFPNRRLARWI--SNTIDE-NSFLRLISMEGMLTIKE--SFP-----VENFELFDVWDKGIS-----EQYILDLMDEKFSFGVG-	443
ZoVT:QBS17025.1	RSFPKVRNHF--CKGYKE-SDFEQMLNLSNGFOVFKVRC--EYPKNHL-----VETLESFLGDESELES-----EDDASIKEKGKEOL-	452
ZoVT:QBS17031.1	RSFPKVRNHF--CKGYKE-SDFEQMLNLSNGFOVFKVRC--EYPKNHL-----VETLESFLGDESELES-----EDDASIKEKGKEOL-	452
ChVT:QNG41875.1	ELFPERVDNL--SCSYAS-RKLEKFILEAEPFYLRVRR--SNLQEELNATVNFEDTO-----RFVITKLDEM-FSNEFK-	442
Fita:QED42804.1	ELFPERVDNL--SCSYAS-RKLEKFILEAEPFYLRVRR--SNLQEELNATVNFEDTO-----RFVITKLDEM-FSNEFK-	442
TrTA:QED42822.1	SIIGDRIRLNL--SSIYAS-RKLEKFILEAEPFYLRVRR--SNLQEELNATVNFEDTO-----RFVITKLDEM-FSNEFK-	442
GVA:NP_619662.1	GALGD5L1ID--NSFQK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---LKVNPVIE-----LDKVNFIIE--	446
ASGV:NP_044335.1	DVMPH1IAASFF-EPTEFH-NLNMRLNLDATLKGVEPLPSVII--DVPYPSK-----LQDVRWIE--	435
YaVa:YP_009268859.1	DVMPH1IAASFF-EPTEFH-NLNMRLNLDATLKGVEPLPSVII--DVPYPSK-----LQDVRWIE--	435
RAVA:YP_009553496.1	DVMPH1IAASFF-EPTEFH-NLNMRLNLDATLKGVEPLPSVII--DVPYPSK-----LQDVRWIE--	435
ACLSV:NP_040551.1	DKALPDLQRLF--PMKRHRREVQFLVPLSIPFSDWMLR--A-----VDSNSFEGTS-----KLFCAADGPFLSPIGLVEGLR-	447
GPGV:YP_004732978.2	DKLPL-YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	451
CtChv:1:YP_009103999.1	DLCP--FKKNF--EYRLHIDDFTDRLMSIYK1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---LKVNPVIE-----LDPFDIDFWG-	429
CtChv:2:YP_009103996.1	SILPFPVRLML--GNSFQR-DNMQ1QIAAMEPFSVSIETC--S-----INRNYDNNAL-----WRYIKDLAHVNEQNSDQLKLF-	459
DiVa:YP_006905850.1	SILPLPFFRML--GNSFQR-DNMQ1QIAAMEPFSVSIETC--S-----INRNYDNNAL-----WRYIKDLAHVNEQNSDQLKLF-	460
ObRV1:YP_009408144.1	DCLPDLHASFAMF-RSHFKA-CONLQLMMKTLISVNETE--DFYPSK-----VDFKQV1RKLPPDQ50SAALKRQLSDGYTGPEALFLKLGHIAKA---RFRNGF5F5CSIDPLPCDALLYK	444
CLBV:NP_624333.1	DLLPPIHSLAF-RKDFKA-RENLMLDILKPLTITLPTA--DHYMRS1-----IHRSGVIDGID--	444
AVCa:YP_008997790.1	DLLPDLWLNFG--MTWKS-PQWKK-KNTFFFLSFLGTLVWDRVER--VCFEHVLEEWGFVVIITDENAYLDPLSVFAFLN-----ENFNEDRVDD--GYL-	481
CPrV:YP_009505632.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
WVA:YP_009357235.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
WVA:QEAG9426.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
CRMa:YP_007761581.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
CTLaV:YP_009046478.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
Ph1VB:YP_001552317.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
GCLV:YP_004936159.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
ASPV:NP_604464.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483
APV1:YP_009094347.1	DPKDN--YREVL--EKIGLA-DDFTTLLMKIKPLAFLDIHTT--DRP-----LTVRMIDIQIWEERLS-----SFDNISNIVFGRREWLNGVL-	483

AgVT	-----FFGQTSKORMK--KEKIDGYSYTPENLYAA-----ERFNRFGCKSPVKI--ALKAKEGAK-----LNVLSNPTF--	507
PVT:YP_002019748.1	--DPKKEYSAHLRVI--KDRTPNYPGPKARTPS-----VVLHREYITKV--EFFSKAKK-----VNVLKERLTG-	505
PVT:ADX41471.1	--DPKKEYSAHLRVI--KDRTPNYPGPKARTPS-----VVLHREYITKV--EFFSKAKK-----VNVLKERLTG-	505
PVT:AFU55321.1	--DPKKEYSAHLRVI--KDRTPNYPGPKARTPS-----VVLHREYITKV--EFFSKAKK-----VNVLKERLTG-	505
PVT:AKX90539.1	--DPKKEYSAHLRVI--KDRTPNYPGPKARTPS-----VVLHREYITKV--EFFSKAKK-----VNVLKERLTG-	505
PrVT:YP_009051684.1	--DAKMDTSVSYATS-----RNKNFVLLDFKQWRKARLAKEKEKEPEORIE-----RNKNFVLLDFKQWRKARLAKEKEKEPEORIE	488
PrVT:AHM92766.1	--DPQDTSVSYKVS-----ELPNKR--IRDMMIKK--KTKDEYITKNNN--RIRELIDRRCES	512
ZoVT:QBS17025.1	--RIDRNREEQYLYNEAKLFNKN-----ELPNKR--IRDMMIKK--KTKDEYITKNNN--RIRELIDRRCES	488
ZoVT:QBS17031.1	--RIDSREGEQYLYNKKTLFCEK-----ELPNKR--IRDMMIKK--KTKDEYITKNNN--RIRELIDRRCES	488
ChVT:QNG41875.1	--SGEADTSVSKSTLVC-----ELPNKR--IRDMMIKK--KTKDEYITKNNN--RIRELIDRRCES	488
Fita:QED42804.1	--PGEADTSVSKSTLVC-----ELPNKR--IRDMMIKK--KTKDEYITKNNN--RIRELIDRRCES	488
TrTA:QED42822.1	--KDRSQQAYGKTTLLDR-----ELPNKR--IRDMMIKK--KTKDEYITKNNN--RIRELIDRRCES	497
GVA:NP_619662.1	--ALSEVNFL--DISNDRVPSYPIE-----CITHGEGR-----IRVPLSRILRAH	488
AcVb:YP_004935358.1	--LQEITYHV--VKEGDRERTPYSK-----GDE-----ILDNKERRSD--LMIQCARM--	489
ASGV:NP_044335.1	--TRFHMFDATQATGVN-----FNYNKRIFAIAEAVGK-----LCLLGKRF--	460
YaVa:YP_009268859.1	--PF--KNPAFLHGGENHCIS--RAVSGVSGLYSCGPNSAEE-----TVRNFDK-----DYLEDSPNKR--	502
ACLSV:NP_040551.1	--PKVKKGLAKL-----PGRVEDSHNYPREIYSDL--LSSTS1IWSRYSYDD-----DPRHRSASPL--VILRNSRA--	511
GPGV:YP_004732978.2	--SEKKMIRPVLKVMIE--MGRSEQGSVVPSTSYYQO--AAVC1CFSMDEN-----CIGWNRNGVK--VLLRASRS--	498
CtChv:1:YP_009103999.1	--KEREKGEDEES--RDRRNIVGFTPLPSFSY-----TQAD--LNSIQGVL--SYASTQRSINRLSSD--	486
CtChv:2:YP_009103996.1	--GDDFDCKGKYASQNIEN--SDRANLVHFKTPRFSS-----TQAD--LNSIQGVL--SYASTQRSINRLSSD--	486
DiVa:YP_006905850.1	--FLNSCDYLORDNIK1TRS--SFRGEFYIDYDTSYGSY-----MTSE--INEVFIN--KVKVIERRIKEFKFAD	523
ObRV1:YP_009408144.1	--YLNDEQMFKGVOEQLMNS--KSRGAFLFGSRGNYHI-----ESAOQGPKNKMQLEIENYG	488
CLBV:NP_624333.1	--ERIRLPFWNLNDYDPL--KRKRVNAYN1LSYRFEERKI-----DLRERGPHKMLQIEWYG	534
CLBV:AFU43536.1	--DRVKLKPFWNLNDYDPL--KGRGRANKYDLCYFEEERKN-----DLRERGPHKMLQIEWYG	536
AVCa:YP_008997790.1	--GDRRTVVIKSLDGLIK--FSRSKNUYKMHIIFLLN-----PSLIRGN--IRNFCNSG-	513
CPrV:YP_009505632.1	--FSWTPKNDYDALIK--KSSESHV-----PSLIRCA--	468
WVA:YP_009357235.1	--FSWTPKNDYDALIK--KSSESHV-----PSLIRCA--	468
WVA:QEAG9426.1	--FSWTPKNDYDALIK--KSSESHV-----PSLIRCA--	468
CRMa:YP_007761581.1	--ESYDPLIFNAHTLWFASSHPSITLMLVKSFINNW-----FMLHNESY--	537
CTLaV:YP_009046478.1	--TAYPDCLFHASQVSFSNPHNLIRRLVLFISTW-----GKTEDAYTTSLLSLKK--FRLHDDRY--	535
Ph1VB:YP_001552317.1	--HKFXYGKVASL-----LEROQPSVGLGVQKQPLCEPTECILKFTTAAVYKDLIDVYVAKDVSICWAVFVEHRLRNNTNCVDIGAKFLLLEPNHV--	552
GCLV:YP_004936159.1	--GERIGAAYTVGP-----FC--DYPVIDAQKVFQQLRVRISREWFSFSMVMQYCERGDTYEFM0ASKLI--	528
ASPV:NP_604464.1	--NITTVAHSPYLVSKFESYDHQFHS1LVSKS1SALTRIAKIVL5LYDPCV-----VAFESRSERNLAVN-----VIAANLRA--	544
APV1:YP_009094347.1	--GAPTSLEG--LTGKFKYSSSEAYHGLHVLDCGPHVFRRLVRKIAADFSC--NEFGIYRKSSYVSSVAITV-----LQRKTNNSLNF--	540

AgVT	-PGEIQEL-	SFEEARFYHG1-	-PGMKRAFDsrv-	507
PVT:YP_002019748.1	-PGEMYET-	SLEEARFESGL-	-VGKRTNMFHEI-	505
PVT:ADX41471.1	-FSILEEK-	SIEEMMLILPLIFRSK-	-KEGEMDGIFFKRDP-	505
PVT:AFU55321.1	-LSIILER-	SVEEMMYLILPLIFRSK-	-NKKFKIYFCCKLY-	505
PVT:AKX90539.1	-GILPTEL-	SFEELRFF-	-LGPNELIVSRSKTMYSYHREG-	505
PrVT:YP_000951684.1	-GVLPMEL-	CFEELRFL-	-QMKSVPSPGEF-TYSKSKKAQFERFGQ-	532
PrVT:AHM92766.1	-LSRFKEI-	SFEESRF-	-QTRSMSPHFGEF-TYSKSKRAFQFERFGQ-	532
ZoVT:QBS17025.1	-ELIAGVQTDVIEINPRYVCS-	SRALIHFQVYLKLG-	-GFRGQFYNIIF--	528
ZoVT:QBS17031.1	DLLENTKELPSINEPWFSP-	IDGRFSRMRFMIREG-	--KKRYSFSNSYNDNC-	528
ChVT:QNG41875.1	-DYEAESEYYFSENGYIFMPSKS-	-	-	534
Fita:QED42804.1	-TYDTESESYFSKDKGFVFYE-	-	-	523
Trit:QED42832.1	-NFEASTKDH/F5--VVVSGPSS-	-WRYCMFRYKRNNLGRVDNVSVILGFIYRSDSLTDSPYEGRIGRPLQTVMSDFM-	-	524
GVA:NP_619662.1	-YSEAAK--FS--SNCLSLCAAPC-	-DEVIARTPFEIHNREKKELSKLCDFHKMMK-	-	482
AcVB:YP_004935358.1	-SYTVLRDEFFS--APLLCESE-	-	-PEKLKFTYDDL--PFYQFLSEDQEIDGYFLRESVLDs-	479
ASGV:NP_044335.1	-YSLIDE-	KLIENYNNKLLMAAMKEF--	-GQNCRDRSFRPFFYIEIM--LGSGLPRLRQIC-GDFTASCVHET-	577
VaYa:YP_009268859.1	-YSSLEE--	QINELFRKLKSLAADIKY--	-PGSFQRDKRNFIIPFF--LTKNFRMMPQLCYRDFVQSNOKEA	563
RAVA:YP_009553496.1	-	-	-	533
ACLSV:NP_040551.1	-	-	-	524
GGPV:YP_004732978.2	-	-	-	524
CtchV:1:YP_009103999.1	-	-	-	524
CtchV:2:YP_009103996.1	-	-	-	524
D1Va:YP_006905850.1	-	-	-	524
ObrV1:YP_00948144.1	-IKEFKVDPFIISN-	-	-SITEF--TLEALLGKRIDPKKYSYSQKACT	488
CLBV:NP_624333.1	-IREFD-DPIAN-	-	-GISEF--TILEALIGKRIHKERYSYSQKADV	480
CLBV:AF443536.1	-IRMCCHQHSAD--GVTI-	-	-	575
AVCa:YP_008997790.1	-RSLCANQLES-GPL-	KTSHYKFKLPTFFFSKWSEM--	-PFLKSFVHFRENNIKRDPPIF	576
CPvV:YP_009505632.1	-GAVLIC-	-PFSRSLSYHEI--	-SDMEGLMALARPLRRIKEGETSV	453
WA:YP_009357235.1	-	TKEEARMRGH-	-	507
WVA:YEAG69426.1	-GAVLIC-	-TKEEARMRGH-	-SDMEGLMALARPLRRIKEGETSA	507
CRMa:YP_007761581.1	-NSLVILANLMD-SHLFKNL-	LNREIRKRLRRLNRNSR-	-	573
CTLaV:YP_009046478.1	-FSLTRLANLMD-SFSFKAT-	LKNEMVKRLRRLGGSLR-	-	571
Ph1bV:YP_001552317.1	-NSTIR-	SLVNKALRSLR-	-	571
GLCV:YP_004936159.1	-WFSS-	-KLAGWDVCLATYNKYVHMRHSWDKRRRLS-	-SWFEI--GPWFKLAGR-AHTRFLTS--	592
ASPv:NP_604446.1	-FAVDTLWRIFE-GILLKEC-	KRAQGKMRK--	-SFRSI--GCAWFCMVR-SYERYICA--	583
APV1:YP_008909437.1	-IFGTDLNPMMI-	GFVRNFYFASRRS-	-FHFEI--GIRWFLFVDF-SNQWFPLPPCRDGL--	600

AgVT	-
PVT:YP_002019748.1	-
PVT:ADX41471.1	505
PVT:AFU55321.1	505
PVT:AKX90539.1	505
Pr:VT:YP_009051684.1	-
Pr:VT:AHM92766.1	-
Zo:VT:OB517025.1	-
Zo:VT:OB517031.1	-
Ch:VT:QNG41875.1	-
Fita:QED42804.1	-
Tr:TA:QED42832.1	-
GVA:NP_619662.1	-
Acv:YP_004935358.1	-
ASGV:NP_044335.1	-
Ya:Va:YP_009268859.1	-
RAVA:YP_009553496.1	-
ACLSV:NP_040551.1	-
GGPV:YP_004732978.2	-
Ctchv:1:YP_009103999.1	-
Ctchv:2:YP_009103996.1	-
D1Va:YP_00905850.1	-
Orv1:YP_00948144.1	-
CLBV:NP_624333.1	-
CLBV:AF44356.1	-
AVCa:YP_008997790.1	-
CPv:YP_00905632.1	-
WA:YP_009357235.1	-
WVA:YP_0094624.1	-
CRMvA:YP_007761581.1	-
CTLav:YP_009046478.1	-
Phl:VP_001552317.1	-
GCLV:YP_004936159.1	-
ASPV:NP_604464.1	-
APV1:YP_009094347.1	-
VLLTNYAHWGLPKREG	-IREVVMWDAAEELISOKE
-JFLTNFEHWKLPLVKKG	-IREVTMKDAFOAQEEQAE
-DKLNNCKSFKDIEAE	-EKEKKGKENGFKMMFQEDE
-DKLNNKSFKDIETE	-EKERKNRENFLKKMFKQNE
-LLLTDFPHRDGYLPEI	-RDVEMKQVDSYEADIEVAKG
-LLLTNFSHKDDEYPSEI	-REVEMKQVDPDEANTGVTKK
-LRLKWNNEEPNQISE	-KEDVEMMDAIPHERALK
-RFSFMSERAHKDIE	-DIQAGLEEGGVITEEEAELRLPPT
-PRFGSGLAIGWEN	-DPNIRLKEGRITHEQYENIISG
-RGVSFEVILAGVMAKLDISTE	-NVRRSLLEGLENRKRLIGTLPA
-VKNVLELEVKLRLER	-NTRISLSKKVGKKAGRSMIPVHLLKPTCGEGN
IJKDAFHYSSEGFFDPDILFASSRGTFLGHSEMTDL	-STSLNTLDKVIAENGKSDWPIL
LDDMLDLWSEIK	-DVTKEELIEISANANENEDSVT
IIEEEVIMDLDMII	-SPMPQIVTVEEIKDLSVAEWESSIPDQEGNFQEGA
-ELHGPDSRHLRMSAHDICSYEANIKLF	-GNHHNHEKMRIE
-ENGTISSHVKFNSNGSDYFTDMDLVEGINLPVNRSDFD1K	-
LSNYLTFLCA	-EGLDGFNLEEHLLERRLKAAGHDVS
-LAKCLSFVCE	--DDEEEEL - TSAEQAGP
-EAEVILDVSNSLDGKQSEHHIDDEFVPTPG	-LKGGS
-ESELEGLGKTAESSGEADAANTL	-LETQ-
-KEGDVKDMDIMTEAKD	-IKKMKMAGCNGSEKEGKEEEVVK
-EAEVILDVSNSLDGKQSEHHIDDEFVPTPG	-IKILADPLGFMK
-LKGGS	-ISGLVAFIPTFSDEGESQH
-KEGDVKDMDIMTEAKD	-DGLVTIESIEVDPSEF
-IKKMKMAGCNGSEKEGKEEEVVK	-
-KEGDVKDMDIMTEAKD	-EEEVSKN
-GKEMEACGRSSKEKEKEKEEVK	-
LRNDLPPSCPDAKREVFRFISCYKSLAADFKKMSSECSP	-
LRDYPISIENPSDDKKDQRARSNFSSVSESSLISSECP	-
-ILTLIATGFPQFQLNAMKDKFDVLI	-NOVSQPKFKEVK
YPHDAIVYKEAK	-QWGHSHVLKELAGGSR
-SLKHREMDYWFKEKDRSS	-QAPVNLNEEQKPY
YPDQAKSYKALD	-EAYSTVADLLGSLA
-RNKLIIASAAPKFDKTS	-
IA	-RSVSDQF1ZKGQCDNSLNHG
-RMSLRLQVLKGPKLQAL	-
WPNDLGLVFEF	-RMKRNKLNALAEISNPFDR
-NSNLRLKGSQFQATPNKSNTSSS	-EGASNHQREQRQDCDEATLQVNFRQEIEFCMG
-	-SLPEANSFKSFT

AgVT	-	-	EVSPEEL-	514
PVT:YP_002019748.1	-	-	EVSFEAA-	512
PVT:ADX41471.1	-	-	EVSFEAA-	512
PVT:AFU55321.1	-	-	EVSFEAA-	512
PVT:AKX90539.1	-	-	EVSFEAA-	512
PrVt:YP_000951684.1	--G--GLKVMGEVIPHNTLSSDC	--AEDSECGSGVGNDES	--MSSEEKE-	ECE-
PrVt:AH92765.1	--D--MPPEEOFPKKEERADSC	--GSEEEEEELEHRHNEMD	--LSSDDDE-	ECT-
ZoVt:OB517025.1	--IE--DVEMDEEIDENIEITDSRFS	--IGECSNSRQIREPNDIFDCST	--DESIDEI-	DAE-
ZoVt:QB517031.1	--IE--VMEEMEEENNVLRCFS	--IGECSGSRQIEKGNDIFDCST	--DESIDEI-	EAE-
ChVt:QNG41875.1	--E--VHPSESTKVYQENDNLSVRSGFSGSDEAKGMDEGDEELAVLSIGETSEEEC	-	-	EGEDVEVKALTTPG
Fita:QED42084.1	--E--SHFTEAVEADRRDNEMFTCSFGESGDEARGMDDEEDDEPAVLISIGETSEEEQ	-	-	EGEDVEVKALTTPG
Tra:T4D42832.1	--S--KPRDEELDSKXKEGETKD	--GGVGNRMRMNEEETDQMGLMS	--KTNESDS-	DSEDFTYGCSISR
GVA:NP_619662.1	-	-	-	568
AcVB:YP_004935358.1	-	-	TKQATKK-	567
ASGV:NP_044335.1	-	-	-	482
YaVa:YP_009268859.1	-	-	-	479
RAVA:YP_009553496.1	-	-	PIGTPAA-	DLVSPYAEDSDAD
ACLSV:NP_040551.1	--G--KPEERNKEEAKIPMNE	-	GTSKEEK-G-	SEPPHVKREGVR
GPGV:YP_004732978.2	--SADESSESVNVKLLNESLTY-	-	DAEPSEC-	EVPSVESHEPEQ
CtchV-1:YP_009103999.1	--MVSSSSSSS	-	STSGREI-	EIDTSDLSLDHNL
CtchV-2:YP_009103996.1	-	-	EGSEENL-	FFNSNSDSEMLDN
DiVa:YP_006905850.1	-	-	-NRF-	WF-
ObrV1:YP_00948144.1	-	-	-	DI-
CLBV:NP_624333.1	ECLE--EIPIETEPSLEERGQFST	--DYZHSEKFENINYNDIFNPHNCMNTTHGDEIPTPSDGNCFFSAFTET	-	FEVERPDTLR--SD
CLBV:AF44356.1	RADL--EVESEGEIGKEESEFEGTLS	-CAEGHEAIKFEIDFSDIFPRHNCMNTHGVEIPTPMGDNCFFSAFAAT	-	FDCPDSKDLR--SN
AcVa:YP_008997790.1	-	-	ETGSGPI-S--FC-	-
CrPrV:YP_009505632.1	PASE--LCGLATEPVS	--FFPGDSCSVLMGNPEIAVADEYNICDVEGDDGN	--CFMRALLTS1KGDDRTYPGSRSLNLRSQ1GVNLTDSEAAQILREEQ	744
WVA:YP_009357235.1	OSVL--IIKRTSKNGEEDNKKKE	-	-E-NKKEI-	580
WVA:QE64926.1	-	-	-	581
CRMa:YP_007761581.1	KCIS--KSTADSPDGKKEHKL	--POHSEGZNKACTDEVIPKRV	--DOPPEKT-	693
CTLa:YP_009046478.1	KIPSEREKCSTQAIEKNEEKPCKSEVNSTKGETPPESTSKTTSKFGELLATPE	-	-ATAVSEP-	702
Ph1Vb:YP_001552317.8	--KDSGGTVENDEDDKGCEPVGVSSSSDDGSD	-	-DKSSQEY-	673
GLCV:YP_004936159.1	--KVPREGVAEEIPAHCARSTAASAFAPCG-	-	-STASSEC-	662
ASPV:NP_604464.1	--DVSSELSIHNVEMENAPEGTLADAGIK-	-	-PTSSPL-	675
APV1:YP_009094347.1	PCV-E--AVAETSYEQVPLEPEANGALVLCGTP-	--DASTPAF-	-	724

AgVT			514
PVT:YP_002019748.1			
PVT:ADX41471.1			512
PVT:AFU55321.1			512
PVT:AXK90539.1			512
PrVT:YP_0009051684.1			624
PrVT:AHM2766.1			- YINGRFSPPN-GSFVE
ZoVT:QBS17025.1			- FISGKFKCS-ESFLD
ZoVT:QBS17031.1			- IENNSKFKCS-SNFND
ChVT:QNG41875.1	ID		- IENNRFKCS-DNFND
FiTA:QED42894.1	VN		- -- EFSID-YRDSA
TrTA:QED42832.1	I		- -DFSVd-YQDFV
GVA:NP_619662.1			- GENKF-TYE-GAFKK
AcVB:YP_004935358.1			- HMDDDTPGTSGESDVKE
ASGV:NP_044335.1			- QMQUITCPG-AELKR
YaVa:YP_009268859.1			585
RAVA:YP_009553496.1	ADEADESIP--	-GLVVLGD-	583
ACLSV:NP_040551.1	LDEQHISEPL--	-LSFKLDD-	482
GPVG:YP_004732978.2	IESSGEIIP--	-ESNTFVD-	479
CtChV-1:YP_009103999.1	IRGIK ---PDDRWSDL	--VVEIKD-	-NRFYTYGSG-HGVP
CtChV-2:YP_009103996.1	KIYRKV	-IED-	-CS-AGLIK
DiVA:YP_006905850.1			-NNNKEFYCD-GAFSL
obRV1:YP_009498144.1			-SSFLQCQGID
CLBV:NP_624333.1	FSDWLMEFNCGGSYASLAEMIRPNGVFMEEAELIYLFCVFRGVTLLIHDRTTHEKENYAVHRGFEEGHMVRGNHFGV	--IET-	-YNISTLTSDF-PLLDG
CLBV:AF443536.1	FADWLDTFDGGSYADMGVKIRPNGVFMEEAELIYLCIYREVTLLIMHDRTNDRESVFAIHGLEEFGHMVRQGDHFLG	--IET-	-YRIDGFASD-PNLSE
AVCa:YP_008997790.1	-----SLKMENHFDYLRCLSSGVS	--KEHTG-	-LLG--KTTYPSGP-
CPvR:YP_009505632.1	FDEWMIMFTV-NVMMLSLKIFQGDVSIPR	--TLPKLV--NTHGNDAKEI	-AILHGRNHFLGLLKCTSESGAHDFDGNOVPEASSDHNDFETE-TGFND
WA:YP_009357235.1			-KMMVEFVDDILD-IRMTL
WVA:YP_009469426.1			-KMMVEFVDDILD-IRMTL
CRMvA:YP_007761581.1			597
CTLaV:YP_009046478.1			887
Phl1V:YP_001552317.1			883
GCLV:YP_004936159.1	CVFELN-		-EEG--KTGSSDQFLFISSIIK-VGPFK
ASPV:NP_604464.1	VVPXTEN		-TDN--VLAQSSLDFLISSIIK-TGPFG
APV1:YP_009094347.1	TFNSAN-		-IEVDTKVRMRMTCS-CGVPM

AgVT	-RFFKGPAA	-YRNS	-LFIDTFLNAYAKKIQ	-	-IDGPRFTVD	547
PVT:YP_002019748.1	-RLQMR-	-YSDS	-OFVAGLPLKRYVK-	-	-MLTWKKDQKLFS	548
PVT:ADX41471.1	-RLQRMM-	-YSDS	-QFVAGLPLKRYVK-	-	-MLTWKKDQELFS	548
PVT:AFU55321.1	-RLQRMM-	-YSDS	-QFVAGLPLKRYVK-	-	-MLTWKDQKLFS	548
PVT:AKX90539.1	-RMQRMM-	-YSDS	-OLVIGVPLKRYVK-	-	-MLWTENQKLFD	548
PrVT:YP_000951684.1	S-----	LSMILNLSKAAYL-HGKRKT-----	LFSTVTGLDYGFPKHKYKQTPC-DFMEDLLKK-----	VGFNSCLAQMYEGGS-IGAHYDDKEVYD-----	-DEDEILTWN	711
PrVT:AH92766.1	S-----	LRLMMNLSSAAYP-HGGRTR-----	LFSTVTGLDYGFPKHRYEQVKC-DFMEELKK-----	TGFNSCLQAOKYEEGGS-IGHDFDDEYV-----	-DDELTWNL	711
ZoVT:OB517025.1	G-----	LKVLFKSKEETL-HESFWI-----	YISKIELASINVRGKLFNF-----	-NELLIEPEKILNRENTNSLVLKLIKQKG-EFESSFLNEKEIN-----	-LDLYIELV	757
ZoVT:OB517031.1	G-----	LRLGFKSKETLW-QENLNNAI-----	YISKIESASISIKEKFVS-----	-NELLMPEKEILNRENTNSLVLKLNKEKG-FDPLFKKKEED-----	-SDCIEVQL	757
ChVT:QNG41875.1	S-----	INEMLRSSIAVK-HKGRIAV-----	LDSRVDGLTYFGFDLVYRSAFK-DQLDGLYRTL-----	-RYGYNTCLVQEYKDGGH-IGYHKDDESYYD-----	-PHVVTMIN	732
FiTA:QED42894.1	S-----	INEFIRSSIAVK-HEGRVA-----	LDSRVDGLTYFGFDLVYRSAFK-DQLDGLYTKL-----	-EYGYNTCLVQEYKDGGH-IGYHKDDESYYD-----	-PHVVTMIN	732
TrTA:QED42832.1	L-----	INFMPGVRFGRKHGREC-----	FVSPVIEDLTYGFNNVVYKNCQS-----	ETINEIMAIKFSEYFVNELNSALVQKVEGEGS-IGLHRDEKVDY-----	-DTPVTLN	738
GVA:NP_619662.1	F-----	KCSRSVLRK-EEIYSEK-LKGREVA-----	FYSR-HSEKEYKGNGSSHSLRGSLDEALNTELQEDG-----	-LDDSDYHDLKIQRTYTAGG-IGFHADDEPCYL-PGGSVTVN	680	
AcVB:YP_004935358.1	T-----	KVEGGYIRSLPQGWTDO-LQGRKAA-----	FYSR-HSEEEYSPGGSKTRGPAIERMNRLEG-----	-LGEDFDHCLQIYEKAGG-IPHYADDETCYK--EPSVTVN	679	
ASGV:NP_044335.1	-	-NPERNWNI-----	-LNNSGSCLIDSYRURARRRFRRRDLPSIKG-----	-KSKPRKOLFESTGNIKSNPNAE-----	-KNSSEGEIK	552
YaVa:YP_009268859.1	-	-RSERNRHV-----	-RSERNRHV-----	-KSKPRKOLFESTGNIKSNPNAE-----	-SDDSERIRK	543
RAVA:YP_009553496.1	I-----	-ELDGFEETR-RLNRRAF-----	FCCKDPSLLYGHDSVIYKTNRWSDALD-----	-PGTASNFSCLVOVDEGAG-IPFHDRDDEDYC-----	-NDLVLTN	754
ACLSV:NP_040551.1	TV-----	-GNDYLLLARQIECPLSQ-LRGKAA-----	YFCLCDPMVYHFDSVSYPTFEATGEIRHVMMKARSKGWIDFNALSILQVYNDGCR-LPLHSNDEEYC-----	-DDGILIT	781	
GPGV:YP_004732978.2	E-----	-LDFASTLEGLPKLN-LRGKRAF-----	FFHS-NGLPYFHDSSLVYRTELEPGWMEEIFVFKANEHDFVNFSNCLQVQEYQDGDS-VGMHDDDEDYC-----	-DPPDILT	767	
CtChV-1:YP_009103999.1	-	-LDNNLKGKISQK-LTRKRAF-----	YFCKDANFDYGHDKVQYNGMNPWNFISELNKICACDVTGFKNFSNLINETYRTRGH-IGHMADDENVYDLDRLRNPLV	788		
CtChV-2:YP_009103996.1	LCEG-----	-LOQEIKMGKKG-INKVRKAF-----	YFCNSRFDYGHDKVQYENLKGPKFISDCEGEMKTKGFKNSNLASINSYCRKGK-IYFHADDEHVVYDSDSSPNLVT	782		
DiVA:YP_006905850.1	-	-LNDKEKF-ENAKRESIRCKTTFDYEADLIEEPPDSDSIFKGFKNGVFSKKFTTMRMNECLIMLRGT-YVNKLSNKLINH-VDDPFSTME	619			
obRV1:YP_009408144.1	-	-IRNNKEFQNSNA1NSRLSKSEPIHKKNGVYVIIINELSSPTFVGFKNGYVIMLKGMSGTRLVVIVCAAA-YLHMQLQEYNET-KANEVSKH	619			
CLBV:NP_624333.1	IPCGFSEEITKFHRPDHNFCAQ-FRGRKAA-----	-FITK-DAWDYDHGNYVPHNSWPSLLEEIIQCGG---QDFDNCALINFYEAANS-LGFHDRDNEYVN-----	-DPPDILT	908		
CLBV:FA44356.1	LPCGYSEELRNHFKEPHFNCAQ-FRGRKG-----	-FLTK-VDADYHGNGMHNWPHNAPWPSLDEIIIRC-----	-HGDFFNCALINFYGPNS-LGFHDRDNEYVN-----	-DPPDILT	934	
AVCa:YP_088997790.1	-	-IINALQGLKPKS-FRGRSSF-----	FFARSNEIDYHGNGFKYRTENFNFAELDDFIPS-----	-DLIFNACLVQVYDGKSG-IGFHHDNEQCYA-GYPILT	586	
CPvP:YP_009505632.1	F-----	-EELRKVGWSISMFKTPP-LKNRDAF-----	FFSESKSISDGHYRNIKAYAHNNW-HGNDVQLLPS-----	-SLRDNYLQIYVQEYEGS-IGMHDREKVD-----	-NDSLISLN	933
WA:YP_009357235.1	T-----	-NLLVKVL-ISKRMQLTR-FTSRDAY-----	YVVED1RLDLYGHMINGYMKKNLADERVRVFMKVERTYKGKNTM-1QRTYKQKSS-INFHSDDEPMIP-RGSSVLT	696		
WVA:YE064926.1	T-----	-NLLKKVL-ISKRMQLTR-FTSRDAY-----	YVVED1RLDLYGHMINGYMKKNLADERVRVFMKVERTYKGKNTM-1QRTYKQKSS-INFHSDDEPMIP-RGSSVLT	697		
CRMvA:YP_007761581.1	E-----	-PSTSISFVEGLDFSKGHN-HGKGRKS-----	FFSE-GGFSYFGSISVYPSQGPNFAKEF-----	-YGDFRNSCLVQYKYNADAT-LGFHADDEQCYQD-QHDEVLT	807	
CTLaV:YP_009046478.1	D-----	-HGVIIFFIRSTLSDFGHS-NHGRKAL-----	FFSR-GGFAFYVFSNTSYQSGSPFAEEI-----	-YGDFRNSCLVQYKESAK-LGLHDDDEDYC-----	-YGDFRNSCLVQYKESAK-LGLHDDDEDYC-----	816
PhLBV:YP_001552317.1	E-----	-IKTLLGSDMHDFAKAR-LKGRRVGG-----	-WYSK-DGTPVLYTGHTSISQGWPDLEWLWMOINK-----	-VPDKVNSCQYIYEAGES-YGHYADDEPFCYK-GEEIEHT	789	
GCLV:YP_004936159.1	A-----	-VLVNLAYEALELEFPDQ-LPGCRAG-----	WYVKGQPQADVGGFLGCQQLRWLDFDFSFLELH-QAPGSYNSCFAQVFLDLS-TFEYHSGDGGVFE-EGAPAYLFQ	783		
ASPvP:NP_604464.1	Q-----	-ADPNSLHGNVLFDLFIGG-SKRGAS-----	FYSR-DLGDYTSVSHSRRGPWFLDKFLDSND-1PLNFTYQNLQVQEYESTG-HSMKHDDESDYD-INDHQVTL	797		
APV1:YP_009094347.1	I-----	-GILSPMELVPLPSSEAT-LNGRQCY-----	FPTRCGCDIYGHNKYRIPKWNPK-SGLSILKD-----ESTYNNACPLQIYEAGAG-IGFHSDNEVKWH--RSP1KTN	842		

AgVT	ADGDA	-EMDCSSD-	-EHEET-HDQOAADKEPEEDSHNETEEEAFTSENSETLSE--	--FFDTKCDSFQIK-	-YDLL-	617
PTV:YP_002019748.1	EFPSEESNEVEME	-DAFEL-RKGRLTKRGERDENGANSECEQLQSEDDVGFSF-	-YEETKADSYEID-	-FEAI-		618
PVT:ADX41471.1	EFPSEESNEVEME	-DAFEL-RKRRTLXXXKKERDENGANSECEQLQSEDDVGFSF-	-YEETKADSYEID-	-FEAI-		618
PTV:AFU55321.1	ELPSEESNEVEME	-DAFECCEKEENSEEGSKERDENGANSECEQLQSEDDVGFSF-	-YEETKADSYEID-	-FEAI-		619
PTV:AXK90539.1	GFTSEESDEVEME	-DAFEEYQEDEADEKEGSEKEDEAGDEAKLERDERSSEDDVGFSF-	-YEETKADSYEID-	-FEAI-		619
PrTV:YP_009051684.1	LEGEADFT-TMFKTKGT-	-ESVHL-TRNVOLVMPKCGSRGE-EKFHKHAVENCTEGRISITF-	--RHOKRFMNGEVP-	-EIEEN-		783
PrTV:AH92766.1	VEGEADFL-VMLKREGT-	-ETIVHL-TPGSVLMPKCGSSRP- EFKHVKHSGCCTKGRVSITF-	--RHOKRFMNGDPV-	-EIEINY-		783
ZoTV:OBS17025.1	LKGAYIAL-SIEENGTC-	-VNRDL-KLEEIEVRSLNEEFTS- -KFRN---LEEVIMMM-	--FKOTHRADGSS-	-VDSL-		823
ZoTV:OBS17031.1	LKGHVVL-SVMESGTY-	-VNRFS-KSEEETEIKLNKTSF- EFRN---FEEDAIIIMVM-	--FKOTHRADGSS-	-VDSL-		823
chVT:ONG41875.1	LRGQASF-EIEGQ-	-PPFEL-NGAQALQFGS-----	--HNNRHRLLYASEGRISLTF-	--RKQVRLLMDGRQ-	-IKDF-	793
Fita:QED42804.1	LKGRAFS-EIEGQ-	-PLFKL-DGAQVLQFGS-----	--HSDRHLRHASEGSRISLTF-	--RKQVRLLMDGRQ-	-IKDS-	793
TrTA:QED42832.1	LFGEANF-KIERAGLV-	-QTFLN-HDGDIVYMKRQEORTS-	--KHSVSELSGRVSITM-	--RNQVRYMGNP-	-IKKG-	805
GRA:NP_619662.1	LHGDAFT-EVKENOSGKI-	-EKKEKL-HDGDVYVMPGMGPQMOHT-	--KHRVTSHTDGRCSSTL-	--RNMKTVDYEARKG-	-DEDSE-	752
AcvB:YP_004935358.1	LFGEADFT-KTCKTNE	-LSFLR-TDGGDVLTMGKGFOSNH-	--KHSVONTGPGRSVSLTF-	--RNSIIISNQADED-	-DLSEY-	747
ASGV:NP_044335.1	IEG--SAENDQPHEV-	-SHTSM-ETED-----	--GGFEGIPSVDLINCF-	--EPEEIKLPK--		600
YaVa:YP_009268859.1	IEELRNLNNSSVEDELNS	-SEVKL-NSED-----	--KHGFEGLSPBDVNDLSSREEQRFVTERK-			600
RAVA:YP_009553496.1	GKGSAAK-HISGDER-	-LSFDL-VEGSSFIIMKADFQKHY-	--RHSVSDCSAGRISFSY-	--RFQYRTPSFILKGKFPMTVPDVAFP-		830
ACLSV:NP_044551.1	VVGDAAK-HTTCHD-	-EVIDL-KQGNEILMPAGYQKHN-	--RHADEVASEGRSFTVTL-	--RVHKRDFSFESK--	-LRFI-	847
GPGV:YP_00473297.2	FNGTALF-EIKNV-	-VSSKL-DHKDFILMKSGLQKRE-	--KHRVQYTESGRISLTL-	--RVQKRPPNHHG--	-LRFI-	832
CtChV-1:YP_00103999.1	MIEGEGMF-SVVKMGKYE-	-HSFPM-SPGDMILMKNGAOKRM-	--KHSVIAKDR-RSFLTF-	--REQIRSKSLIS-	-LASS-	854
CtChV-2:YP_00103996.1	ARGRGIF-YKVKYNTKAVG-	-TECLL-DEGEAILEMKGAEQRLR-	--KHSVHAISQ-RISITL-	--RDDQRKRSFSKLN-	-ESCN-	850
DiVA:YP_006905850.1	KHKRDRDLN-	-KVIKYIIGVVEYEMPSSQVSEL--	--EETTEITPPIRNLSSN--			665
orbRV:YP_009408144.1	MNKKEMKE	-MILDFTMKTGDTDDHVSKSRTSD-	--EQTKEQTNLICESCSK-			665
CLBV:NP_E24333.1	TFFGEGRF-TIEFKDQV-	-TSFL-TMAGSFFLMPKGFQPKA-	--RHSVSN-EMRSVSTIF-	--RKHVRRLLNGSP--	-IAIR-	974
CLBV:AF44356.1	TEGEFFG-SIEFEKEQ-	-ASFLM-TAGSFLLMPMRGFQPKA-	--RHSVRN-ELPRSIFT-	--RKHIRRLLDGSP-	-IAIR-	1000
AVCa:YP_008997790.1	F-GLALF-EFDSG-	-EAFNL-TDGGDTILLSLGYDRKLK-	--RHRVTSLSDSRSITL-	--RHRVCRMNKP-	-LEFF-	649
CPvP:YP_009505632.1	LNGDALD-QIEAKSKR-	-YSFMRD-KGDDYFLMKRQDFQAKF-	--RHGVQGATEGRINVTF-	--RKHVRNSRNEP-	-IYLG-	1001
wva:WP_009357235.1	VEGSATF-RIVEKENKEKKKKKKHENHPCDEFSL-	-NMFVFCKMKGEOFQELF-	--RHSIDVHSEGRMSITF-	--REIKPTFIKGK-	-E-	775
WVA:EA64924.1	VEGSATF-RIVKKGNE-KNNKKNKENHPCDEFSL-	-NMFVFCKMKGEOFQELF-	--RHSIDVHSEGRMSITF-	--REIKPTFIKGK-	-E-	775
CRMvA:YP_007761581.1	LFGSATI-CFTGDKFALSNT-	-NPKLYLVEWL-DHCDWLLMPRGFORNY-	--KHSIKGTSEGRISLTF-	--RKQRRTLEGSL-	-IQSRA--ESGDSN-	891
CTLaV:YP_009046478.1	LFTGATF-IIFTADGAKGLERA-	-DPSKFL-EITL-SHGEYLLMPNGFOKF-	--KHGVSCTASGRISLTL-	--RKQARMSMGT-	-LHAGA--DGGNNNG-	901
PhlVB:YP_001552317.1	LSGKAVF-EIKCRNGA-	-GGEYL-EGPMQFTMPMDFGQTH-	--KHSVSGTTKGRESVTF-	--RVLRACTEAQEK	-EVDAE-	858
GLCV:YP_004936159.1	TRGTSRV-HVQGLGCC-	-GERAL-LGPMQFTMPASLLEH-	--RWKIKSSTGCTIMTF-	--RKLTRQEPPWVTTAPT-	-VQKGV-	857
ASPV:NP_604464.1	YSGDAF-CIECLGSG-	-FEIPL-SQGPQMLMPMGPQFKEH-	--RHGIKSPSKGRISLTF-	--RKLTRQEPPWVTTAPT-	-VQKGV-	878
APV1:YP_009094347.1	FCGEADFT-VVAKKGKRDGVVN-	-ATCHM-KTGFQFTMDMSNFQSY-	--QHSVNCSEGRSITL-	--RHYHNNIAGLP-	-IKHTCG--EFGDTS-	923

AgVT			617
PVT:YP_002019748.1			618
PVT:ADX41471.1			618
PVT:AFU55321.1			619
PVT:AXK90539.1			619
PrVT:YP_009051684.1	KRS		786
PrVT:AHM92766.1	KRT		786
ZoVT:OBS17025.1	KVR		826
ZoVT:OBS17031.1	KVR		826
ChVT:QNG41875.1	RSD		796
FiT:QED42804.1	RSD		796
TrTA:QED42832.1	RSD		888
GVA:NP_619662.1	EED		755
AcVB:YP_004935358.1	EET		750
ASGV:NP_044335.1			600
YaVa:YP_009268859.1			600
RAVA:YP_009553496.1	-QSEGNE	-TDSMSVG-	844
ACLSV:NP_040551.1			847
GPGV:YP_004732978.2			832
CtChV-1:YP_009103999.1			854
CtChV-2:YP_009103996.1			850
DiVA:YP_006905850.1			665
ObRV1:YP_009408144.1			665
CLBV:NP_624333.1			974
CLBV:AFA43536.1			1000
AVCaV:YP_008997790.1			649
CPvV:YP_009505632.1			1001
WVA:YP_009357235.1	-KED		778
WVA:QEAE69426.1	-KED		778
CRMvA:YP_007761581.1	-SDDGGGFYFEEINK		996
CTLaV:YP_009046478.1	-SGNEEDDSYYEEMNK		916
Phl1BV:YP_001552317.1	-QEPESPDTDEENELDKEKLSEDEAGGSEEKE	-VEAEPGSSD--QSGECCGSEASRDETLA---VDMEC	922
GCLV:YP_004936159.1		-GVDFSSFT-	864
ASPV:NP_604464.1	LKALERRSHQSRRPAVELEGHEREKVNDSDSAPVQEFLIQIDSSLLEYALKSLSGLSKNVNCDMLCNSPWLKEELRFSEALRDLAFAQGLIQLDFLCLKVLRCAEVNR		993
APV1:YP_009094347.1			923

AgVT		617
PVT:YP_002019748.1		618
PVT:ADX41471.1		618
PVT:AFU55321.1		619
PVT:AXK90539.1		619
PrVT:YP_009051684.1		786
PrVT:AHM92766.1		786
ZoVT:QBS17025.1		826
ZoVT:QBS17031.1		826
ChVT:QNG41875.1		796
FiT:QED42804.1		796
TrTA:QED42832.1		808
GVA:NP_619662.1		755
AcVB:YP_004935358.1		750
ASGV:NP_044335.1		600
YaVA:YP_009268859.1		600
RAVA:YP_009553496.1		844
ACLSV:NP_040551.1		847
GPGV:YP_004732978.2		832
CtChv-1:YP_009103999.1		854
CtChv-2:YP_009103996.1		850
DiVA:YP_006905850.1		665
ObrV1:YP_009408144.1		665
CLBV:NP_624333.1		974
CLBV:AF443536.1		1000
AVCaV:YP_008997790.1		649
CPv:YP_009505632.1		1001
WVA:YP_009357235.1		778
WVA:QEAE69426.1		778
CRMvA:YP_007761581.1	CSITSAPDSVKCSLSVFPVKADGDCFWHAVS	937
CTLav:YP_009046478.1	CSISSAPDSAKCSLSSVFPVKADGDCFWHAVS	947
Ph1Vb:YP_001552317.1	CTIEYKEMPKIGKYKVNVDVRGDGNCFWYALE	953
GCLV:YP_004936159.1	-QYGVTLSSHMSKAPDGRIEPQRGDGSCFHHCMC	900
ASPV:NP_604464.1	IISELPVTHVPLRGTMHVLDDEISRGDVKEGSFSGFRRKWVMSCTDLIMLAFLKPKMTLGGERSHEDCECLSDTEKLHGCSVILSRKFEPDLFHFSFDVEADGNCFWHHS	1108
APV1:YP_009094347.1	-LFDVLIRRSFSYSSKNFHTFPVPGDGGSCFHLSG	957

AgVT	VMRVKIEMVLAIL-CGRD--QTWADWFLKDIAE LADVEKALSDLPLAIHTE--DGVHKVD--GQG----FKEVELWLHDHNHFV-----EPLSFAQMKGKSRF-----728	
PVT:YP_002019748.1	ITGTKREITLSSL-LGRD--GTAWDWFLKDKGATFDDFKAVSDDLNCITCK--EGSNFAH--VNR--NYKHNFLYLFDEHVS-----ERPKVMLFEQVRHQK-----730	
PVT:ADX41471.1	ITGTKREITLXXL-LGRD--GTAWDWFLKDKGATFDDFKAVSDDLNCITCK--EGSNFAH--VNR--NYKHNFLYLFDEHVS-----ERPKVMLFEQVRHQK-----730	
PVT:AFU55321.1	ITGTKREITLSSL-LGRD--GTAWDWFLKDKGATFDDFKAVSDDLNCITCK--EGSNFAH--VNR--NYKHNFLYLFDEHVS-----ERPKVMLFEQVRHQK-----731	
PVT:AKX90539.1	ITGTKREITLSSL-LGRD--GTAWDWFLKDKGATFDDFKAVSDDLNCITCK--EGSNFAH--VNR--NYKHNFLYLFDEHVS-----ERPKLMMFEKKHQV-----731	
PrVT:YP_009051684.1	HLCMNRSAVFNL-FDQD--KSVITNLEDKGFTLSEVIDHLMNLDPGRIVSN--GEVINYL-EKG----SFKPIDLMLMRDGHIGL-----NQHDVLYDTKEVKE-----905	
PrVT:AHM92766.1	HLAMNRNGVFNL-FDQD--RSVLTNVVEDKGFTLAEVIDHNTLDLIPGRIVS--GEVINYL-EKG----SFKPIDLMLMRDGHIGL-----NQHDVLYNSKDIRVE-----905	
ZoVT:QBS17025.1	FLKMRSCQTISVM-YSDY--DAILDLIVNDKGFTVAEMINILIKMDIPGVIFDG--KKNIRYL-EHG----SYTDIFLRVREDHVSM-----ESLMDCTETGLNIID-----943	
ZoVT:QBS17031.1	ITSLTRTQVISTL-IALD--GSWISKVINDSLVLESEVISALTALDIPGSINSK--GVRIDYL-REG----AFKPTHLLRVRDEHIC1-----EQTEAGTSLGEFTFK-----915	
ChVT:QNG41875.1	HSLSLTRAOTQISTL-IALD--GSWISKVINDSMVLESEVISTALDIPGSINSK--GVRIDYL-KEG----AFKPTHLLRMRDHEHIC1-----ERTEAGTSLGEFTFK-----915	
Fita:QED42804.1	FLKMSRRESVFSL ISMD-DKWLQKININDVOTSSTEEMINTLVSGLPCKIMMN--GLIMPIN-GEG----SYDPIKLVRDVGHVSS-----ENGFEQEVMKMSFK-----926	
TrTA:QED42822.1	HMQLSTPSVIAIV-NGAS--PQTLREI-EDGGSYLATLVLNSKALDFPIAIEH--RGYAEPT----G-SYRRLHLKITSGHVPEP-----FEGVTSKGGFRE-----867	
GVA:NP_619662.1	AcVb:YP_004935358.1	HMVGKREVCASII-HSKM--PRAIEEF-KEGMSSATIFIHVKQLDLACYIQNE--RGNQIOP----G-KFREMKVATGEHMSA-----VLPGTATSTLAT-----862
ASGV:NP_044335.1	YVa:YP_009268859.1	FLGKDJDKDEFIEEI--ADSDNEDLLECDIEKDGLSHMIEEVLTKLGLSMVYTSF--FEDMSVLRNKFG--LRTGTYCTIRNHNCEL-----VDKACFKLKKLKYEH-----709
RAVA:YP_009553496.1	RAVA:YP_009553496.1	SVGKEVGLMVAE-ETDV--PIWKLLYLLDGLTPVETKMLDGLGVSKIRL--SKDRVIG--SCK----DWTTKVIKISKGHASC-LDIIG--CRPDLSVLRPRVKTV-----963
ACLSV:NP_040551.1	IIHKKPCEEIMMPI--PHIMDCRVNSRCGSLLDAKAIKEYIKECEGD--CGLVCG--TSG----LSIGRMRLGRNHFSS-----ASVRSSRSMDSLANSKEIK-----951	
GPGV:YP_004732978.2	OFVTKFDEVLAIKL--GTYLGDLANWGSVADWQFAEKLGLRVLNL-TNG--FVERAIG--VEG----PEMSMSFNSNHFRS-----NSNSRMNKGKV/ESEF-----930	
CtChv:1:YP_009103999.1	EIRISRSKLNLL-VKED--STFLIKIKDKGLTIDDLSSIANLNLNSVRVLIID--GQWSYFG-VKES-----NYRLSLSLKLKIRHFSV-----YNGEVLKALGDESSDKL1-----971	
CtChv:2:YP_009103996.1	EIKIISKEKLSLNLL-INED--PTFLDIIKDKRDMTIDDLKESNLLCVRVLDID--GOQWSYFG-VKES-----NFGRVSLGRLSNSHFD-----YEKEISKIALGDEVESEKKVQ-----968	
DiVA:YP_006905850.1	CLBV:NP_624333.1	CLNLDLFLVNL--KG--SVFIELLKQDGLLESEFEDLDDLLGNNENVMMA-----CTESSGIFLSSHHNCRF-----ISKEECGDWFVNFKVG-----774
ObrV1:YP_009408144.1	AMRSKQOAIIAKLTKTVNS--PFWNSRSLSGNGGSVSECLAAEGLTVDLFLVND--GKCVVLG--KG----ALRZSMLRNHFSS-----INAQMLERTFVSHL-----L 1081	
CLBV:NP_624333.1	ALNRGMOAIIAKLTKTVNS--PFWNSRSLSGNGGSVSECLAAEGLTVDLFLVND--GKCVVLG--EG----AVRSLSLKDNNHFSS-----VEEHRSLQRFTFVSHL-----A 1107	
AVCa:YP_008997790.1	ALGOTSNVANKI-VAQR--PDLQCVLDDMLDKOTTEITCIVMLHATIVNEDEGETMELN--PEG----LTKFSVLDLDEHMMV-----L 747	
CPrV:YP_009505632.1	CPfV:YP_009505632.1	LEKRPLYDILLAIKKNK--NYWTSFLEFGVGGTLDLNOQAEDLSFRFELYMN--EKWIAAGG--NRG----PIYRLNLSDDHFVSHRELSGNVETDQLNFSKAQS-----1114
WVA:YP_009357235.1	WVA:YP_009357235.1	FFHFEVKFLANKL-AQON--ELLSDWINNSNGADSTIMAISLKMRLNVPFGLD-EKSFE--PDGYDIPESKIVDLINEEHTL-----LNRSDVLRMSNAQKCLMGLE-----915
WVA:QEAG9426.1	CRMa:YP_007761581.1	FFHFEVKFLANKL-AQON--ELLSDWINNSNGADSTIMAISLKMRLNVPFGLD-EKSFE--PDGYDIPESKIVDLINEEHTL-----LNRSDVLRMSNAQKCLMGLE-----915
CRMa:YP_007761581.1	CTLaV:YP_0099046478.1	FLQKNPPTKVLVSLSANCS--KDLNLHMSLQGKQEEFFLEEFYFDFRGINAVNEFE--GKAYNPN--ETG----HLLPAAPFLDKDHGIEF-----IGRNSPSTVPMRMR-----1142
Ph1Vb:YP_001552317.1	Ph1Vb:YP_001552317.1	FLQKNPPTKVLVSLSANCS--KDLNLHMSLQGKQEEFFLEEFYFDFRGINAVNEFE--GKAYNPN--ETG----HLLPAAPFLDKDHGIEF-----IGRNSPSTVPMRMR-----1147
GCLV:YP_004936159.1	GCLV:YP_004936159.1	GLGRKTDIYLVSLRSPH--SDIFQFATGVLLTLELEPIFOCFQDARVLGC--SEFTVTP--TSG----TFALDFELDAGDHLFS-----KSARKEVETVSSLKV-----1094
ASPV:NP_604464.1	ASPV:NP_604464.1	ALNRREVDTVAVLGKPAH--EDLFEEVAEGRGSFISDLTRLFEIFSICGSVDTG--GELIMVN--ENG----RIPAEFSLEKEHLAH-----IPTLSRRKFSPIVSD-----1301
APV1:YP_009094347.1	APV1:YP_009094347.1	TLNQTEAKLISVIGRPNN--RLILEGLVEGEGLNLIEDLEAFAVSFGICARVSTE--RGVFTLN--KEG----NLHANYELSKHIMY-----LKKASSSQFAPTNPI-----1154

AgVT	-----TEKRDIFSKMSGNKCFFLT-----KYPFEEIERADALIKSMKATYGVVMSKFOKTPMLNGAP-----785
PVT:YP_002019748.1	-----IDFLGAFEKCPGAGKF-----RYEALEAERGSLASALKDNLTGVISSKFNWDPKCEFV-----784
PVT:ADX41471.1	-----IDFLGAFEKCPGAGKF-----RYEALEAERGSLASALKDNLTGVISSKFNWDPKCEFV-----784
PVT:AFU55321.1	-----INFLGAFEKCPGAGKF-----RYEALEAERGSLASALKDNLTGVISSKFNWDPKCEFV-----785
PVT:AKX90539.1	-----VNYLGFANECPAGR-----EYEALEAERGSLASALKDNLTGVISSKFNWDPKCSFD-----785
PrVT:YP_009051684.1	-----ELIGADII-----RPHFSVERARVLVKSMSMEGTMGVLNFRKFHAFNELPR-----951
PrVT:AHM92766.1	-----DLIGADVI-----KPNFSVERARVLVKSMSMEGTLGVLNFRKFHAFNELPR-----951
ZoVT:QBS17025.1	-----ESLEMGSANRV-----HPSYSVERARVCVMCKSLQEGATGIVLTKFKFEPFNKILP-----992
ZoVT:QBS17031.1	-----ESLEMGSANRV-----HPSYSVERARICMCKSLQEGATGIVLTKFKFEPFNKILP-----992
ChVT:QNG41875.1	-----KMCERE-LTEV-----KAESYAERARKLKSQEGATGK1LNRFKVGFKVNTM-----963
Fita:QED42804.1	-----EAIKSKNLSNADSLFDLGFLRNFVHRAVLAKSLSNRLQGK1LNRFKVGFKVNTM-----975
TrTA:QED42822.1	-----AMLLGDDGVGV-----HPRFDKADRLAQFMSQEGATGIVLTKFKFEPFNKILP-----M 911
GVA:NP_619662.1	-----ALDFNPDSVRL-----SEITQSRATLESFREGFTGVNNKYYKQRP-----N 906
AcVb:YP_004935358.1	-----AQMNSNENLADSLFDLGFLRNFVHRAVLAKSLSNRLQGK1LNRFKVGFKVNTM-----S 765
ASGV:NP_044335.1	-----VKLNGSNLTPESLFDNGKVK-----SEITQSRATLESFREGFTGVNNKYYKQRP-----C 765
YVa:YP_009268859.1	-----VKLNGSNLTPESLFDNGKVK-----SEITQSRATLESFREGFTGVNNKYYKQRP-----C 765
RAVA:YP_009553496.1	-----SDG--VLDHVTNFNFHRLK--LVEPDLTNA-----DIXDSSRAGKLLKSLMDGTMGIVSHNSTHEGWRMIKGINSTSEM-RSFMMMVNRQGIEEPKSDLFDK-----1043
ACLSV:NP_040551.1	-----PKEFARKVSDE--MSNDANQPIQNLNE--YVGVLNQFT-----IFKLPDKRAORLNLKSLDQGTTGVCNLSKLEGKWMIPNAKSVFVTKNYIN-----SSDI-WK-----1022
GPGV:YP_004732978.2	-----KLDSDGFYNSF-----LNKDID--PRKNFVNFK-----DRMFNFERAALIHSRGSTQVTFSSGNNVGDYFSGRKRNIDP-ESF-----RDPKF-LK 1051
CtChv:1:YP_009103999.1	-----LQRDID--PKNEFVNRF-----ERVIDLDRAKLIIDSQKGTGIVLTCVNC-----KF-----DDPSF-LK 1048
CtChv:2:YP_009103996.1	-----FLDFTGVSSI-----IKNVNDYKRSKLYDLSLSKGTGVSFNMKIKKNDDESEKKDKNRV1-----EMMNF-----FEDEI-NE 844
DiVA:YP_006905850.1	-----GLISLPGDNLVYLN-----LKDINCIKRAGLFLKSLSRGTGKLNFKDNLKNSKIK-----EFLNLI-----FOND-DH 844
ObrV1:YP_009408144.1	-----EKGIVNVLEGFDAMLSGD-----VGAAGVNKI-----OFAANFEFARILANSFLNMTTGICLGLKADNGEKFVHLI-----L 1148
CLBV:NP_624333.1	-----KKSNLVRMVDGLDEMLOSE-----MSTGVNCV-----QFIADEHARVLANSFLNMTTGICLGLKADNGEKFVHLI-----S 1173
AVCa:YP_008997790.1	-----DIPNCRSKKGIDICMSPDLANSNCAANYE--UTCQNQLOV-----QYQADHERA1KLMNSLAGTGTGIVLNLVFGSRSLFMD-----SV 827
CPrV:YP_009505632.1	-----SNFSDDDDNSFDLSDIEH-----VNXS-----LFPFLNDAEELLRQSFNRTTNGK1LSDAFAENGHLRR-----I 1178
WVA:YP_009357235.1	-----DRMEVNIVKVRMEGNSQNNRRQKLVNNVIEE1LNFPSSSE-----KFLAKKENALILMCKSLMSMSTGICLSEHVNHKDQFMKLS-----A 995
WVA:QEAG9426.1	-----CRMVNIVKVGQNEFGSHNRQKLVNNVIEE1LNFPSSSE-----KFLAKKENALILMCKSLMSMSTGICLSEHVNHKDQFMKLS-----A 995
CRMa:YP_007761581.1	-----PSGCPMIAIEKY--DEFRLRNSANV-----PFTPSLPLAKKLADLSLQSGTGWVNSKIVAGQDFWLAN-----1203
CTLaV:YP_0099046478.1	-----PSGGOTIPTEQV-ETFLRGNANV-----PFTPSLIAAKLKLNSLQSGTGWVNSKIVTSQGYDWAD-----1213
Ph1Vb:YP_001552317.1	-----VNTLTVPSNLLIIKAASTG-----EFPDPSRAKCLADCFHTGCTGVNNKIFNNESEHLAH-----V 1207
GCLV:YP_004936159.1	-----VEASPHGRRLVNCAGTGV-----LFEFICNTAHLAEQSLDFTGRTGIVVNSKLFNNRERFEVS-----1150
ASPV:NP_604464.1	-----LNRVNSA--MRFLAINGAEV-----DVRPSIDRASRLLDSEIIGATGVLCOGKIEAQDOLASK-----1358
APV1:YP_009094347.1	-----QNFNGQP--EFLRGLIVSEV-----DVKPSWGRARNLEESLNLNGTGLCDRTNLQKNWLTV-----1211

AgVT	-----DLTVGCLFGFAFGSGSKRELTVLRCYFNR-----HDTLIIISPRKLFIAEFAIHDLTAVA-----STKMN-----843
PVT:YP_002019748.1	-----IEKEILVWAGFGSGKTRGICQIVKSMFNN-----KKTVLSPRKNLADDWVKNLANL-----HRPSH-----842
PVT:ADX41471.1	-----IEKEILVWAGFGSGKTRGICQIVKSMFNN-----KKTVLSPRKNLADDWVKNLANL-----HRPSH-----842
PVT:AFU55321.1	-----IEKEILVWAGFGSGKTRGICQIVKSMFNN-----KKTVLSPRKNLADDWVKNLANL-----HRPSH-----843
PVT:AKX90539.1	-----VKKIEVLSVGFAGSGKTRGICQIVKVRMFK-----KTTVLSPRKNLADDWVKNLANL-----HRPSH-----843
PrVT:YP_009051684.1	-----HENRVMCIAGFGSGKSRALQGVCAVSLNK-----KVNVLSSPRKNLLRDWEKSID-----KLKGKRL-----1011
PrVT:AHM92766.1	-----HGNKVMCIAGFGSGKSRALQGVCAVSLNK-----KVNVLSSPRKNLLRDWEKSID-----KLKGKEMH-----1011
ZoVT:QBS17025.1	-----HSNKTFCISGFAGSGKSRG1QDLCGILNS-----ENVIILSPRSNRLSDWEKKIRN-----GLNNQNFK-----1052
ChVT:QNG41875.1	-----FARTFVSMGFGAGSGKSRG1QDLCGILNS-----KKTVLSPRKNLIEDWRTKVVK-----GLNGQMK-----1022
Fita:QED42804.1	-----FARTFVSMGFGAGSGKSRG1QDLCGILNS-----KKTVLSPRKNLIEDWRTKVVK-----GLNGQMK-----1022
TrTA:QED42822.1	-----KNDCYTISGFAGSGKSRK1QIEIYSTYGNR-----SDVLICSPRKLILLDDWQSKIER-----KLNGKNL-----1034
GVA:NP_619662.1	-----HTGEIEPEKVLTAFFGAGSGKSHWCQTLKHCVS-----KVLVISPRKVLRDDWVAKISK-----969
AcVb:YP_004935358.1	-----GTDIDNLTDIVYGLFGAGSGKSYQPTQLRNCNMK-----DTLVIPRVLKADWKEVKDKD-----964
ASGV:NP_044335.1	-----ELPFENSSVWGLRLFGAGSGKTRGICQIVKSMFNN-----KRMFISPRMALLADEVEPOLKG-----TA 824
YVa:YP_009268859.1	-----NYLDPHFEFSDLGLMRLGFAFGGKTPMLDILKKS-----NNDILILVPRKRLGDSWTSKMGH-----KKN-----1074
RAVA:YP_009553496.1	-----VEFKAIDLMSFSLMGFAFGGKTPMLDILKKS-----SQGIMIVCPRFLAKDWSEKVKD-----KKN-----1093
ACLSV:NP_040551.1	-----EMTKGDAVVKGAVILFGAGGGKSRPVQMALSDMSP-----LNLISPRVNLLLADWKKVNN-----GN 1081
GPGV:YP_004732978.2	-----KLGEIPEKVLTAFFGAGSGKSHWCQTLKHCVS-----M KILLISPRVNLLLADWKKVNN-----GN 1111
CtChv:1:YP_009103999.1	-----EMTKGDAVVKGAVILFGAGGGKSRPVQMALSDMSP-----LNLISPRVNLLLADWKKVNN-----GN 1108
CtChv:2:YP_009103996.1	-----KLIGEEFLTKGAIIIGFAGGGKSRPVQMALSDMSP-----DGCCTVTVSPRVLLELLDWEKKVNN-----ANKK-----907
DiVA:YP_006905850.1	-----KDRVKQIGIDVTMVGFGAGSGKSRKLQSLWHSRKKG-----KGFVIIISPRSELLKDQWSKVKT-----QNKH-----907
ObrV1:YP_009408144.1	-----EERPKLQIGDFDTAICFGAGSGKSRQSLQSLWHSRKKG-----NFCVVSPPRNLNAADWFAKL-----EPNEQ-----1235
CLBV:NP_624333.1	-----NERKSDFVEELSFVPGFAGGGKSLGLNEVKRISREIHLAKEKKGMKGKGSKGKHEKKERNRGLNSKMCIISSPRNLADDWTKLGP-----SALEH-----918
AVCa:YP_008997790.1	-----VKSDDPFPEEVYFSCFGAGSGKSLQSLKLSKNSFL-----LKVLLISPRVNLLLADWKKVNN-----SS 1237
CPrV:YP_009505632.1	-----SKREGDIISDLTVWSGGGGKSRSLQELIKEKKG-----VRFIIISPRNLNAADWFHEKVNDSLDAKENDAEKKGK-----1067
WVA:YP_009357235.1	-----TNKLCFDERIGAIVGTFGSGKSHNIELIRHNLGY-----QNLIIISPRNLKDQFINMLDLVN-----ARSKGKTS-----1271
WVA:QEAG9426.1	-----TNKLCFDERIGAIVGTFGSGKSHNIELIRHNLGY-----QNLIIISPRRLSKEQFINMLDLVQ-----ARSKGKKAS-----1281
CRMa:YP_007761581.1	-----NINDRPTVQINSVLGTFGSGKSSLRFFDANPK-----GTVYSPRRLADEFERQKLENAV-----VRTKRRKGASSKNGAGASTGPDPN-----1298
CTLaV:YP_009046478.1	-----STSLPLRNLTVNCAGTGV-----CIFTVPRRSLAEQMTQLQVOSV-----ETSTS-----1210
Ph1Vb:YP_001552317.1	-----LIPELVHERKLIMILGTFGGGKSSLRFFDANPK-----AIFTVPRRSLAEQMTQLQVOSV-----ARVGGKTKGSKSD-----1428
ASPV:NP_604464.1	-----DRKLNDNSRNLGVGLVGLFGSGKSSLRFFDANPK-----SIVFVSPRSLAEQMTQLQVOSV-----KR--GKSLR-----1277
APV1:YP_009094347.1	-----*: * * *.
	-----*: * * *.

AgVT	- - - - - IJKVFTWGLKSL	- - - - - ITK - AQQVIDEISLPPGGLDCLLAKKK	- - - - - AQVWVLGDPQLQTRYHSKDDALT - - - - - KQDHT	914
PVT: YP_002619748.1	- - - - - KVMTFEAGLRR	- - - - - VQK - SSSLVIDELSMPNGYLDMILNM -	- - - - - NEATFTLFDPLOARYHAKSDVLRV - SPENDV	912
PVT: ADX41471.1	- - - - - KVMTFEAGLRR	- - - - - VQK - SSSLVIDELSMPNGYLDMILNM -	- - - - - NEATFTLFDPLOARYHAKSDVLRV - SPENDV	912
PVT: AFU55321.1	- - - - - KVMTFEAGLRR	- - - - - VQK - SSSLVIDELSMPNGYLDMILNM -	- - - - - NEATFTLFDPLOARYHAKSDVLRV - SPENDV	913
PVT: AXK90539.1	- - - - - KVMTFEAGLRR	- - - - - VQK - SSSLVIDELSMPNGYLDMILNM -	- - - - - NREATFTLFDPLOARYHAKSDVLRV - SPENDV	913
PvT: YP_00451684.1	- - - - - IJKLRTFELAISAIT - RMVKKEQDGKLTVIDEAT	- - - - - LLPGGYLDLNVSLNPEVG	- - - - - STIILFLDPLOSHYSSKSDVR - - - - - VNLPVG	1088
PvT: YP_00451684.1	- - - - - IJKLRTFELAISAIT - RMVKKEQDGKLTVIDEAT	- - - - - LLPGGYLDLNVSLNPEVG	- - - - - STIILFLDPLOSHYSSKSDVR - - - - - VNLPVG	1088
ZoVT: OPS17025.1	- - - - - IJKLRTYETGIIIEINKRDRYTD - - - - -	- - - - - KPIIIIDEVSLLPGGYLDLINSIPIEG	- - - - - STMLVIFIDPLQSSYYSPKAHV - - - - - HSLPDI	1128
ZoVT: OBP17031.1	- - - - - IJKLRTYETGIIIEINKRDRYTD - - - - -	- - - - - KPIIIIDEVSLLPGGYLDLINSIPIEG	- - - - - STMLVIFIDPLQSSYYSPKAHV - - - - - HSLPDI	1128
ChVT: QNG41875.1	- - - - - VKLRTFEIGISALS - RLAIRGE -	- - - - - PLN2IIIDEVTLPMPGGYLIDLCSCLAPEG	- - - - - SIIIVGDPQCAGYYSKDDVG - - - - - RNLGKA	1097
FtIA: QED42804.1	- - - - - VKLRTFEIGISALS - RLAIRGE -	- - - - - PLN2IIIDEVTLPMPGGYLIDLCSCLAPEG	- - - - - SIIIVGDPQCAGYYSKDDVG - - - - - RNLGKA	1097
TrTA: QED42832.1	- - - - - IJKLRTFELAIKTQ-SRSRKRL -	- - - - - ETLFLIDEVSLLPGGYLDLNCNSLVEG	- - - - - SVMIMIFDPLQASFYFSKKDH - - - - - RNLGDV	1109
GVA: NP_619662.1	- - - - - HRVTFVFAVFMDB - - - - -	- - - - - DYG - CKD1IDEIGLPPGYLDLVIAAHQPR	- - - - - TLVLGLDPQLSTYHSKRDNVLEASQEDD	1040
AcBV: YP_004935358.1	- - - - - AIVRTFESAFNG - - - - -	- - - - - RKG - YENIIDEVGLLPPGYLDLVANHQFN	- - - - - TMLLGLDPQLSTYHSKRDNVLEASQEDD	1040
ASGV: NP_044335.1	- - - - - COVHTWETALKK - - - - -	- - - - - IDGT - FMEVFVDEIPLPGYLTLLQMCARFKVQKQSENF - - - - -	- - - - - LKGKLLELSCKTLCNRKFGDPLRYYSAEADTNLL - DKTHD	917
Ya: YP_009268859.1	- - - - - CHCETELEVAKG - - - - -	- - - - - VDLS - YTEYIDIEGLMPGTYLTLAAAMGKSIKSFSDDK -	- - - - - KFEAEKFMCPKLPRFCNLQDPLCQRYCTEDNDALL - KVKDEI	917
RAVA: YP_009553496.1	- - - - - VRVNTYERMKCL - - - - -	- - - - - SFAN - YDYYVIEDEIPLPGSFEDDLTLKWHASA -	- - - - - GANEKKMIVFVDPQLQAGYSSPKDHRL - - - - - VARDA	1149
ACLSV: NP_040551.1	- - - - - KDIKTFESALKS - - - - -	- - - - - DVKG - KRLFILDETSLLPKGFTDMLLMKHM -	- - - - - GILKSTCIVGDPQLQAGYFCKPDNDYL - SREGEI	1180
GPGV: YP_004732978.2	- - - - - LKMTFESAIKG - - - - -	- - - - - CLAG - YKWIILDEVTLPFNGYLDLNLVLAHY	- - - - - NEINLKHITLVDPLQANFYNERDCNL - GSVKVM	1158
CtChV: 1:YP_009103999.1	- - - - - VTFTKYESALKE - - - - -	- - - - - NLSK - FSLIIIDFELTPTRGTYDVIAYKSVD -	- - - - - NLCTRLEKKVTKLTLQDPLQASFYSESSDDLL - AQQGEI	1193
CtChV: 2:YP_009103996.1	- - - - - LILKTYESALKE - - - - -	- - - - - NFAE - FSMIVIDEFLVPPRGYLDVAAFKSKMD -	- - - - - CKVCKSKPRIPKFLLLGDPQLQAGYNNALDDHL - PEKSEM	1199
D1VA: YP_006905850.1	- - - - - IRFSTYEKALTL - - - - -	- - - - - SYEE - DELVWDEIQLPPGYLISLSSLVTAFR - VNKISHNIRLSKRNYSQVYENQNSRSLVLLGDHQLQGRYNNESDFRSL - SQPDEI	- - - - - 1002	
ORv1: YP_00948144.1	- - - - - IRFLTFLERATV - - - - -	- - - - - TYQE - SELVIDEIGLMPGYSMLNIIITSK - FEEVSNFRNLSRNRNFRNFGSPRSRVLVLDGHQLQGRYNNDSDFRSL - DPKDEI	- - - - - 1002	
CLBV: NP_624333.1	- - - - - RKVSTFEKFIFT - - - - -	- - - - - DKSX - LDLVWDELTLPFNGYLDLVLVEYADV -	- - - - - NRHCQILFLDPQLQARYHKMHDSEVL - TFEHDF	1285
CBLV: AF43536.1	- - - - - RKVATFESFIKM - - - - -	- - - - - DKSX - DLMVLDWDELTLPFNGYLDLVLVEYADV -	- - - - - NSHCHLILFLDPQLQARYHKMHDSEVL - FHEFDV	1310
ACVa: YP_008997790.1	- - - - - CCSVTFVFLVKA - - - - -	- - - - - STSK - IKLWVDELTLPFNGYLDLVLVEYADV -	- - - - - SPDKLILFLDPQLQARYSDASQDRAIL - GSEHDF	993
CrPrV: YP_009056532.1	- - - - - HKVCTFVELVALQ - - - - -	- - - - - NLSR - VELIVEDLGLPFPRGYLDDMLFKLRT -	- - - - - KNFKGVKMLVFLDPQLQARYHSDSDFERL - HIEHIC	1313
WVA: YP_009357235.1	- - - - - VIKKTFESALKM - - - - -	- - - - - NLGX - SDVIVLDELSLYPNGYLDDLIHLSLGL -	- - - - - NVNMPLRVVIGCPQFQARYHSLSDEHL - TFDHEI	1143
WVA: QEAG9426.1	- - - - - VIKKTFESALKM - - - - -	- - - - - NLGX - SDIIVLDELSLYPNGYLDDLIHLSLGL -	- - - - - NVNMPLRVVIGCPQFQARYHSLSDEHL - TFDHEI	1143
CRMvA: YP_007761581.1	- - - - - TDVVTFEVALKK - - - - -	- - - - - GLLK - KARIFIDEAQPLLPGYLDLCLTLAGSD -	- - - - - SISLVMGDPQAQSSYSDAESDRMMAGFDGKCL	1345
CTLav: YP_009046478.1	- - - - - TEVATFEVALKKT - - - - -	- - - - - GMKL - KVRIFIDEQQLLPPGYLDLCLTLAGSD -	- - - - - ASILVMGDPQAQSSYSDAESDRMMAGFDGKCL	1355
PhLBV: YP_001552317.1	- - - - - SQAERMKRKNWLVCFTEILKCIH - - - - -	- - - - - LVPK - GMALIDEQTLQYPPGYLDLCLTLAGSD -	- - - - - VHHIVGGDPLQSDYDNEKRNRLWSLNPPCI	1375
GLCV: YP_004936159.1	- - - - - VTIILTFFKLFHOMV - - - - -	- - - - - NVKE - GSTT1IDEFQQLLPPGYLDLCLTLAGSD -	- - - - - ISLHLLGDPQCSDYDNAKDRGFLPGLD	1285
ASPvN: YP_604464.1	- - - - - LKNVRVKTFFELHLHD - - - - -	- - - - - SIKE - GHFTVVIDEQLLPPGYLDLCLTLAGSD -	- - - - - VNIIAAGDPQCSDYDCSSRHFAGFESDII	1506
APV1: YP_009094347.1	- - - - - VRVLTLESFIKAV - - - - -	- - - - - FTFK - AASVVLDEQVLPYPPGYLDLCLMCLSLN -	- - - - - CQIYLAGDPQCSDYDSAKDRAFLDGLKGD	1351

AgVT	PVT:YP_00219748.1	DRT---KJERYLLLSRHLSE--LSYM-----FEPFLSSEKEKLHEHL-GKIQYREQEL--SVDLKGSQDVWLAQVSQNMKRKY-----SHRGVPKTGFGVQTLTFNF-C	1003
PVT	ADX41471.1	DRI---KVPKYLFSKRMSELDF-----FDVRCSDDQKKWELH-GKQYREPAAL--FRDIKGQEFTILSPSFETAREMSKYAD-IDKGCKSMFTGESQGLTVNK-A	1006
PVT	AUFS5521.1	DRI---KVPKYLFSKRMSELDF-----FDVRCSDDQKKWELH-GKQYREPAAL--FRDIKGQEFTILSPSFETAREMSKYAD-IDKGCKSMFTGESQGLTVNK-A	1006
PVT	AXK90539.1	DRI---KVPKYLFSKRLSELDF-----FDIGCSDDQKKWELH-GKQYREPAAL--FRDIKGQEFTILSPSFETAREMSKYAD-IDKGCKSMFTGESQGLTVNK-A	1007
PrVT	YP_000951684.1	DTRPIFG-QEFRRYGRGSYSPFLKFDFE-----DFE-YGHGDDVDPNH-MRVFQAPOQ-----VREA1KRPVFLCPSDDKRSLE-----SNFGEAYTFTGTSQGLTFDF-V	1176
PrVT	AH92766.1	LTPFQY-QEYRYGRYTYRPFELKVE-----GFE-FGGKEDDKNH-MRIFQAPOQ-----VREA1KRPVFLCPSDKRNEL-----SNFGEAYTFTGTSQGLTFDF-V	1176
ZoVT	OB517825.1	FEPLYG-QSFQDYKVVSYRFGLDFKIE-----GLSMMGMEISEHH-MKIFKOPEA-----VVKVFKSDPFIISPSPEAKANEL-----RRYGDSTYFTGTSQGLTFDF-V	1217
ZoVT	OB517831.1	FEPLYG-QSFQDYKVVSYRFGLDFKVE-----GLSMMGMEISEHH-MKIFKOPEA-----VVKIILNDPFIISPSPEAKANEL-----RRYGDSTYFTGTSQGLTFDF-V	1217
ChVT	QNQ41875.1	MDPLNN-CFPYFLRTHRFPLKFDFDVE-----GLQFLGKQEISEFH-MHEFGSPEA-----VLKKIEKPIFLCPSDAKRAEL-----SHYGDAYTFTGTSQGLTFDF-V	1186
Fita	QED42804.1	MDPLNN-CFPYLYRTHRFPLKFDFDIE-----GLQFLGKQEISEFH-MHEFGSPEA-----VLKKIEKPIFLCPSDAKRAEL-----SHYGDAYTFTGTSQGLTFDF-V	1186
TrTA	QED42832.1	FEPLYG-TSKFYLYQTYRFRKFQNFQE-----NLVMSAALDENH-MKFYLQPE-----VRAAIERPIFLCPSEKREEL-----KRYGDAYTFTGTSQGLTFDF-V	1198
GVA	NP_619662.1	FNVRVG-KLPYLYCYSHLRPLRNCL-----FEIEMCGAESKRV-----YRSNRNLDEPTICATRAMKE-----EKGSWMYTVEQTSOLFLSKS-C	1118
AcVB	YP_004935358.1	FDRMLG---KKNLYKLTHRLSPNSQKL-----FDVPSKGSERSENLYK-----GAEGANDNLDIITASRAAKE-----KRQKGKSTIGEQSGLSVRR-V	1113
ASGV	NP_044335.1	DLMIKT-IHKHYKLFGQYRFGW---FOEL-----VNMPTRVDESFKS-----RKFFADIS-----SVKTEDYGLVLAKERDGFV-----AGRVPVATWESQESOMITISKR	1005
VaYA	YP_009268859.1	DIFRSKFNKFQYLFQFRGKFW-----FSEI-----VNIPTRDDESKHS-----RKFFPDMS-----KVDISKYKAVALGVPRREAKISL-----ASGLPVVTMSEQSLFTNGRV	1006
RAVA	YP_009553496.1	GRLIA---KEQPSLSSTRNRNEG---IERT-----FDVSEREGHGHA-----INNWSY-----DFKSVSMDMAVKVLFVPSLFRKELLISEACKIGCVNLLMTYQESGLTFERGV	1243
ACLSV	NP_040551.1	KRLFKG---GVNYKWHYSRINKF---IAKK-----LAITEFMNDIGIDEQ-SSTYKDMPSAHH-MFEGKGNHIEVILVAVSMVKE-----SNVNGVMFTGEQSGLTFNC-G	1274
GPGV	YP_004732978.2	DSVF---KDVKYQYQSYSRIPAN---VAGR-----FDWDKRNHREPIDCH-GTFYSDLSSAKL-HAKRCNQKIDVVLASeleKKYF-----SNQCKCITYGEQSGLTFD-Y	1251
CtChv	1:YP_008103999.1	SSELEI---DYPYRLLYSHRLRPLKG---MKSM-----MDINMLGSFEGETK-----WLKNYNSAAA-----AFSEKAFDVLVAGQRQKETFF-----GNFTVMTFGEQSGLTFNK-V	1280
CtChv	2:YP_009103996.1	ETLEI---RKPKYLYSHRLSS---LGGI-----LDVPMPLVLINEQ-LNLYNSAAA-----AFSERADVLVAGQRQKES-----SNYTMFTGEQSGLTFDK-V	1277
DiVA	YP_00905850.1	DFIMMN-EEILYNNLYSHRLNKHMFY-----PGVEMLGDEDII---SRRFSNFV-----AKKTIPEAQALLVRSARDEQVR-----KELDAKTFGEQSGLTFD-E	1089
OrBVI	YP_009408144.1	VFLMEN-EEILYNNLYSHRMSRSRHYK-----PGVFLNLDADSVP-----TKRFLNTLV-----AKKTSIPNAQVLAQVSHADEQH-----RDLGAKTFGEQSGLTFD-E	1089
CLBV	NP_624333.1	DRILLG-QNIEFYIYSTHRMSRY---FNRF-----FDVPCPNQDARTTEEQRLWIFDVSIPS-----ICSDRQPCPDLVWLSDELEKKAF-----SPINVMTFGEQSGLTFHN-V	1381
CBLV	AF44356.1	DRLIGG-QDLRYYIYSTHRMSKY---FNRF-----FDVPCPNQDATTETEQLWRLLWDVDSITS-----ICD1QDGEPDCVLDLVSDELEKKAF-----SPINVMTFGEQSGLTFHN-V	1406
ACVaV	YP_008997790.1	DLTLDG-SEVDMYOSKRFSEEEFLNEDLKKNEVDAESETRGKAGFR-----PRMTYNTLTMKV-----EEENOQNPIDVLYVGSFDEAGL-----ASSIKTMFTGEQSGLTFDH-A	1097
CrPnV	YP_009505632.1	DRITSG-AKINLYFLFESWRLSKFFGNF-----VDTIELRNSGSVNYE-----LDFPDNNHIVAA-----EAKKRGFPLDILVLASDEKNS-----AGKVNVLTFGEAQGLTVKH-S	1409
wWA	YP_009357235.1	DRIFKGNSAINYLAFLSHRLGTC-----FNCV-----FEGIECLGESEMEGS-----INVFKSFnNAAWA-----MEKQEQFFDLILVDSREKKEY-----SGLINVLTFGEAQGLTVNN-S	1240
WA	QEAG6426.1	DRIFKGNSAINYLAFLSHRLGVC-----FNCV-----FEGIECLGESEMEGS-----INVFKSFnNAAWA-----MEKQEQFFDLILVDSREKKEY-----SGLINVLTFGEAQGLTVNN-S	1240
CRMvA	YP_007761581.1	DRLLKG-KVYYLSELESKFRNPMFVG-----RLPCFTFDSRSLTL-----KEEYAVFDSFKAFAKDYLSPK1KTLVFSSTEKTWKVANM-----GRNVNLSFTGESTMNFVD-Y	1444
CTLav	YP_00946478.1	DRLLDN-KVYYLSELESKFRNPMFGL-----RLPCFTFDSRSLTL-----KEEYAVFDSFKAFAKDYLSPK1KTLVFSSTEKTWKVANM-----GRNVNLSFTGESTMNFVD-Y	1454
PhLBV	YP_001552317.1	DSVLEG-AEYQVYJKSFRNPKNGF-----RLPCFEGTQMGEOQA-TEEHLLYSLGHEH-LH1VQPFESKVFVLFSEEEKK1TEIHEAP-----GSNPTVLTGEFTGLNFKY-G	1474
GCLV	YP_004936159.1	QRILOG-IQFRYATRSYRFNSPNFVG-----RLPCAINSTNEDD-----EVOQE-IDCEVYCLVSIKFIQEAVRAL-----GLDKVQVFTGESTGLTYD-V	1379
ASPvN	NP_604464.1	MRLISG-RSYKFNLZSFRNPFVY-----RLPCNLNKLTRTL-----EEEYLTWDSIQF-----FSMGRKRDPCPVVLSEEEKK1IVAAHL-----KMCCKTGYESTGLNFKQ-G	1604
APV1	YP_009094347.1	FEVLSG-KKYKFNVNSSLRFQSEMFG-----RLPCRMDTKAMTE-----NENFHWLESIES-AAEVSNTEYDVVLVSSFEKK1IVWAHL-----GRDLEVLTGESTGLTFNR-G	1448

AgVT	VV/ICSDAHLVNSFAHNVVAL TRGRSGCCFLVDSVNDEKAVRINLQRLIEKAMSKKVNTFLRAMGVSLETAEFIG -	- VETFKTTEWEEKLEGDPWLKSVPVLPEYEF	1115
PVT:	VVQDDQLVLATSVLHWIIVAL TRSRQGVFVLVHKVFDMLTIQPVNSIIGLVRGVKQVENIFINTAGKLSEAEIVE -	- LETFKRTEDEDLLEGDPWLKGQLFCQSVELD	1118
PVT:	VVQDDQLVLATSVLHWIIVAL TRSRQGVFVLVHKVFDMLTIQPVNSIIGLVRGVKVSREHLINTAGKLSEAEIVE -	- LETFKRTEDEDLLEGDPWLKGQLFCQSVELD	1118
PVT:	VVQDDQLVLATSVLHWIIVAL TRSRQGVFVLVHKVFDMLTIQPVNSIIGLVRGVKVSREHLINTAGKLSEAEIVE -	- LETFKRTEDEDLLEGDPWLKGQLFCQSVELD	1118
PVT:	VVQDDQLVLATSVLHWIIVAL TRSRQGVFVLVHKVFDMLTIQPVNSIIGLVRGVKVSREHLINTAGKLSEAEIVE -	- LETFKRTEDEDLLEGDPWLKGQLFCQSVELD	1119
PVT:	VVQDDQLVLATSVLHWIIVAL TRSRQGVFVLVHKVFDMLTIQPVNSIIGLVRGVKVSREHLINTAGKLSEAEIVE -	- LETFKRTEDEDLLEGDPWLKGQLFCQSVELD	1119
PVT:	CISIDMDGSVTSDFHMVAL TRARRGCFCLTCASTMSDMNRAKLLVNLKEQKSFNFNLWNLGRALGARVARKGKDEFSLKGKTREEFESLESQEDGPWLKGMLNYLEGDDAN	- CISLDMDGSVTSDFHMVAL TRARRGCFCLTCASTMSDMNRAKLLVNLKEQKSFNFNLWNLGRALGARVARKGKDEFSLKGKTREEFESLESQEDGPWLKGMLNYLEGDDAN	1291
PVT:	CISLDMDGSVTSDFHMVAL TRARRGCFCLTCASTMSDMNRAKLLVNLKEQKSFNFNLWNLGRALGARVARKGKDEFSLKGKTREEFESLESQEDGPWLKGMLNYLEGDDAN	- CISLDMDGSVTSDFHMVAL TRARRGCFCLTCASTLSRNFKESNRAKLLVNLKEQKSFNFNLWNLGRALGARVARKGKDEFSLKGKTREEFESLESQEDGPWLKGMLNYLEGDDAN	1291
ZoVT:	VISVDMGDPVLVSNAHMVAL TRARKRGAFVVCSSITLNDKAKVTKIIKGVLVKAWSKDFMRASGKGMIDHANLIGO -	- SKGGRTREEFEDTLENDPWFQLTQLFLENPELQ	1329
ZoVT:	VISVDMGDPVLVSNAHMVAL TRARKRGAFVVCSSITLNDKAKVTKIIKGVLVKAWSKDFMRASGKGMIDHANLIGO -	- SKGGRTREEFEDTLENDPWFQLTQLFLENPELQ	1329
ChVT:	IISIDMDGPVTDNCNMVAL TRAKRGAFALNPCTIRRCDFLQRQSEGKGLHILKKQKVSMDFIKFMGGKIMRKARML -	- EAVGRTRREEFEEACEDGPWMKAQSLFLENIPIE	1296
Fita:	IISIDMDGPVTDNCNMVAL TRAKRGAFALNPCTIRRCDFLQRQSEGKGLHILKKQKVSMDFIKFMGGKIMRKARML -	- EAVGRTRREEFEEACEDGPWMKAQSLFLENIPIE	1296
TrTA:	VISLDLDPGTFISDAHMVAL TRRSRGKGFALPSCTIPLKKDFDTRLEGKLNVLNKVMGKLSLISYRLGQGVKMVENTYDNE -	- EAVGRTRREEFEEACEDGPWMKAQSLFLENIPIE	1310
GVA:	LITYLDEHWAKEEDVMVAL TRSRSGEIHGT -PALKKLITNATAKSTLLKKVGETYRREISEVRAKRH1PETTVLE -	- ESRLAETVYEARLADGPDYLKSSLALYDEIEM	1229
ACBvY:	KLV1DRDNGLNNKDVAKMVAL TRARLNTSVEVD -MSKMEHLVKHAKSSLLKLMFRGQMKIRELIMEMGTDGDLVIELE -	- ETRFADSDMDMLEKLSQDPLGKLLRLYDQDVE	1224
ASGV:	LCILDNLFGAGANAAVITATRSKVGFFDLK -GNSLKEVORMAQTIQFIEIIGKSQIPMVERINM -	- DVGNSLSQDKASNDLFPMIPINLAEEEVDP	1111
YaVA:	VAP_009268859.1	- NPQASFYESP -	1111
RAVA:	VAP_009553496.1	- NVGNSLSQDKASNDLFPMIPINLAEEEVDP	1112
ACLSV:	VAVMSDETKVFSFGHLLVAL TRASRVRSPPLIWTTRRTFDL -	- VMRGNPLLDAERRRIVKVSME -	1344
GPGV:	VAVMSDETKVFSFGHLLVAL TRASRVRSPPLIWTTRRTFDL -	- VDKMGKFVDF - EKIGRLE - FAEKKLHGDEHL LCMIDINESALPE	1386
Ctchv-1:	VIVLSEEEAKLCSDAHIMVAITRFRRGFCFALGSKGSKEDYMRMSKGSQRLICSGVGASKEFILGSSV -	- NLISKEKDIAKGAGIDEMOREARLEGDWLVLKSMIYLGKRYHM	1360
Ctchv-2:	LISLSEESRLCSNDNHYVALTRFKGGFFQNFRGDLGFTKNSLGSKLLGRYINLRLDNLKPFMMQMLDI -	- NLIQDFMD - RNQVGAGIEEMNKGMSDPLWKGLLDLQQAEEVE	1387
Diva:	AIALTEDSLASNDNHMMVLTRAKETFNFKGGFYPNLNEYVKKGANKL1GKVLQGVKQVRAELEMNSGM -	- EDVTFLITEPP -	1387
Orv1:	EDVTFLITEPP -	- TFGHQEDVQGPDPWMSLTLTTRDQESDQ	1387
CLBV:	CLTALKSLLKCFGEDEKKFTRAGTKLGVKLNNKKKVRQVLEMLNLL -	- KFGTQEERTEGDPWMKGLLTHIQEVIME	1384
CBLV:	EKIKRIV -	- CRLGMSNEVEMKLMGDPFLKSIISPLDEGSLI	1198
CBLV:	CLVSPPNCNSMINVMATVARKRGHVFAHLNGDFDVTDFNRVKGTPVNAILGSPSFEIHTRPGKDKD -	- CRLGMSNEVEMKLMGDPFLKSIISPLDEGSLI	1198
CBLV:	CLVSPPNCNSLMFNVIMVARSIKGVHFAFLNGDSIDFPNRVKGTPVAAIMLKGMDFIHQAPMSTPE -	- DCKCIIKS - DRCLLSSDVEENLKGDPFLKSIISPLDEGSLI	1198
CBLV:	CILSESSAASNEFRRMVALTRARTRFSCLSFLTGGIEEIKVKRKSESLITSLQIYEKTFINRLNRLML -	- KCNLIRREK - ENGRCDERDEERLLEGDPFLKPIIFLQGRVKED	1490
CBLV:	CILSESSAASNEFRRMVALTRARTRFSCLSFLTGGIEEIKVKRKSESLITSLQIYEKTFINRLNRLML -	- KCNLIRREK - ENGRCDERDEERLLEGDPFLKPIIFLQGRVKED	1490
CBLV:	CILSESSAASNEFRRMVALTRARTRFSCLSFLTGGIEEIKVKRKSESLITSLQIYEKTFINRLNRLML -	- KCNLIRREK - ENGRCDERDEERLLEGDPFLKPIIFLQGRVKED	1490
CBLV:	CILSESSAASNEFRRMVALTRARTRFSCLSFLTGGIEEIKVKRKSESLITSLQIYEKTFINRLNRLML -	- KCNLIRREK - ENGRCDERDEERLLEGDPFLKPIIFLQGRVKED	1490
CBLV:	AILSESENALSDHDRLWVALTRARKVTFCLLHLSLNGLFLSTMENRLVAHAVINLGLVTKRLRSSMVR -	- KLNVVFK - GLAGKDEVOREDRLEGDLFLKGIVFLGRCEIM	1207
CBLV:	AILSESENALSDHDRLWVALTRARKVTFCLLHLSLNGLFLSTMENRLVAHAVINLGLVTKRLRSSMVR -	- KLNVVFK - GLAGKDEVOREDRLEGDLFLKGIVFLGRCEIM	1207
CBLV:	AILSESENALSDHDRLWVALTRARKVTFCLLHLSLNGLFLSTMENRLVAHAVINLGLVTKRLRSSMVR -	- KLNVVFK - GLAGKDEVOREDRLEGDLFLKGIVFLGRCEIM	1207
CBLV:	LIVLSENSANSEFRMVVALTRARTRLTSFLVFLWHLDIGEFGMAETDGKMINALLGKEVNVKELSKKGF -	- NCELVECHR - ATGRDEVDRDRLEGDPFLKPFVFLGRQINSE	1518
CBLV:	LIVLSENSANSEFRMVVALTRARTRLTSFLVFLWHLDIGEFGMAETDGKMINALLGKEVNVKELSKKGF -	- NCELVECHR - ATGRDEVDRDRLEGDPFLKPFVFLGRQINSE	1518
CBLV:	NLNLFIEFEIINKNGNDQEORLLEGDPFLKPFVFLGRQINSE	- NLNLFIEFEIINKNGNDQEORLLEGDPFLKPFVFLGRQINSE	1352
CBLV:	NLNLFIEFEIINKNGNDQEORLLEGDPFLKPFVFLGRQINSE	- NLNLFIEFEIINKNGNDQEORLLEGDPFLKPFVFLGRQINSE	1352
CBLV:	CVLLTQDSMLVDERRVMVALSRAKINSLFNTSGLSLPTEFCCTQMGVGVHFKTFGTATFDNLRLLELPGD -	- PIFSKRF - QRLGKDEVDRERLLEGDPFLKWLKAVFLGRQEKKI	1553
CBLV:	CVLLTQDSMLVDERRVMVALSRAKINSLFNTSGLSLPTEFCCTQMGVGVHFKTFGTATFDNLRLLELPGD -	- PIFSKRF - QRLGKDEVDRERLLEGDPFLKWLKAVFLGRQEKKI	1553
CBLV:	TIIITNTVSASKEKRMVTAFLSRSENFICFVNWLWSLSEARMAYTRVFLGRKLAKSLDLEHLPGV -	- AIFTDSDTGY - ENIGKDEVGRERVQGPDPWLKGMLDFQLEDEV	1563
CBLV:	AIVVSEASKLASERWRITALTRARKRVFTFTNLGCSKHLIAEIFSNRALGRFLSCTASIDNLRCLLPGE -	- AIVVSEASKLASERWRITALTRARKRVFTFTNLGCSKHLIAEIFSNRALGRFLSCTASIDNLRCLLPGE -	1563
CBLV:	PNFVEELV - PTIGANLGVEEKVSGDPWLKTMFLFGOAVADVA -	- PELIEFGO - SQVGADEGVREAKLYGDPWLKTKIFLQGONPDE	1489
CBLV:	ALVYTESLTSRDRWWTALSRFSHDHIFINGWMTDWAITHVFGPKLHFPTKRAKTNCDIIDLPGR -	- PELIEFGO - SQVGADEGVREAKLYGDPWLKTKIFLQGONPDE	1714
CBLV:	ILILSHESTLTSRDRWWTALSRFLNIIFTVFLVNLQCEDACQVFHDRTLDRFLTRAKTIANVZDQLPGL -	- PELTNDPG - DKVGRSEGVMEALSGPSLWKLTEIDLQDDEQD	1552

AgVT		DIE--PHEELKDHSSPKTHLCKMSKAHT--SILMNEAKGREGREFRSIS--	--GWSEQSFDDLHKKG--KFPDVSYAEEFITYPKHTLSDDVFTWAAIQRKVSKNSPKREAR	1219
PVT:YP_002019748.1		EVT--PEEPLRHESPPRTHLPLVGELT--PLLMSNVKAREDREFITPS-	--GWSKQFRDKEVN--DWRNVSYADAFETIYPKHEASDDITLWAAIQRKVIMADPFRNAME	1220
PVT:ADX41471.1		EVT--PEEPLRHESPPRTHLPLVGELT--PLLMSNVKAREDREFITPS-	--GWSKQFRDKEVN--DWRNVSYADAFETIYPKHEASDDITLWAAIQRKVIMADPFRNAME	1220
PVT:APU55321.1		EVT--PEEPLRHESPPRTHLPLVGELT--PLLMSNVKAREDREFITPS-	--GWSKQFRDKEVN--DWRNVSYADAFETIYPKHEASDDITLWAAIQRKVIMADPFRNAI	1221
PVT:AXK90539.1		EAV--PEEPLRHESPPRTHLPLVGEKV--PLLMSDIIKAREEFVFPC-	--GWSKQFRDKEVN--DWRNVSYADAFETIYPKHEASDDITLWAAIQRKVIMADPFRNAME	1221
PrVT:YP_000951684.1		DPE--PEEPLRKDSDSPRTHLMLIAPIHQAEEHMHLRAREFRFRNSN--	--LWSEQFDCCDRTRKVI--IHNRAETFEQYIPKSNSDTLFWAAIQRKMKMSDPYSVER	1393
PrVT:AH92766.1		DPE--PEEPLRKDSDSPRTHLMLIAPIHQAEEHMHLRAREFRFRNSN--	--MWSDFDDSRTRKVI--IHNRAETFEQYIPKSNSDTLFWAAIQRKMKMSDPYSERR	1393
ZoVT:QBS17025.1		DPE--PEEPLRKDSDSPRTHLMLIAPIHQAEEHMHLRAREFRFRNSN--	--MWSEQFDCCDRTRKVI--IHNRAETFEQYIPKSNSDTLFWAAIQRKMKMSDPYSERR	1393
ZoVT:QBS17031.1		DPE--PEEPLRKDSDSPRTHLMLIAPIHQAEEHMHLRAREFRFRNSN--	--MWSEQFDCCDRTRKVI--IHNRAETFEQYIPKSNSDTLFWAAIQRKMKMSDPYSERR	1393
chVT:QNG41875.1		KEE--MNEMVFKSPPRTHLMSISNEGNAFINGPHLNRAREFRFKGRG--	--KYNRAETFTIYPNHNGTDSLTWMAAIKRKLKMSDPYTER	1431
Fita:QED24804.1		KEE--MNEMVFKSPPRTHLMSISNEGNAFINGPHLNRAREFRFKGRG--	--MNSEQFDCCDRTRKVI--RYNRRAETFTIYPNHNGTDSLTWMAAIKRKLKMSDPYTER	1431
TrTA:QED42832.1		EEP--VEEPVRKDSPPRTHLHGCESTAQIOPGPMKRNAREFKFSKD--	--TWSSQFQDDNSRRN--LDNSAESFESIYPKHNSVSLTMVAAIQLRKLFKSDNSERR	1397
GVA:NP_619662.1		EEP--VEEPVRKDSPPRTHLHGCESTAQIOPGPMKRNAREFKFSKD--	--TWSSQFQDDNSRRN--LDNSAESFESIYPKHNSVSLTMVAAIQLRKLFKSDNSERR	1397
acVB:YP_004935358.1		EVE--VEEPNRKESPPRTHLSIOPQEOFVDPGSLKRSREFRGLG--	--LWSEQFDLKKGRR--LNNEVERFENIYPRHNSADSLTFWAAIQLRKLFKSNALTER	1412
ASGV:NP_044335.1		DIE--IEEPVTLE--PTKTHALSTKMNELAP--FDLKRAEHRQHTEA--	--GRTEQIDEN--GYQEYGDPMTHKALYLRHSTSDDTTFMWSVKKVRLRNFYRNEAN	1326
YaVa:YP_009268859.1		DIE--IEEPVTLE--PTKTHALSTKMNELAP--FDLKRAEHRQHTEA--	--GTTEQIDEN--GYKMEPENPMTHKALYLRHNSDATTFFLVSVKRLRFMDREKNH	1321
RAVA:YP_009553496.1		EEE--VPDVLSP--PKTLPKLIPTKNELEN--SLLRRAEHRARTPA--	--EVEARLDMNLIIQTHSPVPIEKSGLAKLDSLRAEERQMVVGSPDPSYYTNTNNDM--	1451
ACLSV:NP_040551.1		EEE--VPDVLSP--PKTLPKLIPTKNELEN--SLLRRAEHRARTPA--	--DYEKDNNAVTSFVTPRHKCEDDTTFMAMVRKRLRFADPSVNAH	1451
GPGV:YP_004732978.2		EVE--VEAFLRDLMIQTHSPVPIEKSGLAKLDSLRAEERQMVVGSPDPSYYTNTNNDM--	--EVEAFLRDLMIQTHSPVPIEKSGLAKLDSLRAEERQMVVGSPDPSYYTNTNNDM--	1451
CtChV:1-YP_009103999.1		EVE--VEAFLRDLMIQTHSPVPIEKSGLAKLDSLRAEERQMVVGSPDPSYYTNTNNDM--	--DYEKDNNAVTSFVTPRHKCEDDTTFMAMVRKRLRFADPSVNAH	1451
CtChV:2-YP_009103996.1		EVE--LIEDPIVESCMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	--EPL--GQVILKTDAIICPKVPCSSLT--GPELDNIQRAEYREFFKGN--	1490
DiVA:YP_00695850.1		EVE--LIEDPIVESCMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	--GWSNOFQDLMEMK--GSNIDVYPMSSRSVPPFHNSDFTFWAGVQKRIRKNSNWRREKS	1214
OBRV1:YP_00948144.1		EVE--LIEDPIVESCMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	--GWSNOFQDLMEMK--GSNIDVYPMSSRSVPPFHNSDFTFWAGVQKRIRKNSNWRREKS	1214
CLBV:NP_624333.1		EDE--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	--DFM--FEDVNLIEPTKVKHPLLSARDNE--FEKRAESENRFKSKD--	1461
CLBV:NP_624333.1		EDE--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	--DFWNSMDFEDCVGCKV--RLVNLNCENFSAVYVPHQACDTEMFLAALKVRKFNSPNAKLT	1461
CLBV:NP_624333.1		EDE--VEEVKIREPTCQTHLYITEPNCFLGCLYNYDFIREKEQREYREDM--	--DFWNSMDFEDCVGCKV--RLVNLNCENFSAVYVPHQACDTEMFLAALKVRKFNSPNAKLT	1461
CLBV:NP_624333.1		HDE--EVEEVKIREPTCQTHLYITEPNCFLGCLYNYDFIREKEQREYREDM--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
CLBV:NP_624333.1		HDE--EVEEVKIREPTCQTHLYITEPNCFLGCLYNYDFIREKEQREYREDM--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
CLBV:NP_624333.1		EPE--IIEPVEMAKDMTHFFVQCNFQACYQCNFDRKIRAELEFRERIGH--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
CLBV:NP_624333.1		EPE--IIEPVEMAKDMTHFFVQCNFQACYQCNFDRKIRAELEFRERIGH--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
acVA:YP_008997790.1		EVE--IIEPVEMAKDMTHFFVQCNFQACYQCNFDRKIRAELEFRERIGH--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
CPvV:YP_00955632.1		EYE--IIEPEVIEPKGRVHLCLIQSENYALARNFLIRAKEYREAKLMG--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
WVA:YP_009357235.1		EYE--IIEPEVIEPKGRVHLCLIQSENYALARNFLIRAKEYREAKLMG--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
WVA:QEA69426.1		EVEI--VDEVFVKEDEKETHLYLAEPNFQSQALNFDLILDKVEFRERLGE--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
CRMvV:YP_007716581.1		EVEI--VDEVFVKEDEKETHLYLAEPNFQSQALNFDLILDKVEFRERLGE--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
CTLAv:YP_009046478.1		ESEIH--NEDEGLDKIIVKVKHPIGSISSLTADIQAVGRVKEAREFRIDN--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
Ph1vB:YP_001552317.1		VEEPISVNLNDKIIVKHCPVGMATFGAFTEVQSKLVKVEAREHRIDN--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
GCLV:YP_004936159.1		EEE--EQLEEMOTEWFVVKHPLQAELESVRKAWHVKLILAKEFREVRIGHT--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
ASPvN:DP_604464.1		EEE--EQLEEMOTEWFVVKHPLQAELESVRKAWHVKLILAKEFREVRIGHT--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
APV1:YP_009094347.1		DEI--DVEALDQFEPKTHVARSNLNEGRVLAIRWLHKIRLEKREKRMGY--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
		IEI--ADEVEAAADEFKTHIPIMSLAEVRAQOWHVKLISREDREFRIGD--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
		MEE--LAEEVKHEPWFKTHLPLFELESIRASWHRIMREYREVRCGS--	--EFEQ--PQMAPDDVKMVKHINYITDKSVALMIINDQLRAEKENRFKSKD--	1461
		* * * * *	* * * * *	1662

AgVT	PVT:YP_002019748.1	KLERDPMIGK----EILNEFLVKVPLNIEI--VLDLAEHKNNFKRVEKGSKLQGHSNSRDPWDLKFLMFSQLCTKKEKFRCDAKAGOTLACFASHQGLCRFGVPFRVFE	1327
	KLKQKVEPIA-----EINFEMNKILLNPHV-SVDRDVQYKEFLRKRLNKSKKLIESHSERSSDWPIDHFFLMFKSOLCTKFEKFRVDAKAGOTLACFSHKLTRFGPAFREFE	1329	
	KLKQKVEPIA-----EINFEMNKILLNPHV-NVRDQVYKEFLRKRLNKSKKLIESHSERSSDWPIDHFFLMFKSOLCTKFEKFRVDAKAGOTLACFSHKLTRFGPAFREFE	1329	
	KLKQKVEAISA-----EINFEMNKILCNLNPHV-SVDRDVQYKEFLRKRLNKSKKLIESHSERSSDWPIDHFFLMFKSOLCTKFEKFRVDAKADAGOTLACFSHKLTRFGPAFREFE	1330	
	KLKQKVEAISA-----EINFEMNKILCNLNPHV-SVDRDVQYKEFLRKRLNKSKKLIESHSERSSDWPIDHFFLMFKSOLCTKFEKFRVDAKADAGOTLACFSHKLTRFGPAFREFE	1330	
PrVT:YP_000951684.1		KLERCPMVG-----NLCLRCLVEEYGLKRGW-QVIDESTEREFLLKRVEAKMTEAHESRSPDWVNMFHFLMFKTQLCTKFEKFRSDAKAGOTLACFSHQLWRFGVPIRVAE	1502
PrVT:AHM92766.1		KLERCPMIGE-----NLCLKIFIVEEYGLKRGV-TIVDESTEREFLLKRVEAKMTEAHESRSPDWLNVFHFLMFKTQLCTKFEKFRSDAKAGOTLACFSHQLWRFGVPIRIAE	1502
ZoVT:QPS17025.1		KLERLSTMKG-----SLFEIFKKEYGLRDRV-RVNTEDETYAFDIDRRLNKSALKSAHSERSPDWICNHLFMLKTLCTKFEKFRSDAKAGOTLACFSHVLTRFGVPIKEVE	1540
ZoVT:QBS17031.1		KLERLSTMKG-----SLFEIFKKEYGLRDRV-RINRDETYAFDIDRRLNKSALKSAHSERSPDWVNCHNFMLKMTQKTYEFSRDKADAGOTLACFSHVLTRFGVPIKEVE	1540
ChVT:QNG41875.1		RLERARSVGM-----SLFEIFCKEYGIKRRR-FRDVEVMVEQTFFIEKRLSLSKKMIECHATRSDPWPWKHFFLMFKSOLCTKFEKFRVDAKAGOTLACFSHVLWRFGIPIRAFe	1506
FiTA:QED42894.1		RLERVKSVGI-----SLFEIFCKEYGIKRRR-FRDVEVMVEQTFFIEKRLSLSKKMIECHATRSDPWSIKHFFLMFKSOLCTKFEKFRVDAKAGOTLACFSHVLWRFGIPIRAFe	1506
TrTA:QED42832.1		KLESLRGAGE-----NLLEIFKTYTIEENI-LPMDLIEKTFFIEKRLNKSKKMIEAHESRSPDWVNHFMLFKMQLSTKTYEFSRDKADAGOTLACFSHVLWRMGFIKIREA	1521
GVA:NP_619662.1		KYTKTCGHIGH-----QMFSVFSKTDYOLKEIDSPLERCEMFMMKRIKESTGLIEKHAGRSRDPWNSPYNLKIFLQKQCTTMKEGRVDAKAGOTIACFAHVSUFLRGFLPILRQE	1436
AcVB:YP_004935358.1		RFNFKVGFGGK-----OLFVLKVETKNYLQRPDKLPLDRIEAEEFARKRLNKSNLIEKHSYRSRDPWSPHYLKIFLQKQCTTMKEGRVDAKAGOTIACFAHCVLCKFGPRLRTE	1431
ASGV:NP_044335.1		KFFEESQK-----ELLQEFISMLPPEFKVNTKIEDEGEKSFLERKRLKSEKMWANHSERSDIDWLKFLHAFMLFSQSYCTKEGKMFTEAKAGOTLACFQHVLFRFGPMLRAIE	1323
YaVa:YP_009268859.1		KLESVQDGK-----ALLREFLMLPKDQFKVNTDNDIAGEKSFLERKRLKQTKETMEWAHSNRSRDIWDLHVFMLFKMSQYCTKEAKMFTEAKAGOTLACFQHVLFRFGPMLRAIE	1324
RAVA:YP_009553496.1		DFEADMAGGNGMVADMLLCNLLKVLRPSKLNVQDFLEEAQIELVEKKILRSAEMIANQSERSDPNWLSTEI1LLFMKSQYCKVDMKVMVDAKAGOTLACFHHQILVRFGPWCRALE	1566
ACLSV:NP_045551.1		KFKAAEERSGK-----YLTLCFLKHPVKICGRDQLRQQFEEFTKLSSAATIGHQHSRDSWDLPKFLMFKSOLCTKFEKFRFEAKAGOTLACFPHQILVEFPPWCRTYE	1600
GPGV:YP_004732978.2		KFRGATAAAGK-----ILNKNFLKFIPIPSETTPEALKSEAREFOEQVKLHKSGEETIAGNSRSPDWNSDRVFLFMKSQCTKFEKFRCEAKAGOTLACFSHEILCHFPSCRYME	1571
CtChV-1:YP_00103999.1		KLNAKWAIGKS-----ILHKFEKTRLRNVSFHRSRDFPLKFALEKALFDNDFFVRMRKSEKLMHAHGRSDPQWIRNFLLFKMSOLCKKAEEKAFCDAKAGOTIACFAHVGFLFKSACRWAYA	1600
CtChV-2:YP_00103996.1		KLKSAFKVKG-----ILYKEFKRIRVQGDFPRDPLFKDALSKDFERVYAKSLLKIEAHAGRSRDPDWVDKFLMFKSOLCKKAEEKAFCDAKAGOTIACFAHVGFLFKSACRWAYA	1597
DiVA:YP_00905850.1		RFEKVRHLG-----EMLDFLFDKICIDNLNLEMSEMMARSYNEYLLKKVSKTANTIASHSRSPDWLKFMLKTLCTKFEKFRSDAKAGOTLACFSHILNRFAPARYTRE	1412
orbRV1:YP_009408144.1		KFVKVRHLGS-----EMFELLEKIPLDKNNKDLDDMLQMCIVNZEYERKVKSPAGTICKHSRSDCWDLKFNDVFLFIKTOQKTYEFSRDKADAGOTLACFHVILNRFAAPARYIE	1412
CLBV:NP_624333.1		RLSRAHLVGG-----LLYTNTFKKMMGLEFTFDQGLLEESINAFEEKKKLEKSGCTIKSHSIRSIDIWALNDVFLFMKSQSLCTKYEQFVDAKAGOTLACFQHLLVLFQFAPWCRLYE	1706
CLBV:AF443536.1		RLSRAHLVGG-----LLYRNFKNKLGLLEFTFDQGLLEESINAFEEKKKLEKSGCTIKSHSIRSIDIWALNDVFLFMKSQSLCTKYEQFVDAKAGOTLACFQHLLVLFQFAPWCRLYE	1731
AVCaV:YP_008997790.1		KLERAHGTG-----ILFHNLQIQLKGLNFTMDNQFLFEVCNDFECKLLEKSAVLAHNSRSDWNSPNWFVLFMKSQSLCTKYEQFVDAKAGOTLACFQHMLVTFVAPCRYME	1423
CPvP:YP_00050632.1		KLKDSDSYSVG-----LLYQNLNEKKLSLSFWSDGDLQDCLNDFTFKLKLKSATLHNRSIDWMDKCFLFLMFKSOLCTKYEQFVDAKAGOTLACFSHVLVLAFKPACYRYME	1734
wVA:YP_009357235.1		KYMEARCTGR-----LYMEHFCKEMGFWHNDQALLECCRDFEVFKLQKSAETIKCHNSRSDCWDLNFMLKTLCTKYEQFVDAKAGOTLACFQHLLAHFPAPCYRYME	1568
WVA:AE64924.1		KYMEARCTGR-----LYMEHFCKETFGIEWNHQDQALLECCRDFEVFKLQKSAETIKCHNSRSDCWDLNFMLKTLCTKYEQFVDAKAGOTLACFQHLLAHFPAPCYRYME	1568
CRMvA:YP_007761581.1		KYMAAIYPGV-----SMLOVFLRKLQKOSNFHDRLFEARADFEKKKLQSMATLENHSRSPDWNSVEKAIFMKSOLCTKFDNFRNAKAGOTLACFHVILNRFAAPARYIE	1767
CTLvA:YP_009046478.1		KFMSAIPYGD-----TMLKVLFLNKRVLKPFDHRLFEARADFEKKKLQSMATLENHSRSPDWWEIKEALIFMKSOLCTKFDNFRDAKAGOTLACFHHNVLRLCRLAPYIYIE	1777
Ph1vB:YP_001552317.1		KLVEAMPGYK-----FMKELFKLKPIMKRSRDLTQMMEQSKLLEFEKKKLQSMATLENHSRSPDWLIDGLYIFLKSQSLCTKFDNFRVAQAKQSFVCFQHAPYMYRIE	1798
GLCV:YP_004936159.1		KLMDASNFSE-----MLQFELKFHVLPKLPKHNQAFMDASLDEEEKKKTSKAAATIANGHSRSCRDWLIDGLVFMKSQSLCTKFDNFRDAKAGOTLACFQHLLAHFPAPCYRYIE	1703
ASPV:NP_604464.1		KLRRAKPFGK-----FLDFTFLKRVLPRVLSNSHKEEMQMOAEEFAHVEEKKLKSMTIENHSRSCRDWLIDGLVFMKSQSLCTKFDNFRDAKAGOTLACFQHLLAHFPAPCYRYIE	1928
APV1:YP_009094347.1		KLNRKAPYKG-----FLVSFELKRLPRLRGNLDPFLFAKARDFEKKKTSKAAATIENGHSRSCRDWLADGVFIFMKSOKCSKWDNRFDAKAGOTLACFQHLLAHFPAPCYRYIE	1772

AgVT	EKVKQQLPKNVIYIHTMKNFDQLDNLWVKEVN - DEHL - GTESDYEA FDRS QD S D L I L A F E L H L L K H M G W D E N L Q D Y V K I Y M M G C R L G S L A I M R F T G E F G T F F N T M A N L A F T V R L	1439	
PVT:YP_002019748.1	KKFTANLPSSWIYIHTMKNFDQLNNVVINVY - DQE E - GTESDYEA FDRS QD A I L G L E I C L K L G F W Q D D L I D D Y R K L L M R G R C W G A I A I M R F T G E F G T F F N T I A N I A F T C L R	1441	
PVT:ADX41471.1	KKFTANLPSSWIYIHTMKNFDQLNNVVINVY - DQE E - GTESDYEA FDRS QD A I L G L E I C L K L G F W Q D D L I D D Y R K L L M R G R C W G A I A I M R F T G E F G T F F N T I A N I A F T C L R	1441	
PVT:AFU55321.1	KKFTANLPSSWIYIHTMKNFDQLNNVVINVY - DQE E - GTESDYEA FDRS QD A I L G L E I C L K L G F W Q D D L I D D Y R K L L M R G R C W G A I A I M R F T G E F G T F F N T I A N I A F T C L R	1442	
PVT:AKX9539.1	KKFTANLPSSWIYIHTMKNFDQLNNVVINVY - DQE E - GTESDYEA FDRS QD A I L G L E I C L K L G F W Q D D L I D D Y R K L L M R G R C W G A I A I M R F T G E F G T F F N T I A N I A F T C L R	1442	
PrVT:YP_009051684.1	KKLRAOLGENIYIHSQKGLDELNEMCGMA - - GKY - GTDSDYESFDRS QD A I L A F E L H L L R L G F W Q D V D O E V D Y T L L R L G R L G L Y L A I M R F T G E F G T F F L N T C C N M L F T C L R	1613	
PrVT:AHM2766.1	KKLRSQSLNDNIYIHSQKGLDELNEMCIRYS - - QGY - GTDSDYESFDRS QD A I L A F E L H L L R L G F W Q D V D O E L D D Y V A I L R L G R L G L Y L A I M R F T G E F G T F F L N T C C N M L F T C L R	1613	
Zo:QTS17025.1	EKMRFLCKLDNIIYIHSQKGLDELNNCIKYA - - TGY - GTDSDYESFDRS QD A I L A F E I H L L E F F G W Q T K D L I D Y D Y V S I K L R L G R L G L N A I M R F T G E F G T F F L N T C C N M L F T C L R	1651	
Zo:QTS17031.1	EKMRFLCKLDNIIYIHSQKGLDELNNCIKYA - - TGY - GTDSDYESFDRS QD A I L A F E I H L L E F F G W Q T K D L I D Y D Y V S I K L R L G R L G L N A I M R F T G E F G T F F L N T C C N M L F T C L R	1651	
CHVT:ONG41875.1	QNLREQLSDKIIYIHSQKGLDELNNEAIKYC - - KVN - GTDSDYESFDRS QD A I L A F E I P L L E H L G W Q S D Q L I D Y V E M K L N Q L G R L G L N A I M R F T G E F G T F F L N T C C N M L F T C L R	1617	
FITA:QED42804.1	QNLREQLSDKIIYIHSQKGLDELNNEAIKYC - - KVN - GTDSDYESFDRS QD A I L A F E I P L L E H L G W Q S D Q L I D Y V E M K L N Q L G R L G L N A I M R F T G E F G T F F L N T C C N M L F T C L R	1617	
TrTA:QED42832.1	AKLRAOLGENIYIHSQKGLDELNNEAISKRYC - - SDC - GTDSDYESFDRS QD A I L A F E I P L L R F L G W D E S L V A E Y I D I K L N L Q R G L G L Y L A I M R F T G E F G T F F L N T C C N M L F T C L R	1632	
GA:NP_619662.1	KALRLEPPEKLIMSYOKYMDLDAHKAWT - - ESM - GTDSDYESFDRS QD E K V D L L E V F R L F L W P E D L I R E Y E E L K L M G M C G A L D V A M R F S G E F G T F F T C V N M V F S C M R	1548	
AcVb:YP_004935358.1	KALRQAOLGDNVLYISQNLNYTDLKNCNKNFV - - PSML - GTDSDYESFDRS QD E R D E R I L D F E M E V L K F L W P E E V I N E Y E K I L L M Q M G S S M S L A V M R F S G E F G T F F N T I C N M A F T C L R	1543	
ASGV:NP_044335.1	S A F L R S C G D S Y I I H S G K N F F L C D S F V T K N A S F D G E - S I E S D Y T A F D Q S S Q D H T L A F E I E L L K H L G V S N E F I M D Y K K I L T L G R C L G S L A I M R F T G E F C T F L N T F A N M L F T C L R	1437	
Ya:VA:YP_009268859.1	A A F L R A C G D S Y I I H S G K N F F A L D T F V T R N A S F D G E - S I E S D Y T A F D Q S S Q D H T L A F E I E L L K H L G V S N E F I M D Y K K I L T L G R C L G S L A I M R F T G E F C T F L N T F A N M L F T C L R	1438	
RAVA:YP_009553496.1	K L L E M P L V N Y Y I H S G K N F F N C L D F V K T H L - - K D G M E C V E N D Y A F E Q D S Q D H S I L A F E V K F L R L G I P W D A P V V D D Y I H L K T G L G Q L G L A I M R F T G E F C T F L N T S L N S N A F C T O	1679	
ACLSV:NP_040551.1	K V L T A N L P D N N Y Y I H S K N F E L D E A F F R R G S - - N S T - C V E S D Y T A F D V S Q D H T L A F E V L E F F R H G W D D R V L O Z Y I K M T C L G R L G F A I M R F T G E F C T F L N T A N M V F F C R	1712	
GPGV:YP_004732978.2	K V F K S V C P E N Y I H S K N F D K L A E F R S K Y C - - K G F F - C I E S D Y V A F D V S Q D H N V L A F V Q M L E H R I P E C V I S D Y R M K T E L G C K L G N F A I M R F T G E F C T F L N T C N M A F T C R	1683	
CtChv-1:YP_009103999.1	CtChv-2:YP_009103999.1	K I N L E V M P A F V Y H S K N F D E L R M V K G H N F G I - - I G P I - C V E S D Y E A F D A S Q D A T I L A F E V O F L K E V G W P Q D L I E D Y I E L K V N L G C K L G N L A I M R F T G E F G T F F L N T A N M A F T C R	1712
CtChv-2:YP_009103999.1	K L M K E M K P D S F Y I H S R K N F D E L E K W K M N F I - - I G P I - C V E S D Y E A F D A S Q D A T I L A F E V O F L K E V G W P Q D L I E D Y I E L K V N L G C K L G N L A I M R F T G E F G T F F L N T A N M A F T C R	1709	
D i V A : Y P _ 0 0 6 9 0 5 8 5 0 . 1	K K I S E G L K F N Y I H Q K K N F D L V N D W V A N N - - F D S Y - C L E S D Y E A F D Q S D Q C D L I L A F E Y E K L Y L G W Q D S S Q L L D D Y L D K L F N L G R C L G N L A I M R F T G E F G T F F L N T A N M V F F T M	1524	
R b R V Y : Y P _ 0 0 9 4 0 8 1 4 . 1	K K L S L C L P D N N Y Y I H S K N F D M L N A V W R N D - - F D S D E - C L E S D Y E A F D Q S D Q C D L I L A F E Y E K L Y M G W Q S S Q L L D D Y L D K L F N L G R C L G N L A I M R F T G E F G T F F L N T A N M V F F T M	1524	
CLBV:NP_624333.1	T Q I R N Q L P E E Y I H S K N F D P D L N A V W R N K F F - - Q R D T - C V E S D Y E A F D Q S D Q C D L I L A F E Y E K L Y M G W Q S S Q L L D D Y L D K L F N L G R C L G N L A I M R F T G E F C T F L N T A N M A F T C R	1818	
CBLV:AF43536.1	A Q J R N Q L P E E Y I H S K N F D M D L Y R W K N F F - - Q K D T - C V E S D Y E A F D Q C D E Y I L S F E I H L M K D H A P F O K T I D A Y I D L K C K L G K L G H F S I M R F T G E F C T F L N T A N M A F T C R	1843	
AVCaV:YP_008997790.1	K K L R A O L P G E Y I H S K N F D L N E W W K K H A - - G D D L - C V E S D Y E A F D Q S D Q O Y I L S F E I H L M K D H A P F O K T I D A Y I D L K C K L G K L G H F S I M R F T G E F C T F L N T A N M A F T C R	1535	
CPvP:YP_009505632.1	K M R K R N L E E Y I I Y I H S K N F D N L D W V V K F F - - E G E E - K V E S D Y E A F D Q S D Q H Y V L A F E V C V M E D M G L P N W F I D Y I D U K L C T L G K L G H F A I M R F T G E F S T F L N T A N M A F T C R	1846	
WA:YP_009357235.1	K Q L T R M P L D E I Y I H S K N F D E L N E W V I K H F - - Q N D I - C V E S D Y E A F D Q S D Q Y I L F A E M F A L M K D A G M P D H L I D D Y L D K L C E L G K L G F A I M R F T G E F C T F L N T A N M A F T I S R	1680	
WA:YP_009357235.1	K Q L V R M P L D E I Y I H S K N F D E L N E W V I K H F - - Q N D I - C V E S D Y E A F D Q S D Q Y I L F A E M F A L M K D A G M P D H L I D D Y L D K L C E L G K L G F A I M R F T G E F C T F L N T A N M A F T I S R	1680	
CRMvA:YP_007761581.1	K K V F K A L P S N Y I H S K N F D R A L D R W V I K N F T G V - C T E S D Y E A F D Q S D Q V N I L A F E V S L M E Y L R P L R D L I E D Y K Y L F H T H S K L Q G A F V M R F T G E A G T F F L N T A N M V F F T M R	1879	
CTLaV:YP_009046478.1	K K V F D A L P R N Y I H S K N F D R D L W V I N S N - - F S G M - C T E S D Y E A F D Q S D Q D A N I L A F E V S L M N Y L P R L D L I E D Y K Y L F K N T H S K L Q G A F V M R F T G E A G T F F L N T A N M V F F T M R	1889	
Ph1LB:YP_001552317.1	K K L H Q A L P G N F Y I H S K G K G L E E L N E W M R B R G F - - D F G D - C T E S D Y E A F D Q S D Q O Y I M A F E M I K Y L G P L A D I S D Y E F K I T H L G S K L G N F A I M R F S G E A S T F L N T M A N L F T F L R	1910	
GCLV:YP_004936159.1	R K I A E V L P E K F Y I H S K G K G L E E L N A W V T R G R - - F E G V - C T E S D Y E A F D Q S D Q O Y I L A F E L H V M K Y L G P L R D L I E D Y K F I K M H L G S K L G N F A I M R F S G E A S T F L N T M A N L F T F L R	1815	
ASPV:NP_604464.1	S K V E V L P K N L Y I H S K N F D L N A W V I T S K - - F N G V - C T E S D Y E A F D Q S D Q H Y I L A F E L H V M K Y L G P L R D L I E D Y K F I K M H L G S K L G N F A I M R F S G E A S T F L N T M A N L F T F L R	2040	
APV1:YP_009094347.1	Y K L Q A A P S N Y I H S K N F D L N A W V I T S K - - F N G V - C T E S D Y E A F D Q S D Q H Y I L A F E L H V M K Y L G P L R D L I E D Y K F I K M H L G S K L G N F A I M R F S G E A S T F L N T M A N L F T F L R	1884	

Fig. S2. Alignment of movement protein sequences of AgVT and related viruses

AgVT	MA-----	LPVPNTFLKKWESSQSITDA-----	-VDSSVIYTESPFFNLKGKMSVNSKTEFKMPNLNTE-DGRGISEAVPLFDRSEVQTMILNDKETEYVHI	87	
PVT:YP_002019749.1	ME-----	LISVEKFRRQWEERESTITGP-----	-LISGAITYTNSAFHNLTKWVKYKSECSIGLDPD-NGKIIKSDIPLFDQEEDIDNIMKDDKQVFVHL	87	
PVT:ADX41472.1	ME-----	LISVEKFRRQWEERESTITGP-----	-LISGAITYTNSAFHNLTKWVKYKSECSIGLDPD-NGKIIKSDIPLFDQEEDIDNIMKDDKQVFVHL	87	
PVT:AFU55322.1	ME-----	LISVEKFRRQWEERESTITGP-----	-LISGAITYTNSAFHNLTKWVKYKSECSIGLDPD-NGKIIKSDIPLFDQEEDIDNIMKDDKQVFVHL	87	
PVT:AKX90540.1	ME-----	LISVEKFRRQWEERESTITGP-----	-LISGAITYTNSAFHNLTKWVKYKSECSIGLDPD-NGKIIKSDIPLFDQEEDIDNIMKDDKQVFVHL	87	
PrVT:YP_009051685.1	MS-----	LVDVQFRRKVNATGSIASA-----	-VDSSAIYKLSPFHALQSDTVVRKSEFKVMMQQTG-ERGVACMSVPLFDDHDKQT-IRESKLPVYHZ	86	
PrVT:AHM92767.1	MS-----	LVEVNQFRKKVNATGSIASA-----	-VDSSAIYKLSPFHALQSDTVVRKSEFKVMMQQTG-ERGVACMSVPLFDDHDKQT-IRESKLPVYHZ	86	
ChVT:QNG41876.1	MS-----	LVDVQFRRKVNATGSIASA-----	-VDSNAVYKLSPFHSLKNDTIVRKTIFVKVLQOSS-ERGVASISVPLFDDLDKNN-IRESKLPVYHZ	86	
FiT:QED42805.1	MS-----	LVDVQFRRKVNATGSIASA-----	-VDSNAVYKLSPFHSLKNDTIVRKTIFVKVLQOSS-ERGVASISVPLFDDLDKNN-IRESKLPVYHZ	86	
ZoVT:QBS17026.1	MN-----	LVDVQFRRKVNATGSIASA-----	-VDSAAVYKLSPFHSLKNDTIVRKTIFVKVLQOSS-ERGVCSMAINLFDESDKAV-IRESKLPVYHZ	86	
ZoVT:QBS17032.1	MN-----	LVDVQFRRKVNATGSIASA-----	-VDSAAVYKLSPFHSLKNDTIVRKTIFVKVLQOSS-ERGVCSMAINLFDESDKAV-IRESKLPVYHZ	86	
TrTA:QED42833.1	MS-----	LVDVQFRRKVNATGSIASA-----	-VDSAAVYKLSPFHSLKNDTIVRKTIFVKVLQOSS-ERGVCSMAINLFDESDKAV-IRESKLPVYHZ	86	
GVA:NP_619664.1	MS-----	QEGLSLGTKASSFEPQ-----	-DIKVKFVKRSTRDLETLNKS-----LHRGDVYNTTELIEKVFP-----RTKCKV1HKD4V-KDGRVCDLDIMDEG-LDD-INEEEFLYHZ	97	
AcVB:YP_004935360.1	MS-----	MSISRGSSMTSSSTVPIRAKSTIKDFVPKG-EDGRSVARA-----	-LNRNRYVKMDAFEKFHQ---STLKSCHDELIV-ENGVDONIDLVDEKTIQD-LNEEKOPYHZ	103	
GPGV:YP_004732979.2	MA-----	*-----L-----MKRIAKVSGRIATGATPIAELPSSFIYNDTSKLKGSAILLERNEVYQVEPSSISEDFRTTIPIVPMEQKL-----LNGSNMNYHZ	88		
AgVT	GA-----	GA-----	-----	*	
PVT:YP_002019749.1	GA-----	GA-----	-----	*	
PVT:ADX41472.1	GA-----	GA-----	-----	*	
PVT:AFU55322.1	GA-----	GA-----	-----	*	
PVT:AKX90540.1	GA-----	GA-----	-----	*	
PrVT:YP_009051685.1	AVALI-----	AVLQISCLFDWA1SEGMEGTFAL-----	-MDTFLFDNVQDNVTDMEGTFAL-----MDTFLFDNVQDNVTDMEGTFAL-----	197	
PrVT:AHM92767.1	AVALI-----	AVLQISCLFDWSMTNGMEGTFAL-----	-MDTFLFDNVQDNVTDMEGTFAL-----MDTFLFDNVQDNVTDMEGTFAL-----	197	
ChVT:QNG41876.1	AVALI-----	AVLQISCLFDWSMTNGMEGTFAL-----	-MDTFLFDNVQDNVTDMEGTFAL-----MDTFLFDNVQDNVTDMEGTFAL-----	197	
FiT:QED42805.1	AVALI-----	AVLQISCLFDWSMTNGMEGTFAL-----	-MDTFLFDNVQDNVTDMEGTFAL-----MDTFLFDNVQDNVTDMEGTFAL-----	197	
ZoVT:QBS17026.1	AAVLI-----	AVLQISCLFDWA1SEGMEGTFAL-----	-MDTFLFDPEDEENVRACNF-----MDTFLFDPEDEENVRACNF-----	197	
ZoVT:QBS17032.1	AAVLI-----	AVLQISCLFDWA1SEGMEGTFAL-----	-MDTFLFDPEDEENVRACNF-----MDTFLFDPEDEENVRACNF-----	197	
TrTA:QED42833.1	AAVVI-----	AVVVI-----	-----	*	
GVA:NP_619664.1	GCIVVALM-----	PHGKMLQGVSVSVEVLTDRVQGA-SRISRTLMDMSKPLSACADFPFGYFISTSFLNQGYTLHLS-----	-RDSRQV-----	206	
AcVB:YP_004935360.1	GCIVVALI-----	PHGKMLQGVSVSVEVLTDRVQGA-SRISRTLMDMSKPLSACADFPFGYFISTSFLNQGYTLHLS-----	-RDSRQV-----	212	
GPGV:YP_004732979.2	GALSI-----	RDRSGVGKVAFAV-----	-YDSRWDNAQSALLQAFHDLNNGTASMVCPNSVQLSDPLSTCLSAVLFENLNFKSGSYAISVRIGITYRPFNSIGRSLMS-----	196	
AgVT	SACSVDDLLQSEILELSDLSDEVSNL-----	REDVERRVPLLEY-----	-PDEKDY-----	-IPRRGLFRTPKPSITRRTYGR-----	272
PVT:YP_002019749.1	ASRTV-----	HLDVGTDLQLDQATLED-----	-EE-----	-VRRSPILRLTAPDERVM-----	284
PVT:ADX41472.1	ASRTV-----	HLDVGTDLQLDQATLED-----	-EE-----	-VRRSPILRLTAPDERVM-----	284
PVT:AFU55322.1	ASRTV-----	HLDVGTDLQLDQATLED-----	-EE-----	-VRRSPILRLTAPDERVM-----	284
PVT:AKX90540.1	ASRTV-----	HLDVGTDLQLDQATLED-----	-EE-----	-VRRSPILRLTAPDERVM-----	284
PrVT:YP_009051685.1	-DHDHFVNIYGTTEFLPKKEKSELCEEI-----	-SDSFQLRQLT-----	-PKPVT-----	-SLPRG-----	287
PrVT:AHM92767.1	-EHDHFVNIYGTTEFLPKKEKSELCEEI-----	-SDSFQLRQLT-----	-PKPVT-----	-RKEPTRIRDYSVMSQDGLIEKDGSNKEGVGNATGG-----	287
ChVT:QNG41876.1	-SNDNFNIVYGTTEFLPKKEKSELCEEI-----	-SESFSSQQOL-----	-PAPVPT-----	-TISRG-----	287
FiT:QED42805.1	-NNDNFNIVYGTTEFLPKKEKSELCEEI-----	-SESFSSQQOL-----	-PAPVPT-----	-TISRG-----	286
ZoVT:QBS17026.1	-KDEYMDIVGTDPLDKSISDELINEM-----	-TEAQTEMQAL-----	-PNPVT-----	-CVSRG-----	287
ZoVT:QBS17032.1	-KDEYMDIVGTDPLDKSISDELINEM-----	-TEAQTEMQAL-----	-PNPVT-----	-CVSRG-----	287
TrTA:QED42833.1	-EDNFIDINGSDLMLNEELKKRDRRL-----	-EFACMYKTNL-----	-PSPKIK-----	-QIKRG-----	286
GVA:NP_619664.1	SKMLHQNILET-----	-PRGVQV-----	-Q-----	-VPTDLMPEVFTIKKFLGKTNGTLRQEGRD-----	263
AcVB:YP_004935360.1	KPGAYQELLNSQNVQPGFEI-----	-PYKROM-----	-NNETG1KDTLPMVNVDYAIRKLHPNHVGYIKDQG-----	274	
GPGV:YP_004732979.2	-DQTNYKIDGKD-----	-INDLDFKEFLQPGDNIDRYSFL-----	-PSDSSIVKSFDVSYRKGLFTLKS D V R L -----	-HRNDVGPL-----	268
AgVT	-----	-----	-----	-----	*
PVT:YP_002019749.1	DLGRRLLSIKDGPNSNSORSEGRSSGGDHNV-----	-----	-GDAVPSR-----	-IHIRDDSDQSERESQVGEGLGHVRDFQL-----	355
PVT:ADX41472.1	RLERGFES-----	ESLAGLVLQDQYGPNNFCADKRRSPESDGS-----	-LQ05MGRSSHSGSEG-----	-GKGTDVA-----	358
PVT:AFU55322.1	RLERGFES-----	ESLAGLVLQDQYGPNNFCADKRRSPESDGS-----	-LQ05MGRSSHSGSEG-----	-IPLRKRNRFSE-----	358
PVT:AKX90540.1	RLERGFES-----	ESLAGLVLQDQYGPNNFCADKRRSPESDGS-----	-LQ05MGRSSHSGSEG-----	-GKGTDVA-----	358
PrVT:YP_009051685.1	KVOTSSKTPGAVLRRCSSFSQGDDLWEHTEGSKTRNVR-----	-RSGSVKRLVRSGVRA-----	-PRADPGKKGISRG-----	-GEQSSSGRSLSQIQGEFLQSGSES-----	381
PrVT:AHM92767.1	KVQTAQEAGSTLIRRSSSI-----	SENGNVREHRSERGKRTDRIR-----	-GRRGHLRKVGKQ-HRF-----	-SHTKEPQGTTSRG-----	381
ChVT:QNG41876.1	KI0QGTSTGAAVLNRNSASFSSG-----	GHFREYSSEGGVH-----	-SHTKEPQGTTSRG-----	-DOSGAEGSSQFOLOSESAHSDSES-----	379
FiT:QED42805.1	KI0QGTSTGAAVLNRNSASFSSG-----	GHFREYSSEGGVH-----	-SHTKEPQGTTSRG-----	-DOSGAEGSSQFOLOSESAHSDSES-----	379
ZoVT:QBS17026.1	EVWKS-----	ASRFLSLDKRPVLA-----	-ELCSGERRV-----	-REQNSEGGIOIQSEFFQPGSES-----	396
ZoVT:QBS17032.1	EVWKS-----	ASRFLSLDKRPVLA-----	-ELCSGERRV-----	-REQNSEGGIOIQSEFFQPGSES-----	396
TrTA:QED42833.1	EVQTS-----	DASRHSRSLRNSA-----	-EVGKHSSEGSFKFNGMG-----	-REQNEGCLFQTEGKLPSPNDYEPDS-----	380
GVA:NP_619664.1	-----	-KGDNRRVVG-----	-GKGT-----	-KGDNEAEFERYLKQDYNFGRYVDSGAEINSQERADRVERGES-----	278
AcVB:YP_004935360.1	-----	-EEGDRGVGADRG-----	-GPGT-----	-GPGT-----	290
GPGV:YP_004732979.2	-----	SFKGNSL-----	-SGCAENSAE-----	-SGCAENSAE-----	361
AgVT	-----	355	-----	-----	
PVT:YP_002019749.1	-----	358	-----	-----	
PVT:ADX41472.1	-----	358	-----	-----	
PVT:AFU55322.1	-----	358	-----	-----	
PVT:AKX90540.1	-----	358	-----	-----	
PrVT:YP_009051685.1	AA-----	383	-----	-----	
PrVT:AHM92767.1	AA-----	383	-----	-----	
ChVT:QNG41876.1	AC-----	381	-----	-----	
FiT:QED42805.1	AC-----	381	-----	-----	
ZoVT:QBS17026.1	-----	IF	398	-----	
ZoVT:QBS17032.1	-----	IF	398	-----	
TrTA:QED42833.1	AA-----	382	-----	-----	
GVA:NP_619664.1	-----	278	-----	-----	
AcVB:YP_004935360.1	-----	290	-----	-----	
GPGV:YP_004732979.2	STSWADRR	369	-----	-----	

Fig. S3. Alignment of coat protein sequences of AgVT and related viruses

AgVT	M--DPQTLLKDLKAEVLEMMATMYSGSFKSIEGKNDLEELAMQYLLEFIFGTMIAIRGASEKVK-WENSGIESETFN-FEVERKKTPGAGAASAVTI	93
PVT:YP_002019750.1	M--DPTTFLQVIRDEVLNLTVAAAYSQSDQ-QATQALKDGAEQMRLFGLGRIAIISSRNTI-WPD--TEIASLDLQIGMSAASA-----GPPPV-	84
PVT:AFU55323.1	M--DPTTFLQVIRDEVLNLTVAAAYSQSDQ-QATQALKDGAEQMRLFGLGRIAIISSRNTI-WPD--TEIASLDLQIGMSAASA-----GPPPV-	84
PVT:ADX41473.1	M--DPTTFLQVIRDEVLNLTVAAAYSQSDQ-QATQALKNGAKEMQLRFGLGRIAIISSRNTI-WPD--TEIASLDLQIGMSAASA-----GPPPV-	84
PVT:AXK90541.1	M--DPTTFLQVIRDEVLNLTVAAAYSQSDQ-QATQALKDGAEQMRLFGLGRIAIISSRNTI-WPD--TEISSEDLQIGMTAASA-----GPPPV-	84
PrVT:AHM2768.1	MGLTKRSRKMRKEVDLWLLTTKFKPQV---KQGQFSQDAAOFLAKEMWFGNIALKGASEQTE-FED-----QEVSQGWVFPLGGRHGMDFEAEFPGEENR-	93
PrVT:YP_009051686.1	MGLTKRSEMRERFWDALIITTFKPQV---KQGQFSQDAAOFLAKEMFGTNTAIKGASQFTF-FED-----QEVSQGWVFPLGGRHGMDFEAEFPGEENK-	93
ChVT:QNG41877.1	MGITTKERQEIMKVEDGVLLTTKFKGQV---POGQFSVEVLHLFQEYIEFGNIALKGASESTE-WED-----VEVSSGKWWANNT-GFTHTARNLDELPGETSR-	92
FiT:AQDE42806.1	MGITTKERLEIMKVEDGVLLTTKFKGQV---POGQFSVEVLHLFQEYIEFGNIALKGASESTE-WED-----VEVTSGKWWANNT-GFTHTARNLDELPGETRN-	92
TrTA:QED42834.1	MGVTTKRDVMRREVRTSLLILKFKPQM---POGIPPFDEATLQFLEYIEFGNIALKGASSSTE-WED-----IEVQTYGLYTPOVGVGAHHFTRSLEELPGEENK-	93
ZoVT:QBS17027.1	MGLLLEKEEMRKEVSNLRRKFGNQL---QGLVWTNDLFHLQAOFVGNTALKGASQSTE-FGNVYULESEGCLVAEEAQAGSSQEQAGQTSDEEPTEGAVATTTRRSRQV	110
ZoVT:QBS17033.1	MGLLLEKEEMRKEVSNLRRKFGNQL---QGLVWTNDLFHLQAOFVGNTALKGASQSTE-FGNVYULESEGCLVAEEAQAGSSQEQAGQTSDEEPTEGAAATTTRRSRQ	110
gNA:NP_619665.1	MA-HYAKRVERIARIAEELVLAQAPQTDAA---SESGYDRMLNTLFYGYALVGTGKSIIAHYE-----VDIVGPKAS-----	60
AcVB:YP_004935361.1	MSGATSTRNLRKCEEEELVLTGVLAPDA---KTAGDVKGDMYRLTFGYALNGTSKTTKTHYYD-----VDIIGNNIT-----	70
GPGV:YP_004732980.2	M---SIRQELRSTVRRELIAKLSEAN---QVLHGLTEGNKLVDLHIFANIZVEGTSGETI-YPT-----TMVKCYES-----	66
	*	*

AgVT	--EKETVGVSFKVNFLTQYQAVRVLTTSSKNKRKGKTFTRQACIPFAEHAKNYLGHPEC--KTAIFAKAPSAGRAPHFVAFDAEGLNYY--ILKNEEKSVIQWMSARLFKTQ	201
PTV:YP_002019750.1	--AAAPISL1FVRNFNSVVKMLIALSNTSNSFVKNLTRQMCMPFAYQAYGSL---EMGYATWEYKMPKLCKRAKWFVAFDGFSLGLIDTTLMLNDEKTVIQLGRLFKTQ	194
PTV:AFU55323.1	--AAAPVSL1FVRNFNSVVKMLIALSNTSNSFVKNLTRQMCMPFAYQAYGSL---EMGYATWEYKMPKLCKRAKWFVAFDGFSLGLIDTTLMLNDEKTVIQLGRLFKTQ	194
PTV:ADX41473.1	--AAAPISL1FVRNFNSVVKMLIALSNTSNSFVKNLTRQMCMPFAXXXYGLS---EMGYATWEYKMPKLCKRAKWFVAFDGFSLGLIDTTLMLNDEKTVIQLGRLFKTQ	194
PTV:AXK90541.1	--PAAPPSL1FVRNFNSVVKMLIALSNTSNSFVKNLTRQMCIPFAYQAYGSL---EMGYATWEYKMPKLCKRAKWFVAFDGFSLGLIDTTLMLNDEKTVIQLGRLFKTQ	194
PrTV:AMH2768.1	--TLREGAYKFVNFKVNSLVSOLITLVRSSGSVFHNKHPEFRMVCAYAEEAKLEYKKDVEGEFTNLV1LKMPATCKHAPEVCFDFNEGLDVL---RLTDVQAQMWSRLLRFATE	203
PrTV:YP_009051686.1	--ALRDGAYRFVNFKVNSLVSOLITLRSGSNSVFVNKKPFLRRVLAAYASEAKLEYKKDVEGEFSNLV1LKMPATCKHAPEVCFDFNEGLDVL---RLTDVQAQMWSRLLRFATE	203
ChTV:QNG41877.1	--ELRAAAFNFKVNHLTLTQS1LTALANSSNVFVSNSLRLCPVYAEAKTYL1SIRKVDGEYTNL1VQKMPDTCR1LAPEVCFDFNEGLDVL---KLTDVQARVMQKQLRRRFATE	202
F1TA:QED42861.1	--ELRAAAFNFKVNHLTLTQS1LTALANSSNVFVSNSLRLCPVYAEAKTYL1SIRKVDGEYTNL1VQKMPDTCR1LAPEVCFDFNEGLDVL---KLTDVQARVMQKQLRRRFATE	202
TrTA:QED42834.1	--AMRDASFKLVNHOMIMSLTALLKSSNSPVVRN1FTRRCAFPAAEAMYLYNTRTEGEYNSLN1VLMKPCTRCAPEVCFDFNEGLDVL---RLSATQV1KVMQKQLRRRFATE	203
ZoTV:QBS17827.1	1IPVPREVNVRVFRNFTLVKSNSNMLLSTS1ENTFRNKLTRRLCLPFADEAKTYLEIAKGYGEYTTL1VTPKGTCKHAPCEVCFDFNEGLDVL---RLTDVOTSVQMKIQ1RRRFHTE	222
ZoTV:QBS17833.1	VAPPREVNVRVFRNFTLVKSNSNMLLSTS1ENTFRNKLTRRLCLPFADEAKTYLEIAKGYGEYTTL1VTPKGTCKHAPCEVCFDFNEGLDVG---RLTDVOTSVQMKIQ1RRRFHTE	222
GVA:NP_619665.1	--KKTG1DPRGMKVSSEVLGRMR1TLSVASVEGPVKATLROMC1PFAQNAFYDVLVMAEQMGTYSQSLAT1MTRSGKFKEPVDFASGLDK---ALTLQEAETVQYQHMSRFRTE	179
AcVB:YP_004935361.1	--ETSLDRSKG1INVATVARQFNSR1TTP1GAAGK1TR1ROMCPEFAAEAREC1LA1LASKG1YSQSLAT1L5KLQGK1PQVPMFNGGLDGM---SLATEFAAT1TQSLNSRLFTE	179
GPGV:YP_004732980.2	--FNPSLPVKEYSLAEVNKIRVYKESEHTNNDIKLMTFRQVCAFAID1AQGLVFKVFRNLNMHTNIYKKHPKLCKDCAPEVAFDFNEGLNN---NLTPNQKSV1ONRLRFLHVE	176

AgVT		GTIETQNAYESQDSGREL	220
PVT:YP_002019750.1		QSIQIADSTMGEAINREI	213
PVT:AFU55323.1		QSIQIADSTMGEAINREI	213
PVT:ADX41473.1		QSIQIADSTMGEAINREI	213
PVT:AKX90541.1		OSIHIAIDSTMGEAINREI	213
PrVT:AHM02768.1		IKKRESERASEDH-VGDQV	221
PrVT:YP_009051686.1		LKKRESERSVADH-IGDQV	221
ChVT:QNG41877.1		LKKRESDRVSEDH-IGDQL	220
FtTA:QED42806.1		LKKRESDRVSEDH-IGDQL	220
TrTA:QED42834.1		LKKNESDKLTNDH-VGDQV	221
ZoVT:OBS17927.1		KAKRESEARINEG-VGEEV	240
ZoVT:OBS17933.1		KAKRESEARINEG-VGE--	238
GVA:NP_619665.1		GAKGVFNAQSSIGEQAVEI	198
A:VB:YP_004935361.1		GAKAVFAQSIVGEQAVEI	198
GPGV:YP_004732980.2		SEKOKTNAATSGESAFSM	195