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Identification of a novel member of the family *Betaflexiviridae* from the hallucinogenic plant *Salvia divinorum*

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Summary. – *Betaflexiviridae* is a family of plant-infecting RNA viruses with 11 recognized genera, of which genomes have diverse organization with three to six open reading frames (ORFs). A genome sequence of a novel *Betaflexiviridae* species, named Salvia divinorum RNA virus 1 (SdRV1), was identified in *Salvia divinorum*, herbal mint plant with hallucinogenic properties. The SdRV1 genome was predicted to have four ORFs encoding a replicase polyprotein (REP), a movement protein (MP), a coat protein (CP), and a putative nucleic acid-binding protein (NBP). Phylogenetic analyses based on the REP, MP, and CP sequences indicated that SdRV1 is most closely related to members of the genus *Citrivirus*. However, the genome organization of SdRV1 is the same as that of the genus *Prunevirus*. Moreover, the SdRV1 NBP had greatest sequence similarity with members of the genus *Carlavirus*. A complex evolutionary history involving ancestors of these three genera might have resulted in the unique phylogenetic position of SdRV1, which could be considered the founding member of a new genus in the family *Betaflexiviridae*. The genome sequence of SdRV1 might be useful for studies on the evolution of *Betaflexiviridae*.

Keywords: Salvia divinorum RNA virus 1; Betaflexiviridae; Salvia divinorum

Introduction

Betaflexiviridae is a family of plant-infecting viruses of the order *Tymovirales*, and consists of 11 approved genera: *Capillovirus*, *Carlavirus*, *Chordovirus*, *Citrivirus*, *Divavirus*, *Foveavirus*, *Prunevirus*, *Robigovirus*, *Tepovirus*, *Trichovirus*, and *Vitivirus* (Adams *et al.*, 2012, 2016). *Betaflexiviridae* viruses have a flexuous particle and a positive-sense single-stranded RNA genome of approximately 6–9 kb. The genome contains three to six open reading frames (ORFs) depending on the genus (Adams *et al.*, 2012). The 11 genera can be classified into five groups based on genome organization. The viruses of six of the genera (*Capillovirus*, *Chordovirus*, *Citrivirus*, *Divavirus*, *Tepovirus*, and *Trichovirus*) have three ORFs. ORF1 encodes a replicase polyprotein (REP), which has viral methyltransferase, 2OG-Fe(II) oxygenase superfamily, viral RNA helicase, and RNA-dependent RNA polymerase (RdRp) domains. ORF2 and ORF3 encode a movement protein (MP) and a coat protein (CP), respectively (Adams *et al.*, 2012; Rubino *et al.*, 2012; Chavan *et al.*, 2013; Marais *et al.*, 2015). Viruses of the genus *Prunevirus* have four ORFs encoding REP, MP, CP, and a nucleic acid-binding protein (NBP) (Veerakone *et al.*, 2018). Viruses of the genus *Vitivirus* have five ORFs encoding REP, a 20-K protein, MP, CP, and NBP (Martelli *et al.*, 1997; Adams *et al.*, 2012; Diaz-Lara *et al.*, 2018). Viruses of the genera *Foveavirus* and *Robigovirus* have five ORFs encoding REP, three triple gene block proteins (TGB1, TGB2, and TGB3), and CP (Morozov and Solovyev, 2003; Prosser *et al.*, 2015; Jo *et al.*, 2017). Viruses of the genus *Carlavirus* have six ORFs encoding REP, TGB1, TGB2, TGB3, CP, and NBP (Adams *et al.*, 2012; Li *et al.*, 2013).

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Abbreviations: CLBV = citrus leaf blotch virus; CP = coat protein; MP = movement protein; NCBI = National Center for Biotechnology Information; NBP = nucleic acid-binding protein; ORF = open reading frame; REP = replicase polyprotein; RdRp = RNA-dependent RNA polymerase; SdRV1 = Salvia divinorum RNA virus 1; TGB = triple gene block

Table 1. ORFs and functional domains of the SdRV1 genome

ORF	nt position	nt length	aa length	Domain	Pfam	aa position
Replicase polyprotein	76–6219	6144	2047	Viral methyltransferase	PF01660	44–347
				2OG-Fe(II) oxygenase superfamily	PF13532	939–1047
				Viral (superfamily 1) RNA helicase	PF01443	1249–1500
				RNA-dependent RNA polymerase	PF00978	1622–2024
Movement protein	6228–7253	1026	341	Viral movement protein	PF01107	14–196
Coat protein	7500–8591	1092	363	Viral coat protein	PF00286	169–315
Putative nucleic acid-binding protein	8705–9067	363	120	Viral nucleic acid-binding	PF05515	1–89

Salvia divinorum, which belongs to the *Lamiaceae* family, is a herbal mint plant with transient psychoactive properties. Owing to its hallucinogenic effects, for many centuries the Mazatec people of Oaxaca, Mexico, have ingested it as a tea or smoked it in traditional spiritual practices (Valdes, 1994; Chavkin *et al.*, 2004). The hallucinatory compound found in *S. divinorum* is called salvinorin A; it has a highly selective and efficient agonistic effect on kappa-opioid receptors in humans (Roth *et al.*, 2002; Chavkin *et al.*, 2004). These receptors are located in parts of the central nervous system, and are known to be involved in psychiatric disorders such as anxiety, depression, and addiction (Butelman and Kreek, 2015; Anderson and Becker, 2017).

Salvinorin A from *S. divinorum* is considered a new medical substance for the treatment of mental disorders (Kivell *et al.*, 2014; Riley *et al.*, 2014). Several transcriptomic analyses using next-generation sequencing technology have been conducted to investigate the genetic features and biochemistry of *S. divinorum* (Chen *et al.*, 2017; Pelot *et al.*, 2017). Plant transcriptome data often contain sequences from RNA viruses that infect the plant samples, which may be identified as novel RNA viruses (Goh *et al.*, 2018; Kim *et al.*, 2018). In the present study, we analyzed a previously reported transcriptome dataset from the leaf trichomes of *S. divinorum* (Pelot *et al.*, 2017), and identified a novel RNA virus of the family *Betaflexiviridae*.

Materials and Methods

Transcriptome dataset. We analyzed a previously reported plant transcriptome dataset isolated from the leaf trichomes of *S. divinorum* (6.8 gigabases of paired-end reads with a single run) (Pelot *et al.*, 2017). The transcriptome dataset is available from the Sequence Read Archive (SRA) at the National Center for Biotechnology Information (NCBI; Acc. No. SRR3716680). Raw RNA-seq reads were filtered to collect high-quality reads using the Sickle program (version 1.33; https://github.com/najoshi/sickle) with the option "-q 30 -l 55." *De novo* assembly was conducted using the SPAdes Genome Assembler (version 3.10.1; http://cab.spbu.ru/software/spades) with the "--rna" option (Bankevich *et al.*, 2012).

Identification of viral genome contig. All the RNA contigs were examined to determine whether they contain a viral RdRp motif. The Pfam database (release 31.0; http://pfam.xfam.org) was parsed to collect reference sequences of viral RdRp motifs. Pfam Acc. Nos. with viral RdRp motifs include PF00602, PF00603, PF00604, PF00680, PF00946, PF00972, PF00978, PF00998, PF02123, PF03431, PF04196, PF04197, PF05788, PF05919, PF07925, PF08467, PF08716, PF08717, and PF12426. Representative viral RdRp motif sequences derived from 394 viruses were converted to a BLAST-searchable database. A BLASTX search was performed with the parameter "-evalue e-5" to compare the assembled contigs with the custom-built viral RdRp database. RNA-seq reads were mapped to a viral contig using the BWA program (version 0.7.16a-r1181;

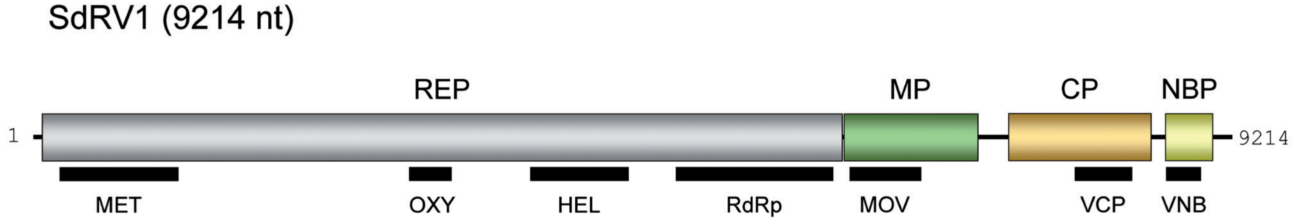


Fig. 1

Schematic representation of SdRV1 genome organization
Open reading frames (ORFs) are depicted as gray boxes: REP, replicase polyprotein; MP, movement protein; CP, coat protein; and NBP, putative nucleic acid-binding protein. Predicted Pfam domains are marked by lines below proteins: MET, viral methyltransferase; OXY, 2OG-Fe(II) oxygenase superfamily; HEL, viral RNA helicase; RdRp, RNA-dependent RNA polymerase; MOV, viral movement protein; VCP, viral coat protein; and VNB, viral nucleic acid-binding. The coordinates and lengths of ORFs and domains are presented in Table 1.

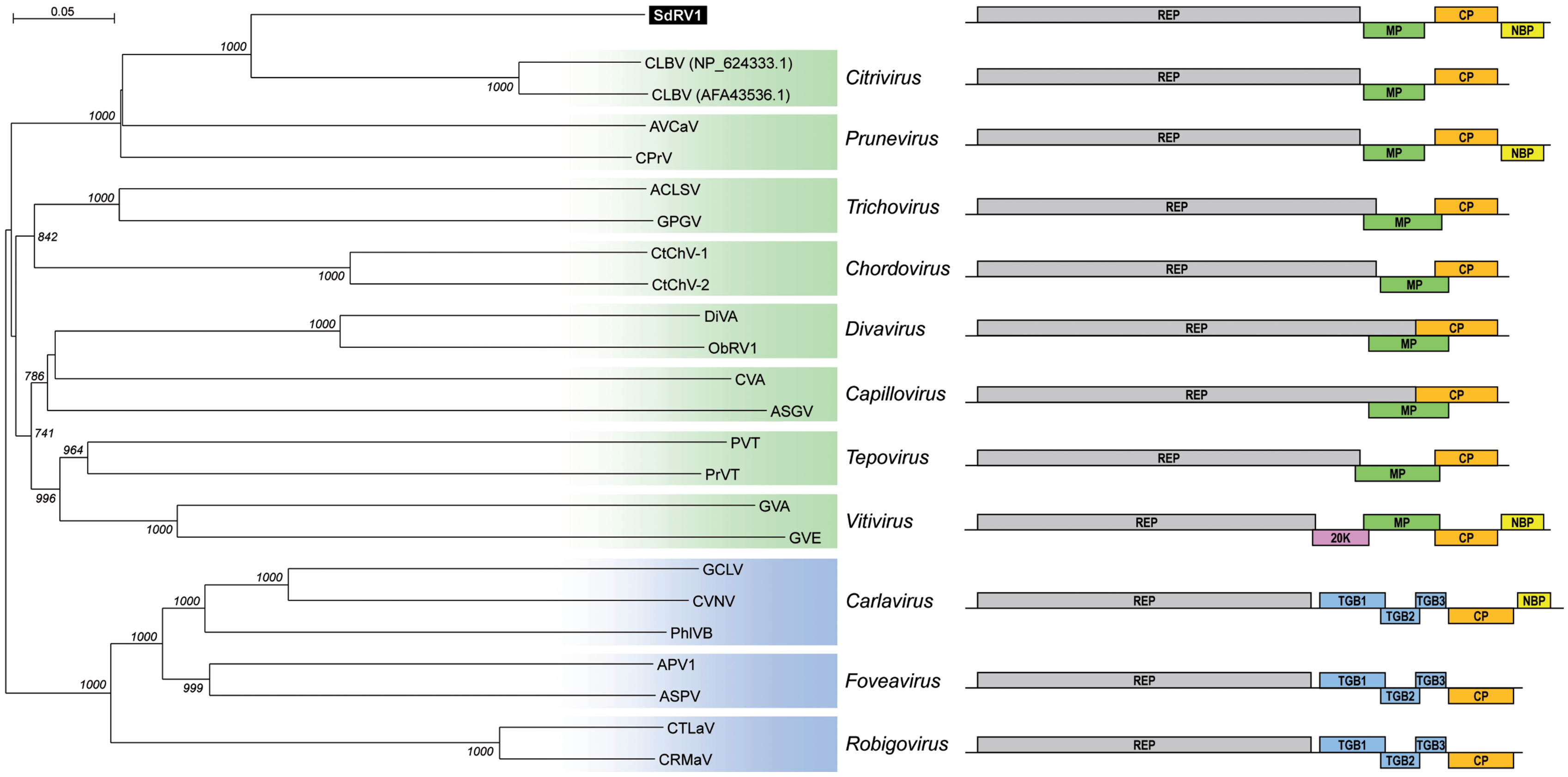


Fig. 2

Phylogenetic tree of SdRV1 and related viruses based on replicase polyprotein (REP) sequences

The phylogenetic tree was inferred from the multiple sequence alignment of REP sequences using the neighbor-joining method. Bootstrap values of 70% or higher, computed from 1000 replicates, are shown at the tree nodes. The full names of viruses and NCBI Acc. Nos. are presented in Table 2. The schematic genome organizations depicted at the right are borrowed from the ViralZone web resource (not to scale).

Table 2. Comparison of the sequence of replicase polyprotein (REP) from SdRV1 with REP sequences from representative members of *Betaflexiviridae*

No.	Acronym	Full name	Genus	NCBI	Identity	Similarity	Overlap length
1	CLBV	Citrus leaf blotch virus	*Citrivirus*	NP_624333.1	48.8%	71.9%	2085
2	CLBV	Citrus leaf blotch virus	*Citrivirus*	AFA43536.1	48.2%	71.9%	2084
3	AVCaV	Apricot vein clearing associated virus	*Prunevirus*	YP_008997790.1	36.7%	57.7%	2104
4	CPrV	Caucasus prunus virus	*Prunevirus*	AKN08994.1	38.2%	67.3%	2093
5	ACLSV	Apple chlorotic leaf spot virus	*Trichovirus*	NP_040551.1	30.8%	56.9%	2107
6	GPGV	Grapevine Pinot gris virus	*Trichovirus*	YP_004732978.2	32.0%	57.5%	2089
7	CtChV-1	Carrot Ch virus 1	*Chordovirus*	YP_009103999.1	31.1%	58.6%	2093
8	CtChV-2	Carrot Ch virus 2	*Chordovirus*	YP_009103996.1	30.4%	57.7%	2100
9	DiVA	Diuris virus A	*Divavirus*	YP_006905850.1	26.5%	51.1%	2084
10	ObRV1	Ocimum basilicum RNA virus 1	*Divavirus*	YP_009408144.1	27.2%	51.3%	2073
11	CVA	Cherry virus A	*Capillovirus*	NP_620106.1	32.4%	62.3%	1052
12	ASGV	Apple stem grooving virus	*Capillovirus*	NP_044335.1	31.9%	60.9%	1026
13	PVT	Potato virus T	*Tepovirus*	YP_002019748.1	34.5%	64.0%	989
14	PrVT	Prunus virus T	*Tepovirus*	YP_009051684.1	28.6%	54.6%	2084
15	GVA	Grapevine virus A	*Vitivirus*	NP_619662.1	27.0%	52.5%	2077
16	GCLV	Garlic common latent virus	*Carlavirus*	YP_004936159.1	29.4%	56.0%	2116
17	CVNV	Coleus vein necrosis virus	*Carlavirus*	YP_001430021.1	27.6%	56.0%	2106
18	PhlVB	Phlox virus B	*Carlavirus*	YP_001552317.1	28.6%	55.8%	2177
19	APV1	Asian prunus virus 1	*Foveavirus*	YP_009094347.1	28.8%	58.2%	2125
20	ASPV	Apple stem pitting virus	*Foveavirus*	NP_604464.1	28.8%	56.7%	2243
21	CTLaV	Cherry twisted leaf associated virus	*Robigovirus*	YP_009046478.1	29.5%	58.4%	2123
22	CRMaV	Cherry rusty mottle associated virus	*Robigovirus*	YP_007761581.1	29.6%	57.6%	2117

https://github.com/lh3/bwa) (Li and Durbin, 2009). Sequence variants were identified using SAMtools/BCFtools programs (version 1.6; http://www.htslib.org) (Li *et al.*, 2009).

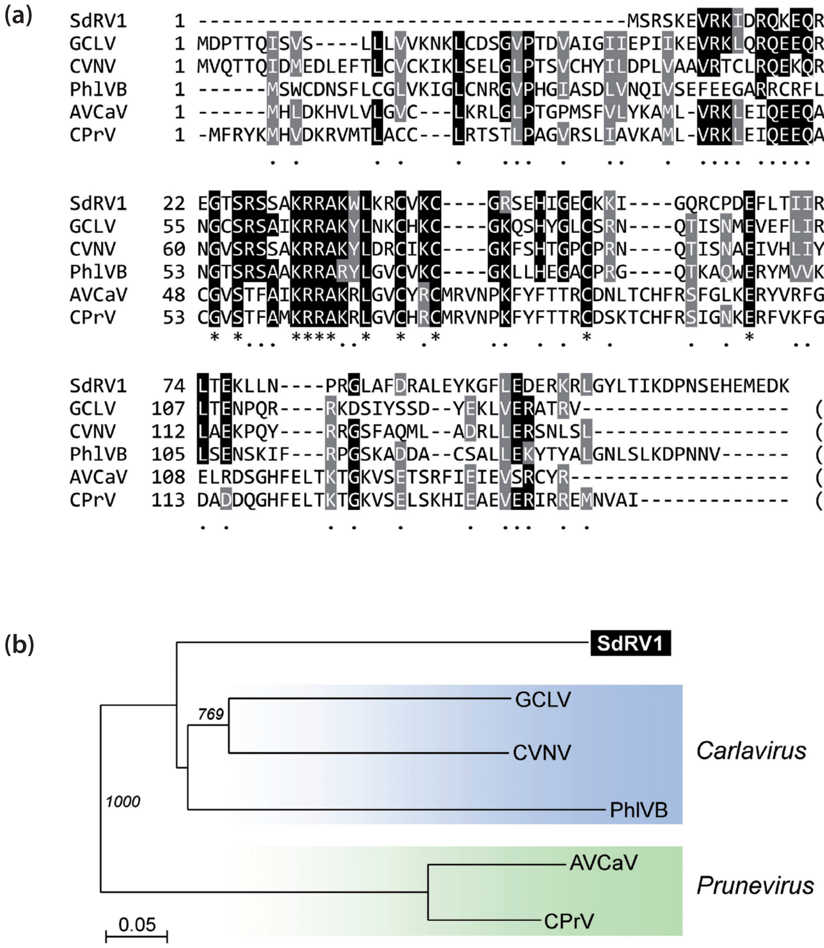
Sequence comparison and phylogenetic analysis. NCBI BLAST searches were performed to identify and collect closely related viruses (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Protein coding regions were predicted based on the outputs of BLASTX and ORFfinder (https://www.ncbi.nlm.nih.gov/orffinder). Functional domains were predicted by Pfam. Pair-wise identities among protein sequences were calculated using the FASTA program (version 36.3.6; https://fasta.bioch.virginia.edu/fasta_www2/fasta_down.shtml). Multiple sequence alignments of sequences were generated using the MUSCLE program (version 3.8.425; https://www.drive5.com/muscle) (Edgar, 2004). Phylogenetic trees were inferred using the neighbor-joining method implemented in ClustalW2 software (version 2.1; http://www.clustal.org) (Larkin *et al.*, 2007). We referred to the ViralZone web resource (https://viralzone.expasy.org) for the genome organizations of viruses (Hulo *et al.*, 2011).

Results and Discussion

A BLASTX search was performed to compare the assembled contigs of the *S. divinorum* transcriptome dataset (SRR3716680) against the custom-built viral RNA-dependent RNA polymerase (RdRp) database. A 9214 nucleotide (nt) contig had sequence similarity with the RdRp motif sequence of the citrus leaf blotch virus (CLBV) (UniProt Acc. No. Q91QZ3). A BLASTX search of the contig against the NCBI non-redundant protein database confirmed that it is a viral genome closely related to CLBV, the type species of the genus *Citrivirus* of the family *Betaflexiviridae* (Vives *et al.*, 2001). The contig was considered a novel *Betaflexiviridae* virus and named as Salvia divinorum RNA virus 1 (SdRV1).

A total of 26,102 reads from the RNA-seq data SRR3716680 were assembled for the SdRV1 genome contig. There were five single-nucleotide polymorphisms at nt positions 2748, 4892, 6506, 6984, and 8054 (Supplementary Table S1), indicating that the SdRV1 genome contig is a composite sequence derived from a rather homogeneous viral population.

The SdRV1 genome was predicted to have four open reading frames (ORFs) (Table 1 and Fig. 1). ORF1 encodes a 2047 amino acid (aa) replicase polyprotein (REP). REP is composed of four functional domains predicted by Pfam: a viral methyltransferase (Pfam Acc. No. PF01660) at aa position 44–347, 2OG-Fe(II) oxygenase superfamily (PF13532) at 939–1047, viral (superfamily 1) RNA helicase (PF01443) at 1249–1500, and RdRp (PF00978) at 1622–2024. ORF2 encodes a 341 aa movement protein (MP), which has a viral movement protein domain (PF01107) at 14–196. ORF3 en-



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SdRV1    1 -------------------------------------MSRSKEVRKIDRQKEQRV--KFG
GCLV     1 MDPTTQISVS----LLLVVKNKLCDSGVPTDVAIGIIEPIIKEVRKLQRQEEQRL-LRF-
CVNV     1 MVQTTQIDMEDLEFTLCVCKIKLSELGLPTSVCHYILDPLVAAVRTCLRQEKQRQNAPF-
PhlVB    1 ------MSWCDNSFLCGLVKIGLCNRGVPHGIASDLVNQIVSEFEEGARRCRFLK--EFH
AVCaV    1 ------MHLDKHVLVLGVC---LKRLGLPTGPMSFVLYKAML-VRKLEIQEEQAK--PL-
CPrV     1 -MFRYKMHVDKRVMTLACC---LRTSTLPAGVRSLIAVKAML-VRKLEIQEEQAR--PL-
                 . .      . .    .   ...  .   ..   .  .... .....     .

SdRV1   22 EGTSRSSAKRRAKWLKRCVKC----GRSEHIGECKKI----GQRCPDEFLTIIRAGPNRS
GCLV    55 NGCSRSAIKRRAKYLNKCHKC----GKQSHYGLCSRN----QTISNMEVEFLIRCGTIRY
CVNV    60 NGVSRSSAKRRAKYLDRCIKC----GKFSHTGPCPRN----QTISNAEIVHLIYNGTTRF
PhlVB   53 NGTSRSAAKRRARYLGVCVKC----GKLLHEGACPRG----QTKAQWERYMVVKEGSISF
AVCaV   48 CGVSTFAIKRRAKRLGVCYRCMRVNPKFYFTTRCDNLTCHFRSFGLKERYVRFGLGKNGV
CPrV    53 CGVSTFAMKRRAKRLGVCHRCMRVNPKFYFTTRCDSKTCHFRSIGNKERFVKFGLGKNGL
            * *... ****..*  * .*    ..  . . * .      .  . *   ..  *

SdRV1   74 LTEKLLN----PRGLAFDRALEYKGFLEDERKRLGYLTIKDPNSEHEMEDK
GCLV   107 LTENPQR----RKDSIYSSD--YEKLVERATRV------------------  (38)
CVNV   112 LAEKPQY----RRGSFAQML--ADRLLERSNLSL-----------------  (39)
PhlVB  105 LSENSKIF---RPGSKADDA--CSALLEKYTYALGNLSLKDPNNV------  (38)
AVCaV  108 ELRDSGHFELTKTGKVSETSRFIEIEVSRCYR-------------------  (21)
CPrV   113 DADDQGHFELTKTGKVSELSKHIEAEVERIRREMNVAI-------------  (23)
           . .        . .   .     .  ...  . .
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Fig. 3

Multiple sequence alignment and phylogenetic tree of nucleic acid-binding protein (NBP) sequences

(a) The NBP sequences of SdRV1, carlaviruses (GCLV, CVNV, and PhlVB), and pruneviruses (AVCaV and CPrV) were multiply aligned. **(b)** The phylogenetic tree inferred from multiple sequence alignment of NBP sequences is shown. The full names of the viruses are presented in Table 2. The NCBI Acc. Nos. of the NBP sequences are: SdRV1, AYE54587.1; GCLV, YP_004936164.1; CVNV, YP_001430026.1; PhlVB, YP_001552322.1; AVCaV, YP_008997793.1; and CPrV, AKN08997.1.

codes a 363 aa coat protein (CP), which contains a viral coat protein domain (PF00286) at 169–315. ORF4 encodes a 120 aa putative nucleic acid-binding protein (NBP) with a viral nucleic acid binding domain (PF05515) at 1–89.

NCBI BLAST searches were performed to identify and collect viruses related to SdRV1. A total of 23 viruses from 11 genera of the family *Betaflexiviridae* were selected including CLBV (*Citrivirus*), apricot vein clearing associated virus (AVCaV) (*Prunevirus*) (Elbeaino *et al.*, 2014), apple chlorotic leaf spot virus (ACLSV) (*Trichovirus*), carrot Ch virus 1 (CtChV-1) (*Chordovirus*), Diuris virus A (DiVA) (*Divavirus*), cherry virus A (CVA) (*Capillovirus*), potato virus T (PVT) (*Tepovirus*), and grapevine virus A (GVA) (*Vitivirus*), garlic common latent virus (GCLV) (*Carlavirus*), apple stem pitting virus (ASPV) (*Foveavirus*), cherry twisted leaf associated virus (CTLaV) (*Robigovirus*).

A sequence comparison of REP sequences of SdRV1 and representative *Betaflexiviridae* viruses was conducted using the FASTA program (Table 2). The SdRV1 REP had the highest sequence similarity with the CLBV REP (NCBI Acc. No. NP_624333.1), which is a member of the genus *Citrivirus*, with 48.8% identity and 2085 aa overlap. The SdRV1 REP also had high sequence similarity with viruses of the genus *Prunevirus*: AVCaV with 36.7% identity and 2104 aa overlap; and Caucasus prunus virus (CPrV) (Marais *et al.*, 2015) with 38.2% identity and 2093 aa overlap. Other members of the family *Betaflexiviridae* also had significant sequence similarity. The sequence comparison indicated that SdRV1 is closely related to the genus *Citrivirus*.

A multiple sequence alignment of full-length REP sequences of SdRV1 and representative *Betaflexiviridae* viruses was generated by MUSCLE (Supplementary Fig. S1). The

SdRV1 REP had greatest sequence similarity with the REPs of citriviruses and pruneviruses. The SdRV1 MP and CP sequences also had greatest sequence similarity with the MPs and CPs of citriviruses (Supplementary Figs. S2 and S3).

We conducted a phylogenetic analysis using the multiply aligned REP sequences of SdRV1 and selected viruses of the family *Betaflexiviridae* using ClustalW2 (Fig. 2). SdRV1 formed a clade with members of the genus *Citrivirus* (CLBV), in agreement with the protein sequence comparisons. The next closest viruses were members of the genus *Prunevirus* (AVCaV and CPrV). The phylogenetic analysis implied that SdRV1 is a novel species that is most closely related to the genus *Citrivirus* in the family *Betaflexiviridae*.

However, citriviruses have only three ORFs encoding REP, MP, and CP (Hajeri *et al.*, 2010; Elbeaino *et al.*, 2014; Marais *et al.*, 2015). In addition to REP, MP, and CP, the SdRV1 genome was predicted to have an additional fourth ORF encoding a 120 aa NBP. NBP is commonly found in viruses of the genera *Prunevirus*, *Vitivirus*, and *Carlavirus* (Adams *et al.*, 2012; Rubino *et al.*, 2012; Veerakone *et al.*, 2018), but not in the genus *Citrivirus*. Among these viruses, only pruneviruses have the same genome organization as SdRV1, implying a possible affiliation between SdRV1 and pruneviruses (Fig. 2).

More interestingly, the SdRV1 NBP had greatest sequence similarity with the NBPs of carlaviruses, with 38–39 identical residues (Fig. 3a). The NBP sequences of SdRV1 and pruneviruses had the next greatest sequence similarity, with 21–23 identical residues. A phylogenetic analysis of NBP sequences also confirmed the closest relationship of SdRV1 and carlaviruses (Fig. 3b). It is worth noting that the SdRV1 NBP is most similar to the NBPs of carlaviruses, which have six ORFs with triple gene block (TGB) proteins instead of MP.

Phylogenetic analysis of SdRV1 proteins and comparison of genome organization revealed conflicting phylogenetic relationships. The sequences of SdRV1 REP, MP, and CP support the closest relationship with the genus *Citrivirus*. However, the genome organization of SdRV1 is the same as that found in the genus *Prunevirus*. Moreover, SdRV1 NBP had the highest sequence similarity with the NBPs of the genus *Carlavirus*. The uniqueness of the SdRV1 genome might be due to a complex evolutionary history involving the ancestors of the genera *Citrivirus*, *Prunevirus*, and *Carlavirus*. SdRV1 may be classified as a novel genus in the family *Betaflexiviridae*.

In conclusion, we identified a novel RNA virus named SdRV1 from *S. divinorum*. The genome organization and protein sequences revealed that SdRV1 has a unique phylogenetic position. SdRV1 could be considered the founding species of a novel genus in the family *Betaflexiviridae*. The genome sequence of SdRV1 identified in the present study might be useful for inferring the evolution of *Betaflexiviridae* viruses.

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

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SUPPLEMENTARY INFORMATION

Identification of a novel member of the family *Betaflexiviridae* from the hallucinogenic plant *Salvia divinorum*

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Table S1. Sequence variations of SdRV1

Position	Con[a]	Alt[b]	Quality[c]	Con #	Alt #	Con %	Alt %
2748	A	G	201	146	51	74.11	25.89
4892	G	A	222	186	198	48.44	51.56
6506	C	T	39.1421	215	48	81.75	18.25
6984	T	C	222	148	123	54.61	45.39
8054	C	T	130	188	55	77.37	22.63

[a]Sequence of the assembled contig. [b]Alternative sequence observed in RNA-seq reads. [c]Phred-scaled quality score for the assertion made in Alt by BCFtools.

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Fig. S1

Multiple sequence alignment of replicase polyprotein (REP) sequences of SdRV1 and representative members of *Betaflexiviridae*

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SdRV1:AYE54584          --MSLLVSKTPVECMLGNFEKSDIKRIYEPAVNYISSTA-IFRNKHFAYAMEPFLKKKLSS--IGIELYPNGYIVHSHPFSKTLENHLLFDVLPGIIHDQ    95
CLBV:NP_624333.1        --MALMSNKTAIESILGNFEKKHVDAIYNAAAQTILSHS-EFRNKHFAYSLNSYQKKIASK--VGIELYPNGYLPHSHPLSKIFENHLLFDVLPGVVNTS    95
CLBV:AFA43536.1         --MALMSNKTAIESILGNFEKKHVDAVYNAAAQTIISHS-EFRNKHFAYALTSYQKKIASK--VGIELYPNGYMPHSHPLSKIFENHILFDVLPDVVSTS    95
AVCaV:YP_008997790.1    ---MALLYRTPQVNLLGSFPQKHVEIIYNLQFERFKKICICRFCIFLTHSEKNQKKVASIRGWLGVPLHPTPYLAHSHPFSKMLENHILLNVLPGHITG-    96
CPrV:AKN08994.1         --MASVTVRTPMEKFFAANDKNDQRSILTSGVNFVKKFC-DDKGIHFAYYVNDRKKEALTN--LGVTLHPIPFLTHSHPFCKTLENHLLINVLPNLLGNG    95
ACLSV:NP_040551.1       ---MAFSYRTPQEELLSRLPQSQQEVISGFQYERIQKEE-EKKVENFSFYLPEKTREWFTK--SGVYLSPFAYVNHSHPGCKTLENHLLFNVVASYISK-    93
GPGV:YP_004732978.2     ---MTFFYRTPTEELISKFTSEEQARIYAPSQRYIENTEIGSNSLFFSYNLKEIQKKFFIS--NGIELSPFSFKAHSHPACKTLENYFLFSFLPSFISH-    94
CtChV-1:YP_009103999.1  ---MSYGFRTPQEKILSTFSPSFIDNVQSTSGRTFEDEE-NRIGKFFNFNLDDRKKEFASN--SGIYLSPYSYKSHSHPLCKTIENHLLYVVIPPLIQN-    93
CtChV-2:YP_009103996.1  ---MSYSYRTPQEKILSTLNPTLIDGVASFSGRIFEENE-SRLGKYFNYHLSDKKKEFAAQ--AGIYLSPYSFQSHSHPLCKTIENYLLYVVMPPMIAN-    93
DiVA:YP_006905850.1     ---MALSYRTPTEYLINQLPARLTDNIAVKQVDLIQSDE-DCYGSYLNYNLSKEQKKFLVD--KGLYLSPYSWRHHSHPACKTIENWLLYKEIGSYAKHV    94
ObRV1:YP_009408144.1    ---MSLIYRTPVENLINQLPSRLTENVAVKQVDILQNME-ESIGKYFNFNLSKEQKKFLVD--KGVYLSPFSWKHHSHPGCKTIENWLLYNEIGFHIRHI    94
CVA:NP_620106.1         ---MAFVAKFAEENYFNSLPSNVTDAFLRDGFNAEHNRF-EILSRHFAFALKPSQRTYLND--CGIQLAPIASKTHPHPVSKIIENHLLYCVVSNMISN-    93
ASGV:NP_044335.1        ---MAFTYRNPLEIAINKLPSKQSDQLLSLTTDEIEKTL-EVTNRFFSFSITPEDQELLTK--HGLTLAPIGFKSHSHPISKMIENHLLYICVPSLLSS-    93
PVT:YP_002019748.1      ---MSFSFRTPAELFVQSLPKEYAEACFKSHAANFQIRS-DKGVGLFDFACSSVVKERLTK--AGIPVSAFCNQEHSHPASKMIENHLLYNILPNYLNLK    94
PrVT:YP_009051684.1     ---MAFSYRTPAEEFLSKLPSASQETVDEYALRSLRDQE-KASSRNYSYHLTDTQKSFCSK--VGVPLSVNNFMVHPHPYCKTMENFLLHDNLFHYRNLI    94
GVA:NP_619662.1         MSISVSSQRVAVSNLYTNGSEESVKAIKELKSKRLLETE-TRLDGLFDYYIPDTLREILTG--YGMEFSVHSFQGHAHPVSKMIENHMLYRVAPNYFSS-    96
GVE:YP_002117775.1      MSLGASSQRVAYANLYANIGSDKLSEVRDRKASTVNSIE-AYASGLFDYYVSDDVYDFLAS--KGLPLSINCFRTHSHPISKMIENHFIFNLIGNNLAK-    96
GCLV:YP_004936159.1     ---MALTYRSPLEEVLTSFSASEQSLIAEPAITSYRGLE-RDLFHFFNYNVGPYAKEKLIG--AGVYLSPFSGVPHSHPVCKTLENHLLYRVLPSILDN-    93
CVNV:YP_001430021.1     ---MALTFRSPLEEVLTNFSSTEQSLISKTAINHYSNLE-SSLFNFFNLNVDAYSKEKLIN--SGIYLSPFSGVPHSHPVCKTLENHILYRVLPSLIDS-    93
PhlVB:YP_001552317.1    ---MALTYRSPLEENVAAYDASVQSTIASTSACYYKDTE-ADKFRFFNYFVNPTAKKKLIE--AGLYLSPYSAMPHSHPVCKTLENYFLFEVIPSKIDN-    93
APV1:YP_009094347.1     ---MALTYRSPIGEVLNRFTSEEQSRVSSTSVSRLTQFE-VNNHKLFSFAMSEKAKEKLIK--VGIYLSPFSFEPHSHPVCKTLENHILYNILVNKLDN-    93
ASPV:NP_604464.1        ---MALLSRTAAEEVIASFTSEEQSRISTQAVLALTNVE-KDKHDLFNYALPELAKMRLFN--SGIYLSPHSYRPHSHPVCKTLENNILFNILPSYLDN-    93
CTLaV:YP_009046478.1    ---MALHTITPAENVLAQFSSEEASRIGASAISNFSKLE-ADYHNLFHFHLPAYAKKKLSE--RGFYLSPFSYETHSHPVSKTIESHLINIKLPNYINE-    93
CRMaV:YP_007761581.1    ---MALHTITPAEGVLAQFSSEEASRIGASAISNFSKLE-SEYHSLFHFHLPAYAKSKLSN--RGFYLSPFSYETHSHPVSKTIESHLINVKLPNYITE-    93
                                  .                                                     *. .       *.** .* :*. ::

SdRV1:AYE54584          A----FIFCSIKECKIRTFKA-----------------KSTSANISFLNRLIDGRDVARYPEVTH------------SSESQYLKGNSDSSPFSNSFKRT   162
CLBV:NP_624333.1        R----LVMCSIKESKVLVFKGIRDKSRRQ-VSDLNALNSLNNSHTSFINRLVASKDVSRYTEEAD---------------AFFQSKKGSPELFSRNFIKS   175
CLBV:AFA43536.1         K----LIMCSIKESKVLIFKNIRDRKKDNGALGFCGKDTSASDHTSFVNRLVAPKDIRRYTEEAD--------------AFFSSKKKNDPELFSNNFIRC   177
AVCaV:YP_008997790.1    S----WVFSSIKPSKVESLAT-----------------KGKKSVLKTINRLLCAKDFGRYDVDTD-------------SSVIRSISREAPDILPEPFVRA   162
CPrV:AKN08994.1         H----WVFTSVKKAKVNSVIKLA---------------GGVSNNVDIVNRCICAKDFGRYDFEPG-------------SVDQKINILSKDHLFPKNFIRS   163
ACLSV:NP_040551.1       YSY--VACLSIKSNKMSKMER------LG---------PNSVKTYDILNRLVTAKDKARYGPLAK------------------------PERSPCP----   148
GPGV:YP_004732978.2     SGIRELFLFSIKKAKVTRLKN-----------------LVDNVQLNHLNRLVEVKDKMRYGMDVS----------------------------PERIEKR   149
CtChV-1:YP_009103999.1  FNN--LNVVSMKESKLKILHE-----SSD---------APKKMSINLINRLMDVKDSFRYKSGDG---------------LSIKYPTQLLESNTRDYDPL   162
CtChV-2:YP_009103996.1  FNN--LYVVSMKESKLRILHS------NS---------QLTGISLNLINRLVDVKDSFRYKDGGD-----------YSVKYPTDLLKWNSDKKYDPLLDC   165
DiVA:YP_006905850.1     SKQQTIAFISLREGKLNAIKKIHFEKKNN---------KVACEKICSFNRYYHTKDRLRYSDSSG------------------------REIIYKSFDKI   161
ObRV1:YP_009408144.1    CRDSSVAFLSLREGKLKNLEKIHFRQGNH---------DQTNDKIRSFNKIHSPKDCLRYSSFSD------------------------RETLYQSFRDI   161
CVA:NP_620106.1         FKF--LVFLSIKEVKAEYIWN-------K---------NTADTVREISNRILDIKDAFRYGPTNT-----------------VNGGINNFSFFCANLNRR   158
ASGV:NP_044335.1        FKS--VAFFSLRENKVDSFLK--MHSVFS---------HGKIKSLGMYNAIIDGKDKYRYGDVEF---------------------SSFRDRVIGLRDQC   159
PVT:YP_002019748.1      N----YTAISIKDSKVRKLLK------------------NGVDSLETFNRLFSCKDALRYVDPET------------------------------CDMDK   142
PrVT:YP_009051684.1     D-----TYVSIKEEKVGLLNR-----------------SRGLNFHRVINRCVADRDNIRYKNCVS------------------------KSFFEDTRNHA   148
GVA:NP_619662.1         N----TLVVSCKESKIKRLRL-----KNA---------NNRNLNFTQYNRLVHANHHHRYENAFR-------------------------ELDVGNLTNL   153
GVE:YP_002117775.1      D----STFISFKEDKLVLLEN------KK---------SRIDGNTCIINRLVHAKDALRYKDPLR-------------------------NLWFDEDQKT   152
GCLV:YP_004936159.1     S----FLFVGIKESKLNFLRA-------R---------HQNLSMVELVNRYVTSADRTRYPNDFH--LSITAEQCFNRYDGFKHLGPGLRKLLPHCITV-   170
CVNV:YP_001430021.1     T----FTFVGIKEAKLQFLRQ-------R---------HSHLNLVQLINRYVTSADRLRYPSEFH--ITPSKAIEVCEKWGRFGKSDSLRELLPACITH-   170
PhlVB:YP_001552317.1    R----FFFVGIKNEKLSMLKA-------R---------NTHLSTVEKVNRYVTSADKVRYGSDFV--VRPTEKIPGLIRQRPCLDGVTLKDLVPELMRK-   170
APV1:YP_009094347.1     S----FYAIGIKGSKVNFLKS-------R---------SKNLSMLEYMNRIVTSADKYRYGSDFT--TLSTQQIDNLCSKQSLEKCGTLRELVPLVKMSK   171
ASPV:NP_604464.1        S----FYLVSIKKNKVDFLKR-------R---------HPDLQMVETINRYISSIDKTRYGGFFHVSPSKISAKFKCDRRTGFEDDASLIDLIPGCMEG-   172
CTLaV:YP_009046478.1    D----FLIVGIKDNKLSVLRK-----------------EKKLRFLEAVNRCVTSHDIQRYGPSFH---FEKAKSNWKTDFSEVNLSAGVQSLLPRVLFDK   169
CRMaV:YP_007761591.1    D----FLIVGIKENKLSVLRK-----------------DKKMRFLEALNRCVTSHDIQRYGPSFH---FEKARSNWRSDFSGVNLSAGVQSLLPRILFDK   169
                                 . :  *   .                             *      .  **

SdRV1:AYE54584          VG----QGKNFFFHDEVHHWSQKDIFRFLKDFSP-KRLVFTVVYPAELLAGYANSQNPKMYKFK-IDG---D--KLFFFPDGVTSEGYQQPL-NLNWLFK   250
CLBV:NP_624333.1        LE----NKEAVFFHDEVHHWTKAQMFSFLKSTKV-KRFIFTVVYPPEILKKFANSQNPKVYDFK-VDK---G--RLFFFPDGVKTEAYEQKL-NMEWLFS   263
CLBV:AFA43536.1         IS----NKEAVFFHDEVHHWTKAQMFSFLKRTKV-RRFIFTIVYPPELLKKFANSQNPKVYDFK-VDK---G--RLFFFPDGVKTEAYEQKL-NMEWLFS   265
AVCaV:YP_008997790.1    V-----KGRNVMIHDEVHHWTLDDMLGFLDRARP-NRFVFSVVYPVELLAGILESQNPKMYKFQDSKS---D--KIVFFPDGRASEGYEQRA-NLRWLFC   250
CPrV:AKN08994.1         V-----RKKKIFIHDEVHHWSHLNMIQFLEETAT-PLLLCSVVFPPELLGGIKTPQNSALYGFQ-VDG---D--KLFFFPDGSRSEMYEQPS-NLNWLFE   250
ACLSV:NP_040551.1       ------KKTNIFIHDEIHYWSRDQLETFLQVHRP-KNLWATLVFPPEILAGYKSSVLPFLYQFE-IHG---K--DLVYMPDGVRSESYTQPL-ENGFLLS   234
GPGV:YP_004732978.2     K-----TGLDIFIHDEIHHWSKAQLISFLEVHRP-RNIMATVVFPIEILGGFKSSVLKFLYEFE-CRN---G--KLFYYPDGVMSEAYVQTL-ESSYLFK   236
CtChV-1:YP_009103999.1  MDVRIEKGSNFLFHDELHYWTFSMMLDFLEKFEP-SHVICTAVFPVEILEGIKQSLYPEVYSFEILQT---G--NFVFAPDGVYSESYEQSV-NMKWLFS   255
CtChV-2:YP_009103996.1  SIE---KGRNFLFHDEMHYWSFDMMLDFLRKFEP-DNVLCTVIFPVEIFSGVKQSLFPDVYSFQIIKN---K--RFVFAPDGCYSESYEQSV-DMKWLFS   255
DiVA:YP_006905850.1     GDQIG-PRASFYIHDECHYWSPNDLSNFLSRTKA-ESILATVIHPTEIDVGKDCSHLPFLYEFE-VSD---N--NIFFFPDGNRSEGYEQPK-TAGWWLK   252
ObRV1:YP_009408144.1    GMKME-KRSCYFIHDECHYWNPADLDRFIRYTDA-ESIMFTVIHPVEVDVGKTSSHLPFLYEFC-IDG---E--TLHFFPDGNKSEGYEQPL-SAGWWLK   252
CVA:NP_620106.1         FNNRAIKPDCFFIHDEVHFWSPAELCEFLFTVEP-KNVLATVVIPPELLEGLDYSFNSVAYDFKKVDG---N---LYYFPDKSKGKPYQQPM-DP-WLLK   249
ASGV:NP_044335.1        LTRNK-FPKVLFLHDELHFLSPFDMAFLFETIPEIDRVVATTVFPIELLFGDKVSKEPRVYTYK-VHG---S--SFSFYPDGVASECYEQNLANSKWPFT   252
PVT:YP_002019748.1      FIARVHHSTRIFLFDELHYWSMNSLSDFLDRSNV-KELLATIVFPIEILLGSKRSLNPELYEFE-ISR---G--KLHFFPDGCTSESYSQP--KDCDILK   233
PrVT:YP_009051684.1     PN----QSKSWFFHDELHHWDVNEFADFLGNFKP-KKVIASCVFPVEVFSS-DESCNPSFYRYL-IHEKKKGEVRFTFFPDGSKESSYFQR--SSDWIFR   239
GVA:NP_619662.1         INKED-QSECIFIHDEVQYWSLDEMQRFLGSLSKVDRVVYSIIYPSEVEAGYSQSLFPEAYTFD-LKD---R--RLVWYPDGKAEGAYTQPV-NP-WLLR   244
GVE:YP_002117775.1      MKGLA-EPDRVIIHDEVHYWNLKDFQRFLSYINC--PLIYTVIYPAELHAGYPFSLYPELYDFR-VSE---DGKTFTWMPDGKCCGSYKQPV-NP-WLLS   243
GCLV:YP_004936159.1     ------KPRRLFLHDELHYWCERDLVTFLSAVKP-EKVLGTVVYPPELLKGVKFSLNKWCYDFD-VEG---D--DLIFYPDGVRTESYTQPL-SGCFYLK   256
CVNV:YP_001430021.1     ------KPRALFLHDELHYWNLKELKVFLLAVKP-EKLLGTLVFPPELLQGVHESLNPWCYTFE-VDD---K--WLHYYPDGVKTEGYTQPR-NSGYLLR   256
PhlVB:YP_001552317.1    ------SAKHLFMHDEIHYWSARDLITFLEVIQP-EVMYATMVYPPELLVGSKFSLFKWCYEFD-VIG---N--DFFFYPDGVRTEGYLQPL-KNGYLLK   256
APV1:YP_009094347.1     ------KKRNFFLHDELHYWSSHDLMLFLDSINP-DHLLATIVFPPEILAGAQESLNPWCYSFQ-RHG---S--KLTFFPDGVQSESYTQPL-SAGYILQ   257
ASPV:NP_604464.1        ------ARKRFFFHDELHYWTKEALITFLDHVKP-EVMLASIVFPPEILAGAKESLNPWCYTFR-IVG---K--DLVFFPDGEQSEAYIQPV-AGSYLLR   258
CTLaV:YP_009046478.1    GRI---QDAQIFLYDELHYWSMRDIVDFLEITRA-KTLIGSFVFPTEILAGSDRSLNPWAYDFK-IQG---D--KLIYAPDGVWAESYEQPL-AAGQILK   258
CRMaV:YP_007761581.1    GKM---FDSQIFLYDELHYWSMKDIVDFLEISKA-KTIIGSFVFPSEILAGARTSLNPWAYEFK-IKG---D--KLIYAPDGVWSESYEQPL-SAGQLLK   258
                                    :.** :.     :  ::        .  : : * *:      .     * :            : : **      * *        :
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SdRV1:AYE54584            A---SHLVDGDK-V-----WTVVRHCSKFSHHLFEILPGE-LHTDSTFFFNDFDVVNMSIMFKNR-FRYYDL--FPVNYQHLFKVYSYLNCLKNADVQSG   337
CLBV:NP_624333.1          A---SHLRSGDC-V-----WTVTRHKSIYAHHLFEISIGE-LVTDSKLFFSDYNSIDMSKIFLDR-FRSYEV--FPISIEHLYKVYSYLLCLKKPDLESG   350
CLBV:AFA43536.1           A---SHFKSGDQ-T-----WTVTRHKSIYSHHLFEVSMGE-LISDSKIFFSDYGSIDMSKIFLDR-FRSYEV--FPIAIEHLYKVYSYLLCLKKPDLESG   352
AVCaV:YP_008997790.1      A---SHFRTSGS-I-----WTVKRIYSAYSHHLFEVVPGN-YFTDEIRFFNDFETIDLQCIFKSR-FLCRDF--VPISKDLVERVYSYLICLKKPDMQSA   337
CPrV:AKN08994.1           A---SYIHTSAG-T-----YTVKMVGSFYAHHLFQISKGE-KITDSVRFFADFNTIDMSVIHKER-FKYYDL--IPIKKSHIEKIYTYLLCLKKPDVESA   337
ACLSV:NP_040551.1         S---SSIIIKNRVTGVEIRYQVSLVYSLGSHHLFHIYPAEDLMKEEVRRFGPYDLFDVGSLFVKP-VRV-PI--QDFPLSVFKKIFIYMSSLKKPDVQSA   327
GPGV:YP_004732978.2       T---NLIKTSKG-H-----YSVSLHRSVGSHHFFQISKYESEILQSHRAFGPYDVLDVGSLFRGK-VRV-SI--EGVSLTHFKKILIYLMSLKKPDVNSA   323
CtChV-1:YP_009103999.1    A---SSFKVRDQ-I-----YSVDLIKTIGAHHLFTIVKGR-RISRSIRLFKGFDTLDMSAFLGTK-YKM-PI--ADVHFSFFKKIVIYLKSLKKPDTQSA   341
CtChV-2:YP_009103996.1    A---ASFVVDDL-L-----YSVDLIKTVGAHHLFAITKGK-RIVKEIRFFREFDILDLSAFSGTE-YKL-PV--VDVHFSFFKKIVIYLKSLKKPDSQSA   341
DiVA:YP_006905850.1       M---RRFYSDGE-V-----YSVTLLRTIGPFHLIYISRGS-LASESRRFFDDFNILDLPVKYAKNNLIKKMK--LLLRNNFMIKIVSYIKSLKKPDKESA   340
ObRV1:YP_009408144.1      M---SRFISRGE-V-----YNVTLLRSIGPFHLMFLSRGG-RVVESKRFFTDFNILDIPSRFNHQHFTRDVN--MILRANFIKKIISYIKSLKKPDRESA   340
CVA:NP_620106.1           CNKISMIKNGEIFS-----YSIGLLESVGANHLFSFQRNK--VVESTRFFNDFDCLDMRKLLPIN-VENGKIKGYNIRTWVFKKILSYIVCLKKGDSESS   341
ASGV:NP_044335.1          C---SGIQWANR-K-----IRVTKLQSLFAHHVFSFDRGR--ACNEFNHFDKPSCLLAEEMRLLT--KRFDK--AVINRSTVSSLSTYMACLKTANAASA   337
PVT:YP_002019748.1        V---NRIVTKTGKI-----FSVELIHTIGANHMVMIKEGS-FDVDSERFFDRSSALTTSLLMPTR---AGKA--LRIRRKFLLRLIIYLFSLKKPDHHSA   319
PrVT:YP_009051684.1       F---KYFEIGSE-I-----YTLSFLRSIKCHHLILIEKGK-LETNDYYISDEAECASLRMFGTAV-AGK-IT--APIRVEVLKREMIYLLSLKKSDMNSA   325
GVA:NP_619662.1           C---SKTEDSKGRS-----WTITKLQTIGAHHLFSAIKGS-YLTEESYKYDNFTIINPNDVLKGK--RGGKP--LYLRARMIKPTLLYLLALKKSDSNSA   331
GVE:YP_002117775.1        T---NKTMDLKGRT-----WTLTKLESVGSHHLFLCTPGD-LVTEDEAVYNDFTLVDPKLFSSLT-QRM-----PKLRAGYMHKVIHYLMALRKPDAASA   328
GCLV:YP_004936159.1       V---GTLKLLDGSV-----YHIDVVHSTFCHHLISITAGE-AVRAPTNSFSNFDATTCRGLPNIAFRSLGPC--IAVPYPVISRVYRYLRTLQKPDLQSA   345
CVNV:YP_001430021.1       L---SKIHLSDGST-----YCVDLVYSCYSHHIIALTLGD-AVRKPFNAFSGFDATTFQGLKKLDLRGIGPC--LPISFSVVNRIYRYLRTLQKPDLASA   345
PhlVB:YP_001552317.1      A---KRILLPDGGV-----YHVDVVQSKFAHHLIAITRGE-SMGPNVRAFGPFDATTCQGLEPLT-SDVSHC--FPVSFEVVSRVYRYLRTLKKPDVQSA   344
APV1:YP_009094347.1       A---SKIVCPSGQV-----YSVDLVYSAFAHHIVSITKGD-LPGLERRFFSNFEATGVKHLSGLS-YSVRDC--IPVSSELISKLYRYIRTLKKPDLQSC   345
ASPV:NP_604464.1          T---GKITTPSGDI-----FQLDLLKSSFSHHLISITKGE-AIGQKMRFFNGFEAVAMKGLNPLR-RKVESC--LPISKNTILKIYRYLRTLKKPDLQSA   346
CTLaV:YP_009046478.1      Y---NKIITQQG-V-----YSVQVRDSIYSHCLVIINRDN-LLNEEFRVYSEFDAVSIRRLNYLG-GNSDDI--IPVRYEVILSVFKYIRTLKKPDLQSG   345
CRMaV:YP_007761581.1      F---NKIMTRNG-S-----YSVQVRDSIYSHCLVIINRDE-LLCEEFRVFSDFDAISIRKIGYLG-GNADDI--IPVRHEVVLSIFKYIRTLKKPDLQSG   345
                                               :    :     ..                                          .    .     *:  *:. :  *

SdRV1:AYE54584            LAKLRQILGEDIEVKEFLFFEKFCTRVIEKGT--SYGLFGHSLFEKLS-CNFIKCLPNSVARLF--PSWRKMN-TFDFLYNLDTLNIEVKRGKVFRDVLE   431
CLBV:NP_624333.1          LAKLRQIIGDDVEIKEFLFFEQFCKRLIERQT--SWGLFGHSFFEKLT-DMALSSLPNSIARIF--PQWKKKN-TFEFLFSLGTLVVDVERKVCFEHVLE   444
CLBV:AFA43536.1           LAKLRQIIGDDVEIKEFLFFEQFCKRLIERQT--SWGLFGYSFFDKLT-DLALSKMPNVVARMF--PQWKKKN-TFEFLFSLGTLVVEIERRVCFEHILE   446
AVCaV:YP_008997790.1      MAKLKQLMGDDLDVRVQVFFRSLVHRILNESE--CFSLFDVSIVNKWK-KKFLDFAPDWLLNGF--MTWKSGN-FIKKLGEHEAAR-QVQEGAYPEGWMI   430
CPrV:AKN08994.1           IAKLRQLMEDEQDCRVVEFFCTFAKKLITDTK-GAINLFGDSFLQKAK-DSFIMALPNSIASCF--DRWHGLN-IFHFLFTLDTIRVKVETKVVDRGYRT   432
ACLSV:NP_040551.1         VAKLRQLSDADISIESVFMIQEFASRIEKNGV----ESWSCSFWGCMK-DWFFDKLP--YREVL--EKIGLADDFTRRLMKIKPLAFDIHTTDRPLTVRM   418
GPGV:YP_004732978.2       VAKLRQLSNEDVDTNEMWVIRDLAERITH-----GVSKWSNVGIRTILRDWMVDLCP--FKKNF--ERYHLIDDFDRYLMSIKPLSFSFNCSDDVDYAFE   414
CtChV-1:YP_009103999.1    VAKLRQLVGDSISLTEVLFIEDFASRFQEHGA---AKLSNDGIFDQFI-HSLKSILPEFVRRLM--GSFQRDN-LLKQISEAKAFEVRIETCSINRNYDN   434
CtChV-2:YP_009103996.1    VAKLRQLVGDNISLTEMLFIEDFAERFQQLGS---AKFSIDGIFDQMA-ESLKSLLPLFFRKML--GSFGRDN-IMKQIAMAEPFSVSIETCRVDKNYDN   434
DiVA:YP_006905850.1       IAKLRMLSEDEFSLEEMIFVDGLVDTLLKNGY---KSIWENGWVEWFI-CGLKDCLPDALHSAMFRSHFKAKQ-NLDLLMNMKTLSIVVETEDFYPYSKV   435
ObRV1:YP_009408144.1      IAKLRMMSEDDFSIEEMLFVEGLIESMLKDGI---RSIWEKGWMDGFM-ATLRDLLPPSIHSALFRKDFKARE-NLMVLIDLKPLTITLPTADYHMR---   432
CVA:NP_620106.1           LAKLRQLSDSSPSSDELLLIGDFFDLMTRVKIFNKRSPWSFLSDAKNYVDSWIIQSP-FLRRIFPVGSRAITELIRDWIANAESLKIQTTCSSL------   434
ASGV:NP_044335.1          VAKLRQLEKRDLYPDELNFVYSFGEHFKNFGM---RDDFDVSVLQWVK-DKFCQVMPHFIAASFFEPTEFHLN-MRKLLNDLATKGIEVPLSVIILDKV-   431
PVT:YP_002019748.1        IAKIRQSSDDSIFCDEIMLADHVGKIFEKLDP---ASPFGVKGVFDLLTSIFKDIF--LLDGLFNWSDRRKSEKFVEFMRALDYQTNKVVTCTFSGGVMR   414
PrVT:YP_009051684.1       AAKLRQLSQEDYHPQELCFFLNLAGRIESV-----KGIFKDRGLVSTVIDCFAQTFPDRIARWI--SKTTDENSFLRLISSMEGMKLTIKRESFPVENFL   418
GVA:NP_619662.1           VAKLRMLSSREENMDEALFVAQLAKQIKDTAL---YDKMGNPNLRSILSESFYDIAGSLFTRLFNRPEYDARC-LEKFIRSCETTEIHVERR-YMEGIRR   426
GVE:YP_002117775.1        VSKLRQLSKGDETTDEMIFSGTIATQIAELKY--FTEVGGLIDLTRALKVGFARLFGQSI-EYFSNKKWYHLDCFTNTVQFMVKAEVRIKMGYR------   419
GCLV:YP_004936159.1       MAKLSQIMPEPTGY-QIKFMTEFSKMVIDTPV--GASFFQVAIFEKFK-GFLTTFFPKYVAARF--DVARIRS-LDEFVEHMCPYTFKIKAVVHDMRLHQ   438
CVNV:YP_001430021.1       MAKLSQILPEPTSF-QIKFIREFSELVIKTET--CSNLFQNNVLLDIK-NFFASQLPKRLAATV--DAYKISS-LDEFLEKMEPYSFTIKLVEATALM--   436
PhlVB:YP_001552317.1      MAKLSQLIPEPSGV-EIKFLQDFASLIISTNT--IKSILCPSRLPLFL-GGWLRKLPKPLAQRF--KTVAEVS-LDDFISIMEPFSFRQELCDVDWNYFH   437
APV1:YP_009094347.1       MAKLSQIVPNPTGT-EIKFTEDFARLTMDVQP---MRSMLMPETAKLIGSLFSSFLPFKMARFF--DCYKACS-LDKFIHDLEPFSFSVETKVINSRSNP   438
ASPV:NP_604464.1          MAKLSQVCKDPNGY-EIKFFEEFSKLCLKCDT---LNTNMIPDMKRIVQGFFLKLFPNPISRNF--KVVQQLH-LDNFIETLEEFNFSINTESLSLNWKD   439
CTLaV:YP_009046478.1      MAKHRQLVDEPTGF-EVRFIEDFVQFILENHE--KFNLIGQKFSNFLS-SACIEVLPRYMQRFF--KSFKGYS-LGKFIEEIEPFSFTVKCRTYSRFSFK   438
CRMaV:YP_007761581.1      MAKHRQLVDNPTGF-EIRFIEDFVQFILEHHE--KFNLIEQKFSNFFS-SACINLLPRYMQRFF--NSFKGYS-LGKFIEEIEPFSFTLRCSTYSRFGFK   438
                           :*               .   .                                        .              :

SdRV1:AYE54584            KC----PIEIIR-LNCEVFLDPLPFFSENENF----NDERVD--DVVLETVILRGWNHQKRFNPENSCYRESAFDILSRTINSKDGISQGTSGSLKGGVV   520
CLBV:NP_624333.1          EW----GFEVVI-TDENAYLDPLSIFAINENF----NEDRVD--DGYLERIRLPFWNLNDYDLKRKRVNAYNILSYRFEEERKIESAQKGPNK-------   526
CLBV:AFA43536.1           EW----GFEVVI-TDENAYLDPLSVFALNENF----NEERVD--DGYLDRVKLPFWNLKDYDPKRGRANKYDLLCYKFEEERKNDLRERGPHK-------   528
AVCaV:YP_008997790.1      N-----LFLANY----------------------------------------------------------------------------------------   437
CPrV:AKN08994.1           Q-----MFDDLE-VKDDVMSTKLPEAIDTLFF----GGQLVK--GGDRRTVVIKSLDGLIKFSRSKNLYKMHIIFLLNPSLIRGN---------------   505
ACLSV:NP_040551.1         II----DQIWEERLSSFDNISNIVFYGRREWLNNGVLPKVKK--KGLAKLIPGREVDSHNYPREIYSDLLSSTSIWRSYDDDFRHRSA------------   500
GPGV:YP_004732978.2       PEEDLPDFIDDFWFGSEKKMIRDPLVKMIEMGRESQGYSVVP--TSYQQAAVCIFSMDENCIGWRNRGVKVLLRASRSSYT-------------------   493
CtChV-1:YP_009103999.1    NALW--RYIKDLAFHDVNELQSDKLLFKEREK-GEDEESRDR--RNIVNGFTPSFYSYPGGDNTKFKKIKIGLLKEEPGVLRD-----------------   512
CtChV-2:YP_009103996.1    NSVF--RFLNGF-FSCSIDPLPCDALLYKGDD---------------FDCSKGKYASQNIENSDRANLVHKFTPRFFSSKSDDK----------------   500
DiVA:YP_006905850.1       DCI---KEIKEYFLNSCDYLQRDNIDK-------------------------------------------------------------------------   459
ObRV1:YP_009408144.1      ------SIIHRSVGIDIQYLN-------------------------------------------------------------------------------   447
CVA:NP_620106.1           ------TFSDSFEMIKTDSISEFGEHILGNIS--------------------------------------------------------------------   460
ASGV:NP_044335.1          ------NFIETR-FHARMFDIAQAIGVNLDLL--------------------------------------------------------------------   456
PVT:YP_002019748.1        S-----GFLAEF-FLDNDCEASEGL---------------------------------------------------------------------------   433
PrVT:YP_009051684.1       EFDVKDGISEQFILDLMEEKMSGGTDAKMDT-------------SYSVATSRNKNFVLLDFKQRKWARLAEKEEKEP-----------------------   482
GVA:NP_619662.1           ------GASFKV-QNVMDWVEDDSANALSEVN--------------------------------------------------------------------   451
GVE:YP_002117775.1        ------PMVDGL-GPEHEVVEPAGL---------------------------------------------------------------------------   437
GCLV:YP_004936159.1       LLF---PRDEEM-PRDEDFDTIRALEMQWG------GGANGE--RIGAAYTVGPFCDYPVIDAQKVFQLLRVISREWSFSFS------------------   508
CVNV:YP_001430021.1       ------DIIFNFDRDIEGFEHEVDIVAELEAFANPKNPHAHN--AKTTPYFCEPYCDAVEFCVQKMAKLVLVK---------------------------   501
PhlVB:YP_001552317.1      ------TFBFFE-FTEADFGIEMAALMDHKFXYGKVASLLER--QSQPYSGLVNGVKQPLLECPTECILKGFTTAIYKDLIDVYAK--------------   514
APV1:YP_009094347.1       ------MFEAVTLGETMSSEEVLKILAKLDMGAPTSLEGLTGKFKYSSEAYHGLHHVLDGCGPHVFRRLVRKIADSFCNEFGIYRKSSYVSSVAITVLQR   532
ASPV:NP_604464.1          DL----EFVNLT-FGDTDFNVEDSFAEAWGTK-----KDVVN--ITTVHHSPYLVKSKFESYDHQFHSILSVKSISALTRIAKIVLSLYDPCV-------   519
CTLaV:YP_009046478.1      N-----SFIEEEEARERDGDPIYKQFSKSQSF-------NST--AYPDCLFHASQSVFSNPHPNLIRRLVTLFISTWVGKTEADYYTSLLSL--------   516
CRMaV:YP_007761581.1      T-----SFIEEE-EAAVADKDPLCLTLKLANN----KPSCFE--SYPDLIFNAHTLVFASSHPSITLMLVKSFINMWVGKTNDRYYQSLVAL--------   518
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SdRV1:AYE54584          PTIKRICW-VSGGPFLTGLDSILGYEVQLSNKRKNFLFDFVCHILREEKIHIDHQDSKFLENMNVCLSIEKLGIIEAVIKMGERAAIINRSMIDFGAKLL   619
CLBV:NP_624333.1        --MLQIEW-YG--------IKEF-------KVDPFISNSITEFTLLEALLGKRIDPKKYSYSKQACTLSNYLTFLCAEGLDGFNLEEHLERRL-------   601
CLBV:AFA43536.1         --MLQIEW-YG--------IREF--------DDPFIANGISEFTILEALIGKRIHKERYSYSKQADVLAKCLSFVCEIGGGGEGLEFVLERRL-------   602
AVCaV:YP_008997790.1    --GIRMCC-HQ--------HSAD-----------------------------------------------------------------------------   449
CPrV:AKN08994.1         --IRNFCS-NG--------RSLC---------ANDQLESGPLKTSHYKFKLPTFFSKWSEMPFSRSLSYHEIPFLKSFVHFRENNIKRFVDPI-------   578
ACLSV:NP_040551.1       --SPLVIL-RS--------NRAY--------------------------------------SEAAKFSSNCLSLCAAPCDEVIARTPFELN---------   542
GPGV:YP_004732978.2     --VLRDEF-FS--------APLL---------------------------------LECSEPEKLKFTYDDLPFYQFLSEDQEIDGYFLRESV-------   542
CtChV-1:YP_009103999.1  --ITMIEL-KS--------NKGY------------------------------------SLIDEKLIEYNNKKLMAAMKEFGQNCQRDRRSF--------   557
CtChV-2:YP_009103996.1  --MSKSDF-YR--------IKIY---------------------------------------DERTDITKGASFILKSNRSYSSLEEQINELF-------   543
DiVA:YP_006905850.1     --IIRSSF-RG--------EYIY-----------------------------------------------------------------------------   471
ObRV1:YP_009408144.1    --DEQMEF-KG--------VQED-----------------------------------------------------------------------------   459
CVA:NP_620106.1         ---------GG-----------------------------------------------------------------------------------------   462
ASGV:NP_044335.1        --GKRFDY--------------------------------------------------------------------------------------------   462
PVT:YP_002019748.1      --DEVISR-FD-----------------------------------------------------------------------------------------   441
PrVT:YP_009051684.1     --EQRIEI-PG---------------------------------------------------EIQELSFEEARFYHGIPGMKRAFD--------------   514
GVA:NP_619662.1         --FLDISW-ND--------RVSE------------------------------------------------PYGIECIHGEGSRIRVPLSRIL-------   485
GVE:YP_002117775.1      --EKRREY-QG--------LRGV-----------------------------------------------------------------------------   449
GCLV:YP_004936159.1     --MVQYCE-RG--------DYTE--------------------------------------------------FMQASKLIWFSSKLAGWDVC-------   540
CVNV:YP_001430021.1     --AAGLLY-HG--------MPVM---------------------------------GGHQAHDIFLDVARRIPLVDYCCGFGLEEEIRLVFIE-------   550
PhlVB:YP_001552317.1    --DVISCW-VA--------VDVE---------------------------------------------HRLRNNTNYCVDIGAFKKLLLEPNH-------   551
APV1:YP_009094347.1     KTNSNLSFIFG--------TDLN--------------------------------------PMIIGFVRNYFASRRSSLLIWFHDRPESWFQFSRLRANQ   586
ASPV:NP_604464.1        --VEAFSE-SR--------VTNL---------------------------------------AVNVIIAANLRACFAVTDLWRIFEGILLKEC-------   562
CTLaV:YP_009046478.1    --KKSLSQ-KG--------LKLF---------------------------------------RLHDDRYFSLTRLANLMDSFSFKATLKNEVM-------   559
CRMaV:YP_007761581.1    --RQALNQ-KG--------AKLF---------------------------------------MLHNESYNSLVILANLMDSHLFKNLLRNEIR-------   561


SdRV1:AYE54584          IKERNDLRLMSKSNYDFLIESGGLSKTCFDCFFEAQLEADPFLEEYADCFSSNPCSHFFNCDIDVDG-NLKEVTFCRDGEFVQLIWENSLKTRGTVPDFP   718
CLBV:NP_624333.1        --KAAGHDVSDDEEEELTSAEQA---------------------------------GPIKILADPLG-FMKECLE---EIPIET----------------   646
CLBV:AFA43536.1         --QSAGRDPIESELEGLGKKTAESSGEADAANTLLETQISGLVAFIPTFSDEGESQHRADLEVESEG-EIGKEES---FEEGTL----------------   680
AVCaV:YP_008997790.1    --------------------------------------------------------------------GVTIETG---SGPISF----------------   462
CPrV:AKN08994.1         --FDMIIDEMNQLDLDIMNDGEEAAVEILDVNSNLDGKQSEHHDEEFV--------TPTGLKGGDGL-VTIESIE---VDPSEF--RTPASELCGLATEP   662
ACLSV:NP_040551.1       --HRREKKELSLKCLDFHI-------------------------------------KKMKVKNVLEL-EVKLRER---NTRISL----------------   583
GPGV:YP_004732978.2     --LDSIKDKAFHYSEGFF--------------------------------------DPILFASSRGT-FLGHSEM---TDLSTS----------------   582
CtChV-1:YP_009103999.1  --------------------------------------------------------RPFYIEIMLSGSFLPLRQI---CGDFTA----------------   582
CtChV-2:YP_009103996.1  --RKLSLAADIK--------------------------------------------YPGSFQRDRKN-FIPFFLT---KNFRMM----------------   577
DiVA:YP_006905850.1     -------------------------------------------------------------DYDTSG-YYSIRTT---SGKMEL----------------   490
ObRV1:YP_009408144.1    --------------------------------------------------------------------LMNSKS----RGAFLF----------------   471
CVA:NP_620106.1         --------------------------------------------------------LSSAIEACRNW-LTSKRFS---GGSYSM----------------   486
ASGV:NP_044335.1        ----------------------------------------------------------------------------------------------------   462
PVT:YP_002019748.1      -----------------------------------------------------------------TF-FDPKKEY-------------------------   450
PrVT:YP_009051684.1     --------------------------------------------------------SRVEHDSITGS-FTKRRDP-------------------------   532
GVA:NP_619662.1         --RAHELI------------------------------------------------AGVQTDVEINF-PRYVCSS---RALIHF----------------   515
GVE:YP_002117775.1      -------------------------------------------------------------EAIADG-GVPERK----RQPYSM----------------   467
GCLV:YP_004936159.1     --LATYNKYVHMRHSDWKRR------------------------------------LKSFRSIGCAW-FCMRVRS---YERYI-----------------   581
CVNV:YP_001430021.1     --KFIGLVRKHSRS------------------------------------------NVLEIPTGLDW-FMFPRRR---NVFYLT----------------   586
PhlVB:YP_001552317.1    --VNSTIRSLVNKALRSR--------------------------------------LSSWFEIGPAW-FLKAGRA---HTRFLT----------------   591
APV1:YP_009094347.1     KFLRSPIWPNDLGLVEFR--------------------------------------MRKNLALEISN-FDRNSNL---RKLGSF----------------   628
ASPV:NP_604464.1        --KRAQGKMRKRFHFELGIR------------------------------------WFLFVDVSNQW-FLPPCRDGLIARSVSF----------------   607
CTLaV:YP_009046478.1    --KRLRLGGSLR--------------------------------------------GLLRYDPISEN-PSDKKDQ---RARSNF----------------   593
CRMaV:YP_007761581.1    --KRLRLRNS----------------------------------------------VRGLLRNDLPP-SCPDAKR---EVRFIS----------------   593


SdRV1:AYE54584          TLNRTPSNDVCTSSSSDVSSCFGENVDDDCQNVDYSKMFCRVECDSLLGDIIDVPADGDCFLWSYKKAMNIES-TCDEIRSAFSEWL--AH--SKNLGVL   813
CLBV:NP_624333.1        ------------EPSLEERGQFSTDYHSEKFEINYNDIFNPHNCMNTHGDEIPTPSDGNCFFSAFTETFEVE--RPDTLRSDFSDWLMEFN--GGSYASL   730
CLBV:AFA43536.1         --------------------SCAEGHEAIKFEIDFSDIFRPHNCMNTHGYEIPTPMDGNCFFSAFAATFDCP--DSKDLRSNFADWLDTFD--GGSYADM   756
AVCaV:YP_008997790.1    --------------------------------------------------------------------------CSLKMENH-----------FDYLRCL   477
CPrV:AKN08994.1         VSFPGDSCSVLMGNEPIAVADE--------------------------YNICDVEGDGNCFMRALLTSIKGDDRTYPGSRSRLLNLSRQIG--VNLTDSE   734
ACLSV:NP_040551.1       --------------------------------------------------------------------------SKKGVKKAGRSRMIPVH--LLKPTCG   607
GPGV:YP_004732978.2     ---------------------------------------------------------------------------LNTLDKVIAENGEKSD--VPILSAD   605
CtChV-1:YP_009103999.1  -------------------------------------------------------------------------SCVHETLDDMLDVLSEIKMAYPLTTDV   609
CtChV-2:YP_009103996.1  ------------------------------------------------------------------------PQLCYRDFVQSNQKEAIEE--VIDMLDM   603
DiVA:YP_006905850.1     --------------------------------------------------------------------------HGPDSRHLMRSAHDCIS--YEANIKL   514
ObRV1:YP_009408144.1    --------------------------------------------------------------------------GSNRGNYHIENGITSSH--IVKFSNG   495
CVA:NP_620106.1         ---------------------------------------------------------------------------------------------VSRNGLL   493
ASGV:NP_044335.1        ----------------------------------------------------------------------------------------------------   462
PVT:YP_002019748.1      --------------------------------------------------------------------------SAHALRVNIKDRT------PNPYGPM   470
PrVT:YP_009051684.1     -----------------------------------------------------------------------------VLLTNYAHWGLPKR--EGIREVV   553
GVA:NP_619662.1         --------------------------------------------------------------------------RQYLIKLGRFSFMESRA--IKDIEDI   539
GVE:YP_002117775.1      ------------------------------------------------------------------------------------------V--FSDCERM   475
GCLV:YP_004936159.1     --------------------------------------------------------------------------CAYPDQAKSYKALDEAY--STVVADL   605
CVNV:YP_001430021.1     --------------------------------------------------------------------------CTPEAIVATKLMRGMWDNVVNELAAS   612
PhlVB:YP_001552317.1    --------------------------------------------------------------------------SYPHDAIVYKEAKQGWS--HVLKELA   615
APV1:YP_009094347.1     -------------------------------------------------------QTAPTNSKSNTSSSEGASNHQREQRDQCDEATLQVN--FQREIEF   671
ASPV:NP_604464.1        --------------------------------------------------------------------------DQFIKGCQRDNSLHNGR--MSLRQVL   631
CTLaV:YP_009046478.1    -------------------------------------------------------------SSVVSELLSISSECPPSSTLTKTSGLQQEL--WKMKKEV   630
CRMaV:YP_007761581.1    --------------------------------------------------------------------------CYKSLLADFKKMSEECS--PILTLIA   617
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SdRV1:AYE54584          ADSVSVSNTFFEHEHVYFFAE----FAQVTICVHSVEATFLFGDSGCKIHLNCDGTHFSPIILYNEKKKTFDQ---------------------------   882
CLBV:NP_624333.1        AEMIRPNGVFMEAELIYLFCVFRGVTLIIHDRTHEKENVYAVHRGFEEGHMVHRGNHFVGIETYNISTLTSDP---------------------------   803
CLBV:AFA43536.1         GVKIRPNGVFMEAELIYLFCIYREVTLIMHDRTNDRESVFAIHLGFEEGHMVQRGDHFLGIETYRIDGFASDP---------------------------   829
AVCaV:YP_008997790.1    SSGVSKEHTGLLGKTTYPSGP-------------------------------------------------------------------------------   498
CPrV:AKN08994.1         EAQILREGEQFDEWMIMFTVN----VMNLSLKIFQGDVSIPRTLSPKLVNTHGNDAKEIAILH-RGNHFLGLLKKCTSESGAHDFDGNQPVEASSDNHFD   829
ACLSV:NP_040551.1       EGNGKPEERNKEEAKIPMNEG----TSKEEKGSEPPHSEVKREGVRLDEQHISEPLLSFKLDDFVGREKLCSA---------------------------   676
GPGV:YP_004732978.2     ESSESVNVKLLNESLTYDAEP----SECEVPSVESKHEPEQIESSGEIIPESWTFVDNNNKEFYCDGAFSLEL---------------------------   674
CtChV-1:YP_009103999.1  IQLEKDVETKLEEISANANEN----EDSVTMVSVSSSSSSSTSGREIEIDTSDLSDHLNDIRGIKPDDRWSDL---------------------------   678
CtChV-2:YP_009103996.1  IISPMPQIVTVEEIKDCLSVA----EVESSIDPQEGNFQEKAEGSEENLFFSNSDDSEMLDNIKRVKIEDENL---------LSYGYSHRIDSLCE----   686
DiVA:YP_006905850.1     FGNNHMEKMRIENRFWFLNDE-------------------------------------------------------------------------------   535
ObRV1:YP_009408144.1    SSDYFDTMDLVEGINPLVNRS----FDFIKNCYPDSFDIIRNNKEFQ-----------------------------------------------------   538
CVA:NP_620106.1         VDSMRQNTSFSCEVFVDLFPS-------------------------------------------------------------------------------   514
ASGV:NP_044335.1        --EAESEEYFSENGYIFMPSK-------------------------------------------------------------------------------   481
PVT:YP_002019748.1      KARTPSVVLHREYITKVEFSS-------------------------------------------------------------------------------   491
PrVT:YP_009051684.1     MWDAEEEISQKEGGLKVMEGV-IHPNTLSSDCAEDSESCGSVSGNDESMSSEEKEECEYINGRFSPNG--------------------------------   620
GVA:NP_619662.1         QAGLEEGVITEEEAELRLLPT----TKPKITEIHMDDDTPGTSGE------SDVEKFKSVRSLCREEIYSEKL---------------------------   602
GVE:YP_002117775.1      CDAGDPVGELNEFKRMLGHPN-------------------------------------------------------------------------------   496
GCLV:YP_004936159.1     LGSLARNKLIISAAAPKFDKT----SKVPREGVAEEIPAHCARTSAAFASAPCGSTASSECCVFELNPPAQIA---------------------------   674
CVNV:YP_001430021.1     SALIKRIGITLSDRNTPVAPL---------EVVLPPAPEPIKQEGSNGSVGVSNELAEDAIANFTPPAFIRNF---------------------------   676
PhlVB:YP_001552317.1    GGSRSLKHREMDYWFEKDRSS----KDSGGTVENDEDDKGEPEGVVSSSSDDGSDDKSSQEYIEVDTKVVRRM---------------------------   684
APV1:YP_009094347.1     CMGSLPEANSFKSFTPCVEAVAETSYEVQPLEPEPEANGLVLGCIPDASTPAFTFNSANQKDRLFSSVVEENI---------------------------   744
ASPV:NP_604464.1        KGPKLQALFDVSELSIIHNVE----MENAPEAGSTLDAGIKPTSSPLEVVPIENARCNLAPCKCDLNCFIQPA---------------------------   700
CTLaV:YP_009046478.1    VTKQAPVLNEEQKPYKIPSER----EKCSTQAIEKNEEPKSEVVSTKGETPPETSKTTSKFGELLATPEATAV-----------SEPTDNVLASSDLFIS   715
CRMaV:YP_007761581.1    TGGPFEQLNAMKKDFVLINQPSVGKFEKVKKCISKSTDASPDGGKEHKLEPQHSEGVNAKTDEVIPKRVDQPE-----------PKTEEGKTGSSDQFIS   706

SdRV1:AYE54584          SEIDGCFKVMNDGRLSQFNFDSSDSLNFKW--RGRESAFFSKVDA-DYGHNGMIYPHNGWVDDFDKIVQICD--PSG--NYNSVLVQW-YKKGAGIGLHR   974
CLBV:NP_624333.1        LLGDIPCGFSEEITKFHFRPDHFNCAQF----RGRKAAFITKVDA-DYGHNGMVYPHNSWVPSLEEIIQICG--QGD--DFNCALINF-YEANSSLGFHR   893
CLBV:AFA43536.1         NLSELPCGYSEELRNFHFKPEHFNCAQF----RGRKGAFLTKVDA-DYGHNGMVYPHNAWVPSLDEIIRICD--HGD--DFNCALINF-YGPNSSLGFHR   919
AVCaV:YP_008997790.1    ---------------IINALQGLKPKSF----RGRSSFFFARSNEIDYGHNGFKYRTENWFAELDDFIPSDL-------IFNACLVQV-YDKGSKIGFHK   571
CPrV:AKN08994.1         ETFETGFNDFEELRKVVGSISMFKKTPL----KNRDAFFFSESKSIDYGHNRIKYAHNHW-NGVDQLLPSSL---RN--DYNAMLIQV-YKEGGSIGMHR   918
ACLSV:NP_040551.1       ------GLIKTVGNDYLLLARQIECMPLSQL-RGKKAAYFCLDFPMVYFHDKVSYPTFEATGEIRHVMMKARSKWGI--DFNSALIQV-YNDGCRLPLHS   766
GPGV:YP_004732978.2     --------------DFASILEGLKPLNL----RGRKAFFFHSNGL-PYFHDSVLYRTLEVPGWLEEIFFKANEHFDV--NFNSCLMQV-YEQDGSVGWHF   752
CtChV-1:YP_009103999.1  VVEIKDSSFLQCGIDLDNLLKGIKSQKL----KTRKAFYFCKDANFDYGHDKVKYQNMGWPNFISELNKIACDVTGF--KFNSVLINE-YTRGGRIHWHA   771
CtChV-2:YP_009103996.1  --------------GLQEKIEGMKGKKI----NVRKAFYFCKNSRFDYGHDKYKYENLGWPKFISDICDEGEKMTGK--KFNSALINS-YCRGGKIYFHA   765
DiVA:YP_006905850.1     -------------------------KRF----ENAKRESISRCKTIFDEYDAILEEELPDDSIFKGFNKGVSFFKKKTMRMNECLIMLRTGVYNKSKLIS   606
ObRV1:YP_009408144.1    --------------------------------SNAINRSLKKSEPIHKNYGVVIINELSSPTVFEGFNKGYIMVLKG--SMSGTRLIV-YIVCAAYLMHK   603
CVA:NP_620106.1         ---------------------------------TIRPAFYS-----DPNFTKVESFEPEWDFLLGSW------------IFNHKQVRLCYEPSNS---HA   561
ASGV:NP_044335.1        --------------------------------SNPERNWILNSGSLKIDYSRLVRARR--FRLRRDFLDPIS-------KGKSPRKQLFLESTGNIKSNP   540
PVT:YP_002019748.1      --------------------------------KAKKVNVLKERLTGEVSFEEARLQRMRYSDS----------------QFVAGLAPK-LRYVKMLTWKK   542
PrVT:YP_009051684.1     --------------SFVESLSMLLNSKAAYLHGGRKTILFSTVTGLDYGFGPHKYKQIP-CDFMEDLLKKVG--------FNSCLAQM-YGEGGSIGAHY   696
GVA:NP_619662.1         --------------------------------KGREVAFYSRHSK-EYKYNGGSHRSLGWDEALNELTQELG--LDD--SYDHCLIQR-YTAGGSIGFHA   664
GVE:YP_002117775.1      --------------------------------NCENQKWMY--------FEATPTPGQNFV-------------------YQEVAKDI-YI---------   527
GCLV:YP_004936159.1     ---DLSCSCDRTLAVLNVLAYEALELEFPDQLPGCRAGWYVKGPQVADVGGFLGCQQLRWLDFFDSFLELHG-AQPG--SYNSCFAQV-FDLDSTFEYHS   767
CVNV:YP_001430021.1     -----SCSCGLEMPISSVVGGDFVYFDLPDVLPGRRAAWFTKDGSTAYTYKGGKHASMGWDERLDLLLEIHG-FEGS--LFDSALVQE-YEQGARIGFHS   767
PhlVB:YP_001552317.1    -----TCSCGVSMEIKTLLGSDMHAFKAKDRLKGRVGGWYSKDGT-PYLYTGGSHISQGWPDWLELWMQINK--VPD--KYNSCLYQI-YEEGASVGYHA   773
APV1:YP_009094347.1     ------TDIGILSPMELVLPSSAEATPL----NGRQCYFFTRCGCIDYGHNKIRYKPNKWFSGLDSILKDEST------YYNACPLQI-YEAGAGIGFHS   827
ASPV:NP_604464.1        --------------DVNSLHGNLVFLDFIGGSKGRGASFYSRDLK-GYSYTGFSHVSRGWPAFLDKFLSDNK-IPLN--FYNQCLVQE-YSTGHGLSMHK   781
CTLaV:YP_009046478.1    SIIKTGPFGDHGVIEFIRSLSFNDGHSH----NGRKALFFSRGGF-AYGFNSVTYQSSGWPSAFEEI-------YGD--RFNSCLVQK-YEKSAKLGLHK   800
CRMaV:YP_007761581.1    SIIKVGPFKEPSTISFVEGLDFSKGHNH----KGRKSLFFSEGGF-SYGFGSIVYPSQGWPNAFKEL-------YGD--RFNSCLVQK-YNADATLGFHA   791

SdRV1:AYE54584          DNESVYG--DDPILTVNLSGKCTFSVEVEGNLK----------SFELSDFDYFVMPHNFQK---RARHSVHAI-DARVSLTFRLHKR-------------  1045
CLBV:NP_624333.1        DNERVYN--DDPILTVCTFGEGRFTIEFKDQVT----------SFLMTAGSFFLMPKGFQK---KARHSVSNE-MSRVSITFRKHVR-------------   964
CLBV:AFA43536.1         DNERVYN--DDPILTVCTEGEGFFSIEFKEQTA----------SFLMTAGSFFLMPRGFQR---KARHSVRNE-LPRVSITFRKHIR-------------   990
AVCaV:YP_008997790.1    DNEQCYA--GYPILTVNF-GLALFEFDSGE-------------AFNLTDGDTILLSGDYLR---KKRHRVTSLSDSRISLTFRRHVC-------------   639
CPrV:AKN08994.1         DNEKVYD--NDSILSINLNGDALFQIEAKSSKRY---------SFRMKDGDYFLMKRDFQA---KFRHGVQGATEGRINVTFRKHVR-------------   991
ACLSV:NP_040551.1       DNEECYD--DDGILTINVVGDAKFHTTCHDE------------VIDLKQGNEILMPAGYQK---KNRHAVEVASEGRTSVTLRVHKR-------------   836
GPGV:YP_004732978.2     DDEDCYD--DDPILTMNFNGTALFEIKNVV-------------SSKLDHKDFILMKSGLQK---REKHRVQYTSEGRISLTLRVQKR-------------   821
CtChV-1:YP_009103999.1  DDENVYDLDRNPVLTVNMIGEGMFSVKMGKYEH----------SFPMSPGDMILMKNGAQK---RMKHSVIAK-DRRVSLTFREQIR-------------   844
CtChV-2:YP_009103996.1  DDEHVYDSSDNPVLTINARGRGIFKYKVNKTGAVT--------ECLLDEGEAILMKEGAQL---RGKHSVHAISQ-RISITLRDQKR-------------   840
DiVA:YP_006905850.1     NIKHV----DDPFSTMEKHKRDRLNKV----------------IKYYIGGVEYEMPSSQVS---ELEEITEITPINRLSSSNPMDEK-------------   670
ObRV1:YP_009408144.1    QLE--YN--ETKANEVS--------------------------SKHMNKKEKEMMILDFM----KTGDTDDHVSKSRSTDEQKTKEQ-------------   656
CVA:NP_620106.1         DSE------EDVNRTSETSSPEKTIADSSS-------------VSPFVSSNH------------EEGTSSQQSEEKPISEQEKKETR-------------   617
ASGV:NP_044335.1        NAEK-----NSESGEIKIEGSAENDQPHEVSHT----------SMETEDGQ------GFEG---SIPVDLINCFEPE-EIKLPKRRR-------------   602
PVT:YP_002019748.1      D-QKLFS---------EFPSEESNEVEMED-------------AFELRKGRTLKRGT-------KERDEDGANSEECEQLDSEDDVG-------------   599
PrVT:YP_009051684.1     DDEKVYD--DDEILTWNLEGEADFTMFKKTGTE----------SVHLTRNQVLVMPKGCSRGEEKFKHAVENCTEGRISITFRHQKR-------------   771
GVA:NP_619662.1         DDEPCYL-PGGSVVTVNLHGDATFEVKENQSGKIE--------KKELHDGDVYVMGPGMQQ---THKHRVTSHTDGRCSITLRNKTV-------------   739
GVE:YP_002117775.1      ---KVYLITNPPLHELLLEGLITLE---------------------------------------EYKSMRGQLPGTETSIVVRKDEV-------------   572
GCLV:YP_004936159.1     GDGGVFE-EGAPAYLFQTRGTSRVHVQGLGCCG----------ERALLGPMCFEMPASLLL---EHRWKISKSSTGCTIMTFRKLRQ-------------   840
CVNV:YP_001430021.1     DDESIFK-VGSEILTMQLKGTSRFAIQGSRCYG----------SSALLGGCHFTMPAGFQE---THKHSVAECSSGRTSITFRVLKG-------------   840
PhlVB:YP_001552317.1    DDEPIFK-KGEEIHTCNLSGKAVFEIKCRNGAG----------GEYLEGPMQFTMPMDFQG---THKHSVSGTTKGRESVTFRVLRA-------------   846
APV1:YP_009094347.1     DNEKVYH--RSPIKTINFCGEADFVVKAKGKRDVGVNA-----TCHMKTGQFFTMDSNFQS---YYQHSVQNCSEGRVSLTFRYHVN-------------   904
ASPV:NP_604464.1        DDESIYD-INHQVLTVNYSGDAIFCIECLGSGF----------EIPLSGPQMLLMPFGFQK---EHRHGIKSPSKGRISLTFRLTKEGDSQVPIQEVVTI   867
CTLaV:YP_009046478.1    DDEDCYD-DEHEVMTVNLFGTATLIFTADGAKGLERADPSKFLEITLSHGEYLLMPNGFQK---KFKHGVSCTSAGRISLTLRKQAR-------------   883
CRMaV:YP_007761581.1    DDEQCYD-QDHEVLTINLFGSATICFTKGDFSALNTSNPKLYLEVGLDHCDWLLMPRGFQR---NYKHSIKGTSEGRISLTFRKQRR-------------   874
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SdRV1:AYE54584          ----------------------------------------------------------------------------------------------------  1045
CLBV:NP_624333.1        ----------------------------------------------------------------------------------------------------   964
CLBV:AFA43536.1         ----------------------------------------------------------------------------------------------------   990
AVCaV:YP_008997790.1    ----------------------------------------------------------------------------------------------------   639
CPrV:AKN08994.1         ----------------------------------------------------------------------------------------------------   991
ACLSV:NP_040551.1       ----------------------------------------------------------------------------------------------------   836
GPGV:YP_004732978.2     ----------------------------------------------------------------------------------------------------   821
CtChV-1:YP_009103999.1  ----------------------------------------------------------------------------------------------------   844
CtChV-2:YP_009103996.1  ----------------------------------------------------------------------------------------------------   840
DiVA:YP_006905850.1     ----------------------------------------------------------------------------------------------------   670
ObRV1:YP_009408144.1    ----------------------------------------------------------------------------------------------------   656
CVA:NP_620106.1         ----------------------------------------------------------------------------------------------------   617
ASGV:NP_044335.1        ----------------------------------------------------------------------------------------------------   602
PVT:YP_002019748.1      ----------------------------------------------------------------------------------------------------   599
PrVT:YP_009051684.1     ----------------------------------------------------------------------------------------------------   771
GVA:NP_619662.1         ----------------------------------------------------------------------------------------------------   739
GVE:YP_002117775.1      ----------------------------------------------------------------------------------------------------   572
GCLV:YP_004936159.1     ----------------------------------------------------------------------------------------------------   840
CVNV:YP_001430021.1     ----------------------------------------------------------------------------------------------------   840
PhlVB:YP_001552317.1    ----------------------------------------------------------------------------------------------------   846
APV1:YP_009094347.1     ----------------------------------------------------------------------------------------------------   904
ASPV:NP_604464.1        CDHGDSDDRAALKALERRSHQSGGRPAVELEGHEREKVNSDSSDSAPVQEFLIQIDSSLLEYALKSLSGLSKNVVNCDMCLCNSPWLKNEELRFSEALRD   967
CTLaV:YP_009046478.1    ----------------------------------------------------------------------------------------------------   883
CRMaV:YP_007761581.1    ----------------------------------------------------------------------------------------------------   874


SdRV1:AYE54584          ----------------------------------------------------------------------------------------------------  1045
CLBV:NP_624333.1        ----------------------------------------------------------------------------------------------------   964
CLBV:AFA43536.1         ----------------------------------------------------------------------------------------------------   990
AVCaV:YP_008997790.1    ----------------------------------------------------------------------------------------------------   639
CPrV:AKN08994.1         ----------------------------------------------------------------------------------------------------   991
ACLSV:NP_040551.1       ----------------------------------------------------------------------------------------------------   836
GPGV:YP_004732978.2     ----------------------------------------------------------------------------------------------------   821
CtChV-1:YP_009103999.1  ----------------------------------------------------------------------------------------------------   844
CtChV-2:YP_009103996.1  ----------------------------------------------------------------------------------------------------   840
DiVA:YP_006905850.1     ----------------------------------------------------------------------------------------------------   670
ObRV1:YP_009408144.1    ----------------------------------------------------------------------------------------------------   656
CVA:NP_620106.1         ----------------------------------------------------------------------------------------------------   617
ASGV:NP_044335.1        ----------------------------------------------------------------------------------------------------   602
PVT:YP_002019748.1      ----------------------------------------------------------------------------------------------------   599
PrVT:YP_009051684.1     ----------------------------------------------------------------------------------------------------   771
GVA:NP_619662.1         ----------------------------------------------------------------------------------------------------   739
GVE:YP_002117775.1      ----------------------------------------------------------------------------------------------------   572
GCLV:YP_004936159.1     ---------------------------------------------------------------------------------GEPPVVETTAPTVQKGVGV   859
CVNV:YP_001430021.1     ---------------------------------------------------------------------TEQPSAPLHPTNEKVEPGGGAVSSRLGAPEE   871
PhlVB:YP_001552317.1    -----------------------------------CETAQEKEVDAEQEPESPPDTDEENELDKEKLSEDEAGGSEEKEVEAPCGSSDQSGECGGSEASR   912
APV1:YP_009094347.1     ----------------------------------------------------------------------------------------NIAGLPIKHTCG   916
ASPV:NP_604464.1        LAFAQGLIQLIDFLCLKVLRCAEVNRIISELPTHVFPLRGTMHIVDLDDESIRGDVKEGSFSGFRRWKVMSCSTDLIMLAFLKPKMTLGGELRSHEDECE  1067
CTLaV:YP_009046478.1    -----------------------------------------------------------------------------SMSGATLHAGADGGNNNGSGNEE   906
CRMaV:YP_007761581.1    ------------------------------------------------------------------------------TLEGSLIQSRAESGDSNSDDGE   896


SdRV1:AYE54584          ---------------------------------------------------------------------------------KLSGKAIIGAPSKADIEER  1064
CLBV:NP_624333.1        --------------------------------------------------------------------------------------RLNGSPIAIREENY   978
CLBV:AFA43536.1         --------------------------------------------------------------------------------------RLDGSPIAIRQDNY  1004
AVCaV:YP_008997790.1    --------------------------------------------------------------------------------------RMNKSPLEFFSNNG   653
CPrV:AKN08994.1         --------------------------------------------------------------------------------------NSRNEPIYLGISKF  1005
ACLSV:NP_040551.1       -----------------------------------------------------------------------------------------DFSFESKLRFI   847
GPGV:YP_004732978.2     -----------------------------------------------------------------------------------------PPNFHHGLRFL   832
CtChV-1:YP_009103999.1  ---------------------------------------------------------------------------------SKSLISLASSIEEEEINDL   863
CtChV-2:YP_009103996.1  -----------------------------------------------------------------------------------SFSKLNESCNLKEEDLL   857
DiVA:YP_006905850.1     -----------------------------------------------------------------------------------------------TFRNL   675
ObRV1:YP_009408144.1    --------------------------------------------------------------------------------------TNLSICESKPIDER   670
CVA:NP_620106.1         ----------------------------------------------------------------------------------------------------   617
ASGV:NP_044335.1        ----------------------------------------------------------------------------------------------------   602
PVT:YP_002019748.1      ---------------------------------------------------------------------------------SFDYEETKADSYEIDFEAI   618
PrVT:YP_009051684.1     ---------------------------------------------------------------------------------FMNGEPVEIENFKRSFIQL   790
GVA:NP_619662.1         -------------------------------------------------------------------------DYEARKGDEDSEYEEDKAELDEGIDYL   766
GVE:YP_002117775.1      ------------------------------------------------------------------------------------QETEADDSFDNDMVKL   588
GCLV:YP_004936159.1     DSSFTWEQYGVTILSSHMSKAPDGRIEPQRGDGSCFFHCMEPFTNLEASLLRRTIAKEMARDSKVL---------ESDLVECQGNGPVSDGVIAYTIRFL   950
CVNV:YP_001430021.1     LSAFDYQIGPVRVENVGGPRAGSYTLTDVPGDGSCFFHAVGLSFNLTGLALRRALLDAAPEIGGMFPAEAF--------AELRGGGAVSDVCVCYVAHAL   963
PhlVB:YP_001552317.1    DETLAVDMECCTIEYKEMPKGIKYNKVDVRGDGNCFWYALECALGLDPMEMKRLCKQVKYKDPTKQRKLND----QLQTGAYAEDEIISAATHIFNFQLI  1008
APV1:YP_009094347.1     EFGDTESLFDVLIRRSFSYSSKNFHTFPVPGDGSCFWHSLGALLGVDGEELKKISAREILKNEVLSRNLSL--SAQMENKQYAERESIAAFCRIQSIHLV  1014
ASPV:NP_604464.1        LSDLTEKLHGCSVILSRKFEPDLFHSFDVEADGNCFWHSVGPLIGVDGEYLKRILHDQAKKDGVKCPRLSK----QLEGNTWAEREAVAYFCSHYGIRLN  1163
CTLaV:YP_009046478.1    DDSYYEEMNKCSISSAPDSAKCSLSVFPVKADGDCFWHAVSSIFGLDALELKNLVKERAIEEGCVDQKHMKDFLHEMEAKVYASNASITATCFLMNIKLI  1006
CRMaV:YP_007761581.1    GGFYFEEINKCSITSAPDSVKCSLSVFPVKADGDCFWHAVSSIFGLEAKELKQLVHDRAIAEGCIDKCHMKDFLHEMEPKVYASNASLAATCYLMNLKLI   996
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SdRV1:AYE54584          ---------------------------------------LSKKENMCLIDSISESLKVESFKVVQALMNKD-RPFWEKFMTD---DAGGDLMDCEKAASD  1121
CLBV:NP_624333.1        -------------------------------------------KNTCLINAFSKAMKRSKQAIIAKLKTVN-SPFWSRYLSE---GNGGSIEDCQSACEA  1031
CLBV:AFA43536.1         -------------------------------------------RNVCLIRALSKALNRGMQAIIAKLKTVN-NPFWSRFLSD---GNGGSVEDCLAACEA  1057
AVCaV:YP_008997790.1    ----------------------------------------KLGKNKCIIHAVAMALGQTSNTVANKIVAQ--RPDLLQCLVD---DEMLDKQTTETICVI   708
CPrV:AKN08994.1         -------------------------------------------KNICLMRSLSILEKRPLYDILLALIKKN-KNYWTSFLEF---GVGGTLADLNQAAED  1058
ACLSV:NP_040551.1       -----------------------------------------KGKFDCLFVSVAEIIHKKPEEIMMFI-----PHIMDRCVS----NRGCSLDDAKAICEK   897
GPGV:YP_004732978.2     ------------------------------------------PKVGCFLQAVSEQVFTKVEDLAIKLGTLY-GDILANW--------GVSLADVDKFAEK   881
CtChV-1:YP_009103999.1  -------------------------------------------KESCLIDSLAEEIRISRSKLINLLVKED-STFLIKIKD----DKGLTIDDLSIIANL   915
CtChV-2:YP_009103996.1  -----------------------------------------DLKESCLIKALAKEIKISELKLSNLIINED--PTYLDKIKK---DRGMTIDDLEKISNL   911
DiVA:YP_006905850.1     -------------------------------------------ANKCCFDCIMEIKKIDHVALVNYI---T-ETKFMDLLLK---DNGLLQKELIELCNF   725
ObRV1:YP_009408144.1    --------------------------------------TFCNLKNKCCFDSVLKCLNIDLFELVDRL---K-GSVFIELLIK---DQGLLESEFLDLLDL   725
CVA:NP_620106.1         -------------------------------------------KNDCFFKAVGETIGIPANSLIERILCSD-SEDLKPVIEQLNLDHPISSKLLEVCCKF   673
ASGV:NP_044335.1        -------------------------------------------KNDCVFKAISAHLGIDSQDLLNFLVNEDISDELLDCIEE---DKGLSHEMIEEVLIT   656
PVT:YP_002019748.1      ----------------------------------LNRVNSGGLRGVCLLDALAKITGTKREITLSILLGRD--GTWADWFLK---DKGATFDDVFKAVSD   679
PrVT:YP_009051684.1     --------------------------------PDNLCDLISKMSNACFLDCLADHLCMNRSAVFNLLFDQD-KSVITNVLE----DKGFTLSEVIDHLMN   853
GVA:NP_619662.1         ---------------------------------------QKNQGNMCSLKAFADHMQLSTPSVIAIVNGA--SPQTLREIE----DGGYSLATLVNLSKA   821
GVE:YP_002117775.1      ---------------------------------------KEIKKNLCLIQPIAEHFALKAPVLISKATVE--IPNFARYLS----DKGLSMPGLYMLCKN   643
GCLV:YP_004936159.1     --GLKVRFFSPELNEVRKFSTCTATNFWVDVLHHGNHFDLLYPTNDCVLIALEQGLGRKRGDILKVLSRPQ-HSDIFQIATG---GVGLTLELLEPIFQC  1044
CVNV:YP_001430021.1     ---KSSIAVISHHEGCMRVFCPDNWENKIDLLHKDGHYNVVNYKNDCALLAVAETLGRTKREVTEVVCKAK-HGGLLRSMRT---GEGLKVELLGELFKI  1056
PhlVB:YP_001552317.1    -------CLSAGDTGLVVYSPKREFSQVVYMHIENQHFNWVEPKNNCLVRAIAVSLNRKTSEVLKVLEEGS-CVGSVGTLWR---GEGVALEDLDFYFDR  1097
APV1:YP_009094347.1     ------VLLPDQNFSYEFLPMQNAEVTQLFVKLSGEHFEPALPINGCVVKSIAETLNQTEAKILSVIGRPN-NRLILEGLVE---GEGLNIEDLEAAFSV  1104
ASPV:NP_604464.1        ------VLYTREECTWIFKPHEVLKAATLICQD--NHFKPCMPVNGCVIRAISSALNRREVDVLAVLGKPA-HEDLFEEVAE---GRGFSIFDLTRLFEI  1251
CTLaV:YP_009046478.1    IKLVESKHSGWVVVEPLNSSNEKISLGYLVLNQRVQHFDLAVPKEGCVIRAISEFLKQNPTKVLSVLSANC-SKELLHELMS---GLGIQEFFLEEIFKV  1102
CRMaV:YP_007761581.1    IKLTGLEDDSWVVVEPLALSNERASIGYLVLNQKCHHFDLAVPKEGCVVRAVSEFLKQNPTKILSVLSANC-SKDLLHELMS---GLGIQEFHLEEIFSI  1092
                                                                      * .  .

SdRV1:AYE54584          LLLNLEVHC-Q-DRINVFKFGQTIVKIT---LTNGHFSK---LEEIKELPRSLVSQFKGKTRIDVVEGLVESLESE--------SH--YNLFNFEANMSF  1203
CLBV:NP_624333.1        LDVTVDLNV-N-GKCVVLGKGALRISMA---LRNNHFSV---INAAQLMERTFVSHLLEKGNVNVLEGFDAMLSGDV-----GAAG--VNKIQFAANFEF  1116
CLBV:AFA43536.1         LGITVDLFV-D-GKCLVLGEGAVRVSLA---LKDNHFSV---VEEHRSIQRTFVSHLAKKSNLRVMDGLDEMLQSEM------STG--VNCVQFIADFEH  1141
AVCaV:YP_008997790.1    MNLHATIVNEDEGETMELNPEGLIKSSFS--VLDEHMMVLSDIPNCRSKKGIDICMSPDLANSNCAANYEVTCQN-------------LQVIQYQADHER   793
CPrV:AKN08994.1         LSFRFELYM-N-EKWIAGGNRGPIYRLN---LSDDHFSV------HRELSGNVEDTQLNFSKAKSKQSNFSSSDDDNSFDLDSIEH--VNKSLFEPLNDA  1145
ACLSV:NP_040551.1       YEIKIECEG-D-CGLVECGTSGLSIGRML--LRGNHFSV---ASVRRSSMDSLANSSKEIKSDGVLDHVTFNFHKRLKLVEPD-----LTNADIKVDSSR   985
GPGV:YP_004732978.2     LGIRLVLTN-G-FEVIRAGVEGPEVSMS---FSNGHFRS---NSNSRMNKGKGVESFPKEFARKVSDEMSNDANPQIIQNLNEVYGVFLNQTIFKLDPKR   973
CtChV-1:YP_009103999.1  LNLSVRVLI-D-GQWSYFGVKESNYRLISLKLIKRHFSV---YNGEVLKLALGDESSDKLIKLSDSGFYNSFLNKI------DPRNKFVNKFDRMINFER  1004
CtChV-2:YP_009103996.1  LCLKVRVLI-D-GQWQYFGVKESNFRGVSLRLSGSHFDA---YEKESIKIALGDEVSEKKVQKSADGAFFEGFLQRIDPKNEF-----VNRFERVIDLDR  1001
DiVA:YP_006905850.1     LNIKVNIIN-Q-SGTRLIYENDNDNTLI---LTERHCKL---VKTESISDWLLDDN-----------KDFLDVTGV------------SSIIKNVFDYKR   794
ObRV1:YP_009408144.1    LGLNENVMN-A-AGFLVKECTESSGIFI---LSSNHCRF---ISKEECGDWFNKVK-----------GGLISLPGV------------NYLLKDINCIKR   794
CVA:NP_620106.1         LGYRVHIYY-G-DSIIKLNDDINMHAIHIGGKPGHLFCI---NQERSKIPKDSQIKVPEVGPQSFIGSIFSKTYGS---------GSSAPIHLGQIDITK   759
ASGV:NP_044335.1        KGLSMVYTS-DFKEMAVLNRKYGVNGKMYCTIKGNHCEL---------SSKECFIRLLKEGGEAQMSNENLNADSL------------FDLGRFVHNRDR   734
PVT:YP_002019748.1      LDLNCTICT-KEGSFNAHVNRNYKHNFLY--LFDEHVSL---ERPKVMLFEQVRHQKIDFL------GAFEKCPG-------------AGKFRYEALAER   754
PrVT:YP_009051684.1     LDIPGRIVS-N-GEVINYLEKGSFKPIDLL-MRDGHIGL---NVQHDVLYDTKEVKVEELIG--------------------------ADIIRPHFSVER   921
GVA:NP_619662.1         LDFPIAIHG-E-RGYAETPGSYRRLHLK---ITSGHVEP---FEGVTSKGGFREAMLLGDG---------------------------VGVGHFRVDKAK   886
GVE:YP_002117775.1      MGLTLSILS-D-EGYLHLQGSYKPLGLV---IKDDHATP---GRYIQRQNRPAEALAVNPG---------------------------VGQMEIEVVSEN   708
GCLV:YP_004936159.1     FQIDARVLC-G-SEVFTYPTSGTFALDFE--LADGHLSF---KSARRKETVSSCLKVVEASP---HGRLVLNCA--------------GTGVLFEICSNT  1120
CVNV:YP_001430021.1     FSIKALVKC-N-GQLHRLNPEGKILGHYR--LEDGHIQV---DKGLIKQLGSAPVKVIEHP---VHGSGMVLIAAV------------ATQLSFEINAEI  1134
PhlVB:YP_001552317.1    FGINAMVEF-E-GKAYNFNETGHLPAAFT--LKDGHIEF-----IGRNSPSTVPMMRGRVNTLTVSPNSLLIIKAA------------GSTIEFRPDYSR  1176
APV1:YP_009094347.1     FGICARVST-E-RGVFTLNKEGNLHANYE--LKSGHIMY---LKKASSSQFAPTNPIQNFNGQ----GPEIFLRGI------------VSEVDYKPSWGR  1181
ASPV:NP_604464.1        FSICGSVDT-G-GELIMVNENGRIPAEFS--LEKEHLAH---IPTLSRRKFSPIVSDLNRVSNSAMRFLAIN----------------GAEVDYRPSIDR  1328
CTLaV:YP_009046478.1    FDICAEVSD-G-EKSRILNANGSRSAKFT--VEQDHFSF---SPGVKASTNLGSFKAPSGGQTIPIEQYETFLRGN------------ANVIPFTPSLIA  1183
CRMaV:YP_007761581.1    FDICAEVSD-G-ASSRVLNKKGSRSAKFI--VDKDHFSF---CPGTKASTNLGVFKAPSGCPMIAIEKYDEFLRSS------------ANVVPFTPSLPL  1173

SdRV1:AYE54584          AGPLMNSFLNRSTG-------ICLGSVINNGGKYF------EDVFSLDESSYRICS------------------AIHALNGFAGSGKSKVMQNWLSKRRC  1272
CLBV:NP_624333.1        ARILANSFLNMTTG-------ICLGKALDNGEKYF--------LHILKDRVKQIGI------------------DVTMVCGFAGSGKSRKLQSWLHSRKK  1183
CLBV:AFA43536.1         ARVLANSFLNMTTG-------ICLSRALDNGEKYF--------LHMSEERPKQIGF------------------DVTAICGFAGSGKSRQLQSWLHARKR  1208
AVCaV:YP_008997790.1    AIKLMNSFLAGTTG-------AVLNELVFKGSRFF------TFMDSVNERKSDFVE------------------ELSFVPGFAGSGKSLGLLNEVKRISR   862
CPrV:AKN08994.1         AELLRQSFLNRTTG------KILSDAFGENGAHLR--------RIRIVKSDDPFPE------------------EVYFSCGFAGSGKSLSLQSKLKSNFK  1213
ACLSV:NP_040551.1       AGKLLKSLMDGMTG-------IVSHNSTHEGWRMIKGINSTSEMRSFMNMVRGQIEEPKSDLFDKVQELNFMKVKIYGIFGFAGSGKSHAIQNLIQTEFK  1078
GPGV:YP_004732978.2     AQRLLKSLLDGSTG-------VHCNSSLKEGWKMI------PNAKSSEFVTKNYIN--SSDIWKGSALWN-AKINISGIFGFAGSGKSHGIQRLLNEKFS  1057
CtChV-1:YP_009103999.1  AALLIHSFLRGSTG-------VVTSSGFNNGVDYF--SGRKRNIDPESFRDPKFLK---------EMTKGDAVVKGAVILGFAGCGKSRPVQMALDSMDS  1086
CtChV-2:YP_009103996.1  AAKLIDSFQKGTTG-------VICSENFGLGVKPF--SGREKNLDSSKFDDPSFLK---------KLIGEEFLIKGAAIIGFAGCGKSRPVQMALSNMDS  1083
DiVA:YP_006905850.1     SKKLYDSLSKGTSG-------VFFNMIKKKNDESE--------KKKDKNRVIEMMNFFFEDEINEKRKLTGRSEPIYGFFGFAGSGKSREIQNYINTNYN   879
ObRV1:YP_009408144.1    AGRLFKSLSRGNTG-------ILFNSIKKKSDESE--------KRKDKNRVIEFLNLIFDNDDDHEVEIVKRDEPIYGFFGFAGSGKSRAIQGFINSEFN   879
CVA:NP_620106.1         ALVLVSAFESMNLGVRVDRKAILEGQLISNGFLAF--------LKRKNNEGHKVIK--------------IQSLPVYPFIGFAGSGKSFGLTEKLINGDC   837
ASGV:NP_044335.1        AVKLAKSMARGTTG--------LLNEFDLEFCKNM--------VTLSELFPENFSS------------------VVGLRLGFAGSGKTHKVLQWINYTPS   800
PVT:YP_002019748.1      GSLLASALKDNLTG-------VISSKFNWDPKCEF----------------VDIEK------------------EILVVAGFAGSGKTRGICQIVKSMFN   813
PrVT:YP_009051684.1     ARVLVKSMMEGMTG-------VILNRFKHAFNELL----------------PRHEN------------------RVMCIAGFAGSGKSRALQGVCASVLN   980
GVA:NP_619662.1         ADRLAQSFYNGNTG-------VLLGKYNKGKMHTG---------------EIEEPK------------------EVLTAFGFAGSGKSHWCQTILKHCSV   946
GVE:YP_002117775.1      ARALQASFEKGFTG-------LILN---DHRGKWA-------------AKIPQGAR---------------AQLTVSMCLGFAGSGKTSSITQMLKLGHQ   770
GCLV:YP_004936159.1     AHKLAESLFDGRTG-------IVSSKLFNNRERFE------------VSSTSLLPR------------------TLNVICGVFGCGKSTLLCKALEKGLG  1183
CVNV:YP_001430021.1     GDKLAECLVSGRTG-------VISSQLFNGRQKLT-----------IPAGSDGKSR------------------AVNLITGVFGCGKSTLMKRSFESGLG  1198
PhlVB:YP_001552317.1    AKCLADCFHTGCTG-------VMNSKIFNNSEHLL--------AHVNINDRPNTVQ-------------------INSVLGTFGSGKSSLFRRFFDANPG  1242
APV1:YP_009094347.1     ARNLEESLLNGTTG-------ILCDRTINLQKNWL----------TVDRKLNDNSR------------------NLGVVLGTFGSGKSSLFKRFIVKNPS  1246
ASPV:NP_604464.1        ASTLLDSFEIGATG-------VLCQGIKEAQKDLA------------SKLIPELVH----------------ERKLIMILGTFGCGKSSLFKKFIEKSPG  1393
CTLaV:YP_009046478.1    AKKLANSFLSGQTG-------VINSKIISGQYDWL----------ADTNKLCFDER------------------KIGAIVGTFGSGKSHNVIELLRHNLG  1248
CRMaV:YP_007761581.1    AKKLADSFLSGQTG-------VINSKIVAGQYDWL----------ANTNKLCFEER------------------RVGAIVGTFGSGKSHNVIELIRHNLG  1238
                        .  *  .:     *                                                                  *  *.**:
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SdRV1:AYE54584           GNY-----------------------------CVVCPRVNLAHDWKLKLGLTEK-------------------------------MA---GKVPTFETFV  1309
CLBV:NP_624333.1         GNF-----------------------------CVVSPRTNLAADWAFKLELEPN-------------------------------EQ---RKVSTFEKFI  1220
CLBV:AFA43536.1          GNF-----------------------------CVVSPRNNLAADWSFKLELEPN-------------------------------EK---RKVATFESFI  1245
AVCaV:YP_008997790.1     EIHLAKEKKGMGKGSGKGHEKKERNRGNLKSMCIISPRRNLADDWETKLGPSAL-------------------------------EH---CSVTTFEVLF   928
CPrV:AKN08994.1          LKF-----------------------------LVICPRVELKEDWERKVKC----------------------------------SS---HKVCTFEVAL  1247
ACLSV:NP_040551.1        GSQ---------------------------GIMVICPRRFLAKDWSEKGV-----------------------------------DE---KDIKTFESAL  1113
GPGV:YP_004732978.2      GSN---------------------------EILLISPRVLLAEDWRDKV------------------------------------KH---LKTMTFESAI  1091
CtChV-1:YP_009103999.1   PMK----------------------------ILLISPRVNLLADWKLKVSN----------------------------------KN---VTFKTYESAL  1121
CtChV-2:YP_009103996.1   PLK----------------------------VLLISPRVNLLDDWKKKVNN----------------------------------GN---LILKTYESAL  1118
DiVA:YP_006905850.1      MDG---------------------------CVTVVSPRVELLKDWEKKISVAN--------------------------------KK---IRFSTYEKAL   917
ObRV1:YP_009408144.1     KKG---------------------------FVTIISPRSELLKDWQSKVKTQN--------------------------------KH---IRFLTFERAL   917
CVA:NP_620106.1          SQN----------------------------FMFTAPRKKIIGQIHERIDSRQYDDKLKIS------------------------RK---KNFSTFENTL   882
ASGV:NP_044335.1         VKR-----------------------------MFISPRRMLADEVEPQLKG----------------------------------TA---CQVHTWETAL   834
PVT:YP_002019748.1       NKK----------------------------TLVLSPRKNLADDWVKNLANLHRP------------------------------SH---VKVMTFEAGL   852
PrVT:YP_009051684.1      KKN----------------------------VILSSPRKNLLRDWESKIDEKLK-------------------------------GKERLIKLKTFELAI  1021
GVA:NP_619662.1          EKV-----------------------------LVISPRKVLRDDWVAKIS-----------------------------------KK---HRVVTFEVAF   979
GVE:YP_002117775.1       MAV-----------------------------AVVSPRKNLCEEWKKELLD----------------------------------TD---VCVYTYESFL   804
GCLV:YP_004936159.1      VCI------------------------------FVTPRRSLAEQMTQLVQSVETS------------------------------TS---VTILTFEKFL  1220
CVNV:YP_001430021.1      SKC-----------------------------YFVTPRRSLADIFSDELTSGRIKTK----------------------------TT---VVVQTYEKFL  1238
PhlVB:YP_001552317.1     KGV-----------------------------FYVSPRRALADEFRQKLENAVVRTKRKKGASSKNGAGASTGPDPNSQAERMKRKN---WLVCTFEIIL  1310
APV1:YP_009094347.1      RSI-----------------------------VFVSPRRSLADQIKDDLGLNTKR------------------------------GKSLRVRVLTLESFI  1287
ASPV:NP_604464.1         KAI-----------------------------TFVSPRRSLAESINHDLGLARVGGKKTGKSKDL--------------------KN---VRVKTFELFI  1441
CTLaV:YP_009046478.1     YQN-----------------------------LIISPRRSLKEQFINMLDLVQARSKGKK-------------------------AS---TEVATFEVAL  1291
CRMaV:YP_007761581.1     YQN-----------------------------LIISPRRNLKDQFINMLDLVNARSKGKK-------------------------TS---TDVVTFEVAL  1281
                                                            **  :                                                     * *  .

SdRV1:AYE54584           -------KMEKKNLDLIVLDELTLFPNGYLDWLV--------------------LHLEANSIM-------AKIVVIFDPLQSRYHNEQDCHVL-NFDHEV  1374
CLBV:NP_624333.1         -------KTDKSKLDLIVIDELTLFPNGYLDLLV--------------------YELADVNRH-------CQIILLFDPLQARYHNKMDESIL-TFEHDV  1285
CLBV:AFA43536.1          -------KMDKSKLDMIVLDELTLFPNGYLDLLI--------------------YELDKFNSH-------CHLILLFDPLQARYHNKMDEAVL-NFEHDV  1310
AVCaV:YP_008997790.1     -------KASISKIKLIVVDELTLFPNGYIDLLI--------------------FRIRTESPD-------CKLILIFDPLQARYDSAQDRAIL-GSEHDV   993
CPrV:AKN08994.1          -------LQNLSRVELIVIDELGLFPRGYLDLMI--------------------FKLRTEKNFK------GKVMLLFDPLQARYHSDSDERFL-HEIHEC  1313
ACLSV:NP_040551.1        -------KSDVKGKRLFILDEISLLPKGFTDLLM--------------------LKMHMEGILKK-----STIVCIGDPLQAGYFCPKDDNYL-SREGEI  1180
GPGV:YP_004732978.2      -------KGCLAGYKWIILDEVTLFPNGYLDLLV--------------------LKLAHYNEINL-----KHITLVGDPLQANYFNERDCNLL-GSVKMV  1158
CtChV-1:YP_009103999.1   -------KENLSKFSLIIIDEFPLTPRGYTDVIA--------------------YKSKVDNLTCRLEKKVTKLLLIGDPLQASYYSESDDDLL-AQGGEL  1193
CtChV-2:YP_009103996.1   -------KENFAEFSMIVIDEFLLVPRGYLDVAA--------------------FKSKMDCKVCKSKPRIPKFLLLGDPLQAGYYNALDDHLI-PEKSEM  1190
DiVA:YP_006905850.1      -------TLSYYEDELVVVDEIGLLPPGYISLLSLVTAFRVNKISHN-------IRLSKRNYSKYVENQSSRLVLLGDHLQGRYYNESDFRSL-SQPDEI  1002
ObRV1:YP_009408144.1     -------TVTYQESELIVIDEIGLMPPGYMSLLNIITSIKFEEVSNN-------FRLSRRNFRNFIGSPRSRLVVLGDHLQCRYYNDSDVRSL-DPKDEI  1002
CVA:NP_620106.1          --------LSLVNKPLVIMDECSLNPPGFIDLVLIKSLDSIIRKSNKDFDHFFSSSVLSEGIIANVASPIACIAVTGDTLQSSFYSESCGKLM-QYKNDI   973
ASGV:NP_044335.1         -------KKIDGTFMEVFVDEIGLYPPGYLTLLQMCAFRKIVKGQSENFLKGKLLELSKTC---------LNIRCFGDPLQLRYYSAEDTNLL-DKTHDI   917
PVT:YP_002019748.1       --------RRVQKSSLIVIDELSLMPNGYLDMLI---------------------NMNEE----------ATFITLFDPLQARYHAKSDVLRV-SPENDV   912
PrVT:YP_009051684.1      SAITRMVKKEQDGKLTVIIDEATLLPGGYLDLVN--------------------SLVPEG----------STIILLFDPLQSHYYSKSDVRV--NLGPVL  1089
GVA:NP_619662.1          -------MDDYGCKDIVI-DEIGLLPPGYIDLVI--------------------AAHQPR-----------TLVLLGDPLQSTYHSKRDNVVLEASQEDV  1040
GVE:YP_002117775.1       -------LNHKHKLDLLILDEIPLFPPGYIDLVH--------------------FIKSVE-----------HILLLGDPLQTSYHADGDALTLSGVEGDI   866
GCLV:YP_004936159.1      HQ-----MVNVKEGSTIIFDEFQLYPPGYFDLVC--------------------SQLTDG----------ISLHLLGDPCQSDYDNAKDRGVFEGLLPDH  1285
CVNV:YP_001430021.1      RM-----LESVEPRDVVIFDEMQLFPHGYFDLTF--------------------SIMSQE----------VPTVCLGDLCQSDYDCATDRSELGCYQSDM  1303
PhlVB:YP_001552317.1     KK-----IHLVKPGMALILDEIQLYPPGYLDLIC--------------------ALCAEG----------VHIVIGGDPIQSDYDNEKDRNWLSNLPPCI  1375
APV1:YP_009094347.1      K------AVFTFKAASVVLDEVQLYPPGYLDLVM--------------------LCLSLN----------CQIYLAGDPCQSDYDSAKDRALFDGLKGDI  1351
ASPV:NP_604464.1         LH-----LDSIKEGHTVVIDEIQLFPPGYIDLII--------------------LGLKPN----------VNIIIAGDPCQSDYDCSSDRHIFAGSESDI  1506
CTLaV:YP_009046478.1     K------KTGMLKKVRIFIDETQLLPPGYLDLVC--------------------LIAGPD----------ASILVMGDPAQSSYDSADDRMAFIGDRGCL  1355
CRMaV:YP_007761581.1     K------KNGLLKKARIFIDEAQLLPPGYLDLIC--------------------LIAGSD----------SSILVMGDPAQSSYDSAEDRMMFAGDKGCL  1345
                                         .. **  * * *:                                                *  *  :

SdRV1:AYE54584           DRM--ISGQR------------------------------------------------------------------------------------------  1382
CLBV:NP_624333.1         DRL--IGGQN------------------------------------------------------------------------------------------  1293
CLBV:AFA43536.1          DRL--IGGQD------------------------------------------------------------------------------------------  1318
AVCaV:YP_008997790.1     DLI--LGDSE------------------------------------------------------------------------------------------  1001
CPrV:AKN08994.1          DRI--TSGAK------------------------------------------------------------------------------------------  1321
ACLSV:NP_040551.1        KRL--FKGG-------------------------------------------------------------------------------------------  1187
GPGV:YP_004732978.2      DSV--FKD--------------------------------------------------------------------------------------------  1164
CtChV-1:YP_009103999.1   SSL---EIDY------------------------------------------------------------------------------------------  1200
CtChV-2:YP_009103996.1   ETL---EIRK------------------------------------------------------------------------------------------  1197
DiVA:YP_006905850.1      DFI--MMNEE------------------------------------------------------------------------------------------  1010
ObRV1:YP_009408144.1     VFL--MENEE------------------------------------------------------------------------------------------  1010
CVA:NP_620106.1          KTLCALSHTR------------------------------------------------------------------------------------------   983
ASGV:NP_044335.1         DLM--IKTIK------------------------------------------------------------------------------------------   925
PVT:YP_002019748.1       DRI-----KV------------------------------------------------------------------------------------------   917
PrVT:YP_009051684.1      TPI---FGQE------------------------------------------------------------------------------------------  1096
GVA:NP_619662.1          FNR--VRGK-------------------------------------------------------------------------------------------  1047
GVE:YP_002117775.1       FRR--LQAKKSGICPCGMHFKPSRYMGPNVEFDFDEADKLKGREAIFFSRGGEGYKYNGGDHKSSGWVGELDQIIDACNINADSFDHCLVQRYIPGGSIK   964
GCLV:YP_004936159.1      QRI--LQGIQ------------------------------------------------------------------------------------------  1293
CVNV:YP_001430021.1      QRL--LQSAK------------------------------------------------------------------------------------------  1311
PhlVB:YP_001552317.1     DSV--LEGAE------------------------------------------------------------------------------------------  1383
APV1:YP_009094347.1      FEV--LSGKK------------------------------------------------------------------------------------------  1359
ASPV:NP_604464.1         MRI--LSGRS------------------------------------------------------------------------------------------  1514
CTLaV:YP_009046478.1     DVL--LDNKR------------------------------------------------------------------------------------------  1363
CRMaV:YP_007761581.1     DRL--LEGKK------------------------------------------------------------------------------------------  1353
```

```
SdRV1:AYE54584          -------------------------------------------------------------------------------------MNYLYTSYRLCNGFF  1397
CLBV:NP_624333.1        -------------------------------------------------------------------------------------IEYIYSTHRMSR-YF  1307
CLBV:AFA43536.1         -------------------------------------------------------------------------------------LRYIYSSHRMSK-YF  1332
AVCaV:YP_008997790.1    -------------------------------------------------------------------------------------VDYMYQSKRFESEEL  1016
CPrV:AKN08994.1         -------------------------------------------------------------------------------------INYLFESWRLSKKFF  1336
ACLSV:NP_040551.1       -------------------------------------------------------------------------------------VNYKWYSYRINK-FI  1201
GPGV:YP_004732978.2     -------------------------------------------------------------------------------------VKYQYQSYRIPA-NV  1178
CtChV-1:YP_009103999.1  -------------------------------------------------------------------------------------PRYLLYSHRLPK-GM  1214
CtChV-2:YP_009103996.1  -------------------------------------------------------------------------------------PKYLYYSHRLSS-SL  1211
DiVA:YP_006905850.1     -------------------------------------------------------------------------------------ILYLNYSHRLNKMHF  1025
ObRV1:YP_009408144.1    -------------------------------------------------------------------------------------IIYLNYSHRMSRSHH  1025
CVA:NP_620106.1         -------------------------------------------------------------------------------------LPYLFGSKRFG--YF   996
ASGV:NP_044335.1        -------------------------------------------------------------------------------------HKYLFQGYRFGQ-WF   939
PVT:YP_002019748.1      -------------------------------------------------------------------------------------PKYLFFSKRMSS--E   930
PrVT:YP_009051684.1     -------------------------------------------------------------------------------------FRYRGYSYRFPKLFD  1111
GVA:NP_619662.1         -------------------------------------------------------------------------------------LPYLCYSHRLPR--N  1060
GVE:YP_002117775.1      PHADNEPIYPVNNPILTVQLTGSCTFTLSCRKGDTSLHLEGAQFFLMPNGRQKGHKHSVVAHDHRVSLTFRSTRPLELMSGKIQAVPYLFLTNRLSS--K  1062
GCLV:YP_004936159.1     -------------------------------------------------------------------------------------FRYATRSYRFSNPNF  1308
CVNV:YP_001430021.1     -------------------------------------------------------------------------------------YTYYTRSHRFQNSNF  1326
PhlVB:YP_001552317.1    -------------------------------------------------------------------------------------YKYVIKSRRFKNGNF  1398
APV1:YP_009094347.1     -------------------------------------------------------------------------------------YKFNVSSRRFQSEMF  1374
ASPV:NP_604464.1        -------------------------------------------------------------------------------------YKFNILSQRFRNPVF  1529
CTLaV:YP_009046478.1    -------------------------------------------------------------------------------------YVYLSESKRFRNPMF  1378
CRMaV:YP_007761581.1    -------------------------------------------------------------------------------------YVYLSESKRFRNPMF  1368
                                                                                                               :     *:

SdRV1:AYE54584          KDVFEKLQLPIKQ---------GDEERRFLYHNPFRIQEDSSETIK-VDVLIVESQLEKK-----TFGSAIKCMTFGESQGLTF-DHVCILLSESSANSC  1481
CLBV:NP_624333.1        NRFF-DVPCFNQADR-------TEEQRLWIFDDVYSIPSICSDRQEPCDVLLVESDLEKK-----AFSPIINVMTFGESQGLTF-NHVCILLSESSAASN  1393
CLBV:AFA43536.1         NRFF-DVPCFNQAET-------TKEQRLWILDDVYSITSVCIDQGEPCDVLLVESDLEKK-----AFSPVINVMTFGESQGLTF-NHVCILLSESSAASN  1418
AVCaV:YP_008997790.1    FNLF-EDLKKNEVDAESRETGKGAKFRPRMYTNLLTMKVEEENQGNPIDVLLVGSFDEAG-----LFASSIKTMTFGESQGLTV-DHAAILLSENSALSD  1109
CPrV:AKN08994.1         GNFFVDIELRNSG---------SVNYELDFFDNHIVAANEAKKRGFPIDLILVASRDEKN-----SFAGKVNVLTFGEAQGLTV-KHSCIVLSEYAEKQD  1421
ACLSV:NP_040551.1       AKKL-AIETMNDFI--------GIDEQSSIYKDMPSAHHFMEKKGNHIEVILVASMVEKE-----LYSNYGNVMTFGESQGLTF-NCGVIVLSEEAKLCS  1286
GPGV:YP_004732978.2     AGRF-DVWDKNRHE--------PIDCHGTFYSDLSSAKLHAKRCNQKIDVVLVASELEKK-----YFSNQCKCITYGESQGLTF-DYGLISLSEESRLCS  1263
CtChV-1:YP_009103999.1  KSMM-DINMLGSF---------EGETKWKLYNSAAAAFSEKA-----FDVILVAGRQEK------TFFGNFTVMTFGESQGLTF-NKVCIALTEDSLLAS  1292
CtChV-2:YP_009103996.1  GGIL-DVPMLGPI---------NELNQLNLYNSAAAAFSERA-----FDVILVAGRQEK------SFFSNYTVMTFGESQGLTF-DKVAIALSEDTLLCS  1289
DiVA:YP_006905850.1     YKP--GVEMLGE----------DENIISRRFSNVFSAKKTIP-----EAQLLVASRDEQ------VRFKELDAKTFGESQGLTF-DEIIIVLSPPAVNCS  1101
ObRV1:YP_009408144.1    YKP--GVVFLND----------ADSVPTKRFLNTLVAKKSIP-----NAQVLVASHDEQ------IRFRDLGAKTFGESQGLTF-DESIIVLSPPSTNCS  1101
CVA:NP_620106.1         TGFL-KLGYYN-----------QMESKAFTIDNMETLQKAIGTSMDKFGVLVTSRADKSD-----FELDFPNVCTINEAQGSTF-NSVILIVTRDFFSNP  1078
ASGV:NP_044335.1        QELV-NMPTRVD----------ESKFSRKFFADISSVKTED------YGLILVAKREDKG-----VFAGRVPVATVSESQGMTISKRVLICLDQNLFAGG  1017
PVT:YP_002019748.1      LDFF-DVRCSSDQK--------KWELHGKQYREPAALFRDIKGQE--FTILSPSFETAREMSKYADIKDGCKSMTFGESQGLTV-NKAVIVVDQDLVATS  1018
PrVT:YP_009051684.1     LEDF-EYGHGD-----------VDPNHMRVFAQPQAVREAIK-----RPVFLCPSDDKRS-----ELSNFGEAYTFGTSQGLTF-DFVCISIDMDGSVTS  1188
GVA:NP_619662.1         CKLF-EIECM------------GAESEKRVVYRSNRLKDEPT---------ICATRAMKE-----EKGSG--WYTVSETQGLSF-KSCLIYLDEHWAKKE  1130
GVE:YP_002117775.1      QKIM-EVPSYG-----------VSDFEVKEIKKLNK-----------ETLTICFSRATVE-----EERDNLTICTVGQAQGLSR-DVVQIMFDHGSLKCA  1133
GCLV:YP_004936159.1     VG---RLPCA------------ISNTNEDDFEDFEILEGIEQVQEIDVECYLVSSFIEKQAVRA-LVGLDKVVQTFGESTGLTY-DCVAVVVSEASKLAS  1391
CVNV:YP_001430021.1     AG---RLPCQFQPEYF------TNHEDFTILHGFESLNDIAG-----LDCILVSSFNEKTAVKALTFGR-VSVQTFGESTGLTF-NSGAIFISEVSKLAS  1410
PhlVB:YP_001552317.1    QG---RLPCEFGTQMEG-----QATEEHLLYSGLEHLHVIPQEF---SKVFLVSSFEEKKIVEAHFPGSNPTVLTFGESTGLNF-KYGTIIITNVSAHTS  1486
APV1:YP_009094347.1     VG---RLPCRMDTKAM------TENENFHWLESIESAAEVSNTE---YDVVLVSSFEEKKIVWA-HLGRDLEVLTFGESTGLTF-NRGIILISHESTLTS  1460
ASPV:NP_604464.1        YG---RLPCNLNKTRLT-----LDEEEYTLWDSIQEFSMMGRKD---CPVVLVSSFEEKKIVAA-HLGLKMKCITYGESTGLNF-QKGAILVTYESALTS  1616
CTLaV:YP_009046478.1    LG---RLPCTFDQSRMT-----LEKEEYAVFSSFKDFKNDYLSPK--IKTFLVSSFTEKTVVKA-NMGRNVLVYTFGKSTGMNF-DYVCVLLTQDSMLVD  1466
CRMaV:YP_007761581.1    VG---RLPCTFDSSRLT-----LEKEEYAVFDSFKAFKADYLSPK--IKTFLVSSFTEKTVVKA-NMGRNVSIFTFGESTGMNF-DYVCVLLTQDSMLVD  1456
                                                                                                  * . : * .  .   : .

SdRV1:AYE54584          EFRWMVALTRAKK--RLSFCCTHLGGIEDFTTNCKSQLFKSFFSRQT---IKVDFLRSLCQAKMNMVKKE--IGGKIDEVDREERLSGDPFLKPFIFLGK  1574
CLBV:NP_624333.1        EFRWMVALTRART--RFSLCSTFLGGIEEFKVKRKESLITSILQG-----EKITFNRLNLMLKCNLIRRE-KENGCRDEVDREERLEGDPFLKPFIFLGQ  1485
CLBV:AFA43536.1         EFRWMVALTRAKT--RLSFCSTFLGGMDEFKIKRGESLVTSILEG-----KQITFERSNMMVKCNLIKQE-KKNGCSDEVDREERLEGDPFLKPFIFLGH  1510
AVCaV:YP_008997790.1    DHRWLVALTRARK--KVTFLCLHLSGLNGFLSTMENRLVAAVINKGLVTKKRLSSMVRAKLNYVKFKGLA-----GKDEVDREDRLEGDLFLKGVIFLGQ  1202
CPrV:AKN08994.1         DYRWVVALTRAKE--KISFITSHRSGLTGFMSSMIGRPIHAFLTG-----LPFTSNRMNWMVNCELVECH-RATGGRDEVDREDRLEGDPFLKPFVFLGQ  1513
ACLSV:NP_040551.1       DAHIMVAITRFRR--GFCFALGSKGSKEDYMRSMKSGLLQRICSGVG---ASKEFILGSSSVNLILSEKDIAKGAGIDEMDREARLEGDVWLKSMIYLGK  1381
GPGV:YP_004732978.2     DNHIYVALTRFKK--GFGFFQNFRGDLGTFKSNLGSKLLGRYINLRD---NLKPFMMQMLDINLDFMDDR---NQVGAGIEMENKMSGDPWLKGLLDLQA  1355
CtChV-1:YP_009103999.1  DNHMMVGLTRAKE--TINFIKGFGYPLNEYVKKAGNKLIGKVLQGKVIKRAELENMSG--MEDVTFITEP------PTFGGHEDKVQGDPWMKSLLTLTQ  1382
CtChV-2:YP_009103996.1  DNHIVVALTRARK--QISLIKCFGYDEKEFFKRAGTKLIGKVLNKKKIKRVQLENM--LALEDLKLISSE------PKFGTQEERTEGDPWMKGLLTHIQ  1379
DiVA:YP_006905850.1     INMWNVAMTRARK--GVHFALNGFDTVDDFINRVKGTPVNAMILGSP---FEIHRTPGGKDKEIKIIKVC---RLGMSNEDVEMKLMGDPFLKSIIPSLD  1193
ObRV1:YP_009408144.1    LFMWNVAMSRSIK--GVHFALNGFDSIDDFLNRVKGTPVAAMILGMK---FDIHAQPMSTPEDCKIICSD---RLCLSSSDVENKLEGDPFLKSIIPSMD  1193
CVA:NP_620106.1         IESIIVAITRHQKNLLIYFPAAIQGEMDFLSRRF--PIHSNVVLKNF---SVLDNLIKDKLNPFQLIQED------PFGHDFEVKLEGDPFLKSELSLVN  1167
ASGV:NP_044335.1        ANAAIVAITRSKV--GFDFILK-GNSLKEVQRMAQKTIWQFIIEGKS---IPMERIVNMNPGASFYESPL-----DVGNSSIQDKASNDLFIMPFINLAE  1106
PVT:YP_002019748.1      VLHWIVALTRSRQ--GFVILVHKVFDMKTLIQPVQNSIIGLVLRGVKVQENIFINTAGKCLSEAEIVEEL--ETFKRTEED-EDLLEGDPWLKGQLFLCQ  1113
PrVT:YP_009051684.1     DFHWMVALTRARR--GFCFLTCASTSMRTFMDNNRAKLIGKVLKKEQISKKFWWNLGGRALEGARAVKKDEFSKLGKTREEFEESLEGDPWLKGMLNYLE  1286
GVA:NP_619662.1         DEDVMVALTRSRGEIGIHVTPALK---KKLITNAKSTLLKKVLKGETYRRSEIVAMVRKHIPETTVLFEE---SRLAETVDYEARLAGDPYLKSLLALYD  1224
GVE:YP_002117775.1      DETIIIALTRARK--AVHLFYKIG---KTDLKNCSSPILRAFISNGKIPEKLLVDKVRGKLGDCRLLTEN--VFIGADSATIGDHLAGDPGLKAMLLILE  1226
GCLV:YP_004936159.1     ERRWITALTRARK--RVTFITNLGCSKHLIAEIFSNRALGRFLSCT----ASIDNLRCLLPGEPNFVEEL-VPTIGANLGVVEEKVSGDPWLKTMLFLGQ  1484
CVNV:YP_001430021.1     EQRWLTALSRFRM--NLTFVSDLGCDSSMLAEVFSGRVLGRFLSGK----ANVCDLRGLLAGSPDLQEDF-PTTVGKNQGLVEEKVVGDPWLKAMLFLGQ  1503
PhlVB:YP_001552317.1    EKRWVTALSRFSE--NICFVNLVNLSWSELARMYATRVLGRFLGKR----AKLSDLLEHLPGVAVFTDSY-DENIGKDEGVREEKVQGDPWLKGMVDLFQ  1579
APV1:YP_009094347.1     ERRWITALSRFRL--NIIFVNLVGNCLEDACQVFHDRTLDRFLTKR----ATIANIVDQLPGLPELTNDF-GDKVGRSEGVMEAKLSGDPWLKTEIDLLQ  1553
ASPV:NP_604464.1        DRRWWTALSRFSH--DIHFINGMGVTWDNAITHFVGKPLHKFFTKR----ACNDDIIDLLPGRPELIEGF-QSQVGADEGVREAKLVGDPWLKTKIFLGQ  1709
CTLaV:YP_009046478.1    ERRWVVALSRAKI--NMSFVNLSGLSLPEFCTQMVGGVVHKFFTGT----ATFNDLRSLLPGDPIFSKKF--QRLGSDEVDREARLSGDPWLKTKVFLGQ  1558
CRMaV:YP_007761581.1    ERRWVVALSRAKI--NISFINLSGLTLPEFCTQMMGGVVHKFFTST----ATFNDLRELLPGDPIFSKRF--QRLGKDEVDREARLLGDPWLKAKVFLGQ  1548
                              .::*       . .                                                                   .*  :   :
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SdRV1:AYE54584          RVEDREIV-IDECDPEEVKCKTHLYLSEPNFAGAYNFDLIREKESREYRESM-MSTDQFCDNYNKKHPKACMRTVGPMRFKSIYPKHSSDDDMTFWMAVK  1672
CLBV:NP_624333.1        RVEKDEDE-VEEVKIREPTCQTHLYITEPNFGLCYNFDFIREKEQREYREDM-LVTNQFCDSYDKVHINGKRETPGPLRFKAIYPKHSADDDMTFWMAVR  1583
CLBV:AFA43536.1         RIQKSHDE-VGEIEVREPTCQTHLYITEPNFGLCYNFDFIREKEQREYREDM-LVTNQFCDSYDKVHINGKRETPGPLRFKAIYPKHSADDDMTFWMAVK  1608
AVCaV:YP_008997790.1    RCEIMEPE-IVEPVMAKEDMKTHFFVCQENFAQCYNFDNIRAKELREFRIGH-RVTNQFIDNYEIVQHVQKKHTAGPLRFEAIYPRHCADDDVTFLMAVH  1300
CPrV:AKN08994.1         RINSEEYE-IIEPEVIEPKGRVHLCISQENYALARNFDLIRAKEYREAKLMG-LETNQFCHDYNRVGAQGSRHVASPLRFESIFPRHRSDDDLTFWMAVK  1611
ACLSV:NP_040551.1       RYHMVEPL-GQVIKLTDDAIKCHIPVCSSQ-TLGPELDNIQAREYREFKGKN-GWSNQFREEAG-PNWKFPYKVNQAMSYEAVYPRHKMDDDLTFLAAIK  1477
GPGV:YP_004732978.2     VEEVEDMF-FEDLNIIEPTGKVHLPLASRN----DEFEKIRARESRELKKLDFDWSMQFEDCGV--KIKRVLNGNLCENFSAVYPVHQACDEMTFLAAVK  1448
CtChV-1:YP_009103999.1  REDSQEVE-LIEPDIVESKMKVHINITDKSYALMIINDQLRAKENREFKSKD-SWSNQFKDNDQ---NLNLETSTGPVNFEAIFPRHQTFDDVTFWMAVK  1477
CtChV-2:YP_009103996.1  EVIMEECE-PQMAKPDDVKMKVHVPITDKSFALTIINDQIRAREYREFKVGD-SWSTQFKDDNK---NLKLESSTGPVNFESIFPRHTSFDDVTFWAAVK  1474
DiVA:YP_006905850.1     EGLSIEQE-YHDIICESPVPKIHLPIESIQGHVSYVSSMLKERGEREFKGDG-CMSEQFPDFWK--TGEPGHYLSQSERFQSIFPKHQNSDSLTFLAAVK  1289
ObRV1:YP_009408144.1    EGLCVHHE-YQDVNFELPTPKIHLPIESIQSHVAFVSSMIRNREFREFIGDG-EMSEQFPDFFK--QSETGSFLSQAERFQAIFPKHSNGDSLTFFAAVK  1289
CVA:NP_620106.1         EIKLQQIE-ENSIESKENL-KTHLPI-SYSGLWNLEISEMRAREDREFKKFGVGWSKQFKDEPN---QKDQVEDNCAMLPEAVFPRHFANDDLTFWSAVK  1261
ASGV:NP_044335.1        EEVDPEEV-VGDVIQPVEWFKCHVPVFDTDPTLAEIFDKVAAKEKREFQSVL-GLSNQFLDMEK----NGCKIDILPFARQNVFPHHQASDDVTFWAGVQ  1200
PVT:YP_002019748.1      SVELDEVT-PEEPLRHESPPRTHLPL-PVEGLTPLLMSNVKAREDREFITPS-GWSKQFRDDKE---NVDWRNVSYADAFETIYPKHEASDDITLWAAIQ  1207
PrVT:YP_009051684.1     GDDANDPE-PEEPIRKDSPPRTHLMIAPVEHQFAEEMHLLRAREFREFRNSN-LWSEQFDDCRK----TRKVIHNRAETFEQIYPSHKNSDTLTFWAAIK  1380
GVA:NP_619662.1         EIEMEDIE-IEEPVTLEPT-KTHLALSTKMNELAPF--DLKAKEHREQHTEA-GRTEQIDENGY------QGEVGDPMTHKALYLRHTSDDTATFMMSVK  1313
GVE:YP_002117775.1      AEEMEPEI-FEEETVPETI-RTHLGVTT--FANEQFAFGLKAKEEREHHIHGTGFSTQIRDNIA------SEFHPGPSAPSSIYLHHTAEDDVLFILSIK  1316
GCLV:YP_004936159.1     VADVADEI-DVDEALQIEPFKTHVARSNLEGVRALWHDKIRLKEHREKRMGY-LVSEQFTDMHS--KNMGKKLTNAAERFETIYPKHKGSDTVTFIMGAR  1580
CVNV:YP_001430021.1     ETDEQEVA-PEVAEVALEVFKTHAPRCELEGVRARWHEKIQAKEFREKRMGY-LVSEQFTDEHS--KNNGKKLTNAAERFETIYPKHKNSDTVTFIMGAR  1599
PhlVB:YP_001552317.1    IEDVEEEE-EQLEEMQTEWFKVHLPQAELESVRAKWVHKILAKEFREVRIGH-LVSEQFTDEHP--REQGKQLTNAAERFEAIYPRHKANDTVTFMMAVK  1675
APV1:YP_009094347.1     DEDQEMEE-LAEEVKHEPWFKTHLPLFELESIRASWVHRIMNREYREVRCGS-ETTTQFPDDHP--SGAKITLANAAERFEAIYPRHRGSDSVTFLMAVK  1649
ASPV:NP_604464.1        NPDFEIEI-ADEVEAAEDWFKTHIPIMSLEAVRAQWVHKLISREDREFRIGD-ITTEQFTDDHS--KNRGQELTNAAERYEAIYPRHKGTDTATFLMAVK  1805
CTLaV:YP_009046478.1    REVRPVEEPISVENLKDIKIKVHCPVGSMGATFAEVQSKLKVKEAREHRIDT-IVTEQFAEVHK---GRGKILTAAPDNFEAIYPRHKAGDTATFVMAAR  1654
CRMaV:YP_007761581.1    REEKIESIHVNDEGLKDIKVKVHCPIGSIGSTLADIQAGVRVKEAREFRIDN-LVTEQFSEVHK---GKGKVLTAAPDNFEAIYPRHKAGDTATFVMAAR  1644
                                            : *                :  :  **        : *: .                   . ::  *   *   :  . :

SdRV1:AYE54584          KRLRFQSEEENRMKLSEAHLIGGILYQNFKEKFD-LDFSHDQGLFERCVN-EFEEKKLGKSQAVIKSHSNRSDTDWKINDIFLFMKNQLCTKFEKQYVDA  1770
CLBV:NP_624333.1        KRLVFREEEENYQRLSRAHLVGGLLYTNFKKKMG-LEFTFDQGLLEESIN-AFEKKKLEKSCGTIKSHSIRSDIDWALNDVFLFMKSQLCTKYEKQFVDA  1681
CLBV:AFA43536.1         KRLVFREEEENYQRLSRAHLVGGLLYRNFKNKLG-LEFTFDQGLFEESVN-AFEKKKLEKSCGTIKSHSIRSDVDWALNDVFLFMKSQLCTKYEKQFVDA  1706
AVCaV:YP_008997790.1    KRLRFSNEMKEREKLERAHGTGSILFHNLIQKLG-LNFTWDNQLFEECVN-DFECKKLEKSKAVLANHSIRSDNDWSPNWVFLFMKSQLCTKYEKQYVDA  1398
CPrV:AKN08994.1         KRLRFSEEFLERAKLKDSYSVGNLLYQNLKEKLS-LSFSWDQGLLDECLN-DFETKKLLKSKATLANHSIRSDIDWSMDKIFLFMKSQLCTKYEKQYVDA  1709
ACLSV:NP_040551.1       KRLRFDNVANNYAKFKAAESRGKYLTKIFLKHVP-IKCGRDQRLLDQCRQ-EFEETKLSKSAATIGAHSQRSDSDWPLDKIFLFMKSQLCTKFEKRFTEA  1575
GPGV:YP_004732978.2     KRLRFSNPAKNLTKFRGATAAGKILLKNFLKFIP-IPSETFPELLSEAKR-EFQEVKLKKSEGTIAGNSGRSDPDWSWDRVFLFMKSQQCTKFEKRFCEA  1546
CtChV-1:YP_009103999.1  KRLSFSNPLVESEKLNKAWIKGSILHKEFTRLIR-VNSHFRPDLFEKALN-DFEDVRMRKSEKLIMAHAGRSDPDWDIRNFLLFMKSQLCKKAEKAFCDA  1575
CtChV-2:YP_009103996.1  KRLSFSNPITEGEKLKSAFVKGSILYKEFRKIIR-VQGDFRPDLFDKALS-DFERVRVAKSKKLIEAHAGRSDPDWDVKKFLLFMKSQLCKKAEKAFSDA  1572
DiVA:YP_006905850.1     KRLKFSSPSVERERFEKVRHLGNEMLDIFLDKIK-IDNKLNSEMMARSYN-EYVLKKVSKTANTIASHSSRSEPDWKLNEIFLFMKTQLCTKFEKRFSDA  1387
ObRV1:YP_009408144.1    KRLKFSSPQIEREKFEKVRHLGSEMFELLLEKIP-LDNKNDDLMMQICVN-EYIERKVSKPAGTIKSHSGRSDCDWKLNDVFLFIKTQLCTKYEKRFSDA  1387
CVA:NP_620106.1         KRLVFKNPLSNAHDFEKAKPFGKELLNIFLRKVP-LMPNFDQRMYDESVS-EFEEKKISKNAAMIGAHHDRSTTDWPTNEIFLFIKSQLCTKKEKMFCDA  1359
ASGV:NP_044335.1        KRIRKSNWRREKSKFEEFESQGKELLQEFISMLP-FEFKVNIKEIEDGEK-SFLEKRKLKSEKMWANHSERSDIDWKLDHAFLFMKSQYCTKEGKMFTEA  1298
PVT:YP_002019748.1      KRIVMADPFRNAMKLQKVEPISAEIFNEMNKILL-LNPHVSVDR-DQVYK-EFLRKRLNKSKKLIESHSERSSDDWPIDHFFLFMKSQLCTKFEKRFVDA  1304
PrVT:YP_009051684.1     KRMKMSDPYSERRKLERCMPVGENLCRLFVEEYG-LKRGWQVDI-ESTER-EFLLKRVEKAKKMIEAHSERSDPDWMVNHFFLFMKTQLCTKFEKRFSDA  1477
GVA:NP_619662.1         KRLRFRNYEANRRKYKTCHGIGHQMFSVFKDTYQ-LKEIDSLPELERCEM-EFMKKRIEKSTGLIEKHAGRSDPDWPSNYLKIFLKQQTCTKMEKRGVDA  1411
GVE:YP_002117775.1      KRLRFADFEKNCASFERKKKLGESIFTEFLKRADFMNFTYPPQVDETSMELDFTMKRIQKSARILEAHSYRSDADWPSNYLKIFIKNQDCTKMEKRGSDA  1416
GCLV:YP_004936159.1     KRLRFSKPAVEARKLMDASNFSEFMLQEFLKHVP-LKKPHNQAFMDASLA-DFEEKKTSKSAATIANHAGRSCRDWLIDTGLVFMKSQHCTKFDNRFRDA  1678
CVNV:YP_001430021.1     KRLRFSKPLVEARKLQDAKVYGEFMLQNFPKYVP-LRKQHNKGFMDKALR-DFESKKVSKSAAIIANHAGRSCRDWLADVGLVFMKSQHCTKFDNRFRDA  1697
PhlVB:YP_001552317.1    KRLKFSRPATEKAKLVEAMPYGKFMLKEFLKKIP-MNKSRDTKMMEQSKL-EFEEKKLSKSAATIENHSGRSCRDWLIDIGLIFSKSQLCTKFDNRFRVA  1773
APV1:YP_009094347.1     KRLSFSQPSKESAKLNRAKPYGKFLVSEFLKRIP-LRGNLDPILFAKAKR-DFEEKKTSKSAAVIENHSGRSCRDWLADVGFIFMKSQFCSKWDNRFRDA  1747
ASPV:NP_604464.1        KRLSFSSPAAEHAKLRRAKPFGKFLLDTFLKRVP-LNSSHDEKMMQEAVH-AFEEKKLSKSMATIENHSGRSCEDWPVDKALIFMKSQLCTKFDNRFRSA  1903
CTLaV:YP_009046478.1    KRLKFSLPAKEKQKFMSAIPYGDTMLKVFLNKVR-LKPNFDHRLFEEARN-DFEEKKLQKSMATLENHSGRSDPDWEIEKALIFMKSQLCTKFDNRFRDA  1752
CRMaV:YP_007761581.1    KRLKFSFPARERQKYMAAIPYGVSMLQVFLKRIK-LQSNFDHRLFEEARA-DFEEKKLQKSMATLENHSGRSDPDWSVEKALIFMKSQLCTKFDNRFRNA  1742
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SdRV1:AYE54584          KAGQTLACFQHLILVFFAPWCRYMEHQIRSQLPEEIYIHSNKNFDDLNEWTKKFF--ARDICVESDYEAFDASQDEYILSFEMHLMEDMGIPRKVIDAYV  1868
CLBV:NP_624333.1        KAGQTLACFQHLILVQFAPWCRYLETQIRNQLPEEIYIHSNKNFDDLNAWVKKFF--QRDICVESDYEAFDASQDEYILSFEIHLMKDAHFPQKIIDAYI  1779
CLBV:AFA43536.1         KAGQTLACFQHLILVQFAPWCRYLEAQIRNQLPEEIYIHSNKNFDDLYRWVKNFF--QKDICVESDYEAFDVCQDEYILSFEIHLMKDAHFPQRVIDAYI  1804
AVCaV:YP_008997790.1    KAGQTLACFQHMILVTFAPYCRYMEKQLRAQLPGEIYIHSNKNFNDLNEWVKKHA--GDDLCVESDYEAFDASQDQYILSFELFMMRHMHIPEQIIQAYI  1496
CPrV:AKN08994.1         KAGQTLACFSHLVLAKFAPYCRYMEKMLRRNLKEEIYIHSNKNFNDLNDWVVKFF--EEGEKVESDYEAFDASQDHYVLAFEVCVMEDMGLPNWFINDYI  1807
ACLSV:NP_040551.1       KAGQTLACFPHKILVEFSPWCRYTEKVLTANLPDNYYIHQRKNFSELEDFARRFS--NGSICVESDYTAFDVSQDHTILAFEVELLRHFGWDDRVLQSYI  1673
GPGV:YP_004732978.2     KAGQTLACFSHEILCHFSPWCRYMEKVFSKYCPENFYIHQRKDFDKLAEFSRKYC--KGGFCIESDYVAFDVSQDHNVLAFEVQLMEHIRIPECVISDYI  1644
CtChV-1:YP_009103999.1  KAGQTIACFAHGVLFKFSAWCRYAELKINEVMPEAFYVHSKKNFDELERWVKGNF--IGPICVESDYEAFDASQDSTILAFECLILKDVGWPHDLIEDYK  1673
CtChV-2:YP_009103996.1  KAGQTIACFAHGVLFKFSAWARYAELKMMEKMPDSFYIHSRKNFDELEKWVKMNF--IGPICVESDYEAFDASQDATILAFEVQFLKEVGWPQDLIEDYI  1670
DiVA:YP_006905850.1     KAGQTLACFSHIILNRFAAPTRYVEKKISEGLGKNFYIHQKKNFDVLNDWVVANN--FDSYCLESDYEAFDSSQDCLILAFEYELLKYLGWDQSLLDDYL  1485
ObRV1:YP_009408144.1    KAGQTLACFSHVILNRFAAPARYIEKKLSLCLPDNYYIHQKKNFDMLNAWVVRND--FSDECLESDYEAFDSSQDCLILAFEYELLKYMGWSQSLLDDYL  1485
CVA:NP_620106.1         KAGQTLACFSHLILCKFAPLNRYIEKKVTQSLPGNFYIHQKKNFDELERWVKSYN--FSGVCTESDYKAYDASQDSCTLAFEYKLLRYLAFSNSLIEDYL  1457
ASGV:NP_044335.1        KAGQTLACFQHIVLFRFGPMLRAIESAFLRSCGDSYYIHSGKNFFCLDSFVTKNASVFDGFSIESDYTAFDSSQDHVILAFEMALLQYLGVSKEFQLDYL  1398
PVT:YP_002019748.1      KAGQTLACFSHKLLTRFGPAFREFEKKFTANLPPSWYIHTMKNFDQLNNWVINYV--DQEEGTESDYEAFDRSQDAIILGLEIECLKLFGWDQDLIDDYR  1402
PrVT:YP_009051684.1     KAGQTLACFSHQVLARFGVPIRVAEKKLRAQLGENIYIHSGKQLDELNEWCMGYA---KGYGTDSDYESFDRSQDALILAFELHLLRFLGWSVDQVEDYV  1574
GVA:NP_619662.1         KAGQTIACFAHSVLCRFGPILRQTEKALRELLPEKLMIYSQKKYMDLDKWAKTWV--ESMMGTDSDYEAFDRSQDEKVLDLEVEVLRFFLWPEDLIREYE  1509
GVE:YP_002117775.1      KAGQTIACFSHAVLCKFGPILRKTEAQLRKILPPHVMIFSQKNYEDLDKWSKDYF--NDHSGTDSDYEAFDRSQDGAILAFEICLLRHFLWPEELIEEYK  1514
GCLV:YP_004936159.1     KAAQAIVCFQHAVLCRLAPFVRYIERKIAEVLPEKFYIHSGKGLEELNAWVTRGR--FEGVCTESDYEAFDASQDQYILAFELHVMKYLGLPRDLIEDYK  1776
CVNV:YP_001430021.1     KAAQSIVCFQHAVLCRFAPYMRYIEMKLQEVLPSNFYVHSGKGLDELSEWVKKGK--FEGICTESDYEAFDASQDQYIMAFELKVMEYLGIPKDLIADYV  1795
PhlVB:YP_001552317.1    KAAQSIVCFQHEVLCRFAPYMRYIEKKLHQALPGNFYIHSGKGLEELNEWVMRGR--FDGVCTESDYEAFDASQDQYIMAFEIEMIKYLGLPADLISDYE  1871
APV1:YP_009094347.1     KAGQTLACFHHSILCRFAPYMRYIEYKLQAASPSNLYIHSGKNLEDLNEWVIRNK--FSGMSTESDYEAFDSSQDHFILSFEIEIMKHLQLPWDLIEDYV  1845
ASPV:NP_604464.1        KAGQTLACFQHSVLCRFAPYMRYIESKVTEVLPKNLYIHSGKNIDDLAAWVTTSK--FNGVCTESDYEAFDASQDHFILAFELEVMKFLGLPSDLIADYT  2001
CTLaV:YP_009046478.1    KAGQTLACFHHNVLCRLAPYIRYIEKKVFDALPRNLYIHSGKNFDDLRDWVINSN--FSGMCTESDYEAFDSSQDANILAFEVSLMNYLNLPRDLIEDYK  1850
CRMaV:YP_007761581.1    KAGQTLACFHHDVLCRLAPYIRYIEKKVFKALPSNLYIHSARNFDDLRDWVIKNN--FTGVCTESDYEAFDSSQDVNILAFEVSLMEYLRLPRDLIEDYK  1840
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SdRV1:AYE54584          DLKCTLGCKLGHFAIMRFTGEFCTFLFNTTANMAFTMCRYEWR-RGQPIAFAGDDMCALNNLPLNHD--FDDLFDKLSLKAKVERTDCPMFCGWRLTQYG  1965
CLBV:NP_624333.1        DLKCKLGCKLGHFSIMRFTGEFCTFLFNTLANMAFTMCRYEWR-RGQPIAFAGDDMCALNNLAVCHD--FDDLFELISLKAKVERTETPMFCGWRLTPYG  1876
CLBV:AFA43536.1         DLKCKLGCKLGHFSIMRFTGEFCTFLFNTLANIAFTLCRYEWR-RGQPIAFAGDDMCALNNLPICHD--FDDLFELISLKAKVERTESPMFCGWRLTPYG  1901
AVCaV:YP_008997790.1    DLKVNLGCKLGHFAIMRFTGEFSTFLFNTLANMAFTMCRYEWN-SGDPIAFAGDDMCALKNLKVTDQ--FNNVFEKISLKAKTQITEVPMFCGWRLSRFG  1593
CPrV:AKN08994.1         DLKCTLGCKLGHFAIMRFTGEFSTFLFNTLANMAFTFARYECD-HKTPIAFAGDDMCMLKACKVSDK--FEDVLSKLSLKAKVIRTEMPMFCGWNLSRYG  1904
ACLSV:NP_040551.1       KMKCTLGCRLGGFAIMRFTGEFSTFLFNTLANMVFTFCRYEVP-DGTPICFAGDDMCALRNLREIDT--HEFILSKLSLKAKVNRTKVPMFCGWRLCCDG  1770
GPGV:YP_004732978.2     RMKTELGCKLGNFAIMRFTGEFCTFLFNTFCNMAFTFMRYQMS-GHEPICFAGDDMCALADLKESDE--YNAFFKSFSLKAKVCRTVKPLFCGWRLTKFG  1741
CtChV-1:YP_009103999.1  TLKLELGCKLGMLAIMRFTGEFGTFFFNTLANMAFTFCRYNVN-RTTPICFAGDDMCILTNAKIRNE--MNDFIGSLKLKAKVEWKINPIFCGWILSRRG  1770
CtChV-2:YP_009103996.1  ELKVNLGCKLGNLAIMRFTGEFGTFFLNTLANMAFTFCRYNVN-RTTPICFAGDDMCILTDAKVRHD--LDEFINSLKLKAKVEWKINPIFCGWILSRYG  1767
DiVA:YP_006905850.1     DLKFNLGCRLGNLAVMRFTGEFGTFLFNTLANMVFTFMTYDLN-GTESICFAGDDMCCNRGIKARVDGKYDHILKRLTLKAKAVITKEPTFCGWRLTKYG  1584
ObRV1:YP_009408144.1    DLKFNLGCRLGNLAVMRFTGEFGTFLFNTLANMVFTFMSYDLT-GKEAICFAGDDMCCNKGIRRRTDGRFDHILNRLSLKAKAVITTEPTFCGWRLTKYG  1584
CVA:NP_620106.1         YLKMHLNCKLGNLAIIRFTGEFCTFLFNTLTNMLFTFMKYDVR-KTHAICFAGDDMCANVRLPENHE--YSSLLKKFSLKAKVDFTRSPTFCGWNLSRYG  1554
ASGV:NP_044335.1        RLKLTLGCRLGSLAIMRFTGEFCTFLFNTFANMLFTQLKYKIDPRRHRILFAGDDMCSLSSLKRRRGERATRLMKSFSLTAVEEVRKFPMFCGWYLSPYG  1498
PVT:YP_002019748.1      KLKLRMGCRWGAIAIMRFTGEFGTFFFNTIANIAFTCLRYNIT-RDTVIAFAGDDMYASGKLEIRKD--REDLLAHLTLKAKVQFTEKPMFCGWYIKKMG  1499
PrVT:YP_009051684.1     TLKLRLGCRLGYLAIMRFTGEFGTFFLNTCCNMLFTCLRYKIN-KNTPIAFAGDDMFSPGRLEVRRD--REFLLNRFSLKAKVNFSKEPMFCGWRMTPYG  1671
GVA:NP_619662.1         ELKLMMGCALGDLAVMRFSGEFGTFFFNTVCNMVFSCMRYHID-RNTPMCFAGDDMYSPGILRVKKD--YEATLDQLTLKAKVHISEEPLFCGWRMSPFG  1606
GVE:YP_002117775.1      TLKLMMGCQLGDLAVMRFSGEFGTFFFNTMCNMAFSYLRYQLG-PYQPIAFAGDDMVAPGRLVVNES--MNSVLNQLELKAKVNYSDSPLFCGWRMSPYG  1611
GCLV:YP_004936159.1     FIKMHLGSKLGNFAIMRFSGEASTFLFNTMANMLFTFLRYEIK-GHERICFAGDDMCANARLRHRLD--QEKFLGLLKLKAKVSFTQKPTFCGWNLCSDG  1873
CVNV:YP_001430021.1     YIKTHLGSKLGNFAIMRYSGEASTFLFNTMANMLFTFLRYDVK-GNEFICFAGDDMCANTKLRKVDT--HESFLSKLKLKAKVGFVNKPTFCGWNLCSDG  1892
PhlVB:YP_001552317.1    FIKTHLGSKLGNFAIMRFSGEASTFLFNTMANMLFTFLRYEIR-GNEFICFAGDDMCASKRLPLSRA--YEGFLSKLKLKAKVFFVKSPTFCGWHLSPDG  1968
APV1:YP_009094347.1     YIKTHLGSKLGNFAIMRFTGEASTFLFNTMANMLFTFLRYDLN-GSEAICFAGDDMCANRRLRVSKK--NENFLGKIKLKAKVQFTEKPTFCGWNLCMDG  1942
ASPV:NP_604464.1        FIKTHLGSKLGSFAIMRFTGEASTFLFNTMANMLFTFLRYDLN-GREAICFAGDDMCANSRLKVTNR--FSNFLDKIKLKAKVQFTATPTFCGWGLCEHG  2098
CTLaV:YP_009046478.1    HLKFNTHSKLGQFAVMRFTGEAGTFLFNTLANMVFTFMRYETN-GRESICFAGDDMCANKLLRKKKE--YEHVLDRMTLKAKMQHTTEPTFCGWRLGPFG  1947
CRMaV:YP_007761581.1    YLKFHTHSKLGQFAVMRFTGEAGTFLFNTLANMVFTFMRYEIN-GREAICFAGDDMCANKLLRKKSE--FEHILDRMTLKAKVQHTTEPTFCGWRLGNFG  1937
                         :*    .  * ::::*::**  **::**  *: *:   *.       : ******                 :  : *.*       * **** :   *

SdRV1:AYE54584          IIKEPELVYNRFQVAIEEGKVAECLENYAIEVSYAYKLSERLFEVLKSEKQLQYHQAVVRFIVKNIRKLKTNVK--------------------------  2039
CLBV:NP_624333.1        IVKEPELVYNRFQVAIEEGKVLECLENYAIEVSYAYSLSERLYEVLKSERQVQYHQAVVRFIVTHIDKLKTKVR--------------------------  1950
CLBV:AFA43536.1         IVKEPELVYNRFQIAIEEGKVMECLENYAIEVSYAYSLSERLYEVLKSERQIQYHQAVVRFIVTHIDKLKTRVK--------------------------  1975
AVCaV:YP_008997790.1    IVKEPELVYNRFMVALERGNVKDCLENYAIEVSYAYSLGERLFDILKREEQLEYHQAVVRFIVKHLGNLRTKVK--------------------------  1667
CPrV:AKN08994.1         IVKEPELVFNRFMVAKKRGNIDECLENYAIEVSYAYSLGEKLYEVLKREEQVEYHQAVVRFIVQRLDKLKTKVK--------------------------  1978
ACLSV:NP_040551.1       LIKEPCLIYERLQVAIENGRLMDVIDSYFLEFSFAYKLGERLYSHLE-IEQLNYHQVLTRFFIRNKHLLRGDSRHNISEL--------------------  1849
GPGV:YP_004732978.2     LYKEPVLVYERLKIAIEKDKLDLVIDSYFLEFCYAYKLGSWLDWVLD-EEQADYQQRLSRFFVKKRHLLKGKSLDYITHC--------------------  1820
CtChV-1:YP_009103999.1  ILKLPSLVYYRLNIAKEKGNLKDCIDSYMIEAGYAYRKGAFIEELLD-EDQMSFHQLVIRSMIKSKHLMKGSSI--------------------------  1843
CtChV-2:YP_009103996.1  ILKLPSLVYYRLCIALEKGNLKDCIDSYMIEAGYAYRKGAFIDELLT-EEQMNFHQLVIRRMIKAKHLMKGSSV--------------------------  1840
DiVA:YP_006905850.1     IFKKPELVLERFLIAIEKGRLLDVIDSYYIECSYAYNLGERLFECFS-EKDFSAHYCCIRIVHKNKSLLKGLSLERYRENR-------------------  1664
ObRV1:YP_009408144.1    IFKKPELVLERFLIAIEKNKLKDVIDSYYLECSYAYSLGERLFECFS-EKDFVAHYCCIRLVHLHKDLLRGQSLDKYISNQ-------------------  1664
CVA:NP_620106.1         IVKKPELIAARLAVARQKGEVNLVLDSYFLEHLYAYNKGDHLFEILS-EKELEHHYNLTRFFVKNSKLLKGESKKKFMETKEIEGGLFGECDFGNDSIFK  1653
ASGV:NP_044335.1        IIKSPKLLWARIKMMSERQLLKECVDNYLFEAIFAYRLGERLYTILK-EEDFEYHYLVIRFFVRNSKLLTGLSK--------------------------  1571
PVT:YP_002019748.1      IVKEPRLVLERWLIAERKKVIDQCFINYSIEVSYGYRLGEYLWEYFD---NLEDFQAIVRLVIKKKKQLPPAIR--------------------------  1570
PrVT:YP_009051684.1     IVKEPKLVLERFKIAEERGCFKECLINYCLEVSFAYRLGERLYDVIK---NIQDKQALVRIVVKNKKFLPKKIRKEF-----------------------  1745
GVA:NP_619662.1         IIKEPNLILDRWKIALRSGNLSLCLVNYAIEASFGYRLSEHLYDV---NIDVDAQQELVREIVIKKHLLPKKIS--------------------------  1677
GVE:YP_002117775.1      IVKDPNLLLDRLEMKRAEGKLDDCIANYALEASYGYRLSDHLYDL---NIDLDAFQELIRKIVMLKHKLPPAIA--------------------------  1682
GCLV:YP_004936159.1     IYKKPQLVLERLCIAKETNNLACCIDNYALEVAFAYKMGERAVLRMD-EEELQSHYNCVRIILQNKNLIKSNVL--------------------------  1946
CVNV:YP_001430021.1     IYKKPQLVLERLCIAKETNNLTSCIDNYAIEVSYAYRMSEKATMRMS-EEELDSHYNCLRIIIKNKHLMKSEAA--------------------------  1965
PhlVB:YP_001552317.1    IYKKPQLVMERMCIAKEKGNLIDCIDNYAIELSYAYKMGELALCRMD-EEETEAFYNCVRIVVKNKHLLKSDIK--------------------------  2041
APV1:YP_009094347.1     IFKRPQLVLERLCVAREKDNLANCLDSYAIEVGYAFALGEKILQYMD-EEALQNHYNCVRFIIKHSHLLKSSVR--------------------------  2015
ASPV:NP_604464.1        VFKKPDLVLERLQIARETRNLENCIDNYAIEVSCAYKMGENLNLYLT-PQEVDAHYNCVRFIVQHNHLLKSNIR--------------------------  2171
CTLaV:YP_009046478.1    IIKRPQLVQERIPIALEKGNFNECIDNYAIEVSHAYNLGDRLISIMS-EKELDAHYFCVRTFLQHKSLFSSNAL--------------------------  2020
CRMaV:YP_007761581.1    IVKRPQLVQERILIALEKGNFHECIDNYAIEVSYAYNLGERLISIMS-EKELDAHYFCVRTFLQNKKLFSSNAL--------------------------  2010
                        : * * *:  *  :      .   . .* :*   .:  .                    * .      :

SdRV1:AYE54584          ----------------------------------------------------------------------------------------------------  2039
CLBV:NP_624333.1        ----------------------------------------------------------------------------------------------------  1950
CLBV:AFA43536.1         ----------------------------------------------------------------------------------------------------  1975
AVCaV:YP_008997790.1    ----------------------------------------------------------------------------------------------------  1667
CPrV:AKN08994.1         ----------------------------------------------------------------------------------------------------  1978
ACLSV:NP_040551.1       ----------------------------------------------------------------------------------------------------  1849
GPGV:YP_004732978.2     ----------------------------------------------------------------------------------------------------  1820
CtChV-1:YP_009103999.1  ----------------------------------------------------------------------------------------------------  1843
CtChV-2:YP_009103996.1  ----------------------------------------------------------------------------------------------------  1840
DiVA:YP_006905850.1     ----------------------------------------------------------------------------------------------------  1664
ObRV1:YP_009408144.1    ----------------------------------------------------------------------------------------------------  1664
CVA:NP_620106.1         DYINRVKNKVEIDLLNERILRINTEMNQFDPRIYMMNKIGFVTSTSMFEAGHIASNESNQVKSLPPQTSWPYDEVKPYMPLSLRNSYESRTKGNRLLSIL  1753
ASGV:NP_044335.1        ----------------------------------------------------------------------------------------------------  1571
PVT:YP_002019748.1      ----------------------------------------------------------------------------------------------------  1570
PrVT:YP_009051684.1     ----------------------------------------------------------------------------------------------------  1745
GVA:NP_619662.1         ----------------------------------------------------------------------------------------------------  1677
GVE:YP_002117775.1      ----------------------------------------------------------------------------------------------------  1682
GCLV:YP_004936159.1     ----------------------------------------------------------------------------------------------------  1946
CVNV:YP_001430021.1     ----------------------------------------------------------------------------------------------------  1965
PhlVB:YP_001552317.1    ----------------------------------------------------------------------------------------------------  2041
APV1:YP_009094347.1     ----------------------------------------------------------------------------------------------------  2015
ASPV:NP_604464.1        ----------------------------------------------------------------------------------------------------  2171
CTLaV:YP_009046478.1    ----------------------------------------------------------------------------------------------------  2020
CRMaV:YP_007761581.1    ----------------------------------------------------------------------------------------------------  2010
```

```
SdRV1:AYE54584            -------LL-------------------------------------------------------------------------------------------  2041
CLBV:NP_624333.1          -------DL-------------------------------------------------------------------------------------------  1952
CLBV:AFA43536.1           -------DL-------------------------------------------------------------------------------------------  1977
AVCaV:YP_008997790.1      -------DL-------------------------------------------------------------------------------------------  1669
CPrV:AKN08994.1           -------DL-------------------------------------------------------------------------------------------  1980
ACLSV:NP_040551.1         -------EW-------------------------------------------------------------------------------------------  1851
GPGV:YP_004732978.2       -------DY-------------------------------------------------------------------------------------------  1822
CtChV-1:YP_009103999.1    -------HI-------------------------------------------------------------------------------------------  1845
CtChV-2:YP_009103996.1    -------EI-------------------------------------------------------------------------------------------  1842
DiVA:YP_006905850.1       -------RFKHSCKSWIQRPSYRSSTMEDETLIASGSVRCTQMGVSSKTRRLTQFREQKVQFQLNQLMGSPGLLKEYLLLTQMLLMRRETRRSIQKSILE  1757
ObRV1:YP_009408144.1      -------RFGLGCKLLGQKHLSKSLMEVKRTSTASVLVVSTPMEVTHKIQRLMLHRNLRVPYLSECQKGGLVLSREYQSLTQRLCVMREQRKSIKKLTLV  1757
CVA:NP_620106.1           RNQKHLCDLGSGSILGLRVLEGLKMFKEECRSYQSRSFFKESQETNQEFSLMQFVPRTFTVMQMPSIPKCSQLLKDFSLQLLYLQAALAKAMLHSSIFLM  1853
ASGV:NP_044335.1          -------SL-----------IFEIGEGIGSKWLSSTSTASSRRSNLQTSKLMLSRPQSFTRMQPFSNQTCLIASKGLNQTSRFPLDLVTASSCLISNCLM  1653
PVT:YP_002019748.1        -------RI-------------------------------------------------------------------------------------------  1572
PrVT:YP_009051684.1       -------ES-------------------------------------------------------------------------------------------  1747
GVA:NP_619662.1           -------DL-------------------------------------------------------------------------------------------  1679
GVE:YP_002117775.1        -------SL-------------------------------------------------------------------------------------------  1684
GCLV:YP_004936159.1       -------TY-------------------------------------------------------------------------------------------  1948
CVNV:YP_001430021.1       -------NI-------------------------------------------------------------------------------------------  1967
PhlVB:YP_001552317.1      -------NL-------------------------------------------------------------------------------------------  2043
APV1:YP_009094347.1       -------DL-------------------------------------------------------------------------------------------  2017
ASPV:NP_604464.1          -------DL-------------------------------------------------------------------------------------------  2173
CTLaV:YP_009046478.1      -------EF-------------------------------------------------------------------------------------------  2022
CRMaV:YP_007761581.1      -------EF-------------------------------------------------------------------------------------------  2012


SdRV1:AYE54584            ----------------------------------------------------------------------------------------------------  2041
CLBV:NP_624333.1          ----------------------------------------------------------------------------------------------------  1952
CLBV:AFA43536.1           ----------------------------------------------------------------------------------------------------  1977
AVCaV:YP_008997790.1      ----------------------------------------------------------------------------------------------------  1669
CPrV:AKN08994.1           ----------------------------------------------------------------------------------------------------  1980
ACLSV:NP_040551.1         ----------------------------------------------------------------------------------------------------  1851
GPGV:YP_004732978.2       ----------------------------------------------------------------------------------------------------  1822
CtChV-1:YP_009103999.1    ----------------------------------------------------------------------------------------------------  1845
CtChV-2:YP_009103996.1    ----------------------------------------------------------------------------------------------------  1842
DiVA:YP_006905850.1       QLSSVSTSLVIMNVRCQEEDVCWLTVEEVEEVELSKPLSLIYPKDQPTSCSYQMQSLTFMMSYLTGPVKCSSSLTMLITVVVPTHLLLRLGQYIACLMSS  1857
ObRV1:YP_009408144.1      QLLSVYTSMATMTKKPAKENACWLMEGEMMKMVSLTPSGLMFQKVQLILSLHQMLFLISMMSCLTRPVSCTFHLKVLSTEKVQDRLLLRLELSTGCQMHS  1857
CVA:NP_620106.1           KLSWRLSKKPLLSTQCFILGQSSYVLHAFSSLKSRSMAELYTLIPGFWTKMMHAKQVLVSSCKLDQPITFIGQIIQCPHMIQTCIGLLESSLNSMQSMLL  1953
ASGV:NP_044335.1          TPKLIQSGRKATSTNTYTMESSWLGSKQCCQTLEAWKGESLYMMEPAWIRKEATFARIFSSLSLTVATLVSGQSTVCLPQTQIWPKGLDFVWTLIVHNMN  1753
PVT:YP_002019748.1        ----------------------------------------------------------------------------------------------------  1572
PrVT:YP_009051684.1       ----------------------------------------------------------------------------------------------------  1747
GVA:NP_619662.1           ----------------------------------------------------------------------------------------------------  1679
GVE:YP_002117775.1        ----------------------------------------------------------------------------------------------------  1684
GCLV:YP_004936159.1       ----------------------------------------------------------------------------------------------------  1948
CVNV:YP_001430021.1       ----------------------------------------------------------------------------------------------------  1967
PhlVB:YP_001552317.1      ----------------------------------------------------------------------------------------------------  2043
APV1:YP_009094347.1       ----------------------------------------------------------------------------------------------------  2017
ASPV:NP_604464.1          ----------------------------------------------------------------------------------------------------  2173
CTLaV:YP_009046478.1      ----------------------------------------------------------------------------------------------------  2022
CRMaV:YP_007761581.1      ----------------------------------------------------------------------------------------------------  2012


SdRV1:AYE54584            -------FEDQVI---------------------------------------------------------------------------------------  2047
CLBV:NP_624333.1          -------FLEQSSDEDI-----------------------------------------------------------------------------------  1962
CLBV:AFA43536.1           -------FLEQSSDEDI-----------------------------------------------------------------------------------  1987
AVCaV:YP_008997790.1      -------FAEQSNEDSC-----------------------------------------------------------------------------------  1679
CPrV:AKN08994.1           -------FSDQNV---------------------------------------------------------------------------------------  1986
ACLSV:NP_040551.1         -------LSDEDGDND--KGSQIEDRR--RGYSNCWGEKLQNLF--------------------------------------------------------  1884
GPGV:YP_004732978.2       -------LSDGSDEED--SKGFWEDCN--RGYSNC-GVAFKFYIQ-------------------------------------------------------  1855
CtChV-1:YP_009103999.1    -------LEDLVDSYSDGV---------------------------------------------------------------------------------  1857
CtChV-2:YP_009103996.1    -------LKEIQDCFSDGVDD-------------------------------------------------------------------------------  1856
DiVA:YP_006905850.1       IAITEWEFQEERVPLEVSIRKYIALRP--YQRKMRSQCCQRCVSQERLEEYLMLREALALNLKGVREVLS---------CLGEKEALL----SFEIIVSE  1942
ObRV1:YP_009408144.1      TVIISWEFQGGGEILVAPFRKFMAQAL--YNQEM-------CIRQ--LKKWLKPKERVELVRLELNQVWNYHRGQGKKLCLGKKEDLAFIGNTLWIVTFL  1946
CVA:NP_620106.1           TIPTYSSLTLESCTSSVIRALQRRQLPQMLGHSFKHFLGLLDYQILNPFLRMKILSILQLWHSLTSVLTRVSGKVVSLKAHHVQQEPEGIMPEARDRVLS  2053
ASGV:NP_044335.1          RTLSCLLLTLELHTDASTLQGFWKPKLAIQDGLHRQSAAVKHLNSMRKSRWPSWIADPRCFWKKVHQTCTLKRDCSEVTRLEGHAQFPLKGGQTQGCKKR  1853
PVT:YP_002019748.1        -------FETSNGVDF--SGEVQETMG--GEGEHHGSCGLWCNLH-------------------------------------------------------  1606
PrVT:YP_009051684.1       -------FDHEFGGCGSVQEEGE------CDRVHRFGCGLECNI--------------------------------------------------------  1778
GVA:NP_619662.1           -------FSEDECERHSDGDEDFLSND--VARLYRIE---------------------------------------------------------------  1707
GVE:YP_002117775.1        -------FKEEEDIVSSDEEA-------------------------------------------------------------------------------  1698
GCLV:YP_004936159.1       -------FSA------------------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1       -------FKASDVGLGI-----------------------------------------------------------------------------------  1977
PhlVB:YP_001552317.1      -------FTTRALEE-------------------------------------------------------------------------------------  2051
APV1:YP_009094347.1       -------FLSGM----------------------------------------------------------------------------------------  2022
ASPV:NP_604464.1          -------FKGESLPASS-----------------------------------------------------------------------------------  2183
CTLaV:YP_009046478.1      -------FSEGESCKSPDRNFG------------------------------------------------------------------------------  2037
CRMaV:YP_007761581.1      -------FSESEGCLSPERNFG------------------------------------------------------------------------------  2027
                                 :
```

```
SdRV1:AYE54584            ----------------------------------------------------------------------------------------------------  2047
CLBV:NP_624333.1          ----------------------------------------------------------------------------------------------------  1962
CLBV:AFA43536.1           ----------------------------------------------------------------------------------------------------  1987
AVCaV:YP_008997790.1      ----------------------------------------------------------------------------------------------------  1679
CPrV:AKN08994.1           ----------------------------------------------------------------------------------------------------  1986
ACLSV:NP_040551.1         ----------------------------------------------------------------------------------------------------  1884
GPGV:YP_004732978.2       ----------------------------------------------------------------------------------------------------  1855
CtChV-1:YP_009103999.1    ----------------------------------------------------------------------------------------------------  1857
CtChV-2:YP_009103996.1    ----------------------------------------------------------------------------------------------------  1856
DiVA:YP_006905850.1       KGLVKLRKIYAGLGQAQEVLMKETFLKRFWIINLGLPVNAENFKVTSGKQAMVDQAANLALSNWINETTGFQGEAYGVRLRKLRRRTLLRQHWVSVFKEY  2042
ObRV1:YP_009408144.1      KSLMK----GATLGQAQVTLMKEEFLKTYWAVRLALPYNHQTHRVTSGKMAGAEAQANQALRNWIDDATGFQGEAYGVRMRKLRRRTLLRDYWVSHMKAE  2042
CVA:NP_620106.1           QSQKLLVKILNNKKEICLGQIHVGLKIFSSIQNRGFQLIKNSSTDLISAILKGGTQISSMALSIVEQNYNEIRRGLGNYIWENMIDPRDLLHLTAKPAVE  2153
ASGV:NP_044335.1          EDLGPSRLELKDLEKMSLEDVLQQARRHRVGVYLWKTHIDPAKELLTVPPPEGFKEGESFEGKELYLLLCNHYCKYLFGNIAVFGSSDKTQFPAVGFDTP  1953
PVT:YP_002019748.1        ----------------------------------------------------------------------------------------------------  1606
PrVT:YP_009051684.1       ----------------------------------------------------------------------------------------------------  1778
GVA:NP_619662.1           ----------------------------------------------------------------------------------------------------  1707
GVE:YP_002117775.1        ----------------------------------------------------------------------------------------------------  1698
GCLV:YP_004936159.1       ----------------------------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1       ----------------------------------------------------------------------------------------------------  1977
PhlVB:YP_001552317.1      ----------------------------------------------------------------------------------------------------  2051
APV1:YP_009094347.1       ----------------------------------------------------------------------------------------------------  2022
ASPV:NP_604464.1          ----------------------------------------------------------------------------------------------------  2183
CTLaV:YP_009046478.1      ----------------------------------------------------------------------------------------------------  2037
CRMaV:YP_007761581.1      ----------------------------------------------------------------------------------------------------  2027

SdRV1:AYE54584            ----------------------------------------------------------------------------------------------------  2047
CLBV:NP_624333.1          ----------------------------------------------------------------------------------------------------  1962
CLBV:AFA43536.1           ----------------------------------------------------------------------------------------------------  1987
AVCaV:YP_008997790.1      ----------------------------------------------------------------------------------------------------  1679
CPrV:AKN08994.1           ----------------------------------------------------------------------------------------------------  1986
ACLSV:NP_040551.1         ----------------------------------------------------------------------------------------------------  1884
GPGV:YP_004732978.2       ----------------------------------------------------------------------------------------------------  1855
CtChV-1:YP_009103999.1    ----------------------------------------------------------------------------------------------------  1857
CtChV-2:YP_009103996.1    ----------------------------------------------------------------------------------------------------  1856
DiVA:YP_006905850.1       VKNLGHANTPAEFTAAESEIYGRVMSDFAAYAFGIMAEEGFSPATIYN----EVPASYTIEYPQPVGALNVSFSPAEVSRQFKYYANSSGNSCFANITWR  2138
ObRV1:YP_009408144.1      FQNLGHANEPQSFTAAESTLYGNIMSDFASHAFGVLAEDGFSPATVYS----SVNASYTVDYRAPVGNKTVEFSPAEVARVFKYLYQSSANPIFENMTWR  2138
CVA:NP_620106.1           ASEGVAATPAITLSENQRAVKNTIRNYYLRIMFGNLAVMGTSEQTDYPGEHLAIPRPVIENQEALTAHLPAGMSLLTFATNVKAWGVVGAEGKFAGLTFR  2253
ASGV:NP_044335.1          PVHYNLTTTPKEGETDEGRKARAGSSGEKTKIWRIDLSNVVPELKTFA-------------------------------------ATSRQNSLNECTFRK  2016
PVT:YP_002019748.1        ----------------------------------------------------------------------------------------------------  1606
PrVT:YP_009051684.1       ----------------------------------------------------------------------------------------------------  1778
GVA:NP_619662.1           ----------------------------------------------------------------------------------------------------  1707
GVE:YP_002117775.1        ----------------------------------------------------------------------------------------------------  1698
GCLV:YP_004936159.1       ----------------------------------------------------------------------------------------------------  1951
CVNV:YP_001430021.1       ----------------------------------------------------------------------------------------------------  1977
PhlVB:YP_001552317.1      ----------------------------------------------------------------------------------------------------  2051
APV1:YP_009094347.1       ----------------------------------------------------------------------------------------------------  2022
ASPV:NP_604464.1          ----------------------------------------------------------------------------------------------------  2183
CTLaV:YP_009046478.1      ----------------------------------------------------------------------------------------------------  2037
CRMaV:YP_007761581.1      ----------------------------------------------------------------------------------------------------  2027

SdRV1:AYE54584            -----------------------------------------------------------------------------------------             2047
CLBV:NP_624333.1          -----------------------------------------------------------------------------------------             1962
CLBV:AFA43536.1           -----------------------------------------------------------------------------------------             1987
AVCaV:YP_008997790.1      -----------------------------------------------------------------------------------------             1679
CPrV:AKN08994.1           -----------------------------------------------------------------------------------------             1986
ACLSV:NP_040551.1         -----------------------------------------------------------------------------------------             1884
GPGV:YP_004732978.2       -----------------------------------------------------------------------------------------             1855
CtChV-1:YP_009103999.1    -----------------------------------------------------------------------------------------             1857
CtChV-2:YP_009103996.1    -----------------------------------------------------------------------------------------             1856
DiVA:YP_006905850.1       QIGESFAEDIVRYFKELQVDAQSWLVRSNPVLAGNAPWVALDVTDGLDVRRLNPEEKKVIARAKNHLLKSMQLKGRESLSAEALLES--             2225
ObRV1:YP_009408144.1      QCGEAFAGDIVRYFKELQPDAQSWLVKSNPVLAGNAPWVALDVTDGLDIRHLNPEEKKVIARAKNHLLRSMQLKGRESLSAEALLES--             2225
CVA:NP_620106.1           QLCEPFAEQAYNFFRENHGAVSFIYLKNPGAYFNCPAVVFDFNKGLPLTIIKIGKNANAISACNQRLFNREGKKAVFAAQGEVNLSFDA             2342
ASGV:NP_044335.1          LCEPFADLAREFLHERWSKGLATNIYKKWPKAFEKSPWVAFDFATGLKMNRLTPDEKQVIDRMTKRLFRTEGQKGVFEAGSESNLELEG             2105
PVT:YP_002019748.1        -----------------------------------------------------------------------------------------             1606
PrVT:YP_009051684.1       -----------------------------------------------------------------------------------------             1778
GVA:NP_619662.1           -----------------------------------------------------------------------------------------             1707
GVE:YP_002117775.1        -----------------------------------------------------------------------------------------             1698
GCLV:YP_004936159.1       -----------------------------------------------------------------------------------------             1951
CVNV:YP_001430021.1       -----------------------------------------------------------------------------------------             1977
PhlVB:YP_001552317.1      -----------------------------------------------------------------------------------------             2051
APV1:YP_009094347.1       -----------------------------------------------------------------------------------------             2022
ASPV:NP_604464.1          -----------------------------------------------------------------------------------------             2183
CTLaV:YP_009046478.1      -----------------------------------------------------------------------------------------             2037
CRMaV:YP_007761581.1      -----------------------------------------------------------------------------------------             2027
```

Fig. S2

Multiple sequence alignment of movement protein (MP) sequences of SdRV1 and representative members of *Citrivirus* and *Prunevirus*

```
SdRV1:AYE54585       MASLIRVDRLVSRIENNQSMLGSNEINNLYGSE-CARVFKDEVKLIVPGNLDGSPVVMQAPILTDERIEEIRATRIKHRGVHKRPCYLHLGFVPIAINSL    99
CLBV:NP_624334.1     MASLINVSSLVNRVKLDQSIIGSDEINKLYGSD-APLVFKDEVKMVIPGNAEGEAIKLQANILTADRLQSIRNAKVNGKEA----AYLHLGFVPIAIRSL    95
CLBV:AFA43557.1      MASLINVSSLVNRVKLDQSIIGSDEISKLYGSD-APLVFKDEVKMVIPGNAEGEAIKLQANILTADRLQSIRNAKVDGKEA----AYLHLGFVPIAIRSL    95
AVCaV:YP_008997791.1 -MALINVQSLCEKLSLDESILGSSEINKLYPKDHHEFIFKDEVKLMIGGNLDGSLVSLQAPILTSERLSQIKTAKPKS-------AYLHLGFVPIVLQSL    92
CPrV:AKN08995.1      MSKAIKVSSFVNRVNLDKSLLGSNEINALYGNGFAPLVFKDEIKMTIPGNVLGKPIKVQANVLTKKRLEQIRAQKFKGKAC----SYIHLGVVPIAIQSL    96
                         *.*. : .::. ::*::**.**. ** .     :****:*: : **  *. : :** :** .*:..*:  : .        .*:***.***.:.**

SdRV1:AYE54585.1     LPSGNDDVTGICALVDTSRSSYKNAVIDAFNFKWTKDEPYAAKLLTINAAIDIDCDVSVRSLQIIFKISGIDLDKERSVAAITVGLSCVPTVDMFQLPRL   199
CLBV:NP_624334.1     LPSGNEQIWGRCALVDTSRTRAETAVIDEFEFKFTKKQPFAAKLLTINAAVDINCKVSVGSIQVLLELHGVDLREERSVAAIITGLTCTPTNKMVLLHKI   195
CLBV:AFA43557.1      LPSGNEQIWGRCALVDTSRTRAETAVIDEFEFKFTKKQPFAAKLLTINAAVDINCKVSVGSIQVLLELHGVDLREERSVAAIITGLTCTPTNKMVLLHKI   195
AVCaV:YP_008997791.1 LPSGNDLIKGTCALIDTSRCSLSTGLIDIFKFKFTSKNPRAGKLLTINAPIDINDEVSVGSVQLLLQVEGVDLREKRSVMSITVGMSCVPTTNASLLHKL   192
CPrV:AKN08995.1      LVSGHENVWGRCSLVDLSRGSEETALIDRFKFRFTNDEPYAAKILTINAAVDINCDTSVGSLQVLLEIHGIDVRSERSVAAITVGLSCVPTNNMVMLPGL   196
                     * **:: : * *:*:* **   ...:** *:*::*..:* *.*:*****.:**: ..** *:*::::: *:*: .:*** :* .*::*.** .   *  :

SdRV1:AYE54585.1     KRECPKISIMNIISSIESDVESREAFVEMFNAKKIDLLGSGKSEMLDKGKRWGF--------FGPVVKPVSRRNLTSANRLKN--VQIKSERC-------   282
CLBV:NP_624334.1     ECDTPKWSLCNIIEQVEDEEESKKAFENMFNASSSNLIDLGQEQWLDEGKRTPLIGSLAIKGFGRKVMPVRRRNLTTRNLMKDYVSHVKSETA-------   288
CLBV:AFA43557.1      ECDTPKWSLCDIIEQVEDEEESKKAFENMFNASSSNLIDLGQEQWLDEGKRVPIIGNLAIKGFGKKVMPVRRRNLTTKNLMKDYVSHVKSETA-------   288
AVCaV:YP_008997791.1 SGERPSWNLLNVESLSSEDKESEQAFQDLFLNCKTGVVETGKIEYLKGGRKLPF--------FGKRFQPVFRRDIKTTGLLE-----IPTESR-------   272
CPrV:AKN08995.1      KRSTPKWSLVNVFNVPEDSEAEKNAFENLFDAANPGLVDMGNDKLLETGKRMHL--------WGNSLKPVYRRELSTRNLIKEQLSHVMSETAKSLKSEG   288
                     . . *. .: :: .  ...  ..:** ::*   . .::  *: : *. *::  :        :*  . ** **::.: . ::     : :*

SdRV1:AYE54585.1     SLKRNGSLN-----------------------------------------------------------LDRSISNARLSLSQIESEILKIRSNELKDK--   321
CLBV:NP_624334.1     SLKRSQSGRD-------------------------------------WGNDRLRKYL-----------EEQALEQARSSTDHQLVKAPKFKTIEVTGLET   340
CLBV:AFA43557.1      SLKRSQSGGD-------------------------------------WGNDRLRKYL-----------EEQASEQARHSVDQQVARVPKLKTIEVTGLET   340
AVCaV:YP_008997791.1 SLSRSLSQR-------------------------------------------------------------------------------------------   281
CPrV:AKN08995.1      SISRCCSSRDVSQIGKEALHLQRGIRMGMEEFHRPRGSDASMGDGCWWRGKEFDTTFARAKGESFGGQAENFIRQHSRSLSRPINRLPE-HGCELHETDS   387
                     *:.*  *

SdRV1:AYE54585.1     -------------FSRANHEEDDGLNELFTGEK------------------                                                 341
CLBV:NP_624334.1     VH-----------DLKDKIDKAESSTASDTGTK------------------                                                 362
CLBV:AFA43557.1      VH-----------DLKSKIDKAESSTASDTGTK------------------                                                 362
AVCaV:YP_008997791.1 ----------------------SIGSEYNSGFV------------------                                                 292
CPrV:AKN08995.1      ARCGWSAGDGGFIQPQNLCGKSEDTCSDTSGQENDGSDAKGSLPEFCKLCP                                                 438
                                           .      :*
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Fig. S3

Multiple sequence alignment of coat protein (CP) sequences of SdRV1 and representative members of *Citrivirus*

```
SdRV1:AYE54586.1  MSEFKLMDRAKWPFWSSLIDGLIRFAEENDSMSEGVVEEF--LLGSLGKNTIEEDPKKNELVYLRLCMKLISRIISNNARHKEEIRKIESDLGKRPRKEV    98
CLBV:NP_624335.1  -MKITNDNAATINYWLAIVEPFLTSDEDRN--SDDIIRKFRAVVAEHG-DTEEVDPEVFFAIFSILATKY-GRVYS---------KKVE-ELNESLKAAI    85
CLBV:AFA43538.1   -MKITNDNATTINYWLAIVEPFLTSDEERN--SDDIIQKFRAVVAEHG-DTEEVDPEVFFTIFAILATKY-GRVYS---------KRVE-ELNESLKVAI    85
                    ::.  : :.  :* :::: ::   *:.:  *:.::.:*  ::.. * :* * **:    ::  *. *  .*: *         :::* :*.:  :  :

SdRV1:AYE54586.1  EVESENEKLKKIIAELHMK-ISDMEKESERSES-ETEKDRNAERRFFAGGTRS-------------LTNDLSCFYLGEDEFPAVTQSISTEKIATAEQIK   183
CLBV:NP_624335.1  LAGAEAEDLRNKLKDISQRYASQLEITADREQQLESLKKKGHEQPLTGSGSSEPVHAESAHAPQLHVVNDLQQFYIPFNEYPSLTQSIGTSDIANDEHLK   185
CLBV:AFA43538.1   LAGAEAEDLRNKLKDISQKYASQVEITADRELQIENLRKKGHEQPLAGSGSSEP-----AHTPQLHVVNDLQQFYIPFNEYPSLTQSIGTSDVANDEHLK   180
                   . :* *.*:: : ::  :  *::*  ::*. . *. :.:. *: : ..*: .             :.***. **:  :*:*::****.*..:*. *::*

SdRV1:AYE54586.1  RVMKALNIVDEKKFSRMAFEFVISCGSKSTSSKSQYAGTFSIDNISYKRSDIAYAITGTGLTVRRFCAAYANLYWNYNIRRNQAPENWRDKNFTDETKFA   283
CLBV:NP_624335.1  RVQLTLKITDTKVFSRTGFEFAISCGSRSTSDKDPYDGIIKISGKSHMRKDIAYAIRTSGITVRQFCAAFANLYWNFNLARNTPPENWRKKGFTEGTKFA   285
CLBV:AFA43538.1   RVQLTLKVTDTKVFSRTGFEFAISCGSRSTSDKDPYDGIIKISGKSHTRKDIAYAIRTSGITVRQFCAAFANLYWNFNLARNTPPENWRKKGFTEGTKFA   280
                  **  :*::.* * *** .***.*****:***.*. * * :.*.. *: *.******  :*:***:****:******:*: ** .*****.*.**: ****

SdRV1:AYE54586.1  AFDFFYAVGSNAAIPTEPNGDVNLIRNPTKEENEANDAVKWVKIAKAKSQSMGHVTSSMFLNKGVAYNVPKSGSLSITEI                        363
CLBV:NP_624335.1  AFDFFYAVGSNAAIPTEADGSVRLIRPPTNEENEANSAMRYADIYEQNSKTAGHVTSSPLYNRGSSYESKNKAKL--LEM                        363
CLBV:AFA43538.1   AFDFFYAVGSNAAIPTEADGSVRLIRPPTNEENEANSAMRYADIYEQNAKTAGHVTSSPLYNRGSSYESKNKAKL--IEM                        358
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