

A

RNA1 5'UTR

```

BdMoV 1 aaattcacatcccgatcccatcatttacaactcgttaccacgaatcacaggattgagg
BNYVV 1 aaattcgattctcccatcgccatcattgaaatcattactctg--tactggaacgcag
BSBMV 1 aaa-----ttctcccatcgccatcattgaaatcgttattctgta--tactggaacgcag
RSNV 1 -----catagacgaacga-----aatcggaccacc
          *** * * * * *

BdMoV ttaggagtggtc--catatcacgtacc--atattgcgt--tgaagtgattcaccct
BNYVV ttaggagtggtc--caaagcatctctcttgaaaatagatt--gcaagtgattcaccct
BSBMV ttaggagtggtc--caaagcgtctctcttgaaaatagatt--gcaagtgattcaccct
RSNV ccggagtggtcattatctgacatcattgaagaagtccaagtgagagcgggtcaccct
          ***** * * * * *

BdMoV acaccggcaactagtgtaagt--ttttattgtgttgtg
BNYVV aagacagctcggtgttttaacagatgtttacataatacaac
BSBMV aagacagctcggtgttttaacagatgtttataatacaag
RSNV aaggtaacggcaagagatagc--tttcaactctcca--
    
```

RNA2 5'UTR

```

BdMoV 1 aaattcaatataatccatccccaataagaatttcaactat----attatctctgagacg
BNYVV 1 aaattcaactatattctccattgaaatagaatttcaaccgtc---tcttggttcttatttt
BSBMV 1 ggattcctaattattctccattgaaatagaatttcaaccaac---tattgctgatctctt
RSNV -----tatacactctgac--gaattcaccctacgttagttaaactcgatctg
          **** * * * * *

BdMoV agtgtggcggtcttctcgaacgatcaatcaaatctctatacaagt-----aaagaagtat
BNYVV gtctcggggcaatttattcaggccct-actttaaaataggtgcgagtataagtag
BSBMV gtctcggggcaatttattcagtgcctaaccttggaaaatcgtgagagtataagtag
RSNV gcccggaccattctcaaccgacacctc--cctttaaatttggtgtcagagcgtgagg
          **** * * * * *

BdMoV ttgcttgacgaacacctttcaaggattttattttg-----
BNYVV cgcctgtcagagaga-----agatagtagt-----
BSBMV ccccgtcaggaga-----agtgcttac-----
RSNV gtgtaccctgaagattttttcogaataactactcgggtgtatttttcaaacatttatcataa
          * * *

BdMoV -----aga
BNYVV -----aac
BSBMV -----aat
RSNV tatcatctttgctcag
    
```

B

RNAs 1 and 2 3'UTR

```

BdMoV1 gtgttttagttaaagttaagag-----ggtataatt
BdMoV2 -----gag-----ggtatagtt
BNYVV1 tegtataatagtaataataacg-----ttgtatact
BSBMV1 -----atg
BNYVV2 -tagggtttattcaagagactatg-----ttaaattt
BSBMV2 -----actctttaaagagactgtt-----gatatata-t
RSNV1 atgttctactctaatcagataat-----gcaatatta
RSNV2 ttccaaagctctatggaggttaatcgatataatgtgtgtgtgtgtgtatcataaata

BdMoV1 ag-----ttcaggggccatgcc--acaggctcctacacgggtt
BdMoV2 ag-----ttcaggggccatgcc--acaggctcctacacgggtt
BNYVV1 tggagtagtataagtttgaagaataaaggccatgcc--acaggctcctacatctgat
BSBMV1 cttgtttgcttattttgtgttttaataaaggccatgcc--acaggctcctacac----
BNYVV2 aat-----aatcaggggccatgcc--acaggctcctacacgggtt
BSBMV2 aat-----aatcaggggccatgcc--acaggctcctacacgggtt
RSNV1 aaagaataaccaatttgg-----gtttt-aaacccctcggttagat
RSNV2 taaagaataaataagtagtgaagggctaatatcaagtgcacgaacctaacacgggta
          * * * * *

BdMoV1 actccagggttagttgtggttttggtt-----ggtatggtggtttttgt
BdMoV2 actccagggttagttgtggttttagtttaagtttgaataaattgtctattttactt
BNYVV1 -----gaaggtgtgtggt-----ttctcactactgtttatattgtttgagtt
BSBMV1 -tccgaaggtgtgtggt-----ttctcactactgtttatattgtttgagtt
BNYVV2 gttccgaaggtgtgtggt-----ttatatt
BSBMV2 gttccgaaggtgtgtggt-----gatataaagtat
RSNV1 gttgggaccactagagggt-----
RSNV2 gttccgaaggtttactcact-----
          **

BdMoV1 ttggttatatttttaatttagatttgttgatgtaata---ttgttat--ttatggtt
BdMoV2 taattaagttagttttagtttaatttgaatattagta---ttaaata--ttatggtt
BNYVV1 tggattatgctggttcttgaatggtgataaattatgaactaattgtttgttgggtt
BSBMV1 -----ttctttcccttgggttttctt---ttagtttcttttgggtt
BNYVV2 tgcttat-----ttctttcccttgggttttctt---ttagtttcttttgggtt
BSBMV2 tattaaataaataatagtgcatcggttaataattattg---ttactggtgtaaggtt
RSNV1 -----gatactctgg---gttttagtcacatcgtg
RSNV2 -----gttggtc
          **

BdMoV1 ttaactactgactgggtggaattgtacagtcactgtaggtttaaaggtgttttat-
BdMoV2 ttaactactgactgggtggaattgtacagtcactgtaggtttaaaggtgttttat-
BNYVV1 gtaactactgactgggtggaattgtacagtcactgtaggtttaaaggtgttttat-
BSBMV1 gtaactactgactgggtggaattgtacagtcactgtaggtttaaaggtgttttat-
BNYVV2 gtaactactgactgggtggaattgtacagtcactgtaggtttaaaggtgttttat-
BSBMV2 gtagtgggtgtagtaggtggaattgtacagtcactgtaggtttaaaggtgttttat-
RSNV1 gtagtgggtgtagtaggtggaattgtacagtcactgtaggtttaaaggtgttttat-
RSNV2 gtagtgggtgtagtaggtggaattgtacagtcactgtaggtttaaaggtgttttat-
          ** * * * * *

BdMoV1 -acac
BdMoV2 -acac
BNYVV1 gatata
BSBMV1 gatata
BNYVV2 g---
BSBMV2 g---
RSNV1 -acac
RSNV2 -----
    
```

C

Benyavirus RNA2 (CP read-through region)

```

BdMoV AAA UAG CAG UUA GCG GCG GGC GAU CUG CAG CAA CGC AUU UCG GCC GCC AAG
BNYVV AAA UAG CAA UUA GCG GCU GCU CGG GUG ACG GCA CAC AUU CGA GCG GCC AAG
BSBMV AAU UAG CAA UUA AAU GCU GCU CGA ACU AUG GCA CAU AUU CGA GCA GCA UUA
RSNV GCA UAG GGG UAC GGG GCA GCG GCA CUG AGU GAU CUG GUU GCA GCU GCC CAA
          |
          CP-stop codon
    
```

A

Replicase-associated protein

Table with 4 columns: BdmV, BNYVV, BSBMV, RSNV amino acid sequences and domain annotations. Domains include Helicase, Protease, Methyltransferase, AlkB-like domain, Y-domain, and RdRp. Sequence alignment is shown with gaps and domain boundaries indicated by arrows and labels.

B

CP-RT

Coat protein
 BdMoV M-----LNWNNDITHHMHSGRWVRLSEAVAFVFKQAQDLKSKASLEFVKSSFDIMF5K
 BNYVV MSSEGRMTWKDMSHNFMTDRWARVSDVVSVIKQSHAMDLKSKAANLSIIK1TALAGLGG
 BSBMV MVDEGRMTWKDATHNKLMTDRWARVSSVQATINQALSLDLKAALSPVIAKFNFSGLG
 RSNV MS-----MPDWT-DTHDVLVSRWVRTSEAMSAVTRARVSDLVAPSLGEIKAAILSLGDR
 * * * * * : : : : : * * * * * : * : : : *

BdMoV WTTD-NPPFVHKRFAEVSQKWDITLWVNFDEPPLSLVAASIIITGSDGGSAAANASAGTR
 BNYVV WT-DNNPFVSPMTRFPQTLTMYGALVLYVNLSDPEFALIMTKVSTLTDGSLADNASANVR
 BSBMV WSEDGDFVAPMVRFPVTLNQFGALVLYVNLSDPAFALIMTKVFTLNAGGADNASASSR
 RSNV HNTD-DPFAVYRFPFHITTEKGTHTYVNLSDNVFKQVLAIEVCTDKDNVAVNSAVNVR
 : : * * * * * : : : : : * * * * * : * : : : *

BdMoV RDVSDGKFAE-KKVGTD-----SAYNLHRSVAALQVMLSSRELYDAFPEKQYGLK
 BNYVV RDVVSNGKAESSGKTAGTNE-----SAYTLTVSLAGLAQALRLEELMWRDKFEDRLKLP
 BSBMV REVVAGSRPETSQKSGVTDES-----GSYTLTTLQAFNQAIRLPEVLWTRDKFEREWNL
 RSNV RD-----GAINSS-SDAKTDKDNIIIGYQLQALRFEELGSGPNLWNRKRFETQYRLK
 * * * * * : : : : : * * * * * : * : : : *

Coat protein RT domain
 BdMoV WGGP-PLPAT--GENKDLAAGDLQORI SAAKVAAGLPPGCGPEWD--NHTSLIP--PGHF
 BNYVV WTPV-QGRTS--PPGDLAARVTAHRAAKRALLYPGDSPEWV--GWKHFPY--PPPY
 BSBMV WTPV-RGVTFAVPRTNLNAARMTLNAARVTAHRAAKRALLYPGDSPEWV--GWVHSYP--PPPY
 RSNV WVDDRGRSP--AEAKYGAALSDLVAAQSDMYPGYGEWNLPPFKHGQIQTPAPW
 * * * * * : : : : : * * * * * : * : : : *

BdMoV RDYDLPSRADVMAALEASLQV-----PEHKEDMVEQKTAESAQETDSTDSLV
 BNYVV DVYDVP-LDIINA-----KLAADDVGLVTPPASSHGLPFEVSEVEQANRNSIWL
 BSBMV DGVDYPS-LDIINE-----KLAADDVGLVTPPDIPGGNFEVSEDEIQKGENGLWLM
 RSNV NEFDLPS-VDYIAEETERKRLKQD--GNLQAPRL-----APSHKTNWPELTA
 * * * * * : : : : : * * * * * : * : : : *

TM1
 BdMoV ILFTLLSIAAGGSLFFARAKVKEFLKMKGNLFRKRDSEPDNTGGTGDWFSRSSGEISL
 BNYVV VGLLLAALAVGIVAAVHRKLLQSRLEKLLWGST--GSGGGGGDFTELYMRATDVSL
 BSBMV VGLLLAALAVGIVAAVHRKLLQSRLEKLLWFSR--GSGGGGGDFTELYMRATDVSL
 RSNV VMLAL-CVGAAGPLGMYRRLRQCAKNIIGYLRPRRRP-----RYHVPYPSLELDTFSC
 : * * * * * : : : : : * * * * * : * : : : *

BdMoV ---QELSRPSEFQAPRPLSPVRDILDDRHLVLYALRNL-----AY-----
 BNYVV GTTLESHAASAPGSLRHRP--AATDSGPEALPFEVWFNDLAV-----VYD-----
 BSBMV GTTISEHAPPVGTMRHRTATDS--HEALPFTVWVNLNLSR-----VYF-----
 RSNV GSTKTELESPQARQEGRTKQADMEVTLRR--FMVAMDFSLDECEVVSFYARDEISK
 * * * * * : : : : : * * * * * : * : : : *

BdMoV ---CAGLYGTFDKFLAISVALQTDKTLISLLE---DDSPDLAIPSEDAI-----
 BNYVV ---SIGMSDLFYTVREFFVGFNG--EFGELIELLESPPDDDGVTNAPRDTAIDAYES---
 BSBMV ---SIGSDLFYATREFVTVFNG--EFGELIELLESDEDDGVYDAESAVIVGTSAI---
 RSNV ALSNCDNLVLEPDGYTLGDAP--DIYEPGLLPIQQEQ---FVHAEVSDPIGEDVAGRS
 * * * * * : : : : : * * * * * : * : : : *

BdMoV ---LANHES---EIALLORELELEKLNELAL-----ERARAEIETL-----
 BNYVV ---QENYDRIDIEITVLERINLKLLEEAELERRERDMTMIADBEQRTLLHRELESSRV
 BSBMV ---VNDHDFQDLNITVLEKRIKFKRLSLEEAELNRQESVTEIFADEERTLHKLESRL
 RSNV LSGISDYES--RMLDLEK---ERLRELESIRTRD-----LEERRDAERLAFER-
 : : * * * * * : : : : : * * * * * : * : : : *

KTER motif
 BdMoV -----KMRKDVQAQELNELAIKEQRLKAEAEFNRKKEALTKLAQMDADSYQAR--
 BNYVV EATHAVAKAADAARAAMALASKEANDYDSKMAFDRCCKEQLRLRELEVNSMPSKTE
 BSBMV EATHVKNKAADAARAAVLAKEARVYDDKLAADRACKELRLRELEVNSMPSKTE
 RSNV -----EKADREYQMLRQDTP-IREQG--DRTAAQAEAFNKQIELREREISMGSTAGE
 * * * * * : : : : : * * * * * : * : : : *

TM2
 BdMoV ---HIT-SVASITGGYLMKAM-----RGPKMSAYTAGVQGVNSLSSIDSSR
 BNYVV EYVHTSIQ-GGAQLAGAMAVKML-----R-----RGAGSSQTVSSG
 BSBMV EYVHTSIQ-GGAQLAGALAVKML-----R-----TRGVNITPSNAG
 RSNV RWGQKQTAGSVAGSLFYKAMRGAGGLKMPFRSRRGNPSSGPRGQGLRSQSISSGNS
 : * * * * * : : : : : * * * * * : * : : : *

BdMoV AR-ANSQVSLGSRASVAAS--VPI-----QPVTASTASSSRAGS
 BNYVV ANIGSRQSLTRGRSASQPL--SSVGGSTRGVNINNTNLVRAAGNSAEVAGRSNAGS
 BSBMV SPTG-----IGRVRSASQVPTSLSGSVLGNANN--NSVGSVSSGSRVESLGYNSAIRNH
 RSNV QS-GSAGGSVARQRSVLETT--IPGSSMRGVQXQGTSSVGRPNPLTANNVSDKIGN
 : * * * * * : : : : : * * * * * : * : : : *

BdMoV NVE-----TIKDLGSGRLHPT---PPFSFAG 606
 BNYVV SNWFSKLRVGEWSKYSEVAATRAQRAIVLPAAPSARAF 689
 BSBMV NTWFSKLRVGEWSKYSEVAATRAQRAIVLPAAPSARAF 686
 RSNV SNS-----QLVRLTP-----INFGPAA 672
 * * * * * : : : : : * * * * * : * : : : *

TGB1

N-terminal positively charged residues
 BdMoV MT-----EWASENPHDFVSLERNCGNAGFSWTVG
 BNYVV MVQVQRRTGGDKAKGNRASSAPVRSRRMQDDWSRTHPDDIFSVIEKTLVEDGYKNGV
 BSBMV MAPEQHKQNASETASGRNRS--VRSRGMKDDWSVTHPDDVFSIIIEKTLVEDGYKNGV
 RSNV MT-----SEWAREHPTDVAIFETCAREAGFTWVNDV
 * * * * * : : : : : * * * * * : * : : : *

Helicase domain
 BdMoV RPRTITYSDLMSGALVNLQSLLESSEFSGCVRSQDIAAVKSDVVSQMD-GKDQWQRCGL
 BNYVV KPGHCDWGLKESGAINFRGTLELGLKNCCLTCNAAAVKLDLTKQVMSDWTARVGI
 BSBMV KPGHCDWGLKESGAINFRGTLELGLKNCCLTCNAAAVKLDLTKQVMSDWTARVGI
 RSNV PPHVVFDSLEKSKAINLTDLENEVAKGCKEKGDAVIAIKLENVGM--TKEYNARVGV
 * * * * * : : * * * * * : * * * * * : * : : : *

I Ia
 BdMoV VILGAFSGKSTLTKLTLTS--GEGRVVLGLPNSLSLKGVSQCPNAFLIDDLFTSEIHLQ
 BNYVV VILGAFSGKSTIKNLLDKFGAKHKWVLCVLPFSQLLEGVFAGRLDFTLVDDLCRQSVYGG
 BSBMV VILGAFSGKSTIKHLLDTSYGRYKWLCLVLPFSQLLEGVFAGRLDFTLVDDLCRQSVYGG
 RSNV CVLAFSGKSTLTKLTKVMSK--ASRVVIAVNSLTKNVSQCPNAFLIDDLFSPRVFEFA
 * * * * * : : * * * * * : * * * * * : * : : : *

II III IV
 BdMoV RVQTMVLDFTVHMCEVMCLVLLGVKNLVCVCFDPSQNSLYKAGSVVNYGLFVLAKSDT
 BNYVV KYNTMLVDEFTVHMCEVMCLVLLGVKNLVCVCFDPSQNSLYKAGSVVNYGLFVLAKSDT
 BSBMV KYHTMLVDEFTVHMCEVMCLVLLGVKNLVCVCFDPSQNSLYKAGSVVNYGLFVLAKSDT
 RSNV KYETIILDEFTVHMCEVMCLVLLGVKNLVCVCFDPSQNSLYKAGSVVNYGLFVLAKSDT
 * * * * * : : * * * * * : * * * * * : * : : : *

BdMoV SKRFGKKIAGLMSGSGC--NVRGSDVNDVDFEDLGMKLRDMSTVLVASESQKELAD
 BNYVV SRRFGKATADLINSNGGKPVVGNNDVNDVDFEDLGMKLRDMSTVLVASESQKELAD
 BSBMV SRRFGVATADLINSNGGKPVVGNNDVNDVDFEDLGMKLRDMSTVLVASESQKELAD
 RSNV SHRFPQAIQEAYN--NAMGTKIEPKSSQGEPEIKDLGLMIRDKRKLKSLKTSQSLDD
 * * * * * : : * * * * * : * * * * * : * : : : *

V VI
 BdMoV CDIDSLVSEVGGTDFVVEVLYDEYDCKLICSNIRTVLSRARKCNVLRFGPNIRAR
 BNYVV DNIESILYSDAAGQTYDVVTVLLEDEFDDAACDPNVRVALLTSRARKGMIKMGPNIAAR
 BSBMV DGIEAVYDEADAGQTYDVVTVLLEDEFDDAACDPNVRVALLTSRARKGMIKMGPNIAAR
 RSNV CGISAEVLSKVGCEFAAVTLLEEPQDIAPFCNKISRCVALSKAEKVLIIQATPYFKSM
 * * * * * : : * * * * * : * * * * * : * : : : *

BdMoV FESGNF-GCGGNDSSYSGDTLREER 349
 BNYVV FKNQDF-NSRQVSKCTGDTFCEDR 384
 BSBMV FKNQDF-NSRQVSKCTGDTFCEDR 382
 RSNV LCNAEFVDPYEVDSQSGDTLREER 349
 : * * * * * : : * * * * * : * * * * * : * : : : *

TGB2

TM1
 BdMoV MTRE-IRARESNTRYIVLGVVAFICFLGFSQQKHATHSGLVGVPRFANSGSRDGR
 BNYVV MSRE-ITARPKNVPIVVGCVVAFVLLAFMQKHKHSGDGVVFTFNSGGRDGR
 BSBMV MSRE-ITARPKNVPIVVGCVVAFVLLAFMQKHKHSGDGVVFTFNSGGRDGR
 RSNV MSGVYSARPNKPIPICIGVVCVAVCLVLAIPRKHHTSAGVGFVFANSGSRDGR
 * * * * * : : * * * * * : * * * * * : * : : : *

TM2
 BdMoV SMNFSNNPNAYGC--KSEGFPGFEKALLFLVLGIIIVAGGCG-AGGD--HVCNGGC
 BNYVV SADFNNSNNRAYCGGSGSVSRVQQLVLLVAVLIVLIVLQRLRSPPE--HICNGAC
 BSBMV SADFNNSNNRAYCGGSGSVSRVQQLVLLVAVLIVLIVLQRLRSPPE--HICNGAC
 RSNV RAKFNCNDRAYG-----SSQPMQSMNFVAVIIVLIVLIVLQRLRSPPE--HICNGAC
 * * * * * : : * * * * * : * * * * * : * : : : *

BdMoV CKV 116
 BNYVV --G 118
 BSBMV --G 118
 RSNV CKN 117

TGB3

TM1
 BdMoV MAVVVRFDVTLVLYIVCGVIVVVCVH--SPVFPQHPVSRVGDVAVFLGDGYSQDQHTV
 BNYVV MVLVVKVLDLNIIVLYIVAGCVVSMVLY--SPFNSNDVKSASYAGAVFKGSGCIMDRNSF
 BSBMV MVLVVKVDFSTIVLYIVAGVIVVSVLY--SPFNSNEVKAGYAGAVFKGSGCIMDRNSF
 RSNV MAVVVRIDVSEIVLCHGGIVVTVLWSTVQRHEPP-PGVAGAM-PYGLLELNRASLN
 * * * * * : * * * * * : * * * * * : * : : : *

TM2
 BdMoV VFG--NFDASRVNTEHISIAKSEHLVDIVGS----MRSFAGDIAPTLVVIC-----
 BNYVV QFG--SCDIQHVAEISITKVA--GHSDIMVKRGE--VTVRVVTLETPLFIIIL--SRLF
 BSBMV QFG--GCDIQLKVADSIKVA--GHSDIMVKRGE--VTVRVVTLETPLFIIIL--SRLF
 RSNV VYNHPSFDSAAAIKEMKTA--GHSDIMVKRGE--VTVRVVTLETPLFIIIL--SRLF
 : * * * * * : : * * * * * : * * * * * : * : : : *

BdMoV --LVLLGQRIKNIIVGSG--G 123
 BNYVV GLAVFLFMICL--MSIWMF--R 132
 BSBMV SWLVVLFMICL--MLFVWFM--R 132
 RSNV --WLVVIFWFI--VVPC--R 132
 * * * * * : : * * * * * : * * * * * : * : : : *

CRP

BdMoV MG-----GVSIFV-----EGDCVFSISC-----ELPVALAYWPRINIVKVCNA
 BNYVV MSMGMVDSLVCVGRVITEGSEVVEGVERFSIKFSDWKLFTTAVVYVYQLGEKESLKD
 BSBMV MEKS--NSIGVYKDPIT-----NDCLRFVSKGNWCLFTNHFVITYRGNKNDKRVKMD
 RSNV MSRSLSTVNIHV--LVDG--KLVYSFAVRGFWPCNGSVTNRVQVLP--GNSTNASSA
 * * * * * : : * * * * * : * * * * * : * : : : *

BdMoV VCLHGQIPNSFHLGLCNE--NSW-LVVRVTLGHTLIVDGGFCRVAKSTVQVQVCSLIG
 BNYVV VG-----RLHFNMCSVCCQKL--KCKKQNNKSKHVQNGYLKRVNRFNFIILGCDICDCE
 BSBMV TC-----RLHFHVRVCSKSV--TFKANNRDLHELSKGFVVRNRFNFIILGCDICDCE
 RSNV SR-----ALSFWRVCLVCSHVGDIKKYIRLHRRLLRNNYCRMQHKTFTTEVCSKIC
 : * * * * * : : * * * * * : * * * * * : * : : : *

BdMoV AE-----SKELVTTGTFETSVRKVKLS----- 119
 BNYVV SF-----TLADEKHVIVDPEV----- 129
 BSBMV VF-----DSCAQQDELNNVV----- 120
 RSNV TYGLKVPVCEAITARPAKGGSEHVHKTGEMDCSEVVPSDSTSSDS----- 153

A. Concatenate (MTR+HEL+RdRp)

CLUSTAL format alignment by MAFFT (v7.032b)

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MTR domain
BdMoV      HRAPRNHP ELAALREVL RQ EYNATNKL VNTK LKTLV VVGAASREVV RYSS-----NPMVHY
BNYVV      SRA-RNH PVL AALREVM RQ EYSASCN ILN TKL KTLV VVGAASREVN CYSS-----NPSVHY
BSBMV      TRAPRNHP VLAALREVM RQ EYAASN ILN TKL KTLV IGAAASREVN CYSS-----NPSVHY
RNYV       GKPPRDH AVLAALREAI RQ DYDATY G VARTS I KTLV VVGA AAREV KRYCS-----NPMVHY
aHEV       PRDNWAHPV----QRV VHDAL E QYVR-RAAG PNCLE V GAHPRS INRHQA-----SHR
sHEV       PEVLWNHPI----QRV IRNELE QYCR-ARAG-RCLE V GAHPWS INDNPN-----VLHR
HeVt1      PEVLWNHPI----QRV IHNELE QYCR-ARAG-RCLE E GAHPRS INDDPN-----VLHR
HEVmex     PEVFWNHPI----QRV IHNELE QYCR-ARSG-RCLE I GAHPRS INDNPN-----VLHR
HEVsar55   PEVFWNHPI----QRV IHNELE QYCR-ARSG-RCLE I GAHPRS INDNPN-----VVHR
DpTV       GI-PTQHP VLAGHQ RVAEAAL HGFAT-RQA--SILE I GPSLH SAARLSH-----LRYHG
HasV       TLPPTQHP ILAGHQ RVAEEVL HNFAR-GRS--TVLE I GPSLH SALKLHGAPNAPVADYHG
NbetaV     TKLPSTHI KLALDLRVA EKDLRRHV K-NVP--TVLE I GPSV ESVRYAVQ--TRDKERVHG
SsRV-L     SYAHAHHP STQAARHALE--LLTWKLV DPA--HTTE I GPSY SSSLFRRAR-----PAFAHY
ReMV       NTQNAVHSL AGGLRSLE LEYLMMQVP-YGS--LTYD I GGNFASHL FKGR-----AYVHC
ToMV       NTQNAVHSL AGGLRSLE LEYLMMQIP-YGS--LTYD I GGNFASHL FKGR-----AYVHC
TRV        DDKNMVHG FAAAERK LQALLLDRVP-ALQ--EVDD I GGQW SFWVTRGE-----KRIHS
PEBV       DDKNMVHG FAAAERK LQALLMARVP-KLE--PVDD I GGQW SFWLSRGD-----KRVHS
SBWMV      NCERGTHS FAAA SRKIETD LLSRIP-KRS--WVYD I GGNWATHV KRND-----GRKVHC
CWMV       NCERGTHS FAAA SRKIETD LLSRIP-KKS--WVYD I GGNWATHI KRND-----GRRVHC
SBCMv      NCERGTHS FAAA SRKIETD LLSRIP-KRA--WVYD I GGNWATHV KRND-----GRKVHC
OGSV       NCERGTHS FAAA SRKIETD LILSRIP-KNA--NVYD I GGNWATHL KRKD-----LRKVHC
srCSV      SYERGTHN FAAA SRI IELDIL LSKFP-KDK--FVYD I GGNWASHV KRND-----NRRVHC
BVQ        SVHRGTHS MAAAMRK IETD LVLS SFP-SE---VIYD VGGN WATHAMRSD-----KRFVHC
PMTV       SVHRGTHS MAAAMRK IETD VIFTSFP-KNG--VIYD I GGNWATHA KRDD-----GGFVHC
BSBV       NSERGTHS MAAAMRK IETD LVLS LFP-KNS--VIYD I GGNWATHA KCND-----GRKVHC
BBNV       GSSRGTHN MAAASRK IETD ILSWFP-TGA--WIFD I GGNWATHA CRRD-----ERKIHC
PCV        NCERGSHT MAAVCRTLE TLYIKSLL PVKHT--VVWD VGGN WLTHV KYAS-----DQNVHC
IPCV       NREGRSHT MAAVCRTLE TLYIKSLL PVNDT--VVWD VGGN WLTHV KYST-----NQDVHC
BSMV       ACESGTHS MAACFR FLETEY LLDMVPMKET--FVYD I GGNWFSHM KFRA-----DREIHC
RubV       QMQVSDHP ALHAISRY TRRH WIEWGP-KEA--LHVLI D P SPGLL-----

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BdMoV      YFADKDSK DLVRTTLD LLENNLAA KYKNMESA ER-ELMNQL KRGGK I V KSRVGDKEYE I V
BNYVV      YFANKDSK DLVRTTLE LLHSALATKY RNMESGER-ELMNNLKG CGYI V KRSVENAVYEVV
BSBMV      YFANKDSK DLVRTTLE LLHSALATKY RNMESDETGEHMINLKG CGYI V KRSTDSGVYEVV
RNYV       HFSASEPK DMNRIAIEFLKESTRTK IANMERQEK-ELMRALRDGGYI VTKRVENTNF EYE
aHEV       CFLPPVGR DEQRWQV-----APRRGLCN LI RRALLNG-
sHEV       CFLKPVGR DVQRWYT-----APTRGPAANCRRSALRG-
HeVt1      CFLKPVGR DVQRWYT-----APTRGPAANCRRSALRG-
HEVmex     CFLHPVGR DVQRWYT-----APTRGPAANCRRSALRG-
HEVsar55   CFLRPAGR DVQRWYT-----APTRGPAANCRRSALRG-
DpTV       C-TKTGTRD QARHIAALHSS FVRGVSPQFQA-----DATLLA-
HasV       C-TKYGTRD GSRHITALESR SVATGRPEFKA-----DASLLA-
NbetaV     C-TFSDARD NLRHNKIGYEAHYDRKIGP-----DAALLA-
SsRV-L     DMPLLTVR DGARRNLAMLSRHKTL DERETRALDALR-----
ReMV       CMPNLDVR DIMRHESQKDS IELYL S-----RLDRGNKV VPSFQKEAFDRY-
ToMV       CMPNLDVR DIMRHEGQKDS IELYL S-----RLERGNKHVP NFQKEAFDRY-
TRV        CCPNLDIR DDQREISRQIFLTAIGDQARSGK-----RQMS ENELW MYDQFREN-----
PEBV       SCPLIDMR DKQRELQRQNF LRVFRDNATTSE-----SRISDDQFDMYNAFKGD-----
SBWMV      CCPTVDIR DSARKTVRWASIE KYLDEKEEIPPE IGERIKRLQADE DRIYANLKSEKAQP-
CWMV       CCPTIDIR DSARKTVSWASIE KYLDEKDEIPTEVGERIKRVQADE IKIYENLNKNRAQP-
SBCMv      CCPTLDIR DAGRKTTRWASIE KYQDEKETIPVEVGEK LKRIQEDENSTYANLKAGRCQP-
OGSV       CCPILDFR DAQRKTTRWLSVEKFI TDRNELMPEVGEK LKEIQEDENFISGNLRKGLV E P-
srCSV      CCPILDFR DAQRKSVRWASIEK FVAEKESIPEDLGNKIKQLYSDESRIRENVRKQDLRA-
BVQ        CCPILDFR DAQRKMTRMINYTKFIESSKELDPATAERAERIRDDTKRIKDQVDAGLLSH-
PMTV       CCPILDFR DAQRKMTRLIDFNRFIDDAKVVS AEAKA AVAAQIKKDCDLISENAKKDAYDA-
BSBV       CCPILDYR DAQRKMTRMLNFHKFTSDSSEIPPDIREKAEMIAEDNAIITANVREGDLNS-
BBNV       CCPILDYR DAQRKTTRVLRIEKLVEEINMV-TSTGRKIQRI LEDEEIISSNIKAGKFNS-
PCV        CCPLLDYR DAMRKQERLLSLELFARNGKEKTEEFDECYKQIKAFELQRRALNAGT----
IPCV       CCPLLDYR DAMRKQERILSLELFARNGKEKTEEFDACYQQIRNFENTRRTAISAGK----
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BSMV CCPILSMRDSERLETRMMAMQKYMRGSKDKPLRLLSRYQNILREQAARTTAFMAGEVNA-
RubV -----REVARVERRWVALCLHRTARKLATAL-----

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BdMoV SRAPRLAEMDSVMEFAKSISVSKSQA-----KTKSKTSTTARKGWF-----
BNYVV SD---KDVAEVLRYAQTVASTKKEA-----KK---KPNTGKRKMVM-----
BSBMV SD---KDVAEVLRYAKTVASTKRDA-----KQ---KP-VGKRKMIM-----
RNYV RVAS--GDLENIVEIAKGLAASKRTS-----KQLKGMVRVPAPGALY-----
aHEV -----VKVA-REFCQLGFGACSHQC-----EVGIALYLSH---DMRPAD
sHEV -----LPPADRTYCFDGFSGCTFAA-----ETGIALYLSH---DLWPAD
HeVt1 -----LPPVDRTYCFDGFSGCTFAA-----ETGVALYLSH---DLWPAD
HEVmex -----LPPADRTYCFDGFAGCRFAA-----ETGVALYLSH---DLQPAD
HEVsar55 -----LPAADRTYCFDGFSGCNFPA-----ETGIALYLSH---DMSPSD
DpTV -----AGIPSETFCVDGVGACAFQA-----QLGISNHSLY---DVELEE
HasV -----NGIASRTFCVDGVGSCAFKS-----RVGIANHSLY---DVTLEE
NbetaV -----AGIPTDTFCVDGFSNCEYQS-----PLAIACHSLYPDGESNSIMD
SsRV-L -----TGMPSGEFCPLSGEDCSHKS-----SALVSFFSLH---DASPAV
ReMV -----AESPQDVVCHNTFQTCHEHQ-----FQNSGRVYAIALHSIY---DIPADE
ToMV -----AEMPNEVVCHDTFQTCGHSQ-----ECYTGRVYAIALHSIY---DIPADE
TRV -----IAAPNAVRCNNTYQGCCTCRG---F-SDGKKKGAQYAIALHSLY---DFKDKD
PEBV -----IDVANFVRCNNTFQDCNCRG---YRADGTRIGATNAIALHSLY---DFKLDD
SBWMV -----EDLDGKWYCGNRFEDCVFRA-----DRAYAMAIHSIY---DIDLSD
CWMV -----EDLDGKWYCGNKFEECVFRA-----ERAYAMAIHSIY---DIDLMD
SBCMv -----EDLNGKWYCGNKFEECVFTA-----ERAYAMAIHSIY---DIDLMD
OGSV -----KFLTGWYECENKFEDCVFKA-----EKAYAMAIHSIY---DIALDD
srCSV -----EAMDGVWYQCQNFEDCVHNV-----ANAAIAIHSIY---DIEIED
BVQ -----HDLNGKWYQCQNFEDCVFEP---FSDDTLKKDALVCGMAIHSIY---DIHLVD
PMTV -----NDLNGTWFCQNKFCVYDHSTLGDGK---KEAYGMAIHSIY---DIHLVD
BSBV -----SALNGRWFCQNKFCVDFPRDILTGTAKDNVMVYAMAIHSIY---DINVYE
BBNV -----EDMNGMWYQCQNFENCVFVKP-----EGRAYAMAIHSIY---DIDLHE
PCV -----AASCNNKYCCDVFQDCAYPE-----EEGKMRVAMGVHSVY---DMTLQD
IPCV -----NVVMNDRYCCDVFQNCAYEP-----DSGKLRVAMGVHSVY---DMTLQE
BSMV -----GVLGDVFCENTFQDCVRRV-----PEGFLKTAIAVHSIY---DIKVEE
RubV -----AETASEAWHADYVICALRGAPSGPFYVHPEDVPHGGRAVADRCLL---YYTPMQ

BdMoV --SPATEKTIELHMLAAEVAERKQIPG-----
BNYVV --SEATRRTIELHELRSRIVAEKKIPN-----
BSBMV --SEATRRTIELHELRSRVAAEKKIPN-----
RNYV --TDSVRKTTLEFMTIAKDVAEENKIPD-----
aHEV VACAMARHNMRTMYVVLHLPPEAMLPPGS-----
sHEV VAEAMARHGMRTRYAALHLPPEVLLPPGT-----
HeVt1 VAEAMARHGMRTRYAALHLPPEVLLPPGT-----
HEVmex VAEAMARHGMRTRYAALHLPPEVLLPPGT-----
HEVsar55 VAEAMFRHGMRTRYAALHLPPEVLLPPGT-----
DpTV LANAFNNHGLHMVKAFMHIPELLYMDDEVNDELGYRFKVVDDDFRLRDVEYTLGDVRRAR
HasV LANAFENHGLHMVRAFMMHPEELLYMDNVVNAELGYRFHVIEEPMVAKDCAFQGGDLRLH
NbetaV VAKGMALHGTHVIYAWMHLPEVLLTLTDADNIFEGYSYSIR-----
SsRV-L LDAMMARKDALVAYVAMHLPVALLATSSFFDDVATGAHCRRDDDTG-----
ReMV FGAALLRKNVHTCYAAFHFAEGLLLEDSYVN-----
ToMV FGAALLRKNVHVCYAAFHFSENLLLEDShVN-----
TRV LMATMVEKKTkvVHAAMLFAPEMML-VDEGP-----
PEBV VADAMIEKGTkFLHAAMLFAPEAEI-EKEGP-----
SBWMV LANALEEKRIKVMsGTFLFSVDLLLGKKSgt-----
CWMV LANALEEKRIKIMsGTFLFSVDLLLGKKSgs-----
SBCMv LANALEEKRVrIMsGTFLFSVDLLLGKkQGR-----
OGSV LANAMEEKRIKYLMGTFLFSVDMLIGKkrGE-----
srCSV LVDALEEKQIKQLTGTFLFSVELLMGSKRGE-----
BVQ LVAAMQRKGIrVLTGTFLFAVDMLLGKKEGE-----
PMTV LVSAMERKKVrVLKGTFLFSADIIIGKkrGE-----
BSBV LATALQRKGIKRMVGTFLFSVDMLLGRKSge-----
BBNV LVDALEEKEIKLMyGTFLFNVDMLLGKQSGV-----
PCV LVNGLERKGIeHFIGCFLFSPKLLLGQEEGE-----
IPCV LVDGLERKKIeHFIGCFLFSPKLLLGQEEGE-----
BSMV FASALKRKGITQAYGCFLFPpAVLIGQKEGI-----

RubV MCELMRTIDATLLVAVDLWLPVALAAHVGDWDDLGIAWHLHDHGGCPADC-----

BdMoV -----HFHFSRDSFIKSGP-FTQLVCEVDVGYN
BNYVV -----HFHFDESDFASVGN-FTQLVCEVDVGYN
BSBMV -----HFHFDERSFGSVGS-FTQLVCEVDVGYN
RNYV -----HFLFTKPDCAVTGQVYTQLVFEDVGYN
aHEV -----YSNKFYNTVNTAD-----KCIITYADDSC-----AGYV
sHEV -----YHTTSYLLIHDGD-----RAVITYEGDSS-----AGYN
HeVt1 -----YHTTSYLLIHDGD-----RAVITYEGDSS-----AGYN
HEVmex -----YRTSSYLLIHDGK-----RAVVITYEGDTS-----AGYN
HEVsar55 -----YRTASYLLIHDGR-----RVVVITYEGDTS-----AGYN
DpTV APKLQFLPESQRRRIERLVGRGSYSRR-----CVIFSGNDDWA-----DAYC
HasV FPELDFINESQERRIERLAARGSYSRR-----AVIFSGDDDWG-----DAYL
NbetaV -----FEETGALPCTKRR-----KAIFSGYNDFG-----SAYV
SsRV-L -----HWHMSFPGSGA-----AGYT
ReMV -----LDEINACFSRDGD-----RLTFSFAEST-----LNYS
ToMV -----LDEINACFQRDGD-----RLTFSFAEST-----LNYS
TRV -----LPSVDGYMKKNG-----KIYFGFEKDPS-----FSYI
PEBV -----LPSVDGYERKEGSLISSEKIFFGFNNDPS-----YAYI
SBWMV -----LPTMDGFFEVEDG-----YVKYGFHNDTN-----PGYK
CWMV -----LPTMDGFFEVEGD-----YVKYGFKNDTN-----PGYK
SBCMv -----LPTMDGFFEVEGD-----YVKYGFHNDTN-----PGYK
OGSV -----MTTVDGFYEIDGE-----DVKYGFYDDTN-----CGYK
srCSV -----LPTVNGFFEVEGD-----KVKYGFYDDPN-----CGYT
BVQ -----LPTVNGFYRVNGN-----KVKYGFYDDPN-----CGYE
PMTV -----LPSVNGFYIIDGE-----SIKYSFYDDPN-----CGYE
BSBV -----LPSVNGFYKLEGE-----YIKYGFYDDPN-----CGYR
BBNV -----MKSFDGMYRIEGE-----YVKYWFGDDPN-----CGYK
PCV -----LPFVNGRFVKVKG-----KIRFFFLDDTT-----HGYE
IPCV -----LPFVNGRFVKVKG-----KIRFFFLDDTT-----HGYE
BSMV -----LPSVDGHYLVENG-----RIKFFFANDPN-----AGYS
RubV -----R-----GAGAGPT-----PGYT

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MTR domain/Hel domain

BdMoV FS----SFDWLVEYIKGGPGTGKSYIIRALADPNDS--LVVAPFLKLRSDYQNVVDGKT
BNYVV FS----VDAWLEEVKGGPGTGKSFILIRSLADPIRD--LVVAPFIKLRSDYQNRVGDDEL
BSBMV FS----VDAWLEEVKGGPGTGKSFILIRSLADPIRD--LVVAPFIKLRSDYQNRVGDV
RNYV FS----PEDWLEEVKGGPGTGKSFILIRALADPVRD--LVVAPFLKLRSDYQNVQGPVGG
aHEV HKREV-LQDWIYALIAGVPGSGKSSVDHRGA-----VVTPTKTLAREWSAR-----
sHEV HDVSI-LRAWIYQFTAGVPGSGKRSRISQGGDVD-----VVVPTRELNSWRRR-----
HeVt1 HDVSI-LRAWIYQFTAGVPGSGKRSRISQGGDVD-----VIVVPTRELNSWRRR-----
HEVmex HDVAT-LRTWIYQFTAGVPGSGKSKSVQADVD-----VVVPTRELNAWRRR-----
HEVsar55 HDVSN-LRSWIYQFTAGVPGSGKRSITQADVD-----VVVPTRELNAWRRR-----
DpTV HD----YHTWLELEYTGPPGSGKTRKLLAAVEAVSTRMLFIAPTSELRSEMEKSIK---
HasV HD----FHTWLELEYEGPPGSGKTGTLIAALEAAGGKALYVAPTRELREAMDRIK---
NbetaV HD----AHHWAIEYWTGPPGSGKSRAAKPRFADLQGGVLYCAPTRTLRDLDESVDH---
SsRV-L HSLAS-LSAWSLAAIVGPPGSGKTHGLRALVGNLD--AVIVPTNQLADSWRAHAP----
ReMV HSYSN-ILKYVVVLVDGVP GCGKTKEILSRVNFEED--LILVPGQAAEMI KRRANASGV
ToMV HSYSN-ILKYVVVLVDGVP GCGKTKEILSRVNFEED--LILVPGQAAEMIRRRANASGI
TRV HDWEE-YKKYLFELVDGVP GCGKSTMI VNSANPCVD--VVLSTGRAATDDLIERFASKGF
PEBV HNLNQ-LMKYLITL RDGVP GCGKSTWILNANPMKD--MVL CVGKEATEDLKEKFMKKHK
SBWMV HNLNQ-LMKYLITL RDGVP GCGKSTWILNANPMKD--MVL CVGKEATEDLKEKFMKKHK
CWMV HKLSQ-LMKYLITL RDGVP GCGKSTWILNANPMKD--MILSVGKEATEDLKEKFMKKHR
SBCMv HKLSQ-LMKYLITL RDGVP GCGKSTWIVENANPMKD--MVL SMCKEATEDLKEKFAKRLR
OGSV HNMQQ-LMEYLIMLKD GVP GCGKSTWILNANHVKD--VVL SMGREATL DLKDKFARKYK
srCSV HNLQQ-LKKYLVVLKDGVP GCGKSTWILNANLKR--VVL SMGKEATVDLREKFEKEYA
BVQ HDLDS-LLLYIVTLIDGVP GCGKSTHIVKEANLVDH--YVLTMGKEASDLKERFMRERG
PMTV HNLNS-LMLYVITLVDGVP GCGKSTYVVKANLVNQ--YVVTIGREAAEDLRRERFKSERN
BSBV HKFSS-LKAYLVTLIDGVP GCGKSTHIVKEARLENQ--YVLTMGREAAAELRRERFKTVRG
BBNV HNLQN-LLKYIITLIDGVP GCGKSTYIVNADVRTD--LILSMGKEATEDLKRRTKEKG
PCV HDLND-YLDYIVRLIDGVP GCGKSTWILSNCDLDRQ--IVLAEGREATDDLRRRFTKEGF
IPCV HDLND-YLEYIVRLIDGVP GCGKSTWILNCDLKDQ--VVLAE GREATDDLKRRTKEGF
BSMV HDLKD-YLKYV FELIDGVP GCGKSTMILNSCDIRRE--VVVGEGRNATDDLRRERFKRKN
RubV RPTTRIYQVLRVWNMAAGAGKTTRILAAFTRED---LYVCPTNALLHEIQAKLRARDI

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BdMoV V-----NWDFQTQHAAL-----KCGREVI FVDEFTAYDWRL LAVLVHRSQAHTIYL
 BNYVV L-----SWDFHTPHKAL-----DVTGKQI IFVDEFTAYDWRL LAVLAYRNHAHTIYL
 BSBMV V-----SWDFHTPHKAL-----DITGKQV IFVDEFTAYDWRL LAVLAYRNHAHTIYL
 RNYV T-----TWNFHTQHKAL-----EQSGKLT IFVDEFTAYDWRL LAVLVHRCGAETVYL
 aHEV -----GATAVTPHVAA-----SAAPEGRVIVDEAYAI PPHL--LVASLRRRARDVVM
 sHEV -----FAAYTPHTAA-----RVTRGRRVVIDEAPSL PPHL--LLLHMQRASSVHL
 HeVt1 -----GFAAYTPHTAV-----RVTRGRRVVIDEAPSL PPHL--LLLHMQRASSVHL
 HEVmex -----GFAAYTPHTAA-----RVTSGRRVVIDEAPSL PPHL--LLLHMQRAASVHL
 HEVsar55 -----GFAAYTPHTAA-----RVTQGRRVVIDEAPSL PPHL--LLLHMQRAATVHL
 DpTV -----PSDAATQHNALSMLRRATAASRPYELVVIDECFML PLVYVSIVAAISPESKIVL
 HasV -----PSASRTQHVALAILRRATAEGAPFATVVIDECFMP L VYVAIVHALSPSSRIVL
 NbetaV -----PSRVCTYHNALHVAAKES--GNRPFVIVIDEAET P PACYVGTMMHASPSSRIVC
 SsRV-L -----DTAVFTVERFL-----ADPPAEPYRRLVVIDECF KLAPSH--LIRALAHGKTCYI
 ReMV I--VATKDNVRTVDSFM--MNYGKVARCQFKRLF IDEGLMLHTGCVNFLVSM SLCEIAYV
 ToMV I--VATKDNVRTVDSFL--MNYGKGARCQFKRLF IDEGLMLHTGCVNFLVEMSLSDIAYV
 TRV P--CKLKRVRVTVDSFL--MHCVD--GSLTGDVLHFDEALMAHAGMVYFCAQIAGAKRCIC
 PEBV G--INLKKRVKTVDSFL--MHCSD--GNCVGDLLHFDEALMAHAGMVYFCAQIAGAKKVIC
 SBWMV C--AESDLKRIRTVDSFL--MHDYD--K-FRAATVHFDEALMAHAGIVYFCADILGAKKVIC
 CWMV C--VESDLKRIRTVDSFL--MHDYD--K-YRAATVHFDEALMAHAGMVYFCADILGAKKVIC
 SBCMVC--TESALRRVRTVDSFL--MHDYD--K-FRAATVHFDEALMAHAGMVYFCADILGAKRVLC
 OGSV C--QERELKRIRTVDSYL--MHDYD--KTLRASVVFHFDEALMAHAGMVYFCADLLGAKKVIC
 srCSV F--GKKELNRVRTVDSYL--MHDYD--KEMTCNTLHFDEALMAHAGMVYFCADLLGARKLIC
 BVQ A--TESDVKRVRTVDSFI--MND---RFSRANVLHFDEALMAHAGTVYFCADML SARTVIC
 PMTV A--TATQLKRVRTVDSYL--LND---TQSRANVLHFDEALMAHAGMVYFCADLLSARSVIC
 BSBV S--TEEQLKRVRTVDSFL--MND---KDSRAKILHFDEALMAHAGMVYFCADNLSARTI IC
 BBNV A--RQEDMKRVRTVDSYL--LNDYD--NKL RADTVHFDEALMAHAGMVYFIAMMCSAKRIKC
 PCV P--KKRCEERVTVHSFM--LKP---LSRRFNSFHFDEALMAHAGMIYICGRMLNAREVIC
 IPCV P--RKRCEERVTVHSFM--LKP---LTRGFNSFHFDEALMAHAGMIYICGRMLRAREVIC
 BSMV LNSKTANHRVRTLDSLL--LAEGP--CVPQADRFFHFDEALKVHYGAIMFCADKLGASEILA
 RubV D-----IKNAATYERRL-----TKPLAAYRRIYIDEAFTLGGEYCAFVASQTTA--EVIC

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BdMoV VGDEQQTGIQESRGEIGIYIPNKIDL--TKIST--HVPFKNFRNPRL DVKVLNLYLFASR--
 BNYVV VGDEQQTGIQEGRGEIGISILNKVDL--SKVST--HVPIMNFRNPVR DVKVLNLYLFGSR--
 BSBMV VGDEQQTGIQEGRGEIGVSILNRIDL--SKIST--HVPIMNFRNPVR DVKVLNLYLFGAR--
 RNYV VGDEQQTGIRESENEIGISILNKLP--SDYSM--HVPLFNRYRNP RKDVSVINHLFGTR--
 aHEV LGDPHQIPALDFDGRG--LTSAVDL--GLQPT--SWRTVSHRCPW--DVCIFLRT--DY
 sHEV LGDPNQIPAI DFEHAG--LVP AIRP--ELVPT--KWWHLTHRCPA--DVCELIRG--AY
 HeVt1 LGDPNQIPAI DFEHAG--LVP AIRP--ELVPT--KWWHLTYRCPA--DVCELIRG--AY
 HEVmex LGDPNQIPAI DFEHTG--LVP AIRP--ELVPT--SWWHVTHRCPA--DVCELVRG--AY
 HEVsar55 LGDPNQIPAI DFEHAG--LVP AIRP--DLAPT--SWWHVTHRCPA--DVCELIRG--AY
 DpTV VGDENQIGFIDFEGLMPTVTKDIL--KECVI--HRYDKTHRSPA--DVVSSAFYQRLY
 HasV VGDVHQIGFIDFQGT SANMPLVRDVL--KQCR--RTFNQTKRCPA--DVVATFFFQSLY
 NbetaV LGDPHQIGYIDFSDRKDDLKPFIIA--AECRT--RRFNTTYRCPQ--DVNLPFIKTLTY
 SsRV-L AGDPAQPRYEGSLGE--PLTLAEL--PICYL--ARLTKSRRCPK--DVPRFLTSVGE
 ReMV YGDTQQIPYINRVTFPYP AHFAKL--EVDEV--ETRRTTLRCPA--DVTHYLNKR--Y
 ToMV YGDTQQIPYINRVTFPYP AHFAKL--EVDEV--ETRRTTLRCPA--DVTHFLNQR--Y
 TRV QGDQNQISFKPRVSQV--DLRFSSLVGKFDIV--TEKRETYRSPA--DVAAVLNK--YY
 PEBV QGDQKQIAYKPRVSQV--TLRF TSLIGRFDEV--EEKRMSYRCPV--DVALTLDR--FY
 SBWMV QGDSQQIPF INRVESI--TLQYAKL--AIDET--EYVRLTYRSPV--DV AHYLTKKSWY
 CWMV QGDSQQIPF INRVESI--TLQYAKL--VIDET--EHVRLTYRSPV--DV AHYLTKKSWY
 SBCMVC--QGDSQQIPF INRVESI--TLQYAKL--QIDDT--EYVRLTYRSPV--DV AHYLTKKSWY
 OGSV QGDSQQIPF INRVESI--SLQYAKL--VIDRT--ESVRMTYRSPV--DV AHYLNKAYY
 srCSV QGDSQQIPF INRVESI--TLRYANL--VIDKT--DKIRHTYRSPV--DV ACYLTMKGY
 BVQ QGDSQQIPF VPRVEGI--TLQYAKL--KIDNV--VEKRLTYRSPV--DVAAFLTRKGY
 PMTV QGDSQQIPF INRVESI--TLRYAKL--EIDNV--VEKRLTYRSPV--DVASYLTKKNFY
 BSBV QGDSQQIPF INRVESI--TLRYAKL--EITNV--VEKRLTYRSPV--DVACFLTRKNFY
 BBNV QGDSKQIPF INRVESI--KLEYAKL--DIHET--IAKRLTYRSPV--DVAYYLTKKGFY
 PCV QGDSKQIPF INVEQI--SLKYSSF--NVVER--EHVRKTYRCPV--DIVYLNKKNYY
 IPCV QGDSKQIPF INVEQI--TLRYASF--NVVER--EYVRKTYRCPV--DIVYLNKKNYY
 BSMV QGDRAQLPMICRVEGI--ELQFQSP--DYTKTI INPKLRSYRIPG--DVAFYLSAKEFY
 RubV VGDRDQCGPHYANNCRTPVP-----DRWPT--ERSRHTWRFPD--CWAARLRAGLDY

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BdMoV -----MLPTSSVDAGYAF-----DDLNSFQTKVKDSSV--KVIHYSDESGANLMTE
 BNYVV -----MVPMSSEKGFSSF-----GDVKEFSSLSNIPDT--KIIHYSDETGHEMMPD
 BSBMV -----MVPMSSEIQGFCF-----GDIKDFSSLSNIPDT--KIVHYSDETGHEMMPD
 RNYV -----MIPVSDVVSGFVN-----RPLSEFQPLVSDPECRYKIIHYTEATGRALLAG
 aHEV PT-----ITTSRVLRLSVVFTGETIG-----OKIVFTQVAKQ-----
 sHEV PK-----VQTASRVLRLSLFWGEPPIG-----QKLVFTQAAKA-----
 HeVt1 PK-----IQTASRVLRLSLFWEEPVG-----QNLVFTQAAKA-----
 HEVmex PK-----IQTTSKVLRLSLFWGEPAVG-----QKLVFTQAAKA-----
 HEVsar55 PM-----IQTTSRVLRLSLFWGEPAVG-----QKLVFTQAAKA-----
 DpTV PG-----VTTTSSNTHSIEYVPASY-----VNSGA--VTLCFTQEEKS-----
 HasV PG-----CTTTSGCVASISHVAPDY-----RNSQA--OTLCFTQEEKS-----
 NbetaV PD-----AISFSKQLTSIRYLTRARSVTRTR-----HAQTLTQDQKP-----
 SsrV-L S-----FVSI STVDYSFGPVDPDVDPDPR-----QTLHITAHQRN-----
 ReMV EG-----FVMSTSSVKRSVSQ---EMVSGAATINPISKPLHG--KVLFTTQSDKEALL--
 ToMV EG-----HVMCTSSSEKKSVSQ---EMVSGAASINPVSKPLKG--KILFTTQSDKEALL--
 TRV TG-----DVRTHNATANSMTV-----RKIVSKEQVSLKPGA--QYITFLQSEKKELVNL
 PEBV TG-----KVVTKNSVLRSM DV-----KRIGSKEQVEMEHGI--QYLTFLQSEKKDIANL
 SBWMV SG----GRVTTKNSVLRSMKVVGPRDAKPMTSVHCVPYHRDA--QYLTFTQSEKADLYKA
 CWMV SG----GRVTTKNPVMRSMKTVGPRDVKPMTSVHCVPYFKDA--QYLTFTQSEKTDLYKA
 SBCM V SG----GRVLTKN TTLRSMNTVGP RDAKPMTSVHCVPYHRDT--QYLTFTQSEKADLYKA
 OGSV DG----GRVTTKNEVLRSM SVVGP RTRPMNSAYCVPYVKDT--QYLTFTQAEKDDL FKA
 srCSV GA----DRITTTNSDGRSLGVVGP RHEKPMTSVYCVPYLAGV--QYLTFTQAEKEDLHKA
 BVQ GN----SVIMSANETLRSMKTIGPRTG--MTSIY SIPKVANC--QYLTFTQAEKEEMEKY
 PMTV GT----SVVTSANPLVRLKTVGPRDG--MTSIY SIPKIPGT--QYLTFLQSEKEEMRQY
 BSBV WH----FHCYERKSNGRSISVVGPRDG--MTSNYSIPKKGGA--QYLTFTQSEKEDMVR Y
 BBNV GL----DFITSANPLLRSMKTVGPRSSTPMSSIYVIPKTKGA--SYLTFTQTEKDEM KQY
 PCV RG----DDIVGYSKTTHSVDTKSKSSG--FTSLVKLPK-EPV--HYLTFLQAEKEEVSKH
 IPCV QG----DDIVGFSKTTHSVDTKSKTSG--FTSLVKLPK-EPV--HYLTFLQAEKEEVAKH
 BSMV KVKGIPQKVI TSNSVKRSLYARGETTPERFVSLLDVPVRKDT--HYLTFLQAEKESLMSH
 RubV DI-----EGERTGTAFACNLWDGRQVD-----LHLAFSRET VRRLL---

HEL domain/

BdMoV ----YVTGVSKTTVRANQGSTHDSVVLPI--TAADGRLV----EDELNLVALSRHKKS-
 BNYVV ----YVRGVSKTTVRANQGSTYDNVVL PV--LPSDLNLI----NSAELNLVALSRHRNK-
 BSBMV ----YVRGISKTTVRANQGSTYDNVVL PV--LPSDLKLI----NSQELNLVALSRHKNK-
 RNYV ----MTTEL-KTTVRSNQGSTHDYVALPV--TVADAPLL----RNEQLNLVAISRHKKE-
 aHEV ----SNPGSITVHEAQGSTFDQTTI-IATLDARGLIA----SSRAHAI VALTRHRERT
 sHEV ----ANPGAITVHEAQGATFTETTI-IATADARGLIQ----SSRAHAI VALTRHTGK
 HeVt1 ----ANPGAITVHEAQGATFTETTI-IATADARGLIQ----SSRAHAI VALTRHTEK-
 HEVmex ----AHPGSITVHEAQGATFTTTTI-IATADARGLIQ----SSRAHAI VALTRHTEK-
 HEVsar55 ----ANPGSVTVHEAQGATYFTETTI-IATADARGLIQ----SSRAHAI VALTRHTEK-
 DpTV ----RCASEGAATVAEVQGKTFASVILHYNGTAPEQQLI----AADKHLV GITRHTNH-
 HasV ----RHGAEGAMTVHEAQGRTFASVILHYNGSTAEQKLL----AEKSHLLV GITRHTNH-
 NbetaV ----HSEPPVTAHEPQARR--TDVIVHYAGT LPERALL----EKVRHINVALTRHTNA-
 SsrV-L ----TNVHPGTVIDQVQGLEAENVVIHC--FPDDAPMW----LRPGRRVGLTRHRSR-
 ReMV ----SRGYSDVHTVHEVQGETYSDVSL-VRLTPTPVSIIS----GDSPHVLVALSRHTCS-
 ToMV ----SRGYTDVHTVHEVQGETYADVSL-VRLTPTPVSI IA--RDSPHVLVLSRHTKS-
 TRV LAL--RKVAAKVSTVHESQGETFKD VVL-VRLKPTDDSI A----RGREYLIVALSRHTQS-
 PEBV LCQ--RKVKS FVNTVHEAQGKTFK VRL-VRLKPTDDVLA----RGQEQI VALSRHTQS-
 SBWMV L--RAKGPVEVNTVHETQGKTFDDVIV-VRLKTTENEIYPGGRKGQPYEIVATTRHRS-
 CWMV L--RNKGPVTVNTVHETQGKTFDDVIV-VRLKTTENEIYPGGRKGQPYEIVATTRHRS-
 SBCM V L--RNRGPVNVNTVHETQGKTFDDVIV-VRLKTTENEIYPGGRKAQPYEIVATTRHRS-
 OGSV L--RSKGSVSVNTVHEAQGKTFDNVIL-VRLKTTENIYPGGLKSKPYTIVSVTRHRS-
 srCSV L--RSKGPVSVNTVHEAQGKTFDNVIL-VRLKTTENEIYPGGRKSKPYSIVGVTRHRS-
 BVQ L---GKGKVGNTVHECQKTYENVVL-VRLKSTANEIYPGGENSKPYVVVGTTRHRS-
 PMTV L---GRGNWNVNTVHESQKTYDNVVL-CRLKATDNEIYPGGRNSSPYMVVGVTRHRS-
 BSBV L---GKGQWSVNTVHESQKTYDDVIL-VRLKPTDNEIYPGGRKSKPYVVVGTTRHRS-
 BBNV L---GSGDWTVNTVHEAQGKTFDNVIL-VRLKNTENEIYPGGRNSEPYMVTGISRHRS-
 PCV L--AGVKGATVSTVHEAQGKTFERNL-VRLKMTDNELYPGGAKSEPYTIVGLTRHTRS-
 IPCV L--AGVKGATVSTIHEAQGKTFECVNL-VRLKMTDNELYPGGAKAEPYTIVGLTRHTRS-
 BSMV LIPKGVKKESISTIHEAQGGTYENVIL-VRLQRTPN EIYPGGRSAPYIVVGTSRHTKT-
 RubV ----HEAGIRAYTVREAQGM SVGTACIHVGRDGT DVALA----LTRDLAIVSLTRASDA-

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RdRp domain

BdMoV RFQLKDIE----KPLKDP--STDLAKAGQGILAWSKEAHVKFMIAFRVLNDLMLKSV-NPN
 BNYVV RFQLKDIE----KPLKDP--ETDLAKAGQGILAWSKEAHVKFMAFRVLNDLMLKSL-NSN
 BSBMV RFQLKDIE----KPLKDS--ETDLAKAGQGILAWSKEAHVKFMAFRVLNDLMLKSL-NSN
 RNYV RFQLKDIE----KPVKEP--TVDMAKAGQGILAWSKEAHVKFMIAFRVLNDLMLKSV-KEN
 aHEV TFFQKDC-----KFTLDD--PVAHGKVGQGISAWPKTLCALFGPWFRAIEKHLVAGL-PPG
 sHEV TFFQKDCN-----KFTTGE--TIAHGKVGQGISAWSKTFCALFGPWFRAIEKEILAAL-APN
 HeVt1 TFFQKDCN-----KFTTGE--TIAHGKVGQGISAWSKTFCALFGPWFRAIEKEILAAL-APN
 HEVmex TFFQKDCN-----KFTTGE--TIAHGKVGQGISAWKTFCALFGPWFRAIEKAILSL-POA
 HEVsar55 TFFQKDCN-----KFTTGE--TIAHGKVGQGISAWSKTFCALFGPWFRAIEKAILL-POG
 DpTV DFLMKTQQ----KVSTK--PMNSGKVGQIAAHSKSLNFVLAWVVRILDEVLRG--STT
 HasV DFLMKTQQ----KVSPK--PINTGKVGQIAAHSKSLNFVLAAWIRILEEILRTG--SRT
 NbetaV SYHLKGQ-----KVM----DPTKLKGQGISAEKCANIALSAWVRIIQDQMS---SEK
 SsrV-L QFFLKAQA----KAKFGSYGRETIIECGQILATSKGLNAQICPVCATMEVLQGC-LYDE
 ReMV RHMIKAQP----KQKLDTSIQTEYPALQTIIVYHSHKINAIIFGPLFSELTRQLLDSVDSR
 ToMV RHMIKAQP----KQKLDLSIQTEYPALQTIIVYHSHKINAIIFGPLFSELTRQLLDSIDSR
 TRV MYMIKSDV----KPKTDLTPQFEYSALQTVVYHEKLNLSLFGPIFKEINERKLDAM-QPH
 PEBV MFMIKSDV----KPKMDSTPQHEYSALQTVIYHEKLNLSLFGPIFKEINERRLDAI-HPH
 SBWMV NYCIKGDE----KPKMDRSPQHEYGALQTVVFPDKIVNALFGPAMKEINERIRLAL-KPH
 CWMV SYNIKGDE----KPKMDRSPQHEYGALQTVVFPDKIVNALFGPVMKEINERIRMAL-KPH
 SBCM V SHNIKGDE----KPKNDLTPQREYGALQTVVYVDPKIVNALFGPVMKEINERIGMAL-KPH
 OGSV NFMIKNDV----KPKMDTTPQSEYALQTVVYVDPKIVNALFGPVMKEINERIRYAL-KPH
 srCSV NFMIKNDV----KPKMDLTPQSEYALQTVVYVDPKIVNALFGPVMKEINERIRYAL-KPH
 BVQ NFMIKNDV----KPKLDLSPQSEYALQTVVLPDKIVNALFGPIMKINERIRFAL-KPH
 PMTV NFMIKGDV----KPKLDLSPQSEYALQTVVYVDPKIVNALFGPIMKEINERIRVAL-KPH
 BSBV NFMIKNDV----KPKLDLSPQSEYALQTVVYVDPKIVNAIFGPMKEINERILLAL-RPH
 BBNV --MIKRDV----KPKLDLSPQSEYALQTVVYVDPKIVNALFGPVIKEINERIRHAL-KPH
 PCV NFMIKNDV----KPKLDLTPQSEYALQTVVYVPEKIVNGLFGPVIKEINERVLSAL-KPN
 IPCV NFMIKNDV----KPKLDLTPQSEYALQTVVYVPEKIVNGLFGPIIKEINERVLSAL-RPN
 BSMV NFMIKNDV----KPKLDLTPQVEYALQTVVYVDPKIVNAFFGPIIKEINERIRAL-RPH
 RubV ATLKCVDAAALGPRDTEDC-HAAQKGAGLEIRAWAKEWVQVMSPHFRAIQIIMRAL-RPQ

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BdMoV VVYDNAMSEDEFVEKINVAMAAPD-VAINGVIDAAACDSGQGPFTQLIERIY-YAALGI
 BNYVV VVYDNTMSETEFVGKINAAMNIVPD-SAINGVIDAAACDSGQGVFTQLIERHI-YAALGI
 BSBMV VVYDNTMSEVKFVANINAAMSIVPG-SAINGVIDAAACDSGQGVFTQLIERIY-YSALGI
 RNYV VVYDNGMSEKEFTDKINSAMSSVPG-VAINGVIDAAACDSGQGPFTQLIVERYI-YELMGI
 aHEV YYYGDLYTEADLHRSVLC--PAGH-LVFE--NDFSEFDSTQNNVSLDLECEL-MRRFGM
 sHEV VFYGDAYEDTVLAAAVAGA--P-GC-KVFE--NDFSEFDSTQNNVSLGLECII-MEECGM
 HeVt1 VFYGDAYEDTVLAAAVAGA--P-GC-KVFE--NDFSEFDSTQNNVSLGLECII-MEECGM
 HEVmex VFYGDAYDDSVFSAAVAGA--S-HA-MVFE--NDFSEFDSTQNNVSLGLECAI-MEECGM
 HEVsar55 VFYGDADFDDTVFSAAVAAA--K-AS-MVFE--NDFSEFDSTQNNVSLGLECAI-MEECGM
 DpTV VRYSNGLPDEEEAMLLEAAVNKVPNASFTS--ADWTEFDTAHNNVSEIFFAEL-LARVGT
 HasV VRYSNGLPDEEEAMLLEAKINQVPHATFVS--ADWTEFDTAHNNVSELLFAAL-LERIGT
 NbetaV FIFANGQSDRDTMSIIEARLQEKAR-EFKS--IDIKEFDTVHNVSVILVFSWR-CDR-GC
 SsrV-L VLLDCGYNGAIDGHVARHIL--GH-PTTE--TDLTQQDSTHDETCRLLIDEV-LRRLNI
 ReMV FLFFTRKTPAQIEEFFEDLDLSDHVP--EILE--LDISKYDKSQNEFHCAVEYEI-WRRLGF
 ToMV FLFFTRKTPAQIEDFFGDLDLSDHVP--DVLE--LDVSKYDKSQNEFHCAVEYEI-WRRLGL
 TRV FVFNTRMTSSDLNDRVKFLNTEAAY-DFVE--IDMSKFDKSNRFLHLQLQLEI-YRLFGL
 PEBV FVFNTRMTASDLNDRVRCCLHPDADY-DFIE--VDLSKFDKSNRFLHLQLQLEI-YRMFGL
 SBWMV VVYNSRMNAEELNRTVEFLDPEEDF-NAFE--IDFSKFDKSKTSLHIRAVIEL-YKLFGL
 CWMV VVYNSRMNAEELNRTVEFLDPEEY-NAFE--IDFSKFDKSKTSLHIRAVIEL-YKLFGL
 SBCM V VVYNSRMNAEELNRTVEFLDPEDEY-DAFE--IDFSKFDKSKTSLHIRAVIEL-YKLFGL
 OGSV VVYNSRMNAEELNRTVEFLDPEDEL-QSFE--IDFSKFDKSKTSLHIRAVIEF-YKLFGL
 srCSV VVYNSRMNAEELDRTEFLDVKKYY-NAFE--IDFSKFDKSKTSLHIRAVIEL-YKLFGL
 BVQ VIYNTRMTASELDAAVEFLDVREEF-ESVE--IDFSKFDKSKTSLHIRAVLEL-YRMFGL
 PMTV VIYNTRMTSDELDPAVEFLDVREDH-ESVE--IDFSKFDKSKTSLHIRVVIEL-YKLFGL
 BSBV VVYNTRMTAEELDRSVEFLDVREYQ-DAVE--IDFSKFDKSKTSLHIRAVIEL-YKIFGL
 BBNV VIYNTRMTAAEMDRSLEFLNVYEDY-DSVE--IDFRKFDKSKVSLHIKVVIEL-YKLFGL
 PCV VFNTRMTSEELSRTAEYLYPGDEF-EVVE--IDFSKYDKSKTSLHIRMVIKL-YEQFGL
 IPCV VFNTRMTSEELSRTAEYLYPGDEF-EVVE--IDFSKYDKSKTSLHIRMVIRL-YEQFGL
 BSMV VFNTRMTADELNETVAFLTP-HKY-RALE--IDFSKFDKSKTGLHIKAVIGL-YKLFGL
 RubV FLVAAGHTEPEVDAWQA---HYTT-NAIE--VDFTEFDMNQTLATRDVELEISAALLGL

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BdMoV SDFFLDWYFSFRERYVMQSK---YVRANMQFIKTSGEPGTLGNTVLMGALLNAMLRGEG
 BNYVV SDFFLDWYFSFREKYVMQSR---YVRAHMSYVKTSGEPGTLGNTILMGAMLNAMLRGTG
 BSBMV SDFFLDWYFSFRERYIMQSR---YVRAHMSYVKTSGEPGTLGNTILMGAMLNAMLRGTG
 RNYV SDFFLDWYFSFREHYIMQSR---YVRAHMTYVKTSGEPGTLGNTILMGALMNSFLRGDG
 aHEV PDWMVALYHLVRSYWLLVAP-KEALRGC--WKKHSGEPGTLWNTVWNMTVLHHVYEFDR
 sHEV PQWMIRLYHLVRSAWVLQAP-KESLRGF--WKKHSGEPGTLWNTVWNMAVIAHCYEFDR
 HeVt1 PQWMIRLYHLVRSAWILQAP-KESLRGF--WKKHSGEPGTLWNTVWNMAVIAHCYEFDR
 HEVmex PQWLVRLYHAVRSAWILQAP-KESLRGF--WKKHSGEPGSLWNTVWNMAVIAHCYEFDR
 HEVsar55 PQWLIRLYHLIRSAWILQAP-KESLRGF--WKKHSGEPGTLWNTVWNMAVITHCYDFRD
 DpTV PAAAVTLFRQRCGKRTLRAKGLGSVEVD--GLLDSGAVWTLTRNTTFSAGVMLTLFR--G
 HasV PAAAVNLFRERCGKRTLRAKGLGSVEVD--GLLDSGAAWTPCRNTIFSAAVMLTLFR--G
 NbetaV PEHLIEYFEKRSKSRTLSSR-IGSVDVD--FMLDSGAVWTIARNTLFAAGLMLALFV--G
 SsrV-L PLDLISEYLESRSRHSVTGL-SYKVSFDVYERMFSGEPMTLLGNCIMMALVAHRFALPP
 RemV EDFLGEVWKQGHRKTTLKDY-TAGIKTCIWIYQRKSGDVTTFIGNTVIIAACLASMLPMEK
 ToMV EDFLAEVWKQGHRKTTLKDY-TAGIKTCLWYQRKSGDVTTFIGNTVIIASCLASMLPMEK
 TRV DEWAAFLWEVSHSTQTTVRDI-QNGMMAHIWIYQQKSGDADTYNANSRDTLCALLSELPLEK
 PEBV DEWAAFLWEVSHSQTTVRDV-QNGMTAYIWIYQQKSGDADTYNANSRDTMCCALLSELPLEK
 SBWMV NDLFALLWEKSQCQTKIRDF-VNGITAYLLYQQKSGNCDTYGSNTWSAALALLESMPLEK
 CWMV NDLIALLWEKSQSRTKIRDF-VYGITAYLLYQQKSGNCDTYGSNTWSAALALLESMPLEK
 SBCM V DMLSLLWEKSQCQTTVIDR-TNGITAYLLYQQKSGNCDTYGSNTWSAALALLESMPLEK
 OGSV EEMLAFLWEKSQCQTTVKDR-LNGITAYLLYQQKSGNCDTYGSNTWSAALALLETMPLEH
 srCSV EELLAFMWEKSQCQTTVKDR-LNGIVAYLLYQQKSGNCDTYGSNTWSAALALLETMPLEK
 BVQ DDLCAYLWEKSQCQTTIVKDR-VNGLVAHLLYQQKSGNCDTYGSNTWSAALSLESLEPLEK
 PMTV DEMIAYLWEKSQCQTTIKDR-VNGIIAQILYQQESGNCDTYGSNTWSAALSLESLEPLEK
 BSBV DDMLAFLWEKSQCQTTIRDR-QNGLIAHILYQQKSGNCDTYGSNTWSAALALLDALPLER
 BBNV DDMLAVLWEKSQCQTLVKDR-INGVQAYLLYQQKSGNCDTYGSNTWSAALALLDCMPLEK
 PCV NGYMKYLWEKSQTQTVVKDR-NYGVEAYILYQQKSGNCDTYGSNTYSSMFALLDCLPMEK
 IPCV NGYMKYLWEKSQTQTVVKDR-NYGVEAYILYQQKSGNCDTYGSNTYSSMFALLDCLPMEK
 BSMV DGLLKVLWEKSQYQTYVKDR-NFGLAAYLLYQQKSGNCDTYGSNTWSAALALLDCLPLED
 RubV PCAEDYRALRAGSYCTLREL--GSTETG--CERTSGEPATLLHNTTVAMCMAMRMVPGK

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BdMoV PMMAIKGDDGFKRQAN-LKINS---DIVKAISAQTVLEFKLDLDVPIITFCGYVLVQGK-
 BNYVV PFCMAMKGGDDGFKRQAN-LKIND---QMLKLIKKETVLDLFDLNLVPIITFCGYALSNGH-
 BSBMV PFCMAMKGGDDGFKRQAN-LKINT---DILKLIKKETVLDLFDLNLVPIITFCGYALSNGH-
 RNYV PFCMAIKGDDGFKRQMN-LRVNK---DIVQAVKDFTFLEFKLDINVPLTFCGYALVGGGA-
 aHEV PSVLCFKGDDSVVVCES-VRARP----EGVSLVADCGKMKDKTGPCGAFSNLLIFPGAG
 sHEV LKVAAFKGGDDSVVLCGD-YRQSR---NAAALIAGCGLKLVDFRPIGLYAGVVVAPGLG
 HeVt1 LKVAAFKGGDDSVVLCSD-YRQSR---DAAVLIAGCGLKLVDFRPIGLYAGVVVAPGLG
 HEVmex LQVAAFKGGDDSVVLCSE-YRQSP----GAGSLIAGCGLKLVDFRPIGLYAGVVVAPGLG
 HEVsar55 LQVAAFKGGDDSVVLCSE-YRQSP----GAAVLIAGCGLKLVDFRPIGLYAGVVVAPGLG
 DpTV VKFAAFKGGDDSLVSGSPLTFTP---ARLHMGEHYAKAHLKVETEVEVVPYIGLLVSAEQ-
 HasV VKFAAFKGGDDSLVCGSHYLRFDA---SRLHMGERYKTKHLKVEVQKIVPYIGLLVSAEQ-
 NbetaV VDFIAAKGDDVFLAGNN-LYLDL---ERLRMGSYLAANNLIEKTAVVSFIFGIVSQAA-
 SsrV-L RSASVWKGGDGLLRGMHFPSPSA-----ASLLARIGARVKVDHQVPVEFTSRVHLSGR
 RemV IIKGAFCGDDSLVFPK-GCEFP---DVQQAANLMWNFEAKLFKKQYGYFCGRYVVIHHR
 ToMV LIKGAFCGDDSLVFPK-GCEYP---DIQQAANLMWNFEAKLFKKQYGYFCGRYVVIHHR
 TRV AVMVTYGGDDSLIAFPR-GTQFV---DPCPKLATKWNFECKIFKYDVPFMCCKFLLKTS
 PEBV CVLMTYGGDDSLVFPK-GLKLV---DPCPKLATKWNFECKIFKFLVPAFCGKFLIRVQD
 SBWMV AKFMIFGGDDSLILFPK-HLTIE---DPCRRLASLWNFDCKLFDKHNMFCKGFLKLVGD
 CWMV AKFMIFGGDDSLILFPK-QQVVE---DPCRRLASLWNFDCKLFDKHNMFCKGFLKLVGD
 SBCM V AKYMIFGGDDSLILFPK-QLCIE---DPCRRLASLWNFDCKLFDKHNMFCKGFLKLVGD
 OGSV AKFMIFGGDDSLILFPK-KICVE---DPCRRLASLWNFDCKLFDKHNMFCKGFLKLVGD
 srCSV AEFMIFGGDDSLILFPE-EVVVE---DPCRRLASLWNFDCKLFSFNHNLFCGKFLKLVGD
 BVQ ARFMIFGGDDSLIFFPK-RMAIP---DPCRRLAAVWNFDCKMNFENNAFCGKFLIKVGE
 PMTV ATFMIFGGDDSLIFFPK-GMVE---DPCRRLASMWNFDCKLNFKNNSFCGKFLIKVGE
 BSBV AKFMVFGGDDSLVFPK-NMNL---DPCGRLASLWNFDCKFFNFQNNMFCKGFLKLVGD
 BBNV LRPMSIGGDDSLFFFK-GITIE---DPCRRLSLWNFDCKLFDKFNENAFCKGFLKLVGD
 PCV AVYSIFGGDDSLILFPK-GTIN---DPCGRLASLWNFDCKSMKFRVPAFCGKFLIPVGG
 IPCV AVYSIFGGDDSLILFPK-GTVVN---DPCGRLASLWNFDCKSMKFKVPAFCGKFMIPVAG
 BSMV AHFCVFGGDDSLILFDQ-GYIIS---DPCRQLAGTWNLECKVDFKYPFCGKFLLCIDG
 RubV RWAGIFQDDMVIFLPEGARSAAKWTPEVGLFGFHIPVKHVSTPTPSFCGHVGTAAAG-

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BdMoV ---LMPSISRKIIK

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BNYVV      ---LFPSVSRKLTK
BSBMV      ---LFPSVSRKLTK
RNYV       ---MYPNIVRKAIK
aHEV       ---VVCDLLRQWGR
sHEV       ---TLPDVVRFAGR
HeVt1      ---TLPDVVRFAGR
HEVmex     ---ALPDVVRFAGR
HEVsar55   ---ALPDVVRFAGR
DpTV       ---VVPDPVRVALK
HasV       ---VVLDPVRSALK
NbetaV     ---VTADVRLATR
SsRV-L     ---SLPDPAKVLAK
ReMV       GCIVYYDPLKLISK
ToMV       GCIVYYDPLKLISK
TRV        CYEFVDPDPVKVLTk
PEBV       KLVFVDPDPVKTVTK
SBWMV      RFKFAPDPMKLITK
CWMV       RFKFAPDPMKLITK
SBCMv      KFKFAPDPMKLLTK
OGSV       KWKFAPDPMKLITK
srCSV      RYRFSPDPVKLMTK
BVQ        RYRFAPDPYKLLTK
PMTV       KYKFAPDPYKLLTK
BSBV       NYKFAPDPFKLLTK
BBNV       NFRMAPDAIKFLVK
PCV        RYRFEPDPMKLITK
IPCV       RYRFEPDPLKLITK
BSMV       KYQFVPDAAKFITK
RubV       ---LFHDVMHQAIK
          .   :   :

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B. AlkB-like domain

CLUSTAL format alignment by MAFFT (v7.032b)

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BdMoV      RARKELFYSTSGQKDYRHGTIR-RTALEFPQELHKLMVY-----LNTVLNISTNSCVVS
ASPV       KGRGASFYSRDLK-GYSYTGFS-HVSRGWPAFLDKFLSD-----NKIPLNFYNQCLVQ
ASPV*      NHRGVSLYSRDLs-QYSSSGYL-QVSKWPKLLGKIFSE-----NIIPLFKFKQCGNE
AltMV      KNREAFFFSRDGT-PYSYTGGS-HVSRGWPAFLDQILATA----ELVRPIPH-FNQCLIQ
GLRAV3     KGRSAVFFSKLGE-GYTYNGGS-HVSSGWPRALDILTA-----IKYPSV-FDHCLVQ
GVB*       KGRRAAFYSRHSW-NYSYTGAN-HASKGWPEWVSNI AEK-----LGLGED-FDHCLAQ
GVA        KGREVAFYSRHSK-EYSYTGGS-HRSLGWDKALDELIVE-----LGLDES-YDHCLIQ
HpLV      KGRKAGWYSMGDV-PYTYNGGS-HKSQGWDSLLOMWEA-----NAVDPK-YDSCLVQ
BRpNV     RGRMALFYSDGAF-DYAHDKYH-YTSQGWPREVDDLAKK-----LGG-YNSCLVQ
LCHV1     RGRDAWFFSKSGD-AYGHDKVS-YVVLPWAKELDKLVC-----FGD-FNTALVQ
ICRSV     RNRCAWFFGPPH-RYGHNDIE-YHTTEYYPWVERIGNI-----FGK-FNTCLAQ
BVY       HGRTAWFFSKDPTLQYGHHPY-YDTHPWDELDKYLGG-----AK-YNTALVQ
CLBV      RGRKAAFITKVDA-DYGHNGMV-YPHNSWVPSLEEIIQI-----CGQGDD-FNCALIN
ChMLV     KGKKSYYVTLDSPMVYFHNSIS-YPSIEATGLIKDWILS-----KAEDYGVP-FNAALVQ
HipLV*    EYGVVWYSRGEV-ICALDGEH-YKSLGWPEWLQLWCAA-----NDVAQR-YDCCLVQ
PVM*      AGASVGLYTKDRS-NLMWGNSE-LLSNGWPRSLSIWMEV-----NSVSQK-FDVAVRL
PVS*      PGKRAAWYCRGQI-DYISGAIR-LENLGWPRWLSQWMEL-----HEIDETYYNSMLAQ
Ecoli     NCGHLGWTTTHRQ--GYLYSPIDPQTNKPWPAMPQSFHNLQRAATAAGYPDFQPDACLIN
Caulobacter ALGSLGWTSDAR--GYRYVDRHPETGRPWPDMPPALLDLW----TVLGDPEFTPDSCLVN

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BdMoV      KHSDDGNDLWCDVEDGGSD-ATSASVVVSYEGFCVFETT-CQWNSSCNRLPMTAGTCLLL
ASPV       EYSTGHGLSMHKDDESIYD-INHQVLTVNYSGDAlFCIE-CL--GSGFEIPLSGPQMLLM
ASPV*      EYRSGDGGSIQNYDNFIFA-NSRNAFTVNYSGDAlFCIE-CL--GSGFVIRMSGPQMLLI
AltMV      KYQRGASIPFHSDDPECYD-VDHQVLTINLTGEAEFKTS-CK--AGSGSCTLAENQFHLS
GLRAV3     KYKMGGGVVPFHADDEECYP-SDNPILTVNLVGNANFSTK-CRKGKGMVINVASGDYFLM
GVB*       IYEEDKGINFNADDEPCY--TDPEVTVNLNGNANFHLK-C---GSESVPLSDGDVFLIM
GVA       RYSKGGSIGFHADDERCYL-PGGSVVTLNLHGEAIFEVK-ENATGKVQKIKLGDGDVYTM
HpLV      IYTEGAALGYHADDEDLFE-QGESILTLNLSGAAEFGVK-CK--NGKGSVHLRGPQOFEM

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BRpNV      KYDKGAYIPFHADDEPCYD-DNDSVITVNLNGRATFIVR-NKTTGAETRRELHHGSILEM
LCHV1      RYTLGGYVSWHADDEPCYS-HDDSIVTINFNGPAVFSIQ-SG--NVYRSFNLLDRSVLIM
ICRSV      THDQGARIGYHADDEDCYD-KDVTVATVNLGTGNATFSLK-TA--TGTRTWKLPKPGDFIVL
BVY        VYDGTRDLPYHKDDEPCYDITNNPIRTVNVVTGTGDLCS-KDKRRLYETIPMTSGTVITF
CLBV       FYEANSSLGFHRDNERY--NDDPILTVCTFGEGRFTE-FK--DQVTSFLMTAGSFFLM
ChMLV      VYEKDCILGMHKDNESCY--GNHPILTVNVSGKAVFSTD-CC---GNTMELDSGDELML
HipLV*     KFAAEKDIVGSMVSAEQVE-DAEGALWVNLQGLTKFGMN-CT--SGKFELGLKEFECLEV
PVM*       SYSKETQMNVLPLPSLDGIE-RGAGATVVNLKRCGAFIVR-CA--EGGDCAGVDGPHLLVV
PVS*       EFPAGGTLECEVGGGQFI-PGSNVAIAEVGGQSQVSIG-CM--AGTGQLLELGDVIEV
Ecoli      RYAPGAKLSLHQDKDEPD--LRAPIVSVSLGLPAIFQFGGLKRNDPLKRLLEHGDVVVW
Caulobacter LYRDGARMGLHQDRDEAD--PRFPVLSISLGD TAVFRIGGVNRKDPTRSLRLASGDVCR L

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BdMoV      PNGFSSTHQYRVTDCLAGQTFLKFF
ASPV       PFGFQKEHRHGIKSPSKGRISLTFR
ASPV*      PLGFRKNHRLRIKSPSNGR TASTFR
AltMV      PPGFQKTHKHSVVSLSAGRVSLTFR
GLRAV3     PCGFQRTHLHSVNSIDEGRISLTFR
GVB*       PKGFQKTHKHAVTGTSAGRISLTFR
GVA        GPGMQQTHKHRVESCTEGRCSVTLR
HpLV       PAGFQVTHKHSVWGCSRQRESVTLR
BRpNV      LPSCQKLCCKHSVNVRDQGRVSLTFR
LCHV1      KAGLQKI AKHMVRSNFEGRVSVTLR
ICRSV      KPGAQGCTKHAISDCTTNR TSLTFR
BVY        PATMQENFYHAVRNPSAGRISITFR
CLBV       PKGFQKKARHSVSN-EMSRV SITFR
ChMLV      PEDFQRKFRHGVKSITDGRMSVTLR
HipLV*     --GKRSEFEGHSIGSAMCTGNSLSAR
PVM*       MGQDCIGHECYMRGLERENDVVVFL
PVS*       PGPCWSKHHLHMCCSEVRGVTFIFR
Ecoli      -GGESRLFYHGIQPLKAGFHPLTID
Caulobacter -LGPARLAFHGVDRILPGSSSLVPG

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C. Coat protein

CLUSTAL format alignment by MAFFT (v7.032b)

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BdMoV      -----MYLNWNDITH-HTHM
BNYVV      -----MSSEGRYMTWKDMSH-NKFM
BSBMV      -----MVDEGRYMTWKDATH-NKLM
RNYV       -----MSYPDWDTH--DVLS
NVMV       -----MAYRQWNEEA--SKAA
CMMV       -----MAVKSGYTVFNRELN-VMAN
OGSV       -----MPVTPGYTGYNKELN-VMAN
SBWMV      -----MAVNKGYTGYNKELN-AMAA
SBCMV      MDKLTRLKGEVDRSLQKAADKVTAEESTESLQSKVVVQLPQMAVKNGYTGYNKELN-LMAS
SorCSV     -----MAVEAGYDTWNAEIN-RIAV
PMTV       -----MAEIRGERKAAVENRYDSWDHEQA-MKAA
BVQ        -----MVDPRYEHWTAEHA-KAAA
BSBV       -----MVDPRYEGWNQREA-IRAK
BBNV       -----MTAAMEPHYAVFSNKMA-KYAA
CAV        -----MAYTPTYALNYAR
TMV        -----MSYSITTPSQF--VFL
CGMMV     -----MAYNPITPSKL--IAF
PCV        -----MSNIAEVSRGGGHYGVDPWRQHI IKNRIN
IPC        -----MTNISEVARGNGHYNVEGWRNHIVRSRAN
BSMV       -----MPNVSLTAKGGGHYNEDQWDTQVVEAGVF
PoMV       -----MPNISLTTKGGGHYDEDLWFSQVVSQGLY
LyRV       -----MANLGLTVKGGGHYDEDQWNSNIIDSIVI
TRV        -----MGDMYDESFDKSGGPADLM
PEBV       -----MVKGKYEGFSASGA-KDLV

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BdMoV SGRWVRLSEAVAFVKFAQAQDLSKARSLEFVKSSFIDMFSKWT-TDNPFFVHPKRFPAEV
 BNYVV TDRWARVSDVSVIKQSHAMDLSKAANLSIIKTALAGLGGSGWT-DNNPFVSPMTRFPQTL
 BSBMV TDRWARVSSVQATINQALSLDLSKAASLPVIKANFSSLGANWSEGDGVFVAPMVRFPVTL
 RNYV YSRWVRTSEAMSAVRTARVSDLSVAPSLGEIKAAILSLGDRHN-TEDPFVAPYRFPHHI
 NVMV CATWYKRTDLLDTIRKIKKGDLSITAOVVAAKNLISSLTP-----VEWGHATRFPD
 CWMV THAYIRLSALLSQVETWQSTRTSVLSHLGIMLNGVSKLGE-----RNFFSRKRFGTHT
 OGSV THAFIRMSTLMNQIEGWQSTRASVLSHLGIMLNAVSKLGE-----RNFFSRNKRFGTHT
 SBWMV THAYIRLSTLMSQIESWQATRASVLTHTLGVMLNGVSKLGE-----RSFFSRKRFGAHT
 SBCMV IHPFIRLGTLSIQIEGWQATRASILTHTLGVMLNGVSKLGE-----RNFFSRQKRFGTHT
 SorCSV RHAFIRYNTLLATVQDWTKTRTSLVAHVGTVLAALSTLGT-----RDFFSRKKRFAFAE
 PMTV VRKFISYDQFSAQLRNWREARLNIIEHATSVLSQVSNLGR-----THFYSGTERFGSS
 BVQ KNKFGSYETLLSLVKNWREVRLSVVEHSATILTQINEFGK-----QGFYSRTVRFGGPM
 BSBV KRRFVSYDTFMDLIVNWREVRVGIIEHSATILSQVSRLE-----ANFYGRTKRFRGRV
 BBNV AHPFIKYNELSETVKSWMQTRTSVMEHVNFVLGSAANLGT-----RGFFSRNVRFGMTN
 CAV VGNWYEVSDFLDFLDAQAADFVSVQTVRDGLRDSFNLSLPR-----SPPFLDTRFPS--
 TMV SSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWK-----PSPQVTVRFPD--
 CGMMV SASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPS-----SVVDINSRFPD--
 PCV ADWWIRLDHWETLLADLRGVSEFVNSSRSQVADF INRVPK-----DLPAGVSVRFPGPR
 IPCV ADWWIRSDLYDQLLADLRVNFVNTSRSEVSAI INRVPK-----DLPAAVSARFPGAR
 BSMV DDWWVHVEAWNKF LDNLRGINFSVASSRSQVAEYLAALDR-----DLPADVDRRFAGAR
 PoMV AEWWVLSDNWEKFLDNLRGVNFGVSSRSQVSDYVAALDR-----DLPADVDRRFAGPR
 LyRV YDWWISLDSWHSLSITLSKVQTDVSSRRRAIADLIDGVKK-----DLPALDRRFAGSQ
 TRV DDSWVESVSWKDLLKKLHSIKFALQSGRDEITGLLAALNR-----QCPYSPYEQFPD--
 PEBV FSAWVEVGNWNEVLRRLMDLKFALQADRDKIPGVLSDLNM-----ESPFRFKRFS--

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BdMoV SKWDT----ITLWVNFDEPPLSLVA-----ASII TGSDGGSAAANASAGTR
 BNYVV TMYGA----LVLYVNLSDPEFALIM-----TKVSTLTDGLADNASANVR
 BSBMV NQFGA----LVLWNLSDPAFALIM-----TKVFTLTNAGGADNASASSR
 RNYV TEKGC----THTYVNLSDNVFKQVL-----AAIEVCTDKDNANSAVNVR
 NVMV VRTG----PEHYVNANEGPYSDLL-----DTIYASTDKSTCD--SSTNA
 CWMV LDGD----EIFCDLGGEGVSVQVL-----TRLTVALGAAKGEGAQRNA
 OGSV QDGD----EIFCDLGGEAAGVQVL-----GRLTVALQPAKGGGTQTRNS
 SBWMV SDGD----EIFCDLGGEAVTQIL-----SRLTVALQSARGEGAQTRNA
 SBCMV QDGD----EIFCDLGGEAVMQII-----TRLTVSLQSAKGEQSQTRNA
 SorCSV ADGD----IIFCDLSDEGTQAM-----NRLKTVLMAVKGEGLKARNA
 PMTV LVGD----KLYVCLNETRMKTAL-----NNIIVALQTVNGEGRARRLG
 BVQ PAGD----MLFVSMSE-HLRRIM-----SNI IIALQSVRGEGRSKRLG
 BSBV TNGD----VFYVDLSEARIRKIL-----DNI IIALQTSGEGRKRLG
 BBNV VNGD----NLYADLGYLPFQNL-----NALTIVLGAVGGGRKLRNP
 CAV -----DFFYISGFKSKWNQLI-----IQMTTALSYPKSGKDTKSRT
 TMV -----SDFKVYRYNAVLDPV-----TALLGAFDT--RNRIIEVEN
 CGMMV -----AGFYAFLNGPVLRFIF-----VSLLSSTDT--RNRVIEVVD
 PCV GNLGSTNY-TEVYFVRIKSELKQKL-----LSLIAAADQ-GKNRDVEIGR
 IPCV GVLGSPTY-KEYFVRIKPELQRF-----LNLIAAADQ-GKNRDIEVGR
 BSMV GQIGLPNYLPAPKFFRLDKRTIAEL-----TRLSRLTDQPHNNDIELNR
 PoMV GQLGSPNYVSAPIFYRINRSLVGD-----TRLARITDQPSNNRDVELSR
 LyRV GVLGAANYRAPPLFVRLDSAMRANL-----IAIARMGDQPFSLSRDQELSR
 TRV -----KKVYFLLDSRANSALGVIQNASAFKRRADEKNAVAVGTNIPANPNTTVTN
 PEBV -----GEEYALLIKEANIAIAQIQAAAFKRRADEKNAVSGLLTQSAQQPTSSIQG

:

BdMoV RDVVSDG-----KFP-----AE-KKVGTTD----SAYNLHRSVA-ALQVMLSSR
 BNYVV RDVVSGN-----KAE-----SSGKTAGTNEN---SAYTLTVSLA-GLAQALRLE
 BSBMV REVVAGS-----RPE-----TSGKSVGTDES---GSYTLTTTLQ-AFNQAIRLP
 RNYV RDGAINS-----SSDAKTDKDNIIIGKYQLHQALR-RFEELLGSP
 NVMV RGVTPTI-----S-----MPNNSRSRDD-PSLSRHLRRTALS-QMEKALVNG
 CWMV KRGAAPP-----AGQ-----IETEEQGQTD---QSLAISNALG-ELMAYVSSK
 OGSV KRGVPPA-----AGQ-----VEGEEQGQSD---QTLQIANAVS-DLMNYVRTK
 SBWMV KRGAAPG-----TSQ-----VENEEQGQTD---QTLAISNAVA-ELMIFVRTK
 SBCMV MGTTPPT-----TNQ-----FEGEEQGQTD---QTLAISNALA-EFMTFIHTK
 SorCSV GRASGTG-----TQA-----QETEDTSGND---TALAIANALV-EFQTHIDSD
 PMTV PREASAN-----TGGED---SALNVAHQLA-EVDDLLTDE
 BVQ IKDGESS-----TGGED---SALNVAHQLS-ELADLLEDD

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BSBV      -KEASTT-----AGAE-----SALNVAHQLA-ELAEELMTSD
BBNV      KGESSKA-----A-----ATEQINGGSD---GQLNIAHCIM-DINQVMSDP
CAV       VDTTDTT-----FDND---VTQSFFQAIK-AMKETIMQP
TMV      QANPTTA-----E-----TLDATRRVDD---ATVAIRSAIN-NLIVELIRG
CGMMV    PSNPTTA-----E-----SLNAVVRTDD---ASTAARAEID-NLIESISKG
PCV      PNAPVVS---TGAGGNQAIVAQRGVNTVRDQQPLRD---GSLHYRYLVQ-DIELAGAEQ
PCV      PTAPTVT---NSAGGNQAIVAQRGVNAVVRTQPMRD---GALHFRYELR-DIELAVVDQ
BSMV     AKRATTNPSPPAQAPSENL-----TLRDVQPLKD---SALHYQYVLI-DLQSARLPV
PoMV     VKKLSGQPTPPPGTDNQ-M-----AIRDVQSLRD---GSLSFSYTLINELVGAQLAA
LyRV     NRPNTGT---NQQPSNAL-----VARDVQPLRD---SALHFTYDLK-DLVTSDPPV
TRV      QGSTTTTKA--NTGSTLEE-----DLYTYKFD---ASTAFHKSLT-SLENMELKS
PEBV     SSQATVVRPPRESDSAFAE-----DNFSFGKFDD---ASTAFHKARS-YLRGLRLVA

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BdMoV     ELY---YDAFRFEQKYGLKWGDP-----PLPATGENK---
BNYVV     ELM---WTRDKFEDRLKLPWTPV-----QGRSPPGQ---
BSBMV     EVL---WTRDKFEREWNLPWTPT-----RGVTPAVPRTN--
RNYV      GNL---WNRKRFETQYRLKWVDD-----RPGRSPAEEA---
NVMV      ESL---YTRTTIENKLGIVWHAP-----AGGGGNQNG---
CWMV      EYTMNECYTQDSFEAKYNLKWEGS-----S-----
OGSV      DYTMCNECYTQDSFEAKYNLKWEGS-----A-----
SBWMV     DFTMCNECYTQDSFEAKYNLKWEGS-----S-----
SBCM      DFTMCNECYTQDSFEAKFNLKWEGT-----S-----
SorCSV    LFLKNHCFTQDQFEARYNLKWSGK-----S-----
PMTV      SFLREAVFTQDKYELVNLRWAGA-----S-----
BVQ       EFLKSHVFTQDKFELTLGLKWGT-----S-----
BSBV      QFIEDACFTREKFEHEVGLRWVE-----S-----
BBNV      TILQNAVYSQSTFEEAHGLAWVYK-----PTA-----
CAV       PANKDL-FDRDSFEKFFNLWVWNP-----S-----
TMV       TGS---YNRSSFESSSGLVWVWTS-----PAT-----
CGMMV     FDV---YDRASFEEAFSVVWSEA-----TTSKA-----
PCV       -----FDRALFEETFSLNWTVV-----APPAGGGGGGAP-
PCV       -----FDQVIFEDVFKLWTPA-----QPGP-----
BSMV      -----YTRKTFERELALEWIIP-----DAEEA---
PoMV      -----YTVRRFETEFGLQWLPV-----QAQGQRD
LyRV      -----FDRRSFEAKFQLNWWAR-----APGDNA---
TRV       -----YYRRNFEEKVFGIKFPGA-----AASSSAPPASGGPIRPNP-
PEBV      -----LDQEDFEKFKLVWKEPQQQNVGTGPTVPATSSGGGKGPVGA

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* : :

D. TGB1 protein

CLUSTAL format alignment by MAFFT (v7.032b)

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BdMoV     -----
BNYVV     -----
BSBMV     -----
RNYV      -----
NVMV      -----
PoMV     MSDGLRTNHQNETPGVQSEKMELRQTTSDDTQADSGAKSHDNTSRVDETAKTDDVKE
BSMV      -----MDMTKTVEEKKTNGTDS-----VKGVFENSTIPK
LYRV     MNIFLVYN-----
PMTV      -----MESVFNGSRPH
BVQ       -----MERR-PRSRHN
BSBV      -----MEKEKLQKKER
PCV       -----
PCV       -----
IPC       -----
BBNV      -----
RCMV      -----
PVM       -----

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BdMoV -----
BNYVV -----
BSBMV -----
RNYV -----
NVMV -----
PoMV SPSGESLSGVSAVSGGTDKGEKSAVRKEAGESKESPKSVPSDGGEVKHVDTEKAKSKRK
BSMV VPTGQEMGG-----DDSSSTSKLKETLKVADQTPLSV-----DNGAKSKLD
LYRV -----
PMTV RVKKDLPDRVNP-----VNTQGSSGTTGNAFIKNNNNKTQNWKPGSGPGNRNEGDOTKNN
BVQ RKGNSTDSHSNSVWKQRVNSKVAEGSDKVASAKRVSAATRGI-----RSDSVAPKDH
BSBV NLN-----RRTNKKGVR
PCV -----MEWRRAFSCKKLE
IPCV -----MCLLLLLFLAMSWQ-----
BBNV -----AKRIFQRKVCRVFIQLNFRTSNPVKEEF
RCVMV -----
PVM -----

BdMoV -----
BNYVV -----
BSBMV -----
RNYV -----
NVMV -----
PoMV KKNKKTPEKGTSKTTSSESSAK-NVESKESKKQTKPKAVS-----PSSDTSKIASEVGS
BSMV SDRQVPGPKLATTVKEPELKNVKKSKKKRIQKPAQPS-----RPND-----L
LYRV ---TMAIDKIVKSDNRSQKQSSKKNRKHGKVVENS TNVGVPPNE-----
PMTV KSDLQQPSEV-----HPENQVRPES-----
BVQ ESDLKVPQEEELNKDHS CAVDSK GADS NCTGHKS NHSARDS-----
BSBV RLDKKNSEEKTKEDNRKSV EEDVVDGL-----
PCV EKVKNMDAQATDYLLLEKVDEQRNLENKLDKRLQNTTRKKN-----
IPCV -----RRDVLGNALDKEKKKLSRE-----
BBNV EQTPAVECDDTHRDN TSACS-----
RCVMV -----
PVM -----

BdMoV -----
BNYVV -----MVQVQRRRTGGDKGAKGNRASSAPVRSR
BSBMV -----MAPEQHKQNAS ETASGRNRSS--VRSR
RNYV -----
NVMV -----
PoMV KKATKESKKQTKDKGSAEDLNAN-TKLKAKASEQKGP T I PGTSAEASRIDLLQSSTA EK
BSMV KGGTKGSSQ-----VGENVSENYTGISKEAAKQKQKTPKSVK-----MQSNLADK
LYRV -GVTLLRRVRSVESIDEIFTSNQRTPPAAEQLPQKQKQSKPPSV-----AKK
PMTV ---STG-ESVKQQSEPHRVLEDK-----QSGKTAGSSVRIPE-EGGG---GLG---SAN
BVQ ---DTGSEGGEHEKPPVPSKVRKGTETESKTEDSNGRTPV-----NLG---SER
BSBV -----GAHESVAKDRAATCERGKSQRQRVDQETS VKEGAGVDSKLG---SDR
PCV ---KNKEKTRTWA EKYPVDYYSPEFVENFMKDMRREEFEKSEERRGHKQVRLG---SDN
IPCV --LKNKDVDRNAESDYP-----SEEKVGKRDGHDRVRLG---SDN
BBNV ---GIGSNRRKDDIDRLQSDQKVHGTSSADCNTSKRQCKHFILQTECGSLKL---PPR
RCVMV -----
PVM -----

BdMoV ---MTEWASENPHDFFSVLERNCGNAGFSWTGVRPRTITYSDLMSSGALVNLQSLLESES
BNYVV RMTQDDWSRTHPDDIFSVIEKTLVEDGYKWNVGVKPGHCDWGLKESGAI DNFRGTLEGE L
BSBMV GMSKDDWSVTHPDDVFSIIIEKTLVEDGYKWHGVKPGHCDWDKLEQSGAIKNFKGTLEGEV
RNYV --MTSEWAREHPTDVFAIFETCAREAGFTWNDVPPHVNFDSLEKSKAISNLTDLLENEV
NVMV ---MSEWAEQYPNDFFSVLESKRSLGFVYHNKCPINIGHRRLVESGLLQSLNDYLLELF
PoMV FTKN DVRR TALVNEFVAQIHKFCIEQGFPEPTGRQYMRARANL FELVGLRNLYMEHLKKT A
BSMV FKANDTRRSELINKFQQFVHETCLKSDFEYTRQYFRARSNFFEMIKLASLYDKHLKECM
LYRV HAANDKRRYEKADAFMNKIVEASRASGFQPTGQNFKRCPANLFEKCKLRALYDKHLRVLH
PMTV YLGKRQ-----LDFVAKLCVESGFKSTGKPLKRYPAEFFKSSG LLEKFDKYLSSRL
BVQ YTGKRQ-----LEIVSAICADSGFKATGKPLKRHPADFFERSGLLKEFDKYL SGR L
BSBV YAGKRQ-----LEVSRICQESGFVATGKPLKRYPEDYFLKSGLLADFDKYLSDRL

PCV FVGDDP-----LKVLSSEALKAGFQHTGKVMKRF PADVFEKSKFIGMYDRHLTTLR
IPC V FVGDDP-----LKVIAEEAVAAGFQATGKVMKRF PADVFEKSKFIGMYDRHLTALR
BBNV YQGNRE-----APVVIKICVECGFKPTGKPLKPFGRGDHFRSTLLKKFKDKYLSEKS
RCVMV -----MDVLFNVLELFCGFTRSSI-----
PVM -----MDVIVDLLYKYKFERLSN-----

. : .

BdMoV FSG-CVRSGDIAAVKSDVVS KM D-GKDWQARCG---LVTGVAGSGKSTLIKTLTLLTS--GE
BNYVV GKN-CDLTCNAAA VKLDTLQVKMSSDWTARVG---IVLGAPGVGKSTS IKNLLDKFGAK
BSBMV DSS-CSLTCNAAA I KLDIVERLDVSSDWSARVG---IVLGAPGVGKSTS I KHILD TYGSR
RNYV AKG-CKEKGDVAAIKLE NVGM--TKEYNARVG---VCVGAPGAGKTTLIKAVMSK---A
NVMV SNS-CSSMSEAMVASAVVCEFPWPDDWVCRVG---LVTGCAGSGKSRVLKEVYGD----
PoMV AKA-CNFTKDRIRRKLF L TSNHKPSVDF--LVG---IVSGVPGCGKSTLVRKLLDS---P
BSMV ARA-CTLERERLKRKLLLVRLKPAVDF--LTG---IISGVPGSGKSTIVRLLKGG---E
LYRV KDA-CDSEKERIAAKSFLHRS LRPNVDF--KVG---IVSGVAGSGKSTLIRKLCSE----
PMTV DKG-CNISQRESEVVLKNLRSKRAEQSF--LAG---AVTGVPGSGKTTLLRKVQCE--GG
BVQ DKG-CNLSKEETEIVLVHLRRKRETVPF--LAG---TISGVPGSGKTTLLRRIQTE--AG
BSBV DKG-CNLTKSETETV LKHLRQRRPQSF--LAG---SVTGVPGSGKTTLLRRIQTE--AG
PCV EKACCKKERNQIQSKLIQLRQLKPSCDF--LAG---TVSGVPGSGKSTLLKNVQKK---L
IPC V EKACCKQERD HVQSKLIQIRQLPPTCSF--LAG---TITGVPGSGKSTLLKKVQKK---L
BBNV LKGG-CNLTKKENEVVL SKLRARRPEVPF--FAG---VISGVPGSGKTTLLRKLQVE--GC
RCVMV -----RVGNPVVILAVPGAGKTTFLRRLLEDTRF-----
PVM -----KLVCPIVVHCVPGAGKSSLI RELLELDSRF-----

. * ** : : :

BdMoV GRVVLGLPNSSLLKGVFSGCPNAFLIDDLFTSEIHLQ--RYQTMVDFETKVMHCEVMCL
BNYVV HKMVLCLPFSQLEGVFAGRLDTFLVDDDFCRSVGYG--KYNTMLVDEVTRVHMCEILVL
BSBMV YKMVLC LPVKQLLDGVFSGRMDTFLIDDFSRSDYDYG--KYHTMLVDEITRVHMCEVLVL
RNYV SRVVI AVPNSTLLKNVYSGNPN AFLIDDLFSRPVEFA--KYETILIDEFTKVHVCEVLMML
NVMV -DSIILV PNKLM-LDPYRG-KRVFTVWEMLTGKLEFSVRPMRLLVDEFTRYHLGEIFFL
PoMV ISCYVALANPAT-ERDYRGTSNVM TDDLLLAKVPMS---SDLLIVDEYTLAESAEIILL
BSMV FPAVCALANPAL-MNDYSGIEGVYGLD LLLSAVPIT---SDLLI IDEYTLAESAEIILL
LYRV ADAMCVLANPRLKETDYKGSKTFTLQOVLLSIVPMT---SDIVIVDEYTLAESAEIILL
PMTV FNSIVILGNPRS-KTEFSNLPSCYTAKEIILLGIAIK---CEVLLIDEYTLTSGEILL
BVQ LNSAVILGNPRH-KVSFSNLPSCYTAKEIILLRTEAQ---FEVLLIDEYTLTSGEILL
BSBV LNSVVILANERH-KIRFTQLPACYTAKEIILLR TAIK---YDVLLIDEYTLQNGEILL
PCV KNSVCLLANKEL-KGDFAGVPSVFSVEEMLLSAVPSS---FNVMVDEYTLTQSAEILL
IPC V KNSVCLLANKEL-KGDFAGVPSVFSVEEMLLTAVPSK---FNIMLVDEYTLTQSAEILL
BBNV LNSVVILGNPNL-KSSFNSQNSYTVKELLLDLKLV---LRLFSLTNNTLASNGEILL
RCVMV IGCTFGIPDP-----HGVTRHILDARTLGPVEEG---KLVLVDEFQRGDYKAL---
PVM CAYTAGVEDQPRLSGNW-----IRKWSGQOPEGKFVVLDEYTLTTEV-----

: . : :

BdMoV CVLLGVKNLVCFGDFSQSLNYKAGSVVNYGLPVLA KSDTSKRFGKKIAGLMS---GSGCG
BNYVV AGHLGVKNVICFGDPAQGLNYKAGSAVNYNFP IIAECYASRRFGKATADLINSNGGGK-
BSBMV AGYLG IKNVICFGDPAQGINFKAGSAVNYNFPVIAECYSSRRFGVATADLINSNGGGK-
RNYV SALLRVKNILMFGDPQQGMHYRPGSFVYYNFPVLAESHASHRMPQAIGEAYN--NAMGT-
NVMV AAKYGIRNVVLFGDHFORSQRNNGSILLASIPVLAHSNVSHRIPKHTQPLLV---RFGF-
PoMV QRRVRSSLVLLVGDVAQGRSNNASNIEYLTLPVIYRKITSHRIGEETAKACS---KQGN-
BSMV QRRLRASMVLLVGDVAQ GKAT TASSIEYLTLPVIYRSETTYRLGQETASLCS---KQGN-
LYRV QRKLQATFLVLFGDVAQGNATASSLEYLQFPVVFISKTSHRLGKHTAELCK---KHGQ-
PMTV QKITNSRIVILFGDRAQGSSNTLCSPEWLQVPVIFQSLTSRRFGKATANLCR---RQGF-
BVQ QRIVRA-MVILFGDRAQGSSAYLGSPEWVQFPVIYQSDVSHRFGKSTASLCG---KQGF-
BSBV QRILEAKVVVLFGDRAQGNRTADSP EWLQIPVIYSSVKSRRFGKATADFCG---KQGF-
PCV QRKLGAKIVVLFGDREQGN TNKLTSP EWLHVPVIFSSDSSHRFGPETAKFCE---DQGF-
IPC V QRKLEAKIVVLFGDREQGN TNKLTSP EWLHVPVIFSSDSSYRFGSETAKFCG---DQGF-
BBNV QSLLGAKYLALFGDRAQGSSNTCDSP EWLNFVVFHLSRRRFGKAI AALCR---GQGL-
RCVMV -----NPYAILGDVAQ-----FCLAPNLVIEANWFKSSSHRVP SVVCDLLN---TLGF-
PVM -----PPVFALFGDPIQSNTSAVQRAD-----FVCSVSRRFGSATCGLLR---ELGW-

. ** * : * . *

BdMoV NVRGSDSVNDDVS FEDLMGKLR-DMSTVLVASEES-----QKELADCDIDSFLWSEVQGO
BNYVV PVVGNNEVKDSWTFEELCGKIL-DMSTVLVATRET-----QKFLLEDNIESILYSDAHGQ
BSBMV SVVGNNDVKDNWTFEELCGKIE-EMSTVLVATHAT-----KEFLADDGIEAVYEDAQGM
RNYV KIEPKSSQS GFEIKDLLGMIR-DKSKVLC LSEKT-----QSNLDDCGISAE LVSQVQGC


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NVMV      DIVCEGKNKGVTELCCHLYNEEIPYDYFVLAFSDKT-----ASMLVEADISQCQLVAGCQGR
PoMV      RIR-SAGRKDKLILVDYEGETE-ETEKNLAFTEET-----RDDVKDCGYDCSLVSEVQGL
BSMV      RMV-SKGGRTVITDYDGETD-GTEKNIAFTVDT-----VRDVKDCGYDCALAIQVQK
LYRV      AFEPGSPEDEIIVADYLGAAAD-TTEKNIAFTKET-----VEDLRDAGVEASLVLETQK
PMTV      DFE-GGEHEDKVVESPYEGSSP-ATDINIVFSEST-----REDLLECGIESTLVSDVQK
BVQ       DFK-GGDHEDVEEEDYEGSSSRETNDINLVVTEKT-----ANDLLSCGVSSSLVEDVQK
BSBV      DFE-GCDQEDQKLDQDFEGSSP-ETDINLALTEAT-----IEDLKEVGIKSLVKDQVGN
PCV       SLE-GRGGEDKIVKGDYEGEGE-DTEVNLCFTEET-----KADLAEVQVEAFLVSSVQGR
PCV       SLQ-GKGDEKVVVTGDYEGEGE-DTEVNLCFTEET-----KRDLAEVQVEAFLVSSVQK
BBNV      DFE-GCDKEDEC-----EAEAATKVLVTLTLLSTWLLWVLETILLSGKLDITLVYEVQGO
RCVMV     SIT--GSSVGLHILGLFESDL--RGTVITYDPEI-----CQLLTDHTCEHTSLEACAGV
PVM       NVR--SEKADLVQVSDIYTKDP--LGKVVVFSEEEV-----GCLLRSHGVEALSQEIQTGQ

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BdMoV     TFDVVEVVLYDEYDDKLCIDSNIRTVLLSRARKCNVLRFGPNIRARFESGNGF--CG-GN
BNIYV     TYDVVTIILEDEFDDAAICDPNVRVLLTRARKGGMIKMGPNIAARFKNGDFN--SR-GV
BSBMV     TYDVVTIVLKDEFDDAAICDSNVRVLLTRARKGGLLKVDPNIAARFKNGDFN--SR-GV
RNYV      EFAAVTLILEEPQDIAPFCNKSIKRVALSRAKEVLI IQATPYFKSMLCNAEFV--DPYEV
NVMV      EFDNVCLVVCCT-DLVGI-DQEELFVGLTRHKKSLRIMADEDALATLSSGELVKLDGLVS
PoMV      EYESVTLFLRNT-DRAAASDHHKRTVSMTRHKSLLIIRAQEQEIGQPFMGEKLSVSSKRP
BSMV      EFDVTLFLRNE-DRKALADKHLRLVALSRHKSLLIIRAQEQEIGQPFMGEKLSVSSKRP
LYRV      EYESVTLFIRES-DEAAMADSHLRAVALTRHKKLIIRAQEQEIGQPFMGEKLSVSSKRP
PMTV      EYKTVTLFIPDE-DREYLTAHLRSVAFSRHKFVLEIRCNPELQMLINGELT--SKQQP
BVQ       EYNSVTLFVLEC-DREKLDTHLRSVAFTRHKTLLVIRIEKSLFLQLINGELV--SDYQP
BSBV      EYDSVSLFVREE-DRAALSDELRSVAFTRHKKLIVRIPVCLMLSLFNGELN--SDYRP
PCV       TFSVSLFVREN-DKPVFSDPHLRLVAITRHRKLLSIRADPEVWVSFMFATRE---GEEV
PCV       TFSVSLFVREG-DKQAFSDPHLRLVAITRHRKLLSIRADPEVWVSFMFATRE---GEEV
PCV       TFSVSLFVREG-DKQAFSDPHLRLVAITRHRKLLSIRADPEVWVSFMFATRE---GEEV
IPCV      EFESVTLFIHER-DREAYADNHLKGVALSRAEKLLVIRCEPQLWQTLNNVTET--ANSRA
BBNV      EFESVTLFIHER-DREAYADNHLKGVALSRAEKLLVIRCEPQLWQTLNNVTET--ANSRA
RCVMV     EFEEVSLLLNGP--VIPAGDRAKFYLAATRSLRVLNIFLPIISELSI-----AGHAS
PVM       TFEVVTFVTSN---SPVINRAAAYQCMTRHRTALHILCPDATYTAA-----

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BdMoV     DSSYSGDTLREER-----
BNIYV     SKSCTGDTFCEDR-----
BSBMV     SKACTGDTFCEDR-----
RNYV      DSSCSGQTLCSNR-----
NVMV      DGNSTGPFSDPKAR-----
PoMV      NAHVYSSE-----
BSMV      NSHRYSAKPDEDHSWFKTK--
LYRV      DSHKYESSKVSADSSSAAAQ
PMTV      QTDYRGPE-----
BVQ       KTYRYGKE-----
BSBV      QTNHYGKN-----
PCV       DTHCYGEEHRPDEAE-----
IPCV      DTHCYGEEHCSHETE-----
BBNV      LTYQYGKKK-----
RCVMV     DSTT-----
PVM       -----

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E. MTR protein + BRLS1

CLUSTAL format alignment by MAFFT (v7.032b)

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CaBRLS1-1 -----DHALMAAYREIIRSDYKRYVNPDKDKIRTLVLGATDREVR----TYHHNPYFHFQ
BdMV      HRAPRNHPVLAALREVLRLQEYNATNKLKTLVVGAAASREVV----RYSSNPMVHYH
BNIYV     SRA-RNHPVLAALREVMRQEYSASCNINLTKLTLVVGAAASREVN----CYSSNPSVHYH
BSBMV     TRAPRNHPVLAALREVMRQEYAAASNINLTKLTLVIGAAASREVN----CYSSNPSVHYH
RNYV      GKPPRDHAVLAALREAIRQDYDATYGVARTSIKTLVVGAAAREVK----RYCSNPMVHYH
aHEV     PRDNWAHPV----QRVVDHDALEQYVRRRAAGP-NCLEVGAPHSIN-----RH-QASHR
sHEV     PEVLWNHPI----QVIRNELEQYCRARAG--RCLEVGAPHSIN-----DNPVNLHR
HEV_T1    PEVLWNHPI----QVIRHNELEQYCRARAG--RCLEEGAPHSIN-----DDPNVNLHR

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HEVmexico PEVFWNHPI----QRVIHNELEQYCRARSG--RCLEIGAHPRSIN-----DNPVNLHR
HEV_sar55 PEVFWNHPI----QRVIHNELELYCRARSG--RCLEIGAHPRSIN-----DNPVNVHR
DpTV G-IPTQHPVLAGHQRVAAEALHGFATRQA---SILEIGPSLHSAARLSH-----LRYHG
HasV TLPPTQHPILAGHQRVAAEVLHNFARGRS---TVLEIGPSLHSAALKLHGAPNAPVADYHG
NbetaV TKLPSTHIKLAIDLVAEKDLRRHVKNVP---TVLEIGPSVESVR--YAVQTRDKERVHG
SsRV-L SYAHAAHPS----TQAARHALELLTWKLVDPAAHTTEIGPSYSSLF----RRARPAFAHYD
RubV QMQVSDHPALHAISRYYTRRHWIEWGPKEA---LHVLDIDPSPGLLR-----

*

CaBRLS1-1 LANKEA-KDVTURLVRDILEA-----VRKNKLRKLNKVKVKN-HVALNRNLKYVNDVDDAI
BdMV FADKDS-KDLVRTTLDLLEN-----NLAAYKKNMESAER-ELMNQLKRGG-----
BNYVV FANKDS-KDLVRTTLELLHS-----ALATKYRNMESGER-ELMNNLKGGC-----
BSBMV FANKDS-KDLVRTTLELLHS-----ALATKYRNMESDETGEHMNNLKGGC-----
RNYV FSASEP-KDMNR I AIEFLKE-----STRTKIANMERQEK-ELMRALRDGG-----
aHEV CFLPPVGRDEQRWQV-APRR-----GLCNLIRRA-----
sHEV CFLKPVGRDVQRWYT-APTR-----GPAANCRRS-----
HEV_T1 CFLKPVGRDVQRWYT-APTR-----GPAANCRRS-----
HEVmexico CFLHPVGRDVQRWYT-APTR-----GPAANCRRS-----
HEV_sar55 CFLRPAGRDVQRWYT-APTR-----GPAANCRRS-----
DpTV CTKTGT-RDQARHIA-ALHS-----SFVRGVSPQFQADA-----
HasV CTKYGT-RDGSRHIT-ALES-----RSVATGRPEFKADA-----
NbetaV CTFSDA-RDNLRHNKIGYEA-----HYDRKIGP----DA-----
SsRV-L MPLLTV-RDGARRNLAMLSR-----HKTLDERETRALDA-----
RubV ----EVARVERRWVALCLHRTARKLATALAETAASEAWHADY-----

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CaBRLS1-1 AEWIKKRKIPERFLLWEETKNLFEYGVIIHD----NDALSRAQEISTFSSFKRTVNQ----
BdMV --KIVKSRVGDK-----EYEIVSRAPRLAEMDSVMEFAKSISVSKSQAKKTKSK
BNYVV --YIVKRSVENA-----VYEVVSD---KDVAEVLRYAQTVA STKKEAKK---K
BSBMV --YIVKRSTDSG-----VYEVVSD---KDVAEVLRYAKTVA STKRDQAKQ---K
RNYV --YIVTKRVENT-----NFEYERVAS---GDLENIVEIAKGLAASKRTSKQLKGM
aHEV ----LLNGVKVA-----REFCQLGF---GACSHQCEVGIALYSLH---D---
sHEV ----ALRGLPPA-----DRTYCFDGF---SGCTFAAETGIALYSLH---D---
HEV_T1 ----ALRGLPPV-----DRTYCFDGF---SGCTFAAETGVALYSLH---D---
HEVmexico ----ALRGLPPA-----DRTYCFDGF---AGCRFAAETGVALYSLH---D---
HEV_sar55 ----ALRGLPAA-----DRTYCFDGF---SGCNFPAETGIALYSLH---D---
DnTV --TIIAAGTPEF-----TECVDGV---GACAFQAOTGTSNHSTV---D---

		F	Y		
Beta flexiviridae	Carlavirus	HpLV	KGRkAgwYSmgd-vpYtYNGgshkSgG-wdsllqmwceanv---dpkY-----DsCLyQi		
		AHLV	RnReAawYaKng-tcYrYSditHqclG-WPnWIEkwaevndl---disgY-----DcLLaQr		
	Foveavirus	ASPV	KGRGAsFYSRdl-kgySytGfshvSrG-WPaFLDkflsdnki---plnfY-----ngCLVQe		
		GVA	KGREvaFYSRhs-keYstgshrSlG-wdkaLDeLivelgl---desY-----DhCLiQr		
	Unassigned	AcVA	KGRkAcFYSRhs-asYeYNGgnHqSgG-WPeeIEEMakklnl---desY-----DhCLaQv		
		Citrixvirus	ICRSV	RnRcAwFFgppT-hryghndieYhte-yypwvErIgnifgk-----f-----ntCLaQt	
	Alpha flexiviridae	Potexvirus	AltMV	KnReAffFSrdg-tpYstGshvSrG-WPaFLDqIlataelvrpiphf-----ngCLiQk	
		Mandarinivirus	CLBV	RGRkAaFitKvd-adYghNGmvYphns-WvpsLEeIiicgqg---gddf-----ncaLInf	
		Trichovirus	ChMLV	KGkksvYvtldspmvYfhNsisYpSie-atglIkdwilskae-dygvpf-----naaLVQv	
	Potyviridae	Brambyvirus	BVY	hGRtAwFFSkdptlqYghhpiyYdthp-WndeLDkylg-----gakY-----ntaLVQv	
Unassigned		LCHV1	RGRdAwFFSKsg-dayghDkvsYvvlp-WakeLDkLvdcfgd-----f-----ntaLVQr		
Closteroviridae	Ampelovirus	GLRAV3	KGRsAvFFSKlg-egyYNGgshvSsg-WPraLEdIltaiky---psvf-----DhCLVQk		
	Sadwavirus	BRpNV	RGRmAlFYSGga-fdYahDkyhYtSgG-WPevDdLakklgg-----Y-----nsCLVQk		
Secoviridae	Unassigned	BdMoV*	RaRkELFVStsggkYrhgtirrtale-fpgeLhLmvylnvlnis-t-----nscvYsk		
		PVS*	pGkrAawcRgq-idYisgairlenlG-WPrwLsqwmeiheidetyY-----nsmLaQk		
Beta flexiviridae	Carlavirus	PVM*	aGavglYtKdr-snlmwgnseIlSnG-WPrsLsiwmevsv---sqkf-----Dvavr1s		
		HipLV*	eygvvgvYSRge-vicalDheYkSlG-WPewLqLwcaandv---aqryY-----DcCLVQe		
	Foveavirus	ASPV*	nhRgvslYSRdl-sqYSSSGylqvSke-WPkLgkIfsenii---plkfyY-----kgCgnee		
	Vitivirus	GVB*	KGRkAaFYSRhs-wnYstGanHaskG-WPewsvnlaklgl---gedf-----DhCLaQi		
	Proteobacteria (out group)	E.coli K12	tnchg1gwthr-ggYLYSpidpqtNKPWPampqsfhnlcgraataagYpdfqDacLInr		
C.vibrioides		talglsgwtSda-rgYrYvdrhpetgrPWPdmpplaldlwtvlgdpetp---pDsCLVnl			

		H D	H	R	R
HpLV	YteGaaL-GYHaDDEdlFE-ggesILTLnLsGaAeFgVKCkngk---gsVhLrgppqfeMPaGFOvtHKHsVwgcsrcReSvTFR				
AHLV	YreGgaL-GFHaDDEciFE-tggsILTVNlKGrAlFsLagnvcr---kvweLndGecftMPcGFQOtkHKHsVsgcseGRiSfTFR				
ASPV	YstGhgL-smHkDDEsiYD-iNhqVLTvNysGdAIFcIEClgsg---feIpLsgppMLMPfGFQKeHRHhgikSpskGRiSLTFR				
GVA	YskGgsL-GFHaDDErCYl-pggsVvTLNlHGeAIFeVkenatgkv-qkLkLgdGDVytMgpGMQOtkHKHrVeScteGRcSvTLR				
AcVA	YEaGsgL-GYHaDDEdCY--nDpsVvTVNlKGeAvFktKctne----ltdLgaGDVLIHhkgFQKtHKHsVvSktpGRvSLTFR				
ICRSV	hdDqGarL-GYHaDDEdCYD-kdvtVaTVNLTGnatFSLKtatgt---rtwkLkpgDfLvlkpgAqgctKHaisdctnRtSLTFR				
AltMV	YQRGasL-pFHsDDEpCYD-vDhQVLTlNLTGeAePktsCkags---gsctLaengfhlSppGFQKtHKHsVvSlsaGRvSLTFR				
CLBV	YEansL-GFHRdNerY--nDpILTvtcfGegrFtLEfkdqv---tsflmtaGsfllMPkGFQKkarHsVsn-emsRvSITFR				
ChMLV	YEkdciL-GmHkDnEsCY--gNhPILTvnvsGkAvFstdc--cg---ntMeLdsGDeLLMPedFORkfrHgvKsItDGRmSvTLR				
BVY	YDgtrdL-pYHkDDEpCYDitNnPIrTVNvtGtdlcIskdkrrly-etIpmtsGtVtftPatmQEnfyHaVrNpsaGRiSITFR				
LCHV1	YtlGgyV-sWHaDDEpCYs-hddsIvTINfnGpAvFsIQsgnvY---rsfnLldrsVLIkkaG1OKiakHmVrsnfeGRvSvTLR				
GLRAV3	YKmgGgV-pFHaDDEeCyp-sDnPIlTVNlVgkAnPstKrkkgkv-mvInvasGDyflMpcGFQrthLhsVnSideGRiSLTFR				
BRpNV	YdkGayL-pFHaDDEpCYD-dndsVITVNLnGrAtFivRnkttgae-trrelhhGsILeMlpScOKlckHsVnvrDqGRvSLTFR				
BdMoV*	hsdGgn--dlwcDvEdggsdatsasvVsyegfcvPettCqwnscc-nrLpmtaGtclLLPnGfssHqYrvtdclagGtflkff				
PVS*	fpaGgtL-ecevGdgqfi-pgsnVaiaevgGsqvsIgcMagt---gqLLeLGDfLevPgpCwskHhlmccsevrqvtfiFR				
PVM*	Ysketqm-nvllpsldgie-rgagatvVNLrkcgaFiVRCAegg---dcagvdgphLLvmmgqdcigHEcyrmrqlerendvvvFl				
HipLV*	faaekdlvGsmvsaEqve--daegaLwVNLqGtLkPgmnCts----gkfeLgkEfecLevGkrSfegHsigSamctgnSLsaR				
ASPV*	YrsGdgg-siqnyDnfiFa-nsrnafTVNysGdAIFcIEClgsg---fvIrmSgppMLliPlGFrKnHrLrikSpsnCRtasTFR				
GVB*	YEedkgL-nFnaDDEpCY--tDpeVvTVNlNgnAnPhLkCgse---svVpLsdGDVLImpkGFQKtHKHAvTgtSaGRiSLTFR				
E.coli K12	YapGakL-slHqDkdepd--lraPIvsVsLglpAifGfgglkrndplkrllLehGDVvVw-gGesRlfyHgiqplkaGfhpLtid				
C.vibrioides	YrdGarm-GlHqDdead--prfPVLsLsgdtAvrIggvnrkdptrsLrLasGDVcrLlgparlaf-Hg drilpGssSLVpg				

Average BLOSUM62 score: Max: 3.0 Low: 0.5