

Supplementary Figure S1. Alignment of the complete polyprotein sequences of *Apis mellifera* solinivirus-1 (AmSV1) and classified and putative soliniviruses. GenBank accession numbers are shown, for Rosy apple aphid virus and Solenopsis invicta virus-3, the putative ORF1-ORF2 fusion products were used.

DQ286292	Rosy apple aphid virus	-----	0
OP265432	Penaeus vannamei solinivirus	-----MQSEEL-----	6
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	-----	24
KX024775	Nylanderia fulva virus 1	-----MTSEKVMRIRGERA-----GTPKIGDIME	24
KY070327	Diabrotica virgifera virgifera virus 2	-----MFNPCKLT--PKVNITSVMQTPKVATPKVATPKVNEIDPTIN-KITAILMI	52
OQ540582	Apis mellifera solinivirus-1	MSYIDMNAEKQTNAEKHTNAERHMAEKQQNA-----EKHTNAEKHMAEKHKQTKNAEMH	56
MN918666	Picornavirales [unknown host]	-----	0
MW251313	Icha Creek insect virus	-----	0
MZ822083	Apis picorna-like virus-4	-----	0
FJ528584	Solenopsis invicta virus-3	-----	0
MW314636	Myrmica rubra picorna-like virus	-----	0
OL569508	Corparats virus-2	MPYVRDLEDYE-----FWEVEPE-----PISFEVE	25
DQ286292	Rosy apple aphid virus	-----	0
OP265432	Penaeus vannamei solinivirus	-----YKLSHCVKKSCISFALYKRHSC-----	28
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	-----MRDCLKRFY-STFIGIYSALVGTSKQQNSTSNGIENSTSIGNYNS	44
KX024775	Nylanderia fulva virus 1	LNS-----FETI-----F-----	32
KY070327	Diabrotica virgifera virgifera virus 2	MQIGTILLFKTTNSIFSCLOQTY-SKFSL-Y-----	82
OQ540582	Apis mellifera solinivirus-1	MKAGKHCVSKHILSRARVLQARKY-KRKEL-NLPWNE-----	91
MN918666	Picornavirales [unknown host]	-----	0
MW251313	Icha Creek insect virus	-----	0
MZ822083	Apis picorna-like virus-4	-----	0
FJ528584	Solenopsis invicta virus-3	-----	0
MW314636	Myrmica rubra picorna-like virus	-----	0
OL569508	Corparats virus-2	VVHNTMPYFKHLQHTVKEWKGWTR-EEASFFISEWID-----	61
DQ286292	Rosy apple aphid virus	-----	0
OP265432	Penaeus vannamei solinivirus	-----TRMTPHPSNLKPLPDLDALA-----DANIQEATLEY-----FEEDFLCLQHIPS	72
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	TSNGTFVHRRPKHIFNGSGIHTRLMMYTFIMTMAMKRTMKYRQIPSSIGLFDHRTIPIS	104
KX024775	Nylanderia fulva virus 1	-----VMVPLVVAHVRSFVTRMFS-----TQFTVGGVRQ--KS	63
KY070327	Diabrotica virgifera virgifera virus 2	-----IR-----SELAIFGTFITLCV	96
OQ540582	Apis mellifera solinivirus-1	-----IR-----DKITPDAFIFILGCS	107
MN918666	Picornavirales [unknown host]	-----	0
MW251313	Icha Creek insect virus	-----MCLMI-----PQLTFVFCFV-----	15
MZ822083	Apis picorna-like virus-4	-----	0
FJ528584	Solenopsis invicta virus-3	-----	0
MW314636	Myrmica rubra picorna-like virus	-----	0
OL569508	Corparats virus-2	-----HPSFFNPKNYADFVEKSWM-----AQDFFFAFV-----	90
DQ286292	Rosy apple aphid virus	-----	0
OP265432	Penaeus vannamei solinivirus	SSDLEFLADNES-----ARALCESMDEMGEH	98
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	TIALQMYNIRWKTLPPWPKFKIRKLR-----K	132
KX024775	Nylanderia fulva virus 1	SRTLAFQPKRTGS-----VVRVKYMRNTNEMVEKVVPEQNSEPFVLD-----GVN	109
KY070327	Diabrotica virgifera virgifera virus 2	LPSVGFLSLIITAP-----IIVKKIKKTK-IQKHPLHNF-----TC	131
OQ540582	Apis mellifera solinivirus-1	I-----YPFLLPAS-----KLFERFDKRR-QMIKNFNNLQ-----NEAN	140
MN918666	Picornavirales [unknown host]	-----	0
MW251313	Icha Creek insect virus	-I-----FAALL-----P-----EYRYKIALKNRKR-EVFDDSGKDPGKGLFQ-----D	52
MZ822083	Apis picorna-like virus-4	-----	0
FJ528584	Solenopsis invicta virus-3	-----	0
MW314636	Myrmica rubra picorna-like virus	-----	0
OL569508	Corparats virus-2	-SNLGFQNLK-----P--IHFKKEKPPQYSIAIPVHENRFSILPESSGGDVNNGWKA-----S	140
DQ286292	Rosy apple aphid virus	-----	0
OP265432	Penaeus vannamei solinivirus	LCHPAVEHLDHVPCEFPPQNLSPA-----TSAW-QALLLDEHIARWAHVPLRHRT	147
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	QSES-----LIDTLKDYFISNRVDLALSILATSIQVMSTIV-----EMFRYKN-----AKQQ	181
KX024775	Nylanderia fulva virus 1	QANE-----PMSVVDTLISAAVLIGIPLSTACTISSMLVNIISMLLWEFLT-DK-----TSIK	161
KY070327	Diabrotica virgifera virgifera virus 2	EGDN-----LITDLKNFLVPMLETYALPVAYIATLASSLVTFALTQHYISTPK-----KKRT	184
OQ540582	Apis mellifera solinivirus-1	QETL-----EVKSITQFIMTCLTFALPIIYITTLTSSLIIGLITSIKTYLIMRK-----DSPK	193
MN918666	Picornavirales [unknown host]	-----	0
MW251313	Icha Creek insect virus	FFQE-----MIKHFEVTITPCFTVANFPVTAVANLVSASTMVYVFGQIIRTWS-----KSKE	105
MZ822083	Apis picorna-like virus-4	-----MECVNSLNP-SDT-----H-----H-----	14
FJ528584	Solenopsis invicta virus-3	-----	0
MW314636	Myrmica rubra picorna-like virus	-----	0
OL569508	Corparats virus-2	LSKP-----K-----VVYKKRTKKLNP-RKVNYRLKSKIKIKNIQLVHQGLLSW-----	182
DQ286292	Rosy apple aphid virus	-----	0
OP265432	Penaeus vannamei solinivirus	LARNNSTFHETCAELNLPFYFTPTVQRQSISDIILDVIKSELVDTVKESAKNFAKSVNVV	207
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	IT-----SFLKTNLI-----LSVTNLA-----MSILGLVSISEETVKAVINNLCETPEYT	227
KX024775	Nylanderia fulva virus 1	IK-----IALGSAIL-----SFVSMFL-----QL-----F-DYEPT-----EN	188
KY070327	Diabrotica virgifera virgifera virus 2	TT-----L-VVAMV-----SAFVNLV-----ST-----ALLGIAGTVT-----AEFPWQQ	218
OQ540582	Apis mellifera solinivirus-1	-V-----G-KVLLI-----NSIVNFI-----ST-----LLLGIAGVTT-----AEFPPELP	226
MN918666	Picornavirales [unknown host]	-----	0
MW251313	Icha Creek insect virus	LKHVLGAFGLSLI-----QFVNLNL-----MI-----INVEIEPE-----EVT	138
MZ822083	Apis picorna-like virus-4	-----FENYDEY-S-----QFFDNLE-----KK-----RF-----DN-----R	36
FJ528584	Solenopsis invicta virus-3	-----MSE-----	0
MW314636	Myrmica rubra picorna-like virus	-----	0
OL569508	Corparats virus-2	-----SSEVSEK-S-----RLFENII-----KD-----NKLKLEEQ-----SLP	210

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----- 0
EVTSTKTIQFV---AACDALANAVTRGKA-----A 234
TFDNFIVD-----VKARKFIGHDL---EKLIREARKNDEF--- 260
EISDVKTQFSELLTDEKVDLDGIV-----AFQEMCLKARYSPDKI--- 229
TLDTLQ---DE---IVEEIGKVEDE---KKFVYINEKKKQYVLMCKE---YKSDAF---K 263
SFSDDIQQATEL---IIEENLEPVKPSPSKREEFIKHVL-----DHQF---T 266
----- 0
EIKKA-----LEQTSNLVTDPPFKTTYASKE----- 164
-----IPQSARYQ--RREDSDSG--Q 53
-----KTQTFVQNEETHVL--DMTSD--FKSDLSLEKVT 32
----- 0
PHDKP-----C-----SSKDTYYNPEQFILEDTKSQ--FHEDDSINIGK 247

----- 0
-----VALHVASFVSHLLPFAVFVCDLA-----GILPEQGLFTFFKEKAT--EF 276
-----VVPKSPSLSMKVL-----QKRNDKWEEFNRSQAL 287
-----QKLYSSF---KVRKNVPYCLPSVNEAQ-----LVVDSKFWT--- 262
LEQ-AKKIFQSIYADFFSMDMFILPRVDPFPLIVGGKFRAPVSHNSCLVFKAMLEW--- 320
TPMQINEYFRANY-----SEDFLLPPSRAPLKLP-----QPIR-----DAKDSFDNY--- 309
-----MNCIVLPANSAPANGT-----LQVK-----DQWM--DFRY--- 28
-----EFLNHYHV---AGKDVSLPLNSPALLQRA--LNGQ---TGRNFRPCFATYS--- 208
VVINTG---LAPIVS---EDKIPSMGTGNFLEDM--IVGVISKFSNDKLLTSLVAMQI 102
SSVEQTDDLVSKEIIN-----NNDLDIKDLSFLRNL--LLSTLQYLGLIAKFVAINITLSI 84
----- 0
LVIDQNELFENHMEI-----REESPYEDPSIINNFI---KSIIMEFVSKFNFDAFVSVAIV 299

----- 0
FNPKNLS-----ELSHSATVDTDY--LFNELTSQP-VHQKLDWSNVLKPEYIFR 322
LHIRSIMQWNEEDYYAFILFHDQGMDELVSRYFNKLEINVVVMTHTPKGTAPESF--R 345
-----KEYI--IFYLGLT---ENLYNLIKANPQAPENTFTWEGAEYSGE--- 303
--P-----IWI--AAYGVVEE---HDEI-----ELWNGAKPTTF--- 348
--P-----DEFL--IIWNNTNP--RYLFSRSLIKMISPK----- 338
--P-----DWFL-AKFWDISY--EAIKLRFRVNMSSPQRSSSSWEIQPPMPNIR 73
-----DEVL-ALYWQQPV--EVVKRFRKAVKECV-----NLR 237
VSL-----LTVV-FSLWHIK-----KFSKGLLA----- 124
LSI-----LM---LLINSCA-----KF----- 98
----- 0
SQL-----LVVF-GLIWSLRR--SRINRQLKVIII----- 326

-----MSL 3
AAVVLV-----LSIFAG-----TSFAKNKNMNA-----GMLY 349
EDM-----TPTEWRIELENTAMTSPCIPSTPHVQKFFKFPILKSNMVTLENALQSMDF 399
--DPPID-----LQT-----QMDQF 316
--MDYPEESEQSDG----- 360
-----PMNEDVRTDDEPK----- 351
TVPLPSDEDTPDEYK----- 88
DDPKPKVSVVDEAYVKNVYQN-----IRQ-----RVDDY 266
----- 124
----- 98
----- 0
----- 326

SKASDLEQVKPASLWITTY-----HTIKQL-----IKEWFIKL-VET--- 39
TAINAGTTLASKATTAGSFLICSLFGI-----EMPHTLEKK--- 386
SLVSL-DEWEYVPDWHCHYLLCESNGWLEKNVSQLTNEDEKRNLOKMKDEYFYFARNKKPD 458
QIVTV-PSDGNCMFWSMLA-----SDAKELTMTNLTKLDSFNALSLTKE--- 360
-----N-MGQE--- 365
-----STWRELS-----SDEEVKA-----VKDSFKKK-KQEQA 379
-----ADWKDP-----SKLPKNA-----HIPRHAYKKT-LGRR--- 116
Q-----GVGKDPYQAI--SELGT-----IYFLVT-VKHE--- 295
-----AITLQIT-----SVISTF-----SVIFGFPLN--RKE--- 149
-----TRIVNLS-----SHILNII---TTLLGLYFQVS--SME--- 125
----- 0
-----SSFVGLC-----STIL-----YASKLSFPKK-TIKD--- 351

-----VLDPGEIFFALTAIV-NTLTGIVLSTVTLFR--- 69
-----A-----EELETKTKIT-HSDY-----ATQA---A 407
FYWPPETPIINAIVDIVKLDLTIEEGTV--KEEIVKVYHAVE-----S 499
-----EMQIV-----NTYGAWGTSMDLFWCETHYRSLY-----LAQMNGKI 398
-----KESIERINQLA-DGGD--ST--- 382
VKVTMRKPKFDLEKPNFF--IRDH-----KQNKDDWEEIA-RGMD--A--- 416
-----QTF--L-----NKVRRHWQKIK-REEP-----RPEIQSEES 144
-----SKENAKLLKQYQEV----- 309
-----MQDI--ISES--ISSSVNSKF--SLQEHINWLN-VNAR---T 181
-----IEEI-TQTF--E--NEFGTYDDDKILSHY--IKI--CNLP---N 157
-----MLNL-FKSF-----TNKNDNKIIDLSSHL-EII--QNLN---S 31
-----MENI-VRSV--LLSKKEEDVVMNDISSHK--RII--SQFR---S 385

DQ286292 Rosy apple aphid virus
OP265432 Penaeus vannamei solinivirus
MZ210029 Fushun monoleptalauta Solinvi-like virus 1
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KGTGYLMKIISGVN-----LLSTFELLIIQIARDNSFVPEHAREH-AERR 114
YEDATLKEYIVQCDDLALCKCTPETA-TLKSRTQTKRDIKAVTNLSQSASAP---MYLQ 463
RVDQFVNLVLPVKNVVDIDHLDPEQMLYIESQLSTLLRIAIGPREVIEYNDK--- 552
GHT--VY--FDGG-----MRKTGPPLKIYYPIQEHFNAPIEKKN---VPMK 439
GHD-----BQELATA-----TVDEGEKTPAEQKPLDNF----- 403
-----BQELATA-----LDSHVKVPEDVKELQAE----- 441
GED--MYETLANT-----AIWNH--EPTGF--SQS----- 168
EED--LLSFATATN-----VE--T--YALGTQGLPPKYEHLND--TEIAT 347
KRD--ILEYLSRN-----YLNRVSLPIVSFHELAKEP----- 211
RKD--VVEYISLN-----DLKYIKLPLDISFYELKNDILSKNN 194
RLE--VHNYYIYKE-----NLFLHLVKMPSCTFDELKNN---KNH 64
RLA--VRKYIFDN-----KLENSIKLPSCTFMELEDK---FDD 418

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LSEYLDYSDTEE-----V-----YA-----NTEQEAESMMVSSL 143
MVQWNEYTFPSEKDLNFASWTQDTLE-----KCMQFNTFMSVTAL-I 505
-----IRIIQQVISFYRYLRAQKLRQMEHFPMV---KQFFESISPG-L 592
GEQWYNGTKIDP--TTTDWAEAAANK--QDE--QKPV--EGVNGQSDSMKDKFDL-A 486
-----TKE--LEITEEDGKTT-----AYDEPFRISKI-I 429
-----IKE--IEDALKPKPVE--EPIPLQQENFF--EDSFVSMDSLNKF-A 480
-----VDN--MEFIELPGNTR--RVASLNLDDYVVKQDSDDELSMKMKWKI-F 212
LKQWIRGQHVVGK-----MV--REDWFDNSVVPV-V 374
ENDWIWNEYSDS--FLAAWYGKTVS--FVLEQRRIPIYVREK--QT---QHTVMRS-G 259
LHLWIFQKFTDE--FLAMWFGVQPY--RISNLRMLVIS--RQGFIPKDLNE-I 242
LLDWVFETFNDK--FLAMWFGVEVY--KLVLHRRPANIQLINQ--DFSNMKGKETYKM-V 115
NYYWIFKNFDEE--FLAMWFGVALW--KLESIRS KIPVE--L--EKQSFIDQYVVF-L 467

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STILTTLFGALLAGFGLSTKGLE-----GLTTTFRAATTTKNGVFCIKELVDNALKLI 196
P-----ERHPVSPLYRSLKAKS-----EVVRRILESR 532
QKLGAWLIVI--LLSISHKILPKFGLFDSAKFAANYMSFSKLR-----TEATKSFTEI 644
VEIFDKIFGL-LFGIYIK--TTKTNAPLRDLATSFSGLKLLK-----EGAVDTKAAV 536
DIMFSKVIAL-FASITSCIL--LEKKKITPRITIITALAEAEKVE-----GVVGDFFKEIL 479
EKIMIQVGCII-IMAIGDAF--VTKKTNLNFSIVDYLSSLKSKIN-----TIGGDLKEAI 530
KRIGLRITAI-CIYVEDTC--TTKQFSLAGLVKSLRMVDTLG-----KSTEAQEP 262
KKVISMVIGI-ITSILFAK--ATGSKLSSREIVSGISIGKSLA-----DVGDNDIEKVI 424
IEFAQRFLGI-VLSWMLHL--IDGKPFVS SVSDGIMIGNITIS-----NCSDDLKIDF 309
RKLCNMGVSV--IISFIQSK--LFDEPFKKRDCQALKDASVIS-----SPFDTLWNLI 292
KEFLFRAPGI-LTSYVSHK--VSGERFKASSFMGGIATGKDIA-----SFTGDFPDSV 165
KQLALRLFGI-TTSWILT K--IHGENFTKRDIMDGIQAKDFN-----TFSGDIIDTI 517

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AEEKYDPVY-----FERKAITELEEAQELLRLNIGAIASDNKVRDRIYTIIDKINLAL 250
QRLWSE--GGD--LCTQPYDRILAKLDSWLQTTAAAFHTPEPRYDFFADLNMAQALL 586
AELFGMETDRS--KYQKKCADMIELLNSFLAKPAYIYASDVSKISDFKAAETAEAIL 700
EKIFLEKDPK---QFIAQCEAISKKLHLYMEIPPYKMANSAATLYNEWKNYQREVETFR 592
KVVKGDPPTDE--NLKRTVTDISTELTKFNEMPTHQFALHPNRTQRFREVIDKAQIVL 535
YVLLNKETPD---SLSNQAAEFALQFNQFLEQPSHVILARSHLVAKINDTLGDYERKQ 586
NLIVGRDTHK---TFNKKAEEFRTYFNKFMEIPTFEFAATPTTVYKAKERCEEFDWKY 318
CGKGFEDVSEAAKEQEGKDLITKYCNVCNEISETEPHVFEKQPHKIKETIGPGQINLFL 484
IDTFDS--DIKK--YFEKQVTKYVDDLEKFLTEPNYFESSNNLRVYVDISDELKEIRTFI 363
SKQKDNDAEE---RFTQTILDFTSEFDNFLGIPNYKFAKNQKLVNTISKSLDACAFTI 348
TKNFFK--HDD---PILDITISKYQKDFDEFNATPTHQFMNKNRIYDIDSKLNAKCEFTI 219
TGISVN--KRS---FYRIQSEYVVKHFNFSLEIPTYDFVRNQRKIHIDINSMLEDCKFTI 571

RNA helicase
(P-loop NTPase domain)
(AmSV1: 630-750)

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TT-YRH---QDSANMRSLLATMAGELNKKLAEVESLIPTQVTAQGVYLQGERGVGKSSLC 306
KNPINDHTRAHSMILTSSYVKA-KQHLAELVK-DAAQASRPPTVVIQLVSEFGHGKSRIT 644
AEAITPEFKAISQVMNGVYTSAN-KKKRLEITSSSTLLSTARPEPIVYCFQGLAGVKTQLA 759
LN-APKEYANTVRSLSSLDAS-SNLITQITACMQHKSLEPQEPVAVLFTGTGGIGKTQAL 650
NS-MEPKIRAKFPILLQTAITTS-TVRRKNELLTTELPSPLOQREPFLVLLRGPEPVGKTELS 593
RA-LKNEDQKHFTGLHGLYAAA-SKKRFNFITSEMPILSRQEPFVLLQGGTGVGKTNLIA 644
HG-LVQEEKQKIASVYTLNATT-RTRIQQFFQTEIKQMARQEPFLILIQPGGIGKTQLA 376
NE-OPKQQSNLIALRGLYQAA-NIFKNQLLTNKMPSFVRQEPFIVCLSGPSGIGKSQLA 542
SD-YPKEQQQIIPILMSIFAAA-SKKRKNELLTSMSEFHRQEPFILLRGPGLGKITYFA 421
RD-CPKDKQTEIFPPLQGLHTAT-VKRRNEILTVMKPFARQEPFVVLFQPGGIGKTHLV 406
RS-VPRDRQHELEPLQGLYNSV-CQRNNDILQNAIEFKRQEPFCVLVTKGGIGKTRLI 277
RE-APKEYKLLPYIQLSTAV-YKRNKELLTSSIPNFKRQEPFVVLFQGGIGKTSFI 629

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MW314636 Myrmica rubra picorna-like virus
OL569508 Corparats virus-2

NYLSAYLAEVF---DWSPAVYNISPGVRFYEPYLNED-FGVLFNEFGS--TVDRDAFSVD 359
TDLHIPDVANLLGI-SPSTYFINI-SENGHWSRYLGQN-FAICDEYLK--CMSKDALFKH 699
LELAKQGLGEKLFHPVSETRIIHVTSVDKYWPRINGQP-IAFFDESASTADLERCLLWLN 818
MNLAYKVKEKLYPGMTYHEAIGTYPPSQKYWPTLHGEP-IGIYDEVASCTTFADEPLLD 709
LQLSRWFAKEILQK-DYHGSFVQITPSDKYWPPLGGQE-IALFDAAATNLDLTLDFSN 651
DEIVYRAARDILRV-SPASAAVDITPSDKYWPPLGGMKDIYKFEACATTDIEKDLDFSN 703
KLARKVCTEILKC-DPNNDIAEVTPTDKYWPSPGGHA-VAIFDEAASADLKLDFLKN 434
NYLIKFDITSVLKQIEGLNNVISINSQDKYFPPLSGQR-IAFFDEAGTVKDFSKDLFLGN 601
QHLAKRIVRELIPDGLKRDYIEVRHDDKYWPPLAGQR-VAFFDEAGTVNRNIADLLFSN 480
QQLATKCVNSFYQDH--EDDYIEISPDCKYWPPLSGQR-VAFFDEAGNLDLKLDFLKN 463
QDYLSETLKFMDNATSAHDYIEIRHDDKYWPPLSGQR-VAFFDEAGTYQNIENDLLFSN 336
QQLAGKCTTKLINDGSMRDYIEIRHDDKYWPPLAGQR-VAFFDEAGTVADIKDDLFSN 688

DQ286292 Rosy apple aphid virus
OP265432 Penaeus vannamei solinivirus
MZ210029 Fushun monoleptalauta Solinvi-like virus 1
KX024775 Nylanderia fulva virus 1
KY070327 Diabrotica virgifera virgifera virus 2
OQ540582 Apis mellifera solinivirus-1
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MW251313 Icha Creek insect virus
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ANRICSSDPNFESAGLSGKVMCQLKALFVTTNVLNPDIKELM-----PNAVSFAWDRF 414
IAETIASARFDVNSAEIAGKGVFPQSQVLFINSNQRTCTFFELS-----PDHVDALHSRI 754
IRALASPASFNCEAAAVDLKMQPCPFKVIITTTNTQLEKLRLIAEYNGMDAIVPAFSKV 878
IKSIVSAVHFNCEGAALSQKQNPQMQLHICMSSNQLEGLQKMASDQFDKSSVPSFWRR 769
LKIGICSPAYFNASAAADIAHKINPIHFQVIFATINSTFDNLAAARVTEFSDNVWAAMCRRA 711
MKGICSPAYFNACAGADVEHKTNPTAKIIVATSNITDSDMAARVSEKTDPTTQAYCRRM 763
KTSICSPVLENAAGADIAHKLNPIFYKVIIATMNTSLQNFSDRVSMYDQESMDACARRI 494
IKGICSRNFFNAAAAADIIHKTNPTFYFVIIAATNTTPDDLVKRYGATDSSSIPAMYRRM 661
IKGLCSAYFNCPAADVEHKVTPCPFHVIIATNTSLELDDIQGKYAGAFAPASVYSMWRR 540
IKSICSPAYFNCAAADIEHKISPCPFELVFATVNTDLTLQSKISSFTGQASVFPPIWRR 523
MQSICSSAYFNCPAALTKVTPCPFQVVIATNTDLYTLQGRVSSGMSANSVYFWRRC 396
IKGICSPAYFNMPAADIEHKVTPCFHILFASVNRRLDLQAKLSLAFSSDSVYPIWRR 748
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IIIKVIDPLVTDRRK-----Q-VNHFEPDFSHLSFKIYELHSDGELPKFKML 461
MTIQVFNPEWAKY-----VADCKQRGTVPPIRTHPVNRDPKRVKFCALCSFGTANE-IVSKKFL 810
RVY---SCSATEA-YGPFVLDNRNS--I-RYDSTGKFRHLTLHRMKIDSQESRQFVADQL 931
QTY---ECARPDN-MPPFDP--NN-PQ-PGDFRKDYSHIYFNKHVDVKTGTTRFLQL 820
IVI---DMTWDQKM-VGNLSKSDTLGK-DKPKKKNFSHANLSQRMD--GGKLQYKHI 764
III---QVER--VSK-HFD--PNYPEQ-DTFDAENYSHLKSQFEHR--DGKLITKQL 811
IVL---TTEWNPKAG-HHN--PNEPWS-NAYDKKNFTHLNKIKQKN--KGVYVDDKPV 544
IFI---NVSHVNEFDPTRC-----S-EQDYKSDFSHLRLNKNINDIGSNKVSILGNYV 710
LVV---DCKWAGE--TKLNL--ND-PTGHRSDFSHIEFTCEWDDSKSRMVKTEI 588
IVV---ECSWNEKELGPFNY--KN-PSGHRSDYSHIIMNYSYDDKTQRLALEKEI 573
LAI---EVEWNADLMGEFNY--RE-PTGHRSDMKHLRIKIMDQNKQRMVFSKL 446
IVI---TTEWNEQRFKGFNF-----VN-PQGYQSDFSHLKFKINQWQQTQRLAESDI 798
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-YEKL-----HINDILQILRTK-----LALETRAF-----YHRLNHFM 493
DYDNLVKFIARLIQDNDTQRSTALTITDDLDADQITQVTPAPVNYQFQPDMSRQGVAFED 870
-----STSFQDLLEALA-----WYDIKEI-----EH--953
-----TMDEVIADTVS-----RQTQKN--R-HQVEM--844
-----SVSOLKTLIQD-----AHRHECG-----EF--784
-----DLKRLMRMIED-----KENFMAN-----KH--831
-----QVKDIMEMAKQ-----REAHFSK-----DF--564
-----STAALKDMIVD-----RYGKAAT-----EF--730
-----GPEKLFNIAAK-----MYQKKYI-----EH--608
-----NFDTLFDMIRL-----RFRKKQQ-----EH--593
-----SREELLEMIRK-----RYRKMEA-----EH--466
-----SVEDIYELIRN-----RYRKMES-----DH--818
: : : :

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PEVLQKIVEAETNPV--GSYAFKYF-----GQEKVEENSSGRDFC 533
LRPVTM-IEA-KNKTVKNGALSCIFCKGGHLSCTCTQFVQGPHEAPRWQAGPVDSCVNLH 928
-----AALLRKNFY-----AKKQSKTARLHL 975
-----DKLLET-A-----ISGVNQSDSADHF 865
-----ERRIRLD-Q-----CIQESPAARHTF 805
-----RAHLA-K-----MALVKENSITHY 849
-----TNWLHLK-----NQKPESSGSKSHY 583
-----DQN-CL-N-----SMKESNTNVQHF 749
-----KRNIDLO-R-----VEKQAEHRMHY 627
-----DTKISIL-N-----NEIQRSNSKQHF 614
-----VFRLNMQ-G-----LVKQV-DQRIHY 485
-----SRVIDNM-N-----MLKQSNLHSHY 838
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ILRLQGPETGKTTL-AMKLAEKWTELTAFEGKSRKYIKQSSNLQFVPSDSTSTIYVLD 592
VFHLYGKPGFGKSHTTINHIHPALQTLTKL---HSVILDSFDEI---FETPMIVFID 979
SVCIFGLPGGKSTL-VEKILEPDLVSATTL---PIVNLSEDTII---PKHKCIFVVD 1025
VVNINGRAAAGSKRL-LEAAVSDFKVLNLY---QVVRYCDLEKRMAGGKRLKKRVILVD 920
SVVIHGRTGQGTYYT-LEQQLANLTAFAY---PLIRINNVYDIKNLPVQRSRAIVVMD 860
SMVIHGQQGQKSYF-IEYLIRNMPSAFNF---PIHYIKESDLLKFRKQTKRCILCID 904
SVVFHGRAGQKSAF-AMESFVRLSESLHF---DGFVAKSFAEL-SKLVFKKRCVLLID 637
SVVMHAGGGHKTP-L-IGQISNNLSKVLRL---PILKLFSENDINNLTQNSRSIVVID 804
TLHMHGPPGQKTPA-LLNLASKLSSLYSM---PVFVIKELRDFQQLRPFKNPSIFVFD 682
SVCLYGEPPGQKTYN-LNKLITT-----FANATNLKI-GSEEEKPSIHF 657
SCHLRGPSSAGKTPQ-LEQISKQLSINFKY---PIINEEFNQLKQ-T-YDFRIIATVD 538
CVHLHSGPQGKTPS-ILEYAKSLKRIYSM---PVKIFTSWDEVK-N-HHSNTRSYIILD 892
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DWVSSNLQESSAYVTKMNATNNDLSFIITTNVEIKRRLPWCELPTRIIMGL-IGNPYN 651
DMVLD-----DAQYLRWWSAQ-P-VSHIVVLCNMMKAKTDKWKTRKDYFRRLSKSVEDS 1033
DYLVPQADPIREKQFMDLYNNQMENNIIIIACTNKIPWRIPTGVFTFVLE-GFTIEPVYI 1084
DDIF-LNSPEIEQKYMHCYNNILANGSVIFVATNISPGYSR-----IPVIG-T-----NGY 969
DVVKENPSSLEQEAEMEMFNKLVHASIIVTVNVSPKFG-----SFTLV-G-----RDF 909
DVIRNTADPEIENAFMDIYNNRLAPCSIVVNATNVSPKFT-----IPYLV-G-----THF 953
DLLRETMIAEENILMDLYNERLHDSSVVFITNVSPKFT-----IPIFD-A-----LSI 686
DVIKIGSDLSLEKSLMDLYNNKLYPNSIILSATNLSPKYSA-----FKF-T-T-----KGI 853
DIFDNNSVELQHEFMNIYNNIMPNNISVLVSSNISSTGYSM-----KPYLN-L-----TNI 732
DYI-KDENDENCSEKFDIYNNKLPNNSVIFSAITNVYKTHF-----FPTFF-L-----TNL 706
DIFHSRNTAEELDLFMKFYNLRCADGSIFLFASNLNYSR-----IPKVS-Q-----LTL 588
DMFINQLSSENQIYLDWYNNRIIDSSIILICSNLKIYK-----LPIIR-G-----TNL 941
* : : *

YPYDMNPFKGLYPGILIGIDDLYSVNGKVKHSVTSPEYCMVVTDEKCVLTATGKKN-VG 710
 RFFKKILKE-KVPGVLRRLGIVGVKFDNNW-ESTQS-GRCFHVGSGCI-T 1079
 KQQOYLPT-YPEGLIRRVYWGQDFLFS-DTNLGNLNLICLD-NRTYQNVQQQ-LT 1135
 KIIRTSPF-INEGMVRMRVYIGSFVDLT-GSSKHGIEFAH-EEELHYIPKQDV-Q 1020
 TISRKLKP-QNEGVARRLYGKGVINGI-VMTIANIELHVE-NFRFHVVQSGSLGRF 961
 CANRKLPLF-TNEGMRGRMYVGCMDGN-YLPTNLTIEIVS-NQTTYKRDNSNLT 1005
 VPQRSLPF-NEGLIRIRAGFGKYYHGA-LAPSTGLEIRCN-MNRYSYFDQVRSIL 738
 LLLKNHFF-VNIGVTRRLGFMGAFDTG-YTPNPNLDYKVV-KSKLIPEDFI-IP 904
 YFPRTLPF-KVTGILIRRLGFCGRFDGLDGMGNAPRYCYCL-NNSFNRSPQH-N 784
 IYAFIQQF-KQVGLYRRLGFDGYTIDP-NSSVNAPIFVQ-NKFKYERQK-HE 753
 AIDRRHPF-DLPGITRRIGLGNFNAGE-VMPSYNDEIFIN-NBQQGTPEPVTY-IP 639
 AIDRRHPF-ENLSLIRTRIGLGRFANE-LVFNVYNVEFIFK-NDQAXYRIDEIS-FF 992

[illegible]

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----- PYIIVENIKKKRFISMIENRYNIVTIGRRPENELPTVDFEIKAAANK 755
----- SINDPNKADIMLMDFSDYSIENKAVGASFSTM ----- SVLKAASK 1124
----- SSQQKLRQIQVGAASMLVYKYNKAISLNDADGTGVKIQSVPTDRPNAMINIFYAESI 1127
AGVSPALFAFNMASTYRDAKDMITYKQMKWLDSSRKDYLVVYVEPTPTVDNFIKIFANRA 1130
----- CPEFEYQEGLTPQDLPNLYVTKYGAFTIEETKTSVQHGLVTKPDDCNFEIYAKSS 1133
----- LWTQDKQQGGFEKRLDLQAQVEYKGRDFDMSRTEPIHYHRTFKMDDNLLIKATRT 1101
----- YLGMTETEIRLEDLVPAFYEGYKAVILAKKDVAVRYNVLRIETGTYNLLIDESA 828
----- NHFTKFKHSICSGDIEKVVLSYQNFNELHTGLKTIYDQELTGDFNMILMAERA 989
----- SLRLRLDMLVDIVEDAYSSYKFLSMRHRDPTINIVD-ELPNAEYVFCITKPR 867
----- LKFIKIDILDKVDVNYKYVRYNFISSLKQTEIVYEYPPNLEVEDFFNMKNKF 833
----- KKRNLKFLTKPLTPNLENYVRYNMAFYKKSDDFVVEGEIPTSDSFYSQLEADSI 737
----- KNSIDSPPEOYIFDRSDYDFIKMKRDOCTIEGSRD-TIGEYDYILOSESI 1074

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DILF-----KKLSTSLG-----AASLYLKPDAEASLYVSERVISGIAEVNPDKAIRPSD 1202
GKIVTRPGLSGTANVLSDMLKPLE-EYFISNLETRFAFVS--VSRVTSYARSFVSFI 804
KNTIK-----IPADVYIQLPHIFSGE--TIDKAVVWPWKIRIDNISILVLPNMSKFLVSSQ 1278
CDVR-----LSHNYLEMNNIFIDYV-KFDKCDLPAWKLIFTRDVFACMKDRSKFSIN 1184
DVVE-----FKADPYMEKHYFLYDRA-EYACDLWLKYLDKFLVAFALMDNNKKFMIEK 1107
DDVI-----MSGDIADLSKHVFCNKS-LYDRCDLPKWLKYSISPETCSFKSNKYELFMCN 1155
NCFM-----KYNTISELDKHVFLHNS-EFDRSVANWKKLHPLISVCRGISLQQLNRLVSSY 882
SDTK-----ITTNPFDYIDNVFYSKE-KFDNSNPGWKKFFLDYLNLYKKMYDHSENFINID 1043
QETI-----LPRNIQLDQYVITISKQ-VYDSDHSHWKKMYFNSDIAKKLRKVYHKFINDT 921
HRSV-----FNNFP-ELDKYIHFKNNSYENLHFDWRMYLSPRVKRLALSVEKFITISI 887
KQVD-----FKILDCSTQKTYITKNLFSK-NATDPKWLYISDRLTAFPTDQYFEVNC 792
EKLN-----FSTDKISNTIRHLS-KLHEFDKDNSSWKKMYVTNLIETFFNNYELFELDS 1128

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FICKEVFDEITIPTEERYTTIVERVSVLLQYFKDP-TFRV-----VIQDE-KRVVYSE 855
      GDDIVFDAL-AMRKLIKNSNLSPVQIFSTRDKKQVILIRDSASGRKYTYD 1249
VKTREDLVLMKIKSYVNLQSNLVNDIVISV-----VIRDL-G-KFYLE 1319
NFTEDVLINVVRRYVDGFTALGIEP-KLLA-----DIGDQ-G-VXAFV 1224
GLDYGKIKLAIIVQRYVMGLTGQIGIAP-RFYV-----IQDGT-G-KFSFL 1147
GFSEELMYTITVRKYVNALDSGIEP-KFYV-----EIDDL-G-RLEF 1195
NFDEESIIISLIKRYSGAFAMSGLEP-RFYA-----EFRDI-G-RQFE 922
EFNTDTIFSLVQQYAMEFAKLGIPA-RFKV-----HVGDL-G-KFYLE 1083
NLSDEVVTRELRRKCAISMLEYGVQV-VMLI-----NLNL-G-RYAF 961
EVNKEIIIEELKRYVLLFGQNIPD-NMEI-----NLGEY-G-SFYI 927
GFYDLACIELKRLAIRIMSSNNIN-NIRV-----FFKDV-G-EFSVC 832
QFSDHLLIKELORIALRITFOYGISP-KIKI-----TVKNL-G-EYYLK 1168

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NGVYYYYEDKEDTR-----ISFEGYNLIINVSTPKMVFYPDFAMALNE--DRIEK 903
SEKFIITVTTTTL-----QDVSWYQ--GLPL 1272
QGVLYMDVQVQNNNTVITPQQAIVITNENADV--LRRYDYDSFFN-AFKFNILP 1371
NGKILHVGKERVVVNYCYFTSKDD-----EWFVEMFNKVMKWNLSILGHNGEHSIPT 1277
GNCVMAEVENPAKNEICLVHTD-----GT--RVAIMEEMQWQFCDPVDIYNP--QHA 1198
DGEISSDLRTETPA--LLN-FA--IVKTELYLMLFGE--HTVPVVRMIK-EP--ELAE 1244
NGVLSISKFNEGNEHQLN-LIPRIHVFEQEPRIFFMD--KTVNPGKLNGYTA--DDAF 975
NNFNFINLNT--HTNSNIHTVHQDRIILHVSNNVTECLTDVMD-YA--TWWS 1130
QGAIIYQKYNDS--NNDNDIAFCISHTSIVLNSNTNLIPLIDFVFGN-NI--NVAI 1012
NGKILHMTINIESNV--SEI--PVPTDGVVY-I--SEHKIPITLDFD-NI--NINS 974
DNLINLKLINKI--NKTNSYIAHTNSVLIYGCCTINIPIDLEIFAKT--NIAT 884
DESVIVHYTESISRV--DTASDLYLATNENGLIFDNNCKRVDISFEDVLY-CS--NIP 1222

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KFVGTLSLTITETIETIIEKYYKRAIL-NK-----VCNPFVAVATRELQL---KRMKDP 953
EA-----IIYL---MKNHQVIEEHFPLTLK-LKKKARRDRNM-----QIV 1310
AN---ITKDDLETAIRIQEAVRDQKIETDP---AYIHNLNKNWKNKETKTIVLVEALKLK 1424
EH---NLNLQETEIFV---NQFQQLK-ATQEFVNLQNVSGNLFEGKVQRAVAVK 1326
DN---SKMQLTSVIAIRFVKTPRFLNHP---SIKLLLNWQQEEIQDLAMVKSFA 1250
TL---NLSYNESIENNYIKSDTFLSSE---AYIQTHKVVVEEIASFAAAKWKLT 1295
KD---GLTFDESAILFKYRTSSEFLHP---NVVKETRIQAKEDAKVEAALIAKMK 1026
TN---KLNATAREISTFIDSIQFAQNP---HFIAPIKNYRRQKMNQDQLLARGIEVK 1181
KY---ELTLLEALEYSKFVKSSKFLSLD---HIRKFLVEKQKQDFQDWSMRKYKLT 1063
KY---NLSFDQSIALNSFKTGDSFYSNA---KVRKSLSKFVLLNLYQTKFKLYLKEAK 1025
KY---KLNVEQIREFVITYIESSEFVNPN---MITKLHNFYSQQCTRRKQQQKFKELK 935
KY---KLDIRQSKLIYAYIDSNQFQNSV---DYKNFLNNRYQQISFLTQNIREFKT 1273

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SYVRGLMRLQNNYLLKGLCGLAGVGSVALLYGVYKLIVSTMKQEKITDNANFVGST 1013
QQITNSKAFQVGF-----PIAVIGVAATAIFGIAKL-SS-KKK-----EES--- 1349
DKFTEFSGTMVGKVFSLVGLALFFVTKGVFLFGSNETAL-----QKGRKEF--- 1473
EKVSLFLETQPKIVRFLLYIFLVSGTIAVVYKLVKSFNG-DKMEQ-VAKGARKV--- 1380
EYRSFKHEPLGKVVMIETIWWGLKIIRKLTSGLGILEGKSKR---RRQAKQV--- 1303
DTIKKWKSHPIFKIVLIIFTIVATATIIIRIISFING-NSMEQR---RKGSKKGN--- 1347
DQFMFAVHPLGLITIVIVGIITSVVLLKAISAAFSGDDEQVPEK---RRTGKRAS--- 1079
QTIEGFLSGPYGKIVKVLAAILASIAVITAIV---HIREFVLEKQKQDFQDWSMRKYKLT 1216
DKVEEIKRQPFYKFLICLYSILALFLVSAVAYKIFGYFFKTRKRVNN-IC----- 1112
DKVRNFKETPIGHLISILITIFVICYASFKIYSKFSNFFSKDQAIED-QRKGEKKI--- 1080
DKLTNFFITPTGFFIRSLMEIIITLITLIL-----IMKMV--- 970
RLLIKFFGTPEGRLGEFFIVGMIFFLFSMYRVFNIGSSFLKSKRVQDD-PELEAQIF--- 1328

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PKRAMNSQSKDKRKLGVTLTEPIIENSPHQ---K-----HR----- 1048
-PKSK-----P-----SHHSDS----- 1361
-IAKFHGLKSKNQRPDLILLIDPEFICSECSNNWNWSCVHIIEKHPERQWVCYNCENK 1532
-RAS-----KANTDE-----D----- 1391
-VES-----ETSS----- 1310
-PKS-----KYDSDD-----DH----- 1359
-PKS-----RNYSDDD-----DR----- 1091
-----KYFNE-----N----- 1223
-----D-----T----- 1114
-KKI-----TNYSDSG----- 1090
-IKV-----INWFNTD-----N----- 981
-AKV-----KTWNKEK-----RDQFWSIWANRE- 1350

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-----GRII-----PNKKRV 1058
----- 1361
VNWTATPISCEYSCSWQYFMMHVLVYXNVCDDDYDKYFTDFC-FMCQGEQTSQ----- 1584
----- 1391
----- 1310
----- 1359
----- 1091
----- 1223
----- 1114
----- 1090
-FKDK-----DMII----- 989
DDYLLD-----ERSLDEQFALRKMHYVPS-----HYTDVRRRVLVGPKDSRPPLNDKV 1399

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SKRQYTSSNTSSSSSSSSNCSESSDSSDSSNLSHPSEHSIKITDNSPHTKRRGKIIPNNK 1118
-----SSSE-----SESDDEQSAPOK-SEK-----SQTR 1384
-----RVVKLRK-RAP-----GTRK 1598
-----SDDHFDPRANAR-----LAQL 1408
-ESET-----E-SEVENQSKLGSKK-----PSKK 1333
-YRRQAD-----SSDDEEDQRKSGSK-----GNPK 1385
-RREVNT-----SSDEDDYYEKRTSRK-----AAPK 1117
-----EKEAIGDRKR-R-----PKKK 1238
-----DSECIDIEQDFGK-G-----GKKR 1131
-----VQPQRKGEK-----PKKK 1103
-----YDEGNNVDEAKK-NK-----PRKK 1008
NPSEYSPTDI-----SDNEENIIGHQQLDQN-----EINY 1429

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IEQIKQPDNDQETQKEDYTKL-PHEHV-CTTCGCLFTHIHFNKNF---LHPTQYACPNY 1173
--VA---RKSKQSAPEKKERPNTKVL-----RKQKQSEPHNLKSSTKVARKKQPS 1430
--VKKVTTDDCKHQGKW---DSSSDESDF---GIQKKRQPKNKR 1637
--QARYPNHNSNEE---LQAA-----M--- 1424
--VG-QASDLDKKVQ---KKKLTKGAKPKA 1358
--SKKYDSDDKKRQC---LQEG---RKKATKKGNNPT 1415
--NRRESDDRRREF---LDSVYS---ERKKSRAKAMPN 1149
--VIHSDTEEEAVGDRKRKPKRKVIHSG---SEDEEAV---GDRK---KRGTK 1282
--NPKYYSVDEQDKGKSGRRKNPKV-YSD---IQDNF---RSRI 1167
--VTNYDSGVPQPSNVKEVEEIKLVFDPGKLLFGNDFTSEL---ETLVELEKDDDEF 1158
--TVKYDTDEDRQAPKR---P---VKK---VNPT 1034
--ILGYKHDL---KKGKKR---P---VLFDGNDTEPER---RSHKK-GKKRPIL 1468

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KCS--NYHSGHNKYSANLIQVDFISSANEPLTPNAMTKLMGEEYAPVRVSLDDFFSTLEFE 1232
EP---QKS--DKS-----ST-----KVARKLMGT 1449
PRDYSTDFDNRKN-----EKEKKRTFGQPK-----TVKDYDIDYEN 1673
---A-QADEKG-----MRV---ET-----CLLWQKRLNPE 1447
KT---GDIS-----DDDK 1368
KK---YSDDD-----RTP---QN 1428
RR---FESDD-----RKREITQN 1165
---VVHSDDD-----S-----PVRQLKIVIG 1299
STEEVSRAE-VKQ-----LAS-----LIDCKRQG 1190
T---KSKID-NKS-----MAGLRREVR-----RRRYARSKRAQ 1187
SD---ADNGKQ-----MKQ---L-----LDEFLTRQGS 1056
KNGNDTDIEKEKH-----ISGPI--SL-----TQRYQLKLQSS 1499

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ERKRVDYINQARDANDKTFYRLCKRYPGLENCIMKVHANMLTDADMI-----VNDTDL 1288
---ILEEDEVPSQSLYDFEVT-----SRNPES-VDTTI-----RL 1481
---RRKQSVLALPDMNAWSMFD-----STQD-VISR-SHKNLAM-LCMFPKGMYEADSL 1722
---LQDQSVNNQEPMSRFDNTR-----LSNNVIYPV-IHRLCH-VYMSN-----SDL 1490
---KQKQTVNMKMDMNSYDAFK-----AHIDACRKQ-ALKAMVQ-IYVLP-----DDG 1411
---CQNEDEVTLCDMNDFTPYK-----LYMQNAYLR-ARTNMLQ-VTVVY-----DDR 1471
---STKEDVLKLRDMNDHTSFL-----PIMENAFKR-ARKNLQ-MYCSN-----STA 1208
---PEREDVLTLTDMNGFDSYV-----PIIKNSWTK-TRKNMTM-AK 1342
---LEKQDVLTLCDMNDYDAYK-----KYIENAYTK-ATKNLAQ-VYMA-SDV 1233
---LEKQEVTLTCDMNGFEGGK-----PYFQIAEEK-ARKNLQ-VYMA-NNE 1230
---IQRDQVTLTDMNSYDAYK-----PYIDVAVTK-ARKNMTQ-LYFVH-----SQE 1099
---KRKQYIKDLENMNNYDSYM-----PYCENAHNK-VTKNLVQ-VYIND-----AKE 1542

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EILHKKLNKAYVQISYAGFRAYALHVGEKFLSVAHCFDGVGK---SLVLSD---GK- 1340
AENYVKV-----KGFSGNFGIILGNGFILTTLTHTVFMNTI---DSLIEIDSDTLF--- 1528
KINPSTV-----SGFLSVYALFVAENYFVTVNHALQN---NYNIFVA-EDFGVAD 1768
GDTTQED-----LKAVNYGIFVKSRLLITVAHSFDEKHD---WYWVGCDDELGEK- 1537
EILHYEP-----RGNQSCYGLIVGDDMLVTVGHVVDSVEERPGSSVYACCDPEEEA 1463
DIIDFEP-----IGKQSCYGLFLTGTMTFATVGHSVFA---AGNLVYACSDSFDKA- 1517
QILQREP-----DYNCCYGLFLGKNMLVTVGHLVDV---DMGVYVGHDDLEGF- 1253
DILTKPE-----AGKQACYGMINDKLMVTVGHYETWKQ-SGMSLHMGADLNNK- 1392
PVMNVEP-----IGQMCYALFLRGNMFEVTVGHIADNTSG-WHLLVVGCDSPFGK- 1282
NCIASKF-----SDHIVCYGLFVFKRLASVGHIVEALKCAPGYNLYAGCDQFNGK- 1281
SKLYSEP-----IGQACYGLFIRKNNLLVTVGHVARDTKRMPAYNLVVGCDSPNGV- 1150
DIINYEP-----KDLANYAVFIKKNLLVTVGHLVDQMKLYIGCRLYVGCDQFKGK- 1593

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---NYPGVVVSITR---ERDLSIIYCKELS--NL--KSARSAFVKDS--SDL----- 1380
---SAPATIHTTWE---GSDLALLKCPKATG---KALLKHWWTNDIDIKLYEGAMISP 1577
NVITLYPVKVHQENA-LKDVAFCSCT--MPKSF--KNITSNFISRKIHEDLA----- 1815
---KYKVKLTNKFVGTNRDLAMCEIISSKAPQF--SDITKHFPSPRAEMGRW----- 1583
GSFKSVRLSLIHRYP--SPDISVWYLNPKL-ANYKQPSLRKRFVYRKKIYDE----- 1512
---HCHILLYKYE--YRDLISWYIPSLK-KKFCASKIRKHFLSQYVYDD----- 1561
---HCTLLLLKYP--PRDISVYVPSVR-YAF--PDISKHFLPRHVYSEQ----- 1295
---FYKMRPVQYK--HDISVWTPIPKESLPF--KSANLFLPKRKEVYVQW----- 1436
---FYRCKLLKTYK--SPDLSFWSCD--IKQSF--PDITKFLFLTRKQMDY----- 1324
---LYKMNLVVRNRY--KRELSVWDVD--CPNDF--VDLTSFFPIKKEELYDA----- 1323
---FYKAVCRNVFK--ARDLSAWTVE-GIP-DF--PDISNLFVKKKEIYEMT----- 1193
---FYKARLLRNK--LRLSVWVEVE-RCPFDF--PDISNLFSSRDEIRDG----- 1636

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---TLGGYFMR---CGPSVTIVAGNIEYREYQEFIDGSCSNSEYRPSM----- 1422
NSSRGVDTFNGRFILEPQ-----KR---RLGQ---YH 1603
--SRKHETAFAR--YAK-----NKQLETSLGVE--FFIRKTDISYFDGSEVEE 1857
-T-TRSFHVQFFRYFGVPEAL-----NKVTVQQAHVQ--KMTAHFNNTSVKTSRV 1631
-T-VISAVLER--FGT-----NKQREYHCGDLN--FFTGPD--ACGKG--T 1548
-I-TANAVIQR--FGP-----NKTEEFHSGECT--MFRTPF--YFGKNSKK 1599
-N-VWDSVIQR--FAP-----GKKEEFQSSTFE--YVCGPT--PFGSGSTT 1333
-H-ELSAFFQR--FGS-----NKKEEFARGPLA--IQTDPT--SDGFG-GV 1473
-Q-MVNAVIGR--YAP-----NKEKIWIQGCCD--IVQPYF--STGS--GG 1360
-E-NCNTVIGR--FGM-----NKREVLVYGNCE--FIQEPF--KVDN--KG 1359
-E-GVNTALQR--FGP-----NKEEIWVQGSAAE--MISEYY--QLDK--DG 1229
-Y-MINSVICR--YGP-----NKEKIWLLGME--FVKPFM--PLTE--GG 1672

Protease domain

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---EVKLKRVGLVVTETIKKGDCGFFVARIHG---TMRIIGHNAYKTHT---VVFSGFI 1475
DERTVSDFVRSQ-IVT-RAGDCGSAYISTQKD--VFGHIFALHACLQNGR---SHGAYI 1656
AKDAFAETITFNGSKTPRSTAGDCGLPHYLVTGKLDYSNKLILGHFAGTGTGHTSQMNSSLI 1917
KADYA-MAMVEGNHAYTSFGDCGLPYFAISSQ--FQNKCVGIHCGMSGVQGTSPKGMASMV 1688
LSDYGYQLEYGTFGIKLITVYGDGCLPYACEPQA-CEQKILGIHCGMNGEYTSQGVVATI 1607
MGDYAQLSFGTSNKLITLTFGDCGLPYFCEQDPKYHDKIIGIHCMNQGLGYTSLGISCM 1659
LRDWAGCYFASTGIKVTAGDCGLPYYSIENHPILKDKIFGIHCGMNGEYTSQSAVAVI 1393
ISDFGMSFGTFTGKATTYGDCGLPYFAEPH--FNDFILGIHCGMNGEYNTTSIAALL 1531
ISEFGYVDFATIGIQITLYYGDGCLPYVAEKDF-AHDKILGLHGMNVDGYSSVGVIALI 1419
AQEFGYIDWATVDITLTTGDCGLPYICERKK-FHNKIMGLHFAGNVNHKTIGMSALI 1418
IQEFGYVDFATFDLMLTNAAGDCGLPYPAETRR-LHNRLILGIHCGMNGVYNTSIGIMALI 1288
IEQAGIMDFGIFGTPLITTYGDCGLPHLSIDKC--HQNKIIGIHCMSGTEAHPISIGVSSLI 1730

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-----SQ-----PLIDELCSVVVPNADV----- 1493
GREDLQDAMQSTPR-----RIPQSCPTPAEGV----- 1683
FKEELEEWIEGLSKKK-----NSNEPVECPGCKVVKSGDLVSLPL 1957
FLEDPEGLKNQSWG-----D-----IGVTESDSTCNICDNTS----- 1721
FEEDYAVWLKQKET-----FLEKAAQQSQCCKMA-TKKWQLLP----- 1643
FKEDVVDWEALYQKVRSSQVSSQSWNNPIVRAEADGEGPGKSPCCFED-VKITITKA----- 1714
TKEDITDWRRLGQ-----KEIIMGENACCKFH-VDPRTEKP----- 1429
YEEDIRAWSKINLK-----E-ERKVCDDFAADDTYIQUIP----- 1564
MQEDFDALD-----R-----QTACDFCSVTKTRLAP----- 1445
YKEDLVVWKGAEKQ-----SKCKFCDDVDIIIAQPPID 1451
YLEDIQWQSQFCQDV-----ISCRHCGETNVMISP----- 1319
WKEDIVEWMGDISKPL-----NKQG-SLQEPDCFQCDLPVIKRAKVS 1772

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---PS---TAVVV-----KVPIVERDYG-----SGYVEMSPM 1520
-----SHI-----EINGHEMLGTT---SQVD 1701
PEKEVCENHTIRWDEDDHNSFTCSRHLLTFLK---DTFSGSCEMNHGHEVPHSVHHPHTH 2014
--VTQDCGNIIWDSLHTFPKMSWQNHVRSYLRMFNSTHAVVFTYNNGTLWGSVKHQHTK 1779
DTTTPKGDGHVTLWNSTHSTRGSFANEFAYLITLQNKQGRYIKNSG-KLHGSIEHSHLQ 1702
FKDKPKCEGHEIWHHMHLSSTISTFVDEVMTFANQRQLRGVIKNSG-KLYGTVEHSHTQ 1773
DDHPKAKGHVNVHSEHTSTWMTFSEEIKELYLTKHPRYEGGILKNSG-IMYGTIEHSHTQ 1488
-TVKKCPDQFNVFSSQHNSSNRTFSEELAAGLEFQPGFNGVILKNSGQIAYGSVKHSHQ 1623
ASIPKCDNHEIVWNGNHNESNAKAFVELKFHDELRTSFTGMVINKSGPTLLRGVSVSHSTQ 1505
KEKYKGNHEIVWNSLHESSTPTLNEELEHYLNIFFKFTGTITIKHSGDKFYGSVSHSTQ 1511
SLTKPCDTHLAIWSPVHSSPATFSEELNGYFKLRGNFTGTQIKNSGPRFYGSVEHSHTQ 1379
KSQDKNKKHEVLEFGVDHSSPATFYREIKQFLDVNKTFTGTVLKNTGNKLGGSVEHSHTQ 1832

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EYAQEFKKC---VTDDPYMPR-----NSGL----- 1542
FLVPQKFGST---DAPRMPL--PKDAIELGRLAKTPPETTKSRKIPITQPMQMT--- 1750
CMPFYFKPEYKYAQNSSRWVK-HPTGEYSYWIYA-----QTTATISAIQNKYLYK 2063
FYADHTRWM---DDTKEGV---YPAHEVGLDHRTKD---ETTVMKFNVSMAITLQEFLLR 1829
FIPNTYTHDL---EV-PHDWLL-TTAGELEIANGME-SSQKLSMKTATITGNFADHLLR 1755
FLPNQRLELV---TS-PHGWL-I-KSTTDMGIDRLP---NTKVFVRTSALFFASFASHFSR 1824
FLPEQDPST---NHDVSPWKV-VDAKDWDWRGTG---QCELITVEIGGSSSLTKYLK 1540
FLPDETT-S---FNKEPGFKGSMTFGEYGEDSSHIPPNTKVVINKNIELVNMPSFTK- 1677
FLSGMRDET---FVVTRGWVT-TTASELGFDSPRINPNSTFSYRVVDVSYGGYLCILN- 1559
FIS-KFKTE---LVTINGWKL-STAGDCQFESNHISPTETVMYRVVDVQFNSIFKAFK- 1564
FLHNVFVRDN---VKVTNGWRT-STAEDLDMHGRIDAGETISYCVKDVFPFAIYNMFN- 1433
FIFNEFE-N---LKISNGWKT-ATASEIGFNKLHVSFKETVSYVVDQCIIESIYSTFN- 1885

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---TSIGFNLFKNYN---RMKEKH-----YT-----HELQLE--- 1569
----- 1750
LHSTKQILRSSPTRNKKTGEIQKMRREYFLIAYPDSKNGY---MELKEP 2110
-NDTIIIGFRFDGFV---RLRNDNILITTDIYVHYETNFNQSCDI----- 1870
NKYWGDDFCNFNVT---DIKSLPMVKYCIITTH-----INKFDPKSQPE 1798
LTDLGNDFRIKGCYIN---EPVTKRLMFRFTLVLFDVSVQ-KRCEIITALNTIQCINES 1880
YWERSSDFRIRAYRYK---HFKTNAFVIRMTIIVPYDKDYK-Q-EIADF---FIETEQP 1591
-KIKTSNFRILNCLSS---GEKMMKFIEI-IEFPV-----TKLESYK- 1715
NIGYASNFRIYANVYN---KG-HKRAALIK-IIIPMEVPS-----RESQFSLSK- 1604
SQPYIKNFRIIANVYE---KDGKQRTVILT-IIFVSDFNVK-----QQTVR- 1606
AISFAKNFRINIDVFI---NKENKRRALIS-LFVPADEAQK-K-QIIEYGPLLNFR- 1484
VVPHVKDFRIRINIYI---TESLKRRATIG-LYILHNSKLP-Q-----TELDLTK- 1930

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-----NE----- 1571
-----CSKVPVSTDLRYVLE----- 1765
QIGMKDRILTVKQKVVVPPCVENIEILEEPIQ-NIDNGIPWDIPFQE---GGKVSMTGS 2166
-----FSKVNLPBGDSGYILTELMPIYRGAQI-NFLNGKLNDDPFDQIKDNETVKVFGT 1923
QIY---MSALPELPFGNQVYASEVKDIITTSLM-EKQGVSEDMPIYKLVSSNETVRVIGV 1855
N-E-DTFAIEPPFPGPVYVSQAVKEIIDTATL-TRRGHPEDVPYENVDKNETVRVLGS 1936
N-D-TYVFTSNFAGPVYVPLEVNQVLQATIR-NRERKLEDPVFARVPNETVRVLGA 1647
-R-RYVFHQFNDRKEAYVCEELKEILVEAKANLENQKLEDPFVQDENNDTINIVIGV 1771
-Q-AIVPLININDEQVVHVNGDIFDVMNQHM-Q-RLRRGMLPDIAIEDIPDNETVQVIGV 1659
-Q-AIVPLINNEDEEVYVTEVDSDIFKTAIK-RKQRGILPDVPYETVEN-ETVEILGI 1660
-Q-GNIPHLPISETEEVYVSGDISDIANQYIA-RKRRGFTLPDIPFKEIKNNMTSVTGI 1539
-Q-GMIPGLTDDQETACDDIKTITGIYQK-RYQREGFPDIPYKMDNSNVQIVGI 1985

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-----N-----TCLPAAFSNRY---VTDTSSELVNGYGQP 1598
-----FDQMAKELNGKP 1777
FRYNQSHTPKNDYKRIGLST---NLPI---EKVPFDDDEKAPPDQYEKLITDNFGKK 2218
FNRFTSHVPKSPFYQTPWFDDLKSDGKPLLPKLPENDITLLTDEQIASLSTDDRDGNP 1983
FRGDKHKPNTFKMTTFFAKHIDKAFKL---EHKKFPSTDMKNIPEDLEKIVMDLNGEK 1912
FHQSQSHTPKDHYLSPFSSIVKDLPI---EKRCIYELGKIPQIQDTLARNNYDL 1992
FSQSQSHVNNHYQLSPFSPIVKDIPI---EKKPCVYDMSLVDPQEKIEVMVKNYGEK 1703
LPYNASRPPGDQSLVSPYSSLSKIPI---TKVPFNKNSLAPAEQKEKMAINTWGLL 1827
AHRNMSPLPPNSYMPPTPFHMAVGDTLGA---YKLPVRFDANNAPQEVKDRMFCRCGNP 1715
THRNMTEPPAQMKPTTFFYKLALKFNLD---HKLNVNEMKDCPCQKQDMMDVRLGQP 1716
AHRNMSQPNNAVYKVTPTFNRLQN-IQP---YKVPVRFDSNAPQEVRTDLALDRAGFP 1594
AHRNMSPLPDGKFPYTPFSLRLEDETSF---HKYPARFDGENAPESKQKMDCLFGRP 2041

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DPLWTQACKYGRNKNYDKHIFRHAVEMAL-----DYNRMTCYADKPKFKLTFEALN 1651
SHLATQIAKHG---MTPPLSIDEGCLRRATSLVAYRYVSAMAKNG--RQLSTLSLQQTFFG 1832
SARATQSIQWDDGFRDVPAAALR-----THVTEQVAYGMHEVY--AGLRVLSDHEVLH 2268
SARVTQALQWAHLLHEPDINFF-----DEVSQEFMKYVNLIIY--GKMSLLTDEQVLQ 2033
SGLATQSIQWAHNNHNPGLNLF-----KEITNEFQSKVLQYY--SNMDEMTQDEVLE 1962
CQRRTQALQWAHPNYVIDEELG-----KVIDDEFQSKTLRY--SGRLRLSDEEVLE 2042
CQRRTLSVAAHAKIGGER-HFT-----AEVGRFQKKIMQYY--SGTLTLDDEQVLE 1752
CPRRTQALQWAHAKHYPASDIR-----NYVKEQMYSKAKAYY--ADMKVCNDEFVFK 1877
DPRITQSIWAHNPFPDIELR-----KPVKSEYMANILESY--SGMNLITDHLQFLH 1765
FJ528584 Solenopsis invicta virus-3
SARITAAKNAHPITSPIDLR-----KYVLNQFRSNILEYY--ANLNLLTDKQVLS 1644
DALITQARRWAHRIVAPNPYLR-----SFAKSEYRSNLAHY--SNMSLLTDHQLH 2091

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DQ286292 Rosy apple aphid virus
OP265432 Penaeus vannamei solinivirus
MZ210029 Fushun monoleptalauta Solinvi-like virus 1
KX024775 Nylanderia fulva virus 1
KY070327 Diabrotica virgifera virgifera virus 2
OQ540582 Apis mellifera solinivirus-1
MN918666 Picornavirales [unknown host]
MW251313 Icha Creek insect virus
MZ822083 Apis picorna-like virus-4
FJ528584 Solenopsis invicta virus-3
MW314636 Myrmica rubra picorna-like virus
OL569508 Corparats virus-2

GRTE-----PFLSNVDISTSAGPYAKYFHNITKREILDTELADGKPIYRFSQNRAGQ 1704
GIKA-----KGVKVLTKLNTDTSAGFLSLYLNAKAPLDAVKV---HDDGQVE-----PTE 1880
GTGD-----GGLERLNLDSIGWTMSSLYEVKKKSDVLSV---DNLGKSVWVDFPAGR 2318
GFPPKKH---PYVDCLGSLQINASIGWSMKALFNVKRNDIFTK---DNLGLITLNNNDAAK 2088
GCSLTARPKDAPYFCGMALDQSVGFTMKELFYVQKRSIDLTV---DELBGHYKWLNEAAH 2019
GLPK---SDPDHDYFKGMELDSSIGFTMKNLKYVMKRSVDVHC---DENGXYTWNPPASA 2097
GIRY---PDDPAQFFKGMEINTSIGFTMRQLFYVTKKSDVIGC---KEDGTYFWQHNAAD 1807
GYPITH---RFRKGKMLELDSSIGFSLKSLFCVNRKSDVITC---NESGBYFWKNDNEASL 1932
YSGSGH---LRRGGLQPLEIDSSIGWTLKQIFNVTHKSDVILH---SDKGYSWKNDNECAD 1820
GYGNH---RLYGALGMEIDSSIGWTKELRYVTKKSDVINL---DSNGNYSPLNNEAAQ 1821
GYENKH---RLRNLGLQGMELDSSIGFTMKQLYTVQKSDVIDL---SATGEYSWADNEASE 1699
GYQSTH---SLGRGLDGLTDSACGWTLKQLYTVNKKSDLISV---DMKGNAYWEDNEAAQ 2146

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**RNA-dependent RNA polymerase (RdRp) from the positive-sense
single-stranded RNA [(+)ssRNA] AmSV1: 2103-2418**

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CIRNHLKTKQNLNLTATYIPCLISQDN----AKVENIEKEKAQKGVRLFNVDPAVNA 1759
LGIKTFQDANNILA-RGKDYPNATLLSIGHCKLKSSELLPAQKIEQGGLRFCVAGIESII 1939
FAKQFYQEGVELIK-NGIRPWSVFLEM-----MKMEKLLKAKQY--IGRIFCSEDIHGV 2370
NPRITQSLKNAHKKDYSPDYELR-----KYVKEQYMCNIMEYY--AGCNLLTEQQLIK 1766
WLREQFQALASVYA-RGEQYFIAFLEL-----LKMEKLLKSKRF--VGRFTFLAQDILGVL 2071
YLKQEQYQALDLSG-QGKNYVYVAYLEL-----LKMEKLLKSKRIY--TGRTFVVQDITLGLV 2149
YLKQRFQEAQVLAS-EGKRYVSIFTEM-----LKMEKLLKTKIF--RGRTFVAQDVLGVL 1859
YTQNLKFKEYKELSD-QGKDYTVCFNEL-----LKMEKLLPPHKNF--LGRFTFQVQDLIGVM 1984
FYSKSNH---LRRGGLQPLEIDSSIGWTLKQIFNVTHKSDVILH---SDKGYSWKNDNECAD 1820
YTQELLKISMEQAH-NGQRYTYAFNEL-----MKMEKLLKSKRF--VGRFTFLAQDILGVL 1873
FLQEMYHDSKQVLS-DGKRPIAFNEL-----LKMEKLLKPEKQF--LPRFTFQDQLLGLV 1751
YLKMYYYQAQELAK-QGKRYWSVFNEL-----LKAELKLLKEMW--LPRSFVADQLGLIL 2198

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ILKIMFGDWFSRAMAKSSDGYAIGQNPYTTSTETIWHRFSTKQKILNTDFKAFDKLLIT 1819
PCRSKLGFSFVAMQNELRHDLFFCIGIDFTESSYLLHRLLSVNDTIQGGDFKRFDKTMPI 1999
WGRKFMGDVFRRA---TLYDDGIGVGVDSNADFRIYHK-LVEKGLYTGDSYRKTPTVL 2427
LERYVMGYFSAKA---MRDDDYCAVGIDPYANFHDMEVE-LRRFDHVAIDYKRFDKTIPG 2197
LERYMGEFAIRA---MRDDPNCGVGVDAHDKFNRYVNY-LNHFTQWADYKRFDRITPG 2128
MERRILGMIAVRA---MKDDITCGVGTDPFKNFHQYYLQ-LSQFQNIWAGDYKRFDRITEPA 2206
MERRILGGMCIATA---YKDDPNCGIGCDPAVDNFRFFIR-MNKFSLNLAGDYKRFDRITPG 1916
MERRNLGEFSARA---MILDPTCGVGTNAYSDFKIKYLR-LRKHNFLETDGYKRFDRITVEM 2041
MERKILGEFTARA---MLWDKTCGVGINVYSDFDQLTRE-MSKFNQFTIDYSYKRFDRITPA 1929
MERWILGEFTARA---LAWDENCAVGCNYPATFHKFATK-PFKFKNFSCDYKRFDRITIPK 1930
LERNVLGEFTARA---MLWDKNCGVGINPYTFEDKLFYR-LSQHFNPFVTDGYKRFDRITIPV 1808
MQRVILGEFCARA---KLNDPNVGINPYTQFDKHANY-LMKHFNMFDTGYKRFDRITIP 2255

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ELIEAFICYG-GLSTFKNEKNPHSELMYEAISLTLIHAVHILNGSVYVNVNNGNESGTFVT 1878
ELKRAACEVVEKCYMKNPLNRYDAPARRVLYNTWCSPLYLARDLLMTTGNQPSGNAMTA 2059
WLYRIACDVLTKL-----NPHLEKEIRITVDMSSTIKHVSGRSMFYVSGGMPSGSFWTA 2481
FLIDLVDCLIGV-----NKKMEKPLKSMKKSFHRIRIQSIGNSLFETIGGMPSGSFITA 2251
CVFQVQVDMVLVKH-----NPKIGQIYSVFNSLIYRFQITGRITLSQVYGGMPSGCGLTA 2182
DVFLRISKLLQKA-----NPHMAQIKSAFNAIVYRFQVSGTTLAHVQGGMPSGCGLTA 2260
LVMLEVMQCLKRA-----NPHMANDIDSCMRNTIERLQVSGTTFEYVFGGLSGSCFSTA 1970
VAFEDMKILVRV-----NPYIQNQITSTIKAIYNRIVSVSGSVTAAGVGMPSGCVITA 2095
CVFEDICELLIGA-----NPHLKHHLNLSCKFTLVNRVQVSGNTIALVKGMPSGCIPITA 1983
CVFEDFDMILQIA-----NPHMKNEIYACFQTIIDRIQVSGNSILLVHGGMPSGCVPITA 1984
SVFDDIRDLLIEA-----NPHIKNEITSTFNSISKRIQISGTALTCTIGGMPSGCVPITA 1862
CAFDDIRDLLIEA-----NPHMANEIQVCIDCISRFQIAANTLSVYVGGMPSGCGLTA 2309

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LLNCVSVHIIFNYSFIV-C-WNKVPDYIHIKPLMKDIMSRSELAILEDKTKQVVSKDIFM 1936
TLNSIVSEIATYTCLEFRA-----D---EHNLRINTGDFMTIYIGDDVVAATKTMLMP 2109
PMNSFINRCLIIYTVYCVLFAEKFG--C---FPDWDQFTITNYYVMAYGDDIVAVATPE-RN 2535
PLNSVFNLLITFAAFVYIL-KLHG-I---DATWEDFQRLVVCRFYGGDDGVYSVHESIAK 2305
PLNSLVNDYIIFSCFASIC-SDNG-M---EWNWQLYDKNVRIRFYGGDDVYLSVSAKYS 2236
PLNSIVNDYLLFSSYVALM-RKFN-L---AFSWEHYEANKVRFYGGDDVYLSVSDSELS 2314
AFNSLNNEFLMYACFYLLG-QKFN--L---DCSWEDYEANIERLYYGGDDVLIASDAWRE 2024
TGNCFTINEYLIYTCFVLLG-NVAQ--F---DVSWSKSYNHRVRFYGGDDVIVSCSDVAK 2149
PLNSKNDYMIITAYISIC-WKNDRE---LATYARFVCLVHIFVYGGDDVIVTVSNEIKN 1918
PLNSKNDYMIITAYISIC-WKNDRE---LATYARFVCLVHIFVYGGDDVIVTVSNEIKN 1918
PLNSKNDYMIITAYISIC-WKNDRE---LATYARFVCLVHIFVYGGDDVIVTVSNEIKN 1918

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-- EEDDLIDLAASLGMECTKAK - G -- GLDDGQCNFCNSRVLVNDEVS-EQ-IVYPRLK 1986
 -- NADKLISYMSEIGLTLTSPKIDPEKDFPIEMEESRSTFHEHTS -- LVVLARLK 2166
 FFTQE-AAARIINIIRGLGVMSKDGKGNLVDPEFPMNKLISWISRYFPLQGN-YP-VIVGALK 2592
 FFRNVRILAKAVAHFLFGMNMSSANKDLKPDFTWETGNWISRYFPLFLNG-RS-VVLGALK 2363
 VFTRETVASKLVLGIFVMVIDSVSDGGVDSDFTWETGNWISRYFKRLDR-YPHFVGALK 2295
 IFTDRKISVLMVELEFGMVLDSAAKDGSVATFDNNETAWSISRFFRKIDQ-PP-FITGALK 2372
 YFTDRBISILLITQFGMVLDSAAKDTSAKDTWESASWISRFFRKLRG-PP-ITCGALK 2082
 FFDRIITLSQOMLETFGMVLDSQKDGTVVRVFTFEQASWISRYPFKLKH-YP-FFVGALK 2207
 FFNSVTVARKAKQLFGMTTIPPSRKQIGLPDEPDQISIFSRFFRKLRD-YN-FYVGALK 2097
 IFNCQTLISEEMKILFGLNMDDGSKSDIPKTEFTLISIFSRFFPLKHQEN-FYVGALK 2099
 FFLNVLISLELTKLIFGMIMTSSDKSGEGLYFESNDEASWISRFFRKLDN-YP-FYVGALK 1976
 FFLNVLISLSDLETKLIFGMEMTASSKEGKFFFTYDEASWISRFFRKADQ-PP-FYFGALK 2422

KSSIIGLLHYWFAASLDNRQVNDNLMIATLFEASLHEREFYDLSVLRDHMLVSWLEFGDITR T 2044
KSSIEALLHYHCYSLTETAVQDNRITLQAFVSYDEEYNNLDHMQILVHAWGQVLPQY 2222
KSSIANWLWHYCHETAIQIGSQSTALYAESLWKDFYFQIYADVKLGIKEFFQGVN - Y 2650
KETILSYFFKTKLEPQHLSLLEKAAEEASWEGEEFYNNVEDLTRCIDCPPLKRL - H 2421
KSSINSHFYVYVTSLDATHIASLLEAMAEALWDEEYNYNLTCEVRLAKMSPRLRA - H 2353
KSSIGANFYHYVTSDDLHIGDMLTKALFEASFWDMEYQITLTARRAISKPKALG - H 2430
KSSIEANFYHYVTSIDYSHGLSGLMTKAFYQEAASFQKYEYLLQISAIRKEICEPLRGR - F 2140
KESIFAYFYHYVSETTPSHIGDLLTTAQFESALWDDDTFFEKVQEGIKFVLEKNPNILKHNY 2267
KSSISTHFWHWDICSPKQGEQTLIAQLAESFWSESYFNINVOEQIRVAIRKVPKIR - Y 2155
KSSIQTHFYXATDDTPEHFQGVFKTKIEEAAALWEEFYFNKQISYQTEIRKPFSEK - F 2157
KSSINSHFCYVYSSLKPKHLEALFTVAWEAALWDEEYFNQINQETRIAIRKYKPNIGL - Y 2034
KSIITHFOFHYLTSLSPHMGDDYITTLIEEAAALWDEEYFNKQIRCHVHAWGQVNNKDILN - H 2481

VAFITVNYQSGKKRLKSLMLMNDFFEYQQISALA-----DRKTKESDYSDDLIRLILKTAQLLES 2098
 EM-AFSALLGKIINKTKIKREF-----KRATEKQSLRPKDPKRLDSSLC 2266
 VVLQPYEAYHDDIFHNSAIAALFQLSLTLCQE-----SDFTNSV 2689
 LALRTFNLTITQDKQNVKSL-ENQEHLEL 2449
 LTLRDLRLVQHSIMKAALPKLCDROETT-----ENLN-NEDKVRVRP 2394
 VRLIDRAVIGKEIIVFALPYSLG-S-RHQ-----QNLINWADVEVEREALTKQEV 2478
 QDITLYETMIETDTHFNYSPLLTFFQKEI-----PKSTSWADEIETGEFQSAHYL 2190
 FQYRSQHDIEREVVKMTTKS-----LHPEIATPEVPEIPIKDP-----NCLTK-S 2311
 FCFRTREFLQQQTIFEGAYLSGGVKRRHQGINLVD-----SE 2189
 FNESYKSIQKRYIM-----NGWNEFVKLEIKDLNLNLN 2190
 FNFERSRLDIQSEIFSGSVMMNKVITHG-IDLSEINKIKATSEDDWNAKCAQDTQNTSNT 2093
 FSPKSLRDIQEOFFYSALGTGLLIRNT-KDPT-DIPTGKSMHNDTLDVNDPEYSADQ 2538

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D I Q K A I S D I T N F S V V K D R A L A I Q K - - - - - Y T T T S T P P - - 2131
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 2266
- - - - - N I I R S G A L D N R L N I I L K A I N S E K - Q S V N E - - - - - F - K 2719
- - - - - P G - - - - - G - - - - - Q - - - - - L Y P D L L R E Y Y L S K Q F - K 2470
- - - - - S V P R T Q D - - - - - - - - - - - E K Y P F - - - - - Q R Y - H Q K E Y Y E Q V T K P K 2231
E - - - - - A Q P I T Q E Q V T E D N L N A T R F G Q L T K D T Q N F - - - - - I D I E S N A Y K R R V I Q S L 2527
L - - - - - N - - - - - - - - - - - Y N F F - - - - - E K P L F T K T Y K R R I M M K A T 2214
I - - - - - I - - - - - D F G V V A G - - - - - S - - - - - Q - N F F - - - - - E R K H N S Y Y R H I I R F I K 2342
L - - - - - Y - - - - - E K R I V D K - - - - - - - - - - - T R E I L L R - - - - - Y T Q T E N E - Y K L F I E R I N 2221
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 2212
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 2212
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 2216
I - - - - - S - - - - - E H O I V P O L E K T O D - - - - - K N L Y D K I L R F N N R K F R K O G R R - - - - - Y S E L N S L T 2584

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ITGSL-----VHESEMAPLTTNSNPISACLELISKLTAGTIEHFERTGPP 2177
-----PDLTLLNTGSHSTIPTCTQVIVDDPP 2178
-----MTA-----QPVYRNQNLDAKQLENL-AEKSFISLLNEAWQAGHTIKPLYDWF--QS 2167
ALRLAL-----NDQSFDDST-MEFSSVSLLNELEKQGTSPRPKYTR-LAPS 2515
S-KQSA-----MGS-NPKSYISQISQSGIITVLITWVMQ-ENAS 2461
TIYHNK-----LKD-LAMSYRKLNLLEKFKGEIGPVHISNK--R 2563
TSLDCE-----LNK-LGAYSQSKLNDLTSGSKISKPIIDVTSAGDP 2254
AYKGNDADELRLEQDKIWTQKQTNVDYR-MSHSNVGLKLNELFQSGRITKPNYSFE-- 2396
LILYKLR-----TDLITYINSEEY-KRMSFKSLHNLHFGVLRSPVDYE--A 2267
RIENEKAL-EGNFN-KESVNTVY-FKMSKAMHLEIFQGLISKLPAEYFY-N 2263
KLPEKVELE-EKY--MNRKSSYFK-IRKMSYIKLMEKFGQEVTKPELTFM--R 2164
RLPDFVAFS-AEAFASLINSLSNLLNLKSLSTOMINELFONGLISKSCPEYT--S 2637

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H - NPTYSCTVITYA - G - RPDFGGEGPSKASSKTAAY - GA 2210
QTSLPNPEPTANDLCAEESRVVHPVQVLLHPQNCESVHQVDSGKDNM - PGHAPA 2340
G - TATNCLASAA - KTG - WCQSVKSSNATGVSQSSKGAEEKL 2808
G - DISWETLHLT - FHEDNSTRPI - TVVGVRGTSSEKKGASFINA 2557
A - SAKKAKLSFK - YTND - ERAPF - EFGYGVGNSKTAKEGAASFA 2502
V - GDEWECEVST - KIA - NSEIF - IAWGRGNSKAEAEVAAASHAI 2603
N - DKTWQCNICK - NLA - TCEDLL - TAVGQCKTKAKAEKEHASLYL 2294
Q - KEFWHCTVTCC - YDS - -RRRI - CCEGRGNSKAEAKEGAASFA 2434
I - GLDWSCKIEVL - LIS - SKRTL - TGIGVSKTIAKEFAEAMT 2307
G - KMWDCNITFR - RSK - DLLPLF - TFSGSGTITKACAREGAEEA 2303
F - LEUEWCEISK - DTG - KDRQY - NVSGQGNCKAVAREQAAAGI 2204
I - OEKWICTITSV - ROS - DNNISI - KGIGKGVTKKAAEEAEERF 2677

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LRQYLEDHIV--CNAACED-----QRTALQKIRKV-----AITAFSFIYED 2250
LPKGN-----PREFPIPGSRQV-DLSSAYAAITPP-----2378
WYLLFPEDKAGTFRQSLLSQRVRFASV-----AGTLTTAQAM-----2846
LKIIGKVPVAVF-----LNGRKKDSAEI-----2579
YCALFV-----KN-----PQRRADLRADK-LQA-----F-----2525
L-----2604
VSKVDPTTKTLVVQKTLNLDNMKECDVPPHVLGQSLSDN-ILAGRDVELTIDHFDKEW 2353
LQQIPITSSR-TETNTDSDQDGRITSNQ---PIPAIRKKIVLQGREKEINPP---2482
CSQLSKLEN-----2316
LVLFSSQDEI-VR-----QINDI-----2320
VELYNSAR-----ISDP-----2216
LEEYVQIK-----LQKQ-----2689

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HINAAIRNAGGKKYIIVIGKR-LADDTVEQVDGFYK-----FHRNGNCYFLSSII 2299
-----EQETR-----ITSRVSKG-GCLPLP 2397
-----TFDERH-----ESLIEQFWYLVPL- 2865
-----TGVNQSDL-----N-----VCRFCGNY- 2596
-----RRITYE-----NTLDKHGDKKVVAML 2545
-----IKMGYL-----2610
ERNNAISLNINGEYEAKESTIKEQKTVYELLDIAYSAIRSDVQEYVDSLSSLGYYIVDI- 2412
-----RSTLSGSSYDNF-----YN-PSS 2499
-----ERSR-----FI-----2322
-----QSDCK-----FC-----2327
-----NTSVR-----F-----2222
-----SY-----2691

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EKL-----GRKTAQ-----2309
GSSTRGS-----DS--ARSNMPASSPRSA 2419
-----IYL-----LYLVIRKTIKYVSINGNEIK--YDQELP-VHYMSQ 2900
-----YDESRYTPQGCPCNKENRPNADYWEDL--TIPIRGGERPMTFRE-----2638
DKCVATSPAIPTTCSCK-----CNRID--ER-----2569
-----K-----2611
GK-PQHYPPLPQVKSIVLDLLVDQKISYFDITHYSEYIEIAGNEKKTYRQAI-ILPREE 2470
SRSDVHYPTVITP-----SI--ERS-----VRSN 2521
-KQ-----2324
-KKMIRY-----2333
-M-----2223
-----2691

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-----CYSYYPGVSFDSSTNEVTL-----DVHASTSNYSLR--EDFEKDYDTD 2350
PLN-SKQRRRLKRRRAERAAEAENATK-----QSSAELDPAPRRFTPSPAE-RQR 2467
-----KEFNRLRRSHYLRKQLAQIAKQQHNRQSDLRKQAGDMNV- 2943
-----IDFPRLAME--IDYV--PTKLTREEMYEIEDLLDSVAGENQND 2678
-----TPTRNSKFRVKSKMALN-----NFRQEMNVT- 2595
-----QQKKMAPQ--MRANLN-----HFVQEMNVA- 2634
VFSTLLDRITIAQIRAPPLDLD-----QMTQEMNV- 2500
-----D--FQRLDFNAVEQE-----RALRERNQSKRRRIDLDGRYQKE 2557
-----SMFME-----P--QMNVS- 2336
-----KRLLSGVSIQ-----R--QMNVS- 2349
-----RQMLLKTFE-----R--QMNVS- 2239
-----RTLFPRLGLK-----L--ESNIS- 2707

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DHLIIANSADKPT-----L-GVMANDDPVTPMPTSVMD- -DK 2386
---LMKRTGALPTAWDKLRVTPLPESPAEKQSLGAPSADAVPQMESGAPAGNGPAPAV 2524
-----GLQLAT-----PAPSGVDVNTTGTSTIFTNRMIGNT 2974
---IPLSTEGNVPT-----E-AQTEPTVTSGNMLWTNVGGKFG 2713
-----PQSVGAIPQ-----APMTQTDVSVVTDGSLFTNTNAPS 2629
-----PQVSNVVPK-----APFLASDVSVVGDAGLYTNTDAPAI 2668
-----AGTVGKIPT-----APMTQTDVSVVADGSLYNTNTVAPSP 2534
-----MMLTPHMGVTT-----GQISSLDPTVVPPQIQATNTTTFPS 2593
-----ASLEHKTIG-----APMIAPDSVTTPDSGLVTNTMTSP 2370
-----KITENHVP- -AGMMATDPSVAPDSGIATNTQTPSI 2383
-----KGVHEAVPG-----ARMVSTDPSISPDGTGIAVNTVSP 2273
-----AGVEHATPG-----APMISADPSIAPDTGIAVNTMTSP 2741

Jelly-roll fold
capsid protein domain
AmSV1: 2705-2864

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ALYQPIIMNRSAPNNSWLRAGGITFNIYDLVYNQFVGC-NKQITVGDGTAAGTILAQIPY 2445
GPVHPSSLQGMIT-----LAG--TAQNLNLSAMEFV--MGTPLOIDPSIAAAWTVKEISL 2576
RLT-----LNNNTTSVINNPAGAGAPYDYLTKIHGIYS--LHLSGTLSSTTASGAEEVFRVSL 3028
YMM-----TNSSESLINPRGTGAPFNLYRSLFEIYR--FEIRTTINGSIARGSLLAIVSL 2767
AKI-----INSVGIALDNPAAGSAPFNKHVSVMYNIYQRWEAKNTVLSPALPSGTIVIRISL 2685
AQD-----VNHTAIALDNPAAGTGAAFSKHQSCYQIYQNWDEKNTTVNPSMANGTEIMRLTL 2724
ARV-----MNSLGIALDNPAAGTGAFFNKHVAVYNIYQRWESKNTSISPSMSQGTETVIRISL 2590
VPD-----FNPGAVALNNPAGTGAPFDKKEVYNIYQEWESKNTSVNGTVPRGAIVCRISL 2649
CRV-----INPGATSLDNPAAGTGAAFDKRDSIYGIYQRWEKSAIVNYSGLQEGAEVVIRISL 2426
SRV-----LNPIARALDNPAAGTGAPFDKHTYVYVNFTRWPEMSTVVNKSIAAGAEVFKISL 2439
VRV-----INPGATSLDNPAAGSAAFDKRDSIYRVYRWSEKNTSINGSLTQGAEEVIRISL 2329
ARV-----INPLAQALDNPAAGTGAAFDKKDAIYGIYRWTERQGTINGSLNQGAEEVFRISL 2797

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DPVDNPFANGYIQLVLLHGRMTGDWMIKTCPGNPGMQCSIGVGWSPSK-IAETVPM 2504
HESKWQN--PVARLFYQLHKNRSPALDIKVEVTGAVFVDGKLATCIVYGGPANGKYS 2634
DPATWPE--E-LQTYVNMHESICPDIDISVMINGAAGALGTMKIGWVPDA-DAMNKYSLA 3084
NPANYEP--Y-QALWAKLHRYFSPQRCLVNLAGAAGSIGVWTFSWHPDE---EDLRF 2820
DPKELPQ--M-IRSYIDFHESEFIPALDIVIAAGAGTIGWIAATGWVKDA-SSTKRYTLQ 2741
DPKTPWK--R-IVDYIMFHDILPALDIVIAGAGTIGWIKSGWVKDA-SSTKRYTSG 2780
DPRDLDP--M-IQSYMQFHDSEFIPALDIVIAGAGTIGWIAATGWVKDA-SPEKKYSL 2646
DPQYYPR--K-ILEYILFHQQIIEIEVGLAIGGAAGTISWLRIGWVQDA-A-KEKITID 2704
DPKTLPA--R-IREYVNFHEYIIPALDIVIAGAGTIGWIKSGWVPDD---TLKYGLD 2480
DPNKLKP--R-ILQYIFHKTIIPQIEVQILIGGAAGTIGWIKSGWVPDA-STAKRYSLD 2495
DPRSLPK--R-IREYIDFHNALIPQIDVQILIGGAAGTIGWIKSGWVPDD---AMKVTL 2383
NPQTLPQ--R-IREYIAFHQSLIPQIDVQILIGGAAGTIGWIKSGWVPDD---SKTYTLD 2851

VITKYAFFTTGVSSEWSHTIVMTDARQNNFYRTIQFNSKKEVEDVANMPHIVIFCETPP 2564
ELQOHYLTATYATNENNTVVTTLTDRRTSHFARTD-E---YDREPESQYKLLVVFVAVPI 2689
DLQSIASDTVTNFQTSVFEGISDLRRANQYRKT-----VGDEPFPPGVALISLFPV 3136
DIDEVTSWTTNLNNHQCMEFILLDDARIQQMRPTAN---PTMNGTEKFFCIAMVQDEPA 2876
DLQGVAMEENMNGTQIKIKILTDDRVRMGLYRRV-----TDDEPFPPGIIMVDAV 2793
DLQQIESKVVNMNGTQVFMKFLINDVRRSGLYRLI-----ENDPEYPGIVFVIESAV 2832
DLQQVSLLEANMNGTQVIRVLLNDIRRGGLYRKM-----LQDPEFPYGIIMMIDHAV 2698
EIQQISMQQINMNGTMTTFFLRDAMRRSFWRV-----KNDPDPYPGIVIMVAPHA 2756
DLQAVACETVNMNGTITMCTLLTDNRQYGMRYKV-----QNDSEFPWALIMVDHPA 2532
DLQVASETINLNTITMSMIINDSRNGMFRIT-----KSDPEFPWPGIVCLVEHPI 2547
DLQLVAEEVNLNLTITMCTMLNDNRSGLYRLV-----KSDPEFPWALVMDHPA 2435
DLQLVAEEVNLNLTITMCTMLNDNRSGMYRVV-----DNDPEFPWALIMIDHPA 2903

TSVYTEKSTYTLFFSKLCSSEDLMFNPSIKPFVLA---DPQQSVTYD-----SK 2611
YNTSGADTPRIRIRVGDRLHPSSIFTMPNLPLVRSIT-----SSGTGMH 2733
GNVGKTGTIEFGQVYMKLGANCFFMNPKSVTITK-----VN 3173
TNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----SGGGGVF 2919
TNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----AT 2831
TNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----SV 2870
TNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----PT 2736
TNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----DS 2794
LNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----EVG 2571
TNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----DGT 2474
LNVQRNDVSYPIQIRTKLGNPAVFVTPSRAGIEGG-----SSG 2942

KGY-----SLNFLAPQL---STR---L-----RGAS-----LGNIFGLAY 2641
TTIPHA---YH-HLKIVIDGAYYISSNER--RHLGPDINGYL---TGPCVPVDE 2779
EKINLDHEITDEIDFLVGSAGIATATD-----QTYDTGVTA---KNAIPGS 3220
NSISLSNYIPT-NFDTVMVGDAGVQAYS---VVSLED-RGLTGNFDFNSDEGNVYVGR 2974
TSFDLGSYFYDTHVDALIGSSAVADDPE--VVVHFD-SGPNVVDKFSVFGHNCVAAIY- 2887
IDFFIGSYFYDDAVDMLVGSVVPNKQPT--ENDIDD-QGWLKGDFQPTFGANVIGMSW 2927
QSFNLGSYFYDDVDALVASSALTSSPTA--TTTFPD-CGYLHDKFQPEYLQSNITYVAY 2793
TAIDLEPLLGGVKPDLVETVQAQPV-LV---KTVEFFD-CGFTGTGTFQIPRTANIHAMNA 2850
DLKSLKFFLNASTVDLIGSSKILNEGIS--LLEYFE-CGWLSDGNPPTDTDNHCNHL 2628
DELDLSKYPNQLIDLLICNSYVFNVSVDLSTYFN-LNFS-----IHNTIDVVV 2657
TRIALSGILQGGSIDLLIGTPNPNCRPTS--TKAYFD-CGMYTQGQFQEFTRDNLCSVGM 2531
TIIDLNRYLKLSFDLLIGTSSICDNVQV--PHSFPD-CGLTGDGFKPKFSKENWCGTFQ 2999

TDYIY-----VHIEGDK-----LT-----D--- 2656
RPHAG-----YVVDGSLADE-ISNLKQED--FTWYQDPDSNKNVLTYSYTHPK 3268
FNAEGAYRFKAVHYGSEPTFTWKPVVDVKIVPETARFDREE-----HGLSVSQ 3025
KQLDGATKAVPTI-SNDTPPSA--D---YLKEIED--MDKFE-----GGPNAQ 2927
NEDMLDAPNKKLV-IVTELPELTPE--IITDFGA-FKEMD-----DDLTTQI 2970
NALAKGKTATQLF-TTETTPGAT---LLAQIDS--LTFTF-----SASDQLS 2834
LECHF-----T-----SNVLE--NVTQENV---DSAP-----EGSLKGF 2879
RRTNY-----I-VPTDN-LSKI-----TLGKTIA-----QYSTQKF 2657
SKRPY-----T-LALFE--TESQINSASVWRGLDT-----QLSVFIQ 2691
SWTSG-----V-IVT-R-EAAYE--V-K-YPLTIKG-----TGTGERY 2562
QAGTV-----I-YTTLS-QSAFQ--T-QVDSGIIKD-FD-----YASVSSI 3035

--LIFQNALTNIPDFTTIS-LF-QHEISSTETNYTFQFCVGYA-----SYY----- 2699
--THFYFFYGAMTDE-ASAIYQDELSVYDASDDIMSFEEAETG----- 2837
AIRSYLLYAFGVIPDMLPA---NQVIDLQGLCNIAIDLGFS-----QPITQCVL 3317
SPISHYIAYGEVPTIYDGGV--EDPFSIMPGTIYIPPTDVTFSKGGRSIFGRIMRVMT 3083
LPPNKLIFSFGTEAPLE--DFHYVNAEPTLLGSTYALSG-AVRVG-IFK---YNITSLVA 2980
LPPNKLIFSFGTEAPLE--FMDYNGKDMPGATVYKTF-SVEIG-NLK---YGNSTTFI 3023
LPPNKLIFSFGTEAPLE--HVVYEEETPTIQTGTVYIISD-TTRLG-LGF---YNCRTLLA 2887
QHVWQIIFSFGTEAPLE--QVFNHLSHDNANLIPASQATEFVSIDITMG-SII---YQNTQLWV 2935
YKFPSSIDFAYGQIPSVFERMTIYPAKF-GSFSNYTIQPLFTING-VFI---YKCTTMV 2712
EKFPTVREAYNKVTTVHDDK---TPNFDGTVYKPVVDVKEHAYG-T---YELTMMWL 2742
YRPSYFVAYGEVDASICEYTYRGEDPPPTGTYYTIPKFTIKFG-SMR---LSCQVNA 2618
TIPGGIVFGYNGIPEAYTGMSTRVSDALQFNSTKYTIKRYTFRSSGLE---YACSQIEM 3092

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QFNGYFVVQSNSSGNFLPLIKD-----YTSSS-----E-YADIRRTI----- 2735
 -----DILDV----- 2842
 YEHGYILLQPVGTPTITTSGLNVRVVDYEKDPYIYGWVANITNVSQTTVCGYKENACCLP 3377
 FEKGLIAETKIGNLAGINDI-----TWVVASQ-----KTG 3114
 QANGCYIVMEIDSSVVVSTKHGK-----LVVYNSCNTNTNFDDQ--TD----- 3020
 YFEGCVIMLEARYALHRTIENIPDC-----IAVVYLDSSVKKNTFFFYQDTQQTIN 3074
 QASGCIIVAEIDHSVIEQSG-----KRYISYNKMNT-----DVV- 2921
 YPNGISLKFNSLPKDFANGIRGIPSV-----RFSD-LNIG-----AWP 2972
 FESGCIHFSIDGNYWEIT-VS-----GSEITTIQ-----AYE 2745
 TSYGLVMEWSLDES RVFYGTYKTD-----NGRRNLIDG-----NTP 2779
 FENGIVMVFRCNDVQRIHCQIES-----NGDITMLGD-----AQD 2653
 FESGCIIMYFLLDNVVYINISYNNNT-----QFTL-TSKGDRNSFGQ-----TIN 3136

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-----YDWNPNPYVEDDYCTFLKVNQVNMFKIEKPVSCVAH-TTFSG-----SK-- 2778
 -----BQFNGVIKYGTYADTRPCY 2861
 -----YG-----FELS-----ELPVQLASNEFLNNFDA----- 3400
 SVIYYLWDG-----VVNG-----ANPV-----SDLFGLSGGP-----SSL 3145
 I-----DH-----AIVYDTR----- 3030
 ISTTYYNWRQTHH-----LFPDPIG----- 3095
 -----TQSDLD-----SFGPDVG----- 2934
 PD-SYYWGTYNMLVAK-----TTDANVVYNKTPLDFFSLNV-FKGGFIYSTY--FGGK 2794
 IARSDHCFIVS-SPD-----LLSDDKAYYNNPIGAKGGKLVDAQIYRIFKTESGGY 2831
 IT--DYVFLYT-VDKA-----E-----QFVNPLDFTSA----- 2678
 VA-----FLQNYMDPG-----KLPISMIDLSTPIGF----- 3162

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-----SEWVFVPSLEVIE--FIKDRVKFR-----ITKLL--LPDNNDRKMSFK 2818
 WVRTRATFLAVQ-----PKNGQQYNT-----T-----VR 2886
 -RKQNVQ-HNWLQ-----GTGYVENGFKYCSQSTDNSFQPVWP-NSSDTLEDIKIP 3449
 AGNGNVVPTGWPVTGGVTGFQVGD-----FARW----- 3172
 -KEVEVN-WIFQEFSSHKIASG-----NPFRRPVRIDQTESIYVT 3068
 -KIGNLG-PDWKEL-----VD 3109
 -QDTKVS-ILWRDPNHNRDVVG-----DDLVRHPIATT-THYVV 2971
 WVPQNDIYICWTGSEWGRHVGGTSYVP-NN-----NTNGQFTTCTPTT----- 3018
 WQALASY-----INLEPIDN-IDGF-----TPRKKWF-----LP 2823
 RSDPFVPETWYP--SETPYNAD----- 2851
 -----TPSYWWSITPTNTPISHNNQNLMPR-----TRPKDFYFAPVY----- 2715
 -----QPLTCWEYRSSSQIFSITSSV--L-----TFSRRYYIAVARDDTR-ISFD 3204

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NLKSFDLNYPPINQIEKALNDVPLANLPQGIQVVFSSYPQ--LSVNNPFRGRQ-TPHI 2874
 NI---TGM--SGLLPQM--SAKDPLTPTGESRCLFQQHSSSITSGNYAGENSPLFAGTL 2939
 FK--VEDG--YFAPASVSSNGSTITSTGLTEFFFAKPGSLNKNNS-YIPL-ASGV 3503
 SVTRQSRRI--LNLTFVLQGNNAATEVLPEGLRAFYFMRPGETSTNLTSGSGFFGLP-VNPA 3229
 DT--QSDK--KPTVVYQGTGNSMPSTTLPTGLKQLSFVRSGTTTQVTEDELFVPLY-KPII 3123
 DIKPTVKE--VTKTFLCTSNAPSTILPTGLKQISFVRKGTSTSDPHDNPSNVPE-KPIL 3166
 NPSTIRSS--VLQTFVTGNSMPATNLPAGLKQLTFVRSGETSTSVSDLPFFVPLE-KPML 3028
 --DMPVT--DIPNVYFTGNSFPFISLPDGLKAFYIARSGQTS--VDSPIVVA-ARGI 3070
 DQKKTTLT--YDWTYVLTGSLPATLGNLKTAFMVRPGETSTTADDAAFAPIT-ARGI 2880
 WSGVKMPY--QIRKVIQTGNLAGKHLGDGLKMCAMIRQSSSTQSTDNFYFYPIY-VHNF 2908
 PGVNDNRF--FQPTYIQSGNNVPTTSLPAGIRFAAMCRPGTSSNISNESGFYPLL-APGI 2772
 NAEQADRL--YVWSFIQTGNTAPATALPNQIKVCSLIREPGTTTQVTDNGFYPMI-VPLG 3261

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APIFLFISRLKQQYGSSETVE---IVFN-----SAFNGQ-QVI---VARIDLSTAVE--- 2918
 DYTFAQEFGEDEDAVVAL-----TDNRTDSTVCYLWWSGTFFSWSIRATPYLAS--NF 2991
 VTLKRLMNLANG--RIM-NFTIFIQDMPDFQVTLNG--ELI--LIKPEVCMARKGV 3554
 WGLLDRLQDIADQLQTNLHFSWVGADGVEIGKLYSS--GFI--VCRCTSRLLIR-AG 3283
 KNAFRAFDEYLVNNGFSNLVRGDLIYAGENKQIGYQN--STF--FVRTDDFKKIF-AN 3177
 KGVILGLEQVQLQGLTNGL-VGNLEINGENIGQVGFAD--ETL--IVRTDDFKVVK-VN 3219
 PNAIAALNKVLSDNGWKAL-KADLYVQNLNLGQVGYQD--GYF--FIKSDLYRQIL-PR 3081
 NNVFDKLDRAQDYQVTLW-KMNLIVDDNIIGQLAYAN-RTF--ICRTNDVLRVR-AS 3123
 HSLYKTLNDYLVTLNTELI-IADLVVAGNILGKVGKVF--NAF--LTRTSVGKVIK-TA 2933
 SALLKQMNLLKERRTKYI-KFDLVQVGGKPFQMGFGD--GAF--IGRTTMRPQIR-AA 2961
 AGVFGNLDLIAHSLKADII-QMDVLVDGRLFTKVAYAD--GTF--LVRTNVRRIR-TA 2825
 EVVYTQLDQIMDNLGALL-QFSVLVQGGVIARLAYTQ--GAF--LGRSSIRLLIR-TA 3314

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-NTFMYIK--TED--DAPLYSTLRFPSSAMLELLSIQTVYNGTQ-----AF-SDASEF 2965
 SLSNICYVSHITRE-FSGKLPTDLSNFSSRV-----ASQGTPTQ-----KIV-- 3031
 RVSETYLSNFTFTSNIEITLQTFNTTQ-IPWT-----TIVATSQ-----SKTF-- 3595
 WVPNSKFVDIEAATSFSALPSLPIASVSWK-----TNTQL-----GVTNRF 3325
 IQGDIKKNLADLPQANAINAFNTTGMSTWI-----SSGKRTR-----R--RL 3218
 VGTNVVLNRNIVGTIDLKGITQFNTKGFSSWV-----SQGLKKT-----KARRFNL 3264
 ITTACILQNTQYLDNVQGLTTFNLSSFSWV-----SASKRL-----RHR--QL 3123
 LTTAMSLTNIEPVDNNTITPMNTNTWSPFK-----QVPTTSLVLVPKAAIKRLPEE 3175
 LTTDQMINITAASNTSAISVLNVGGFASWS-----GSNT-----YFVGKRVFSF 2977
 ITNVILLKNIVGVDDLSGLQALPTS GFADWV-----VKAQ-----STNSKFLND 3005
 LSTNIIIDNQIPDINILPVPVINGFEPWT-----TGAA-----SLSDPFMMN 2869
 LTKDIRLTEIARLDNINVLPLLPQGFSSWN-----SSSSQ-----SFRSKVVD 3359

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DS-----NVITANAGAAAFITGGGILLSGLG-----QGLGAYAGQKMQMMDKTLWS 3012
-----RCRTDLTE--PPAERQGNLISTSMQIHAQQNMLTQQLQAWQNELNREYN 3082
KS-----RKMKQSGAFWG--MAAGSMMSGLG-----GGMSAYFANQQDQQLREIMDT 3641
FVRPQKPISGINQSA--ALAIGGILLSGLG-----SGLGAVYASKRQSKLNAENW-- 3373
DL-----N-NFHQQ--SATVGGAVMTGLG-----NGFSAWGDQLFQ----- 3251
NL-----C-QYES-----FAGIAASGIG-----ALMGSVGQNVNMQYNDKIMEQ 3303
NL-----D-NYTRF--ASAIAGGATISGLG-----QGITAWSNQMFG----- 3156
TFRRKIAIAIKYQRESAIVA-GLGGAMTGLD-----NYLSQQ-----FNFTQ 3216
Q-----SAFMALGMAAQAGSNMMQAIG-----NGLMYNDYKSWQDARLDKQNAL 3021
FYNDKISTIERQASLGIAAAIGAGQGLFGGLS-----AQWQWQQQADWSRQMQRERLDM 3058
KF-----MRQSAALIGASAAGGLFSGLT-----SALQFGEYNQWRNNYLOKQIDA 2914
LF-----QKQSGAFMAVGALGGLFNGLA-----NTMQFQBYNEWKDAYQKRLHDT 3404

DQ286292 Rosy apple aphid virus
OP265432 Penaeus vannamei solinivirus
MZ210029 Fushun monoleptalauta Solinvi-like virus 1
KX024775 Nylanderia fulva virus 1
KY070327 Diabrotica virgifera virgifera virus 2
OQ540582 Apis mellifera solinivirus-1
MN918666 Picornavirales [unknown host]
MW251313 Icha Creek insect virus
MZ822083 Apis picorna-like virus-4
FJ528584 Solenopsis invicta virus-3
MW314636 Myrmica rubra picorna-like virus
OL569508 Corparats virus-2

YEQKQ-----KHDIDNQRYLQQSMFDWKSHMQQDFDYGNEQQRQIDWQRSSQ 3061
-----NAQQD-----RQHSEFLQTRDQHFKA----- 3103
NNKFK-----KQYLAQQDFDQQLAL-----QTQQQNFQR----- 3669
-----HRLSDLQHSLLGINKSQELAKMDKQFQQ----- 3401
-ERMQ-----NAVLANNRAIAGANNAALAEQKAAFER----- 3283
QKLMQ-----SMQLSNQRTIAEANNSAIARQQKAFEN----- 3336
EN-MM-----KQLMANQQALQGANNAAIAKRQQEAFDR----- 3188
QKDLV-----NLQGDNQIRVLQARYAQKQDYQAYLNHL----- 3249
RLQLMEMQNEAAQVQAMRNQNEIDK-----IQKQAEI----- 3054
MEKLA-----NINNQARLNQLTQSGAQQRTITQQAAYQ----- 3091
QKSLA-----MMNNQNQRDL-----SKQNFDDQ----- 2936
LKQLE-----GIRGENQLNL-----SKQNFDDQ----- 3426

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AALFSQQNLYQDTQNKFTKELVETNLDSDIRARNNAQQLSGYRTDATVSGLSNSGRG--G 3119
-----QMRGLR-----LGNLDGRDIPAG 3121
G--NIGLSNGGAVGMMMRGNTASAS 3692
QLELIGKSSSYSAMSGNTYGPFG--E 3424
NLELKGYNSSSSQYGLFGTTPK--R 3306
-----SLILKGYSSASAQSGLGVAE----- 3356
-----NLQITGYNSASSQFGLIGPRHE--N 3211
-----LLTLRLGYSSPGAQMGNIIDSLQH--P 3272
-----KQSLILGYSSGNSAQNGNLEGRSR--G 3077
-----QMNALGAGSVSAQNGMYTPS----- 3111
-----FMELLGRSSSSALSNGNVASS----- 2956
-----FMQLLGFSNVSSQQGHNGQTQT--G 3449

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LG-----HP-----DAPRG--ATLPPRSAS--TQTNSPK----- 3144
TQLSVLPAYSEHDPFTSSAKPKE--GNPSPAKPKEGNHPLGT----- 3162
VG-----PQQQFVQSGKLDYLAD--SGARAPRKPVTVNSQNTIGSTKIRVPELDTKDRQ 3742
LE-----SGKNFSSSGLLSGTASSSRGGPLVDLTNNHTTQR-----VNDM 3465
GG-----TAV-----APPPRLTISSSQVQTESQQ-----TP----- 3331
-----PNKNFVYSHVYQPNQGP-----QPKEV 3378
QM-----NTRP-----YQNMNNFVYSHVTPTSPVPA-----PTGP-- 3240
ET-----PAVEK-----EINNSE--N-SIQLFNYF--R--FE----- 3297
ES-----VQRPP-----ILGVEA--NGMIPRVPLQ-----S-----GKTKE 3106
-----N-----YTFLPSYK-----S-----NTTNY 3126
-----LPPPSYT-----T-----NSLPS 2969
RN-----PND-----PLPDLPYQ-----S-----NLNY 3468

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---VYTT-----RPTGYFTGP 3157
FDDFSLSTY---ASESTPGDEVLSMSDPPIYSEQSQAIMQMGHKEGELGKQSQGITS- 3218
LGDNMYYDDLHNL--NAD--ETP-----STLA-----GTQKGIY-- 3774
LNDFV-GTT--NNNNGMVPG-----EII--AN-----KHFGNL-GSV-HSRHGSISGF 3506
-----RS-----NLEPLQEN----- 3341
LNDKVYRNIS-GEEVSASDD--EASPVLSEG----- 3406
-----QIGNPDS-----RRSSLMSSD----- 3256
FRKPLYAPFFKSAGI-QNPS-----KINPIPSQGENPVPKVNITTEAIEHTETKPRMSGP 3351
LRLDAY-----EQQRTKFKVP 3121
YNNSVYHT--DNNITNNPS--N-----TSLTNNINNFPNPELQQQPFEMPTP 3169
K---YSD--NASN-----TENPAHIPP 2977
P---YYGA--NNST----- 3477

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MSSDNDKI----- 3165
-----PIQPDYSDLA-----G 3229
-LNLHNNLMADGIPGKSDEEKQALVK----- 3799
SDTINDD-----PRFVKALE---QQNISKIAN 3530
-----PGTETS-----EASLTP 3353
-----DEQPIRYPAKEIKTATLLT--NHAPASLQP 3434
-----SSDSL--PEIHVDVTHM-----TENPAHIPP 3280
ESTLNPE-----AKEFTPKINS-----TLNPE-----AAEFK 3378
KDSISNVKVDGATTDETDDVAIPPFLDRFRSVSTAYPEVADRARQSVV-----P 3171
SEAYDNS-----KGFVPQPGTSKIATENINPNYKDEEHIYEPLEQQNHXYA 3216
-----SSV-----SNASTTSYVQPPDIEAN-HYEQINYPEHIYE 3010
-----YKLPFTDSSSSSSQSSIGTRYMTNS-NYS-----SIYN 3509

DQ286292	Rosy apple aphid virus	-----	3165
OP265432	Penaeus vannamei solinivirus	GKRYPVLGSDPT-----PTNPSGTGL-KSAKAEFPPPAT-----	3262
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	---LSTQDIK-----RNTDP-----LLNKKKQGGTQPMDDKA	3827
KX024775	Nylanderia fulva virus 1	PWNYDTRGPF-SDFEREIA--TGTRE-----VKASHLDWAREANRQGRQTLDPK	3576
KY070327	Diabrotica virgifera virgifera virus 2	ASEYTTSPETKAEL-----TQRMKSGP-----ITKLSQSTPNWTPRALELGEASVNNNA	3401
OQ540582	Apis mellifera solinivirus-1	SKGTVIPVKDLNDFAIQFNQTGNL-----FPKASQTFPNAGVTQ-----HA	3477
MN918666	Picornavirales [unknown host]	PRNVVPYDDET-----PTGVDP-----IDP-----ALDKTD-----HA	3307
MW251313	Icha Creek insect virus	PSALMATD-----S-ALNLFGL-----	3394
MZ822083	Apis picorna-like virus-4	NLPMPSKD-----EPDDDENI-----	3187
FJ528584	Solenopsis invicta virus-3	DIDYNAMNISRENK---NSSNFGNVGILDHQYADIDYDAMKIIDQQNSSKFGNVGVNLH	3273
MW314636	Myrmica rubra picorna-like virus	ELNYPTDS-----DKGYDK-IQNSYLNNPAPQKIY-----NS	3041
OL569508	Corparats virus-2	GQNSSTRDSI-----ISGNSRNSS-TRNSFLDIPSVSNQI-----ST	3545
DQ286292	Rosy apple aphid virus	-----	3165
OP265432	Penaeus vannamei solinivirus	-----LA-----	3264
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	SGA-----	3830
KX024775	Nylanderia fulva virus 1	LQAHHNQIKNNA-----GLLKATTPTTVE-----	3601
KY070327	Diabrotica virgifera virgifera virus 2	FNTQPSQDNAMQRTF-----GP-AV--AQ-----	3422
OQ540582	Apis mellifera solinivirus-1	---DQ--RNMPETL-----LP-NDVLAQQ-----	3494
MN918666	Picornavirales [unknown host]	---NFSSTIVHQL-----SP-NAYYNQ-----	3325
MW251313	Icha Creek insect virus	-----	3394
MZ822083	Apis picorna-like virus-4	-----	3187
FJ528584	Solenopsis invicta virus-3	QYAEIDFSGNNTRKN---SQILDNSLYSKTQPSSKIMIDNSLYGINPNKMVENQNYEPAS	3329
MW314636	Myrmica rubra picorna-like virus	GKTDENILEKDSRSFANLLDDSPGNSVYDKTNPLV-----	3076
OL569508	Corparats virus-2	QTNQPSITTENI---AVGTQDLP-----PKTRS-----	3570
DQ286292	Rosy apple aphid virus	-----	3165
OP265432	Penaeus vannamei solinivirus	-----GGTSGRIAARSATKTALKAVSKAHPALIAADVASQVVKANPTSL	3308
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	-----ASHIAPAIGQVN-----DEIMGGM--ADHAYNVLGL	3859
KX024775	Nylanderia fulva virus 1	-----ETAHPDLVP-----ESEA-----	3614
KY070327	Diabrotica virgifera virgifera virus 2	-----LAGAFKNINDTKEGV-----	3437
OQ540582	Apis mellifera solinivirus-1	-----SQQAVNNIAQT-K-----	
3506			
MN918666	Picornavirales [unknown host]	-----	3325
MW251313	Icha Creek insect virus	-----	3394
MZ822083	Apis picorna-like virus-4	-----	3187
FJ528584	Solenopsis invicta virus-3	MERKNSIFYSSNLRSSNNLKFNNIPNFKGPTN--LNISGAKPAGFGSGIIQP-----AI	3380
MW314636	Myrmica rubra picorna-like virus	LG-----DNKPSGSKFNQLNSAMAAHPAGWGAVAGQLEKGFNTVA-	3117
OL569508	Corparats virus-2	IE-----DKMADAKGISNQFSNAIAAHPQGHGAVMAELKSKQMHGSL	3612
DQ286292	Rosy apple aphid virus	-----	3165
OP265432	Penaeus vannamei solinivirus	GHLA---PV--QPMQPTVSLDGR-----	3326
MZ210029	Fushun monoleptalauta Solinvi-like virus 1	SRYENDNSPTMSASPHPNIDFENTYSPADIHNYL	3893
KX024775	Nylanderia fulva virus 1	-----	3614
KY070327	Diabrotica virgifera virgifera virus 2	-----	3437
OQ540582	Apis mellifera solinivirus-1	-----	3506
MN918666	Picornavirales [unknown host]	-----	3325
MW251313	Icha Creek insect virus	-----	3394
MZ822083	Apis picorna-like virus-4	-----	3187
FJ528584	Solenopsis invicta virus-3	NKYTDFSKPN-----	3390
MW314636	Myrmica rubra picorna-like virus	-----	3117
OL569508	Corparats virus-2	NQEQQSSDLPPMLNSS-----	3627