T-Coffee Alignment of Selected SF1 Viral Helicases

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HepEhel    -----------------------------------------------------R------
GAVhel     IKITTPNPSNSLTL----------------WNSISPITPVLNVFRGIQQQVSTYSIDDTG
Bernehel   ------------------------------------------------------------
PRRSVhel   -------------DYASTALL-----------------------PTCKEINMVA------
EAVhel     -------------SHIAVPLQ-----------------------DTLKGVVVNK------
HCoVhel    TKLV-PGMLFILTSHNVAPLRAPTMANQEKYSTIYKLHPSFNVSDAYANLVPYY------
SARShel    YKLN-VGDYFVLTSHTVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANY------

                               I
HepEhel    ---VTPGVVQYQFTAGVPGSGKSRS-------ITQA-----DVDVVVVPTRELRNA----
GAVhel     SLLDKMANNNITVIQGPPGTGKTYTINRFLTKINEILP---NSNIAVLASSHSAVDNIGN
Bernehel   --------ENVTFVMGPPGTGKTTF----VYDTYLSKA-SSSNRFVYCAPTHRLVGDMDE
PRRSVhel   ---VASNVLRSRFIIGPPGAGKTYW-------LLQQVQ---DGDVIYTPTHQTMLDMI--
EAVhel     ---ALKNAAASEYVEGPPGSGKTFH-------LVKDVLAVVGSATLVVPTHASMLDCI--
HCoVhel    ---QLIGKQRITTIQGPPGSGKSHC----SIGIGVYYP---GARIVFTACSHAAVDSLCA
SARShel    ---QKVGMQKYSTLQGPPGTGKSHF----AIGLALYYP---SARIVYTACSHAAVDALCE
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                                                            II
HepEhel    ----------------------WRRRGFAAFTPHTAAR----------VTQGRR-VVIDEA
GAVhel     SVNPSI-FRRCKRLIPQESEEKVRTRFQRYTTGGGIIFATLQSTRGILCPSVEY-MIIDEF
Bernehel   KVDGAVVVSAY-------NDRTYRNPVWNKDDSYGVLLCTHNT---LPFIKSAV-LIADEV
PRRSVhel   RALGTC-----RFNVPAGTTLQFPVPSRTGPWVRILAG----------GWCPGKNSFLDEA
EAVhel     NKLKQAGADP-YFVVPKYTVLDFPRPGSGNITVRLPQV----------GTSEGE-TFVDEV
HCoVhel    KAVTAYSVDKCTRIIPARARVECYSGFKPNNNSAQYVFSTVNA---LPEVNADI-VVVDEV
SARShel    KALKYLPIDKCSRIIPARARVECFDKFKVNSTLEQYVFCTVNA---LPETTADI-VVFDEI
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                                  III
HepEhel    PSLPPHLLLLHMQR---AATVHLLGDPNQIPAIDFEH---AGLVPAIRPD-----------
GAVhel     SMATD-IQIYSAICHLNPRHIIFTGDPCQL--------STQHVYNTDVYHSNIINN---HQ
Bernehel   SLIPPH-VMIKILS-MGFKKVVLLGDPFQLSPVYKNHK----------VHFKYDTF---YL
PRRSVhel   AYCNH-LDVLRLLS---KTTLTCLGDFKQLHPVGFDS---HCYVFDIMPQ-----------
EAVhel     AYFSP-VDLARILT---QGRVKGYGDLNQLGCVGPASVPRNLWLRHFVSL-----------
HCoVhel    SMCTN-YDLSVINQRISYKHIVYVGDPQQL--------PAPRVLISKGVMEPIDYNVVTQR
SARShel    SMATN-YDLSVVNARLRAKHYVYIGDPAQL--------PAPRTLLTKGTLEPEYFNSVCRL
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HepEhel    ---LAPTSWWHVTHRCPADVCELIRGAY-PMIQ----------------------------
GAVhel     LTGKFPTEFLDITYRMGSKINDFISENFYDGKLKTAATYEGEVFQLHLDPINMLSQIHAIW
Bernehel   LQLATQKRYLTACYRCPPQILSAFSKPYCDVGVDLVSFNNKP-------GKFDII-VSKQL
PRRSVhel   -------TQLKTIWRFGQNICDAIQPDYRDKLM----------------------------
EAVhel     -------EPLRVCHRFGAAVCDLIKGIY-PYYE----------------------------
HCoVhel    MCAIGPDVFLHKCYRCPAEIVNTVSELVYENKFVPVKEASKQCFKIFERGSVQVD-NGSSI
SARShel    MKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHD-VSSAI

                                                            V
HepEhel    --TTSRVLRSLFWGEPAVGQKLVFTQAAKAA-------NPGS----VTVHEAQGATY TET-
GAVhel     ESSAQN------------NFAILVTHHEAFSIIRQYFTDIDIQIPIYTVHTSQGRTFDRGIV
Bernehel   ANIQDFSVLSVLSKE--YPGYVILVNYRAAVDYAMQN-GLGD---VTTIDSSQGTTAANHLL
PRRSVhel   --SMVNTTRVTYVEKP-VRYGQVLTPYHRDR-------EDDA----ITIDSSQGATF DVV-
EAVhel     --PAPHTTKVVFVPNPDFEKGVVITAYHKDR-------GLGH----RTIDSIQGCTF PVV-
HCoVhel    NRRQLDVVKRFIHKNSTWSKAVFISPYNSQNYVAARLLGLQT----QTVDSAQGSEYDYVIF
SARShel    NRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPT----QTVDSSQGSEYDYVIF
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                                VI
HepEhel    TIIATADARGLIQSSRAHAIVALTRHTEKCVIIDA-------PGLLR----
GAVhel     VSYRNTAF----TRDPNIVNVAVSRFRFQCICMHQG---NPYYSKLPY---
Bernehel   VLFGASNF----SKTVNRVIVGCSRSTTHLVVVCCPELFKHFQPILNWPEP
PRRSVhel   TLHLPTKD----SLNRQRALVAITRARHAIFVYDPH---RQLQGLFDLPAK
EAVhel     TLRLPTPQ----SLTRPRAVVAVTRASQELYIYDPF---DQLSGLLKFTKE
HCoVhel    AQTSDTAH----ACNANRFNVAITRAKKGIFCIMSD---RTLFDALKFFEI
SARShel    TQTTETAH----SCNVNRFNVAITRAKIGILCIMSD---RDLYDKLQFTSL
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Relative degree of conservation BAD AVG GOOD

The major conserved helicase motifs [Kadare, G., and Haenni, A. L. (1997) *J Virol* **71**, 2583-2590; Gorbalenya, A. E., and Koonin, E. V. (1993) *Curr. Opin. Struct. Biol* **3**, 419-429] are indicated with Roman numerals and are underlined with asterisks.

Sequences were aligned using T-Coffee [Notredame, C., Higgins, D., Heringa, J. (2000) *J. Mol. Biol*, **302**, 205-217. http://www.ch.embnet.org/software/TCoffee.html] and were manually cropped for clarity.

HepEhel = Hepatitis E virus, Orf1 helicase domain (NP_056785.1); **GAVhel** = Gill-associated virus, Orf1ab replicase (locus AF227196.1); **Bernehel** = Berne virus, Orf1b helicase domain (locus P18458); **PRRSVhel** = Porcine reproductive and respiratory syndrome virus, Orf1ab nsP10 helicase domain (NP_066135.1); **EAVhel** = Equine arteritis virus, Orf1ab nsP10 helicase domain (NP_705591); **HCoVhel** = Human coronavirus 229E, Orf1ab nsP10 helicase domain (NP_073549.1); **SARSCoV** = SARS coronavirus, Orf1ab nsP10 helicase domain (NP_828849.2)