

Virus Report

11-01-2015 16:49:07

Secondary structure results

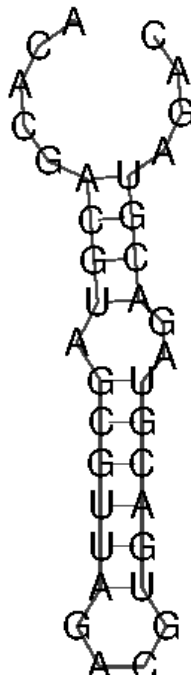
Virus name:
HI-V

Sequence:
ACACGACGUAGCGUUAGACGUGACGUAGACGUAGAC

Structure in dot-bracket format:
.....(((((((.....))))))..))))....

Energy:
-9.4

RNA-Structure:



Virus Domain(s)

Number of proteins:
3

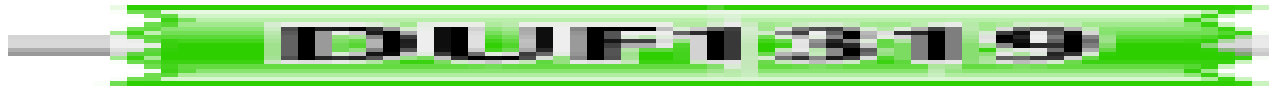
Protein 1

Number of domains:
1

Amino acid sequence:
LDSYWDLEFEKYKNSHKSVDLSYLDLASADKVS NKDLAFNLHINTYRSDLGFKVAIHSLSK
NRELLIQNRKLL EEQKQQLSEINNLSKV VRLQRADLKETLRRQDVLAKELQALRKDYLERPL
SKEDVEELVVRIS EQPKIY

Starting nucleotide position:
753

Ending nucleotide position:
1191



Domain 1

Starting aminoacid position:
15

Ending aminoacid position:
145

Domain description:
Protein of unknown function (DUF1319)

Identifier:
DUF1319

Protein 2

Number of domains:
0

Aminoacidsequence:
MSLAGSKATAIYQEALQSTAAGWEDTGIGFTDKGVISTTTLSRQLNSLLFLVIKQNNQITTISEE
LTQLHNRVKNLEGRTGVSAPLYKSEIESINAKLKSIIQDIQGSHPKETPSGVIKVFEDPYSLR
RL

Starting nucleotide position:
1282

Ending nucleotide position:
1681



Protein 3

Number of domains:
4

Aminoacidsequence:
MASRPRVSGSTTRTMIAEPGVPLVDDQIREYRSAARVAYEAQRIARRTGNI LGRIVGRQPREH
TLAMVVDPNSELERSLAHRARTIPAEVLYMTQRGEPTNRVYRNRTEERMLVTHGQQDRTFIL
PESYEELREAGFEYIHLGVLRVIRIIMHRTYDGTMALVVFRDTRWTQENHQDRSIIATMEADL
SQGHQLIYVIPDIMMTIRDFYQHIQISILTKGYEGFQGEANLLITRSCRCRLSNVPNVGFQYNIQ
NVVEFLKSRGVKALNATKLSTRRFQGGGEWNIRPSEVVVPMQPTTMIVRVNYDSSRSIRFGDY
EASTSSAPRYEQDGDDEALGDIHQVNMITIIEDDAEDDYPRLSALERIIAPESMVGEEDTIAE
FLSNLSLDSSTDEEFYDADNSLFEEEEYDGDSEVSTPRSKYNIFALED EYPKLQQLESVLSTT
ESAISRFRPADTDMTGVGPGYAPATGTAGYTGASSDFPYPRRPRKWDNNSEWFNLPTANA
RQASIFVMPQDFDTKVFERWESSVLLHMSDKVFDDPQDKLTYVENLLGESEKKMFITWRMM
FTAEEEMKNNALGSNGTQNILNQIRMIFFLENPQVGTTNTQDAAYKTLKQLVCTEMSGPAIY
RYLNDYFHAAKSGRAWASDELSKEFFTKLPRGLGDRVEKKFKEKYPNNTIGVAPRITFTRNY
IKEICQEAVFQSQLKRLDFCKGTPVHGLYGKEKAYGRKYGVRKSTSYKGKPKHSHVRIDKKK
HLLMKRKDCKCFACGDIGHFASECPNPKKLMHRVQILQSLELDDGIDVISVGFDESVDIYSV
SEGEDSYQFNNEFDVIGHDVFMFTIEEQRNCLVETTSAWRSAMKVTPPEKNCLHTWSFEK
TTDHCRACKNLALRGSRADCTQCKIIICSLCKPYYFQDGSPIPAQSSTPSGYSYDDWMGSAN
RWKAHYEFSQARRKSLKADLERAEELKFYKQKEKEKAKLKDQIPEAVQAKLDDLEKEKELN
NILRIEAETELKALKESFKEKEEALKEEITAL EEEVRIHKEEAEELQEENQKLKEKIIAFEKDVTQ
GP EEVIELVNNVEEHLVLTGQQKNLLNIKITLEVKEKRITMNAILD TGAAICVCDGQMVNEYFR
RPSMMNAFIKGVNGITNVKEILEEGKIWIGNQWFRIPRTYIMPQLSEGLHFIIGMNFIRAMEGGI
RIEQQGTVTFYKMTQAQAPPMVHDISYLEELELELPIYYDICATNPSGGEINSDLISPSEIRKLKD

LGYIGEEPLKHWAKNQVKCRIEIKNPDLIEDRPLKHVTPAMKESMKKHVDKLLLELKVIRPSTSK
HRTTAIVQSGTEIDPLTGKEKRGKERLVFNKYKRLNDNTEKDQYSLPGINTIISRIGKSKIYSKFD
LKSGFHQVAMDPESIPWTAFAIDGLYEWLVMPFGLKNAPAFQKMDNCFRGTEEFIAVYID
DILIFSDNISDRKHLKFLICKANGLVLSPTKMKIGAKEIDFLGATIGNSKIKLQPHIIKKIETKD
EELKETKGLRKWLGVNLNYARAYIPNLGKTLGPLYSKTSINGEKKMNSQDWKVQQLIKNQVQNL
PDLIPPAEATMVLETDGCMEGWGGVCKWKLHPSDTRLAEKVCAYASGRYHPIKSTIDAEVH
AVINSLEKFKIYYLDKKELIIRTDSSQAIVAFYKKQADHKPSRTRWLMLIDYITGLGINVKFEHIDGK
ENVLADTL SRLVQVLITKVHHPAETQLVEAVMEVISNPKKEALDKVNHFIFLTQQWIAERKEEH
TVNTLLQLEEPQLHCGCRNYETGERRNAILLQSHTSANPNRWFYKCAENKCHIWIWKDILDQ
YAEDYATYTRIGLEALNLEDWFEEPEPDPPNPVDRQRIEDILLNVSND

Starting nucleotide position:
1681

Ending nucleotide position:
7378



Domain 1

Starting aminoacid position:
125

Ending aminoacid position:
246

Domain description:
Viral movement protein (MP)

Identifier:
MP

Domain 2

Starting aminoacid position:
763

Ending aminoacid position:
780

Domain description:
Zinc knuckle

Identifier:
zf-CCHC

Domain 3

Starting aminoacid position:
1090

Ending aminoacid position:
1201

Domain description:
Retroviral aspartyl protease

Identifier:
RVP

Domain 4

Starting aminoacid position:
1349

Ending aminoacid position:
1509

Domain description:
Reverse transcriptase (RNA-dependent DNA polymerase)

Identifier:
RVT_1