

# Virus Report

12-01-2015 10:11:25

## Secondary structure results

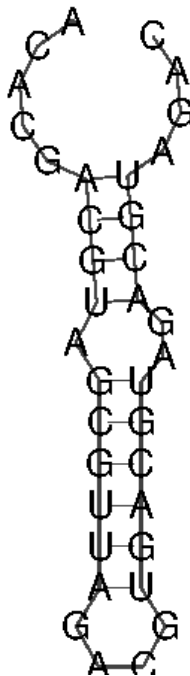
Virus name:  
HI-V

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

Aminoacidsequence:  
VTNNQLAHNLA VTFDRVNLGNRVFIK NLKQIQESILELNTRVDTIEVALRRLTKTFRESKPLTES  
EVRKLV EEEIAQQPKIVEKQALEISQQLEQKLEKVEKLLHKLDQWVGQ

Starting nucleotide position:  
533

Ending nucleotide position:  
872



## Domain 1

Starting aminoacid position:  
1

Ending aminoacid position:  
99

Domain description:  
Protein of unknown function (DUF1319)

Identifier:  
DUF1319

## Protein 2

Number of domains:  
0

Aminoacidsequence:  
MTDSPAYQEALKEAEKVDPPAVGITTSTGVTAVQGFKTVIKQNNVQICLLAVIADKLEELIQDQ  
KKARKDKAKEVAIPEDLITKLQGLSIQEKGEAKVTRKPEPKGTLFGFKDPYKILAAEKAKITLKP  
VKE

Starting nucleotide position:  
868

Ending nucleotide position:  
1267



## Protein 3

Number of domains:  
4

Aminoacidsequence:  
MSRARQPQHPVPSVTTTTSEQNREGPLYEDQIRDYRRGQRRIFNLRRRARRLRRSMMGSTRYQ  
ETLEQEIDPQTTLRLSMQERARLVPAEVLRSRRDTVHHRVYTHRSEESVLCVGGSSQVDRAF  
IQPESLEQLQRTGMSFIHIGILQVRIQILHRQEEGTALVVFRDNRWSGDQSIFAQMEIDLTKG  
SQLVFVIPDTMMTIGDFARNVQLSILTRGYENWQNGEANLLITRGMTGRLSNTPNVAFAYQIA  
SATDYLASHGVKAIAGKKMNLQHLRNQQWILRPPQTDITPMQPRSVETRNLVDGSISIRFHDY  
EAATSASRPHYNEEDEEVESETESEIREHTIAVWIGEEEEIPDQTGRKKVWEESNGNGRFFRY  
YTPPPTFEGQIIATGWGSDDDNEKTPPKWDESPDEEGPTEPIWDQEEEEDEYDPNVYRAYL  
QKEEDEWQEITASLREEMEYPKRRPQTEMAFSETVDYTPPGDTMMTPVGYPASSSRSTVT  
TPSRPPLFEGRTTHVPRFLKRDEYTEWWQLPSSQGTGALFVMPKQMGLFHEVFSRWESIT  
KNYVAAQGFTDPTEKMEFMENLLGETEKLTIQWRMNYEAEYQQLLTQADGRQGTQNILSQI  
KRIFSLEDPASGSTRIQDAAYRDLERLTCHNIKDIVQFLNDYGRLAAGSRLFLGTELSEKLWM  
KMPPELGHRMKEAFQKEYSGNEVGVPFRLFAYRYLEQECKDAAFKRSLSLSFCKDMPLTG  
YYDKTSKYGMRKSRTYKKGPHASHARVEKRKHLIRNKKCKCYLCGDEGHFARECPNQRRDV  
KRVAIFEGIDLPEGFDIVSVEEGEEESDAIYSISENEDGELDTEVVHEKVFMREEDQSYWLG  
KTNHWTAMVRVSSQQYHCHMHQWEHNKEILVVAHINCHFCQPTQLRSRIHCPTCQLTSCFM  
CAPIYCNMIVQQQPKPPVPFNTHLLQQQAAYIQWLEKENQRLTEAVEFYKKEAEELRLERDL  
EQDRRSLEPTLLDKGKKVQILDPEDEDQHTAYLEEDTISRVIHTVEQQEVRKPKVKKGNMLYNL  
DVVLHIPEVGRPIKVKAILDTGATTCCININSVPQTAIEQNTFLVQFRGINSTQSVDDKKLKYGRM  
TISNHQFRIPYCYAFPLSLGDGIEMILGCNFIRGMYGGLRIEGHTITFYKNVTTIQTRLAAMVG  
GTTASELGGGEESKSDSESMFDLSETEEFDSETHQQIVSHVAAQAQQQKLDPKLQQLMVQL

QDQGFIGNPMQHWAKNKILCRLDIKNPDLIEDKPIKHLTPAMEKQFQKHIKALLDIGVIRPSK  
SKHRTTAFIVESGTVIDPVTKKTIHGKERLVFNKYKRLNDNTEKDQYSLPGIQTILKRVGNKKVFS  
KFDLKSGFHQVAMAEESIPWTAFWVPQGLYEWLVMPFGLKNAPAVFQRKMDQCFCFGTEEFI  
AVYIDDILVFSENMAEHTKHIGIMLKICQENGLVLSPSKICLAQREIEFLGTVISQGMKLQAHVI  
KKIVNKANIELETTKGLRSFLGLLNYARIYIPNLGRKLSPLYAKTSPTGEKRFNRQDWHLIKEIKD  
MVQKLPNLAIPPARCYIIIESDGCMEGWGAVCKWKLAKEDSRTTEKICAYASGKFGVVKSTIDA  
EIYALIKALESFKIFYLDKKHLVVRTDCQAIVTFYNKTSSTHKPSRIRWITFSDYITGLGVPVTIEHI  
DGKENQLADTL SRLVYTTWNQSQTHQPEEEEELEKSQHLSFAGLAIPAWPMMGSYNKRRTPL  
LTGQSLWQRNKPSQHSSTASKSRQPRKHYPYVTYRAYSTSRETIWPLLPLETTGLATDCQL  
PNKTQPP

Starting nucleotide position:  
1271

Ending nucleotide position:  
6776



### Domain 1

Starting aminoacid position:  
86

Ending aminoacid position:  
241

Domain description:  
Viral movement protein (MP)

Identifier:  
MP

### Domain 2

Starting aminoacid position:  
786

Ending aminoacid position:  
803

Domain description:  
Zinc knuckle

Identifier:  
zf-CCHC

### Domain 3

Starting aminoacid position:  
1046

Ending aminoacid position:  
1163

Domain description:  
Retroviral aspartyl protease

Identifier:  
RVP

### Domain 4

Starting aminoacid position:  
1333

Ending aminoacid position:  
1494

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

Identifier:  
RVT\_1