Virus Report

20-01-2015 15:28:06

Secondary structure results

Virus name: HI-V

Sequence:

TGĠTATCAGAGCAAGGTTAAACATGGTCATGTCCGGCTAAAAACCTAGTGTTAGGTTCGG GGAAAGAGGTCTACTGTGTTTCAAATATCCATTTGTTATTATCCAAACAGTGTCTGTTC CTTGTGTTTAGGATGGAAACCTGAGGTTGCGAACTACGTGTTCAAAGGAGTGATCATTTC AAAAGGAATGTCATTCTAACTATCGTATGCTCTAGACTTGCCCTGTTATAGCAACAGAGGA TCCTGTCTATCAGAAAATAGTTTGAACAATTCCGATGATCTCTCATACTTTAGGTATAACAA CGCCACGTATAAGGAGCTAATTCTTTTGTAAAAGACGTAACCCAGAAGAGAGTACCCAGA GAGGGGAAGACTTGGGGAGAAGGTGAACAGAAGAGAGAGCTTACTGTACCTGGTACTGT TATAGGAAGATTTTGTTATGTCCAGTCGCTGGGAGAATAGTATACAAGAGTGGTATGAGA AGTCACACACAGCAAACCTTGAGTACCTTGACCTAGCATCTACTAGTAAAGTGACCAACA ACCAGTTAGCACATAACCTTGCAGTAACCTTTGATAGAGTAAATTTAGGTAACCGAGTTTT TATTAAAAACCTGAAGCAGATTCAAGAGTCTATTCTTGAATTAAACACCCGTGTTGATACTA TAGAAGTAGCTCTAAGGAGGTTAACCAAGACCTTCAGAGAAAGCAAACCACTTACCGAAA GTGAAGTCCGTAAGTTGGTTGAAGAAATTGCTCAACAACCTAAGATCGTCGAGAAACAAG CACTCGAGATCTCTCAACAACTTGAGCAGAAACTAGAGAAGGTGGAAAAGCTCTTGCACA AACTTGACCAGTGGGTTGGTCAATGACTGATAGCCCAGCCTATCAAGAAGCTTTAAAGGA AGCAGAAAAGGTTGACCCACCAGCAGTTGGGATAACAACCTCCACCGGAGTAACAGCGG TTCAAGGGTTTAAAACCGTTATTAAGCAGAACAACGTTCAGATCTGCTTACTCGCTGTCAT AGGAAGTTGCCATTCCAGAAGACTTAATCACAAAACTCCAAGGATTATCTATTCAGGAGAA AGGAGAGGCAAAAGTCACAAGAAAACCCGAGCCAAAAGGAACGCTGTTTGGATTCAAAG ATCCTTACAAGATCCTAGCAGCAGAAAAGGCTAAGATCACACTTAAGCCTGTGAAAGAGT AGAAAGATGAGTCGAGCACGACCGCAACACCCAGTTCCTAGTGTGACTACAACCACTAGT GAGCAAAACAGGGAAGGACCTCTATACGAGGATCAGATCAGAGACTACCGAAGAGACA AAGAAGGATCTTTAACCTTCGAAGAAGAGCCAGAAGGTTAAGAAGATCAATGATGGGGTC TAGATATCAAGAGACCCTAGAACAAGAAATAGATCCACAGACAACACTGAGGTTGTCCAT GCAAGAACGAGCAAGACTAGTACCAGCTGAGGTACTGTACAGATCCAGGCGAGACACTG AAGTGGATAGGGCGTTTATACAGCCTGAAAGTCTGGAACAACTCCAAAGGACAGGAATGT CCTTTATTCATATCGGAATTCTGCAAGTGAGGATTCAGATTCTGCACCGACAAGAAGAAG GCACCATGGCCTTGGTAGTATTCAGGGATAACAGATGGTCGGGAGATCAGTCTATTTTCG CTCAAATGGAAATAGACCTAACAAAAGGAAGCCAATTGGTGTTCGTTATACCAGACACCAT AAATTGGCAGAACGGAGAAGCCAATCTCCTGATAACACGTGGCATGACAGGGCGACTGT CCAACACTCCCAATGTCGCCTTTGCTTACCAAATTGCCAGCGCAACAGATTACTTGGCAA GTCACGGTGTAAAAGCTATCGCAGGAAAGAAAATGAATCTGCAACACCTGCGAAACCAAC AGTGGATACTACGTCCACCACAAACGGACATCACTCCAATGCAACCAAGATCGGTTGAAA CAAGAAATCTCGTAGATGGAAGTATCTCCATCAGATTCCATGATTATGAGGCAGCTACTTC AGCTTCAAGACCTCACTACAATGAGGAAGATGAAGAAGTGGAATCAGAAACGGAGTCAGA AATAAGGGAGCATACTATTGCAGTCTGGATAGGAGAAGAAGAAATTCCAGACCAGACAGG GAGAAAGAAGGTATGGGAAGATCTAGTAATGGAAATGGAAGATTCTTCCGGTATTACAC TCCTCCACCAACATTTGAAGGGCAAATCATTGCTACAGGATGGGGAAGTGATGATAA TGAAAAAACTCCTCCAAAATGGGATGAAAGCCCAGATGAAGAAGGACCCACAGAACCCAT ATGGGATCAAGAAGAAGAAGATGAATATGATCCCAATGTCTATAGGGCATACTTACA AAAGGAGGAAGATGAGTGGCAAGAAATCACAGCTAGTCTCAGGGAAGAAATGGAGTACC CAAAAAGACGACCACAAACAGAGATGGCGTTCTCTGAAACAGTCGACTATACTCCACCTG GTGACACTATGATGACACCTGTCGGATACCCCCCGGCCTCGTCATCAAGATCAACAGTCA CAACGCCAAGTAGACCGCCACTTTTTGAAGGAAGGACCACACACGTGCCACGATTCCTAA AAAGGGATGAGTACACAGAATGGTGGCAATTACCATCATCGCAAGGCACAACAGGGGCG TTATTTGTAATGCCTAAACAAATGGGCCTATTCCATGAAGTCTTCTCGAGATGGGAATCCA TCACCAAAAACTACGTTGCGGCCCAAGGTTTTACGGACCCAACAGAAAAGATGGAGTTCA AGGCTGAATACCAGCAGCTGCTAACCCAAGCAGATGGGCGACAAGGAACCCAAAATATC TTGTCCCAGATCAAGAGAATCTTTTCTTTAGAAGACCCAGCCTCTGGATCCACGAGAATAC AAGATGCTGCATACAGAGACCTGGAGAGATTAACCTGCCACAACATAAAAGACATAGTTC

AATTTCTAAATGACTATGGAAGGCTTGCAGCAAAGAGTGGGCGACTGTTCTTAGGAACTG AGCTCAGTGAAAAGTTATGGATGAAGATGCCACCAGAACTAGGGCATCGAATGAAAGAAG CATTTCAAAAGGAGTATTCAGGCAATGAAGTAGGAGTCTTCCCGCGCATCTTGTTTGCCT ACAGATATCTGGAGCAAGAGTGTAAAGATGCAGCTTTTAAGAGAAGCCTGAAGTCATTAA GCTTCTGCAAAGACATGCCATTAACAGGATACTATGATAAAACCTCCAAGTATGGCATGA GAAAGTCAAGAACCTATAAAGGAAAACCACATGCATCACATGCAAGGGTGGAGAAGAGG AAGCACTTGATCAGAAATAAAAAGTGCAAATGTTATCTCTGCGGGGATGAAGGACACTTT GCCCGGGAATGCCCCAATCAGAGGAGAGATGTCAAGAGAGTAGCCATTTTTGAAGGAAT TGATCTTCCTGAAGGCTTTGATATCGTCTCAGTAGAAGAAGAAGAAGAAGAAGATGC TATTTATAGCATATCTGAAAATGAAGACGGAGAACTTGACACTGAAGTAGTCCATGAGAAA GTCTTCATGATGAGAGAGAGACCAGTCCTATTGGTTAGGAAAGACAAACCATTGGACG GAAATATTAGTGGTGGCCCACATCAACTGCCACTTCTGTAAGCAACCCACTCAGTTAAGG AGTCGAATACACTGTCCCACGTGTCAACTCACCAGTTGCTTCATGTGTGCCCCAATATACT GCAATATGATAGTCCAGCAGCAGCCTAAACCACCAGTACCGTTTAATACTCACACACTGC TCCAACAACAAGCGGCTTATATCCAGTGGTTGGAAAAAGAAAATCAGCGGTTAACTGAAG CCGTTGAATTCTATAAAAAGGAGGCTGAAGAATTAAGGCTCGAAAGAGACTTAGAGCAAG ATAGAAGGAGTCTGGAACCTACGTTGTTAGACAAAGGAAAGAAGGTTCAGATTCTTGATC CAGATGAAGATCAGCACACAGCGTATCTTGAAGAAGATACCATCAGCCGTGTTATCGGCC ATACTGTGGAACAACAAGAGGTTAGAAAGCCCCGTTAAAAAGGGGAAACATGCTCTATAACC TCGATGTGGTGTTACATATCCCAGAGGTAGGAAGACCTATCAAAGTCAAAGCAATTCTAG ACACTGGAGCAACCACATGCTGTATAAACATCAACTCTGTACCACAAACAGCAATTGAACA GAACACTTTTCTGGTACAATTCCGAGGCATAAATTCCACGCAATCTGTGGATAAGAAACTC AAATATGGGAGGATGACTATCAGCAATCACCAGTTCAGAATCCCGTACTGTTATGCCTTTC CTCTATCCCTTGGTGATGGAATAGAGATGATCCTAGGGTGTAATTTCATCCGTGGGATGT ATGGCGGTTTGCGTATTGAAGGTCACACAATCACCTTCTACAAAAATGTCACTACAATCCA AACCCGCCTTGCTGCCGTAATGGTTGGTGGTACAACCGCTTCTGAGTTAGGGGGAGGGG AGGAGTCCAAATCCGATTCTGAATCCATGTTTGACCTCTCAGAAACAGAAGAATTTGACTC AGAAACCCACCAGCAGATTGTGAGTCATGTTGCAGCCCAAGCCCAACAACAAAATTGGA TCCAAAACTCCAACAACTAATGGTCCAACTTCAGGATCAGGGCTTTATTGGGGAAAATCCT ATGCAACATTGGGCTAAAAACAAGATCCTATGTCGACTAGATATCAAGAATCCTGATCTTA TAATAGAAGACAAGCCCATCAAGCATCTAACACCGGCCATGGAGAAACAGTTCCAGAAGCACATCAAAGCACTCCTGGACATTGGTGTTATCAGGCCTAGTAAGTCAAAACACAGGACTA CGGCCTTCATTGTGGAATCAGGCACTGTTATTGATCCAGTCACGAAAAAGACTATACACG GTAAAGAACGTTTGGTCTTCAACTACAAACGCCTGAACGACAACACTGAAAAGGACCAGT ACTCGCTACCCGGTATACAGACCATCCTAAAGCGGGTGGGCAACAAGAAGGTCTTCAGC AAGTTCGATCTAAAATCGGGCTTCCATCAAGTTGCCATGGCGGAAGAGTCCATCCCTTGG ACTGCTTTCTGGGTACCGCAGGGCCTTTATGAATGGTTAGTGATGCCCTTTGGGCTCAAA AACGCTCCTGCAGTATTTCAAAGAAAAATGGACCAATGCTTCAAAGGTACAGAAGAATTCA TTGCAGTGTACATTGATGACATTTTGGTCTTCAGCGAAAATATGGCAGAGCATACCAAGCA CATTGGAATCATGCTCAAGATCTGCCAAGAAAATGGGCTGGTACTAAGCCCAAGTAAGAT ATGTCTTGCCCAACGCGAGATTGAATTTTTGGGCACAGTCATCTCACAAGGACAAATGAA GCTTCAGGCCCATGTAATCAAAAAGATAGTCAACAAAGCCAACATAGAGCTAGAAACAAC AAAAGGCCTGAGATCCTTTTTGGGCCTCCTCAACTATGCCCGTATCTACATACCCAACCT GGGTAGAAAGCTAAGTCCACTATATGCCAAGACTAGTCCCACCGGAGAGAAAAGGTTTAA TCGACAAGATTGGCATCTGATAAAGGAAATCAAAGATATGGTCCAAAAGCTCCCAAACCT CGCTATCCCACCAGCAAGATGCTACATTATCATTGAAAGCGATGGCTGCATGGAAGGATG GGGGGCCGTATGTAAGTGGAAATTAGCAAAAGAAGATTCCCGCACTACTGAAAAGATTTG TGCGTACGCTAGTGGGAAATTCGGTGTTGTCAAGTCTACCATCGACGCCGAAATTTACGC ACTCATAAAAGCATTGGAATCTTTTAAAATCTTCTATCTGGACAAAAAACATTTGGTGGTGC GAACAGACTGTCAAGCGATAGTGACATTTTACAACAAGACAAGTACTCATAAACCCAGTA GAATACGTTGGATCACCTTTTCCGACTATATAACGGGGGTTAGGAGTTCCGGTTACTATCG AACACATAGACGGAAAAGAGAACCAGTTGGCTGATACACTAAGCAGACTCGTGTATACAA CATGGAACCAGTCCCAAACTCACCAACCGGAGGAAGAAGAGCTGGAGAAGTCCCAACAT CTCAGCTTCGCGGGGCTAGCTATCCCTATAGCTTGGCCTATGATGGGCTCCTACAACAA AGAAGGACGCCATTACTCACGGGACAATCACTCTGGCAACGGAACAAGCCATCTCAGCA CAGCTCTACCGCATCGAAGAGCAGGCAGCCAAGAAAGCACTATTGGCCCTACGTGACCT ACAGGGCGTACTCCACTTCAAGAGAGACTATTTGGCCGCTACTGCCACTAGAGACAACTG GGCTAGCGACAGACTGCCAGCCCAACAAGACTCAGCCGCCCTAGACCAACATGCTG GCGTGATTAACGCCATTATTGAAAGGGCTGTCCAACCCTAGTTTGGACGGTAGTAGTAGG TGTAATAATAGTTAGGTGTGCTTTACTTTTCCAAGCTGTCACTCATTATAGAGTAGACA TGATGATCGACGATGGGGCCCAATGAGCACCCGGATCACCATTCTCCCATCTATAAATGA GAGTTTGTAAGGCTTAGCCATCAGAGAGTGAAAACTACTCAACTGATCCTAAGTGTTAGA GTTTGTATTTTCCTAAGAGTTTGTAAGATTTTTATGAAATAAAGAGTCTACTTTGTGTTTATC

TCTTTGTTTCACCTGGGATTTAAACAGTTTTTGTTTTTCCGCACCATCGGTTTGCGCCCGA TCGATGT

Structure in dot-bracket format:	
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Energy: -2056.9

RNA-Structure:



Virus Domain(s)

Number of proteins: 3

Protein 1

Number of domains:

Aminoacidsequence: VTNNQLAHNLAVTFDRVNLGNRVFIKNLKQIQESILELNTRVDTIEVALRRLTKTFRESKPLTES EVRKLVEEIAQQPKIVEKQALEISQQLEQKLEKVEKLLHKLDQWVGQ

Starting nucleotide position: 533

Ending nucleotide position: 872

Domain 1

Starting aminoacid position:

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:

MSRARPQHPVPSVTTTTSEQNREGPLYEDQIRDYRRGQRRIFNLRRRARRLRRSMMGSRYQ ETLEQEIDPQTTLRLSMQERARLVPAEVLYRSRRDTVHHRVYTHRSEESVLCVGGSQVDRAF IQPESLEQLQRTGMSFIHIGILQVRIQILHRQEEGTMALVVFRDNRWSGDQSIFAQMEIDLTKG SQLVFVIPDTMMTIGDFARNVQLSILTRGYENWQNGEANLLITRGMTGRLSNTPNVAFAYQIA SATDYLASHGVKAIAGKKMNLQHLRNQQWILRPPQTDITPMQPRSVETRNLVDGSISIRFHDY EAATSASRPHYNEEDEEVESETESEIREHTIAVWIGEEEIPDQTGRKKVWEESSNGNGRFFRY YTPPPTFEGQIIATGWGSDDDNEKTPPKWDESPDEEGPTEPIWDQEEEEDEYDPNVYRAYL QKEEDEWQEITASLREEMEYPKRRPQTEMAFSETVDYTPPGDTMMTPVGYPPASSSRSTVT TPSRPPLFEGRTTHVPRFLKRDEYTEWWQLPSSQGTTGALFVMPKQMGLFHEVFSRWESIT KNYVAAQGFTDPTEKMEFMENLLGETEKLTWIQWRMNYEAEYQQLLTQADGRQGTQNILSQI KRIFSLEDPASGSTRIQDAAYRDLERLTCHNIKDIVQFLNDYGRLAAKSGRLFLGTELSEKLWM KMPPELGHRMKEAFQKEYSGNEVGVFPRILFAYRYLEQECKDAAFKRSLKSLSFCKDMPLTG YYDKTSKYGMRKSRTYKGKPHASHARVEKRKHLIRNKKCKCYLCGDEGHFARECPNQRRDV KRVAIFEGIDLPEGFDIVSVEEGEEESDAIYSISENEDGELDTEVVHEKVFMMREEDQSYWLG KTNHWTAMVRVSSQQYHCMHQWEHNKEILVVAHINCHFCKQPTQLRSRIHCPTCQLTSCFM CAPIYCNMIVQQQPKPPVPFNTHTLLQQQAAYIQWLEKENQRLTEAVEFYKKEAEELRLERDL EQDRRSLEPTLLDKGKKVQILDPDEDQHTAYLEEDTISRVIGHTVEQQEVRKPVKKGNMLYNL DVVLHIPEVGRPIKVKAILDTGATTCCININSVPQTAIEQNTFLVQFRGINSTQSVDKKLKYGRM TISNHQFRIPYCYAFPLSLGDGIEMILGCNFIRGMYGGLRIEGHTITFYKNVTTIQTRLAAVMVG GTTASELGGGEESKSDSESMFDLSETEEFDSETHQQIVSHVAAQAQQQKLDPKLQQLMVQL QDQGFIGENPMQHWAKNKILCRLDIKNPDLIIEDKPIKHLTPAMEKQFQKHIKALLDIGVIRPSK SKHRTTAFIVESGTVIDPVTKKTIHGKERLVFNYKRLNDNTEKDQYSLPGIQTILKRVGNKKVFS KFDLKSGFHQVAMAEESIPWTAFWVPQGLYEWLVMPFGLKNAPAVFQRKMDQCFKGTEEFI AVYIDDILVFSENMAEHTKHIGIMLKICQENGLVLSPSKICLAQREIEFLGTVISQGQMKLQAHVI KKIVNKANIELETTKGLRSFLGLLNYARIYIPNLGRKLSPLYAKTSPTGEKRFNRQDWHLIKEIKD MVQKLPNLAIPPARCYIIIESDGCMEGWGAVCKWKLAKEDSRTTEKICAYASGKFGVVKSTIDA EIYALIKALESFKIFYLDKKHLVVRTDCQAIVTFYNKTSTHKPSRIRWITFSDYITGLGVPVTIEHI DGKENQLADTLSRLVYTTWNQSQTHQPEEEELEKSQHLSFAGLAIPIAWPMMGSYNKRRTPL LTGQSLWQRNKPSQHSSTASKSRQPRKHYWPYVTYRAYSTSRETIWPLLPLETTGLATDCQL **PNKTQPP**

Starting nucleotide position: 1271

Ending nucleotide position: 6776



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