

Virus Report

22-01-2015 21:31:41

Secondary structure results

Virus name:

Sequence:

TGGTATCAGAGCAAGGTTTTCTGTAAGTAATTTATGGCTTTCATGGGGTAAAACCCTTAGA
TAGGAGCCTGAGGGCTCTGCTATGTTCTATTTTGAGAAAATAACTGTGTAAGTAGTAATGC
ATGATAAATCGAATAAGTTCTTTACGGATGGTCCTAAATTTATGAAATCATTCTTTTACTAT
CTGAGTGAGACCCTTGTTTCCAAGTTCTACTGAGAAATCATGAGTAAATGGACGTTGA
CACACTGACTTAAGGAAAAGAAAGATGTGCCTAGGATGAAGTCGAGCACTGTTCTAGGCT
GAAGGGTGAAAAGAAAAATGAGTTGAGTTGGGAGTAAGACTCTGAGAGGCTTGAGGCAA
AAGAACCGGAACCTTACCTAGCAAAGTAAGACCCAAGGGAGGGCAGTAGCTGGAGAACC
CCGGTGTGAGTTTCTTTACCTAGCAGAAGATATACTCTAGTATCCTCAAAACACCGTGAAG
TATTTACAACCCTTTATGAACAAGTATTTTCTGGAGTTAGATGTCAGCCACCAAAGATCAT
GATCTATCACAAACAACTTGAGTCATACAGAGAAGAACTCAGATGTAACCTGAATGACTAA
TGATCAGGGACCTCTATTAAGAGCTTAGTAAGAAGTAAGTGCATAAACTACCTCTGGAAC
TGGTTATAATCTTGAAATGAGCATATGTATCCCAAAGGTTACTCCTATCTGTCCGTGACCA
TAAGAAACCTTCTTTAAAGAAAAACTCTGGATTCTACTGGGATCTTGAATTTGAAAAGTA
CAAAAACCTCTCATTCCAAATCTGTTTCAGATCTTTCTTATTTAGACTTAGCATCTGCTGATA
AGGTCTCTAATAAAGACCTTGCATTTAATTTACATATAAACACTTATCGTAGTGATCTTGGT
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CCAACGAGCTGATTTAAAGGAGACCTTGAGAAGACAGGACGTCCTTGCGAAGGAGCTTC
AGGCTCTTCGTAAAGACTATCTGGAAAGGCGCCCTCTTAGCAAGGAGGACGTGGAAGAA
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GTTACTGGGATGAGCCTGGCCGGAAGCAAGGCCACAGCAATCTATCAAGAAGCCTTGCA
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TACCACTACCCTATCAAGGCAGCTAAATTCGCTGTTATTTCTGGTGATCAAAACAAAATCAG
CAGATCACCACCATCTCGGAAGAACTAACCCAACCTTCACAACCGGGTTAAAAACCTTGAA
GGAAGGACAGGGGTATCTGCAAGCCCCCTGTATAAATCGGAGATTGAATCCATCAACGC
CAAGCTCAAAAGTATTCAAGATATACAAGGGAGTCACCCTCCAAAAGAGACCCCTCCGG
AGTTATCAAAGTTTTTGAGGATCCCTACAGCATCCTCCGCAGACTATAAATGGCGTCAAGA
CCTAGAGTTTCTGGGAGCACTACCAGAACCATGATAGCAGAACCAGGGGTTCCCTGGT
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ATTGCCAGACGCACTGGCAATATTCTTGGAAGAATTGTTGGACGACAACCAAGGGAGCAT
ACCCTTGCGATGGTCGTGGACCCCAACAGTGAGCTGGAACGCTCACTGGCTCACCGGGC
ACGAACAATACCTGCTGAAGTCCTTTACATGACCCAGCGCGGTGAGCCTACAAATCGGGT
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CATCTTGCCAGAGTCATATGAAGAGCTCAGGGAGGCTGGATTTGAGTACATCCATCTAGG
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AAAATCAGGTACAAAATTTACCTGACCTTGACATACCCCTGCGAGAGGCAACTATGGTCTT
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ACAGGGGAAAGAAGGAACGCGATTCTCCTACAAAGTCACACTTCAGCCAACCCGAACAG

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CCAATATGCTGAAGATTATGCTACCTACACCAGGATAGGACTTGAAGCACTTAACCTTGAA
GATTGGTTCGAAGAACCAGAACCCGATCCACCTAACCCTGTGGACCGCCAGAGGATAGA
GGACATCCTGGACCTACTGAACGTCAGCAATGACGACTGAAAGATTCCCAGGACACCGG
CGGAAGTGGTGGACCCAGTCTAGGTGCGATGCTTAGTCGCGCACGATGACTATGTCGGA
AGGCATCTTTGCTTTCGGCAAACCTTTAGTAATACTTTAAGGAAAGTATTGTACAAGTTAGG
TGCAGAGACAATAATGCACCCAGCTTTAGCTTTGTTTATGGAATTATTGTGTCGGTTGCAT
TATTGGATGCCTGCGTGCACCCTAAGCAATCCCCGGCCCTCTTCTCTATAAGAGGAGCCC
TTGCAATCAGTTGCAAGCATGCAAGTTTCCCAGTCAAGCTTACTTCTGAGTTTGAGTTCA
AGTTCAATAAAATTCAAGCTTTCTCTTACATTCTGTTCTTGAAAGGTTGATCTAATCGAG
CGAGTAGAGAACAAGATCTTTTGGGATTTCCGCCGTTCCA

Structure in dot-bracket format:

[illegible]

Ending aminoacid position:
145

Domain description:
Protein of unknown function (DUF1319)

Identifier:
DUF1319

Protein 2

Number of domains:
0

Aminoacidsequence:
MSLAGSKATAIYQEALQSTAAGWEDTGIGFTDKGVISTTTLSRQLNSLLFLVIKQNQQITTISEE
LTQLHNRVKNLEGRTGVVSASPLYKSEIESINAKLKSIQDIQGSHPKETPSGVIKVFEDPYSILR
RL

Starting nucleotide position:
1282

Ending nucleotide position:
1681



Protein 3

Number of domains:
4

Aminoacidsequence:
MASRPRVSGSTTRTMIAEPGVPLVDDQIREYRSAARVAYEAQRIARRTGNI LGRIVGRQPREH
TLAMVVDPNSELESLAHRARTIPAEVLYMTQRGEPTNRVYRNRTTEERMLVTHGQQDRTFIL
PESYEELREAGFEYIHLGVLQVRIQIMHRTYDGTMALVVFRDTRWTQENHQDRSIIATMEADL
SQGHQLIYVIPDIMMTIRDFYQHIQISILTKGYEGFQGEANLLITRSCRCRLSNVPNVGFQYNIQ
NVVEFLKSRGVKALNATKLSTRRFQGGGEWNIRPSEVVVPMQPTTMIVRVNYDSSRSIRFGDY
EASTSSSAPRYEQDGEDEALGDIHQVNMITIIEDDAEDDYPRLSALERIIAPESMVGEEDTIAE
FLSNLSLDSSTDEEFYDADNSLFEEEEYDGDSEVSTPRSKYNIFALEDEYPKLQQLESVLSTT
ESAISRFRPADTDMTGVGPGYAPATGTAGYTGASSDFPYPRRPRKWDNNSEWFNLPTANA
RQASIFVMPQDFDTKVFERWESSVLLHMSDKVFDDPQDKLTYVENLLGESEKKMFITWRMM
FTAEEYEMKNNALGSNGTQNILNQIRMIFFLENPQVGTTNTQDAAYKTLKQLVCTEMSGPAIY
RYLNDYFHAAKSGRAWASDELSKEFFTKLPRGLGDRVEKKFKEKYPNNTIGVAPRITFTRNY
IKEICQEAVFQSQLKRLDFCKGTPVHGLYGKEKAYGRKYGVRKSTSYKGKPKHSHVRIDKKK
HLLMKRKDCKCFACGDIGHFASECPNPKKLMHRVQILQSLELDDGIDVISVGFDESVDIYSV
SEGEDSYQFNNEFDVIGHDVFMFTIEEQRNCLVETTSAWRSAMKVTPPEKNCLHTWSFEEK
TTDHCRACKNLALRGSRADCTQCKIIICSLCKPYYFQDGSPIPAQSSTPSGYSYDDWMGSAN
RWKAHYEFSQARRKSLKADLERAEELKFYKQKEKEKAKLKDQIPEAVQAKLDDLEKEKELN
NILRIEAETELKALKESFKEKEEALKEEITALEEEVRIHKEEAEELQEENQKLKEKIIAFEKDVTQ
GPREEVIELVNNVEEHLVLTGQQKNLLNIKITLEVKEKRITMNAILDGTGAICVCDGQMVNEYFR
RPSMMNAFIKGVNGITNVKEILEEGKIWIGNQWFRIPRTYIMPQLSEGLHFIIGMNFIRAMEGGI
RIEQGTVTIFYKMTQAQAPPMVHDISYLEELELELPIYYDICATNPSGGEINSDLPSEIRKLKD
LGYIGEEPLKHWAKNQVKCRIEIKNPDLIEDRPLKHVTPAMKESMKKHVDKLELKVIRPSTSK
HRTTAIVQSGTEIDPLTGKEKRGKERLVFNKYKRLNDNTEKDQYSLPGINTIISRIGKSKIYSKFD
LKSGFHQVAMDPEIPWTAFAWAIDGLYEWLVMPFGLKNAPAIQQRKMDNCFRGTEEFIAVYID
DILIFSDNISDHRKHLSKFLEICKANGLVLSPTKMKIGAKEIDFLGATIGNSKIQLQPHIIKKIIETKD
EELKETKGLRKWLGVNLNARAYIPNLGKTLGPLYSKTSINGEKKMNSQDWKVVLQIKNQVQNL
PDL DIPPAEATMVLETDGCMEGWGGVCKWKLHPSDTRLAEKVCAAYASGRYHPIKSTIDA EVH
AVINSLEKFKIYYLDKKELIIRTD SQAIVAFYKKQADHKPSRTRWLMLIDYITGLGINVKFEHIDGK
ENVLADTL SRLVQVLITKVHHPAETQLVEAVMEVISNPKKEALDKVNHFIFLTQQWIAERKEEH

TVNTLLQLEEPQLHCGCRNYETGERRNAILLSHTSANPNRWFKCAENKCHIWIWKDILDQ
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