# Virus Report

28-01-2015 11:54:37

# Secondary structure results

Virus name: Banana Virus

Sequence:

TGGTATCAGAGCAAGGTTTTCTGTAAGTAATTTATGGCTTTCATGGGGTAAAACCCTTAGA TAGGAGCCTGAGGGCTCTGCTATGTTCTATTTTGAGAAAATAACTGTGTAAGTAGTAATGC ATGATAAATCGAATAAGTTCTTTACGGATGGTCCTAAATTTATGAAATCATTCTTTTACTAT CTGAGTGAGACCCTTGTGTTTCCAAGTTCTACTGAGAAATCATGAGTAAATGGACGTTGA CACACTGACTTAAGGAAAAGAAGATGTGCCTAGGATGAAGTCGAGCACTGTTCTAGGCT GAAGGGTGAAAAGAAAATGAGTTGAGTTGGGAGTAAGACTCTGAGAGGCTTGAGGCAA CCGGTGTGAGTTTCTTTACCTAGCAGAAGATATACTCTAGTATCCTCAAAACACCGTGAAG TATTTACAACCCTTTATGAACAAGTATTTTCTGGAGTTAGATGTCAGCCACCAAAGATCAT GATCTATCACAAACAAACTTGAGTCATACAGAGAAGAACTCAGATGTAACTGAATGACTAA TGGTTATAATCTTGAAATGAGCATATGTATCCCAAAGGTTACTCCTATCTGTCCGTGACCA TAAGAAACCTTCTTTAAAGAAAACTCTGGATTCCTACTGGGATCTTGAATTTGAAAAGTA CAAAAACTCTCATTCCAAATCTGTTTCAGATCTTTCTTATTTAGACTTAGCATCTGCTGATA AGGTCTCTAATAAAGACCTTGCATTTAATTTACATATAAACACTTATCGTAGTGATCTTGGT TTTAAAGTCGCAATTCACTCTTTATCAAAAAATCGTGAGCTGCTAATACAGAACAGGAAGC TTTTGGAAGAACAAAAGCAGCAGCTGTCTGAAATTAACAACCTATCTAAGGTTGTGCGTCT CCAACGAGCTGATTTAAAGGAGACCTTGAGAAGACAGGACGTCCTTGCGAAGGAGCTTC AGGCTCTTCGTAAAGACTATCTGGAAAGGCGCCCTCTTAGCAAGGAGGACGTGGAAGAA TTGGTTGTCCGCATCTCTGAACAACCAAAAATTTATTGAAAAAACAGACGGAAGCTCTTAC TGAGGAGCTTACAAAGGAGGTTCAGGCACTGAAGCTAATCATCCATAACTTCGAACAGAA GTTACTGGGATGAGCCTGGCCGGAAGCAAGGCCACAGCAATCTATCAAGAAGCCTTGCA ATCTACTGCTGCTGGTTGGGAAGACACCGGCATCGGATTTACTGATAAAGGAGTTATCAG CAGATCACCACCATCTCGGAAGAACTAACCCAACTTCACAACCGGGTTAAAAACCTTGAA GGAAGGACAGGGTATCTGCAAGCCCCCTGTATAAATCGGAGATTGAATCCATCAACGC CAAGCTCAAAAGTATTCAAGATATACAAGGGAGTCACCCTCCAAAAGAGACCCCCTCCGG AGTTATCAAAGTTTTTGAGGATCCCTACAGCATCCTCCGCAGACTATAAATGGCGTCAAGA CCTAGAGTTTCTGGGAGCACTACCAGAACCATGATAGCAGAACCAGGGGTTCCCCTGGT GGATGATCAGATCCGGGAATACCGGAGTGCGGCCCGAGTCGCATACGAAGCACAAAGG ATTGCCAGACGCACTGGCAATATTCTTGGAAGAATTGTTGGACGACAACCAAGGGAGCAT ACCCTTGCGATGGTCGTGGACCCCAACAGTGAGCTGGAACGCTCACTGGCTCACCGGGC ACGAACAATACCTGCTGAAGTCCTTTACATGACCCAGCGCGGTGAGCCTACAAATCGGGT CTATCGGAACAGAACTGAAGAAAGGATGCTAGTGACTCATGGTCAGCAAGATAGGACTTT GGTACTCCAGGTGCGCATCCAAATTATGCACCGAACATATGATGGTACAATGGCATTAGT GGTCTTCCGTGACACCAGATGGACACAGGAGAACCACCAAGACAGATCCATTATAGCAAC CATGGAGGCTGATCTCCCCAAGGGCATCAGCTAATTTACGTCATCCCAGATATAATGAT GACTATTCGGGATTTCTACCAGCACATTCAGATAAGCATCCTTACCAAAGGATATGAAGG CTTTCAAGGAGAAGCAAATCTCCTTATTACAAGAAGCTGCCGGTGCAGATTAAGCAACGT TCCTAACGTTGGCTTCCAATACAACATCCAGAACGTCGTGGAATTCTTAAAATCTAGGGGA GTAAAAGCCCTAAATGCGACGAAATTAAGCACCAGGAGGTTCCAAGGAGGAGAATGGAA CATCCGACCATCAGAAGTGGTGGTCCCTATGCAGCCAACAACTATGATAGTACGAGTTAA TTATGACTCGTCACGAAGCATCAGATTCGGGGGATTATGAAGCTAGCACATCATCAGC CCCGAGATATGAGCAAGACGGTGATGAAGATGAAGCACTTGGTGATATCCATCAAGTAAA TATGATCACCATCATAGAAGATGATGCAGAAGATGACTACCCACGGTTATCAGCTTTAGA GCGAATAATCGCTCCAGAAAGCATGGTGGGAGAGGAGGACACAATTGCTGAATTTTTAAG CAATCTGTCCTTAGATTCCTCCACTGATGAGGAATTCTACGACGCCGACAACTCATTATTC GAAGAAGAAGAATATGATGGGGATTCCGAAGTTAGCACCCCAAGGAGCAAATACAATATA TTTGCGCTAGAAGATGAGTACCCAAAACTTCAACAGCTGGAAAGCCTGGTACTCTCCACA ACAGAGTCTGCTATCAGTCGCTTTAGACCAGCAGACACAGATATGACTGGCGTAGGCCCT GGCTACGCACCAGCAACTGGAACAGCTGGCTATACTGGAGCCAGTTCATCTGATTTCCCT TACCCTAGAAGACCAAGAAAGTGGGACAACAACTCGGAGTGGTTCAACCTACCCACCGC TAACGCGAGGCAAGCATCAATATTCGTTATGCCTCAGGATTTTGACACAAAGGTCTTTGAA

AGATGGGAAAGTTCTGTTCTCCTTCACATGTCTGACAAGGTTTTTGATGATCCACAAGACA AGTTAACTTATGTGGAAAACCTACTAGGAGAATCAGAAAAGAAGATGTTTATCACTTGGAG GATGATGTTCACAGCTGAGTACGAAGAAATGAAGAACAACGCTCTCGGCTCAAATGGAAC TCAAAATATCCTGAACCAGATCAGGATGATATTCTTTCTGGAAAATCCCCAAGTTGGAACC ACCAACACTCAAGACGCAGCATACAAGACACTCAAACAACTAGTCTGCACAGAGATGTCT GGACCTGCGATCTACAGGTACCTAAATGATTACTTCCATTTAGCGGCAAAATCTGGAAGA GCGTGGGCATCTGATGAGCTGTCCAAGGAATTCTTTACAAAACTGCCAAGGGGATTAGG GGACAGAGTTGAAAAGAAATTCAAAGAAAAGTACCCCAACAACACTATTGGAGTAGCCCC CAGAATCACCTTCACAAGAAATTATATAAAGGAAATATGCCAAGAGGCTGTATTCCAAAGC CAACTGAAAAGGCTAGATTTTTGCAAAGGGACACCCGTCCACGGCTTATATGGTAAAGAG AAGGCATATGGGAGGAAATACGGAGTCAGGAAAAGCACTTCGTACAAAGGAAAGCCTCA CAAGTCACATGTGAGGATAGATAAAAAGAAGCACCTCCTGATGAAACGAAAAGACTGCAA GTGTTTTGCTTGCGGAGATATCGGTCACTTCGCATCAGAGTGTCCGAATCCCAAGAAGCT GATGCACCGAGTTCAAATTCTACAATCCTTAGAGCTTGATGACGGAATCGACGTAATCTC CGTAGGATTTGATGAGTCAGATGTCTCAGACATCTATTCGGTATCTGAAGGCGAGGACAG CTACCAGTTCAATAATGAGGATTTTGACGTTATAGGACATGACGTGTTCATGTTCACCATT GAAGAACAAAGAAACTGCCTGGTAGAAACCACGTCAGCCTGGAGAAGTGCAATGAAAGTT ACTCCAGAAGAAAAGAATTGCTTACACACATGGAGCTTTGAGGAAAAGACAACAGACCAC TGCAGAGCCTGCAAAAATCTGGCCCTACGAGGGAGCAGAGCTGACTGCACTCAGTGTAA GATAATCATTTGCTCTTTATGCAAACCATACTATTTCCAGGATGGTTCACCTATCCCAGCA CAAAGTTCAACCCCATCAGGATACTCCTACGATGATTGGATGGGATCAGCAAATAGGTGG AAGGCACACTATGAGTTCTCTCAGGCAAGAAGGAAGAGCCTGAAGGCAGACCTTGAAAG AGCGGAAGAAGAACTAAAATTTTATAAGCAAAAGGAAAAGGAAAAGGCCAAATTAAAGGA TCAAATTCCAGAAGCAGTACAAGCAAAACTGGATGATCTGGAAAAAAGAAAAAGAGCTCAA TAACATCCTAAGAATAGAGGCTGAGACAGAGCTAAAAGCATTAAAGGAAAGCTTCAAAGA AAAGGAAGAAGCCCTGAAGGAAGAAATCACAGCTCTAGAAGAAGAAGTGAGGATACACA AAGAGGAGGCTGAAGAACTTCAGGAAGAAAATCAAAAACTCAAAGAGAAGATCATAGCCT TCGAAAAAGACGTAACACAAGGACCAGAAGAAGTGATCGAATTGGTCAATAACGTGGAGG AGCACCTGGTACTAACAGGACAACAGAAGAACAATCTCCTCAACATCAAGATAACTCTGG AAGTTAAGGAAAAAGGATTACCATGAACGCGATACTAGACACTGGAGCCGCAATCTGTG TCTGTGATGGGCAAATGGTAAACGAATATTTCAGGAGACCATCAATGATGAATGCGTTCAT TGGTAATCAATGGTTCAGAATCCCAAGGACATACATCATGCCCCAGCTATCAGAAGGCCT TCATTTCATCATCGGAATGAACTTTATCAGGGCAATGGAAGGAGGGATTCGAATTGAGCA AGGAACGGTAACCTTCTACAAAATGGTTACACAAGCACAGGCACCCCCTATGGTACACGA TATTTCTTACCTTGAAGAATTAGAATTAGAACTGCCGATTTACTATGATATCTGTGCAACTA ACCCCTCAGGAGGAGAATCAATAGTGACCTAATATCCCCCTCGGAGATCCGGAAACTAA AGGACTTAGGCTACATTGGGGAAGAGCCCTTGAAACATTGGGCTAAGAATCAAGTCAAGT GCCGAATTGAAATCAAGAACCCTGACTTAATCATTGAAGATAGGCCCTTGAAGCACGTCA CCCCAGCAATGAAAGAATCCATGAAGAAACATGTGGACAAGCTGCTGGAACTTAAGGTAA TCAGGCCATCCACAAGCAAACACCGGACGACTGCGATAATTGTTCAATCCGGTACAGAAA TTGACCCCCTCACTGGAAAAGAGAAAAGAGGGGAAAGAGAGGCTTGTATTCAACTACAAAC GCCTCAACGACAATACCGAAAAAGACCAGTATTCACTACCTGGCATCAATACAATTATCAG CAGGATCGGCAAGTCAAAAATTTACAGCAAATTTGACTTAAAATCCGGATTCCACCAGGTA GCCATGGATCCAGAAAGCATCCCATGGACGGCCTTTTGGGCCATAGATGGACTTTATGAA TGGCTAGTTATGCCATTTGGTCTGAAGAATGCGCCCGCTATATTTCAGAGAAAGATGGAC AACTGCTTCCGAGGAACGGAGGAATTCATAGCGGTATATATTGATGATATTTTAATATTCT CTGACAATATCTCTGATCACAGGAAACATCTGTCAAAATTCCTGGAGATCTGCAAGGCGA ATGGGCTGGTATTAAGCCCAACAAAAATGAAGATAGGCGCAAAGGAAATTGATTTCCTAG GAGCAACTATTGGAAACTCCAAGATCAAGCTTCAACCTCATATAATCAAGAAGATCATCGA GACAAAGGACGAGGAGCTAAAGGAAACAAAGGGGCTCAGAAAATGGTTGGGAGTCCTTA ACTATGCACGGGCATACATTCCAAATTTAGGAAAAACATTAGGCCCGCTCTACTCCAAGA CGTCAATTAATGGAGAGAAGAAGATGAACAGCCAAGATTGGAAGGTTGTTCAACTGATCA AAAATCAGGTACAAAATTTACCTGACCTTGACATACCCCCTGCAGAGGCAACTATGGTCTT AGAGACTGACGGGTGTATGGAAGGATGGGAGGAGTATGCAAATGGAAGCTCCATCCCT CTGACACAAGACTGGCAGAAAAGGTCTGTGCGTACGCAAGTGGAAGGTATCACCCCATC AAGAGCACAATTGATGCAGAGGTACACGCAGTGATCAACAGCTTAGAAAAATTCAAAATTT TAAGAAGCAAGCTGATCATAAGCCCTCAAGAACAAGGTGGCTTATGCTAATTGACTACATT GATACTCTATCAAGGCTGGTCCAAGTGCTGATCACCAAGGTTCATCATCCAGCAGAAACC CAGCTAGTCGAAGCCGTCATGGAAGTTATAAGCAATCCAAAGAAGAAGCCTTGGACAAG GTAAACCATTTTATCTTCCTAACCCAACAGTGGATTGCAGAACGCAAGGAGGAGCACACG GTGAACACGCTACTCCAGTTGGAAGAACCACAGCTGCATTGTGGTTGTAGAAACTATGAA

ACAGGGGAAAGAAGGAACGCGATTCTCCTACAAAGTCACACTTCAGCCAACCCGAACAG
ATGGTTCTATAAGTGTGCAGAAAACAAGTGCCACATTTGGATCTGGAAAGACATCCTGGA
CCAATATGCTGAAGATTATGCTACCTACACCAGGATAGGACTTGAAGCACTTAACCTTGAA
GATTGGTTCGAAGAACCAGAACCCGATCCACCTAACCCTGTGGACCGCCAGAGGATAGA
GGACATCCTGGACCTACTGAACGTCAGCAATGACGACTGAAAGATTCCCAGGACACCGG
CGGAAGTGGTGGACCCAGTCTAGGTGCGATGCTTAGTCGCACCGATGACTATGTCGGA
AGGCATCTTTGCTTTCGGCAAACTTTAGTAATACTTTAAGGAAAGTATTGTACAAGTTAGG
TGCAGAGACAATAATGCACCCAGCTTTAGCTTTGTTTATGGAATTATTGTGTCGGTTGCAT
TATTGGATGCCTGCGTGCACCCTAAGCAATCCCCGGCCCTCTTCTCTATAAGAGGAGCCC
TTGCAATCAGTTGCAAGCATGCAAGTTTCCCACTGCAAGCTTACTTCTGAGTTTCAGTTCA
AGTTCAATAAAATTCAAGCTTTCCTCTTACATTCTGTTCTTGAAAAGGTTCGATCTAATCGAG
CGAGTAGAGAACAAGATCTTTTGGGATTTCCGCCGTTCCA

# Structure in dot-bracket format: $(1,\dots,(1)))))(1,\dots,(1))(1,\dots,(1)))(1,\dots,(1)))(1,\dots,(1)))(1,\dots,(1)))(1,\dots,(1)))(1,\dots,(1)))(1,\dots,(1))($

$ \begin{array}{lll} .))).))))))(((((((((((((((((((((((($
Energy: -2272.4
RNA-Structure:
Image of the structure couldn't be produced
Virus Domain(s)
Number of proteins: 3
Protein 1
Number of domains:
Aminoacidsequence: LDSYWDLEFEKYKNSHSKSVSDLSYLDLASADKVSNKDLAFNLHINTYRSDLGFKVAIHSLSK NRELLIQNRKLLEEQKQQLSEINNLSKVVRLQRADLKETLRRQDVLAKELQALRKDYLERRPL SKEDVEELVVRISEQPKIY
Starting nucleotide position: 753
Ending nucleotide position: 1191
Image of the domain isn't available
Domain 1
Starting aminoacid position: 15
Ending aminoacid position: 145
Domain description: Protein of unknown function (DUF1319)
Identifier: DUF1319
Protein 2
Number of domains:
Aminoacidsequence: MSLAGSKATAIYQEALQSTAAGWEDTGIGFTDKGVISTTTLSRQLNSLLFLVIKQNQQITTISEE LTQLHNRVKNLEGRTGVSASPLYKSEIESINAKLKSIQDIQGSHPPKETPSGVIKVFEDPYSILR RL

Starting nucleotide position:

Ending nucleotide position: 1681

Image of the domain isn't available

#### Protein 3

Number of domains:

4

Aminoacidsequence:

MASRPRVSGSTTRTMIAEPGVPLVDDQIREYRSAARVAYEAQRIARRTGNILGRIVGRQPREH TLAMVVDPNSELERSLAHRARTIPAEVLYMTQRGEPTNRVYRNRTEERMLVTHGQQDRTFIL PESYEELREAGFEYIHLGVLQVRIQIMHRTYDGTMALVVFRDTRWTQENHQDRSIIATMEADL SQGHQLIYVIPDIMMTIRDFYQHIQISILTKGYEGFQGEANLLITRSCRCRLSNVPNVGFQYNIQ NVVEFLKSRGVKALNATKLSTRRFQGGEWNIRPSEVVVPMQPTTMIVRVNYDSSRSIRFGDY EASTSSSAPRYEQDGDEDEALGDIHQVNMITIIEDDAEDDYPRLSALERIIAPESMVGEEDTIAE FLSNLSLDSSTDEEFYDADNSLFEEEEYDGDSEVSTPRSKYNIFALEDEYPKLQQLESLVLSTT ESAISRFRPADTDMTGVGPGYAPATGTAGYTGASSSDFPYPRRPRKWDNNSEWFNLPTANA RQASIFVMPQDFDTKVFERWESSVLLHMSDKVFDDPQDKLTYVENLLGESEKKMFITWRMM FTAEYEEMKNNALGSNGTQNILNQIRMIFFLENPQVGTTNTQDAAYKTLKQLVCTEMSGPAIY RYLNDYFHLAAKSGRAWASDELSKEFFTKLPRGLGDRVEKKFKEKYPNNTIGVAPRITFTRNY IKEICQEAVFQSQLKRLDFCKGTPVHGLYGKEKAYGRKYGVRKSTSYKGKPHKSHVRIDKKK HLLMKRKDCKCFACGDIGHFASECPNPKKLMHRVQILQSLELDDGIDVISVGFDESDVSDIYSV SEGEDSYQFNNEDFDVIGHDVFMFTIEEQRNCLVETTSAWRSAMKVTPEEKNCLHTWSFEEK TTDHCRACKNLALRGSRADCTQCKIIICSLCKPYYFQDGSPIPAQSSTPSGYSYDDWMGSAN RWKAHYEFSQARRKSLKADLERAEEELKFYKQKEKEKAKLKDQIPEAVQAKLDDLEKEKELN NILRIEAETELKALKESFKEKEEALKEEITALEEEVRIHKEEAEELQEENQKLKEKIIAFEKDVTQ GPEEVIELVNNVEEHLVLTGQQKNNLLNIKITLEVKEKRITMNAILDTGAAICVCDGQMVNEYFR RPSMMNAFIKGVNGITNVKEILEEGKIWIGNQWFRIPRTYIMPQLSEGLHFIIGMNFIRAMEGGI RIEQGTVTFYKMVTQAQAPPMVHDISYLEELELELPIYYDICATNPSGGEINSDLISPSEIRKLKD LGYIGEEPLKHWAKNQVKCRIEIKNPDLIIEDRPLKHVTPAMKESMKKHVDKLLELKVIRPSTSK HRTTAIIVQSGTEIDPLTGKEKRGKERLVFNYKRLNDNTEKDQYSLPGINTIISRIGKSKIYSKFD LKSGFHQVAMDPESIPWTAFWAIDGLYEWLVMPFGLKNAPAIFQRKMDNCFRGTEEFIAVYID DILIFSDNISDHRKHLSKFLEICKANGLVLSPTKMKIGAKEIDFLGATIGNSKIKLQPHIIKKIIETKD EELKETKGLRKWLGVLNYARAYIPNLGKTLGPLYSKTSINGEKKMNSQDWKVVQLIKNQVQNL PDLDIPPAEATMVLETDGCMEGWGGVCKWKLHPSDTRLAEKVCAYASGRYHPIKSTIDAEVH AVINSLEKFKIYYLDKKELIIRTDSQAIVAFYKKQADHKPSRTRWLMLIDYITGLGINVKFEHIDGK ENVLADTLSRLVQVLITKVHHPAETQLVEAVMEVISNPKKEALDKVNHFIFLTQQWIAERKEEH TVNTLLQLEEPQLHCGCRNYETGERRNAILLQSHTSANPNRWFYKCAENKCHIWIWKDILDQ YAEDYATYTRIGLEALNLEDWFEEPEPDPPNPVDRQRIEDILDLLNVSNDD

Starting nucleotide position: 1681

Ending nucleotide position: 7378

Image of the domain isn't available

#### Domain 1

Starting aminoacid position: 1349

Ending aminoacid position: 1509

Domain description:

Reverse transcriptase (RNA-dependent DNA polymerase)

Identifier:

# RVT\_1

## Domain 2

Starting aminoacid position: 125

Ending aminoacid position: 246

Domain description: Viral movement protein (MP)

Identifier: MP

## Domain 3

Starting aminoacid position: 1090

Ending aminoacid position: 1201

Domain description: Retroviral aspartyl protease

Identifier: RVP

## Domain 4

Starting aminoacid position: 763

Ending aminoacid position: 780

Domain description: Zinc knuckle

Identifier: zf-CCHC