Virus Report

17-01-2015 16:57:34

Secondary structure results

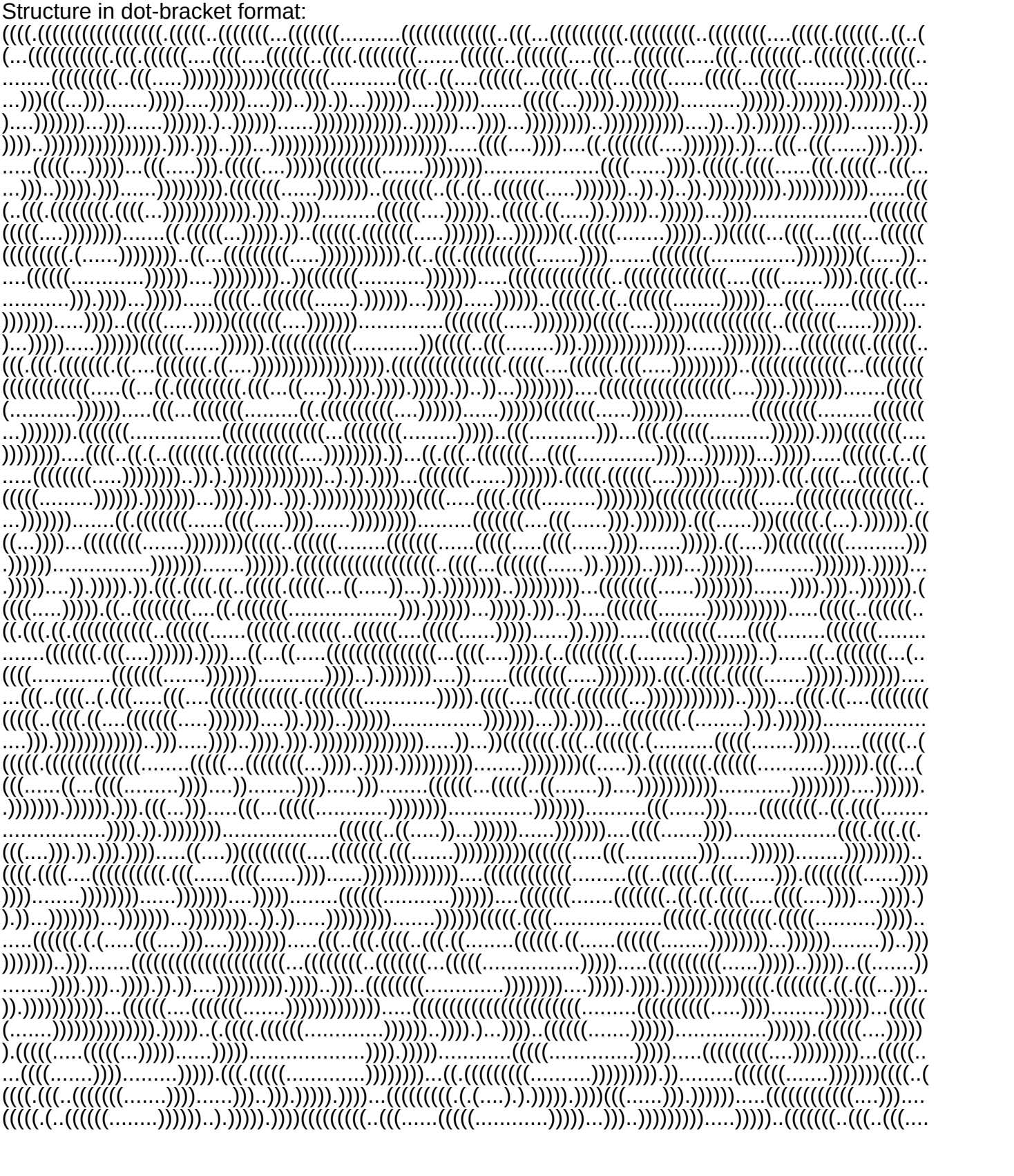
Virus name:
HI-V

Sequence:
TGGTATCAGAGCAAGGTTTTCTGTAAGTAATTTATGGCTTTCATGGGGTAAAACCCTTAGA
TAGGAGCCTGAGGGCTCTGCTATGTTCTATTTTGAGAAAATAACTGTGTAAGTAGTAATGC
ATGATAAATCGAATAAGTTCTTTACGGATGGTCCTAAATTTATGAAATCATTCTTTTACTAT
CTGAGTGAGACCCTTGTGTTTCCAAGTTCTACTGAGAAATCATGAGTAAATGGACGTTGA
CACACTGACTTAAGGAAAAGAAAGATGTGCCTAGGATGAAGTCGAGCACTGTTCTAGGCT
GAAGGGTGAAAAGAAAAATGAGTTGAGTTGGGAGTAAGACTCTGAGAGGCTTGAGGCAA
AAGAACCGGAACCTTACCTAGCAAAGTAAGACCCAAGGGAGGGCAGTAGCTGGAGAACC
CCGGTGTGAGTTTCTTTACCTAGCAGAAGATATACTCTAGTATCCTCAAAACACCGTGAAG
TATTTACAACCCTTTATGAACAAGTATTTTCTGGAGTTAGATGTCAGCCACCAAAGATCAT
GATCTATCACAAACAAACTTGAGTCATACAGAGAAGAACTCAGATGTAACTGAATGACTAA
TGATCAGGGACCTCTATTAAAGAGCTTAGTAAGAAGTAAGTGCATAAACTACCTCTGGAAC
TGGTTATAATCTTGAAATGAGCATATGTATCCCAAAGGTTACTCCTATCTGTCCGTGACCA
TAAGAAACCTTCTTTAAAGAAAAACTCTGGATTCCTACTGGGATCTTGAATTTGAAAAGTA
CAAAAACTCTCATTCCAAATCTGTTTCAGATCTTTCTTATTTAGACTTAGCATCTGCTGATA
AGGTCTCTAATAAAGACCTTGCATTTAATTTACATATAAACACTTATCGTAGTGATCTTGGT
TTTAAAGTCGCAATTCACTCTTTATCAAAAAATCGTGAGCTGCTAATACAGAACAGGAAGC
TTTTGGAAGAACAAAAGCAGCAGCTGTCTGAAATTAACAACCTATCTAAGGTTGTGCGTCT
CCAACGAGCTGATTTAAAGGAGACCTTGAGAAGACAGGACGTCCTTGCGAAGGAGCTTC
AGGCTCTTCGTAAAGACTATCTGGAAAGGCGCCCTCTTAGCAAGGAGGACGTGGAAGAA
TTGGTTGTCCGCATCTCTGAACAACCAAAAATTTATTGAAAAAACAGACGGAAGCTCTTAC
TGAGGAGCTTACAAAGGAGGTTCAGGCACTGAAGCTAATCATCCATAACTTCGAACAGAA
GTTACTGGGATGAGCCTGGCCGGAAGCAAGGCCACAGCAATCTATCAAGAAGCCTTGCA
ATCTACTGCTGCTGGTTGGGAAGACACCGGCATCGGATTTACTGATAAAGGAGTTATCAG
TACCACTACCCTATCAAGGCAGCTAAATTCGCTGTTATTTCTGGTGATCAAACAAAATCAG
CAGATCACCACCATCTCGGAAGAACTAACCCAACTTCACAACCGGGTTAAAAACCTTGAA
GGAAGGACAGGGGTATCTGCAAGCCCCCTGTATAAATCGGAGATTGAATCCATCAACGC
CAAGCTCAAAAGTATTCAAGATATACAAGGGAGTCACCCTCCAAAAGAGACCCCCTCCGG
AGTTATCAAAGTTTTTGAGGATCCCTACAGCATCCTCCGCAGACTATAAATGGCGTCAAGA
CCTAGAGTTTCTGGGAGCACTACCAGAACCATGATAGCAGAACCAGGGGTTCCCCTGGT
GGATGATCAGATCCGGGAATACCGGAGTGCGGCCCGAGTCGCATACGAAGCACAAAGG
ATTGCCAGACGCACTGGCAATATTCTTGGAAGAATTGTTGGACGACAACCAAGGGAGCAT
ACCCTTGCGATGGTCGTGGACCCCAACAGTGAGCTGGAACGCTCACTGGCTCACCGGGC
ACGAACAATACCTGCTGAAGTCCTTTACATGACCCAGCGCGGTGAGCCTACAAATCGGGT
CTATCGGAACAGAACTGAAGAAAGGATGCTAGTGACTCATGGTCAGCAAGATAGGACTTT
CATCTTGCCAGAGTCATATGAAGAGCTCAGGGAGGCTGGATTTGAGTACATCCATCTAGG
GGTACTCCAGGTGCGCATCCAAATTATGCACCGAACATATGATGGTACAATGGCATTAGT
GGTCTTCCGTGACACCAGATGGACACAGGAGAACCACCAAGACAGATCCATTATAGCAAC
CATGGAGGCTGATCTCTCCCAAGGGCATCAGCTAATTTACGTCATCCCAGATATAATGAT
GACTATTCGGGATTTCTACCAGCACATTCAGATAAGCATCCTTACCAAAGGATATGAAGG
CTTTCAAGGAGAAGCAAATCTCCTTATTACAAGAAGCTGCCGGTGCAGATTAAGCAACGT
TCCTAACGTTGGCTTCCAATACAACATCCAGAACGTCGTGGAATTCTTAAAATCTAGGGGA
GTAAAAGCCCTAAATGCGACGAAATTAAGCACCAGGAGGTTCCAAGGAGGAGAATGGAA
CATCCGACCATCAGAAGTGGTGGTCCCTATGCAGCCAACAACTATGATAGTACGAGTTAA
TTATGACTCGTCACGAAGCATCAGATTCGGGGATTATGAAGCTAGCACATCATCATCAGC
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
TCAAATTCCAGAAGCAGTACAAGCAAAACTGGATGATCTGGAAAAAGAAAAAGAGCTCAA
TAACATCCTAAGAATAGAGGCTGAGACAGAGCTAAAAGCATTAAAGGAAAGCTTCAAAGA
AAAGGAAGAAGCCCTGAAGGAAGAAATCACAGCTCTAGAAGAAGAAGTGAGGATACACA
AAGAGGAGGCTGAAGAACTTCAGGAAGAAAATCAAAAACTCAAAGAGAAGATCATAGCCT
TCGAAAAAGACGTAACACAAGGACCAGAAGAAGTGATCGAATTGGTCAATAACGTGGAGG
AGCACCTGGTACTAACAGGACAACAGAAGAACAATCTCCTCAACATCAAGATAACTCTGG
AAGTTAAGGAAAAAAGGATTACCATGAACGCGATACTAGACACTGGAGCCGCAATCTGTG
TCTGTGATGGGCAAATGGTAAACGAATATTTCAGGAGACCATCAATGATGAATGCGTTCAT
AAAGGGAGTTAATGGGATTACCAATGTCAAAGAAATCTTAGAGGAAGGAAAAATCTGGAT
TGGTAATCAATGGTTCAGAATCCCAAGGACATACATCATGCCCCAGCTATCAGAAGGCCT
TCATTTCATCATCGGAATGAACTTTATCAGGGCAATGGAAGGAGGGATTCGAATTGAGCA
AGGAACGGTAACCTTCTACAAAATGGTTACACAAGCACAGGCACCCCCTATGGTACACGA
TATTTCTTACCTTGAAGAATTAGAATTAGAACTGCCGATTTACTATGATATCTGTGCAACTA
ACCCCTCAGGAGGAGAAATCAATAGTGACCTAATATCCCCCTCGGAGATCCGGAAACTAA
AGGACTTAGGCTACATTGGGGAAGAGCCCTTGAAACATTGGGCTAAGAATCAAGTCAAGT
GCCGAATTGAAATCAAGAACCCTGACTTAATCATTGAAGATAGGCCCTTGAAGCACGTCA
CCCCAGCAATGAAAGAATCCATGAAGAAACATGTGGACAAGCTGCTGGAACTTAAGGTAA
TCAGGCCATCCACAAGCAAACACCGGACGACTGCGATAATTGTTCAATCCGGTACAGAAA
TTGACCCCCTCACTGGAAAAGAGAAAAGAGGGAAAGAGAGGCTTGTATTCAACTACAAAC
GCCTCAACGACAATACCGAAAAAGACCAGTATTCACTACCTGGCATCAATACAATTATCAG
CAGGATCGGCAAGTCAAAAATTTACAGCAAATTTGACTTAAAATCCGGATTCCACCAGGTA
GCCATGGATCCAGAAAGCATCCCATGGACGGCCTTTTGGGCCATAGATGGACTTTATGAA
TGGCTAGTTATGCCATTTGGTCTGAAGAATGCGCCCGCTATATTTCAGAGAAAGATGGAC
AACTGCTTCCGAGGAACGGAGGAATTCATAGCGGTATATATTGATGATATTTTAATATTCT
CTGACAATATCTCTGATCACAGGAAACATCTGTCAAAATTCCTGGAGATCTGCAAGGCGA
ATGGGCTGGTATTAAGCCCAACAAAAATGAAGATAGGCGCAAAGGAAATTGATTTCCTAG
GAGCAACTATTGGAAACTCCAAGATCAAGCTTCAACCTCATATAATCAAGAAGATCATCGA
GACAAAGGACGAGGAGCTAAAGGAAACAAAGGGGCTCAGAAAATGGTTGGGAGTCCTTA
ACTATGCACGGGCATACATTCCAAATTTAGGAAAAACATTAGGCCCGCTCTACTCCAAGA
CGTCAATTAATGGAGAGAAGAAGATGAACAGCCAAGATTGGAAGGTTGTTCAACTGATCA
AAAATCAGGTACAAAATTTACCTGACCTTGACATACCCCCTGCAGAGGCAACTATGGTCTT
AGAGACTGACGGGTGTATGGAAGGATGGGGAGGAGTATGCAAATGGAAGCTCCATCCCT
CTGACACAAGACTGGCAGAAAAGGTCTGTGCGTACGCAAGTGGAAGGTATCACCCCATC
AAGAGCACAATTGATGCAGAGGTACACGCAGTGATCAACAGCTTAGAAAAATTCAAAATTT
ATTATCTGGATAAAAAGGAGTTGATCATAAGAACAGACAGCCAGGCTATTGTGGCTTTTTA
TAAGAAGCAAGCTGATCATAAGCCCTCAAGAACAAGGTGGCTTATGCTAATTGACTACATT
ACTGGGCTCGGAATCAACGTCAAATTCGAGCATATTGACGGGAAAGAAAATGTTCTAGCT
GATACTCTATCAAGGCTGGTCCAAGTGCTGATCACCAAGGTTCATCATCCAGCAGAAACC
CAGCTAGTCGAAGCCGTCATGGAAGTTATAAGCAATCCAAAGAAAGAAGCCTTGGACAAG
GTAAACCATTTTATCTTCCTAACCCAACAGTGGATTGCAGAACGCAAGGAGGAGCACACG
GTGAACACGCTACTCCAGTTGGAAGAACCACAGCTGCATTGTGGTTGTAGAAACTATGAA

ACAGGGGAAAGAAGGAACGCGATTCTCCTACAAAGTCACACTTCAGCCAACCCGAACAG
ATGGTTCTATAAGTGTGCAGAAAACAAGTGCCACATTTGGATCTGGAAAGACATCCTGGA
CCAATATGCTGAAGATTATGCTACCTACACCAGGATAGGACTTGAAGCACTTAACCTTGAA
GATTGGTTCGAAGAACCAGAACCCGATCCACCTAACCCTGTGGACCGCCAGAGGATAGA
GGACATCCTGGACCTACTGAACGTCAGCAATGACGACTGAAAGATTCCCAGGACACCGG
CGGAAGTGGTGGACCCAGTCTAGGTGCGATGCTTAGTCGCGCACGATGACTATGTCGGA
AGGCATCTTTGCTTTCGGCAAACTTTAGTAATACTTTAAGGAAAGTATTGTACAAGTTAGG
TGCAGAGACAATAATGCACCCAGCTTTAGCTTTGTTTATGGAATTATTGTGTCGGTTGCAT
TATTGGATGCCTGCGTGCACCCTAAGCAATCCCCGGCCCTCTTCTCTATAAGAGGAGCCC
TTGCAATCAGTTGCAAGCATGCAAGTTTCCCACTGCAAGCTTACTTCTGAGTTTGAGTTCA
AGTTCAATAAAATTCAAGCTTTCCTCTTACATTCTGTTCTTGAAAGGTTCGATCTAATCGAG
CGAGTAGAGAACAAGATCTTTTGGGATTTCCGCCGTTCCA

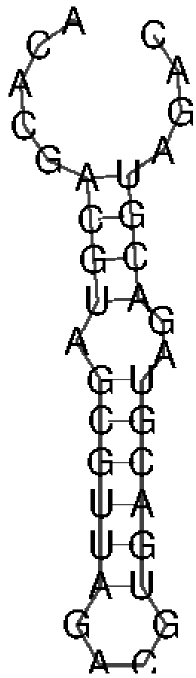
Structure in dot-bracket format:



.)))..))))))....((((((((.((........)).))))))))................))))(((((((............)))))))....((((((....((.......(((((((....(((......((
(((.....(((.(((.(.......).))).)))))))))))....)))))))))....))))))((((.(((...)))..))))...)))))).)))))))))).((....)).......((((((....(((....
))).((((.....))))))))))))).))))))..))))))..))))))))))))..((((((.....))))))((((((((.((((.......(((....((((....((..............))....))))
......)))......))))))))))))(((.(((..........))))))...((((((.((......(((((((.........((...........))........)))))))....(((.(((........))).))).
((((((((...))))))))..)).))))))(((...(((.(((....))).)))....)))...((((((..((.......(((((....)))))......))....)))))))))))))))...))))))))))(
(((..(((((((((.....)))))))).)...)))).((((((.((((((....))))))))))))(((((...(((((((((....)))))))))...))))).((((((..........)))))).(((....))
)...))))))))......))).)))).))))).)))))))).......)))))).)))..))))).((((((((((.......)))))).)))(((((((....)))))))..((((.((.....))))))((((
((....))))))))))))))...))))..........)))..))))))).))))))))))))))..))))))))))..)))))).))))))...)))).))))...)))))....))))))...

Energy:
0

RNA-Structure:



Virus Domain(s)

Number of proteins:
1

Protein 1

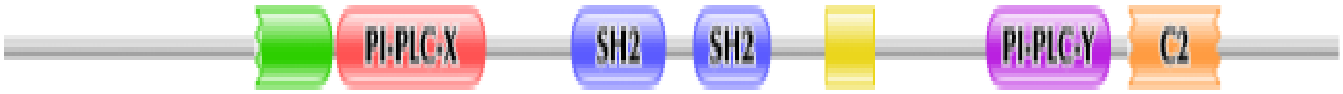
Number of domains:
7

Aminoacidsequence:
MAGAASPCANGCGPSAPSDAEVVHLCRSLEVGTVMTLFYSKKSQRPERKTFQVKLETRQIT
WSRGADKIEGAIDIREIKEIRPGKTSRDFDRYQEDPAFRPDQSHCFVILYGMEFRLKTLSLQAT
SEDEVNMWIRGLTWLMEDTLQAATPLQIERWLRKQFYSVDRNREDRISAKDLKNMLSQVNY
RVPNMRFLRERLTDLEQRTSDITYGQFAQLYRSLMYSAQKTMDLPFLEASALRAGERPELCR
VSLPEFQQFLLEYQGELWAVDRLQVQEFMLSFLRDPLREIEEPYFFLDEFVTFLFSKENSIWN
SQLDEVCPDTMNNPLSHYWISSSHNTYLTGDQFSSESSLEAYARCLRMGCRCIELDCWDGP
DGMPVIYHGHTLTTKIKFSDVLHTIKEHAFVASEYPVILSIEDHCSIAQQRNMAQYFKKVLGDTL
LTKPVDIAADGLPSPNQLKRKILIKHKKLAEGSAYEEVPTSVMYSENDISNSIKNGILYLEDPVN
HEWYPHYFVLTSSKIYYSEETSSDQGNEDEEEPKEASGSTELHSNEKWFHGKLGAGRDGRH
IAERLLTEYCIETGAPDGSFLVRESETFVGDYTLSFWRNGKVQHCRIHSRQDAGTPKFFLTDN
LVFDSLYDLITHYQQVPLRCNEFEMRLSEPVPQTNAHESKEWYHASLTRAQAEHMLMRVPR
DGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQEGQTVMLGNSEFDSLVDLISYYEKHPLYRK
MKLRYPINEEALEKIGTAEPDYGALYEGRNPGFYVEANPMPTFKCAVKALFDYKAQREDELTF
TKSAIIQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVSPAALEPEREHLDENSPLGDLLR
GVLDVPACQIAVRPEGKNNRLFVFSISMASVAHWSLDVAADSQEELQDWVKKIREVAQTADA
RLTEGKMMERRKKIALELSELVVYCRPVPFDEEKIGTERACYRDMSSFPETKAEKYVNKAKG
KKFLQYNRLQLSRIYPKGQRLDSSNYDPLPMWICGSQLVALNFQTPDKPMQMNQALFLAGG

HCGYVLQPSVMRDEAFDPFDKSSLRGLEPCAICIEVLGARHLPKNGRGIVCPFVEIEVAGAEY
DSIKQKTEFVVDNGLNPVWPAKPFHFQISNPEFAFLRFVVYEEDMFSDQNFLAQATFPVKGLK
TGYRAVPLKNNYSEGLELASLLVKIDVFPAKQENGDLSPFGGASLRERSCDASGPLFHGRAR
EGSFEARYQQPFEDFRISQEHLADHFDGRDRRTPRRTRVNGDNRL

Starting nucleotide position:
1

Ending nucleotide position:
1337



Domain 1

Starting aminoacid position:
245

Ending aminoacid position:
318

Domain description:
Phosphoinositide-specific phospholipase C, efhand-like

Identifier:
EF-hand_like

Domain 2

Starting aminoacid position:
322

Ending aminoacid position:
465

Domain description:
Phosphatidylinositol-specific phospholipase C, X domain

Identifier:
PI-PLC-X

Domain 3

Starting aminoacid position:
550

Ending aminoacid position:
639

Domain description:
SH2 domain

Identifier:
SH2

Domain 4

Starting aminoacid position:
668

Ending aminoacid position:
741

Domain description:
SH2 domain

Identifier:
SH2

Domain 5

Starting aminoacid position:
797

Ending aminoacid position:
843

Domain description:
SH3 domain

Identifier:
SH3_1

Domain 6

Starting aminoacid position:
952

Ending aminoacid position:
1070

Domain description:
Phosphatidylinositol-specific phospholipase C, Y domain

Identifier:
PI-PLC-Y

Domain 7

Starting aminoacid position:
1090

Ending aminoacid position:
1177

Domain description:
C2 domain

Identifier:
C2