

Virus Report

25-01-2015 15:17:21

Secondary structure results

Virus name:
aowiuhf

Sequence:

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TGGTATCAGAGCAAGGTTTTCTGTAAGTAATTTATGGCTTTCATGGGGTAAAACCCTTAGA
TAGGAGCCTGAGGGCTCTGCTATGTTCTATTTTGAGAAAATAACTGTGTAAGTAGTAATGC
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CCGGTGTGAGTTTCTTTACCTAGCAGAAGATATACTCTAGTATCCTCAAAACACCGTGAAG
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AGTTCAATAAAATTCAAGCTTTCTCTTACATTCTGTTCTTGAAAGGTTGATCTAATCGAG
CGAGTAGAGAACAAGATCTTTTGGGATTTCCGCCGTTCCA

Structure in dot-bracket format:

This image displays a highly complex, black-and-white fractal pattern. The structure is composed of numerous small, repeating geometric shapes that form a larger, self-similar overall shape. The pattern is dense and intricate, with a high degree of symmetry and repetition. It resembles a Sierpinski triangle or a similar fractal, where the same basic shape is repeated at different scales. The image is rendered in a high-contrast, pixelated style, giving it a digital or printed appearance. The overall effect is one of infinite detail and complexity, with the pattern filling the entire frame.

15

Ending aminoacid position:
145

Domain description:
Protein of unknown function (DUF1319)

Identifier:
DUF1319

Protein 2

Number of domains:
0

Aminoacidsequence:
MSLAGSKATAIYQEALQSTAAGWEDTGIGFTDKGVISTTTLSRQLNSLLFLVIKQNQQITTISEE
LTQLHNRVKNLEGRTGVSASPLYKSEIESINAKLKSIQDIQGSHPKETPSGVIKVFEDPYSILR
RL

Starting nucleotide position:
1282

Ending nucleotide position:
1681

Protein 3

Number of domains:
4

Aminoacidsequence:
MASRPRVSGSTTRTMIAEPGVPLVDDQIREYRSAARVAYEAQRIARRTGNI LGRIVGRQPREH
TLAMVVDPNSELESLAHRARTIPAEVLYMTQRGEPTNRVYRNRTTEERMLVTHGQQDRTFIL
PESYEELREAGFEYIHLGV LQVRIQIMHRTYDGTMALVVFRDTRWTQENHQDRSIIATMEADL
SQGHQLIYVIPDIMMTIRDFYQHIQISILTKGYEGFQGEANLLITRSCRCRLSNVPNVGFQYNIQ
NVVEFLKSRGVKALNATKLSTRRFQGGGEWNIRPSEVVVPMQPTTMIVRVNYDSSRSIRFGDY
EASTSSSAPRYEQDGEDEALGDIHQVNMITIIEDDAEDDYPRLSALERIIAPESMVGEEDTIAE
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RYLNDYFHAAKSGRAWASDELSKEFFTKLPRGLGDRVEKKFKEKYPNNTIGVAPRITFTRNY
IKEICQEA VFQSQLKRLDFCKGTPVHGLYGKEKAYGRKYGVRKSTSYKGKPKH KSHVRIDKKK
HLLMKRKDCKCFACGDIGHFASECPNPKLMHRVQILQSLELDDGIDVISVGFDESVDIYSV
SEGEDSYQFNNEFDVIGHDVFMFTIEEQRNCLVETTSAWRSAMKVTPPEEKNCLHTWSFE EK
TTDHCRACKNLALRGSRADCTQCKIIICSLCKPYYFQDGSPIPAQSSTPSGYSYDDWMGSAN
RWKAHYEFSQARRKSLKADLERAEELKFYKQKEKEKAKLKDQIPEAVQAKLDDLEKEKELN
NILRIEAE TELKALKESFKEKEEALKEEITAL EEEVRIHKEEAEELQEENQKLKEKIIAFEKDVTQ
GP EEVIELVNNVEEHLVLTGQQKNLLNIKITLEVKEKRITMNAILD TGAAICVCDGQMVNEYFR
RPSMMNAFIKGVNGITNVKEILEEGKIWIGNQWFRIPRTYIMPQLSEGLHFIIGMNFIRAMEGGI
RIEQGTVT FYKMVTQAQAPPMVHDISYLEELELELPIYYDICATNPSGGEINSD LISPSEIRKLKD
LGYIGEEPLKHWAKNQVKCR IEIKNPDLIEDRPLKHVTPAMKESMKKHVDK LLELKVIRPSTSK
HRTTAIVQSGTEIDPLTGKEKRGKERLVFN YKRLNDNTEKDQYSLPGINTIISRIGKSKIYSKFD
LKSGFHQVAMD PESIPWTAFAWIDGLYEWLVMPFGLKNAPAI FQRKMDNCFRGTEEFIAVYID
DILIFSDNISDHRKHLSKFLEICKANGLVLSPTKMKIGAKEIDFLGATIGNSKIKLQPHIIKKIIETKD
EELKETKGLR KWLGV LNYARAYIPNLGKTLGPLYSKTSINGEKKMNSQDWKV VQLIKNQVQNL
PDL DIPPAEATMVLETDGCM EGWGGVCKWK LHPSDTRLAEKVCA YASGRYHPIKSTIDAEVH
AVINSLEKFKIYYLDKKELIIR TDSQAIVAFYKKQADHKPSRTRWLMLIDYITGLGINVKFEHIDGK

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