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Download alignment | Download alignment image | Charge | clustal2

Select/type PDB entry:

4v9d

Select a polymer

50S ribosomal protein L2

Download mapped data

- Show ribosomal context in 3D
- Select by ECOD domain
- Select custom range
- Mask/Unmask 2D and 3D residues
- Upload custom mapping data
- Show amino acid frequencies

Structure sequence
Bacteria candidate division WS6 bacterium
Bacteria Candidatus Saccharibacteria bacter
Bacteria candidate division WWE3 bacterium
Bacteria Candidatus Berkelbacteria bacterium
Bacteria Candidatus Peregrinibacteria bacte
Bacteria Candidatus Gottesmanbacteria bac
Bacteria Candidatus Woesebacteria bacteriu
Bacteria Candidatus Falkowbacteria bacteriu
Bacteria Candidatus Harrisonbacteria bacter
Bacteria Candidatus Staskawiczbacteria bact
Bacteria Candidatu
Bacteria Synechoco
Bacteria Crocospha
Bacteria Anabaena
Bacteria Thermosyn
Bacteria Synechocy
Bacteria Blochmann
Bacteria Polaromon

185 190 195 200 205 210 215 220 225 230 235 240

Topology viewer

This is the topology viewer that shows secondary protein structure.

Skip tour | Previous | Next

4v9d | Entity 27 | Chain CC | Select data

1 0 -1

4V9D | Model 1 | Instance ASM_1 | XA [auth CC] | ILE 266

1
00:00:05,990 --> 00:00:03,429
hello

2
00:00:08,390 --> 00:00:06,000
i'm peter from georgia tech and i will

3
00:00:10,150 --> 00:00:08,400
present protovision a web-based tool for

4
00:00:12,150 --> 00:00:10,160
the concerted study of sequence

5
00:00:13,589 --> 00:00:12,160
alignments and structures

6
00:00:16,070 --> 00:00:13,599
in the study

7
00:00:19,510 --> 00:00:16,080
of the origin of life we often compare

8
00:00:21,670 --> 00:00:19,520
sequences of extent species

9
00:00:22,710 --> 00:00:21,680
to learn about ancient evolutionary

10
00:00:24,710 --> 00:00:22,720
events

11
00:00:26,870 --> 00:00:24,720
protovision provides an easy and

12
00:00:32,150 --> 00:00:26,880
intuitive interface to study the

13
00:00:34,310 --> 00:00:32,160

evolution of proteins in 1 2 and 3d

14
00:00:36,389 --> 00:00:34,320
protovision provides a set of alignments

15
00:00:37,750 --> 00:00:36,399
for the most ancient molecular fossil

16
00:00:39,830 --> 00:00:37,760
the ribosome

17
00:00:42,389 --> 00:00:39,840
and it calculates a sequence

18
00:00:45,750 --> 00:00:42,399
conservation it allows for the download

19
00:00:48,229 --> 00:00:45,760
of these alignments and the download of

20
00:00:50,150 --> 00:00:48,239
images and the mapping of different

21
00:00:53,990 --> 00:00:50,160
types of calculated data from these

22
00:00:58,790 --> 00:00:56,069
protovision can calculate amino acid

23
00:01:01,430 --> 00:00:58,800
frequencies based on these alignments

24
00:01:02,709 --> 00:01:01,440
and it allows for the saving of these

25
00:01:06,630 --> 00:01:02,719
frequencies

26
00:01:08,630 --> 00:01:06,640
both as an image and as a data

27
00:01:11,590 --> 00:01:08,640
finally protovision allows the

28
00:01:13,590 --> 00:01:11,600
connection of the alignment to

29
00:01:15,910 --> 00:01:13,600
the structure

30
00:01:19,990 --> 00:01:15,920
and the mapping of the data of the

31
00:01:22,230 --> 00:01:20,000
calculated data on 2d and 3d

32
00:01:26,230 --> 00:01:22,240
prodivision allows the download of high

33
00:01:28,550 --> 00:01:26,240
fidelity images from these viewers and

34
00:01:30,069 --> 00:01:28,560
the use and their use in publication

35
00:01:32,230 --> 00:01:30,079
images

36
00:01:35,270 --> 00:01:32,240
protovision is available at