

Petar Penev

- 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

Download alignment | Download alignment image | Charge | clustal2

Structure sequence

1	185	190	195	200	205	210	215	220	225	230	235	240																																																											
M	R	N	I	P	V	G	S	T	V	H	N	V	E	M	K	P	G	K	G	G	L	A	R	S	A	G	T	Y	V	Q	I	V	A	R	D	-	-	G	A	-	-	Y	V	T	L	R	L	R	S	S	O	E	I	R	R	L	V	P	A	E	A	M	A	T							
V	K	N	I	P	S	G	T	I	V	H	C	I	E	N	R	V	G	K	G	A	T	F	G	R	S	A	G	Q	E	I	V	V	Q	G	I	D	P	T	G	K	-	-	G	D	-	-	Y	V	Q	I	R	L	S	S	O	E	I	R	R	L	V	P	A	E	A	M	A	T			
L	A	K	I	P	V	G	S	Q	I	Y	A	I	E	I	O	V	G	K	G	A	O	M	V	R	S	A	G	T	K	A	Q	L	M	A	K	E	-	-	G	D	-	-	G	D	-	-	Y	A	M	V	R	R	L	P	S	S	G	E	V	R	R	K	V	L	R	L	E	A	T	A	
L	S	N	A	P	L	G	A	L	I	H	N	I	E	L	Y	P	K	G	G	K	L	V	R	G	A	G	L	S	A	V	L	M	A	K	E	-	-	G	D	-	-	G	D	-	-	Y	G	I	I	R	L	P	S	S	G	E	I	R	R	K	V	L	R	L	E	C	M	A	T		
L	A	D	I	P	P	G	O	E	I	H	N	V	E	L	Q	P	G	R	G	G	O	M	I	R	S	A	G	S	W	A	I	L	S	A	K	E	-	-	G	K	-	-	G	D	-	-	Y	A	V	I	R	L	P	S	S	G	E	I	R	K	V	L	L	E	C	M	A	T			
I	G	N	V	P	P	G	F	N	I	F	N	V	E	L	N	P	G	C	G	K	L	V	R	S	A	G	T	C	A	Q	V	V	S	T	D	-	-	S	G	K	-	-	G	D	-	-	Y	V	Q	V	R	L	P	S	S	G	E	I	R	L	I	N	K	E	C	M	A	T			
M	S	K	I	P	I	G	M	P	I	H	N	V	E	L	H	P	G	K	G	G	Q	I	V	R	G	A	G	T	M	A	T	I	L	A	R	E	-	-	G	G	-	-	G	D	-	-	F	V	H	L	R	L	P	S	S	G	E	V	R	R	K	V	R	E	N	G	M	A	T		
L	A	K	I	P	V	G	T	I	H	N	V	E	L	K	P	G	M	G	G	Q	M	V	K	S	A	G	S	A	A	I	L	Q	G	K	E	-	-	E	D	-	-	E	D	-	-	W	V	L	V	R	L	P	S	S	G	E	V	P	R	F	L	P	G	S	K	A	T				
L	E	L	I	P	V	G	T	T	V	H	N	V	E	L	I	Q	E	G	K	G	V	L	V	N	G	A	G	L	G	A	Q	L	V	A	I	D	-	-	G	D	-	-	G	D	-	-	Y	A	Q	M	R	L	P	S	S	G	E	I	R	K	I	R	R	V	S	S	E	G	L	A	T
L	K	N	V	P	I	Q	Y	F	V	H	N	V	E	L	M	R	R	G	S	G	K	I	A	R	S	A	G	S	Y	A	E	V	L	A	H	E	-	-	S	G	-	-	S	G	-	-	L	I	D	L	R	L	P	S	S	G	E	I	R	R	V	S	S	E	G	L	A	T			
L	K	N	I	L	V	G	T	M	V	Y	N	V	E	L	E	P	E	R	G	G	K	I	V	R	S	A	G	S	S	A	Q	V	L	A	H	D	-	-	G	D	-	-	G	D	-	-	Y	T	N	L	K	M	P	S	S	G	E	I	R	K	F	R	G	E	C	F	A	S			
L	K	N	I	L	V	G	T	M	V	Y	N	V	E	L	F	L	P	N	G	A	R	I	A	R	S	A	G	I	Y	A	E	V	V	A	N	N	-	-	E	G	-	-	E	G	-	-	Q	A	H	L	R	M	P	S	S	G	E	I	R	N	V	P	E	Q	C	W	A	S			
B	V	H	N	V	E	L	V	P	G	R	G	G	Q	V	V	R	A	A	G	A	A	A	Q	V	V	A	K	E	-	-	G	N	-	-	G	N	-	-	G	N	-	-	Y	V	T	L	R	L	P	S	S	G	E	V	R	M	I	R	R	B	C	Y	A	T							
S	V	H	N	V	E	L	K	A	G	K	G	G	O	I	V	R	S	A	G	A	T	A	Q	V	V	A	K	E	-	-	G	N	-	-	G	N	-	-	Y	V	T	L	K	L	P	S	S	G	E	V	R	L	I	R	R	E	C	Y	A	T											
S	V	H	N	V	E	L	T	P	G	R	G	A	Q	M	V	R	A	A	G	A	M	A	Q	V	V	A	K	E	-	-	G	D	-	-	G	D	-	-	M	V	T	L	R	L	P	S	S	G	E	V	R	L	F	R	K	E	C	Y	A	T											
I	H	N	V	E	L	V	A	G	R	G	G	Q	M	V	R	S	A	G	A	F	A	Q	V	V	A	K	E	-	-	G	D	-	-	G	D	-	-	Y	V	T	I	R	L	P	S	S	G	E	V	R	M	V	R	K	E	C	Y	A	T												
I	H	N	V	E	M	K	V	G	K	G	G	O	L	A	R	S	A	G	T	Y	V	Q	I	V	S	R	D	-	-	G	E	-	-	G	E	-	-	Y	I	L	R	L	R	S	S	G	E	V	I	R	K	V	R	C	E	C	R	A	T												
I	H	C	I	E	M	O	I	G	S	G	A	O	I	A	R	S	A	G	T	S	A	T	I	L	A	R	E	-	-	G	T	-	-	G	T	-	-	Y	A	O	V	R	M	P	S	S	G	E	V	I	R	K	I	H	I	E	C	R	A	T											

Topology viewer

This is the topology viewer that shows secondary protein structure.

Skip tour Previous Next



4v9d | Entity 27 | Chain CC | Select data



4v9d | Model 1 | Instance ASM_1 | KA [pub. 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 extant 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

provision 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

provision 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

protovision 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