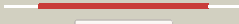



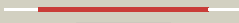




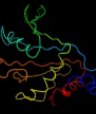







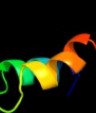


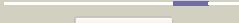


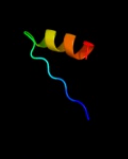
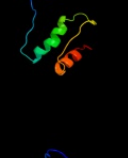





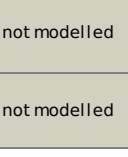


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P62399
Date	Thu Jan 5 12:07:30 GMT 2012
Unique Job ID	f1fee4da9c6b4144

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iq4a_	 Alignment		100.0	61	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
2	d1mjia_	 Alignment		100.0	56	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
3	d2zjrd1	 Alignment		100.0	60	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
4	c3bboH_	 Alignment		100.0	49	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein l5; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
5	d2gycd1	 Alignment		100.0	100	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
6	c4a1cD_	 Alignment		100.0	26	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l11; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
7	c1s1ij_	 Alignment		100.0	34	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l11; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
8	d1vqod1	 Alignment		100.0	42	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
9	c2rf4B_	 Alignment		38.8	38	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
10	d3d37a1	 Alignment		17.9	27	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
11	c2jvfA_	 Alignment		17.5	33	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein

12	c3hxxA_	Alignment		17.5	22	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
13	c1qysA_	Alignment		17.1	24	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
14	c1yfsB_	Alignment		12.8	25	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
15	d1riqa2	Alignment		10.0	24	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
16	c2x6vB_	Alignment		9.2	23	PDB header: transcription/dna Chain: B: PDB Molecule: t-box transcription factor tbx5; PDBTitle: crystal structure of human tbx5 in the dna-bound and dna-2 free form
17	c1vjqB_	Alignment		8.6	24	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
18	c3c25A_	Alignment		6.4	30	PDB header: hydrolase/dna Chain: A: PDB Molecule: noti restriction endonuclease; PDBTitle: crystal structure of noti restriction endonuclease bound to cognate2 dna
19	c2xznH_	Alignment		6.2	26	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein s8 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
20	c1xtzA_	Alignment		5.6	12	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
21	c2ejxA_	Alignment	not modelled	5.5	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: st0812; PDBTitle: crystal structure of the hypothetical protein st0812 from2 sulfolobus tokodaii
22	d1nt2b_	Alignment	not modelled	5.4	25	Fold: Nop domain Superfamily: Nop domain Family: Nop domain