Phyre2

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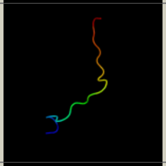
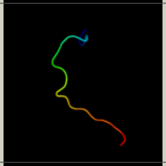
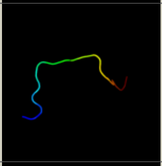
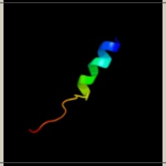
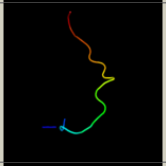
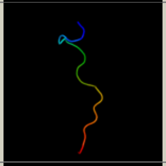
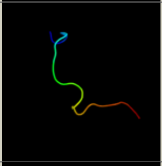
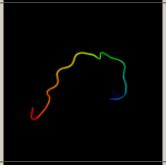
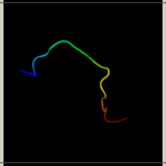
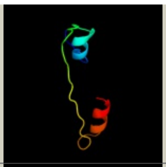
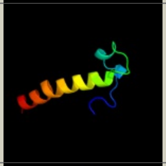
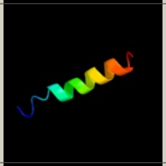
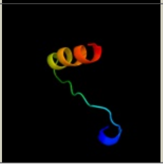
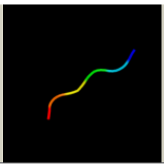
Description	P64459
Date	Thu Jan 5 12:08:32 GMT 2012
Unique Job ID	c51c91935c960550

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bboF_	Alignment		28.1	20	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**ribosomal protein l3; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
2	d2gycb1	Alignment		26.0	45	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
3	d2zjrb1	Alignment		22.4	50	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
4	d2j01e1	Alignment		20.4	50	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
5	c2yqkA_	Alignment		19.7	35	**PDB header:**transcription/apoptosis **Chain:** A: **PDB Molecule:**arginine-glutamic acid dipeptide repeats protein; **PDBTitle:** solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
6	c2ftcC_	Alignment		16.7	20	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**mitochondrial 39s ribosomal protein l3; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
7	d1vqob1	Alignment		16.2	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
8	c3jywC_	Alignment		15.2	20	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
9	c1s1iC_	Alignment		12.6	20	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **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.
10	c2zkrb_	Alignment		10.5	25	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es4; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
11	c2kwzA_	Alignment		10.4	75	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution structure of ns2 [60-99]

12	c1ni5A_	Alignment		6.8	28	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
13	c3du6A_	Alignment		6.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**telomerase reverse transcriptase; **PDBTitle:** structure of the catalytic subunit of telomerase, tert
14	c1odpA_	Alignment		5.9	47	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apoa-i peptide; **PDBTitle:** peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
15	c1odqA_	Alignment		5.9	47	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apoa-i peptide; **PDBTitle:** peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
16	c1odrA_	Alignment		5.9	47	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apoa-i peptide; **PDBTitle:** peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
17	c3mtuD_	Alignment		5.8	38	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**tropomyosin alpha-1 chain, microtubule-associated protein **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
18	c2lciA_	Alignment		5.6	42	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)

19	c3fd9C_	Alignment		5.6	83	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the transcriptional anti-activator exsd2 from pseudomonas aeruginosa