Phyre2

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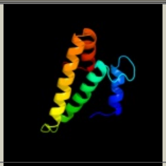
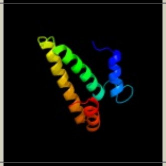
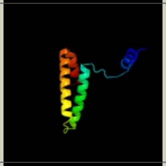
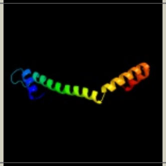
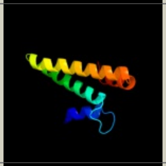
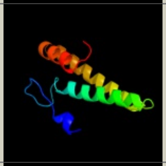
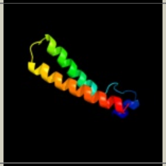
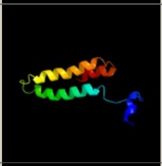
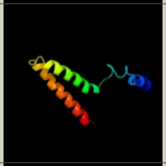
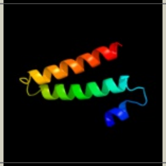
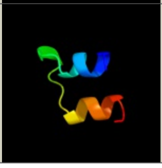
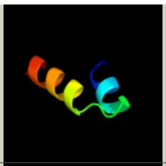
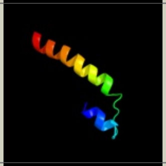
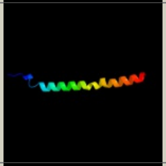
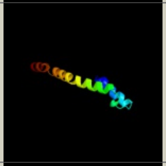
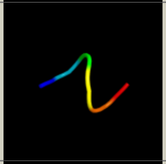
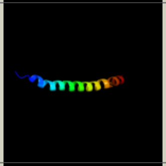
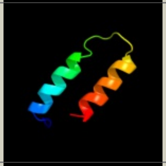
Description	P0ADZ4
Date	Thu Jan 5 11:22:08 GMT 2012
Unique Job ID	61c270b61956df4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vs5o1	Alignment		100.0	99	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
2	d1g1xb_	Alignment		100.0	59	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
3	d1a32a_	Alignment		100.0	59	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
4	c3ulwA_	Alignment		100.0	54	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s15; **PDBTitle:** 30s ribosomal protein s15 from campylobacter jejuni
5	d1kuqa_	Alignment		100.0	61	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
6	c3bbnO_	Alignment		100.0	35	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**ribosomal protein s15; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
7	c2xzmO_	Alignment		99.4	16	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rps13e; **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 1
8	c3izbO_	Alignment		99.4	11	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein rps13 (s15p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
9	c1yshE_	Alignment		98.3	20	**PDB header:**structural protein/rna **Chain:** E: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
10	c1s1hO_	Alignment		96.6	14	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein s13; **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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
11	d1y0ua_	Alignment		32.2	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators

12	c2y50A_	Alignment		25.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**collagenase; **PDBTitle:** crystal structure of collagenase g from clostridium2 histolyticum at 2.80 angstrom resolution
13	c2ke4A_	Alignment		18.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
14	c2zvnF_	Alignment		17.0	16	**PDB header:**signaling protein/transcription **Chain:** F: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cozi domain incomplex with diubiquitin in p2121212 space group
15	c3f1iH_	Alignment		12.4	17	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
16	c2vogB_	Alignment		8.7	67	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-modifying factor; **PDBTitle:** structure of mouse a1 bound to the bmf bh3-domain
17	c2v4hA_	Alignment		8.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
18	d1sxjd1	Alignment		7.1	18	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
19	c2f5xC_	Alignment		6.7	17	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
20	c3nqwB_	Alignment		6.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
21	c2pnvA_	Alignment	not modelled	5.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
22	c3cuoB_	Alignment	not modelled	5.5	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
23	c1m7lA_	Alignment	not modelled	5.5	43	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
24	d3crda_	Alignment	not modelled	5.3	20	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
25	d1biaa1	Alignment	not modelled	5.3	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
26	c2bmmA_	Alignment	not modelled	5.2	6	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca; **PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca