Phyre^2

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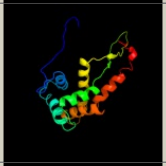
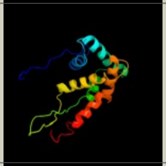
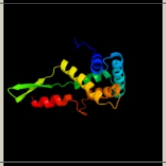
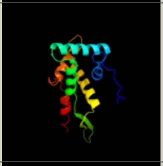
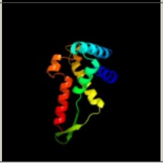
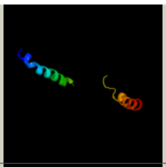
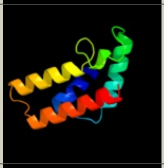
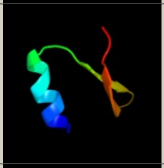
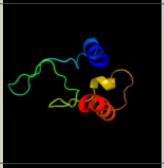
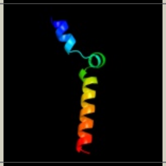
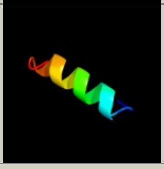
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gtyS_	Alignment		100.0	56	**PDB header:**chaperone/ribosomal protein **Chain:** S: **PDB Molecule:**30s ribosomal protein s7; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
2	c3bbnG_	Alignment		100.0	44	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein s7; **PDBTitle:** homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
3	d2qalg1	Alignment		100.0	59	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
4	c1vs5G_	Alignment		100.0	59	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**30s ribosomal protein s7; **PDBTitle:** crystal structure of the bacterial ribosome from2 escherichia coli in complex with the antibiotic kasugamyin3 at 3.5a resolution. this file contains the 30s subunit of4 one 70s ribosome. the entire crystal structure contains5 two 70s ribosomes and is described in remark 400.
5	d1rssa_	Alignment		100.0	51	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
6	d1husa_	Alignment		100.0	76	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
7	c2xzmG_	Alignment		100.0	27	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein s7 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 1
8	d1iqva_	Alignment		100.0	31	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
9	c1s1hG_	Alignment		100.0	27	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**40s ribosomal protein s5; **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.
10	c3izbF_	Alignment		100.0	28	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**40s ribosomal protein rps5 (s7p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
11	c2zkqg_	Alignment		100.0	28	**PDB header:**ribosomal protein/rna **Chain:** G: **PDB Molecule:**rna helix; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map

12	c2kn8A_	Alignment		28.8	22	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**dna cleavage and packaging protein large subunit, ul89; **PDBTitle:** nmr structure of the c-terminal domain of pul89
13	d3bula1	Alignment		27.9	19	**Fold:**Methionine synthase domain-like **Superfamily:**Methionine synthase domain **Family:**Methionine synthase domain
14	d1u5ta1	Alignment		27.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
15	d1o7fa1	Alignment		21.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
16	c2zmeA_	Alignment		20.4	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
17	c3cuqA_	Alignment		18.9	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
18	c1u5tA_	Alignment		15.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
19	c2hv8D_	Alignment		10.5	26	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of gtp-bound rab11 in complex with fip3
20	d1kx9b_	Alignment		9.2	28	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
21	c3kmpA_	Alignment	not modelled	8.0	18	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**smad1-mh1; **PDBTitle:** crystal structure of smad1-mh1/dna complex
22	c1w7pD_	Alignment	not modelled	7.9	11	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vps36p, ylr417w; **PDBTitle:** the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
23	d1n8va_	Alignment	not modelled	6.2	23	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
24	c3g36D_	Alignment	not modelled	6.2	12	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
25	d1qe6a_	Alignment	not modelled	5.9	17	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
26	d1s16a1	Alignment	not modelled	5.9	17	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
27	d1y6xa1	Alignment	not modelled	5.6	12	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
28	d1pd3a_	Alignment	not modelled	5.3	30	**Fold:**ROP-like **Superfamily:**Nonstructural protein ns2, Nep, M1-binding domain **Family:**Nonstructural protein ns2, Nep, M1-binding domain