Phyre^2

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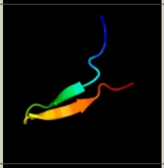
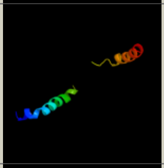
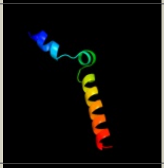
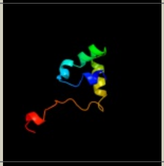
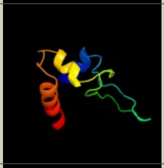
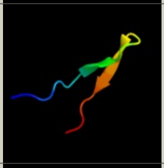
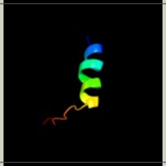
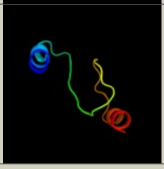
Detailed template information

#	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 subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
3	d2qalg1	Alignment		100.0	100	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
4	c1vs5G_	Alignment		100.0	100	**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	53	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
6	d1husa_	Alignment		100.0	55	**Fold:**Ribosomal protein S7 **Superfamily:**Ribosomal protein S7 **Family:**Ribosomal protein S7
7	c2xzmG_	Alignment		100.0	28	**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	29	**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	29	**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 an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map

12	d1u5ta1	Alignment		26.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
13	d1ahsa_	Alignment		24.1	37	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
14	c2kn8A_	Alignment		20.0	11	**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
15	c2hv8D_	Alignment		17.9	23	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of gtp-bound rab11 in complex with fip3
16	d2cg4a1	Alignment		17.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
17	d1o7fa1	Alignment		13.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
18	d1bvp12	Alignment		13.4	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
19	c2e5zA_	Alignment		11.7	26	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 8; **PDBTitle:** solution structure of the surp2 domain in splicing factor,2 arginine/serine-rich 8
20	c1u5tA_	Alignment		11.4	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
21	d1ojha_	Alignment	not modelled	10.1	36	**Fold:**NblA-like **Superfamily:**NblA-like **Family:**NblA-like
22	c1ojhK_	Alignment	not modelled	9.9	36	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**nbla; **PDBTitle:** crystal structure of nbla from pcc 7120
23	c1w7pD_	Alignment	not modelled	6.3	8	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vps36p, ylr417w; **PDBTitle:** the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
24	d1n8va_	Alignment	not modelled	6.2	31	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
25	c3csxA_	Alignment	not modelled	6.1	40	**PDB header:**metal binding protein,unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structural characterization of a protein in the duf6832 family- crystal structure of cce_0567 from the3 cyanobacterium cyanothece 51142.
26	d1qe6a_	Alignment	not modelled	6.1	17	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
27	d1kx9b_	Alignment	not modelled	6.0	31	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
28	c3g36D_	Alignment	not modelled	6.0	18	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
						PDB header:structural genomics, unknown function

29	c2js5B_	Alignment	not modelled	5.9	37	**Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
30	d1y6xa1	Alignment	not modelled	5.7	12	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
31	d2j5ya1	Alignment	not modelled	5.7	27	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
32	d1yxba1	Alignment	not modelled	5.3	17	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
33	d1ia9a_	Alignment	not modelled	5.2	19	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**MHCK/EF2 kinase
34	d1s16a1	Alignment	not modelled	5.2	13	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
35	d1pd3a_	Alignment	not modelled	5.1	25	**Fold:**ROP-like **Superfamily:**Nonstructural protein ns2, Nep, M1-binding domain **Family:**Nonstructural protein ns2, Nep, M1-binding domain