Phyre2

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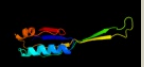
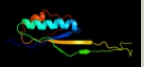
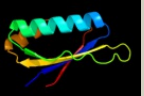
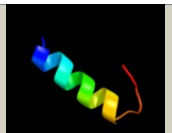
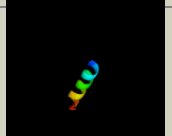
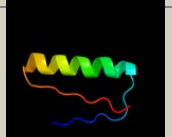
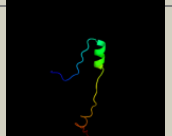
Description	P0A7R5
Date	Thu Jan 5 11:06:06 GMT 2012
Unique Job ID	b5776b7bd06f9eaa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qalj1	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S10 **Family:**Ribosomal protein S10
2	c3bbnJ_	Alignment		100.0	54	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**ribosomal protein s10; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
3	d2uubj1	Alignment		100.0	55	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S10 **Family:**Ribosomal protein S10
4	c2xznJ_	Alignment		100.0	28	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**ribosomal protein s10 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
5	c2zkqj_	Alignment		100.0	27	**PDB header:**ribosomal protein/rna **Chain:** J: **PDB Molecule:** **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
6	c1s1hJ_	Alignment		100.0	25	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**40s ribosomal protein s20; **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.
7	c3iz6J_	Alignment		100.0	27	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**40s ribosomal protein s20 (s10p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
8	c3r2cJ_	Alignment		99.9	55	**PDB header:**transcription/rna **Chain:** J: **PDB Molecule:**30s ribosomal protein s10; **PDBTitle:** crystal structure of antitermination factors nusb and nuse in complex2 with boxa rna
9	d1xbpg1	Alignment		33.6	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
10	d1fnoa3	Alignment		19.9	19	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
11	d1hc8a_	Alignment		15.5	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain

12	d1mmsa1	Alignment		15.2	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
13	c1s1iK_	Alignment		12.6	37	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l12; **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.
14	c1vq8l_	Alignment		11.4	26	**PDB header:**ribosome **Chain:** l: **PDB Molecule:**50s ribosomal protein l11p; **PDBTitle:** the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
15	d1dbda_	Alignment		10.8	12	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
16	c2kl8A_	Alignment		10.3	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
17	c2zkri_	Alignment		9.8	32	**PDB header:**ribosomal protein/rna **Chain:** l: **PDB Molecule:**rna expansion segment es15 part i; **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
18	c1s6xA_	Alignment		9.4	36	**PDB header:**toxin **Chain:** A: **PDB Molecule:**kvap channel; **PDBTitle:** solution structure of vstx
19	c2yqrA_	Alignment		8.5	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein
20	c1jqmA_	Alignment		8.2	37	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid
21	d1a7ge_	Alignment	not modelled	7.8	16	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
22	c2vhml_	Alignment	not modelled	7.8	33	**PDB header:**ribosome **Chain:** l: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** structure of pdf binding helix in complex with the ribosome2 (part 1 of 4)
23	d1f9fa_	Alignment	not modelled	7.7	8	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
24	c3izcn_	Alignment	not modelled	7.6	24	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
25	c3bboK_	Alignment	not modelled	7.6	32	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**ribosomal protein l11; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
26	c3ai4A_	Alignment	not modelled	7.3	20	**PDB header:**fluorescent protein, replication **Chain:** A: **PDB Molecule:**yeast enhanced green fluorescent protein, dna polymerase **PDBTitle:** crystal structure of yeast enhanced green fluorescent protein - mouse2 polymerase iota ubiquitin binding motif fusion protein
27	d1r8ha_	Alignment	not modelled	7.1	8	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
28	d2q79a1	Alignment	not modelled	7.1	15	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain

						Family: Viral DNA-binding domain
29	c3lpeF_	Alignment	not modelled	6.4	38	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
30	d1vqoi1	Alignment	not modelled	6.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
31	c2ko4A_	Alignment	not modelled	6.3	0	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 15; **PDBTitle:** complex structure of the activation domain of gcn4 bound to the2 mediator co-activator domain of gal11/med15
32	d1yvua2	Alignment	not modelled	6.3	7	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
33	c2hxgB_	Alignment	not modelled	6.0	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-arabinose isomerase; **PDBTitle:** crystal structure of mn2+ bound ecai
34	d1iwga2	Alignment	not modelled	5.8	15	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
35	d1vqoe2	Alignment	not modelled	5.4	17	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
36	c4a1eE_	Alignment	not modelled	5.4	21	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**60s ribosomal protein l9; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1