Phyre^2

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Description	P0A7J3
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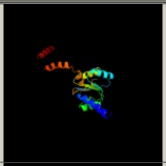
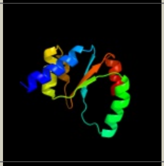
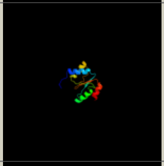
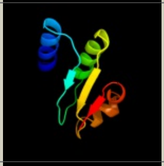
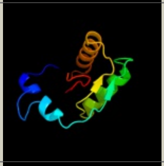
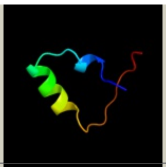
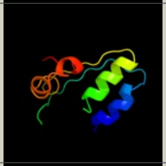
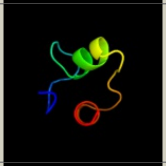
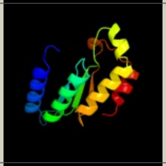
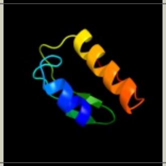
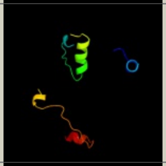
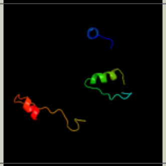
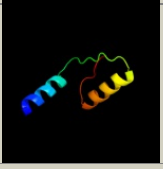
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zava1	Alignment		100.0	36	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein L10-like **Family:**Ribosomal protein L10-like
2	c3a1yG_	Alignment		99.9	21	**PDB header:**ribosomal protein **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0; **PDBTitle:** the structure of protein complex
3	c3jyw8_	Alignment		99.9	23	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**60s ribosomal protein lp0; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
4	c3jsyA_	Alignment		99.9	23	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
5	c3izcs_	Alignment		99.9	24	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
6	c3iz5s_	Alignment		99.9	19	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l18a (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
7	c1keeH_	Alignment		50.9	20	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
8	d1a9xb2	Alignment		40.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
9	d1th8b_	Alignment		26.1	13	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
10	d1ln4a_	Alignment		24.5	20	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
11	d1vc1a_	Alignment		19.1	10	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa

12	d1luza_	Alignment		18.3	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
13	d1auza_	Alignment		17.3	10	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
14	c3oirA_	Alignment		14.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter sulfate transporter family protein; **PDBTitle:** crystal structure of sulfate transporter family protein from wolinella2 succinogenes
15	d1h1js_	Alignment		14.1	23	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
16	d1hl2a_	Alignment		13.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
17	c2qv6D_	Alignment		13.4	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
18	c2fknC_	Alignment		12.2	27	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
19	d1x87a_	Alignment		11.6	30	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
20	c3brcA_	Alignment		11.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein of unknown function; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
21	c3d5bJ_	Alignment	not modelled	11.3	38	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**50s ribosomal protein l10; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
22	d3ceda1	Alignment	not modelled	11.2	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
23	c2y0dB_	Alignment	not modelled	10.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
24	d1zrja1	Alignment	not modelled	10.6	31	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
25	c3rhtB_	Alignment	not modelled	9.2	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
26	c2a1sC_	Alignment	not modelled	8.8	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
27	d1jo0a_	Alignment	not modelled	8.5	18	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
28	c3m20A_	Alignment	not modelled	8.4	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution

29	c3f43A_	Alignment	not modelled	8.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative anti-sigma factor antagonist tm1081; **PDBTitle:** crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
30	d2ohwa1	Alignment	not modelled	8.0	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YueI-like **Family:**YueI-like
31	d1jjga_	Alignment	not modelled	8.0	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
32	c2klnA_	Alignment	not modelled	7.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable sulphate-transport transmembrane protein, cog0659; **PDBTitle:** solution structure of stas domain of rv1739c from m. tuberculosis
33	c2qexG_	Alignment	not modelled	6.7	64	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** negamycin binds to the wall of the nascent chain exit tunnel of the2 50s ribosomal subunit
34	c2zpmA_	Alignment	not modelled	6.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
35	c1ykaA_	Alignment	not modelled	6.6	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
36	c3cxjB_	Alignment	not modelled	6.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
37	d1h4xa_	Alignment	not modelled	6.3	7	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
38	c3lerA_	Alignment	not modelled	6.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
39	d1iioa_	Alignment	not modelled	6.2	11	**Fold:**EF Hand-like **Superfamily:**Hypothetical protein MTH865 **Family:**Hypothetical protein MTH865
40	d1l1sa_	Alignment	not modelled	6.1	27	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
41	d1uwka_	Alignment	not modelled	6.1	27	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
42	c2y9jt_	Alignment	not modelled	6.0	7	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
43	d1gyxa_	Alignment	not modelled	6.0	32	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
44	c1q14A_	Alignment	not modelled	6.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
45	d1wdea_	Alignment	not modelled	5.9	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
46	d1yc5a1	Alignment	not modelled	5.8	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
47	c3mglA_	Alignment	not modelled	5.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate permease family protein; **PDBTitle:** crystal structure of permease family protein from vibrio2 cholerae
48	d1phza1	Alignment	not modelled	5.5	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain