Phyre^2

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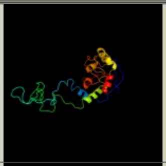
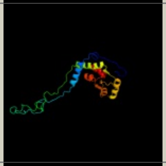
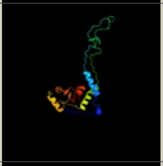
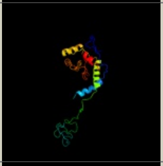
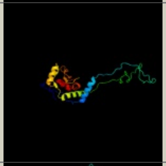
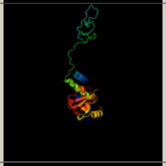
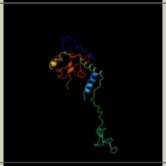
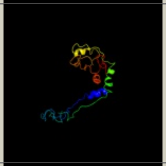
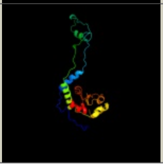
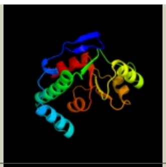
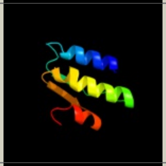
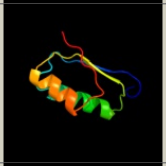
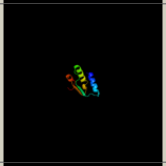
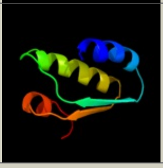
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gycc1	Alignment		100.0	100	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
2	c3bboG_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein l4; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
3	d2j01f1	Alignment		100.0	30	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
4	d2zjrc1	Alignment		100.0	29	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
5	c3jywD_	Alignment		100.0	23	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4(b); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
6	d1vqoc1	Alignment		100.0	20	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
7	c2zkrc_	Alignment		100.0	19	**PDB header:**ribosomal protein/rna **Chain:** C: **PDB Molecule:**rna expansion segment es5; **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
8	c1s1iD_	Alignment		100.0	23	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4-b; **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.
9	c2ftcD_	Alignment		100.0	32	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**mitochondrial ribosomal protein l4 isoform a; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
10	c3iz5D_	Alignment		100.0	27	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4 (l4p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	c4a1aC_	Alignment		100.0	25	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**rpl4; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.

12	d1dmga_	Alignment		100.0	35	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
13	c1f2uD_	Alignment		46.4	16	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
14	d1i5ea_	Alignment		44.5	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
15	d1o5oa_	Alignment		36.3	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
16	d1ecfa1	Alignment		30.2	10	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
17	c2ehjA_	Alignment		29.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
18	c2e55D_	Alignment		28.7	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
19	c1ii8B_	Alignment		27.6	15	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
20	c2vf7B_	Alignment		26.2	16	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
21	d1gph11	Alignment	not modelled	25.7	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
22	d1v9sa1	Alignment	not modelled	24.0	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
23	d1xtta1	Alignment	not modelled	23.4	5	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
24	c3iz5s_	Alignment	not modelled	21.9	10	**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
25	d1zmba1	Alignment	not modelled	21.3	19	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
26	c3izcs_	Alignment	not modelled	19.2	14	**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
27	d2j01p1	Alignment	not modelled	18.1	33	**Fold:**Ribosomal proteins L15p and L18e **Superfamily:**Ribosomal proteins L15p and L18e **Family:**Ribosomal proteins L15p and L18e
28	c3dezA_	Alignment	not modelled	17.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
						PDB header:transferase

29	c1ecjB_	Alignment	not modelled	16.7	10	**Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
30	c1xhbA_	Alignment	not modelled	16.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
31	c2ygrD_	Alignment	not modelled	16.0	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
32	d1z7ga1	Alignment	not modelled	15.7	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
33	c1gpjA_	Alignment	not modelled	14.8	16	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
34	c3nvbA_	Alignment	not modelled	11.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
35	c2p1zA_	Alignment	not modelled	11.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
36	c1gph1_	Alignment	not modelled	10.9	14	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
37	c2v3jA_	Alignment	not modelled	10.9	12	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**essential for mitotic growth 1; **PDBTitle:** the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
38	c3qw4B_	Alignment	not modelled	10.5	17	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
39	c2pcjB_	Alignment	not modelled	9.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
40	d2v3ka1	Alignment	not modelled	9.7	12	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
41	c3dmpD_	Alignment	not modelled	9.7	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
42	d2pmka1	Alignment	not modelled	9.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
43	c2jxoA_	Alignment	not modelled	9.5	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
44	c3jtpB_	Alignment	not modelled	9.3	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
45	d1vpla_	Alignment	not modelled	9.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
46	c3if4C_	Alignment	not modelled	8.7	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**integron cassette protein hfx_cass5; **PDBTitle:** structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
47	c2wnsB_	Alignment	not modelled	8.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
48	c3ozxA_	Alignment	not modelled	8.0	11	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
49	d1l1qa_	Alignment	not modelled	7.7	3	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
50	c2olkD_	Alignment	not modelled	7.7	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
51	d1pf4a1	Alignment	not modelled	7.3	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
52	d1omza_	Alignment	not modelled	7.2	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
53	c3jtoE_	Alignment	not modelled	7.1	18	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**adapter protein meca 2; **PDBTitle:** crystal structure of the c-terminal domain of ypbh
						PDB header:isomerase

54	c3hjbA_	Alignment	not modelled	7.1	17	**Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
55	c2hdnJ_	Alignment	not modelled	7.0	13	**PDB header:**translation **Chain:** J: **PDB Molecule:**elongation factor ef-tu; **PDBTitle:** trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
56	c3nbuC_	Alignment	not modelled	7.0	17	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
57	d3bbda1	Alignment	not modelled	6.8	6	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
58	c2d7iA_	Alignment	not modelled	6.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
59	d1y0ja1	Alignment	not modelled	6.3	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
60	c3kb8A_	Alignment	not modelled	6.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
61	d2gycj1	Alignment	not modelled	6.2	32	**Fold:**Ribosomal proteins L15p and L18e **Superfamily:**Ribosomal proteins L15p and L18e **Family:**Ribosomal proteins L15p and L18e
62	c3b85A_	Alignment	not modelled	6.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
63	d1tc1a_	Alignment	not modelled	6.2	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	c2zkr4_	Alignment	not modelled	6.0	25	**PDB header:**ribosomal protein/rna **Chain:** 4: **PDB Molecule:**60s ribosomal protein l44e; **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
65	d1yfza1	Alignment	not modelled	5.9	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
66	c1yfzA_	Alignment	not modelled	5.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
67	c3gd7C_	Alignment	not modelled	5.7	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fusion complex of cystic fibrosis transmembrane **PDBTitle:** crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
68	c1lkzB_	Alignment	not modelled	5.7	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
69	d1p17b_	Alignment	not modelled	5.6	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
70	d1oeyj_	Alignment	not modelled	5.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
71	d3b60a1	Alignment	not modelled	5.2	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
72	d1gnfa_	Alignment	not modelled	5.2	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
73	d2vuti1	Alignment	not modelled	5.0	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1