Phyre^2

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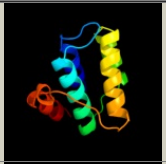
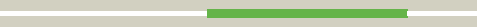
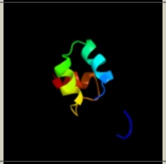
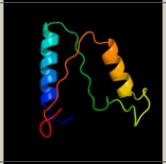
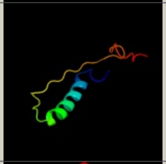
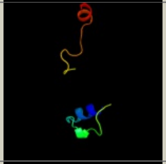
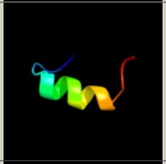
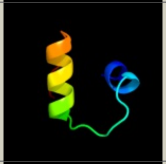
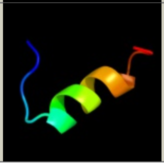
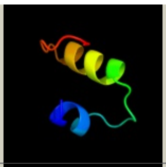
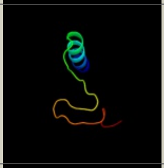
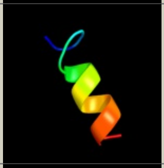
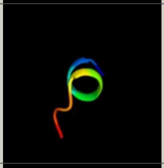
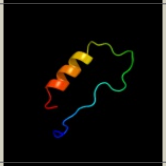
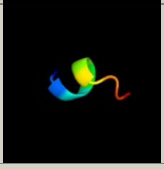
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2es9a1	 Alignment		100.0	63	**Fold:**YoaC-like **Superfamily:**YoaC-like **Family:**YoaC-like
2	c2cosA_	 Alignment		55.2	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase lats2; **PDBTitle:** solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
3	d2cosa1	 Alignment		43.5	45	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
4	d1t8sa_	 Alignment		33.0	35	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
5	c2q62A_	 Alignment		25.3	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
6	d1dpta_	 Alignment		23.4	20	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
7	d2v4ja3	 Alignment		17.8	12	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
8	d1tnsa_	 Alignment		16.5	32	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
9	c2o03A_	 Alignment		14.8	29	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
10	c3n70F_	 Alignment		14.7	26	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**transport activator; **PDBTitle:** the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a
11	d1qpma_	 Alignment		14.2	44	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like

12	d1mzba_	Alignment		14.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
13	d1jbob_	Alignment		10.4	25	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
14	d1opaa_	Alignment		10.1	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
15	d1p6pa_	Alignment		9.4	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
16	c2zv3E_	Alignment		9.4	28	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
17	c2ph5A_	Alignment		9.2	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
18	c3em0A_	Alignment		8.9	33	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**ileal bile acid-binding protein; **PDBTitle:** crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b).
19	c3civA_	Alignment		8.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
20	d2ftba1	Alignment		8.7	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
21	d1d4aa_	Alignment	not modelled	8.7	30	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
22	d1kqwa_	Alignment	not modelled	8.6	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
23	c3ca8B_	Alignment	not modelled	8.6	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
24	d1qrda_	Alignment	not modelled	8.6	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
25	d2fs6a1	Alignment	not modelled	8.4	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
26	c4a5qC_	Alignment	not modelled	8.4	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**chi1; **PDBTitle:** crystal structure of the chitinase chi1 fitted into the 3d structure2 of the yersinia entomophaga toxin complex
27	c3oa5A_	Alignment	not modelled	8.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chi1; **PDBTitle:** the structure of chi1, a chitinase from yersinia entomophaga
28	d1ftpa_	Alignment	not modelled	8.2	44	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
						Fold: Peptidyl-tRNA hydrolase II

29	d1rlka_	Alignment	not modelled	8.2	17	**Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
30	d2cbra_	Alignment	not modelled	8.1	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
31	c3nnkC_	Alignment	not modelled	8.0	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
32	d1ggla_	Alignment	not modelled	8.0	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
33	d1tw4a_	Alignment	not modelled	7.9	44	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
34	d1vyfa_	Alignment	not modelled	7.7	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
35	c2vmlD_	Alignment	not modelled	7.6	20	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**phycocyanin beta chain; **PDBTitle:** the monoclinic structure of phycocyanin from gloeobacter2 violaceus
36	d2fhfa5	Alignment	not modelled	7.6	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	c2lbaA_	Alignment	not modelled	7.6	33	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**babp protein; **PDBTitle:** solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
38	c2c4bB_	Alignment	not modelled	7.6	21	**PDB header:**fusion protein **Chain:** B: **PDB Molecule:**barnase mcoeeti fusion; **PDBTitle:** inhibitor cystine knot protein mcoeeti fused to the2 catalytically inactive barnase mutant h102a
39	d2ogqa1	Alignment	not modelled	7.6	55	**Fold:**Polo-box domain **Superfamily:**Polo-box domain **Family:**Polo-box duplicated region
40	d1fdqa_	Alignment	not modelled	7.6	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
41	d1mdca_	Alignment	not modelled	7.5	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
42	d1g7na_	Alignment	not modelled	7.4	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
43	d1hmsa_	Alignment	not modelled	7.4	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
44	d1o1va_	Alignment	not modelled	7.2	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
45	d1lpja_	Alignment	not modelled	7.2	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
46	d1lfoa_	Alignment	not modelled	7.1	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
47	d2f73a1	Alignment	not modelled	7.1	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
48	c3efeC_	Alignment	not modelled	7.0	50	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
49	d1kzwa_	Alignment	not modelled	7.0	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
50	d1pmpa_	Alignment	not modelled	6.9	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
51	c3pptA_	Alignment	not modelled	6.8	44	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**sodium-calcium exchanger; **PDBTitle:** rep1-nxsq fatty acid transporter
52	d1hfoa_	Alignment	not modelled	6.8	32	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
53	d1yiva1	Alignment	not modelled	6.8	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
54	c3mwmA_	Alignment	not modelled	6.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
55	d1cpcb_	Alignment	not modelled	6.7	25	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins

56	d1ifca_	Alignment	not modelled	6.6	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
57	c2vqpA_	Alignment	not modelled	6.6	75	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** structure of the matrix protein from human respiratory2 syncytial virus
58	d1bwya_	Alignment	not modelled	6.5	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
59	d1eala_	Alignment	not modelled	6.5	33	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
60	d1eyxa_	Alignment	not modelled	6.5	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
61	d2a0aa1	Alignment	not modelled	6.4	44	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
62	d1o8va_	Alignment	not modelled	6.4	44	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
63	d1liaa_	Alignment	not modelled	6.4	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
64	d2hnxa1	Alignment	not modelled	6.3	56	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
65	d1crba_	Alignment	not modelled	6.3	44	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
66	d1b56a_	Alignment	not modelled	6.3	67	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
67	d1uyra2	Alignment	not modelled	6.3	43	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
68	c2crvA_	Alignment	not modelled	6.3	80	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
69	c2vofA_	Alignment	not modelled	6.3	42	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-related protein a1; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
70	d2gdga1	Alignment	not modelled	6.1	17	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
71	d1t0ia_	Alignment	not modelled	6.1	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
72	d2j2za2	Alignment	not modelled	6.1	25	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
73	c2gqsA_	Alignment	not modelled	6.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** saicar synthetase complexed with cair-mg2+ and adp
74	c3kreA_	Alignment	not modelled	6.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
75	c2o8kA_	Alignment	not modelled	5.8	55	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
76	c2q9sA_	Alignment	not modelled	5.8	56	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fatty acid-binding protein; **PDBTitle:** linoleic acid bound to fatty acid binding protein 4
77	c3fwtA_	Alignment	not modelled	5.8	29	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
78	c2z02A_	Alignment	not modelled	5.7	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** crystal structure of2 phosphoribosylaminoimidazolesuccinocarboxamide synthase3 wit atp from methanocaldococcus jannaschii
79	d2fzva1	Alignment	not modelled	5.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
80	c2xtdB_	Alignment	not modelled	5.5	43	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tbl1 f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
81	c3nraA_	Alignment	not modelled	5.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution

82	d1gd0a_	Alignment	not modelled	5.4	21	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
83	c2kuaA_	Alignment	not modelled	5.4	36	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-like protein 10; **PDBTitle:** solution structure of a divergent bcl-2 protein
84	c2xteH_	Alignment	not modelled	5.4	43	**PDB header:**transcription **Chain:** H: **PDB Molecule:**f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
85	d1o82a_	Alignment	not modelled	5.3	50	**Fold:**Saposin-like **Superfamily:**Bacteriocin AS-48 **Family:**Bacteriocin AS-48
86	c2fu4B_	Alignment	not modelled	5.1	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
87	c2xa6B_	Alignment	not modelled	5.0	38	**PDB header:**transcription **Chain:** B: **PDB Molecule:**kh domain-containing\,rna-binding\,signal **PDBTitle:** structural basis for homodimerization of the src-associated2 during mitosis, 68 kd protein (sam68) qua1 domain