Phyre^2

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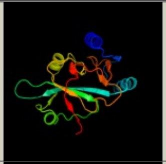
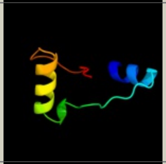
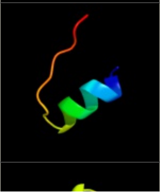
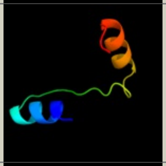
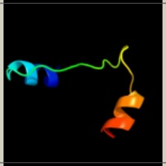
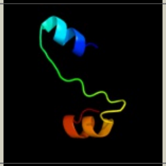
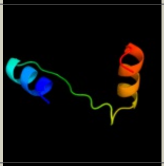
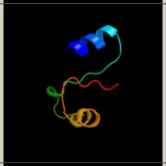
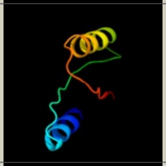
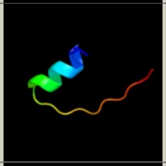
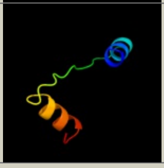
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vjfa_	Alignment		100.0	28	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
2	d1vkia_	Alignment		100.0	23	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
3	c2dxaA_	Alignment		100.0	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein ybak; **PDBTitle:** crystal structure of trans editing enzyme prox from e.coli
4	d1wdva_	Alignment		100.0	17	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
5	d1dbxa_	Alignment		100.0	21	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
6	c2cx5B_	Alignment		100.0	23	**PDB header:**translation **Chain:** B: **PDB Molecule:**a putative trans-editing enzyme; **PDBTitle:** crystal structure of a putative trans-editing enzyme for2 prolyl trna synthetase
7	c3op6B_	Alignment		100.0	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an oligo-nucleotide binding protein (lpg1207)2 from legionella pneumophila subsp. pneumophila str. philadelphia 1 at3 2.00 a resolution
8	c3memA_	Alignment		100.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative signal transduction protein; **PDBTitle:** crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
9	c2j3mA_	Alignment		98.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
10	d1t1va_	Alignment		56.8	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
11	c2ct6A_	Alignment		54.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2

12	c1u6tA_	Alignment		47.7	16	**PDB header:**protein binding, signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like
13	d1h75a_	Alignment		41.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
14	c1nm3B_	Alignment		40.8	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
15	d1nm3a1	Alignment		39.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	d1r7ha_	Alignment		38.5	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
17	c3nznA_	Alignment		36.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
18	c2h31A_	Alignment		28.1	14	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
19	c3lgcA_	Alignment		24.0	5	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
20	c2klxA_	Alignment		23.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
21	c3ic4A_	Alignment	not modelled	19.7	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
22	c3f0iA_	Alignment	not modelled	17.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
23	d1pz4a_	Alignment	not modelled	17.5	7	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
24	d1rw1a_	Alignment	not modelled	16.9	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
25	c2kokA_	Alignment	not modelled	16.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
26	c3gkxB_	Alignment	not modelled	16.4	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
27	d1of5b_	Alignment	not modelled	15.3	30	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
28	d1fova_	Alignment	not modelled	15.3	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
29	c3l78A_	Alignment	not modelled	15.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx;

		Alignment	not modelled			**PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
30	d1abaa_	Alignment	not modelled	14.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
31	d1k0da2	Alignment	not modelled	13.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
32	c2khpA_	Alignment	not modelled	13.3	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
33	d1o6xa_	Alignment	not modelled	13.0	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
34	d1pbaa_	Alignment	not modelled	11.9	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
35	d1dzfa2	Alignment	not modelled	11.7	14	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
36	d1eika_	Alignment	not modelled	11.7	14	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
37	d2obba1	Alignment	not modelled	11.0	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
38	c2auwB_	Alignment	not modelled	10.8	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
39	d1z3ea1	Alignment	not modelled	10.5	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
40	c3h8qB_	Alignment	not modelled	10.5	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
41	d1jlva2	Alignment	not modelled	10.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
42	c3bkrA_	Alignment	not modelled	10.3	26	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**sterol carrier protein-2 like-3; **PDBTitle:** crystal structure of sterol carrier protein-2 like-3 (scp2-2 l3) from aedes aegypti
43	d1hmja_	Alignment	not modelled	10.1	12	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
44	c3rdwB_	Alignment	not modelled	9.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** putative arsenate reductase from yersinia pestis
45	d2boaa2	Alignment	not modelled	9.6	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
46	c3bn8A_	Alignment	not modelled	9.5	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative sterol carrier protein 2; **PDBTitle:** crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
47	d1axda2	Alignment	not modelled	9.3	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
48	d1ayea2	Alignment	not modelled	9.2	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
49	d1pyta_	Alignment	not modelled	9.2	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
50	d1qcza_	Alignment	not modelled	9.1	11	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
51	d1pcaa1	Alignment	not modelled	9.0	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
52	c2ht9A_	Alignment	not modelled	8.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
53	d1k0dd2	Alignment	not modelled	8.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
54	d1jqga2	Alignment	not modelled	8.7	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
55	c2e7pC_	Alignment	not modelled	8.5	25	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides

56	d1kwma2	Alignment	not modelled	8.4	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
57	d1ljra2	Alignment	not modelled	8.2	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
58	d1nsaa2	Alignment	not modelled	8.0	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
59	c2fw9A_	Alignment	not modelled	8.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
60	d1u11a_	Alignment	not modelled	7.9	16	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
61	c3fz4A_	Alignment	not modelled	7.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
62	d1z9ha2	Alignment	not modelled	7.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
63	d1c44a_	Alignment	not modelled	7.1	13	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
64	d1g7oa2	Alignment	not modelled	6.8	0	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
65	c3trhI_	Alignment	not modelled	6.7	16	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
66	d1gnwa2	Alignment	not modelled	6.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
67	d1j9ba_	Alignment	not modelled	6.6	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
68	c3orsD_	Alignment	not modelled	6.2	11	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
69	d1r5aa2	Alignment	not modelled	6.0	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
70	d1wika_	Alignment	not modelled	6.0	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
71	d1pn9a2	Alignment	not modelled	5.7	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
72	d2bvca1	Alignment	not modelled	5.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Glutamine synthetase, N-terminal domain **Family:**Glutamine synthetase, N-terminal domain
73	d1ikta_	Alignment	not modelled	5.3	25	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
74	c1ykaA_	Alignment	not modelled	5.2	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.