Phyre^2

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Description	P0AAR3
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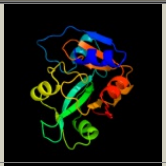
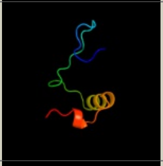
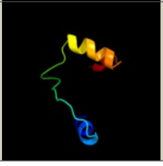
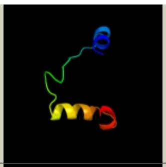
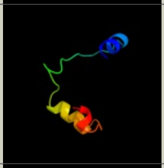
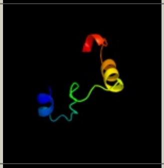
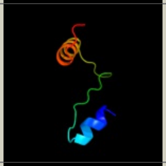
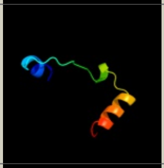
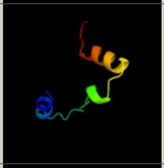
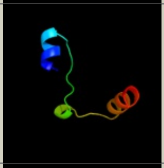
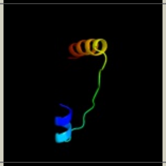
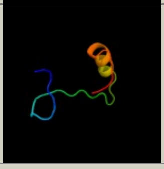
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dxaA_	Alignment		100.0	97	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein ybak; **PDBTitle:** crystal structure of trans editing enzyme prox from e.coli
2	d1dbxa_	Alignment		100.0	62	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
3	d1vjfa_	Alignment		100.0	14	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
4	d1wdva_	Alignment		100.0	21	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
5	d1vkia_	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	18	**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	18	**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		98.5	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
10	d1j9ba_	Alignment		86.2	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
11	c3gkxB_	Alignment		83.9	19	**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

12	d1z3ea1	Alignment		82.2	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
13	c3fz4A_	Alignment		81.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
14	c3l78A_	Alignment		81.3	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
15	c3rdwB_	Alignment		69.1	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** putative arsenate reductase from yersinia pestis
16	c2kokA_	Alignment		66.6	22	**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.
17	c3f0iA_	Alignment		64.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
18	d1rw1a_	Alignment		60.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
19	c3lgcA_	Alignment		46.9	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
20	d1fova_	Alignment		41.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
21	c3nznA_	Alignment	not modelled	34.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
22	d1t1va_	Alignment	not modelled	34.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
23	c2khpA_	Alignment	not modelled	29.7	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
24	c3ic4A_	Alignment	not modelled	24.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
25	d1nm3a1	Alignment	not modelled	23.1	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
26	d1h75a_	Alignment	not modelled	23.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	c3h8qB_	Alignment	not modelled	22.5	3	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
28	c2ct6A_	Alignment	not modelled	21.5	33	**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

29	c2e7pC_	Alignment	not modelled	21.2	11	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
30	c1nm3B_	Alignment	not modelled	20.9	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
31	c1u6tA_	Alignment	not modelled	18.7	29	**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
32	d1wika_	Alignment	not modelled	16.0	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	d1r7ha_	Alignment	not modelled	15.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
34	d1abaa_	Alignment	not modelled	14.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
35	c2ht9A_	Alignment	not modelled	11.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
36	c1ykaA_	Alignment	not modelled	11.4	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
37	d2obba1	Alignment	not modelled	9.2	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
38	c3qmxA_	Alignment	not modelled	8.9	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin a; **PDBTitle:** x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
39	d1gmua2	Alignment	not modelled	7.5	8	**Fold:**Ferredoxin-like **Superfamily:**Urease metallochaperone UreE, C-terminal domain **Family:**Urease metallochaperone UreE, C-terminal domain
40	d1jqga2	Alignment	not modelled	7.0	5	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
41	c3kc2A_	Alignment	not modelled	6.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
42	c2klxA_	Alignment	not modelled	6.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
43	d2v94a1	Alignment	not modelled	6.4	30	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
44	d1pz4a_	Alignment	not modelled	5.8	7	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
45	d1ayea2	Alignment	not modelled	5.5	22	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
46	d2boaa2	Alignment	not modelled	5.5	6	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
47	d1pyta_	Alignment	not modelled	5.4	22	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
48	d1nsaa2	Alignment	not modelled	5.4	17	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
49	d1kwma2	Alignment	not modelled	5.3	11	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
50	c1yj7A_	Alignment	not modelled	5.3	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
51	d1pcaa1	Alignment	not modelled	5.1	22	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain