Phyre2

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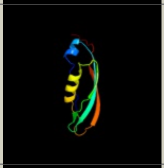
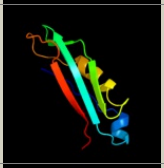
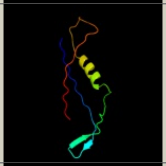
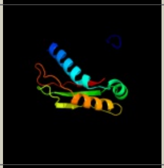
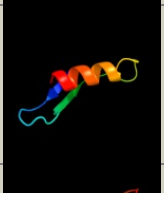
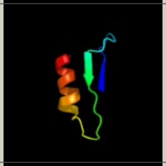
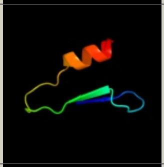
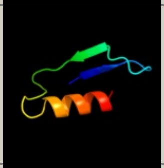
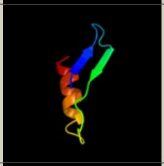
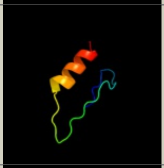
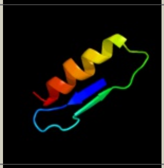
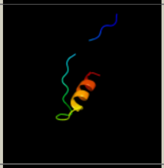
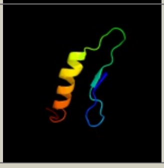
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xx3A_	Alignment		99.8	100	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
2	d1u07a_	Alignment		99.8	100	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
3	c2grxC_	Alignment		99.8	100	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
4	d2gskb1	Alignment		99.8	100	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
5	d1ihra_	Alignment		99.7	100	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
6	c2k9kA_	Alignment		99.7	31	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
7	d1lr0a_	Alignment		99.4	22	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
8	c2x9aB_	Alignment		99.2	11	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**membrane spanning protein, required for outer membrane **PDBTitle:** crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
9	d1tola2	Alignment		99.1	10	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
10	c1tolA_	Alignment		98.7	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (fusion protein consisting of minor coat **PDBTitle:** fusion of n-terminal domain of the minor coat protein from2 gene iii in phage m13, and c-terminal domain of e. coli3 protein-tola
11	c1ybxA_	Alignment		64.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum

12	c3onrl_	Alignment		60.8	21	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
13	c2h66G_	Alignment		60.0	9	**PDB header:**structural genomics/oxidoreductase **Chain:** G: **PDB Molecule:**pv-pf14_0368; **PDBTitle:** the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
14	c3kebB_	Alignment		57.6	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** thiol peroxidase from chromobacterium violaceum
15	d1j8ba_	Alignment		57.6	17	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
16	d1puga_	Alignment		52.2	22	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
17	d2cv4a1	Alignment		50.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
18	c3drnB_	Alignment		47.4	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
19	d2ux9a1	Alignment		45.5	25	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
20	d1we0a1	Alignment		43.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
21	d1zyea1	Alignment	not modelled	42.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
22	d2h01a1	Alignment	not modelled	41.6	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
23	c2vxaL_	Alignment	not modelled	40.3	32	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
24	d1e2ya_	Alignment	not modelled	38.3	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
25	c2bmxB_	Alignment	not modelled	36.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxidase c; **PDBTitle:** mycobacterium tuberculosis ahpc
26	d1qq2a_	Alignment	not modelled	33.8	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
27	d1qmva_	Alignment	not modelled	33.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
28	c3hd7A_	Alignment	not modelled	31.6	15	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
29	d1n8ja_	Alignment	not modelled	31.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like

30	c3oqtP_	Alignment	not modelled	31.1	14	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
31	d1uula_	Alignment	not modelled	30.9	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
32	d1m98a2	Alignment	not modelled	30.5	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Orange carotenoid protein, C-terminal domain
33	c3dtdI_	Alignment	not modelled	29.6	22	**PDB header:**structural genomics, unknown function **Chain:** I: **PDB Molecule:**invasion-associated protein b; **PDBTitle:** crystal structure of invasion associated protein b from bartonella2 henselae
34	d1psqa_	Alignment	not modelled	29.1	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
35	d1xvqa_	Alignment	not modelled	29.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
36	c2ii1A_	Alignment	not modelled	28.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetamidase; **PDBTitle:** crystal structure of acetamidase (10172637) from bacillus halodurans2 at 1.95 a resolution
37	c2kzxA_	Alignment	not modelled	28.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
38	c2yzhD_	Alignment	not modelled	26.1	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** crystal structure of peroxiredoxin-like protein from aquifex aeolicus
39	c2xpdC_	Alignment	not modelled	25.3	6	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol peroxidase; **PDBTitle:** reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
40	d1ijda_	Alignment	not modelled	24.5	21	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
41	d2cx4a1	Alignment	not modelled	23.6	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
42	d1nkza_	Alignment	not modelled	22.1	17	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
43	d2bmxa1	Alignment	not modelled	21.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	d2vnud4	Alignment	not modelled	21.3	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
45	c2c0dA_	Alignment	not modelled	20.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin peroxidase 2; **PDBTitle:** structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
46	d1zofa1	Alignment	not modelled	20.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
47	c3o6uB_	Alignment	not modelled	20.4	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein cpe2226; **PDBTitle:** crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
48	c2r7fA_	Alignment	not modelled	18.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease ii family protein; **PDBTitle:** crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
49	d2r7da2	Alignment	not modelled	18.4	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
50	c3lwxA_	Alignment	not modelled	18.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, **PDBTitle:** crystal structure of na(+)-translocating nadh-quinone2 reductase subunit c (yp_001302508.1) from parabacteroides3 distasonis atcc 8503 at 1.10 a resolution
51	d1knga_	Alignment	not modelled	18.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
52	c1zyeL_	Alignment	not modelled	17.9	15	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**thioredoxin-dependent peroxide reductase; **PDBTitle:** crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
53	c2egtA_	Alignment	not modelled	15.5	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein aq_1549; **PDBTitle:** crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus
54	c2jszA_	Alignment	not modelled	14.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** solution structure of tpx in the reduced state
						Fold: YbaB-like

55	d1pugb_	Alignment	not modelled	13.8	22	**Superfamily:**YbaB-like **Family:**YbaB-like
56	c3eytA_	Alignment	not modelled	13.6	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
57	c1h2aL_	Alignment	not modelled	12.8	30	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
58	d1iwla_	Alignment	not modelled	12.7	10	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**Outer-membrane lipoproteins carrier protein LolA
59	c2ywnA_	Alignment	not modelled	12.3	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin-like protein; **PDBTitle:** crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
60	c1zofB_	Alignment	not modelled	11.1	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide-reductase; **PDBTitle:** crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
61	d2idla1	Alignment	not modelled	11.0	14	**Fold:**eIF1-like **Superfamily:**TM1457-like **Family:**TM1457-like
62	d1xvwa1	Alignment	not modelled	10.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
63	d2zcta1	Alignment	not modelled	10.7	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
64	d1wui1	Alignment	not modelled	10.5	31	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
65	c3mjjD_	Alignment	not modelled	10.3	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted acetamidase/formamidase; **PDBTitle:** crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
66	c2b7kD_	Alignment	not modelled	10.1	6	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
67	d2ix0a4	Alignment	not modelled	9.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RNB domain-like
68	d1xcca_	Alignment	not modelled	9.5	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
69	c3myrB_	Alignment	not modelled	9.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
70	c2fug4_	Alignment	not modelled	8.9	8	**PDB header:**oxidoreductase **Chain:** 4: **PDB Molecule:**nadh-quinone oxidoreductase chain 4; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
71	d2fug41	Alignment	not modelled	8.9	8	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
72	c3gknA_	Alignment	not modelled	8.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
73	c1vqzA_	Alignment	not modelled	8.6	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
74	c2vnuD_	Alignment	not modelled	8.2	14	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
75	c2kl8A_	Alignment	not modelled	8.1	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
76	c3kh7A_	Alignment	not modelled	7.9	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
77	c3razA_	Alignment	not modelled	7.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
78	d2b7ka1	Alignment	not modelled	7.7	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
79	d1yexa1	Alignment	not modelled	7.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
80	c2kncA_	Alignment	not modelled	7.4	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib;

80	c2kncA_	Alignment	not modelled	7.4	19	**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
81	d1qxha_	Alignment	not modelled	7.4	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
82	d1xrda1	Alignment	not modelled	7.2	16	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
83	c2nr1A_	Alignment	not modelled	7.2	39	**PDB header:**receptor **Chain:** A: **PDB Molecule:**nr1 m2; **PDBTitle:** transmembrane segment 2 of nmda receptor nr1, nmr, 102 structures
84	d1rjlc_	Alignment	not modelled	7.1	31	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
85	d1yq9h1	Alignment	not modelled	6.9	30	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
86	c2v1mA_	Alignment	not modelled	6.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
87	d1q98a_	Alignment	not modelled	6.1	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
88	d1frfl_	Alignment	not modelled	6.1	30	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
89	c3f8xD_	Alignment	not modelled	6.0	7	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative delta-5-3-ketosteroid isomerase; **PDBTitle:** crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
90	d1e3db_	Alignment	not modelled	5.8	25	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
91	c2boyC_	Alignment	not modelled	5.7	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
92	c3fljA_	Alignment	not modelled	5.3	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
93	c2qtsA_	Alignment	not modelled	5.1	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acid-sensing ion channel; **PDBTitle:** structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph
94	c2wpnB_	Alignment	not modelled	5.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
95	c2rliA_	Alignment	not modelled	5.0	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
96	d3bzka5	Alignment	not modelled	5.0	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like