Phyre2

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Description	P18472
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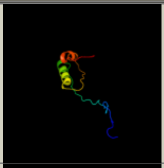
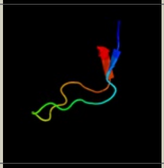
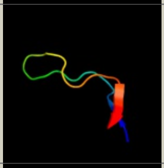
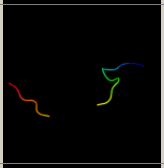
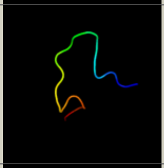
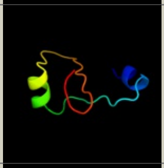
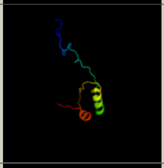
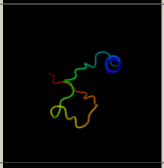
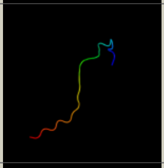
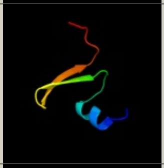
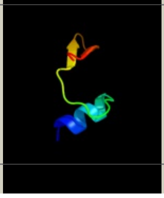
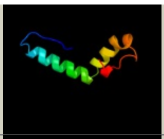
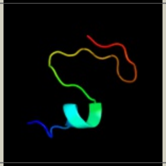
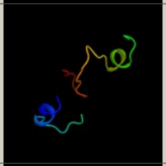
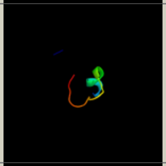
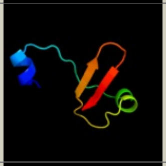
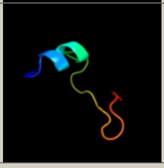
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fu3A_	Alignment		72.2	20	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
2	c2bhvC_	Alignment		60.3	21	**PDB header:**bacterial protein **Chain:** C: **PDB Molecule:**comb10; **PDBTitle:** structure of comb10 of the com type iv secretion system of2 helicobacter pylori
3	c3jqoV_	Alignment		57.7	22	**PDB header:**transport protein **Chain:** V: **PDB Molecule:**traf protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
4	d2gtta1	Alignment		57.5	29	**Fold:**Rhabdovirus nucleoprotein-like **Superfamily:**Rhabdovirus nucleoprotein-like **Family:**Rhabdovirus nucleocapsid protein
5	d2gica1	Alignment		55.1	16	**Fold:**Rhabdovirus nucleoprotein-like **Superfamily:**Rhabdovirus nucleoprotein-like **Family:**Rhabdovirus nucleocapsid protein
6	c3emxB_	Alignment		52.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
7	c2nqqA_	Alignment		51.9	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
8	c2qsiB_	Alignment		50.2	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
9	c3e7hA_	Alignment		47.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor
10	d1j08a2	Alignment		47.2	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
11	d2hfda1	Alignment		43.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like

12	c2yjpB_	Alignment		41.7	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative abc transporter, periplasmic binding protein, **PDBTitle:** crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
13	d1v58a1	Alignment		40.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
14	d1woua_	Alignment		36.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
15	d1v9wa_	Alignment		36.3	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
16	d1hyua4	Alignment		36.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
17	d1nhoa_	Alignment		35.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
18	d1syra_	Alignment		35.3	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
19	d1zmaa1	Alignment		34.1	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
20	c2fgxA_	Alignment		33.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
21	c2vm2C_	Alignment	not modelled	33.2	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin h isoform 1.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 12 crystallized using peg as precipitant
22	d1j08a1	Alignment	not modelled	31.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
23	d2nqra2	Alignment	not modelled	31.4	18	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
24	c2l6dA_	Alignment	not modelled	30.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
25	c2dizA_	Alignment	not modelled	29.8	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 5; **PDBTitle:** the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5
26	d1a8la1	Alignment	not modelled	29.8	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
27	d1fo5a_	Alignment	not modelled	29.8	32	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
28	d1uz5a2	Alignment	not modelled	29.4	29	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
29	c3nvbA_	Alignment	not modelled	29.0	11	**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
30	d1h6ua1	Alignment	not modelled	28.9	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Internalin Ig-like domain
31	c3dmlA_	Alignment	not modelled	28.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
32	c2pptA_	Alignment	not modelled	28.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
33	d1h6ta1	Alignment	not modelled	28.0	5	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Internalin Ig-like domain
34	c1v57A_	Alignment	not modelled	27.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
35	c3gnjD_	Alignment	not modelled	26.9	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
36	c3cxgA_	Alignment	not modelled	26.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
37	d1gh2a_	Alignment	not modelled	26.2	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
38	d1qgva_	Alignment	not modelled	25.7	0	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
39	d1spgb_	Alignment	not modelled	25.5	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
40	c2y7iB_	Alignment	not modelled	25.3	19	**PDB header:**arginine-binding protein **Chain:** B: **PDB Molecule:**stm4351; **PDBTitle:** structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
41	d1wu2a2	Alignment	not modelled	25.2	33	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
42	c2l5lA_	Alignment	not modelled	24.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
43	c2f51B_	Alignment	not modelled	23.9	18	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
44	c3d6iB_	Alignment	not modelled	23.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monothiol glutaredoxin-3; **PDBTitle:** structure of the thioredoxin-like domain of yeast2 glutaredoxin 3
45	d1a8la2	Alignment	not modelled	23.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
46	c2dmlA_	Alignment	not modelled	23.1	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
47	c3gv1A_	Alignment	not modelled	22.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
48	d1wdna_	Alignment	not modelled	22.1	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
49	d2omza1	Alignment	not modelled	21.7	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Internalin Ig-like domain
50	c1j08A_	Alignment	not modelled	21.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
51	c2i9hA_	Alignment	not modelled	20.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin i; **PDBTitle:** nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
52	d2b5ea4	Alignment	not modelled	20.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
53	c3kzqE_	Alignment	not modelled	20.5	21	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein vp2116; **PDBTitle:** the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
54	c2pyyB_	Alignment	not modelled	20.1	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**ionotropic glutamate receptor bacterial homologue; **PDBTitle:** crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
55	c1zypB_	Alignment	not modelled	20.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf

56	c1wu2B_	Alignment	not modelled	19.3	29	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
57	c1w89E_	Alignment	not modelled	19.0	24	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
58	c3h7mA_	Alignment	not modelled	18.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
59	c1yvyA_	Alignment	not modelled	18.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase [atp]; **PDBTitle:** crystal strucutre of anaerobiospirillum succiniciproducens2 phosphoenolpyruvate carboxykinase
60	d1thxa_	Alignment	not modelled	18.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
61	d1dbya_	Alignment	not modelled	18.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
62	c1zu4A_	Alignment	not modelled	18.3	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
63	c3delC_	Alignment	not modelled	18.2	11	**PDB header:**protein binding, transport protein **Chain:** C: **PDB Molecule:**arginine binding protein; **PDBTitle:** the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
64	c3kzgB_	Alignment	not modelled	18.2	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**arginine 3rd transport system periplasmic binding **PDBTitle:** crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
65	d2ftsa2	Alignment	not modelled	18.1	27	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
66	c2vhaB_	Alignment	not modelled	17.9	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**periplasmic binding transport protein; **PDBTitle:** debp
67	d1l1fa2	Alignment	not modelled	17.8	12	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
68	d1eeja1	Alignment	not modelled	17.7	32	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
69	d1r89a1	Alignment	not modelled	17.6	12	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
70	d1lsta_	Alignment	not modelled	17.5	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
71	c2vimA_	Alignment	not modelled	17.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
72	d1hsla_	Alignment	not modelled	17.2	6	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
73	c3apsA_	Alignment	not modelled	17.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of trx4 domain of erdj5
74	c2ieeB_	Alignment	not modelled	17.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable abc transporter extracellular-binding **PDBTitle:** crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
75	c3tcoA_	Alignment	not modelled	17.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
76	d2bv3a4	Alignment	not modelled	16.6	16	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
77	d2es7a1	Alignment	not modelled	16.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
78	d1m7ta_	Alignment	not modelled	16.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
79	c1jzdA_	Alignment	not modelled	16.5	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
80	c2oe0B_	Alignment	not modelled	16.5	16	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
81	c3kbrA_	Alignment	not modelled	16.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase

						precursor from2 pseudomonas aeruginosa pa01
82	d2f34a1	Alignment	not modelled	16.3	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
83	c1t3bA_	Alignment	not modelled	15.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
84	d2cvba1	Alignment	not modelled	15.7	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
85	c2ylnA_	Alignment	not modelled	15.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter, periplasmic binding protein, **PDBTitle:** crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
86	d1xwaa_	Alignment	not modelled	15.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
87	d1ep7a_	Alignment	not modelled	15.6	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
88	c1xbsA_	Alignment	not modelled	15.6	21	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
89	d1ti3a_	Alignment	not modelled	15.5	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
90	d1t3ba1	Alignment	not modelled	15.4	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
91	c2xbqB_	Alignment	not modelled	15.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
92	c3hypB_	Alignment	not modelled	15.3	18	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
93	c3g41A_	Alignment	not modelled	15.1	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amino acid abc transporter, periplasmic amino acid-binding **PDBTitle:** the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
94	c3kp8A_	Alignment	not modelled	15.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
95	c3g9bA_	Alignment	not modelled	15.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide-protein **PDBTitle:** crystal structure of reduced ost6l
96	c2dj1A_	Alignment	not modelled	15.0	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a4
97	c1t00A_	Alignment	not modelled	14.8	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
98	d1dd9a_	Alignment	not modelled	14.7	22	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
99	c1dd9A_	Alignment	not modelled	14.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core