Phyre2

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Description	P75839
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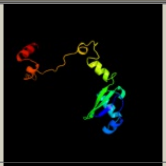
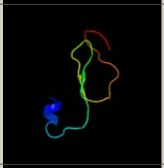
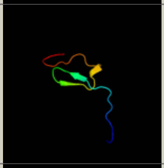
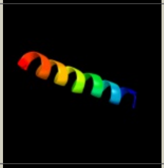
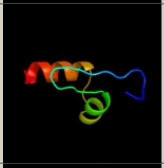
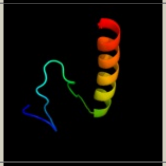
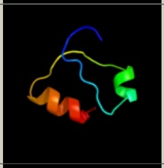
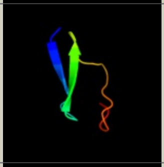
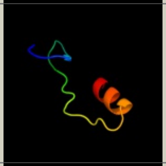
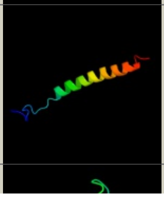
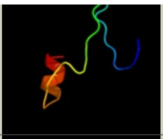
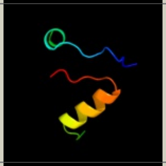
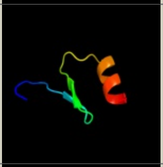
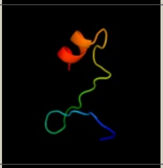
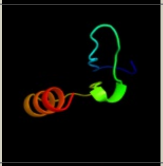
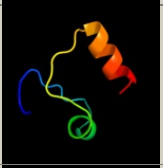
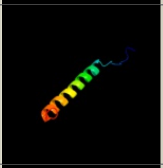
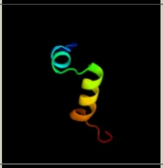
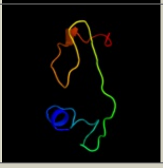
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c6fD_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yetf protein; **PDBTitle:** crystal structure of protein bsu07140 from bacillus subtilis
2	c1yuzB_	Alignment		53.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
3	d2guka1	Alignment		43.5	15	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
4	c2hr5B_	Alignment		39.3	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
5	d2e74d2	Alignment		37.8	26	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
6	c2znmA_	Alignment		33.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** oxidoreductase nmdsba3 from neisseria meningitidis
7	c3dvwA_	Alignment		33.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of reduced dsba1 from neisseria2 meningitidis
8	c3gv1A_	Alignment		30.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
9	c1dvbA_	Alignment		27.0	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
10	d1fvka_	Alignment		25.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
11	c2kncA_	Alignment		25.3	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex

12	c3l9vE_	Alignment		24.9	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
13	d1e42a2	Alignment		20.7	19	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Clathrin adaptor appendage, alpha and beta chain-specific domain
14	d1z6ma1	Alignment		19.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
15	d1un2a_	Alignment		18.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
16	d2fwha1	Alignment		18.2	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
17	d1eeja1	Alignment		18.1	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
18	c2k1aA_	Alignment		17.9	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
19	d1y5ib1	Alignment		17.0	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	c2r77A_	Alignment		15.9	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**phosphatidylethanolamine-binding protein, putative; **PDBTitle:** crystal structure of phosphatidylethanolamine-binding protein,2 pfl0955c, from plasmodium falciparum
21	c3kzqE_	Alignment	not modelled	15.5	6	**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
22	c3feuA_	Alignment	not modelled	15.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
23	c1t3bA_	Alignment	not modelled	15.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
24	d2ewha1	Alignment	not modelled	14.5	23	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
25	c3hd5A_	Alignment	not modelled	13.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
26	c1jzdA_	Alignment	not modelled	13.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
27	d1t3ba1	Alignment	not modelled	13.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
28	d1iwga5	Alignment	not modelled	12.6	12	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
						Fold:DHS-like NAD/FAD-binding domain

29	d1d4oa_	Alignment	not modelled	11.8	19	**Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
30	c1pt9B_	Alignment	not modelled	11.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
31	c3gmfA_	Alignment	not modelled	11.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
32	d1pnoa_	Alignment	not modelled	11.5	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
33	d1aipc1	Alignment	not modelled	11.2	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
34	d1dl6a_	Alignment	not modelled	10.6	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
35	c3h93A_	Alignment	not modelled	10.4	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba
36	d1beda_	Alignment	not modelled	10.4	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
37	c2eelA_	Alignment	not modelled	10.4	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**cell death activator cide-a; **PDBTitle:** solution structure of the cide-n domain of human cell death2 activator cide-a
38	c2bruC_	Alignment	not modelled	10.0	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
39	c3gykC_	Alignment	not modelled	9.8	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**27kda outer membrane protein; **PDBTitle:** the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
40	d1ppva_	Alignment	not modelled	9.6	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
41	d2cp9a1	Alignment	not modelled	9.2	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
42	d1pfta_	Alignment	not modelled	9.2	14	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
43	d1lkoa2	Alignment	not modelled	9.0	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
44	d1ckma1	Alignment	not modelled	8.7	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
45	c3fz5C_	Alignment	not modelled	8.6	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**possible 2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
46	d1thta_	Alignment	not modelled	8.4	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
47	d1ibxa_	Alignment	not modelled	8.4	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
48	d1xb2b1	Alignment	not modelled	8.3	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
49	d1yuza2	Alignment	not modelled	8.0	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
50	d2fwua1	Alignment	not modelled	7.9	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
51	c2d7cD_	Alignment	not modelled	7.8	8	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of human rab11 in complex with fip3 rab-2 binding domain
52	d1efub3	Alignment	not modelled	7.7	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
53	c3gn3B_	Alignment	not modelled	7.7	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative protein-disulfide isomerase; **PDBTitle:** crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
54	d1h6za3	Alignment	not modelled	7.6	9	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Pyruvate phosphate dikinase, N-terminal domain
55	d2i5ia1	Alignment	not modelled	7.5	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**YdjC-like
						Fold:P-loop containing nucleoside triphosphate hydrolases

56	d1t5la1	Alignment	not modelled	7.5	14	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
57	d2b2na1	Alignment	not modelled	7.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
58	c3kcmC_	Alignment	not modelled	7.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
59	d1d4ba_	Alignment	not modelled	7.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
60	d1nnqa2	Alignment	not modelled	7.3	31	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
61	d1zd0a1	Alignment	not modelled	7.2	18	**Fold:**PF0523-like **Superfamily:**PF0523-like **Family:**PF0523-like
62	d2fi0a1	Alignment	not modelled	7.2	8	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
63	d2h7aa1	Alignment	not modelled	7.2	17	**Fold:**YcgL-like **Superfamily:**YcgL-like **Family:**YcgL-like
64	c3bciA_	Alignment	not modelled	7.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond protein a; **PDBTitle:** crystal structure of staphylococcus aureus dsba
65	d2odka1	Alignment	not modelled	6.8	25	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
66	d1meka_	Alignment	not modelled	6.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
67	d2gmga1	Alignment	not modelled	6.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
68	c3rcqA_	Alignment	not modelled	6.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartyl/asparaginyl beta-hydroxylase; **PDBTitle:** crystal structure of human aspartate beta-hydroxylase isoform a
69	c2ivwA_	Alignment	not modelled	6.5	18	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**pilp pilot protein; **PDBTitle:** the solution structure of a domain from the neisseria2 meningitidis pilp pilot protein.
70	c2odkD_	Alignment	not modelled	6.4	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
71	c2x5rA_	Alignment	not modelled	6.3	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hypothetical protein orf126; **PDBTitle:** crystal structure of the hypothetical protein orf126 from2 pyrobaculum spherical virus
72	c1ngmB_	Alignment	not modelled	6.2	23	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription factor iiib brf1 subunit; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
73	c2jugB_	Alignment	not modelled	6.1	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
74	d1szpb1	Alignment	not modelled	6.1	29	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
75	d1cy5a_	Alignment	not modelled	6.0	5	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
76	c2kvsA_	Alignment	not modelled	5.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mw0776; **PDBTitle:** nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215
77	c1b22A_	Alignment	not modelled	5.6	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
78	d1b22a_	Alignment	not modelled	5.6	22	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
79	c3c7mB_	Alignment	not modelled	5.6	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiol:disulfide interchange protein dsba-like; **PDBTitle:** crystal structure of reduced dsbl
80	c1xtzA_	Alignment	not modelled	5.5	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
81	c3ghaA_	Alignment	not modelled	5.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)
82	d1hyua4	Alignment	not modelled	5.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like

83	c1e3hA_	Alignment	not modelled	5.4	26	**PDB header:**polyribonucleotide transferase **Chain:** A: **PDB Molecule:**guanosine pentaphosphate synthetase; **PDBTitle:** semet derivative of streptomyces antibioticus pnpase/gpsi2 enzyme
84	c2jqeA_	Alignment	not modelled	5.3	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
85	c3hryA_	Alignment	not modelled	5.3	35	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
86	d1wpxb1	Alignment	not modelled	5.1	13	**Fold:**PEBP-like **Superfamily:**PEBP-like **Family:**Phosphatidylethanolamine binding protein
87	d1iwga6	Alignment	not modelled	5.1	9	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
88	c2oarA_	Alignment	not modelled	5.1	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)