Phyre^2

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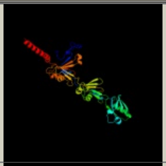
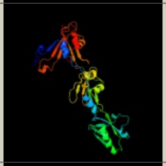
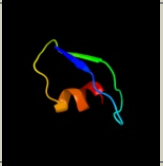
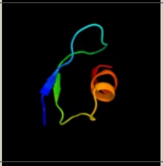
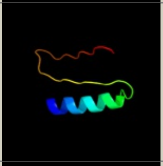
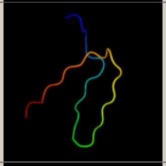
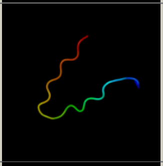
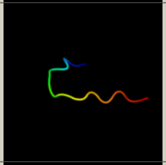
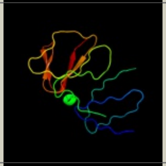
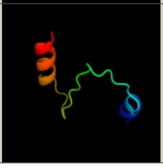
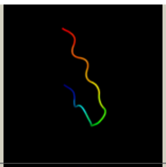
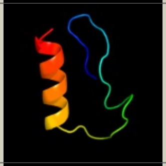
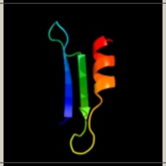
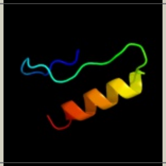
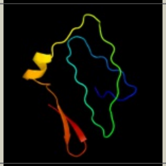
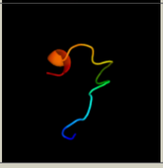
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j58G_	Alignment		100.0	67	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza; **PDBTitle:** the structure of wza
2	c2w8iG_	Alignment		100.0	69	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza; **PDBTitle:** crystal structure of wza24-345.
3	c3p42D_	Alignment		99.8	17	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**predicted protein; **PDBTitle:** structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
4	d2fug13	Alignment		90.0	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Nqo1 middle domain-like **Family:**Nqo1 middle domain-like
5	c2fugA_	Alignment		84.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
6	d1ghha_	Alignment		66.8	10	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
7	c2xdvA_	Alignment		64.8	27	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
8	d1vrba1	Alignment		57.3	37	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
9	c3uyjA_	Alignment		57.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
10	c3rnsA_	Alignment		56.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** cupin 2 conserved barrel domain protein from leptotrichia buccalis
11	c2h8kA_	Alignment		51.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap

12	c3al6A_	Alignment		46.4	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
13	c3eytA_	Alignment		45.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
14	d1q44a_	Alignment		43.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
15	d1zofa1	Alignment		41.9	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
16	d1qmva_	Alignment		41.3	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
17	d1wp0a1	Alignment		40.2	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
18	c3k2oB_	Alignment		40.0	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
19	d1x82a_	Alignment		39.8	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
20	c2zpmA_	Alignment		39.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
21	c3lorB_	Alignment	not modelled	38.8	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**thiol-disulfide isomerase and thioredoxins; **PDBTitle:** the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
22	d1prxa_	Alignment	not modelled	37.7	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
23	c2r37A_	Alignment	not modelled	36.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
24	c2yztA_	Alignment	not modelled	36.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1756; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
25	c2v2gC_	Alignment	not modelled	36.1	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxiredoxin 6; **PDBTitle:** crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
26	c2opkC_	Alignment	not modelled	35.9	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
27	d1xv1a_	Alignment	not modelled	35.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
						Fold: Double-stranded beta-helix

28	d1h2ka_	Alignment	not modelled	35.0	46	**Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
29	c3razA_	Alignment	not modelled	34.2	3	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
30	d1j99a_	Alignment	not modelled	34.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
31	d1fmja_	Alignment	not modelled	34.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
32	d1g3ma_	Alignment	not modelled	32.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
33	d1knga_	Alignment	not modelled	31.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
34	d1q20a_	Alignment	not modelled	31.3	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
35	c2hhzA_	Alignment	not modelled	31.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related; **PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
36	d1we0a1	Alignment	not modelled	30.9	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
37	c2r32A_	Alignment	not modelled	30.6	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
38	d1j3pa_	Alignment	not modelled	30.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
39	c2fhdA_	Alignment	not modelled	30.0	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
40	c2v1mA_	Alignment	not modelled	29.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
41	d2dsya1	Alignment	not modelled	28.6	19	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA0281-like
42	d1xcca_	Alignment	not modelled	26.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
43	d1uula_	Alignment	not modelled	26.1	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	c3cmiA_	Alignment	not modelled	25.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
45	c3or5A_	Alignment	not modelled	25.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein, thioredoxin family **PDBTitle:** crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum tls
46	c3jxoB_	Alignment	not modelled	24.6	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trka-n domain protein; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
47	c3drnB_	Alignment	not modelled	24.2	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
48	d1aqua_	Alignment	not modelled	23.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
49	d1gp1a_	Alignment	not modelled	23.1	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
50	c3kh7A_	Alignment	not modelled	23.0	14	**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
51	d1juha_	Alignment	not modelled	22.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
52	d1sfna_	Alignment	not modelled	22.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
53	c1zd1B_	Alignment	not modelled	22.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1

54	c2gwhA_	Alignment	not modelled	22.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
55	d1uija2	Alignment	not modelled	21.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
56	d1uika2	Alignment	not modelled	21.7	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
57	d1yexa1	Alignment	not modelled	21.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	c3d0fA_	Alignment	not modelled	21.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
59	d1y7ma2	Alignment	not modelled	21.4	4	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
60	c2q30C_	Alignment	not modelled	21.1	7	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
61	d2phla2	Alignment	not modelled	20.6	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
62	d1lr5a_	Alignment	not modelled	20.3	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
63	c2wbqA_	Alignment	not modelled	20.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
64	d1qq2a_	Alignment	not modelled	20.2	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
65	c3lwaA_	Alignment	not modelled	20.1	6	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**secreted thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
66	c1sefA_	Alignment	not modelled	19.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
67	d1sefa_	Alignment	not modelled	19.9	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
68	d1n8ja_	Alignment	not modelled	19.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
69	c3kvaA_	Alignment	not modelled	19.6	31	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1d; **PDBTitle:** structure of kiaa1718 jumonji domain in complex with alpha-2 ketoglutarate
70	c2rqeA_	Alignment	not modelled	19.0	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta-1,3-glucan-binding protein; **PDBTitle:** solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition
71	d1dgwa_	Alignment	not modelled	19.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
72	d2cv4a1	Alignment	not modelled	18.5	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
73	d2d40a1	Alignment	not modelled	18.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
74	d2phna1	Alignment	not modelled	18.4	23	**Fold:**CofE-like **Superfamily:**CofE-like **Family:**CofE-like
75	c2og5A_	Alignment	not modelled	18.3	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
76	d1ds1a_	Alignment	not modelled	18.0	31	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
77	c3gl3D_	Alignment	not modelled	18.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative thiol:disulfide interchange protein **PDBTitle:** crystal structure of a putative thiol:disulfide interchange2 protein dsbe from chlorobium tepidum
78	c2rogA_	Alignment	not modelled	17.5	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
79	c3u7zA_	Alignment	not modelled	17.4	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative metal binding protein rumgna_00854; **PDBTitle:** crystal structure of a putative metal binding protein

						rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
80	d2b7ka1	Alignment	not modelled	17.4	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
81	d1z5ye1	Alignment	not modelled	16.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
82	c2b1kA_	Alignment	not modelled	16.9	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
83	d1uzxa_	Alignment	not modelled	16.9	11	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
84	d1zyea1	Alignment	not modelled	16.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
85	d1te7a_	Alignment	not modelled	16.5	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
86	d1rc6a_	Alignment	not modelled	16.5	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
87	c2yu1A_	Alignment	not modelled	16.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1a; **PDBTitle:** crystal structure of hjhdm1a complexed with a-ketoglutarate
88	c1zofB_	Alignment	not modelled	16.3	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide-reductase; **PDBTitle:** crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
89	c2rliA_	Alignment	not modelled	16.0	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
90	d1sq4a_	Alignment	not modelled	15.9	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
91	d1fe0a_	Alignment	not modelled	15.9	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
92	d3bfxa1	Alignment	not modelled	15.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
93	c2c0dA_	Alignment	not modelled	15.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin peroxidase 2; **PDBTitle:** structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
94	c3h7hA_	Alignment	not modelled	15.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
95	c1zyeL_	Alignment	not modelled	15.6	16	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**thioredoxin-dependent peroxide reductase; **PDBTitle:** crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
96	c2wkdA_	Alignment	not modelled	15.5	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
97	c2vpvA_	Alignment	not modelled	15.5	7	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
98	d1e2ya_	Alignment	not modelled	15.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
99	c2he3A_	Alignment	not modelled	15.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 2; **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)