Phyre^2

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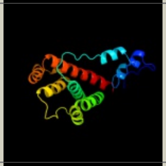
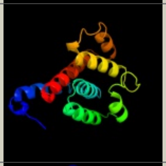
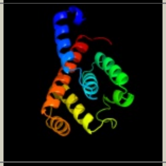
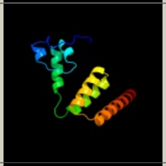
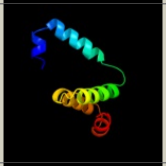
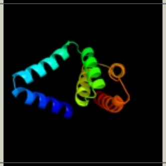
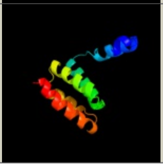
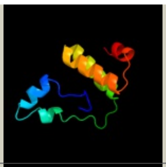
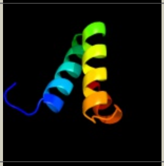
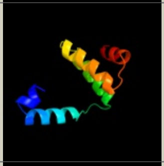
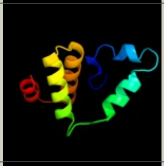
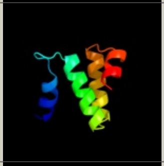
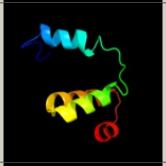
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2prra1	Alignment		100.0	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
2	d2pfxa1	Alignment		100.0	13	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
3	c3c1lB_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative antioxidant defense protein mlr4105; **PDBTitle:** crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
4	c3lvyB_	Alignment		100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
5	d2oyoa1	Alignment		100.0	19	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
6	d2o4da1	Alignment		100.0	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
7	d2gmya1	Alignment		100.0	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
8	d2ouwa1	Alignment		99.7	18	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
9	c3beyC_	Alignment		99.0	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
10	d1vkea_	Alignment		98.9	11	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
11	c1p8cD_	Alignment		98.9	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima

12	c2qeuA_	Alignment		98.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
13	d1knca_	Alignment		98.8	13	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
14	c3d7iB_	Alignment		98.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family protein; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
15	d2q0ta1	Alignment		98.5	12	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
16	d2cwqa1	Alignment		98.4	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
17	d1vkeb_	Alignment		98.3	7	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
18	d2af7a1	Alignment		96.6	7	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
19	d1a9xa1	Alignment		92.1	9	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
20	c3bjxB_	Alignment		68.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**halocarboxylic acid dehalogenase dehi; **PDBTitle:** structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
21	c3cixA_	Alignment	not modelled	54.4	11	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
22	c3iwfA_	Alignment	not modelled	41.4	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
23	d2a1ka1	Alignment	not modelled	39.9	43	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
24	c3omdB_	Alignment	not modelled	39.4	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
25	d1bkra_	Alignment	not modelled	38.9	25	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
26	c2d87A_	Alignment	not modelled	38.2	15	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**smoothelin splice isoform l2; **PDBTitle:** solution structure of the ch domain from human smoothelin2 splice isoform l2
27	c1m6vE_	Alignment	not modelled	36.3	9	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
28	c2vn2B_	Alignment	not modelled	35.9	20	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad

						protein2 from geobacillus kaustophilus hta426
29	d1gpca_	Alignment	not modelled	33.7	43	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
30	c2d89A_	Alignment	not modelled	31.6	18	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**ehbp1 protein; **PDBTitle:** solution structure of the ch domain from human eh domain2 binding protein 1
31	c2krkA_	Alignment	not modelled	31.4	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**26s protease regulatory subunit 8; **PDBTitle:** solution nmr structure of 26s protease regulatory subunit 82 from h.sapiens, northeast structural genomics consortium3 target target hr3102a
32	c1wylA_	Alignment	not modelled	30.5	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** solution structure of the ch domain of human nedd92 interacting protein with calponin homology and lim domains
33	c3mhvC_	Alignment	not modelled	28.6	13	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of vps4 and vta1
34	c3rmsA_	Alignment	not modelled	26.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis
35	d1t3wa_	Alignment	not modelled	24.7	15	**Fold:**DNA primase DnaG, C-terminal domain **Superfamily:**DNA primase DnaG, C-terminal domain **Family:**DNA primase DnaG, C-terminal domain
36	d2csba4	Alignment	not modelled	23.0	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
37	d1t33a2	Alignment	not modelled	22.9	10	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
38	c1wr1B_	Alignment	not modelled	22.7	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
39	c2dt7A_	Alignment	not modelled	20.5	36	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
40	c2v79B_	Alignment	not modelled	20.3	20	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
41	c1t3bA_	Alignment	not modelled	20.2	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
42	c3n7qA_	Alignment	not modelled	19.1	19	**PDB header:**transcription, replication/dna **Chain:** A: **PDB Molecule:**transcription termination factor, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial mterf fragment (aa 99-399) in2 complex with a 12-mer dna encompassing the trnaleu(uur) binding3 sequence
43	d1sh5a2	Alignment	not modelled	18.8	28	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
44	c3l9vE_	Alignment	not modelled	18.7	33	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
45	c3dvwA_	Alignment	not modelled	18.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of reduced dsba1 from neisseria2 meningitidis
46	c2rcyB_	Alignment	not modelled	18.1	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline carboxylate reductase; **PDBTitle:** crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
47	c2d88A_	Alignment	not modelled	18.0	13	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**protein mical-3; **PDBTitle:** solution structure of the ch domain from human mical-32 protein
48	d1bhda_	Alignment	not modelled	17.5	25	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
49	c3bj4B_	Alignment	not modelled	17.0	41	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily kqt **PDBTitle:** the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
50	c3lgcA_	Alignment	not modelled	16.9	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
51	d1sxjd1	Alignment	not modelled	15.8	11	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
52	c1v57A_	Alignment	not modelled	15.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
53	c3hd5A	Alignment	not modelled	15.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba;

53	c3hd3A_	Alignment	not modelled	15.1	11	**PDBTitle:** crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
54	c3gv1A_	Alignment	not modelled	15.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
55	c2jy5A_	Alignment	not modelled	14.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
56	d2ccaa1	Alignment	not modelled	14.5	11	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
57	d1xcca_	Alignment	not modelled	14.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	d1t3ba1	Alignment	not modelled	14.3	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
59	c2remB_	Alignment	not modelled	13.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**disulfide oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase dsba from xylella2 fastidiosa
60	d1m3va1	Alignment	not modelled	13.7	56	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
61	d1rt8a_	Alignment	not modelled	13.7	23	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
62	c3hi2D_	Alignment	not modelled	13.6	11	**PDB header:**dna binding protein/toxin **Chain:** D: **PDB Molecule:**motility quorum-sensing regulator mqsr; **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
63	c3gykC_	Alignment	not modelled	13.1	14	**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
64	c1jzdA_	Alignment	not modelled	13.0	0	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
65	c3riwA_	Alignment	not modelled	12.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ascorbate peroxidase; **PDBTitle:** the crystal structure of leishmania major peroxidase mutant c197t
66	d1eeja1	Alignment	not modelled	12.3	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
67	c2k9hA_	Alignment	not modelled	12.1	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glycoprotein; **PDBTitle:** the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers
68	d2vkva2	Alignment	not modelled	11.8	10	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
69	c3ghaA_	Alignment	not modelled	11.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)
70	c3c7mB_	Alignment	not modelled	11.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiol:disulfide interchange protein dsba-like; **PDBTitle:** crystal structure of reduced dsbl
71	d1prxa_	Alignment	not modelled	11.4	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	d2o3fa1	Alignment	not modelled	11.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
73	c3feuA_	Alignment	not modelled	11.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
74	d2euta1	Alignment	not modelled	11.2	7	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
75	c2v2gC_	Alignment	not modelled	11.2	29	**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
76	c2qjxA_	Alignment	not modelled	11.0	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
77	d1repc1	Alignment	not modelled	10.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
78	d1pxya_	Alignment	not modelled	10.6	19	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
79	d1j2oa1	Alignment	not modelled	10.5	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
						PDB header:oxidoreductase

80	c3mk7B_	Alignment	not modelled	10.5	33	**Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
81	c3bciA_	Alignment	not modelled	10.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond protein a; **PDBTitle:** crystal structure of staphylococcus aureus dsba
82	d2zcta1	Alignment	not modelled	10.3	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
83	c2o3fC_	Alignment	not modelled	10.1	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
84	d1un2a_	Alignment	not modelled	10.1	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
85	d1ehsa_	Alignment	not modelled	10.0	50	**Fold:**Toxic hairpin **Superfamily:**Heat-stable enterotoxin B **Family:**Heat-stable enterotoxin B
86	d1dxxa2	Alignment	not modelled	9.8	25	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
87	c3gmfA_	Alignment	not modelled	9.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
88	d2daha1	Alignment	not modelled	9.1	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
89	d2e39a1	Alignment	not modelled	9.0	15	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
90	d1oqya2	Alignment	not modelled	8.9	9	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
91	d1rutx1	Alignment	not modelled	8.9	63	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
92	d2bwba1	Alignment	not modelled	8.9	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
93	d1h75a_	Alignment	not modelled	8.7	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
94	c1g6uB_	Alignment	not modelled	8.7	15	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**domain swapped dimer; **PDBTitle:** crystal structure of a domain swapped dimer
95	d1mwva1	Alignment	not modelled	8.7	15	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
96	d1fova_	Alignment	not modelled	8.6	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
97	c3nznA_	Alignment	not modelled	8.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
98	c1nm3B_	Alignment	not modelled	8.4	23	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
99	c2agaA_	Alignment	not modelled	8.3	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**machado-joseph disease protein 1; **PDBTitle:** de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain