Phyre2

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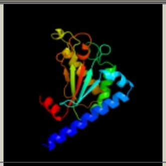
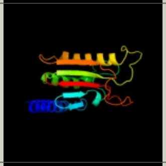
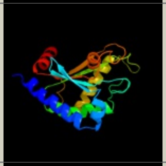
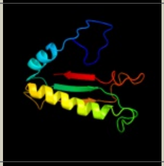
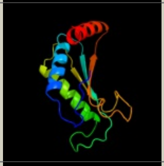
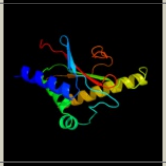
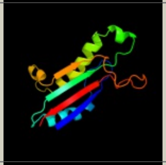
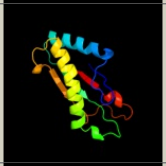
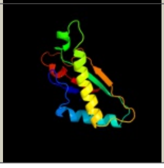
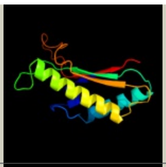
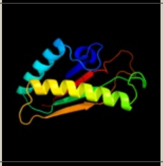
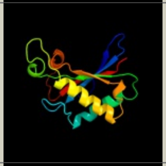
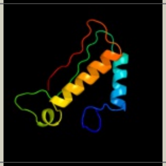
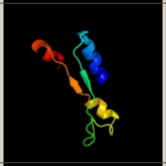
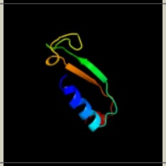
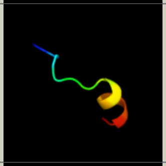
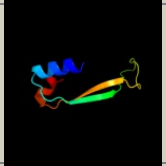
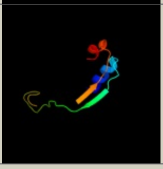
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zvyB_	Alignment		100.0	94	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form ii)
2	c3khnB_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
3	c2zovA_	Alignment		100.0	91	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form i)
4	c2l26A_	Alignment		100.0	27	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
5	c3cyqM_	Alignment		100.0	21	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
6	c2k1sA_	Alignment		100.0	21	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad; **PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
7	c3ldtA_	Alignment		99.9	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein, ompa family protein; **PDBTitle:** crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila
8	c2kgwA_	Alignment		99.9	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
9	c3td4D_	Alignment		99.9	25	**PDB header:**membrane protein,peptide binding protein **Chain:** D: **PDB Molecule:**outer membrane protein omp38; **PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
10	d2aizp1	Alignment		99.9	29	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
11	d2hqsc1	Alignment		99.9	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like

12	d1r1ma_	Alignment		99.9	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
13	c1r1mA_	Alignment		99.9	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein class 4; **PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis
14	c3oonA_	Alignment		99.9	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein (tpn50); **PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31
15	c2zf8A_	Alignment		99.5	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
16	c3l7pA_	Alignment		58.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
17	d2cz4a1	Alignment		42.2	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
18	c2ccaA_	Alignment		34.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxidase/catalase t; **PDBTitle:** crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis
19	c2rd5D_	Alignment		29.4	21	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
20	d1qy7a_	Alignment		28.8	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
21	c2b2qB_	Alignment	not modelled	26.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of native catalase-peroxidase katg at2 ph7.5
22	c3mhyC_	Alignment	not modelled	26.0	18	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
23	c2fxhB_	Alignment	not modelled	25.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase protein; **PDBTitle:** crystal structure of katg at ph 6.5
24	c1itkB_	Alignment	not modelled	25.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of catalase-peroxidase from haloarcula2 marismortui
25	c2j9dG_	Alignment	not modelled	24.8	20	**PDB header:**membrane transport **Chain:** G: **PDB Molecule:**hypothetical nitrogen regulatory pii-like **PDBTitle:** structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
26	d2ns1b1	Alignment	not modelled	23.9	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
27	d2h8pc1	Alignment	not modelled	22.5	13	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
28	d2piia_	Alignment	not modelled	22.0	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
						PDB header:unknown function

29	c1skhA_	Alignment	not modelled	21.7	30	**Chain:** A: **PDB Molecule:**major prion protein 2; **PDBTitle:** n-terminal (1-30) of bovine prion protein
30	d2axla1	Alignment	not modelled	21.7	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
31	d1saza1	Alignment	not modelled	17.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
32	c3o8wA_	Alignment	not modelled	17.1	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-1); **PDBTitle:** archaeoglobus fulgidus glnk1
33	d1ofda2	Alignment	not modelled	17.1	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
34	c1ub2A_	Alignment	not modelled	14.7	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of catalase-peroxidase from synechococcus pcc 7942
35	d2ccaa1	Alignment	not modelled	14.0	33	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
36	d1hwua_	Alignment	not modelled	13.6	26	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
37	d1e5ma2	Alignment	not modelled	13.3	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
38	d1tqya2	Alignment	not modelled	13.3	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
39	c3ncpD_	Alignment	not modelled	13.1	16	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-2); **PDBTitle:** glnk2 from archaeoglobus fulgidus
40	d1vfja_	Alignment	not modelled	13.0	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
41	d1z2la1	Alignment	not modelled	12.6	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
42	d1ul3a_	Alignment	not modelled	11.6	20	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
43	d1ub2a2	Alignment	not modelled	10.5	22	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
44	d1r3na1	Alignment	not modelled	10.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
45	d1danl3	Alignment	not modelled	10.3	67	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
46	d1rbli_	Alignment	not modelled	10.0	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
47	c3mk7F_	Alignment	not modelled	9.7	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
48	c2xqoA_	Alignment	not modelled	9.3	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulosome enzyme, dockerin type i; **PDBTitle:** ctcel124: a cellulase from clostridium thermocellum
49	c3bzqA_	Alignment	not modelled	9.1	19	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
50	d1nh2a1	Alignment	not modelled	9.1	16	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
51	c2kv5A_	Alignment	not modelled	9.0	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**putative uncharacterized protein rnai; **PDBTitle:** solution structure of the par toxin fst in dpc micelles
52	d2gfva2	Alignment	not modelled	8.9	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
53	d2ccaa2	Alignment	not modelled	8.7	22	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
54	c1yr2A_	Alignment	not modelled	8.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
55	d1u5ta2	Alignment	not modelled	8.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
56	d1oywa1	Alignment	not modelled	8.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: RecQ helicase DNA-binding domain-like
57	c3bl6A_	Alignment	not modelled	8.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
58	d1itka1	Alignment	not modelled	7.9	50	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
59	d1ub2a1	Alignment	not modelled	7.8	33	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
60	d1mwva1	Alignment	not modelled	7.8	33	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
61	c2oghA_	Alignment	not modelled	7.7	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
62	c3bzjA_	Alignment	not modelled	7.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
63	d1itka2	Alignment	not modelled	7.5	23	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
64	d1xmeb2	Alignment	not modelled	7.4	37	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
65	d1jqna_	Alignment	not modelled	7.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
66	c2q3vB_	Alignment	not modelled	7.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein at2g34160; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160
67	d1v8da_	Alignment	not modelled	6.8	8	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Hypothetical protein TT1679
68	d2juza1	Alignment	not modelled	6.8	22	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
69	d1cdwa2	Alignment	not modelled	6.7	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
70	d2qtia1	Alignment	not modelled	6.6	25	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
71	c2imoA_	Alignment	not modelled	6.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
72	d1mwva2	Alignment	not modelled	6.3	22	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
73	d2auna2	Alignment	not modelled	6.2	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
74	c3rrwB_	Alignment	not modelled	6.2	44	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**thylakoid lumenal 29 kda protein, chloroplastic; **PDBTitle:** crystal structure of the tl29 protein from arabidopsis thaliana
75	d1uc8a1	Alignment	not modelled	6.1	32	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
76	d1cdwa1	Alignment	not modelled	6.1	16	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
77	d2jrxa1	Alignment	not modelled	6.0	19	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
78	d2cu3a1	Alignment	not modelled	5.8	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
79	d2v7fa1	Alignment	not modelled	5.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rps19E-like
80	c3g23A_	Alignment	not modelled	5.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ld-carboxypeptidase a; **PDBTitle:** crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
81	c3eyiB_	Alignment	not modelled	5.5	28	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
82	d1jqoa_	Alignment	not modelled	5.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase

83	c1jqoA_	Alignment	not modelled	5.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
84	d2if1a_	Alignment	not modelled	5.4	26	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
85	c3iumA_	Alignment	not modelled	5.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
86	d2juwa1	Alignment	not modelled	5.3	25	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
87	d1j3na2	Alignment	not modelled	5.3	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
88	c2latA_	Alignment	not modelled	5.2	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
89	c2h3oA_	Alignment	not modelled	5.2	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
90	c1qysA_	Alignment	not modelled	5.1	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold