Phyre²

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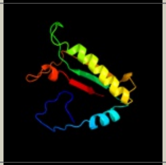
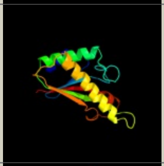
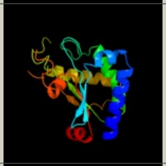
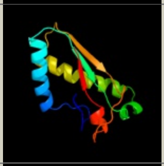
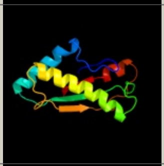
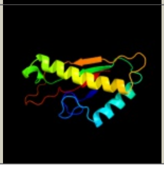
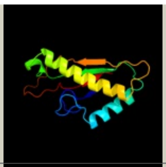
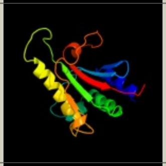
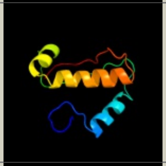
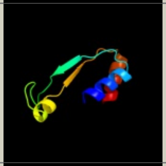
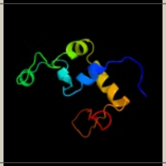
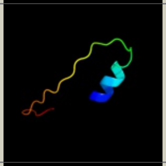
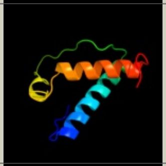
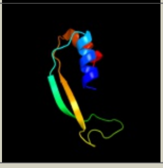
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zvyB_	Alignment		100.0	35	**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	19	**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	c2l26A_	Alignment		100.0	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
4	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.
5	c3cyqM_	Alignment		100.0	20	**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	c2zovA_	Alignment		99.9	34	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form i)
7	c2kgwA_	Alignment		99.9	24	**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
8	d2aizp1	Alignment		99.9	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
9	c3td4D_	Alignment		99.9	21	**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	d2hqsc1	Alignment		99.9	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
11	d1r1ma_	Alignment		99.9	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like

12	c1r1mA_	Alignment		99.9	20	**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
13	c3ldtA_	Alignment		99.9	16	**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
14	c3oonA_	Alignment		99.9	23	**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		99.6	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
16	d2cz4a1	Alignment		39.0	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
17	d2axla1	Alignment		31.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
18	c3l7pA_	Alignment		30.8	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
19	c3latB_	Alignment		29.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bifunctional autolysin; **PDBTitle:** crystal structure of staphylococcus peptidoglycan hydrolase2 amie
20	c3o8wA_	Alignment		29.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-1); **PDBTitle:** archaeoglobus fulgidus glnk1
21	d1qy7a_	Alignment	not modelled	28.7	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
22	c2rd5D_	Alignment	not modelled	27.9	16	**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
23	c3mhyC_	Alignment	not modelled	26.5	11	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
24	c3bzqA_	Alignment	not modelled	23.5	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
25	d2piia_	Alignment	not modelled	21.7	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
26	c2j9dG_	Alignment	not modelled	21.5	17	**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
27	d1hwua_	Alignment	not modelled	21.5	21	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
28	d1ul3a_	Alignment	not modelled	20.7	19	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
						PDB header:signaling protein

29	c3ncpD_	Alignment	not modelled	20.4	21	**Chain:** D: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-2); **PDBTitle:** glnk2 from archaeoglobus fulgidus
30	d2ns1b1	Alignment	not modelled	20.0	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
31	d1z2la1	Alignment	not modelled	18.7	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
32	d1e32a3	Alignment	not modelled	18.2	16	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
33	d1rbli_	Alignment	not modelled	16.4	16	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
34	d1h4pa_	Alignment	not modelled	16.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
35	d1svdm1	Alignment	not modelled	14.9	8	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
36	d1uzhc1	Alignment	not modelled	14.8	8	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
37	d1e5ma2	Alignment	not modelled	13.8	9	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
38	d1ir1s_	Alignment	not modelled	13.4	28	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
39	d1xhja_	Alignment	not modelled	13.2	8	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
40	c2oghA_	Alignment	not modelled	13.2	4	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
41	d1vfja_	Alignment	not modelled	13.1	5	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
42	d1jx4a1	Alignment	not modelled	13.0	16	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
43	d1k1sa1	Alignment	not modelled	13.0	16	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
44	d1bxni_	Alignment	not modelled	12.3	20	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
45	d2if1a_	Alignment	not modelled	12.0	22	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
46	c2qw5B_	Alignment	not modelled	11.7	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
47	c3icgD_	Alignment	not modelled	11.5	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
48	d2gfva2	Alignment	not modelled	11.4	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
49	d1bwvs_	Alignment	not modelled	11.4	20	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
50	c3o0dF_	Alignment	not modelled	11.3	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
51	d1u5ta2	Alignment	not modelled	11.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
52	c3r8kB_	Alignment	not modelled	10.7	22	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul protein (hexagonal form)
53	d2gova1	Alignment	not modelled	10.2	21	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
54	d1tqya2	Alignment	not modelled	10.1	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related

55	c2q3vB_	Alignment	not modelled	9.9	16	**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
56	d1d4oa_	Alignment	not modelled	9.8	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
57	d1qnaa1	Alignment	not modelled	9.8	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
58	d1saza1	Alignment	not modelled	9.8	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
59	c1ir6A_	Alignment	not modelled	9.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
60	d1ir6a_	Alignment	not modelled	9.8	15	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
61	c2cfuA_	Alignment	not modelled	9.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
62	d2ix4a2	Alignment	not modelled	9.5	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
63	c1pt9B_	Alignment	not modelled	9.4	12	**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
64	c3g7nA_	Alignment	not modelled	9.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
65	d1jqna_	Alignment	not modelled	9.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
66	d1xdpa4	Alignment	not modelled	8.5	17	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
67	c3ds8A_	Alignment	not modelled	8.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
68	c1amuB_	Alignment	not modelled	7.8	18	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
69	c1nauA_	Alignment	not modelled	7.6	18	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
70	c1jqoA_	Alignment	not modelled	7.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
71	d1jqoa_	Alignment	not modelled	7.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
72	d2o8ra4	Alignment	not modelled	7.4	27	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
73	c2rodB_	Alignment	not modelled	7.2	22	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**noxa; **PDBTitle:** solution structure of mcl-1 complexed with noxaa
74	c3hluA_	Alignment	not modelled	7.2	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
75	d3tgla_	Alignment	not modelled	7.2	26	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
76	d2j5pa1	Alignment	not modelled	7.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
77	d1ox0a2	Alignment	not modelled	7.0	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
78	c3mmpC_	Alignment	not modelled	7.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
79	d1r3na1	Alignment	not modelled	7.0	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
80	d1tkja1	Alignment	not modelled	6.9	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
						PDB header:lyase

81	c1ydoC_	Alignment	not modelled	6.8	8	**Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
82	d2v7fa1	Alignment	not modelled	6.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rps19E-like
83	c3aysA_	Alignment	not modelled	6.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose
84	d1ybha1	Alignment	not modelled	6.4	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
85	c2cw6B_	Alignment	not modelled	6.1	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
86	d2ve8a1	Alignment	not modelled	6.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
87	c4a1dH_	Alignment	not modelled	6.0	22	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**rpl35a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
88	d1j3na2	Alignment	not modelled	5.8	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
89	d1e5da2	Alignment	not modelled	5.8	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
90	d1nh2a1	Alignment	not modelled	5.8	12	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
91	d1amua_	Alignment	not modelled	5.8	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
92	d1uc8a1	Alignment	not modelled	5.7	42	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
93	c3lubE_	Alignment	not modelled	5.6	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
94	d1fyba1	Alignment	not modelled	5.5	18	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
95	c3bzjA_	Alignment	not modelled	5.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
96	d1nh2a2	Alignment	not modelled	5.2	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
97	c3eyiB_	Alignment	not modelled	5.2	29	**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
98	d1v8da_	Alignment	not modelled	5.1	12	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Hypothetical protein TT1679