Phyre^2

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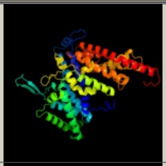
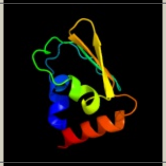
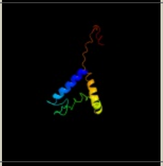
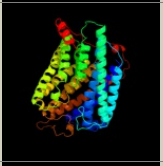
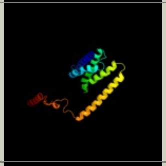
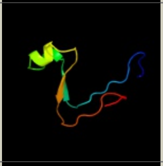
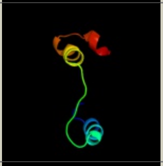
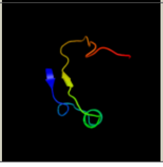
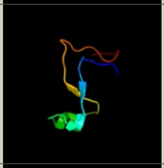
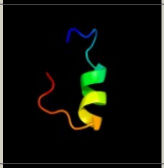
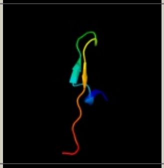
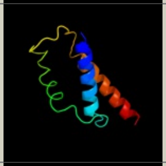
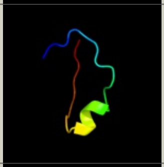
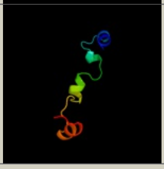
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		100.0	15	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	d3bp8c1	Alignment		99.9	41	**Fold:**Homing endonuclease-like **Superfamily:**Glucose permease domain IIB **Family:**Glucose permease domain IIB
3	c1ibaA_	Alignment		99.9	41	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
4	c3ipjB_	Alignment		99.8	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, iiabc component; **PDBTitle:** the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
5	c3mp7A_	Alignment		47.0	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
6	d1xmea1	Alignment		45.8	13	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
7	c3b9yA_	Alignment		39.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
8	c2hnhA_	Alignment		38.1	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
9	d1gpra_	Alignment		37.8	8	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
10	c2dlaB_	Alignment		36.9	29	**PDB header:**replication **Chain:** B: **PDB Molecule:**397aa long hypothetical protein; **PDBTitle:** primase large subunit amino terminal domain from pyrococcus horikoshii
11	d2gpra_	Alignment		33.6	3	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like

12	d1glaf_	Alignment		27.6	5	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
13	d2f3ga_	Alignment		27.6	9	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
14	c3e0dA_	Alignment		25.9	35	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
15	c2rddB_	Alignment		25.7	39	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
16	d1nh8a2	Alignment		24.9	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
17	c3zqsB_	Alignment		18.8	35	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase fancl; **PDBTitle:** human fancl central domain
18	d2nr9a1	Alignment		18.5	17	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like **Family:**Rhomboid-like
19	d1h3da2	Alignment		16.6	24	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
20	d1l0wa3	Alignment		16.2	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
21	d1osda_	Alignment	not modelled	15.2	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
22	d1cpza_	Alignment	not modelled	14.9	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1st6a5	Alignment	not modelled	14.6	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
24	c2ci2I_	Alignment	not modelled	14.1	30	**PDB header:**proteinase inhibitor (chymotrypsin) **Chain:** I: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** crystal and molecular structure of the serine proteinase2 inhibitor ci-2 from barley seeds
25	c1p68A_	Alignment	not modelled	14.1	55	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein s-824; **PDBTitle:** solution structure of s-824, a de novo designed four helix2 bundle
26	d2cfua2	Alignment	not modelled	13.2	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
27	d1q8la_	Alignment	not modelled	13.0	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	d1kvja_	Alignment	not modelled	12.6	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
29	c2qa7A	Alignment	not modelled	12.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1;

29	c2ga7A_	Alignment	not modelled	12.6	21	**PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
30	d1fzda_	Alignment	not modelled	12.4	29	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
31	d1j7na3	Alignment	not modelled	12.1	15	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
32	c2ldiA_	Alignment	not modelled	11.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
33	d2axtk1	Alignment	not modelled	11.4	40	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein K, PsbK **Family:**PsbK-like
34	c2cfuA_	Alignment	not modelled	11.2	19	**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.
35	c1yjrA_	Alignment	not modelled	11.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
36	c3f2cA_	Alignment	not modelled	10.6	26	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
37	d1u7ga_	Alignment	not modelled	10.3	3	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
38	d2ifqa1	Alignment	not modelled	10.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
39	d1f9qa_	Alignment	not modelled	10.1	10	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
40	c2w2eA_	Alignment	not modelled	10.1	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
41	d2a9da1	Alignment	not modelled	10.0	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
42	d1p6ta1	Alignment	not modelled	9.7	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
43	c3a0bK_	Alignment	not modelled	9.7	33	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
44	c3a0bk_	Alignment	not modelled	9.7	33	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
45	d2qifa1	Alignment	not modelled	9.2	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
46	c2l3mA_	Alignment	not modelled	9.0	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
47	d3pvia_	Alignment	not modelled	9.0	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease PvuII
48	d1afia_	Alignment	not modelled	9.0	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
49	c3e6qL_	Alignment	not modelled	8.9	24	**PDB header:**isomerase **Chain:** L: **PDB Molecule:**putative 5-carboxymethyl-2-hydroxymuconate isomerase; **PDBTitle:** putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa.
50	c3a0hk_	Alignment	not modelled	8.7	33	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
51	d1pfma_	Alignment	not modelled	8.5	10	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
52	d1fida_	Alignment	not modelled	8.3	24	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
53	d2axti1	Alignment	not modelled	7.8	23	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
54	d1plfa_	Alignment	not modelled	7.7	10	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
55	c3eh4A_	Alignment	not modelled	7.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase subunit 1; **PDBTitle:** structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus

56	c1vbwA_	Alignment	not modelled	7.5	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**trypsin inhibitor bgit; **PDBTitle:** crystal structure of bitter gourd trypsin inhibitor
57	d1lwuc1	Alignment	not modelled	7.5	31	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
58	d1wf3a2	Alignment	not modelled	7.4	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
59	d1ypci_	Alignment	not modelled	7.4	29	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
60	d1f9ra_	Alignment	not modelled	7.2	10	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
61	c3l7qD_	Alignment	not modelled	7.2	16	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
62	d1to2i_	Alignment	not modelled	7.0	29	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
63	c1q1kA_	Alignment	not modelled	7.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
64	d1h7sa2	Alignment	not modelled	6.9	37	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
65	c1u5tB_	Alignment	not modelled	6.9	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**defective in vacuolar protein sorting; vps36p; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
66	c1hgvA_	Alignment	not modelled	6.9	10	**PDB header:**virus **Chain:** A: **PDB Molecule:**ph75 inovirus major coat protein; **PDBTitle:** filamentous bacteriophage ph75
67	d2snii_	Alignment	not modelled	6.9	30	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
68	c3dxsX_	Alignment	not modelled	6.8	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
69	d1z9ha1	Alignment	not modelled	6.8	17	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
70	d1dwma_	Alignment	not modelled	6.7	31	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
71	c1y3kA_	Alignment	not modelled	6.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
72	c1tinA_	Alignment	not modelled	6.6	35	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**trypsin inhibitor v; **PDBTitle:** three-dimensional structure in solution of cucurbita maxima2 trypsin inhibitor-v determined by nmr spectroscopy
73	d1bkna2	Alignment	not modelled	6.6	26	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
74	d1s6ua_	Alignment	not modelled	6.5	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
75	d1l0wa2	Alignment	not modelled	6.4	16	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
76	c3hd7A_	Alignment	not modelled	6.4	15	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
77	d1egla_	Alignment	not modelled	6.3	18	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
78	c3qd1X_	Alignment	not modelled	6.3	26	**PDB header:**sugar binding protein **Chain:** X: **PDB Molecule:**platelet binding protein gspb; **PDBTitle:** gspb plus alpha-2,3-sialyl (1-thioethyl)galactose
79	c2j61B_	Alignment	not modelled	6.2	35	**PDB header:**lectin **Chain:** B: **PDB Molecule:**ficolin-2; **PDBTitle:** l-ficolin complexed to n-acetylglucosamine (forme c)
80	d1lwub1	Alignment	not modelled	6.2	19	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
81	d1m1jc1	Alignment	not modelled	6.2	30	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
82	d1wffa_	Alignment	not modelled	6.1	30	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger

						Family:AN1-like Zinc finger
83	d1xrga_	Alignment	not modelled	6.1	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
84	d2aw0a_	Alignment	not modelled	6.1	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
85	d1wgla_	Alignment	not modelled	6.0	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
86	c2hqnA_	Alignment	not modelled	6.0	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
87	c1yg0A_	Alignment	not modelled	5.9	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
88	c3cjsA_	Alignment	not modelled	5.9	15	**PDB header:**transferase/ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** minimal recognition complex between prma and ribosomal protein l11
89	c2ofhX_	Alignment	not modelled	5.8	17	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
90	c1a0oH_	Alignment	not modelled	5.7	15	**PDB header:**chemotaxis **Chain:** H: **PDB Molecule:**chea; **PDBTitle:** chey-binding domain of chea in complex with chey
91	d1jmkc_	Alignment	not modelled	5.7	9	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
92	c2kncA_	Alignment	not modelled	5.7	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
93	c1deqF_	Alignment	not modelled	5.6	24	**PDB header:** **PDB COMPND:**
94	c1w7pD_	Alignment	not modelled	5.6	14	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vps36p, ylr417w; **PDBTitle:** the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
95	d1qaha_	Alignment	not modelled	5.6	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
96	d1p6ta2	Alignment	not modelled	5.6	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
97	c1b9uA_	Alignment	not modelled	5.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
98	c3bvhC_	Alignment	not modelled	5.5	24	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
99	c2hpcF_	Alignment	not modelled	5.5	24	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.