Phyre^2

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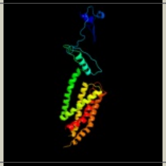
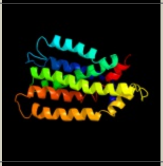
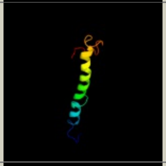
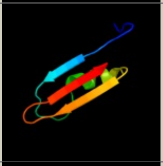
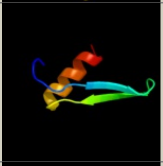
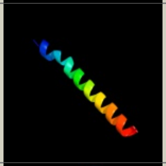
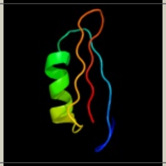
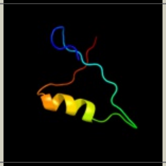
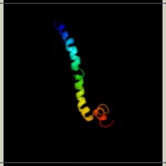
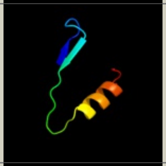
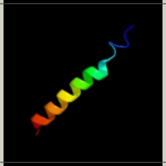
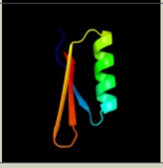
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aqpB_	Alignment		100.0	37	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
2	c3k07A_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
3	c1oy8A_	Alignment		100.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
4	d1iwga8	Alignment		99.9	14	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
5	d1iwga7	Alignment		99.9	15	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
6	c2rrnA_	Alignment		99.1	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** solution structure of secdf periplasmic domain p4
7	c2jo1A_	Alignment		28.9	15	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
8	d1je3a_	Alignment		27.5	15	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
9	d1iwga4	Alignment		22.3	12	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
10	d1in0a1	Alignment		18.6	20	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
11	d2axte1	Alignment		16.0	16	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits

12	d1dcja_	Alignment		15.8	15	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
13	d1m56d_	Alignment		15.2	22	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
14	d1pava_	Alignment		14.1	17	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
15	c2gcfA_	Alignment		14.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
16	c2jp3A_	Alignment		13.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
17	c1yg0A_	Alignment		13.1	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
18	d2ggpb1	Alignment		12.2	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	d1qled_	Alignment		10.7	18	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
20	c3hz7A_	Alignment		9.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
21	c2kt2A_	Alignment	not modelled	9.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
22	c2zxeG_	Alignment	not modelled	9.2	21	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
23	c1ciiA_	Alignment	not modelled	9.1	21	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
24	d1s6ua_	Alignment	not modelled	8.7	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
25	d1cpza_	Alignment	not modelled	8.4	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c1yjrA_	Alignment	not modelled	8.3	8	**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
27	d1osda_	Alignment	not modelled	8.2	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	d1o75a2	Alignment	not modelled	8.1	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
29	c3dxsX_	Alignment	not modelled	8.1	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1;

29	c3dxsX_	Alignment	not modelled	8.1	13	**PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
30	d1jdqa_	Alignment	not modelled	7.6	18	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
31	c1in0B_	Alignment	not modelled	7.5	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yajq protein; **PDBTitle:** yajq protein (hi1034)
32	d1pgya_	Alignment	not modelled	7.0	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
33	c3f1jA_	Alignment	not modelled	7.0	45	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** crystal structure of the borna disease virus matrix protein2 (bdv-m) reveals rna binding properties
34	c2k2pA_	Alignment	not modelled	6.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
35	c2yvxD_	Alignment	not modelled	6.6	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
36	c1y3kA_	Alignment	not modelled	6.5	9	**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
37	c3ipdB_	Alignment	not modelled	6.4	20	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
38	c3n23E_	Alignment	not modelled	6.4	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
39	c2mltA_	Alignment	not modelled	6.4	29	**PDB header:**toxin (hemolytic polypeptide) **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** melittin
40	c2mltB_	Alignment	not modelled	6.4	29	**PDB header:**toxin (hemolytic polypeptide) **Chain:** B: **PDB Molecule:**melittin; **PDBTitle:** melittin
41	c2bbjB_	Alignment	not modelled	6.3	11	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
42	d1afia_	Alignment	not modelled	6.2	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
43	d1pqua2	Alignment	not modelled	6.1	12	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
44	c3fewX_	Alignment	not modelled	6.0	6	**PDB header:**immune system **Chain:** X: **PDB Molecule:**colicin s4; **PDBTitle:** structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
45	d1cola_	Alignment	not modelled	6.0	7	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
46	c3g5uB_	Alignment	not modelled	6.0	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
47	d2qifa1	Alignment	not modelled	5.9	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
48	c1wwuA_	Alignment	not modelled	5.9	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21935; **PDBTitle:** solution structure of the sam_pnt domain of human protein2 flj21935
49	c3lk2T_	Alignment	not modelled	5.9	26	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
50	d1t4ba2	Alignment	not modelled	5.7	18	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
51	c2l3mA_	Alignment	not modelled	5.6	13	**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
52	c1w8xP_	Alignment	not modelled	5.6	25	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
53	c1v06A_	Alignment	not modelled	5.5	23	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** axh domain of the transcription factor hbp1 from m.musculus
54	c2ofhX_	Alignment	not modelled	5.5	9	**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

55	d1mxaa1	Alignment	not modelled	5.5	15	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
56	d1kvja_	Alignment	not modelled	5.3	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
57	d1q7ha2	Alignment	not modelled	5.2	37	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Hypothetical protein Ta1423, N-terminal domain
58	c1bh1A_	Alignment	not modelled	5.1	31	**PDB header:**toxin **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** structural studies of d-pro melittin, nmr, 20 structures
59	d2gz1a2	Alignment	not modelled	5.1	18	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
60	c2rmlA_	Alignment	not modelled	5.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa