Phyre²

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Description	P75870
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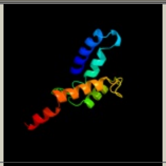
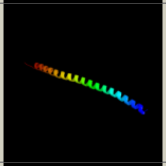
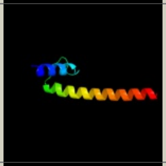
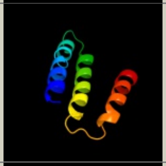
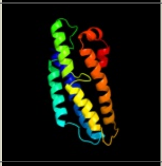
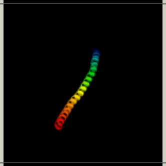
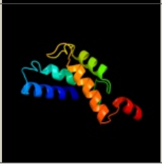
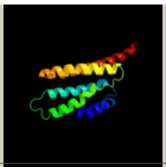
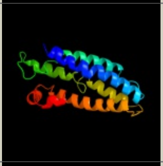
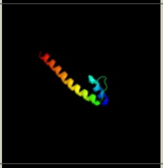
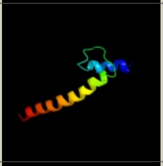
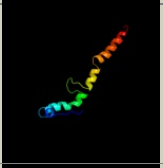
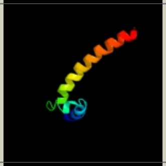
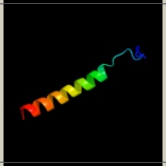
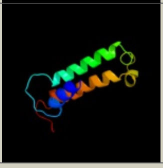
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ht2B_	Alignment		52.5	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
2	c3k3gA_	Alignment		36.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
3	c3cvfA_	Alignment		16.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
4	d1otsa_	Alignment		16.3	16	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
5	d1hloa_	Alignment		14.5	11	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
6	d1nlwe_	Alignment		14.5	11	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
7	d2r6gf1	Alignment		14.3	8	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
8	d3dtua1	Alignment		14.1	10	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
9	d1kpla_	Alignment		13.2	18	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
10	c1ei3E_	Alignment		12.6	11	**PDB header:** **PDB COMPND:**
11	c3nd0A_	Alignment		12.5	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter

12	d1pw4a_	Alignment		12.5	11	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
13	c1m56G_	Alignment		12.2	10	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
14	d1nkpb_	Alignment		10.1	11	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
15	c1deqF_	Alignment		9.7	10	**PDB header:** **PDB COMPND:**
16	d1an2a_	Alignment		9.7	11	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
17	d1k8kd2	Alignment		9.5	11	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits **Family:**Arp2/3 complex subunits
18	d1r05a_	Alignment		9.3	13	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
19	c2kncA_	Alignment		8.3	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
20	d1st6a5	Alignment		8.0	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
21	c1ymgA_	Alignment	not modelled	8.0	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
22	d1ymga1	Alignment	not modelled	8.0	11	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
23	c2yvxD_	Alignment	not modelled	7.9	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
24	c2kbvA_	Alignment	not modelled	7.9	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger
25	c3dwlI_	Alignment	not modelled	7.2	11	**PDB header:**structural protein **Chain:** I: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
26	c2kdcC_	Alignment	not modelled	7.2	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
27	c2k1lA_	Alignment	not modelled	7.1	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
28	c2k1kB_	Alignment	not modelled	7.1	28	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3

29	c2k1lB_	Alignment	not modelled	7.1	28	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
30	c2k1kA_	Alignment	not modelled	7.1	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
31	d1ar1a_	Alignment	not modelled	7.0	12	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
32	c3hfwA_	Alignment	not modelled	6.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
33	c2wocA_	Alignment	not modelled	6.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosyl-[dinitrogen reductase] glycohydrolase; **PDBTitle:** crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
34	c1deqO_	Alignment	not modelled	6.9	3	**PDB header:** **PDB COMPND:**
35	c2oszA_	Alignment	not modelled	6.8	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
36	c3r84O_	Alignment	not modelled	6.7	20	**PDB header:**transcription **Chain:** O: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 11; **PDBTitle:** structure of the mediator head subcomplex med11/22
37	c3ghgK_	Alignment	not modelled	6.7	4	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
38	c3g9dB_	Alignment	not modelled	6.7	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
39	c2jqqA_	Alignment	not modelled	6.6	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**conserved oligomeric golgi complex subunit 2; **PDBTitle:** solution structure of saccharomyces cerevisiae conserved2 oligomeric golgi subunit 2 protein (cog2p)
40	d1v54a_	Alignment	not modelled	6.5	9	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
41	c1iijA_	Alignment	not modelled	6.1	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
42	d1f6ga_	Alignment	not modelled	6.0	17	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
43	c3cveC_	Alignment	not modelled	6.0	13	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**homer protein homolog 1; **PDBTitle:** crystal structure of the carboxy terminus of homer1
44	c2yzwA_	Alignment	not modelled	5.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
45	d1j4na_	Alignment	not modelled	5.8	15	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
46	c2p9lD_	Alignment	not modelled	5.7	12	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of bovine arp2/3 complex
47	d2nwwa1	Alignment	not modelled	5.7	9	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
48	d1h2sa_	Alignment	not modelled	5.7	11	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
49	d2e74d2	Alignment	not modelled	5.6	42	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
50	c1xioA_	Alignment	not modelled	5.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**anabaena sensory rhodopsin; **PDBTitle:** anabaena sensory rhodopsin
51	d1xioa_	Alignment	not modelled	5.5	14	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
52	d1oqwa_	Alignment	not modelled	5.5	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
53	c3ojaB_	Alignment	not modelled	5.5	7	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
54	c2qtyB_	Alignment	not modelled	5.4	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
						PDB header:membrane protein

55	c2kb1A_	Alignment	not modelled	5.3	8	**Chain:** A: **PDB Molecule:**wsk3; **PDBTitle:** nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
56	c2dw3A_	Alignment	not modelled	5.3	28	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**intrinsic membrane protein pufx; **PDBTitle:** solution structure of the rhodobacter sphaeroides pufx2 membrane protein
57	d2pila_	Alignment	not modelled	5.3	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
58	c2xdjF_	Alignment	not modelled	5.2	26	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf