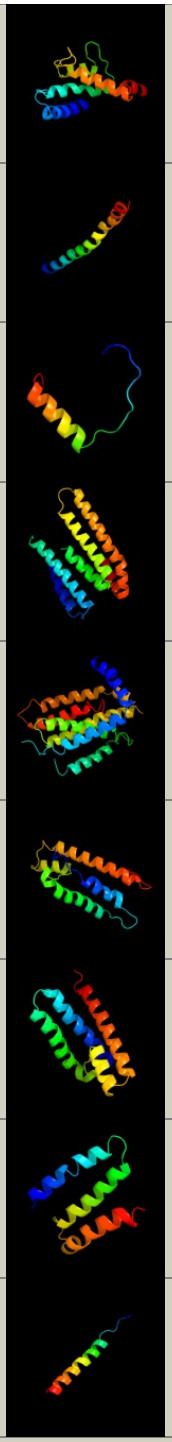
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P45537
Date	Thu Jan 5 12:02:58 GMT 2012
Unique Job ID	ace9cf229ab65d62

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ht2B_	Alignment		44.4	17	**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	d1otsa_	Alignment		41.4	16	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
3	c2yvxD_	Alignment		28.6	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
4	d1kpla_	Alignment		14.7	16	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
5	d1fx8a_	Alignment		12.2	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
6	c1ldaA_	Alignment		12.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycerol uptake facilitator protein; **PDBTitle:** crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
7	c2yggA_	Alignment		11.7	9	**PDB header:**metal binding protein/transport protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** complex of cambr and cam
8	c1ymgA_	Alignment		11.7	8	**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
9	d1ymga1	Alignment		11.7	8	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
10	d1ciya3	Alignment		11.4	10	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
11	d2nefa_	Alignment		11.4	23	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef

12	c3nd0A_	Alignment		11.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
13	c2kncB_	Alignment		11.2	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
14	c3rbbA_	Alignment		10.7	20	**PDB header:**viral protein, protein binding **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** hiv-1 nef protein in complex with engineered hck sh3 domain
15	d1e12a_	Alignment		10.5	11	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
16	d1iwga8	Alignment		10.2	13	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
17	d1rc2a_	Alignment		10.1	12	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
18	d1j4na_	Alignment		9.9	10	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
19	d2r6gf1	Alignment		9.6	10	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
20	c2rmzA_	Alignment		9.4	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
21	c3pltB_	Alignment	not modelled	9.2	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**sphingolipid long chain base-responsive protein lsp1; **PDBTitle:** crystal structure of lsp1 from saccharomyces cerevisiae
22	c3k3gA_	Alignment	not modelled	8.8	14	**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
23	c2jagA_	Alignment	not modelled	8.6	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**halorhodopsin; **PDBTitle:** l1-intermediate of halorhodopsin t203v
24	d1pw4a_	Alignment	not modelled	8.4	7	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
25	c3hfwA_	Alignment	not modelled	8.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
26	c2wocA_	Alignment	not modelled	8.3	25	**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
27	c3msqC_	Alignment	not modelled	8.2	10	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**putative ubiquinone biosynthesis protein; **PDBTitle:** crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
28	c2kbvA_	Alignment	not modelled	8.1	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
29	c1i5pA_	Alignment	not modelled	7.8	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry2aa; **PDBTitle:** insecticidal crystal protein cry2aa
30	c1iijA_	Alignment	not modelled	7.7	21	**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
31	c3k07A_	Alignment	not modelled	7.6	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
32	c3g9dB_	Alignment	not modelled	7.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
33	c2kdcC_	Alignment	not modelled	7.5	5	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
34	c1iojA_	Alignment	not modelled	7.4	21	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
35	d1i5pa3	Alignment	not modelled	7.3	13	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
36	c1ciyA_	Alignment	not modelled	7.0	9	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cryia(a); **PDBTitle:** insecticidal toxin: structure and channel formation
37	c2b5fD_	Alignment	not modelled	7.0	12	**PDB header:**transport protein,membrane protein **Chain:** D: **PDB Molecule:**aquaporin; **PDBTitle:** crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
38	c2kncA_	Alignment	not modelled	6.7	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
39	d2pw6a1	Alignment	not modelled	6.6	7	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
40	c2qtyB_	Alignment	not modelled	6.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
41	c2yzwA_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
42	c3ik5A_	Alignment	not modelled	6.4	21	**PDB header:**viral protein/signaling protein **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** sivmac239 nef in complex with tcr zeta itam 1 polypeptide2 (a63-r80)
43	c2k1lB_	Alignment	not modelled	6.3	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
44	c2k1kA_	Alignment	not modelled	6.3	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
45	c2k1kB_	Alignment	not modelled	6.3	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
46	c2k1lA_	Alignment	not modelled	6.3	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
47	d1t5ja_	Alignment	not modelled	6.3	21	**Fold:**ADP-ribosylglycohydrolase **Superfamily:**ADP-ribosylglycohydrolase **Family:**ADP-ribosylglycohydrolase
48	c3t6gB_	Alignment	not modelled	6.2	7	**PDB header:**signaling protein, cell adhesion **Chain:** B: **PDB Molecule:**breast cancer anti-estrogen resistance protein 1; **PDBTitle:** structure of the complex between nsp3 (shep1) and p130cas
49	c2c9kA_	Alignment	not modelled	6.0	13	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry4aa; **PDBTitle:** structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
50	d1tuka1	Alignment	not modelled	5.3	25	**Fold:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Superfamily:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Family:**Plant lipid-transfer and hydrophobic proteins
51	d2bida_	Alignment	not modelled	5.3	10	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
52	d1t01a1	Alignment	not modelled	5.2	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
53	c2y69Q_	Alignment	not modelled	5.2	6	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
						Fold:7-stranded beta/alpha barrel

54	d1xw8a_	Alignment	not modelled	5.1	15	**Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like