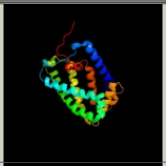
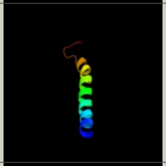
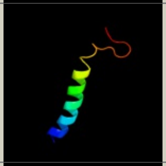
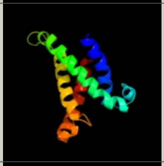
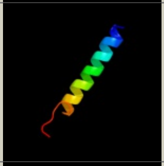
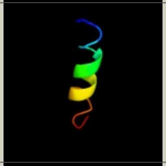
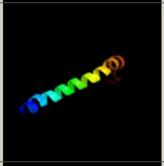
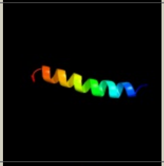
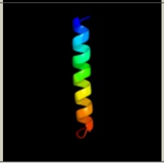
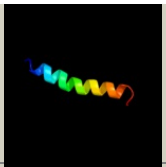
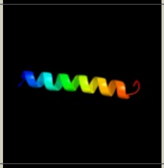
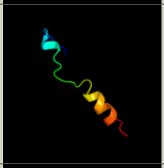
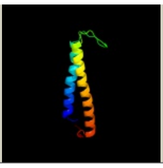
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AF32
Date	Thu Jan 5 11:25:00 GMT 2012
Unique Job ID	f8c183e6908c0ddd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ic1	Alignment		100.0	72	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain
2	c2kncA_	Alignment		75.6	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
3	c2kluA_	Alignment		71.7	34	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
4	d1kqfc_	Alignment		57.7	15	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Formate dehydrogenase N, cytochrome (gamma) subunit
5	c2k1aA_	Alignment		39.1	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
6	c3kdpH_	Alignment		38.9	24	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
7	c3kdpG_	Alignment		38.9	24	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
8	c2w8aC_	Alignment		18.2	11	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
9	c2jp3A_	Alignment		13.0	18	**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
10	c2k1lB_	Alignment		11.9	26	**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
11	c2k1kB_	Alignment		11.9	26	**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

12	c2k1lA_	Alignment		11.9	26	**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
13	c2k1kA_	Alignment		11.9	26	**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
14	c2k9yB_	Alignment		10.2	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
15	c2jo1A_	Alignment		9.8	26	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
16	c2k9yA_	Alignment		7.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
17	c2dyoB_	Alignment		6.7	50	**PDB header:**protein turnover/protein turnover **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex

18	d1ar1a_	Alignment		5.6	16	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like