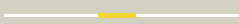
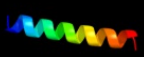
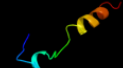
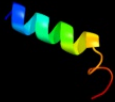
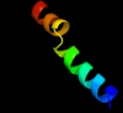


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ic1	 Alignment		100.0	100	Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain
2	c2kncA	 Alignment		73.6	26	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alpha-iiB-beta3 transmembrane-cytoplasmic2 heterocomplex
3	d1kqfc	 Alignment		67.3	11	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit
4	c2klua	 Alignment		58.3	26	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
5	c3kdpG	 Alignment		55.5	15	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
6	c3kdpH	 Alignment		55.5	15	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
7	c2k1aA	 Alignment		46.6	31	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
8	c2jp3A	 Alignment		26.5	19	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
9	c2jo1A	 Alignment		13.3	25	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
10	c2k9yB	 Alignment		9.4	32	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
11	d1ar1a	 Alignment		9.1	17	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like

12	c2zzeG_	Alignment		7.1	29	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
13	c2k9yA_	Alignment		7.0	32	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
14	c3rkoA_	Alignment		5.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
15	c2ww9B_	Alignment		5.7	28	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
16	d1wpga4	Alignment		5.4	12	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
17	c2k1kB_	Alignment		5.3	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
18	c2k1lA_	Alignment		5.3	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
19	c2k1lB_	Alignment		5.3	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
20	c2k1kA_	Alignment		5.3	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
21	c3n23E_	Alignment	not modelled	5.1	8	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