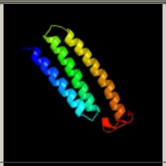
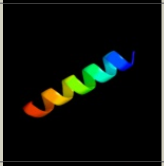
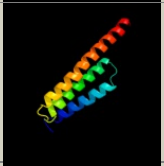
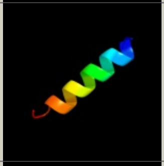
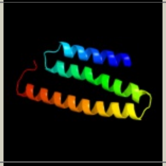
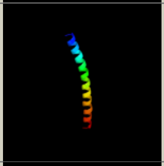
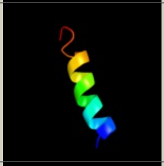
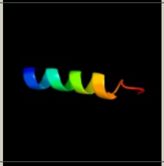
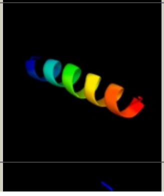
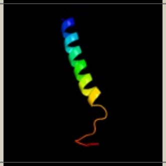
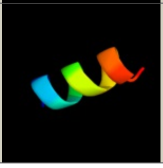
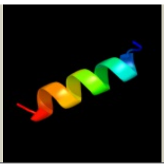
Email	l.a.kelley@imperial.ac.uk
Description	P0AFE4
Date	Thu Jan 5 11:26:02 GMT 2012
Unique Job ID	6fd9c2ef5d4c234e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoK_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c3rkoL_	Alignment		79.7	22	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**nadh-quinone oxidoreductase subunit l; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c2jo1A_	Alignment		54.0	47	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
4	c2jp3A_	Alignment		49.7	21	**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
5	c3rkoM_	Alignment		41.2	13	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
6	c2zxeG_	Alignment		40.6	42	**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
7	c3rkoN_	Alignment		25.2	22	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
8	c1iflA_	Alignment		24.8	10	**PDB header:**virus **Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
9	c3kdpH_	Alignment		22.5	47	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
10	c3kdpG_	Alignment		22.5	47	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
11	d1xmec1	Alignment		15.8	30	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa

12	c3n23E_	Alignment		11.7	41	**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
13	c3mk7F_	Alignment		10.4	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
14	c3ctoE_	Alignment		10.1	33	**PDB header:**toxin inhibitor **Chain:** E: **PDB Molecule:**uncharacterized protein rv3357/mt3465; **PDBTitle:** crystal structure of m. tuberculosis yefm antitoxin

15	d1v54m_	Alignment		8.5	24	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)