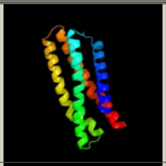
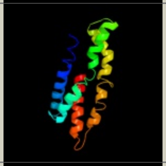
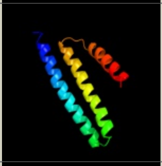
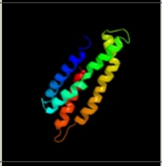
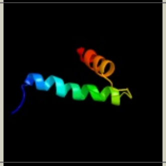
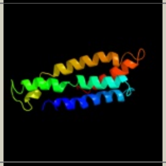
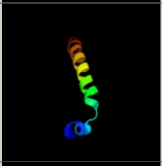
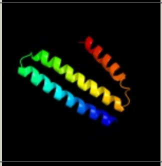
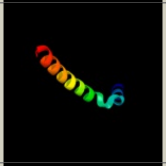
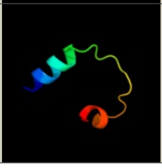
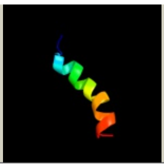
Email	l.a.kelley@imperial.ac.uk
Description	P25743
Date	Thu Jan 5 11:42:30 GMT 2012
Unique Job ID	bbd53a3bd1d97c16

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aqpB_	Alignment		51.8	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
2	c1oy8A_	Alignment		50.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
3	c3k07A_	Alignment		24.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
4	c2vv5D_	Alignment		19.5	12	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
5	d1iwga7	Alignment		15.6	14	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
6	d2nn6h3	Alignment		9.5	14	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
7	d1iwga8	Alignment		9.0	9	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
8	c1qcrD_	Alignment		8.9	13	**PDB header:** **PDB COMPND:**
9	d2vv5a3	Alignment		8.4	12	**Fold:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Superfamily:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Family:**Mechanosensitive channel protein MscS (YggB), transmembrane region
10	c1zrtD_	Alignment		6.7	14	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
11	c2kvsA_	Alignment		6.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mw0776; **PDBTitle:** nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215

12	c1hjiB_	Alignment		6.0	9	**PDB header:**bacteriophage hk022 **Chain:** B: **PDB Molecule:**nun-protein; **PDBTitle:** bacteriophage hk022 nun-protein-nutboxb-rna complex