
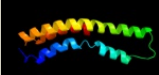



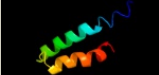

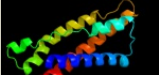



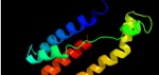


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P67143
Date	Thu Jan 5 12:10:30 GMT 2012
Unique Job ID	5af137fc43fb18c3

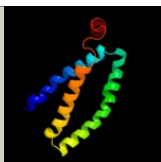
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bl2F_	 Alignment		34.6	9	PDB header: hydrolase Chain: F: PDB Molecule: v-type sodium atp synthase subunit k; PDBTitle: the membrane rotor of the v-type atpase from enterococcus2 hirae
2	c2vv5D_	 Alignment		28.3	14	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of msccs
3	c1oy8A_	 Alignment		20.3	20	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
4	c3aqpB_	 Alignment		10.8	15	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
5	d2nn6h3	 Alignment		8.1	17	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)
6	d1iwga7	 Alignment		7.5	13	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain

7

[d1pv7a_](#)

Alignment



7.4

10

Fold: MFS general substrate transporter
Superfamily: MFS general substrate transporter
Family: LacY-like proton/sugar symporter