








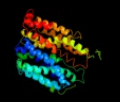






Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P39381
Date	Thu Jan 5 12:00:13 GMT 2012
Unique Job ID	731affe7b0c8820e

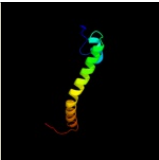
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	d1pv7a_	 Alignment		100.0	13	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
3	c2gfpA_	 Alignment		100.0	12	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
4	c3o7pA_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	c2xutC_	 Alignment		99.9	10	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	d3proc1	 Alignment		21.4	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
7	c2xq2A_	 Alignment		9.3	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsglT

8

[c3qngD_](#)

Alignment



7.0

10

PDB header:membrane protein, transport protein
Chain: D: **PDB Molecule:**pts system, cellobiose-specific iic component;
PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system