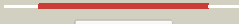



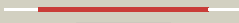










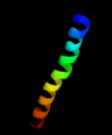











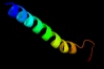



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P32135
Date	Thu Jan 5 11:49:20 GMT 2012
Unique Job ID	625e74c229cfd0b7

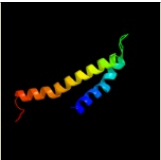
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		100.0	14	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	d1pv7a_	 Alignment		100.0	9	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
3	c3o7pA_	 Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
4	c2gfpA_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
5	c2xutC_	 Alignment		99.9	6	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	c3mkuA_	 Alignment		89.7	8	PDB header: transport protein Chain: A: PDB Molecule: multi antimicrobial extrusion protein (na(+)/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
7	c3qngD_	 Alignment		64.7	19	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
8	c2rddB_	 Alignment		35.7	16	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
9	c3rkoN_	 Alignment		32.6	9	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
10	c2g9pA_	 Alignment		10.6	21	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide latarcin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaei) venom
11	c2k21A_	 Alignment		8.2	17	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c

12	c2kluA_	Alignment		6.8	19	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
13	d3proc1	Alignment		6.6	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
14	c3rkoF_	Alignment		6.3	13	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
15	d1fftb2	Alignment		6.1	15	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
16	c3mk7K_	Alignment		6.0	14	PDB header: oxidoreductase Chain: K: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit n; PDBTitle: the structure of cbb3 cytochrome oxidase
17	c2kncA_	Alignment		6.0	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
18	d2nr9a1	Alignment		5.9	4	Fold: Rhomboid-like Superfamily: Rhomboid-like Family: Rhomboid-like

19 [d2oara1](#)

Alignment



5.2

11

Fold:Gated mechanosensitive channel
Superfamily:Gated mechanosensitive channel
Family:Gated mechanosensitive channel