
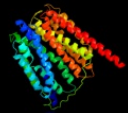








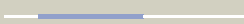


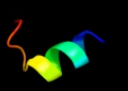

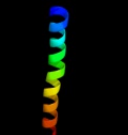


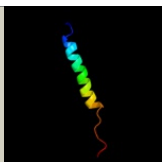


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		100.0	15	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	d1pv7a_	 Alignment		100.0	13	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
3	c3o7pA_	 Alignment		100.0	15	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	16	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	12	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	c2jlnA_	 Alignment		25.0	12	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
7	c2g9pA_	 Alignment		14.7	29	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 tarabaevi) venom
8	c2rddB_	 Alignment		9.4	23	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	d3proc1	 Alignment		7.1	10	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain

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[c3rkoF_](#)

Alignment



6.8

15

PDB header: oxidoreductase
Chain: F: **PDB Molecule:** nadh-quinone oxidoreductase subunit j;
PDB Title: crystal structure of the membrane domain of respiratory complex i from *e. coli* at 3.0 angstrom resolution