











Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P69210
Date	Thu Jan 5 12:11:16 GMT 2012
Unique Job ID	d879d0f16193ab87

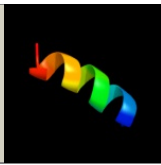
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s7ba_	 Alignment		100.0	35	Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE
2	c2i68B_	 Alignment		99.8	31	PDB header: transport protein Chain: B: PDB Molecule: protein emre; PDBTitle: cryo-em based theoretical model structure of transmembrane2 domain of the multidrug-resistance antiporter from e. coli3 emre
3	c3mp7B_	 Alignment		14.7	29	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase subunit sece; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
4	c2vqcA_	 Alignment		7.6	18	PDB header: dna-binding protein Chain: A: PDB Molecule: hypothetical 13.2 kda protein; PDBTitle: structure of a dna binding winged-helix protein, f-112,2 from sulfolobus spindle-shaped virus 1.
5	d2vqca1	 Alignment		7.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like

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[d2axtj1](#)

Alignment



6.2

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Fold: Single transmembrane helix

Superfamily: Photosystem II reaction center protein J, PsbJ

Family: PsbJ-like