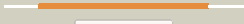

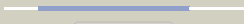



















Phyre2

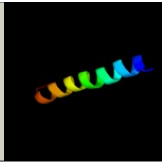
Email	l.a.kelley@imperial.ac.uk
Description	P60643
Date	Tue Jul 17 17:05:12 BST 2012
Unique Job ID	558f6694b425dc5e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yvxD_	 Alignment		84.0	13	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
2	d2yvxa3	 Alignment		26.6	13	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
3	d1z0kb1	 Alignment		19.7	14	Fold: Long alpha-hairpin Superfamily: Rabenosyn-5 Rab-binding domain-like Family: Rabenosyn-5 Rab-binding domain-like
4	d1yzma1	 Alignment		18.3	14	Fold: Long alpha-hairpin Superfamily: Rabenosyn-5 Rab-binding domain-like Family: Rabenosyn-5 Rab-binding domain-like
5	c3p5nA_	 Alignment		16.8	15	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
6	c3zv0A_	 Alignment		14.3	19	PDB header: cell cycle Chain: A: PDB Molecule: protein shq1; PDBTitle: structure of the shq1p-cbf5p complex
7	c1ciiA_	 Alignment		13.5	14	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
8	c3rfuC_	 Alignment		8.1	16	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
9	c1ckxA_	 Alignment		6.9	30	PDB header: metal transport Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance PDBTitle: cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
10	d2akza2	 Alignment		6.5	25	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like

11 [c2l2ta_](#)

Alignment



5.9

14

PDB header:membrane protein
Chain: A; **PDB Molecule:**receptor tyrosine-protein kinase erbb-4;
PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain