



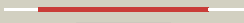



























Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P16701
Date	Thu Jan 5 11:35:47 GMT 2012
Unique Job ID	cb57681ae0a96a5a

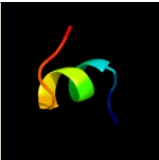
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3d31c1	 Alignment		100.0	28	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
2	c3d31D_	 Alignment		100.0	28	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
3	c2onkC_	 Alignment		100.0	28	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
4	d2onkc1	 Alignment		100.0	28	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
5	c3fh6F_	 Alignment		100.0	18	PDB header: transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli
6	c2r6gF_	 Alignment		100.0	20	PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: the crystal structure of the e. coli maltose transporter
7	d2r6gf2	 Alignment		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d2r6gg1	 Alignment		100.0	22	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d3dhwa1	 Alignment		99.9	19	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c2jwaA_	 Alignment		38.3	21	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
11	c1umqA_	 Alignment		30.3	19	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity

12	d1umqa_	Alignment		30.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	d1ntca_	Alignment		25.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
14	c2hx6A_	Alignment		23.2	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
15	d1fipa_	Alignment		20.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	d1etob_	Alignment		17.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c3e7lD_	Alignment		14.7	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
18	d1etxa_	Alignment		14.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	d1g2ha_	Alignment		13.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

20 [c2cw1A](#)

Alignment



6.8

36

PDB header:de novo protein
Chain: A: **PDB Molecule:**sn4m;
PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein