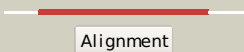

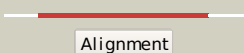

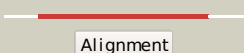

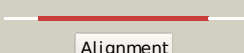



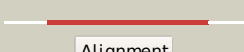

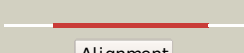

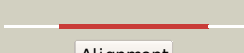

















Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P16683
Date	Thu Jan 5 11:35:28 GMT 2012
Unique Job ID	b31cae06aa5efc9d

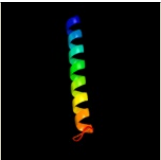
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2onkC_	 Alignment		100.0	12	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
2	d2onkc1	 Alignment		100.0	12	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
3	c3fh6F_	 Alignment		100.0	14	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
4	c3d31D_	 Alignment		100.0	13	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
5	d3d31c1	 Alignment		100.0	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	c2r6gF_	 Alignment		100.0	15	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	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d3dhwa1	 Alignment		100.0	21	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d2r6gg1	 Alignment		100.0	14	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	d1umqa_	 Alignment		29.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
11	c1umqA_	 Alignment		29.1	10	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	d1ntca_	Alignment		26.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	d1fipa_	Alignment		23.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
14	d1etob_	Alignment		21.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1etxa_	Alignment		19.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	d1g2ha_	Alignment		19.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c3e7lD_	Alignment		17.8	6	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
18	d1x8da1	Alignment		11.5	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YjiL-like
19	c2cw1A_	Alignment		9.8	20	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein

20 [c2jwaA](#)

Alignment



7.8

27

PDB header:transferase
Chain: A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2;
PDBTitle: erbb2 transmembrane segment dimer spatial structure