



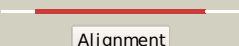



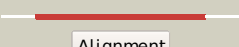

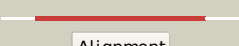





















Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P33359
Date	Thu Jan 5 11:52:01 GMT 2012
Unique Job ID	f596cee90ac5dc83

Detailed template information

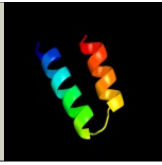
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2onkc1	 Alignment		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
2	c2onkC_	 Alignment		100.0	20	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
3	d3d31c1	 Alignment		100.0	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
4	c3d31D_	 Alignment		100.0	18	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
5	c3fh6F_	 Alignment		100.0	16	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	18	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	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d3dhwa1	 Alignment		99.9	24	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d2r6gg1	 Alignment		99.9	21	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	d1ntca_	 Alignment		26.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
11	c1umqA_	 Alignment		25.1	22	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		25.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	c3rkoF_	Alignment		16.8	10	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
14	d1fipa_	Alignment		14.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1etob_	Alignment		13.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	c3e7lD_	Alignment		12.3	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
17	d1etxa_	Alignment		11.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	c2jwaA_	Alignment		11.6	21	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
19	c2cw1A_	Alignment		10.3	27	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein

20

[c2d7dB](#)

Alignment



7.7

19

PDB header:hydrolase/dna
Chain: B: **PDB Molecule:**40-mer from uvrabc system protein b;
PDB Title: structural insights into the cryptic dna dependent atp-ase2 activity of uvrb