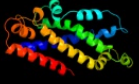
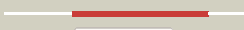
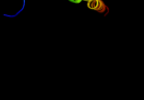
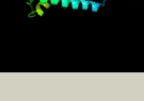


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P75799
Date	Thu Jan 5 12:14:18 GMT 2012
Unique Job ID	213584f01ee6d379

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dhwa1	 Alignment		99.9	21	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
2	c2onkC_	 Alignment		99.9	16	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	d2onkc1	 Alignment		99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
4	c3d31D_	 Alignment		99.8	21	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
5	d3d31c1	 Alignment		99.8	21	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	d2r6gf2	 Alignment		99.8	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	c3fh6F_	 Alignment		99.8	13	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
8	d2r6gg1	 Alignment		99.8	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	c2r6gF_	 Alignment		99.8	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
10	c1wz4A_	 Alignment		36.6	50	PDB header: gene regulation Chain: A: PDB Molecule: major surface antigen; PDBTitle: solution conformation of adr subtype hbv pre-s2 epitope
11	c2jwaA_	 Alignment		34.7	15	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure

12	d1umqa_	Alignment		13.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	c1umqA_	Alignment		13.1	13	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
14	d1ntca_	Alignment		10.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1fipa_	Alignment		10.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	c2cw1A_	Alignment		9.9	32	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
17	d1etob_	Alignment		9.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	d1p7ba2	Alignment		9.1	8	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
19	c2voyB_	Alignment		8.7	10	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
20	c1p7bB_	Alignment		8.5	7	PDB header: metal transport Chain: B: PDB Molecule: integral membrane channel and cytosolic domains; PDBTitle: crystal structure of an inward rectifier potassium channel
21	d1g2ha_	Alignment	not modelled	8.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
22	c2jpwa_	Alignment	not modelled	7.8	21	PDB header: contractile protein Chain: A: PDB Molecule: troponin i, cardiac muscle; PDBTitle: solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
23	d2axtk1	Alignment	not modelled	6.6	31	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
24	d2auwa1	Alignment	not modelled	6.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
25	d1etxa_	Alignment	not modelled	6.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c3a0bk_	Alignment	not modelled	6.1	28	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
27	c3a0bK_	Alignment	not modelled	6.1	28	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
28	d1pjqaz	Alignment	not modelled	5.9	34	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
						Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex

29	d2bs2c1	Alignment	not modelled	5.8	15	transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
30	c3e7lD_	Alignment	not modelled	5.6	13	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain