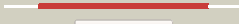
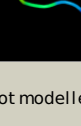


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AEG1
Date	Thu Jan 5 11:23:13 GMT 2012
Unique Job ID	c20052bb460798f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		99.9	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
2	d2onkc1	 Alignment		99.9	11	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
3	c2onkC_	 Alignment		99.9	11	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	d2r6gf2	 Alignment		99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
5	c3d31D_	 Alignment		99.9	16	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
6	d3d31c1	 Alignment		99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	c2r6gF_	 Alignment		99.9	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
8	d2r6gg1	 Alignment		99.9	12	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d3dhwa1	 Alignment		99.8	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c2jwaA_	 Alignment		30.3	14	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
11	c1p7bB_	 Alignment		25.2	10	PDB header: metal transport Chain: B: PDB Molecule: integral membrane channel and cytosolic domains; PDBTitle: crystal structure of an inward rectifier potassium channel

12	dlp7ba2	Alignment		15.9	10	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
13	clwz4A_	Alignment		14.5	50	PDB header: gene regulation Chain: A: PDB Molecule: major surface antigen; PDBTitle: solution conformation of adr subtype hbv pre-s2 epitope
14	c2b9sB_	Alignment		13.8	23	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase i-like protein; PDBTitle: crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
15	dlg2ha_	Alignment		13.6	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	c2lhuA_	Alignment		13.4	13	PDB header: structural protein Chain: A: PDB Molecule: mybpc3 protein; PDBTitle: structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
17	dlntca_	Alignment		13.1	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	clumqA_	Alignment		12.4	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
19	dlumqa_	Alignment		12.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	c2ftcP_	Alignment		11.4	57	PDB header: ribosome Chain: P: PDB Molecule: mitochondrial ribosomal protein l33 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
21	d2gyc11	Alignment	not modelled	8.7	43	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L33p
22	c2hx6A_	Alignment	not modelled	7.9	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
23	dlfipa_	Alignment	not modelled	7.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c2voyB_	Alignment	not modelled	7.3	8	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
25	d1etob_	Alignment	not modelled	6.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	d1etxa_	Alignment	not modelled	6.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
27	c2b9n6_	Alignment	not modelled	6.1	43	PDB header: ribosome Chain: 6: PDB Molecule: 50s ribosomal protein l33; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf2,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400.
28	d2zjr11	Alignment	not modelled	6.1	43	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins

					Family: Ribosomal protein L33p
29	d2ns0a1	Alignment	not modelled	6.0	11 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
30	c3e7lD_	Alignment	not modelled	6.0	13 PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
31	d2axtk1	Alignment	not modelled	5.7	31 Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
32	c1ql1A_	Alignment	not modelled	5.6	12 PDB header: virus Chain: A: PDB Molecule: pf1 bacteriophage coat protein b; PDBTitle: inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
33	c3a0bK_	Alignment	not modelled	5.2	28 PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
34	c3a0bk_	Alignment	not modelled	5.2	28 PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex