
































Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P10905
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		100.0	24	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	c2r6gF_	 Alignment		100.0	30	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
3	d2r6gg1	 Alignment		100.0	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
4	d2r6gf2	 Alignment		100.0	30	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
5	d2onkc1	 Alignment		100.0	19	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	c2onkC_	 Alignment		100.0	19	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
7	d3d31c1	 Alignment		100.0	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	c3d31D_	 Alignment		100.0	18	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
9	d3dhwa1	 Alignment		99.9	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	d2r6gf1	 Alignment		95.5	9	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
11	c1umqA_	 Alignment		46.5	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	d1umqa_	Alignment		46.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	d1fipa_	Alignment		40.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
14	d1ntca_	Alignment		38.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1etob_	Alignment		36.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	d1etxa_	Alignment		36.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c3e7ID_	Alignment		31.7	23	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
18	d1g2ha_	Alignment		24.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	c2hx6A_	Alignment		12.9	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
20	c2cw1A_	Alignment		7.1	20	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
21	d1v54g_	Alignment	not modelled	5.3	21	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
22	c1twcF_	Alignment	not modelled	5.2	29	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
23	d1twff_	Alignment	not modelled	5.2	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6