Phyre^2

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Description	P0AFR7
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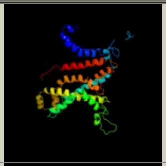
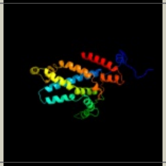
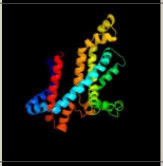
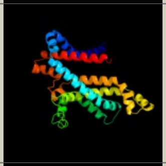
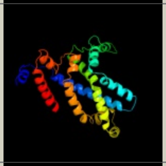
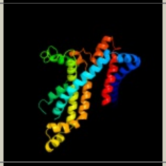
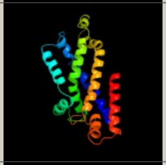
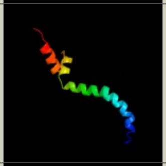
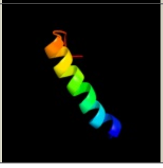
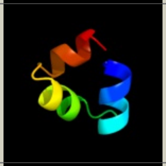
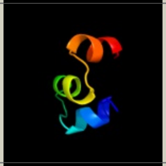
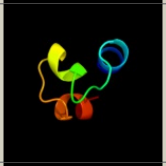
Unique Job ID	e36690bfbbfaf298

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		100.0	27	**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	29	**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	24	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	d2onkc1	 Alignment		100.0	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c2onkC_	 Alignment		100.0	18	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
6	d2r6gf2	 Alignment		100.0	30	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	d3d31c1	 Alignment		100.0	20	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	c3d31D_	 Alignment		100.0	20	**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		95.2	20	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
11	c2hx6A_	 Alignment		29.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb

12	c1umqA_	Alignment		24.1	19	**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
13	d1umqa_	Alignment		24.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d1fipa_	Alignment		22.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
15	d1etob_	Alignment		19.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	d1ntca_	Alignment		18.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	d1etxa_	Alignment		17.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	d1g2ha_	Alignment		17.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	c3e7lD_	Alignment		16.8	23	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
20	c2cw1A_	Alignment		8.3	36	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
21	d1cf7a_	Alignment	not modelled	6.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
22	d1v54g_	Alignment	not modelled	6.2	21	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa