Phyre^2

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Description	P76224
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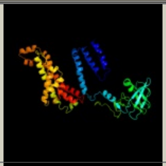
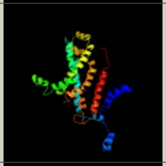
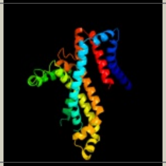
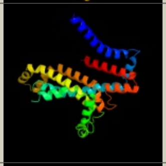
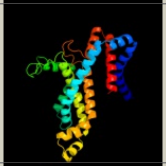
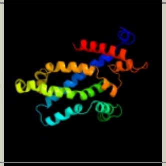
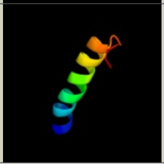
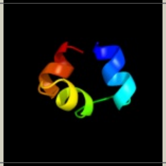
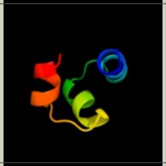
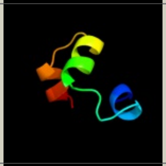
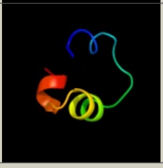
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r6gF_	 Alignment		100.0	14	**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
2	c3fh6F_	 Alignment		100.0	15	**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
3	d3d31c1	 Alignment		100.0	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	c3d31D_	 Alignment		100.0	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
5	d2onkc1	 Alignment		100.0	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c2onkC_	 Alignment		100.0	14	**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	d2r6gf2	 Alignment		100.0	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	d2r6gg1	 Alignment		100.0	20	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3dhwa1	 Alignment		99.9	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d1ntca_	 Alignment		25.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
11	c2hx6A_	 Alignment		22.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb

12	c1umqA_	Alignment		20.7	16	**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		20.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d1iwga8	Alignment		16.7	9	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
15	d1fipa_	Alignment		12.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	d1etxa_	Alignment		11.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	c3e7lD_	Alignment		10.1	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
18	d1etob_	Alignment		9.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	d1i1ga1	Alignment		7.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
20	c2oviA_	Alignment		7.1	10	**PDB header:**ligand binding protein, metal transport **Chain:** A: **PDB Molecule:**hypothetical protein chux; **PDBTitle:** structure of the heme binding protein chux
21	d2cg4a1	Alignment	not modelled	6.0	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
22	d1v54g_	Alignment	not modelled	5.9	12	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
23	d1cf7a_	Alignment	not modelled	5.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
24	d1g2ha_	Alignment	not modelled	5.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
25	d2diia1	Alignment	not modelled	5.5	11	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain