Phyre2

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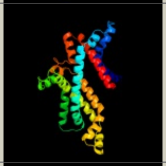
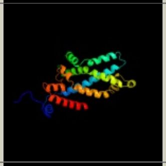
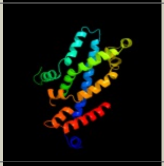
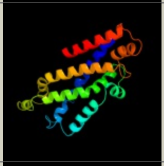
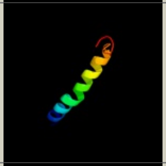
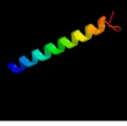
Description	P0AFK6
Date	Thu Jan 5 11:26:36 GMT 2012
Unique Job ID	798fced1422b8d24

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gg1	Alignment		100.0	21	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	c3fh6F_	Alignment		100.0	18	**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	c2onkC_	Alignment		100.0	21	**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	d2onkc1	Alignment		100.0	21	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	d3d31c1	Alignment		100.0	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c3d31D_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
7	c2r6gF_	Alignment		100.0	20	**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	d2r6gf2	Alignment		100.0	20	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3dhwa1	Alignment		99.9	21	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d2r6gf1	Alignment		33.5	12	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
11	d1umqa_	Alignment		30.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

12	c1umqA_	Alignment		30.0	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	d1fipa_	Alignment		27.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d1ntca_	Alignment		25.1	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
15	c2hx6A_	Alignment		23.7	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
16	d1etob_	Alignment		23.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	c3e7lD_	Alignment		17.0	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	d1etxa_	Alignment		16.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	c2jwaA_	Alignment		16.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure

20	d1g2ha_	Alignment		12.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like