Phyre2

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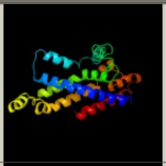
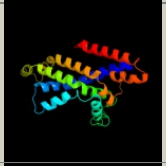
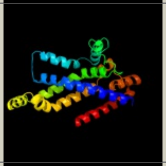
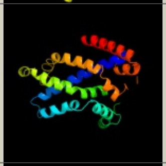
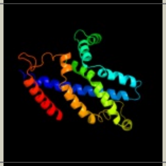
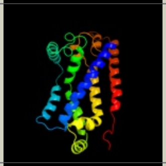
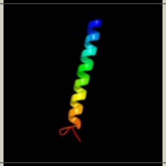
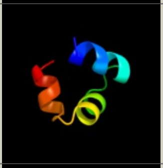
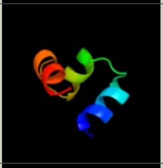
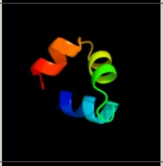
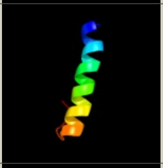
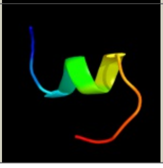
Description	P0AE30
Date	Thu Jan 5 11:22:24 GMT 2012
Unique Job ID	1b41e757a1bd1af6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3d31c1	Alignment		100.0	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	c3d31D_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
3	d2onkc1	Alignment		100.0	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	c2onkC_	Alignment		100.0	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
5	c2r6gF_	Alignment		100.0	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
6	d2r6gf2	Alignment		100.0	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c3fh6F_	Alignment		100.0	13	**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
8	d3dhwa1	Alignment		99.9	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d2r6gg1	Alignment		99.9	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c2jwaA_	Alignment		32.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
11	c1umqA_	Alignment		22.8	13	**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		22.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
13	d1ntca_	Alignment		21.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d1fipa_	Alignment		19.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
15	c3e7lD_	Alignment		17.4	6	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
16	d1etob_	Alignment		17.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	d1etxa_	Alignment		16.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	c2hx6A_	Alignment		13.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
19	c2cw1A_	Alignment		13.1	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein

20	d1g2ha_	Alignment		10.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like