Phyre2

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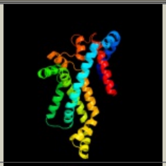
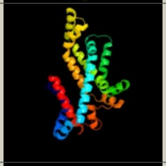
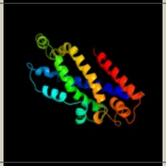
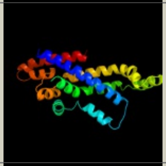
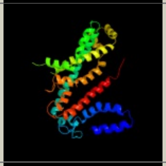
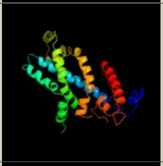
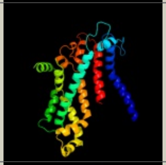
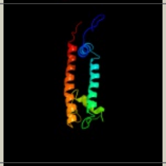
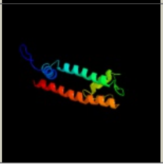
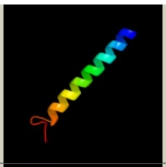
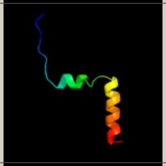
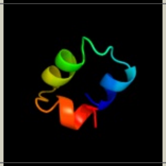
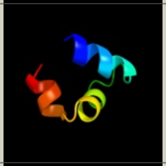
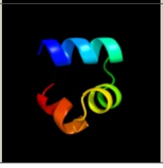
Description	P0AGH5
Date	Thu Jan 5 11:29:11 GMT 2012
Unique Job ID	ddb4fc39a579f408

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2onkC_	Alignment		99.9	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
2	d2onkc1	Alignment		99.9	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	d3dhwa1	Alignment		99.9	21	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	d2r6gf2	Alignment		99.9	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	d3d31c1	Alignment		99.9	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c3d31D_	Alignment		99.9	18	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
7	c3fh6F_	Alignment		99.9	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
8	c2r6gF_	Alignment		99.9	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
9	d2r6gg1	Alignment		99.8	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c1p7bB_	Alignment		73.3	8	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**integral membrane channel and cytosolic domains; **PDBTitle:** crystal structure of an inward rectifier potassium channel
11	d1p7ba2	Alignment		47.0	8	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels

12	c2jwaA_	Alignment		24.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
13	c2voyB_	Alignment		9.2	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
14	c2lhuA_	Alignment		7.6	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
15	c1umqA_	Alignment		7.2	6	**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
16	d1umqa_	Alignment		7.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	d1ntca_	Alignment		6.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	d1fipa_	Alignment		5.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

19	d1etob_	Alignment		5.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like