Phyre2

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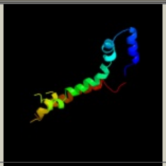
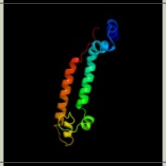
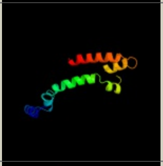
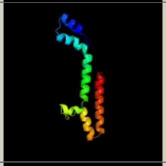
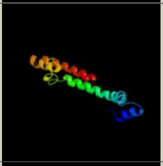
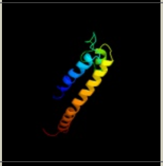
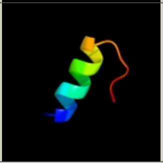
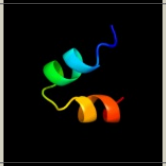
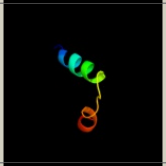
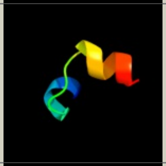
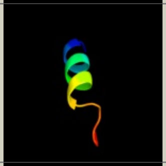
Description	P75681
Date	Thu Jan 5 12:13:01 GMT 2012
Unique Job ID	00fcf4cf044bad6e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	Alignment		99.9	29	**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	d2r6gg1	Alignment		99.8	21	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	c2r6gF_	Alignment		99.8	31	**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
4	d2onkc1	Alignment		99.8	25	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c2onkC_	Alignment		99.8	25	**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		99.8	28	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c3d31D_	Alignment		99.8	25	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
8	d3d31c1	Alignment		99.8	25	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3dhwa1	Alignment		99.5	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c3qnqD_	Alignment		17.7	11	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
11	c2hx6A_	Alignment		11.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb

12	c2d7dB_	Alignment		11.5	25	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**40-mer from uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
13	d2ns0a1	Alignment		10.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
14	c1umqA_	Alignment		9.8	14	**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
15	d1umqa_	Alignment		9.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	c2diiA_	Alignment		9.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
17	d1ntca_	Alignment		7.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	c2ka6B_	Alignment		7.5	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** nmr structure of the cbp-taz2/stat1-tad complex
19	d3fapb_	Alignment		7.3	28	**Fold:**Four-helical up-and-down bundle **Superfamily:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) **Family:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
20	d1g2ha_	Alignment		7.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
21	d2diia1	Alignment	not modelled	7.0	24	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
22	c1ql1A_	Alignment	not modelled	6.7	30	**PDB header:**virus **Chain:** A: **PDB Molecule:**pf1 bacteriophage coat protein b; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
23	c2qksA_	Alignment	not modelled	6.1	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
24	d1v54g_	Alignment	not modelled	5.6	21	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa