Phyre2

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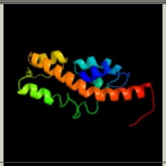
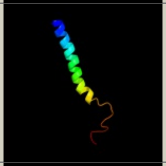
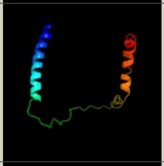
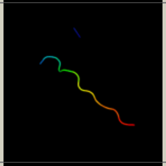
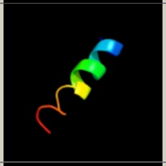
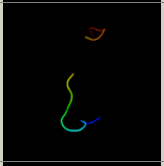
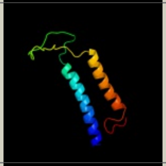
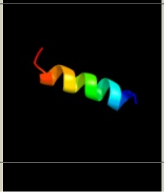
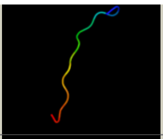
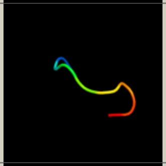
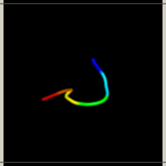
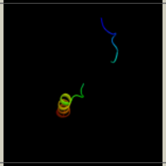
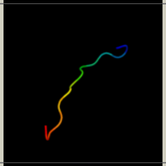
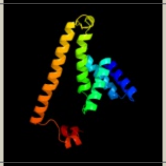
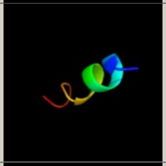
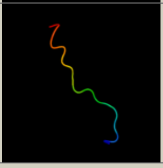
Description	P39263
Date	Thu Jan 5 11:58:35 GMT 2012
Unique Job ID	5e7feb89531d9af9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		46.1	12	**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
2	c2voyE_	Alignment		20.1	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
3	c2kncA_	Alignment		12.1	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
4	c3eh4A_	Alignment		10.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase subunit 1; **PDBTitle:** structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
5	d1jb0f_	Alignment		9.4	24	**Fold:**Single transmembrane helix **Superfamily:**Subunit III of photosystem I reaction centre, PsaF **Family:**Subunit III of photosystem I reaction centre, PsaF
6	c1eysH_	Alignment		9.1	7	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
7	c2wsfF_	Alignment		8.5	12	**PDB header:**photosynthesis **Chain:** F: **PDB Molecule:**photosystem i reaction center subunit iii, **PDBTitle:** improved model of plant photosystem i
8	c2yvxD_	Alignment		8.1	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
9	d2j01c1	Alignment		7.1	18	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
10	c3mk7F_	Alignment		6.5	6	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
11	c1wrgA_	Alignment		6.4	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum

12	d1neea1	Alignment		6.4	29	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
13	d1lghb_	Alignment		6.3	22	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
14	c3kysB_	Alignment		6.3	33	**PDB header:**transcription/protein binding **Chain:** B: **PDB Molecule:**65 kda yes-associated protein; **PDBTitle:** crystal structure of human yap and tead complex
15	d1k8ga2	Alignment		5.7	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
16	c2voyB_	Alignment		5.7	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
17	c1neeA_	Alignment		5.6	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
18	c2b2hA_	Alignment		5.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
19	c2o01F_	Alignment		5.4	15	**PDB header:**photosynthesis **Chain:** F: **PDB Molecule:**photosystem i reaction center subunit iii, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
20	c2gyc2_	Alignment		5.4	24	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** structure of the 50s subunit of a secm-stalled e. coli2 ribosome complex obtained by fitting atomic models for rna3 and protein components into cryo-em map emd-1143
21	c2vdaB_	Alignment	not modelled	5.2	29	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
22	d1fftb2	Alignment	not modelled	5.2	6	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
23	d1jb7a2	Alignment	not modelled	5.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
24	d1wiia_	Alignment	not modelled	5.1	7	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain