Phyre2

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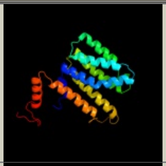
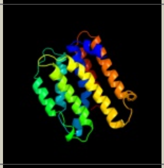
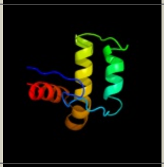
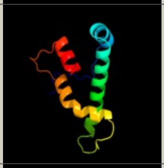
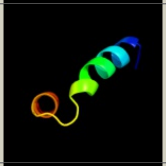
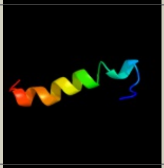
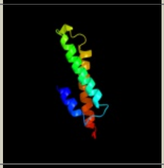
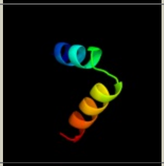
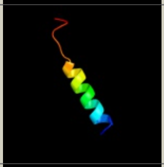
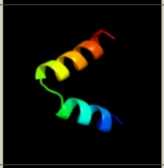
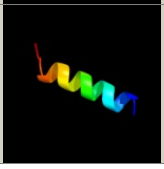
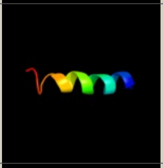
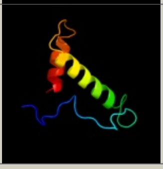
Description	P32680
Date	Thu Jan 5 11:50:06 GMT 2012
Unique Job ID	59e5e961851a2bf8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f7cA_	Alignment		100.0	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf416); **PDBTitle:** crystal structure of a duf416 family protein (maqu_0942) from2 marinobacter aquaeolei vt8 at 2.00 a resolution
2	c2q9rA_	Alignment		100.0	37	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a duf416 family protein (sbal_3149) from2 shewanella baltica os155 at 1.91 a resolution
3	d1pula1	Alignment		64.3	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**p25-alpha
4	c2dpyA_	Alignment		44.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellum-specific atp synthase; **PDBTitle:** crystal structure of the flagellar type iii atpase flii
5	d1z9ha1	Alignment		32.8	26	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
6	c3lj4i_	Alignment		29.0	28	**PDB header:**viral protein **Chain:** I: **PDB Molecule:**portal protein; **PDBTitle:** bacteriophage p22 portal protein bound to middle tail factor gp4. this2 file contain the first biological assembly
7	d1szia_	Alignment		22.9	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain **Family:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
8	d1m98a1	Alignment		21.0	15	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
9	c3t98A_	Alignment		19.2	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup54; **PDBTitle:** molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
10	c1m98A_	Alignment		15.8	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
11	d1iyjb1	Alignment		13.6	11	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain

12	d1fnna1	Alignment		13.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
13	c2an7A_	Alignment		12.7	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
14	c2oblA_	Alignment		12.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**escn; **PDBTitle:** structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
15	c2r4gA_	Alignment		11.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**telomerase reverse transcriptase; **PDBTitle:** the high resolution structure of the rna-binding domain of telomerase
16	d2bjca1	Alignment		11.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
17	d1zoqc1	Alignment		9.7	19	**Fold:**Nuclear receptor coactivator interlocking domain **Superfamily:**Nuclear receptor coactivator interlocking domain **Family:**Nuclear receptor coactivator interlocking domain
18	d1miua1	Alignment		9.7	11	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain
19	d1wlma1	Alignment		9.2	23	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**p25-alpha
20	c1fx0B_	Alignment		8.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase beta chain; **PDBTitle:** crystal structure of the chloroplast f1-atpase from spinach
21	c3ovkD_	Alignment	not modelled	7.6	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**aminopeptidase p, xaa-pro dipeptidase; **PDBTitle:** crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
22	c2h12C_	Alignment	not modelled	7.3	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyldethia coenzyme a (cmx)
23	c2o8kA_	Alignment	not modelled	7.1	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
24	c2qe7C_	Alignment	not modelled	6.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
25	c2jrfA_	Alignment	not modelled	6.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tubulin polymerization-promoting protein family **PDBTitle:** solution nmr structure of tubulin polymerization-promoting2 protein family member 3 from homo sapiens. northeast3 structural genomics target hr387.
26	d2cx6a1	Alignment	not modelled	6.7	32	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
27	c1mjeA_	Alignment	not modelled	6.7	11	**PDB header:**gene regulation/antitumor protein/dna **Chain:** A: **PDB Molecule:**breast cancer 2; **PDBTitle:** structure of a brca2-dss1-ssdna complex
						PDB header:gene regulation/antitumor protein

28	c1iyjB_	Alignment	not modelled	6.6	11	**Chain:** B: **PDB Molecule:**breast cancer susceptibility; **PDBTitle:** structure of a brca2-dss1 complex
29	d1or7a1	Alignment	not modelled	6.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
30	c3a8qB_	Alignment	not modelled	6.4	27	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**t-lymphoma invasion and metastasis-inducing **PDBTitle:** low-resolution crystal structure of the tiam2 phccex domain
31	d1k28a3	Alignment	not modelled	6.4	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
32	d1dd3a2	Alignment	not modelled	6.3	30	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
33	c1miuA_	Alignment	not modelled	6.2	11	**PDB header:**gene regulation/antitumor protein **Chain:** A: **PDB Molecule:**breast cancer type 2 susceptibility protein; **PDBTitle:** structure of a brca2-dss1 complex
34	d1zq1a1	Alignment	not modelled	5.8	57	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
35	c2yufA_	Alignment	not modelled	5.7	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ngfi-a-binding protein 1; **PDBTitle:** solution structure of the ncd2 domain in human2 transcriptional repressor nab1 protein
36	c3lhfC_	Alignment	not modelled	5.6	15	**PDB header:**recombination **Chain:** C: **PDB Molecule:**serine recombinase; **PDBTitle:** the crystal structure of a serine recombinase from2 sulfolobus solfataricus to 2.3a
37	c3a5dM_	Alignment	not modelled	5.5	23	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**v-type atp synthase beta chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
38	d1gx5a_	Alignment	not modelled	5.1	19	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase