Phyre²

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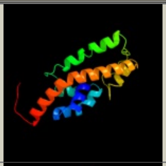
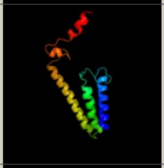
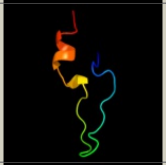
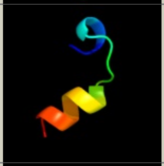
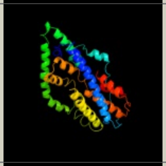
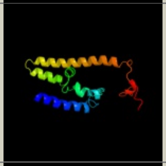
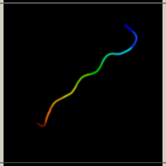
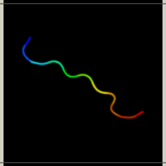
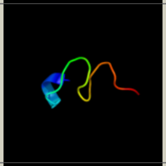
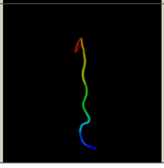
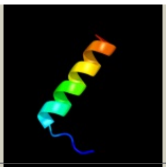
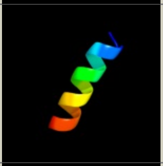
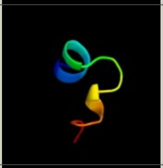
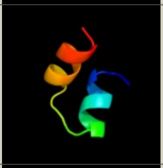
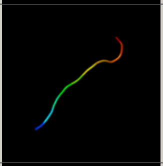
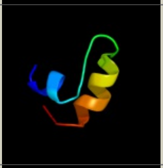
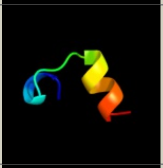
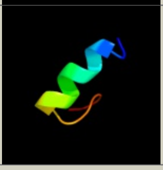
Description	P46133
Date	Thu Jan 5 12:04:06 GMT 2012
Unique Job ID	a6d5f50ae1241294

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		33.8	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	c3b9yA_	Alignment		17.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
3	d1iuqa_	Alignment		13.6	12	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
4	d2b0la1	Alignment		10.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CodY HTH domain
5	c2voyE_	Alignment		10.6	29	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
6	d2nwwa1	Alignment		10.4	16	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
7	c3hd6A_	Alignment		10.3	18	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
8	c2pmzL_	Alignment		8.9	36	**PDB header:**translation, transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerase subunit l; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
9	c3h0gK_	Alignment		8.9	64	**PDB header:**transcription **Chain:** K: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb11; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
10	d1rzsa_	Alignment		8.5	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
11	d1xppa_	Alignment		8.3	25	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL

12	c2l9mA_	Alignment		7.3	18	**PDB header:**apoptosis inhibitor **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 2; **PDBTitle:** structure of ciap1 card
13	c2qupA_	Alignment		7.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh1478 protein; **PDBTitle:** crystal structure of uncharacterized protein bh1478 from bacillus2 halodurans
14	d1iq8a4	Alignment		7.1	6	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Archaeosine tRNA-guanine transglycosylase, C2 domain
15	c3neuA_	Alignment		6.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
16	d1twfk_	Alignment		6.7	45	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL
17	d2b7ea1	Alignment		6.3	11	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
18	c3eetA_	Alignment		6.3	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
19	d1u0ua2	Alignment		5.9	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
20	c3myrB_	Alignment		5.9	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
21	d1n1ea1	Alignment	not modelled	5.8	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Glycerol-3-phosphate dehydrogenase
22	c2p61A_	Alignment	not modelled	5.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein tm_1646; **PDBTitle:** crystal structure of protein tm1646 from thermotoga2 maritima, pfam duf327
23	c2du9A_	Alignment	not modelled	5.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
24	c1hgvA_	Alignment	not modelled	5.7	8	**PDB header:**virus **Chain:** A: **PDB Molecule:**ph75 inovirus major coat protein; **PDBTitle:** filamentous bacteriophage ph75
25	d2p61a1	Alignment	not modelled	5.7	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**TM1646-like **Family:**TM1646-like
26	d1vkya_	Alignment	not modelled	5.6	24	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
27	c3eh4A_	Alignment	not modelled	5.6	9	**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
28	c3d0wD_	Alignment	not modelled	5.5	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yflh protein; **PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326
						Fold: QueA-like

29	d1wdia_	Alignment	not modelled	5.3	29	**Superfamily:**QueA-like **Family:**QueA-like
30	c1yy3A_	Alignment	not modelled	5.3	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
31	c2igrA_	Alignment	not modelled	5.3	21	**PDB header:**de novo protein, lipid binding protein **Chain:** A: **PDB Molecule:**anticancer peptide cb1a; **PDBTitle:** solution structure of cb1a, a novel anticancer peptide derived from2 natural antimicrobial peptide cecropin b
32	d1oqya2	Alignment	not modelled	5.2	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
33	c2jlnA_	Alignment	not modelled	5.1	0	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
34	d1xmea1	Alignment	not modelled	5.1	9	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
35	d1dv0a_	Alignment	not modelled	5.0	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain