Phyre^2

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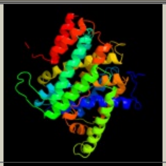
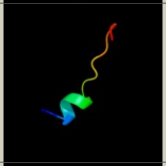
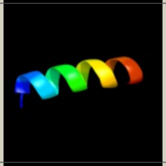
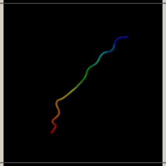
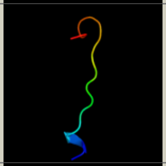
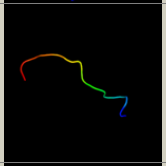
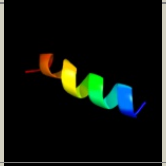
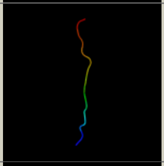
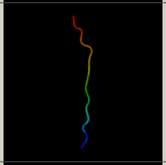
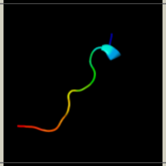
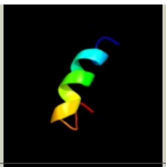
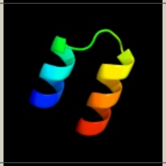
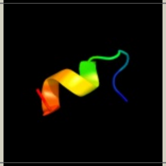
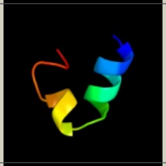
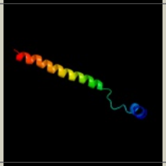
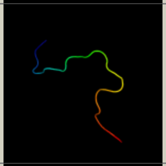
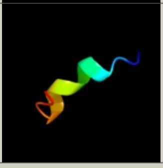
Description	Q46817
Date	Thu Jan 5 12:34:42 GMT 2012
Unique Job ID	7cad0c107f312f1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qe7A_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uracil permease; **PDBTitle:** crystal structure of uracil transporter--uraa
2	c3lpzA_	Alignment		25.2	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
3	d1v54l_	Alignment		19.1	24	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa) **Family:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)
4	c3iysA_	Alignment		16.5	47	**PDB header:**virus **Chain:** A: **PDB Molecule:**major capsid protein vp1; **PDBTitle:** homology model of avian polyomavirus asymmetric unit
5	c1w3gA_	Alignment		13.3	29	**PDB header:**toxin/lectin **Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus; **PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules.
6	c2x7lP_	Alignment		11.2	27	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv rev; **PDBTitle:** implications of the hiv-1 rev dimer structure at 3.2a2 resolution for multimeric binding to the rev response3 element
7	c2y69Y_	Alignment		10.7	25	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**cytochrome c oxidase subunit 7c; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
8	d1sida_	Alignment		10.3	50	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
9	d1sva1_	Alignment		9.9	53	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
10	c3lphD_	Alignment		9.0	31	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**protein rev; **PDBTitle:** crystal structure of the hiv-1 rev dimer
11	c1hynQ_	Alignment		8.6	36	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein

12	d3er7a1	Alignment		8.4	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Exig0174-like
13	d1hynp_	Alignment		8.4	36	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
14	c2elpA_	Alignment		7.5	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
15	c3hfxA_	Alignment		7.5	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
16	c2kkuA_	Alignment		7.4	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
17	d1pv0a_	Alignment		7.4	21	**Fold:**Long alpha-hairpin **Superfamily:**Sporulation inhibitor Sda **Family:**Sporulation inhibitor Sda
18	c3dinD_	Alignment		7.2	10	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
19	c3kihC_	Alignment		7.1	23	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**5-bladed -propeller lectin; **PDBTitle:** the crystal structures of two fragments truncated from 5-bladed -2 propeller lectin, tachylectin-2 (lib2-d2-15)
20	d1txna_	Alignment		6.7	43	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
21	d2gr7a1	Alignment	not modelled	6.5	18	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
22	c2gr7C_	Alignment	not modelled	6.5	18	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
23	c2ziiA_	Alignment	not modelled	6.5	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 74; **PDBTitle:** crystal structure of yeast vps74-n-term truncation variant
24	c2zihC_	Alignment	not modelled	6.4	21	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 74; **PDBTitle:** crystal structure of yeast vps74
25	c2aexA_	Alignment	not modelled	6.3	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen iii oxidase, mitochondrial; **PDBTitle:** the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyria
26	c3ns4A_	Alignment	not modelled	6.2	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 53; **PDBTitle:** structure of a c-terminal fragment of its vps53 subunit suggests2 similarity of garp to a family of tethering complexes
27	c1u7bB_	Alignment	not modelled	6.1	35	**PDB header:**replication **Chain:** B: **PDB Molecule:**srqgstqgrlddffkvtgsl peptide of flap **PDBTitle:** crystal structure of hpcna bound to residues 331-350 of the2 flap endonuclease-1 (fen1)
28	c3hymA_	Alignment	not modelled	6.1	17	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cdc26;

						PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
29	c3hymE_	Alignment	not modelled	6.1	17	**PDB header:**cell cycle, ligase **Chain:** E: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
30	c3hymI_	Alignment	not modelled	6.1	17	**PDB header:**cell cycle, ligase **Chain:** I: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
31	d1tkla_	Alignment	not modelled	6.0	43	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
32	c3omdB_	Alignment	not modelled	6.0	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
33	c2ogfD_	Alignment	not modelled	5.9	36	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
34	d1vjua_	Alignment	not modelled	5.9	35	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
35	d1vqoi1	Alignment	not modelled	5.8	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
36	c1vq8I_	Alignment	not modelled	5.8	32	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l11p; **PDBTitle:** the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
37	c1bmxA_	Alignment	not modelled	5.6	37	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**human immunodeficiency virus type 1 capsid; **PDBTitle:** hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
38	c2ht2B_	Alignment	not modelled	5.5	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
39	c1zv8I_	Alignment	not modelled	5.3	7	**PDB header:**viral protein **Chain:** I: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
40	d1avwb_	Alignment	not modelled	5.3	21	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
41	c1btqA_	Alignment	not modelled	5.2	18	**PDB header:**anion transport **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
42	c1btrA_	Alignment	not modelled	5.2	18	**PDB header:**anion transport **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
43	d1q90m_	Alignment	not modelled	5.2	32	**Fold:**Single transmembrane helix **Superfamily:**PetM subunit of the cytochrome b6f complex **Family:**PetM subunit of the cytochrome b6f complex