Phyre2

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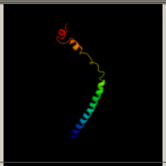
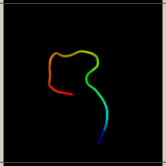
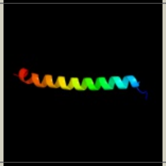
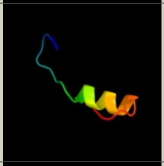
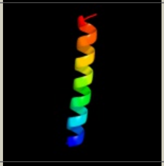
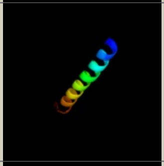
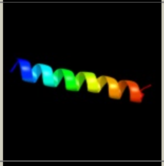
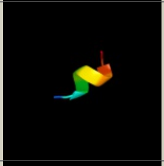
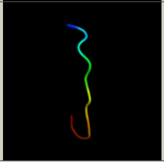
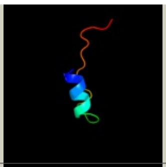
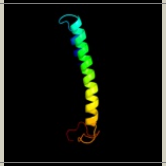
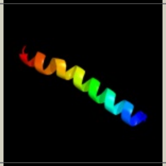
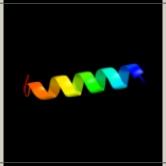
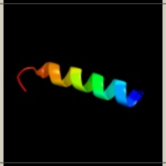
Description	P0AFN2
Date	Thu Jan 5 11:26:50 GMT 2012
Unique Job ID	dc77f459dcf8ff0f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f6ga_	Alignment		51.8	13	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
2	c3r1fO_	Alignment		39.1	31	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
3	c3okqA_	Alignment		23.3	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
4	c2o0cB_	Alignment		18.1	21	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**alr2278 protein; **PDBTitle:** crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
5	c3pp5A_	Alignment		14.7	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
6	d1v54j_	Alignment		13.9	13	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIa **Family:**Mitochondrial cytochrome c oxidase subunit VIIa
7	c1htmB_	Alignment		12.3	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain; **PDBTitle:** structure of influenza haemagglutinin at the ph of membrane2 fusion
8	d3e11a1	Alignment		12.0	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
9	c1zgxB_	Alignment		10.8	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanyl-specific ribonuclease sa; **PDBTitle:** crystal structure of ribonuclease mutant
10	c1emzA_	Alignment		10.0	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein e1; **PDBTitle:** solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1
11	c3f5dA_	Alignment		9.4	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis

12	c2vvyC_	Alignment		9.3	29	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**protein b15; **PDBTitle:** structure of vaccinia virus protein b14
13	c3hd6A_	Alignment		8.8	13	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
14	c1nhlA_	Alignment		8.5	26	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**synaptosomal-associated protein 23; **PDBTitle:** snap-23n structure
15	c1txpA_	Alignment		8.1	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein c **PDBTitle:** heterogeneous nuclear ribonucleoprotein (hnrnp) c2 oligomerization domain tetramer
16	c1txpB_	Alignment		8.1	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein c **PDBTitle:** heterogeneous nuclear ribonucleoprotein (hnrnp) c2 oligomerization domain tetramer
17	c1txpD_	Alignment		8.1	15	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein c **PDBTitle:** heterogeneous nuclear ribonucleoprotein (hnrnp) c2 oligomerization domain tetramer
18	c1txpC_	Alignment		8.1	15	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein c **PDBTitle:** heterogeneous nuclear ribonucleoprotein (hnrnp) c2 oligomerization domain tetramer
19	c3swfA_	Alignment		7.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
20	c2y0nD_	Alignment		7.3	30	**PDB header:**transcription **Chain:** D: **PDB Molecule:**male-specific lethal 3 homolog; **PDBTitle:** crystal structure of the complex between dosage2 compensation factors msl1 and msl3
21	d1ukfa_	Alignment	not modelled	7.1	27	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Avirulence protein Avrpph3
22	c3rmsA_	Alignment	not modelled	7.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis
23	c2vvxA_	Alignment	not modelled	7.1	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein a52; **PDBTitle:** structure of vaccinia virus protein a52
24	c3p8cE_	Alignment	not modelled	7.0	30	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave complex
25	d1r69a_	Alignment	not modelled	6.9	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
26	d2fexa1	Alignment	not modelled	6.7	29	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
27	d1pv0a_	Alignment	not modelled	6.7	25	**Fold:**Long alpha-hairpin **Superfamily:**Sporulation inhibitor Sda **Family:**Sporulation inhibitor Sda
28	c1envA_	Alignment	not modelled	6.5	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 envelope protein chimera consisting of a fragment of **PDBTitle:** atomic structure of the ectodomain from hiv-1 gp41
						PDB header:protein transport

29	c2k6sB_	Alignment	not modelled	6.2	30	**Chain:** B: **PDB Molecule:**rab11fip2 protein; **PDBTitle:** structure of rab11-fip2 c-terminal coiled-coil domain
30	c3i5dC_	Alignment	not modelled	6.2	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**p2x purinoceptor; **PDBTitle:** crystal structure of the atp-gated p2x4 ion channel in the closed, apo2 state at 3.5 angstroms (r3)
31	c2f5jA_	Alignment	not modelled	6.1	60	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**mortality factor 4-like protein 1; **PDBTitle:** crystal structure of mrg domain from human mrg15
32	c3cneD_	Alignment	not modelled	5.8	36	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
33	c3efeC_	Alignment	not modelled	5.8	18	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
34	d2axte1	Alignment	not modelled	5.5	19	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits