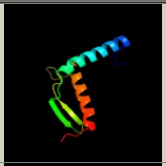
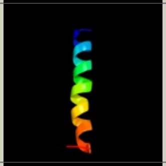
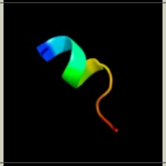
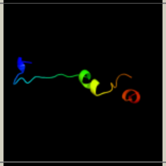
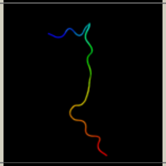
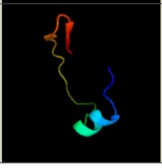
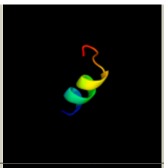
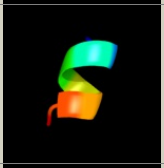
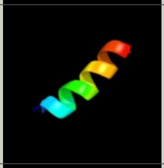
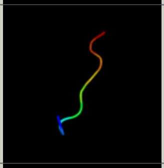
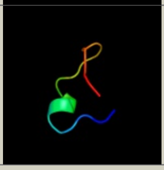
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AB61
Date	Thu Jan 5 11:14:43 GMT 2012
Unique Job ID	ca73c05a38ebafc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m92B_	Alignment		100.0	99	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ycin; **PDBTitle:** the structure of ycin, an unchracterized protein from shigella2 flexneri.
2	c2k5eA_	Alignment		29.3	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
3	c2k6sB_	Alignment		22.2	29	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**rab11fip2 protein; **PDBTitle:** structure of rab11-fip2 c-terminal coiled-coil domain
4	c2rmrA_	Alignment		18.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of msin3a pah1 domain
5	d1jr1a4	Alignment		17.2	55	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
6	c2ld7B_	Alignment		14.9	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
7	c3glsC_	Alignment		10.3	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
8	c2kc2A_	Alignment		9.3	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the f1 domain (residues 86-202) of the2 talin
9	d2a5yb2	Alignment		9.2	44	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
10	d2v9va1	Alignment		7.1	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
11	c3o27B_	Alignment		6.9	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx

12	d1v32a_	Alignment		6.8	14	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
13	c1qhuA_	Alignment		6.0	22	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (hemopexin); **PDBTitle:** mammalian blood serum haemopexin deglycosylated and in2 complex with its ligand haem
14	c2gzdC_	Alignment		6.0	28	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**rab11 family-interacting protein 2; **PDBTitle:** crystal structure of rab11 in complex with rab11-fip2
15	c1zikB_	Alignment		5.6	75	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16lys in the dimeric2 state
16	c1zikA_	Alignment		5.6	75	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16lys in the dimeric2 state
17	d1k1sa1	Alignment		5.5	29	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
18	d1k28d2	Alignment		5.4	33	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
19	d1xg8a_	Alignment		5.4	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YuzD-like
20	c1s1hL_	Alignment		5.4	16	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s23; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
21	c3tsiC_	Alignment	not modelled	5.4	42	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**hemagglutinin-neuraminidase; **PDBTitle:** structure of the parainfluenza virus 5 (piv5) hemagglutinin-2 neuraminidase (hn) stalk domain
22	c2xzmL_	Alignment	not modelled	5.0	16	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
23	c1zilA_	Alignment	not modelled	5.0	63	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
24	c1zilB_	Alignment	not modelled	5.0	63	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the dimeric2 state