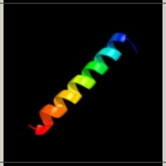
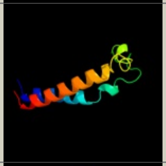
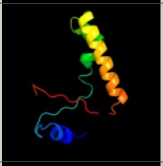
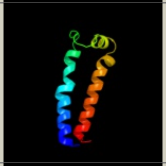
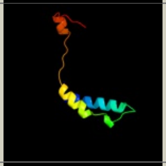
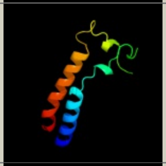
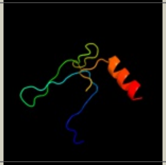
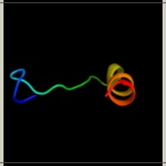
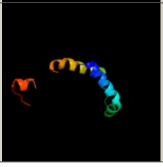
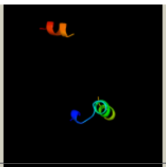
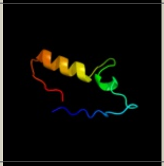
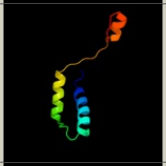
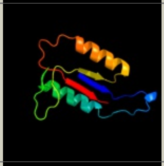
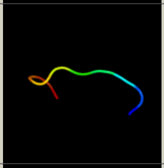
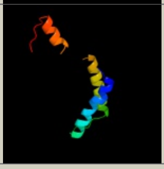
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76483
Date	Thu Jan 5 12:23:26 GMT 2012
Unique Job ID	7d08d6688e9e697c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ryla_	Alignment		100.0	98	**Fold:**Hypothetical protein yfbM **Superfamily:**Hypothetical protein yfbM **Family:**Hypothetical protein yfbM
2	c3tekA_	Alignment		21.6	4	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
3	d1bbha_	Alignment		21.3	7	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
4	d2o3bb1	Alignment		19.7	11	**Fold:**Nuclease A inhibitor (NuiA) **Superfamily:**Nuclease A inhibitor (NuiA) **Family:**Nuclease A inhibitor (NuiA)
5	d1e85a_	Alignment		18.5	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
6	c1iweB_	Alignment		16.2	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** imp complex of the recombinant mouse-muscle2 adenylosuccinate synthetase
7	d1p9ba_	Alignment		16.2	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
8	d1gqaa_	Alignment		16.0	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
9	c2hmaA_	Alignment		13.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
10	d2o0qa1	Alignment		12.4	27	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**CC0527-like
11	c3r7tA_	Alignment		12.2	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni

12	c2derA_	Alignment		11.9	10	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
13	c2p4dA_	Alignment		11.2	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** structure-assisted discovery of variola major h12 phosphatase inhibitors
14	c3p0kA_	Alignment		11.1	50	**PDB header:**oxidoreductase, viral protein **Chain:** A: **PDB Molecule:**sulfhydryl oxidase; **PDBTitle:** structure of baculovirus sulfhydryl oxidase ac92
15	d1dj2a_	Alignment		10.7	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
16	c1cp3B_	Alignment		10.6	8	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**apopain; **PDBTitle:** crystal structure of the complex of apopain with the tetrapeptide2 inhibitor ace-dvad-fmc
17	d2dara2	Alignment		10.4	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
18	d1gxya_	Alignment		10.1	33	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Ecto-ART
19	d1zs3a1	Alignment		10.1	6	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
20	d1dj3a_	Alignment		9.6	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
21	c3a1yF_	Alignment	not modelled	9.5	19	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
22	c3k6gA_	Alignment	not modelled	9.4	5	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**telomeric repeat-binding factor 2-interacting protein 1; **PDBTitle:** crystal structure of rap1 and trf2 complex
23	d1iwea_	Alignment	not modelled	8.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
24	c2fq8A_	Alignment	not modelled	8.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**2f; **PDBTitle:** nmr structure of 2f associated with lipid disc
25	c2fq5A_	Alignment	not modelled	8.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**peptide 2f; **PDBTitle:** nmr structure of 2f associated with lipid disc
26	d1w2ya_	Alignment	not modelled	8.5	50	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**Type II deoxyuridine triphosphatase
27	d1j3sa_	Alignment	not modelled	8.4	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
28	d1u5sb1	Alignment	not modelled	8.4	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
29	d2o3la1	Alignment	not modelled	8.0	14	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like

						Family:BH3980-like
30	d2j8wa1	Alignment	not modelled	8.0	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
31	c1kmcB_	Alignment	not modelled	7.6	8	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of the caspase-7 / xiap-bir2 complex
32	d1zfoa_	Alignment	not modelled	7.5	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LASP-1
33	d1wejf_	Alignment	not modelled	7.2	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
34	d1lfma_	Alignment	not modelled	7.0	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
35	d2btoa2	Alignment	not modelled	6.9	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
36	d1umya_	Alignment	not modelled	6.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
37	c3kd4A_	Alignment	not modelled	6.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative protease; **PDBTitle:** crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
38	d1jdla_	Alignment	not modelled	6.2	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
39	d1zuja1	Alignment	not modelled	6.1	11	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
40	d1nw9b_	Alignment	not modelled	6.1	14	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
41	c1z64A_	Alignment	not modelled	6.0	23	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**pleurocidin; **PDBTitle:** nmr solution structure of pleurocidin in dpc micelles
42	d1bccb1	Alignment	not modelled	6.0	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
43	c2funB_	Alignment	not modelled	5.8	12	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-8; **PDBTitle:** alternative p35-caspase-8 complex
44	d2hh6a1	Alignment	not modelled	5.7	5	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
45	c3l4oB_	Alignment	not modelled	5.7	21	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**methylamine utilization protein maug; **PDBTitle:** crystal structure of the maug/pre-methylamine dehydrogenase complex2 after treatment with hydrogen peroxide
46	d1cxca_	Alignment	not modelled	5.7	10	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
47	d1h32b_	Alignment	not modelled	5.5	12	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
48	d1ccra_	Alignment	not modelled	5.5	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
49	c3n1bA_	Alignment	not modelled	5.4	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 54; **PDBTitle:** c-terminal domain of vps54 subunit of the garp complex
50	c3qfqE_	Alignment	not modelled	5.4	26	**PDB header:**dna binding protein/dna **Chain:** E: **PDB Molecule:**large t antigen; **PDBTitle:** asymmetric assembly of merkel cell polyomavirus large t-antigen origin2 binding domains at the viral origin