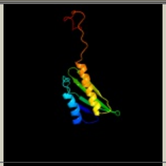
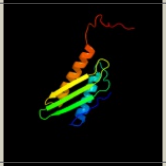
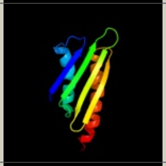
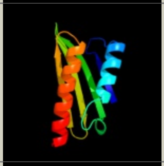
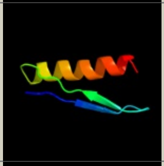
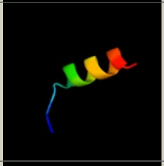
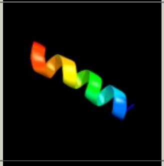
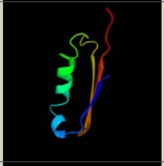
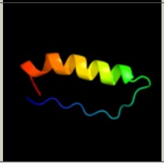
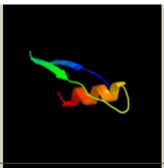
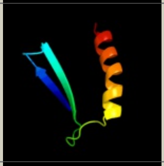
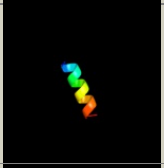
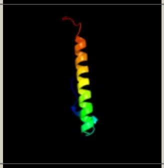
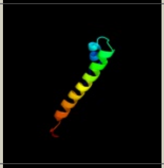
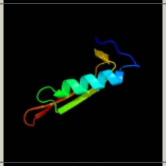
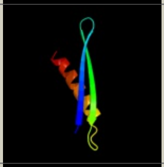
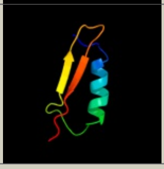
Email	l.a.kelley@imperial.ac.uk
Description	P0AD49
Date	Thu Jan 5 11:20:01 GMT 2012
Unique Job ID	ae181120a0692c0e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l4sa_	Alignment		100.0	100	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
2	d1imua_	Alignment		100.0	64	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
3	c2rqlA_	Alignment		100.0	38	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable sigma-54 modulation protein; **PDBTitle:** solution structure of the e. coli ribosome hibernation2 promoting factor hpf
4	c3tqmD_	Alignment		99.9	26	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** structure of an ribosomal subunit interface protein from coxiella2 burnetii
5	d2ywqa1	Alignment		99.9	27	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
6	d1uila_	Alignment		25.1	27	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
7	c3kxeD_	Alignment		23.0	6	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
8	c1by0A_	Alignment		16.6	44	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
9	c1i7nA_	Alignment		15.7	12	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
10	c2kxoA_	Alignment		13.7	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
11	d1o6da_	Alignment		12.7	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like

12	c3f6hA_	Alignment		12.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
13	c2yh5A_	Alignment		12.1	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
14	d2e9xd1	Alignment		12.1	33	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**SLD5 N-terminal domain-like
15	d1lr0a_	Alignment		10.2	7	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
16	c1hk8A_	Alignment		10.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
17	d1hk8a_	Alignment		10.2	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
18	d2i52a1	Alignment		9.5	13	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
19	c3rd6A_	Alignment		9.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mll3558 protein; **PDBTitle:** crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
20	c3r9jD_	Alignment		8.9	11	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
21	c1pk8D_	Alignment	not modelled	8.3	10	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**rat synapsin i; **PDBTitle:** crystal structure of rat synapsin i c domain complexed to2 ca.atp
22	c3q2oB_	Alignment	not modelled	7.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
23	c1hf9B_	Alignment	not modelled	7.8	13	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
24	c3zqbB_	Alignment	not modelled	7.3	19	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**protein prgi, cell invasion protein sipd; **PDBTitle:** prgi-sipd from salmonella typhimurium
25	d1sr9a3	Alignment	not modelled	6.9	13	**Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
26	c1mx0D_	Alignment	not modelled	6.5	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
27	d1kr4a_	Alignment	not modelled	6.5	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
						PDB header:de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x2 fold protein;

28	c2kpoA_	Alignment	not modelled	6.3	5	**PDBTitle:** solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
29	d2r85a2	Alignment	not modelled	6.0	6	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
30	d1ghha_	Alignment	not modelled	6.0	10	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
31	c2l9pA_	Alignment	not modelled	5.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147
32	d1gsoa3	Alignment	not modelled	5.6	9	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
33	c2l5gB_	Alignment	not modelled	5.3	29	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
34	c2q9qF_	Alignment	not modelled	5.2	33	**PDB header:**replication **Chain:** F: **PDB Molecule:**gins complex subunit 4; **PDBTitle:** the crystal structure of full length human gins complex
35	d1vkza1	Alignment	not modelled	5.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like