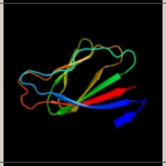
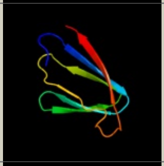
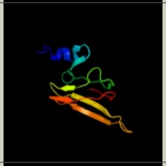
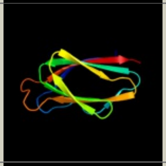
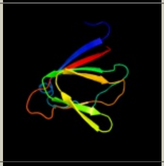
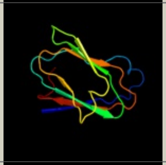
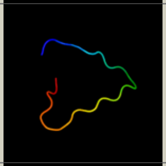
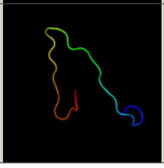
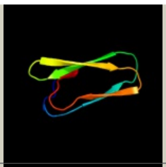
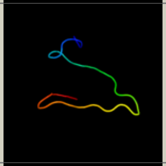
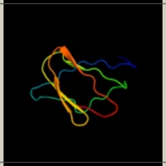
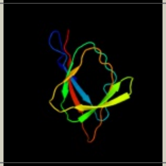
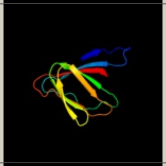
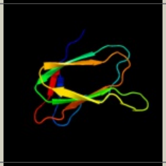
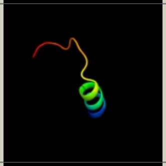
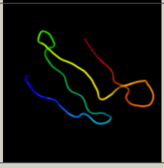
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AF96
Date	Thu Jan 5 11:25:39 GMT 2012
Unique Job ID	bc22ffea64c3676e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s4ca1	Alignment		100.0	28	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YhcH-like
2	d1yfua1	Alignment		85.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
3	d1v70a_	Alignment		76.9	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
4	c3cewA_	Alignment		59.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
5	c2i45C_	Alignment		58.1	22	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
6	d1zvfa1	Alignment		41.8	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
7	d1o4ta_	Alignment		41.2	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
8	d1vj2a_	Alignment		35.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
9	d2pa7a1	Alignment		33.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
10	d2arca_	Alignment		33.7	32	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
11	c2xxzA_	Alignment		33.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain

12	d1j3pa_	Alignment		32.8	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
13	c2xueB_	Alignment		30.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of jmjd3
14	c3d82A_	Alignment		30.4	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
15	c2ozjB_	Alignment		27.7	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
16	c2fqpD_	Alignment		27.4	13	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hypothetical protein bp2299; **PDBTitle:** crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
17	c3kgzA_	Alignment		23.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
18	c2oa2A_	Alignment		22.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2720 protein; **PDBTitle:** crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
19	d1a6qa1	Alignment		21.0	16	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
20	d1y9qa2	Alignment		15.8	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
21	c2w2iC_	Alignment	not modelled	14.6	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate oxygenase; **PDBTitle:** crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
22	c2hdlA_	Alignment	not modelled	13.6	24	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**small inducible cytokine b14; **PDBTitle:** solution structure of brak/cxcl14
23	d3bb6a1	Alignment	not modelled	13.1	24	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
24	c2os2A_	Alignment	not modelled	13.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 3a; **PDBTitle:** crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
25	c2q8eB_	Alignment	not modelled	13.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** specificity and mechanism of jmjd2a, a trimethyllysine-2 specific histone demethylase
26	c3opwA_	Alignment	not modelled	13.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dna damage-responsive transcriptional repressor rph1; **PDBTitle:** crystal structure of the rph1 catalytic core
27	d3dl3a1	Alignment	not modelled	12.9	27	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
28	c3ibmB_	Alignment	not modelled	11.5	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein;

						PDBTitle: crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
29	c3ebrA_	Alignment	not modelled	11.2	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
30	c3fjsC_	Alignment	not modelled	10.8	27	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
31	d2es7a1	Alignment	not modelled	10.3	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
32	c2pyhB_	Alignment	not modelled	10.1	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
33	c3h8uA_	Alignment	not modelled	9.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
34	c2r32A_	Alignment	not modelled	9.8	7	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
35	c2bx6A_	Alignment	not modelled	9.6	24	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
36	c3l2hD_	Alignment	not modelled	9.3	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative sugar phosphate isomerase; **PDBTitle:** crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
37	c2gu9B_	Alignment	not modelled	9.2	15	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
38	c2oziA_	Alignment	not modelled	8.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
39	c3ht2A_	Alignment	not modelled	8.6	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
40	c2q30C_	Alignment	not modelled	7.7	17	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
41	c2pfwB_	Alignment	not modelled	7.6	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
42	c3emrA_	Alignment	not modelled	7.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
43	d2a1xa1	Alignment	not modelled	6.6	27	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
44	d1y3ta1	Alignment	not modelled	6.2	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
45	d1tvfa1	Alignment	not modelled	6.2	27	**Fold:**Penicillin-binding protein associated domain **Superfamily:**Penicillin-binding protein associated domain **Family:**Pencillin binding protein 4 (PbpD), C-terminal domain
46	d2fcta1	Alignment	not modelled	6.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
47	c2lazA_	Alignment	not modelled	5.8	22	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
48	d1rc6a_	Alignment	not modelled	5.6	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
49	d1j0sa_	Alignment	not modelled	5.6	24	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
50	c2nnzA_	Alignment	not modelled	5.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
51	c2opwA_	Alignment	not modelled	5.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)

52	c2kpsA_	Alignment	not modelled	5.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of domain iv from the ybbr family protein of2 desulfitobacterium hafniense
53	c2lb0A_	Alignment	not modelled	5.3	22	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide