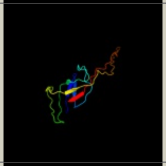
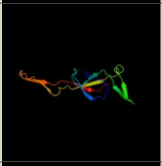
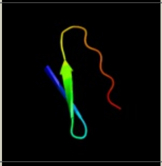
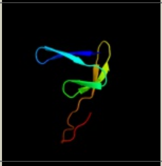
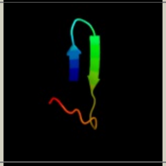
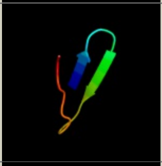
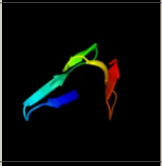
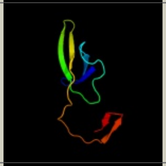
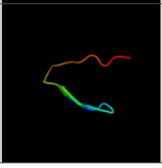
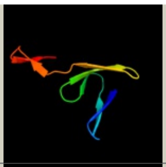
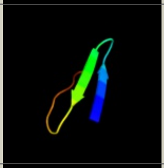
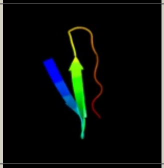
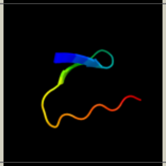
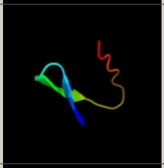
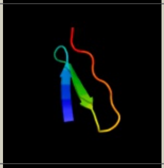
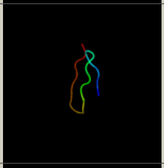
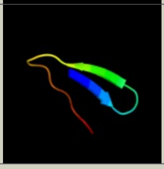
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AG48
Date	Thu Jan 5 11:28:07 GMT 2012
Unique Job ID	75bda8a866578675

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qamr1	Alignment		100.0	100	**Fold:**L21p-like **Superfamily:**L21p-like **Family:**Ribosomal protein L21p
2	c3bboT_	Alignment		100.0	30	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**ribosomal protein l21; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
3	d2j01v1	Alignment		100.0	44	**Fold:**L21p-like **Superfamily:**L21p-like **Family:**Ribosomal protein L21p
4	d2zjro1	Alignment		100.0	44	**Fold:**L21p-like **Superfamily:**L21p-like **Family:**Ribosomal protein L21p
5	c2gu9B_	Alignment		54.7	14	**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
6	c2lc4A_	Alignment		51.2	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**pilp protein; **PDBTitle:** solution structure of pilp from pseudomonas aeruginosa
7	d2arca_	Alignment		50.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
8	c3ibmB_	Alignment		47.0	10	**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
9	c3ossC_	Alignment		43.9	23	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**type 2 secretion system, gspc; **PDBTitle:** the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
10	c3m9bK_	Alignment		41.5	13	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
11	c3d82A_	Alignment		40.3	9	**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

12	c2ivwA_	Alignment		40.2	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**pilp pilot protein; **PDBTitle:** the solution structure of a domain from the neisseria2 meningitidis pilp pilot protein.
13	c3kgzA_	Alignment		39.8	19	**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
14	d1sfna_	Alignment		38.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
15	d1sq4a_	Alignment		38.2	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
16	d1sefa_	Alignment		37.4	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
17	c1sefA_	Alignment		37.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
18	d1rc6a_	Alignment		37.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
19	d1o4ta_	Alignment		36.1	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
20	c2vpvA_	Alignment		36.1	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
21	d1vj2a_	Alignment	not modelled	36.0	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
22	c3cewA_	Alignment	not modelled	34.4	14	**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
23	d1y9qa2	Alignment	not modelled	33.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
24	c3lwcA_	Alignment	not modelled	28.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
25	c2ozjB_	Alignment	not modelled	27.6	10	**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
26	c3h7yA_	Alignment	not modelled	27.1	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**bacilysin biosynthesis protein bacb; **PDBTitle:** crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
27	c3fjsC_	Alignment	not modelled	26.4	24	**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

28	d1yhfa1	Alignment	not modelled	26.0	33	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
29	c3l2hD_	Alignment	not modelled	25.8	14	**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
30	c3jzvA_	Alignment	not modelled	25.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
31	d1wpga1	Alignment	not modelled	22.9	16	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
32	c2pfwB_	Alignment	not modelled	20.1	10	**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
33	c1d8lA_	Alignment	not modelled	19.3	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
34	c3i7dB_	Alignment	not modelled	18.9	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase; **PDBTitle:** crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from silicibacter pomeroyi (yp_168127.1) from3 silicibacter pomeroyi dss-3 at 2.30 a resolution
35	d1cuka3	Alignment	not modelled	18.6	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA helicase RuvA subunit, N-terminal domain
36	d1vqow1	Alignment	not modelled	18.5	44	**Fold:**Ribosomal protein L30p/L7e **Superfamily:**Ribosomal protein L30p/L7e **Family:**Ribosomal protein L30p/L7e
37	d1v70a_	Alignment	not modelled	18.0	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
38	d2pyta1	Alignment	not modelled	15.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
39	d2f4pa1	Alignment	not modelled	15.1	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
40	c2h5xA_	Alignment	not modelled	14.6	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
41	c2q30C_	Alignment	not modelled	13.6	10	**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
42	c1hjpA_	Alignment	not modelled	13.2	17	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
43	c3acgA_	Alignment	not modelled	13.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,4-endoglucanase; **PDBTitle:** crystal structure of carbohydrate-binding module family 282 from clostridium josui cel5a in complex with cellobiose
44	d1o5ua_	Alignment	not modelled	12.7	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
45	d1bvsa3	Alignment	not modelled	12.6	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA helicase RuvA subunit, N-terminal domain
46	d1ixra2	Alignment	not modelled	12.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA helicase RuvA subunit, N-terminal domain
47	c3fp9E_	Alignment	not modelled	12.1	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
48	c3rnsA_	Alignment	not modelled	11.8	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** cupin 2 conserved barrel domain protein from leptotrichia buccalis
49	c2ejgD_	Alignment	not modelled	11.5	13	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
50	d1vcpa_	Alignment	not modelled	10.8	38	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
51	c2wkdA_	Alignment	not modelled	10.5	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
52	d1wyka_	Alignment	not modelled	10.3	38	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases

53	c2i45C_	Alignment	not modelled	10.1	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
54	c1kxfA_	Alignment	not modelled	9.5	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sindbis virus capsid protein; **PDBTitle:** sindbis virus capsid, (wild-type) residues 1-264,2 tetragonal crystal form (form ii)
55	d2b8ma1	Alignment	not modelled	9.3	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
56	d2cqaa1	Alignment	not modelled	9.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
57	d1ep5a_	Alignment	not modelled	9.3	38	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
58	d1uwwa_	Alignment	not modelled	8.3	17	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 28 carbohydrate binding module, CBM28
59	c1b5fD_	Alignment	not modelled	7.7	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (cardosin a); **PDBTitle:** native cardosin a from cynara cardunculus l.
60	c2o8qA_	Alignment	not modelled	7.5	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with a cupin-like fold and unknown2 function (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
61	c2x48B_	Alignment	not modelled	7.2	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
62	c3cw3A_	Alignment	not modelled	7.1	27	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**absent in melanoma 1 protein; **PDBTitle:** crystal structure of aim1g1
63	d2ae8a2	Alignment	not modelled	6.7	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
64	d1dgwa_	Alignment	not modelled	6.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
65	c3a35B_	Alignment	not modelled	6.6	14	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**lumazine protein; **PDBTitle:** crystal structure of lump complexed with riboflavin
66	c3i0mA_	Alignment	not modelled	6.3	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair and telomere maintenance protein nbs1; **PDBTitle:** structure of the s. pombe nbs1 fha/brct-repeat domain
67	d2fug33	Alignment	not modelled	6.3	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
68	c3myxA_	Alignment	not modelled	6.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244; **PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
69	d1rhya2	Alignment	not modelled	6.0	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
70	c2aujD_	Alignment	not modelled	5.9	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
71	d1uija1	Alignment	not modelled	5.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
72	d1uika1	Alignment	not modelled	5.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
73	c2opkC_	Alignment	not modelled	5.5	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
74	c2d40C_	Alignment	not modelled	5.5	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
75	d1u0la1	Alignment	not modelled	5.3	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
76	d1i8da1	Alignment	not modelled	5.1	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase