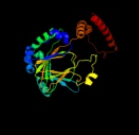
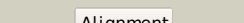
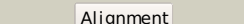
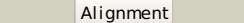
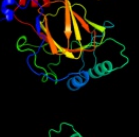
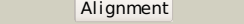
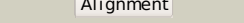
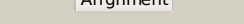
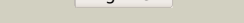


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P27431
Date	Thu Jan 5 11:43:58 GMT 2012
Unique Job ID	8f585b04c2799643

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xdvA_	 Alignment		100.0	14	PDB header: nuclear protein Chain: A: PDB Molecule: myc-induced nuclear antigen; PDBTitle: crystal structure of the catalytic domain of flj14393
2	d1vrba1	 Alignment		100.0	16	Fold: Double-stranded beta-helix Superfamily: Clavaminase synthase-like Family: Asparaginyl hydroxylase-like
3	c3al6A_	 Alignment		100.0	16	PDB header: unknown function Chain: A: PDB Molecule: jmc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
4	c3uyjA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 8; PDBTitle: crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
5	d1h2ka_	 Alignment		100.0	19	Fold: Double-stranded beta-helix Superfamily: Clavaminase synthase-like Family: Hypoxia-inducible factor HIF inhibitor (FIH1)
6	c3k2oB_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional arginine demethylase and lysyl-hydroxylase PDBTitle: structure of an oxygenase
7	c3k3nA_	 Alignment		99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: crystal structure of the catalytic core domain of human phf8
8	c3pu3A_	 Alignment		99.9	12	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 2; PDBTitle: phf2 jumonji domain-nog complex
9	c2yu1A_	 Alignment		99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: jmc domain-containing histone demethylation protein 1a; PDBTitle: crystal structure of hjhdm1a complexed with a-ketoglutarate
10	c3kvaA_	 Alignment		99.8	13	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: jmc domain-containing histone demethylation protein 1d; PDBTitle: structure of kiaa1718 jumonji domain in complex with alpha-2 ketoglutarate
11	c3kv5D_	 Alignment		99.7	12	PDB header: h3k4me3 binding protein, transferase Chain: D: PDB Molecule: jmc domain-containing histone demethylation PDBTitle: structure of kiaa1718, human jumonji demethylase, in complex2 with n-oxalylglycine

12	c3kv4A_	Alignment		99.7	13	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: structure of phf8 in complex with histone h3
13	c3n9mC_	Alignment		99.7	10	PDB header: oxidoreductase Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: cekdm7a from c.elegans, alone
14	c2xxzA_	Alignment		99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of the human jmjd3 jumonji domain
15	c2xueB_	Alignment		98.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of jmjd3
16	d1zvfa1	Alignment		98.4	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
17	d1yfua1	Alignment		98.3	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
18	c2pfbB_	Alignment		98.2	16	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
19	d1yhfa1	Alignment		98.2	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
20	c3fjsC_	Alignment		98.2	25	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
21	d1od5a2	Alignment	not modelled	98.1	29	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
22	d1lr5a_	Alignment	not modelled	98.1	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
23	d1j58a_	Alignment	not modelled	98.1	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
24	d2b8ma1	Alignment	not modelled	98.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
25	c2ozjB_	Alignment	not modelled	98.0	19	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	d1v70a_	Alignment	not modelled	98.0	27	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
27	d2phla2	Alignment	not modelled	98.0	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
28	c2vqaC_	Alignment	not modelled	98.0	21	PDB header: metal-binding protein Chain: C: PDB Molecule: sll1358 protein; PDBTitle: protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
						Fold: Double-stranded beta-helix

29	d1fxza2	Alignment	not modelled	98.0	22	Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
30	c2oa2A	Alignment	not modelled	97.9	20	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
31	d1uika2	Alignment	not modelled	97.9	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
32	d2et1a1	Alignment	not modelled	97.9	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
33	c1fxzC	Alignment	not modelled	97.9	25	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
34	c3h8uA	Alignment	not modelled	97.8	23	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
35	c2gu9B	Alignment	not modelled	97.8	23	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
36	c3cewA	Alignment	not modelled	97.8	20	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
37	c3ehkC	Alignment	not modelled	97.8	20	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
38	c3kglB	Alignment	not modelled	97.8	22	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from2 brassica napus
39	c2d40C	Alignment	not modelled	97.8	11	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
40	c1cauB	Alignment	not modelled	97.8	21	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
41	d2f4pa1	Alignment	not modelled	97.8	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
42	d1y3ta1	Alignment	not modelled	97.8	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
43	c2q30C	Alignment	not modelled	97.8	18	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
44	d1uija2	Alignment	not modelled	97.8	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
45	d2phda1	Alignment	not modelled	97.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
46	d2d40a1	Alignment	not modelled	97.7	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
47	c3qacA	Alignment	not modelled	97.7	23	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin seed storage protein; PDBTitle: structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
48	c3c3vA	Alignment	not modelled	97.7	25	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
49	c3rnsA	Alignment	not modelled	97.7	12	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
50	c2e9qA	Alignment	not modelled	97.7	21	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
51	c3ibmB	Alignment	not modelled	97.7	19	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 hha1_0468 from2 halorhodospira halophila
52	c3kscD	Alignment	not modelled	97.7	23	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
53	c3lwcA	Alignment	not modelled	97.6	23	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

54	c3kgzA_	Alignment	not modelled	97.6	21	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
55	d1uija1	Alignment	not modelled	97.6	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
56	d1juha_	Alignment	not modelled	97.6	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Quercetin 2,3-dioxygenase-like
57	c3jzvA_	Alignment	not modelled	97.6	24	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.
58	d1dgwa_	Alignment	not modelled	97.6	23	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
59	c3h7yA_	Alignment	not modelled	97.6	16	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
60	d1o4ta_	Alignment	not modelled	97.6	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
61	c1uijA_	Alignment	not modelled	97.5	23	PDB header: sugar binding protein Chain: A: PDB Molecule: beta subunit of beta conglycinin; PDBTitle: crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
62	c2d5fB_	Alignment	not modelled	97.5	32	PDB header: plant protein Chain: B: PDB Molecule: glycinin a3b4 subunit; PDBTitle: crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
63	c2cauA_	Alignment	not modelled	97.5	24	PDB header: plant protein Chain: A: PDB Molecule: protein (canavalin); PDBTitle: canavalin from jack bean
64	d1uika1	Alignment	not modelled	97.5	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
65	c2vpvA_	Alignment	not modelled	97.4	11	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
66	c3ht2A_	Alignment	not modelled	97.3	24	PDB header: lyase Chain: A: PDB Molecule: remf protein; PDBTitle: zink containing polyketide cyclase remf from streptomyces2 resistomycificus
67	c3s7eB_	Alignment	not modelled	97.3	18	PDB header: allergen Chain: B: PDB Molecule: allergen ara h 1, clone p41b; PDBTitle: crystal structure of ara h 1
68	c2eaaB_	Alignment	not modelled	97.3	24	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
69	c2q8eB_	Alignment	not modelled	97.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: jmc domain-containing histone demethylation PDBTitle: specificity and mechanism of jmd2a, a trimethyllysine-2 specific histone demethylase
70	d1nxma_	Alignment	not modelled	97.3	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
71	d1j3pa_	Alignment	not modelled	97.3	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
72	c2qnkA_	Alignment	not modelled	97.3	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
73	c2xlfA_	Alignment	not modelled	97.2	17	PDB header: metal binding protein Chain: A: PDB Molecule: sli1785 protein; PDBTitle: structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
74	d1x82a_	Alignment	not modelled	97.2	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
75	c3i7dB_	Alignment	not modelled	97.2	24	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
76	c3l2hD_	Alignment	not modelled	97.2	19	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
77	c2fqpD_	Alignment	not modelled	97.2	20	PDB header: metal binding protein Chain: D: PDB Molecule: hypothetical protein bp2299; PDBTitle: crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohamia i at 1.80 a resolution
78	d1vj2a_	Alignment	not modelled	97.2	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
79	c3i4fC_	Alignment	not modelled	97.1	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein;

79	c2143C	Alignment	not modelled	97.1	15	PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis 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
80	c2oziA	Alignment	not modelled	97.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdosp, 2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
81	c3bu7A	Alignment	not modelled	97.1	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
82	d3bu7a1	Alignment	not modelled	97.1	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
83	d1fxza1	Alignment	not modelled	97.1	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
84	d1sefa	Alignment	not modelled	97.1	22	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
85	c1sefA	Alignment	not modelled	97.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
86	c3d82A	Alignment	not modelled	97.0	23	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
87	c2w2iC	Alignment	not modelled	97.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate oxygenase; PDBTitle: crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
88	d1od5a1	Alignment	not modelled	97.0	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
89	d1rc6a	Alignment	not modelled	97.0	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
90	d1sfna	Alignment	not modelled	97.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
91	c3ejkA	Alignment	not modelled	97.0	11	PDB header: isomerase Chain: A: PDB Molecule: dtdp sugar isomerase; PDBTitle: crystal structure of dtdp sugar isomerase (yp_390184.1) from2 desulfovibrio desulfuricans g20 at 1.95 a resolution
92	d1sq4a	Alignment	not modelled	97.0	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
93	d1y9qa2	Alignment	not modelled	96.9	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
94	c2os2A	Alignment	not modelled	96.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: jmjC domain-containing histone demethylation protein 3a; PDBTitle: crystal structure of jmj2a complexed with histone h3 peptide2 trimethylated at lys36
95	d2ixca1	Alignment	not modelled	96.7	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
96	c2zklA	Alignment	not modelled	96.6	17	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
97	c3opwA	Alignment	not modelled	96.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dna damage-responsive transcriptional repressor rph1; PDBTitle: crystal structure of the rph1 catalytic core
98	c2o8qA	Alignment	not modelled	96.5	16	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 (bx_e_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
99	d2ixha1	Alignment	not modelled	96.4	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
100	d1ep0a	Alignment	not modelled	96.3	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
101	c3bcwB	Alignment	not modelled	96.3	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
102	c2c0zA	Alignment	not modelled	96.3	18	PDB header: isomerase Chain: A: PDB Molecule: novw; PDBTitle: the 1.6 a resolution crystal structure of novw: a 4-keto-6-2 deoxy sugar epimerase from the novobiocin biosynthetic3 gene cluster of streptomyces spheroides
103	d2phla1	Alignment	not modelled	96.3	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
						Fold: Double-stranded beta-helix

104	d2c0za1	Alignment	not modelled	96.3	15	Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
105	c1upiA	Alignment	not modelled	96.2	19	PDB header: epimerase Chain: A: PDB Molecule: ddtp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: mycobacterium tuberculosis rmlc epimerase (rv3465)
106	d1o5ua	Alignment	not modelled	96.1	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
107	d1wita1	Alignment	not modelled	95.9	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
108	c3ebrA	Alignment	not modelled	95.8	20	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
109	d1dzra	Alignment	not modelled	95.7	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
110	c2bnoA	Alignment	not modelled	95.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
111	c3eqeB	Alignment	not modelled	95.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative cystein deoxygenase; PDBTitle: crystal structure of the yubc protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr112.
112	d1oi6a	Alignment	not modelled	95.6	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
113	c2y0oA	Alignment	not modelled	95.5	22	PDB header: isomerase Chain: A: PDB Molecule: probable d-lyxose ketol-isomerase; PDBTitle: the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
114	d2pa7a1	Alignment	not modelled	95.4	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
115	d1zrra1	Alignment	not modelled	95.0	12	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
116	d2bnma2	Alignment	not modelled	94.9	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
117	c3rykB	Alignment	not modelled	94.9	18	PDB header: isomerase Chain: B: PDB Molecule: ddtp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
118	c2opkC	Alignment	not modelled	94.8	19	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
119	d3bb6a1	Alignment	not modelled	94.2	17	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: TehB-like
120	c3cxE	Alignment	not modelled	94.1	21	PDB header: unknown function Chain: E: PDB Molecule: protein of unknown function with a cupin-like fold; PDBTitle: crystal structure of a protein of unknown function with a cupin-like2 fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution