Phyre2

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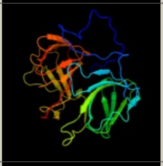
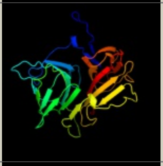
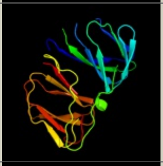
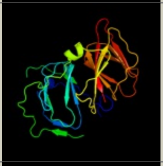
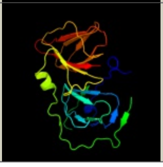
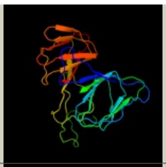
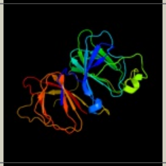
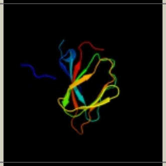
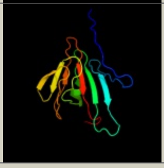
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sefa_	Alignment		100.0	56	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
2	c1sefA_	Alignment		100.0	56	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
3	d1rc6a_	Alignment		100.0	100	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
4	d1sq4a_	Alignment		100.0	28	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
5	d1sfna_	Alignment		100.0	33	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
6	d1y3ta1	Alignment		100.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
7	c3h7yA_	Alignment		100.0	10	**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
8	c3rnsA_	Alignment		100.0	17	**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
9	c2d40C_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
10	c3bu7A_	Alignment		100.0	12	**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
11	d3bu7a1	Alignment		100.0	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like

12	d2phda1	Alignment		100.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
13	d2d40a1	Alignment		100.0	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
14	d1juha_	Alignment		99.9	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
15	c2vqaC_	Alignment		99.9	17	**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.
16	d1j58a_	Alignment		99.9	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
17	c3o14B_	Alignment		99.8	12	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**anti-ecfsigma factor, chrr; **PDBTitle:** crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
18	c3ibmB_	Alignment		99.8	16	**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
19	c3kgzA_	Alignment		99.8	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
20	c3jzvA_	Alignment		99.8	18	**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.
21	d1vj2a_	Alignment	not modelled	99.7	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
22	c3ht2A_	Alignment	not modelled	99.7	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
23	c2cauA_	Alignment	not modelled	99.7	17	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
24	d1y9qa2	Alignment	not modelled	99.7	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
25	c1fxzC_	Alignment	not modelled	99.7	14	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
26	c3kglB_	Alignment	not modelled	99.7	13	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
27	d1lr5a_	Alignment	not modelled	99.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
28	c3kscD_	Alignment	not modelled	99.7	14	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
						PDB header:isomerase

29	c3i7dB_	Alignment	not modelled	99.7	13	**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
30	c3qacA_	Alignment	not modelled	99.7	13	**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.
31	c2vpvA_	Alignment	not modelled	99.7	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
32	c2e9qA_	Alignment	not modelled	99.6	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
33	d2f4pa1	Alignment	not modelled	99.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
34	c3myxA_	Alignment	not modelled	99.6	13	**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
35	d2bnma2	Alignment	not modelled	99.6	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
36	c3ehkC_	Alignment	not modelled	99.6	16	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
37	c3cewA_	Alignment	not modelled	99.6	17	**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
38	c3c3vA_	Alignment	not modelled	99.6	14	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
39	c2d5fB_	Alignment	not modelled	99.6	17	**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
40	c2eaaB_	Alignment	not modelled	99.6	19	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
41	c2gu9B_	Alignment	not modelled	99.6	13	**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
42	d1o4ta_	Alignment	not modelled	99.6	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
43	c3l2hD_	Alignment	not modelled	99.6	15	**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
44	c1uijA_	Alignment	not modelled	99.6	18	**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)
45	c2oa2A_	Alignment	not modelled	99.5	12	**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
46	c3s7eB_	Alignment	not modelled	99.5	20	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
47	c2pfwB_	Alignment	not modelled	99.5	14	**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
48	c3fjsC_	Alignment	not modelled	99.5	12	**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
49	d1v70a_	Alignment	not modelled	99.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
50	d2b8ma1	Alignment	not modelled	99.5	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
51	c2ozjB_	Alignment	not modelled	99.5	21	**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
52	c2qdrA_	Alignment	not modelled	99.4	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f5605)

						from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
53	c3h8uA_	Alignment	not modelled	99.4	13	**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
54	d1yhfa1	Alignment	not modelled	99.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
55	c1y9qA_	Alignment	not modelled	99.4	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
56	c2bnoA_	Alignment	not modelled	99.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
57	d1dgwa_	Alignment	not modelled	99.3	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
58	c2fqpD_	Alignment	not modelled	99.3	10	**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
59	c2xlfA_	Alignment	not modelled	99.3	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sll1785 protein; **PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
60	c3es1A_	Alignment	not modelled	99.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution
61	d1j3pa_	Alignment	not modelled	99.3	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
62	c2o8qA_	Alignment	not modelled	99.3	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 (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
63	c2q30C_	Alignment	not modelled	99.3	12	**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
64	d1uika1	Alignment	not modelled	99.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
65	c2oziA_	Alignment	not modelled	99.2	13	**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
66	c3lwcA_	Alignment	not modelled	99.2	16	**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
67	d1x82a_	Alignment	not modelled	99.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
68	d2et1a1	Alignment	not modelled	99.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
69	d1uija1	Alignment	not modelled	99.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
70	d1yfua1	Alignment	not modelled	99.1	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
71	c3d82A_	Alignment	not modelled	99.1	17	**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
72	c2i45C_	Alignment	not modelled	99.0	23	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
73	c3ebrA_	Alignment	not modelled	99.0	8	**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
74	d1fxza1	Alignment	not modelled	99.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
75	d1j1la_	Alignment	not modelled	98.9	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
76	d1xrua1	Alignment	not modelled	98.9	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like

77	c3cjxE_	Alignment	not modelled	98.9	17	**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
78	c2vecA_	Alignment	not modelled	98.9	13	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**pirin-like protein yhak; **PDBTitle:** the crystal structure of the protein yhak from escherichia2 coli
79	c2qnkA_	Alignment	not modelled	98.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
80	d1tq5a1	Alignment	not modelled	98.8	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
81	c3bcwB_	Alignment	not modelled	98.8	11	**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
82	d1zvfa1	Alignment	not modelled	98.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
83	d1fxza2	Alignment	not modelled	98.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
84	d1od5a1	Alignment	not modelled	98.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
85	d1zrra1	Alignment	not modelled	98.8	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
86	d2phla2	Alignment	not modelled	98.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
87	c1cauB_	Alignment	not modelled	98.7	14	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
88	d1uika2	Alignment	not modelled	98.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
89	d1pmia_	Alignment	not modelled	98.7	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
90	d1uija2	Alignment	not modelled	98.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
91	d2phla1	Alignment	not modelled	98.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
92	d1od5a2	Alignment	not modelled	98.7	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
93	d2o1qa1	Alignment	not modelled	98.7	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acetylacetone-cleaving enzyme-like
94	c3h1yA_	Alignment	not modelled	98.7	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
95	c1ywkE_	Alignment	not modelled	98.6	11	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**4-deoxy-l-threo-5-hexosulose-uronate ketol- **PDBTitle:** crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
96	c3balB_	Alignment	not modelled	98.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acetylacetone-cleaving enzyme; **PDBTitle:** crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
97	d1ywka1	Alignment	not modelled	98.6	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
98	d1qwra_	Alignment	not modelled	98.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
99	c2qjvB_	Alignment	not modelled	98.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**uncharacterized iolb-like protein; **PDBTitle:** crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
100	d2pyta1	Alignment	not modelled	98.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
101	c2p17A_	Alignment	not modelled	98.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pirin-like protein; **PDBTitle:** crystal structure of gk1651 from geobacillus kaustophilus
102	d2arca_	Alignment	not modelled	98.4	10	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC

						Family: Regulatory protein AraC
103	c2opkC_	Alignment	not modelled	98.2	16	**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
104	d1o5ua_	Alignment	not modelled	98.2	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
105	d1vr3a1	Alignment	not modelled	98.2	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
106	c2zklA_	Alignment	not modelled	98.2	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
107	d1zx5a1	Alignment	not modelled	98.1	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
108	c3eqeB_	Alignment	not modelled	98.0	11	**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.
109	c3es4B_	Alignment	not modelled	97.9	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
110	d2gm6a1	Alignment	not modelled	97.7	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
111	c2y0oA_	Alignment	not modelled	97.6	10	**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
112	d2pa7a1	Alignment	not modelled	97.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
113	d1vrba1	Alignment	not modelled	97.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
114	d3elna1	Alignment	not modelled	97.5	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
115	c3mpbA_	Alignment	not modelled	97.4	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
116	c3ejkA_	Alignment	not modelled	97.4	10	**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
117	c1ey2A_	Alignment	not modelled	97.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
118	d1eyba_	Alignment	not modelled	97.2	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
119	c2z2sD_	Alignment	not modelled	97.2	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**anti-sigma factor chrr, transcriptional activator chrr; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
120	d2ic1a1	Alignment	not modelled	97.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I