Phyre^2

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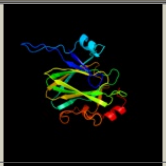
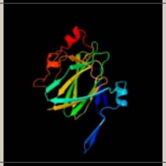
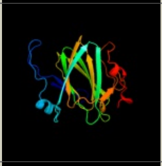
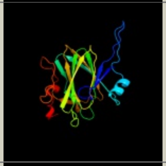
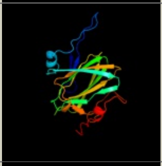
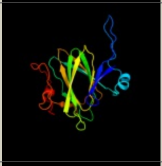
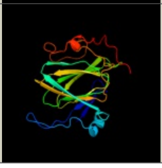
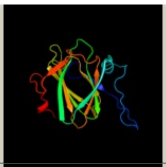
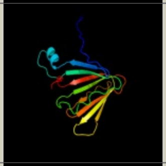
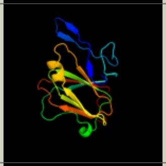
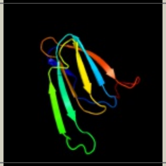
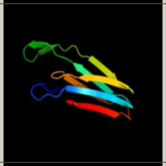
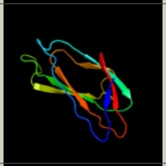
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ixca1	Alignment		100.0	34	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
2	c2c0zA_	Alignment		100.0	34	**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
3	d2c0za1	Alignment		100.0	34	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
4	d1dzra_	Alignment		100.0	65	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
5	d1oi6a_	Alignment		100.0	28	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
6	c1upiA_	Alignment		100.0	34	**PDB header:**epimerase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** mycobacterium tuberculosis rmlc epimerase (rv3465)
7	d2ixha1	Alignment		100.0	59	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
8	d1ep0a_	Alignment		100.0	51	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
9	c3rykB_	Alignment		100.0	51	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dtdp-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
10	d1wlta1	Alignment		100.0	39	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
11	d1nxma_	Alignment		100.0	31	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase

12	c3ejkA_	Alignment		100.0	19	**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
13	c2zklA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
14	d2pa7a1	Alignment		100.0	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
15	c2vqaC_	Alignment		98.0	18	**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		97.9	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
17	d2phla2	Alignment		97.7	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
18	d1juha_	Alignment		97.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
19	d1x82a_	Alignment		97.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
20	c2o8qA_	Alignment		97.5	17	**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
21	d1uija2	Alignment	not modelled	97.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
22	d1j3pa_	Alignment	not modelled	97.4	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
23	d1y3ta1	Alignment	not modelled	97.4	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
24	c1cauB_	Alignment	not modelled	97.3	14	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
25	c2oa2A_	Alignment	not modelled	97.3	15	**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
26	d2et1a1	Alignment	not modelled	97.2	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
27	c2gu9B_	Alignment	not modelled	97.2	17	**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
28	c3kglB_	Alignment	not modelled	97.1	16	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus

29	c3ehkC_	Alignment	not modelled	97.1	12	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
30	c2d5fB_	Alignment	not modelled	97.0	16	**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
31	d1uika2	Alignment	not modelled	97.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
32	d1fxza2	Alignment	not modelled	96.9	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
33	c3c3vA_	Alignment	not modelled	96.9	20	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
34	c3s7eB_	Alignment	not modelled	96.9	13	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
35	d1v70a_	Alignment	not modelled	96.9	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
36	d1zvfa1	Alignment	not modelled	96.9	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
37	d1od5a2	Alignment	not modelled	96.9	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
38	c1fxzC_	Alignment	not modelled	96.9	18	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
39	c3kscD_	Alignment	not modelled	96.8	19	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
40	d1o4ta_	Alignment	not modelled	96.8	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
41	c2e9qA_	Alignment	not modelled	96.5	17	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
42	c1uijA_	Alignment	not modelled	96.5	11	**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)
43	c3qacA_	Alignment	not modelled	96.5	16	**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.
44	c3jzvA_	Alignment	not modelled	96.4	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.
45	c2q30C_	Alignment	not modelled	96.4	13	**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
46	d2f4pa1	Alignment	not modelled	96.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
47	d1yfua1	Alignment	not modelled	96.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
48	c3h8uA_	Alignment	not modelled	96.2	6	**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
49	c2i45C_	Alignment	not modelled	96.1	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
50	d1lr5a_	Alignment	not modelled	95.9	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
51	c2d40C_	Alignment	not modelled	95.9	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
52	c3uyjA_	Alignment	not modelled	95.9	11	**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
53	c2pfwB_	Alignment	not modelled	95.9	15	**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
						PDB header:plant protein

54	c2eaaB_	Alignment	not modelled	95.9	12	**Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
55	c3ibmB_	Alignment	not modelled	95.8	11	**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
56	c3al6A_	Alignment	not modelled	95.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
57	c3fjsC_	Alignment	not modelled	95.7	19	**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
58	d1dgwa_	Alignment	not modelled	95.6	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
59	d2b8ma1	Alignment	not modelled	95.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
60	c2ozjB_	Alignment	not modelled	95.4	14	**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
61	c2y0oA_	Alignment	not modelled	95.3	19	**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
62	d1y9qa2	Alignment	not modelled	95.3	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
63	c3d82A_	Alignment	not modelled	95.2	13	**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
64	d1vj2a_	Alignment	not modelled	95.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
65	c3kgzA_	Alignment	not modelled	95.2	12	**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
66	c3ht2A_	Alignment	not modelled	95.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
67	d1od5a1	Alignment	not modelled	95.1	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
68	c3cewA_	Alignment	not modelled	95.1	13	**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
69	c3i7dB_	Alignment	not modelled	95.0	22	**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
70	d1rc6a_	Alignment	not modelled	95.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
71	d1uija1	Alignment	not modelled	94.9	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
72	d2d40a1	Alignment	not modelled	94.8	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
73	c2xlfA_	Alignment	not modelled	94.5	13	**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)
74	d1uika1	Alignment	not modelled	94.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
75	c3h7yA_	Alignment	not modelled	94.2	11	**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
76	d1yhfa1	Alignment	not modelled	94.1	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
77	d1sfna_	Alignment	not modelled	94.0	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
78	d1fxza1	Alignment	not modelled	93.9	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein

79	c2cauA_	Alignment	not modelled	93.8	12	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
80	d1sq4a_	Alignment	not modelled	93.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
81	c3k2oB_	Alignment	not modelled	93.3	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
82	d1vrba1	Alignment	not modelled	93.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
83	c3rnsA_	Alignment	not modelled	92.8	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
84	d1sefa_	Alignment	not modelled	92.6	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
85	c1sefA_	Alignment	not modelled	92.6	9	**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	c2fqpD_	Alignment	not modelled	92.2	19	**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
87	c3k3nA_	Alignment	not modelled	91.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** crystal structure of the catalytic core domain of human phf8
88	c2eceA_	Alignment	not modelled	91.8	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**462aa long hypothetical selenium-binding protein; **PDBTitle:** x-ray structure of hypothetical selenium-binding protein2 from sulfolobus tokodaii, st0059
89	c3es1A_	Alignment	not modelled	91.8	11	**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
90	c2vpvA_	Alignment	not modelled	91.3	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
91	c3lwcA_	Alignment	not modelled	91.2	19	**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
92	d2phda1	Alignment	not modelled	89.9	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
93	c3l2hD_	Alignment	not modelled	89.3	9	**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
94	c2oziA_	Alignment	not modelled	87.8	14	**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
95	d1h2ka_	Alignment	not modelled	87.8	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
96	d1zrra1	Alignment	not modelled	87.3	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
97	c3bu7A_	Alignment	not modelled	87.0	10	**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
98	d3bu7a1	Alignment	not modelled	87.0	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
99	c3o14B_	Alignment	not modelled	85.5	14	**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
100	c3ebrA_	Alignment	not modelled	83.5	11	**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
101	d1yuda1	Alignment	not modelled	83.2	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YML079-like
102	c3mpbA_	Alignment	not modelled	83.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
103	c3kv5D_	Alignment	not modelled	82.4	20	**PDB header:**h3k4me3 binding protein, transferase **Chain:** D: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** structure of kiaa1718, human jumonji demethylase, in complex2 with n-oxalylglycine

104	c3kvaA_	Alignment	not modelled	81.7	23	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1d; **PDBTitle:** structure of kiaa1718 jumonji domain in complex with alpha-2 ketoglutarate
105	d1znpa1	Alignment	not modelled	80.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YML079-like
106	d1xe7a_	Alignment	not modelled	80.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YML079-like
107	c3pu3A_	Alignment	not modelled	80.0	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 2; **PDBTitle:** phf2 jumonji domain-nog complex
108	c3m3iC_	Alignment	not modelled	79.1	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** hypothetical protein from leishmania major
109	d2bnma2	Alignment	not modelled	78.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
110	c2yu1A_	Alignment	not modelled	77.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1a; **PDBTitle:** crystal structure of hjhdm1a complexed with a-ketoglutarate
111	c3kv4A_	Alignment	not modelled	75.0	22	**PDB header:**h3k4me3 binding protein, transferase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** structure of phf8 in complex with histone h3
112	c3n9mC_	Alignment	not modelled	65.6	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** cekdm7a from c.elegans, alone
113	c2xdvA_	Alignment	not modelled	63.8	14	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
114	c1y9qA_	Alignment	not modelled	62.5	11	**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
115	d1xsqa_	Alignment	not modelled	61.3	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
116	d2phla1	Alignment	not modelled	61.1	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
117	d1rzhh1	Alignment	not modelled	56.1	26	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
118	d1bf2a1	Alignment	not modelled	55.0	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
119	c1dgrX_	Alignment	not modelled	53.9	11	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**canavalin; **PDBTitle:** refined crystal structure of canavalin from jack bean
120	d1vr3a1	Alignment	not modelled	51.5	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase